_SL
SEQUENCE LISTING

<110> NOVARTIS AG
TRUSTEES OF THE UNIVERSITY OF PENNSYLVANIA
UNIVERSITY OF PITTSBURGH - OF THE COMMONWEALTH SYSTEM
OF HIGHER EDUCATION

<120> TREATMENT OF CANCER USING HUMANIZED ANTI-EGFRVIII
CHIMERIC ANTIGEN RECEPTOR

<130> N2067-7000WO

<140>
<141>

<150> 61/888,255
<151> 2013-10-08

<150> 61/767,071
<151> 2013-02-20

<160> 127

<170> PatentIn version 3.5

<210> 1
<211> 535
<212> PRT
<213> Artificial Sequence

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

<400> 1
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

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

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

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                                                _SL
Gly Phe Asn Ile Glu Asp Tyr Tyr Ile His Trp Val Lys Gln Arg Thr
    50                  55                  60

Glu Gln Gly Leu Glu Trp Ile Gly Arg Ile Asp Pro Glu Asn Asp Glu
65                  70                  75                  80

Thr Lys Tyr Gly Pro Ile Phe Gln Gly Arg Ala Thr Ile Thr Ala Asp
                85                  90                  95

Thr Ser Ser Asn Thr Val Tyr Leu Gln Leu Ser Ser Leu Thr Ser Glu
            100                 105                 110

Asp Thr Ala Val Tyr Tyr Cys Ala Phe Arg Gly Gly Val Tyr Trp Gly
        115                 120                 125

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

Gly Gly Ser Gly Gly Gly Gly Ser His Met Asp Val Val Met Thr Gln
145                 150                 155                 160

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

Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu
            180                 185                 190

Asn Trp Leu Leu Gln Arg Pro Gly Gln Ser Pro Lys Arg Leu Ile Ser
        195                 200                 205

Leu Val Ser Lys Leu Asp Ser Gly Val Pro Asp Arg Phe Thr Gly Ser
    210                 215                 220

Gly Ser Gly Thr Asp Phe Thr Leu Arg Ile Ser Arg Val Glu Ala Glu
225                 230                 235                 240
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                                        _SL
Asp Leu Gly Ile Tyr Tyr Cys Trp Gln Gly Thr His Phe Pro Gly Thr
                245                 250                 255

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Ala Ser Thr Thr Thr Pro
            260                 265                 270

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

Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
    290                 295                 300

Thr Arg Gly Leu Asp Phe Ala Cys Asp Phe Trp Val Leu Val Val Val
305                 310                 315                 320

Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile
                325                 330                 335

Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr
            340                 345                 350

Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln
        355                 360                 365

Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Lys Arg Gly
    370                 375                 380

Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val
385                 390                 395                 400

Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu
                405                 410                 415

Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp
            420                 425                 430
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_SL
Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
        435   440   445

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
    450   455   460

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
465   470   475   480

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
                485   490   495

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
            500   505   510

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
        515   520   525

Met Gln Ala Leu Pro Pro Arg
    530   535

<210> 2
<211> 491
<212> PRT
<213> Artificial Sequence

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

<400> 2
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1   5   10   15

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

Glu Leu Val Lys Pro Gly Ala Ser Val Lys Leu Ser Cys Thr Gly Ser

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                                        _SL
        35                  40                  45

Gly Phe Asn Ile Glu Asp Tyr Tyr Ile His Trp Val Lys Gln Arg Thr
    50                  55                  60

Glu Gln Gly Leu Glu Trp Ile Gly Arg Ile Asp Pro Glu Asn Asp Glu
65                  70                  75                  80

Thr Lys Tyr Gly Pro Ile Phe Gln Gly Arg Ala Thr Ile Thr Ala Asp
                85                  90                  95

Thr Ser Ser Asn Thr Val Tyr Leu Gln Leu Ser Ser Leu Thr Ser Glu
            100                 105                 110

Asp Thr Ala Val Tyr Tyr Cys Ala Phe Arg Gly Gly Val Tyr Trp Gly
        115                 120                 125

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

Gly Gly Ser Gly Gly Gly Gly Ser His Met Asp Val Val Met Thr Gln
145                 150                 155                 160

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

Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu
            180                 185                 190

Asn Trp Leu Leu Gln Arg Pro Gly Gln Ser Pro Lys Arg Leu Ile Ser
        195                 200                 205

Leu Val Ser Lys Leu Asp Ser Gly Val Pro Asp Arg Phe Thr Gly Ser
    210                 215                 220

Gly Ser Gly Thr Asp Phe Thr Leu Arg Ile Ser Arg Val Glu Ala Glu
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                                        _SL
225                 230                 235                 240

Asp Leu Gly Ile Tyr Tyr Cys Trp Gln Gly Thr His Phe Pro Gly Thr
                245                 250                 255

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Ala Ser Thr Thr Thr Pro
            260                 265                 270

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

Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
    290                 295                 300

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

Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
                325                 330                 335

Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe
            340                 345                 350

Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg
        355                 360                 365

Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser
    370                 375                 380

Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr
385                 390                 395                 400

Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys
                405                 410                 415

Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn
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_SL
420 425 430

Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
435 440 445

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
450 455 460

His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
465 470 475 480

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 3
<211> 488
<212> PRT
<213> Artificial Sequence

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

<400> 3
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

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

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

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

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

```
Val Pro Ser Arg Phe Thr Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu
                85                  90                  95

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

Gln His His Ser Tyr Pro Leu Thr Ser Gly Gly Gly Thr Lys Val Glu
        115                 120                 125

Ile Lys Arg Thr Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly
    130                 135                 140

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

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
                165                 170                 175

Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
            180                 185                 190

Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Asn Tyr Ala
        195                 200                 205

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
    210                 215                 220

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
225                 230                 235                 240

Tyr Tyr Cys Ala Gly Ser Ser Gly Trp Ser Glu Tyr Trp Gly Gln Gly
                245                 250                 255

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Thr Thr Pro Ala Pro Arg
            260                 265                 270
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Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
        275                 280                 285

Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
    290                 295                 300

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

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

Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro
            340                 345                 350

Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu
        355                 360                 365

Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala
    370                 375                 380

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

Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly
                405                 410                 415

Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu
            420                 425                 430

Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
        435                 440                 445

Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
    450                 455                 460
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Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
465 470 475 480

His Met Gln Ala Leu Pro Pro Arg
485

<210> 4
<211> 729
<212> DNA
<213> Mus sp.

<400> 4
gagattcagc tgcagcaatc tggggcagaa cttgtgaagc caggggcctc agtcaagctg 60

tcctgcacag gttctggctt caacattgaa gactactata ttcactgggt gaagcagagg 120

actgaacagg gcctggaatg gattggaagg attgatcctg agaatgatga aactaaatat 180

ggcccaatat tccagggcag ggccactata acagcagaca catcctccaa cacagtctac 240

ctgcaactca gcagcctgac atctgaggac actgccgtct attactgtgc ctttcgcggt 300

ggagtctact gggggccagg aaccactctc acagtctcct caggaggtgg tggttccggt 360

ggtggtggtt ccggaggtgg tggttcacat atggatgttg tgatgaccca gtctccactc 420

actctatcgg ttgccattgg acaatcagcc tccatctctt gcaagtcaag tcagagcctc 480

ttagatagtg atggaaagac atatttgaat tggttgttac agaggccagg ccagtctcca 540

aagcgcctaa tctctctggt gtctaaactg gactctggag tccctgacag gttcactggc 600

agtggatcag ggacagattt cacactgaga atcagcagag tggaggctga ggatttggga 660

atttattatt gctggcaagg tacacatttt cctgggacgt tcggtggagg gaccaagctg 720

gagataaaa 729

<210> 5
<211> 720
<212> DNA
<213> Artificial Sequence

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

<400> 5
gacatccaga tgacccagag ccctagcagc ctgagcgcca gcgtgggcga cagagtgacc 60

atcacctgtc gggccagcca gggcatcaga aacaacctgg cctggtatca gcagaagccc 120

ggcaaggccc ccaagagact gatctacgct gccagcaatc tgcagagcgg cgtgcccagc 180

agattcaccg gaagcggctc cggcaccgag ttcaccctga tcgtgtccag cctgcagccc 240

gaggacttcg ccacctacta ctgcctgcag caccacagct accctctgac cagcggcgga 300

ggcaccaagg tggagatcaa gcggaccggc agcaccagcg gcagcggcaa gcctggcagc 360

ggcgagggaa gcgaggtcca ggtgctggaa tctggcggcg gactggtgca gcctggcggc 420

agcctgagac tgagctgtgc cgccagcggc ttcaccttca gcagctacgc catgtcttgg 480

gtccggcagg ctcctggaaa gggcctggaa tgggtgtccg ccatcagcgg ctctggcggc 540

tccaccaact acgccgacag cgtgaagggc cggttcacca tcagccggga caacagcaag 600

aacaccctgt atctgcagat gaacagcctg agagccgagg acaccgccgt gtactactgt 660

gccggcagca gcgggtggag cgagtactgg ggccagggca cactggtcac agtgtctagc 720

<210> 6
<211> 63
<212> DNA
<213> Artificial Sequence

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

<400> 6
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccg 63

<210> 7

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

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

<400> 7
accacgacgc cagcgccgcg accaccaaca ccggcgccca ccatcgcgtc gcagcccctg 60

tccctgcgcc cagaggcgtg ccggccagcg gcgggggcg cagtgcacac gagggggctg 120

gacttcgcct gtgat 135

<210> 8
<211> 72
<212> DNA
<213> Artificial Sequence

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

<400> 8
atctacatct gggcgccctt ggccgggact tgtggggtcc ttctcctgtc actggttatc 60

acccttact gc 72

<210> 9
<211> 126
<212> DNA
<213> Artificial Sequence

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

<400> 9
aaacggggca gaaagaaact cctgtatata ttcaaacaac catttatgag accagtacaa 60

actactcaag aggaagatgg ctgtagctgc cgatttccag aagaagaaga aggaggatgt 120

gaactg 126

<210> 10
<211> 336
<212> DNA
<213> Artificial Sequence

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

<400> 10
agagtgaagt tcagcaggag cgcagacgcc cccgcgtaca agcagggcca gaaccagctc 60

tataacgagc tcaatctagg acgaagagag gagtacgatg ttttggacaa gagacgtggc 120

cgggaccctg agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgtacaat 180

gaactgcaga aagataagat ggcggaggcc tacagtgaga ttgggatgaa aggcgagcgc 240

cggaggggca aggggcacga tggcctttac cagggtctca gtacagccac caaggacacc 300

tacgacgccc ttcacatgca ggccctgccc cctcgc 336

<210> 11
<211> 243
<212> PRT
<213> Mus sp.

<400> 11
Glu Ile Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Thr Gly Ser Gly Phe Asn Ile Glu Asp Tyr
20 25 30

Tyr Ile His Trp Val Lys Gln Arg Thr Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Arg Ile Asp Pro Glu Asn Asp Glu Thr Lys Tyr Gly Pro Ile Phe
50 55 60

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Gln Gly Arg Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Val Tyr
65                  70                  75                  80

Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Phe Arg Gly Gly Val Tyr Trp Gly Pro Gly Thr Thr Leu Thr Val
            100                 105                 110

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

Ser His Met Asp Val Val Met Thr Gln Ser Pro Leu Thr Leu Ser Val
    130                 135                 140

Ala Ile Gly Gln Ser Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu
145                 150                 155                 160

Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro
                165                 170                 175

Gly Gln Ser Pro Lys Arg Leu Ile Ser Leu Val Ser Lys Leu Asp Ser
            180                 185                 190

Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Ile Tyr Tyr Cys
    210                 215                 220

Trp Gln Gly Thr His Phe Pro Gly Thr Phe Gly Gly Gly Thr Lys Leu
225                 230                 235                 240

Glu Ile Lys
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<210> 12
<211> 240
<212> PRT
<213> Homo sapiens

<400> 12
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1   5   10   15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asn
            20   25   30

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

Tyr Ala Ala Ser Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Thr Gly
    50   55   60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His His Ser Tyr Pro Leu
                85   90   95

Thr Ser Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Gly Ser Thr
            100   105   110

Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Glu Val Gln Val
        115   120   125

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

Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met Ser Trp
145   150   155   160

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Ser

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                                    _SL
                165                 170                 175


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


Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn
        195                 200                 205


Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Gly Ser Ser
    210                 215                 220


Gly Trp Ser Glu Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
225                 230                 235                 240


<210> 13
<211> 21
<212> PRT
<213> Artificial Sequence

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

<400> 13
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15


His Ala Ala Arg Pro
            20


<210> 14
<211> 45
<212> PRT
<213> Artificial Sequence

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

<400> 14
Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
1   5   10   15

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
            20   25   30

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

<210> 15
<211> 24
<212> PRT
<213> Artificial Sequence

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

<400> 15
Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu
1   5   10   15

Ser Leu Val Ile Thr Leu Tyr Cys
            20

<210> 16
<211> 42
<212> PRT
<213> Artificial Sequence

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

<400> 16
Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
1   5   10   15

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe

_SL
20 25 30

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

<210> 17
<211> 112
<212> PRT
<213> Artificial Sequence

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

<400> 17
Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly
1 5 10 15

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

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
35 40 45

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

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

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

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

<210> 18
<211> 1605

<212> DNA
<213> Artificial Sequence

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

<400> 18
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ccgggatccg agattcagct gcagcaatct ggggcagaac ttgtgaagcc aggggcctca 120

gtcaagctgt cctgcacagg ttctggcttc aacattgaag actactatat tcactgggtg 180

aagcagagga ctgaacaggg cctggaatgg attggaagga ttgatcctga gaatgatgaa 240

actaaatatg gcccaatatt ccagggcagg gccactataa cagcagacac atcctccaac 300

acagtctacc tgcaactcag cagcctgaca tctgaggaca ctgccgtcta ttactgtgcc 360

tttcgcggtg gagtctactg ggggccagga accactctca cagtctcctc aggaggtggt 420

ggttccggtg gtggtggttc cggaggtggt ggttcacata tggatgttgt gatgacccag 480

tctccactca ctctatcggt tgccattgga caatcagcct ccatctcttg caagtcaagt 540

cagagcctct tagatagtga tggaaagaca tatttgaatt ggttgttaca gaggccaggc 600

cagtctccaa agcgcctaat ctctctggtg tctaaactgg actctggagt ccctgacagg 660

ttcactggca gtggatcagg gacagatttc acactgagaa tcagcagagt ggaggctgag 720

gatttgggaa tttattattg ctggcaaggt acacattttc ctgggacgtt cggtggaggg 780

accaagctgg agataaaagc tagcaccacg acgccagcgc cgcgaccacc aacaccggcg 840

cccaccatcg cgtcgcagcc cctgtccctg cgcccagagg cgtgccggcc agcggcgggg 900

ggcgcagtgc acacgagggg gctggacttc gcctgtgatt tttgggtgct ggtggtggtt 960

ggtggagtcc tggcttgcta tagcttgcta gtaacagtgg cctttattat tttctgggtg 1020

aggagtaaga ggagcaggct cctgcacagt gactacatga acatgactcc ccgccgcccc 1080

gggcccaccc gcaagcatta ccagccctat gccccaccac gcgacttcgc agcctatcgc 1140

tccaaacggg gcagaaagaa actcctgtat atattcaaac aaccatttat gagaccagta 1200

caaactactc aagaggaaga tggctgtagc tgccgatttc cagaagaaga agaaggagga 1260

tgtgaactga gagtgaagtt cagcaggagc gcagacgccc ccgcgtacaa gcagggccag 1320

aaccagctct ataacgagct caatctagga cgaagagagg agtacgatgt tttggacaag 1380

agacgtggcc gggaccctga gatgggggga aagccgagaa ggaagaaccc tcaggaaggc 1440

ctgtacaatg aactgcagaa agataagatg gcggaggcct acagtgagat tgggatgaaa 1500

ggcgagcgcc ggaggggcaa ggggcacgat ggcctttacc agggtctcag tacagccacc 1560

aaggacacct acgacgccct tcacatgcag gccctgcccc ctcgc 1605

<210> 19
<211> 1473
<212> DNA
<213> Artificial Sequence

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

<400> 19
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgggatccg agattcagct gcagcaatct ggggcagaac ttgtgaagcc aggggcctca 120

gtcaagctgt cctgcacagg ttctggcttc aacattgaag actactatat tcactgggtg 180

aagcagagga ctgaacaggg cctggaatgg attggaagga ttgatcctga gaatgatgaa 240

actaaatatg gcccaatatt ccagggcagg gccactataa cagcagacac atcctccaac 300

acagtctacc tgcaactcag cagcctgaca tctgaggaca ctgccgtcta ttactgtgcc 360

tttcgcggtg gagtctactg ggggccagga accactctca cagtctcctc aggaggtggt 420

ggttccggtg gtggtggttc cggaggtggt ggttcacata tggatgttgt gatgacccag 480

tctccactca ctctatcggt tgccattgga caatcagcct ccatctcttg caagtcaagt 540

cagagcctct tagatagtga tggaaagaca tatttgaatt ggttgttaca gaggccaggc 600

cagtctccaa agcgcctaat ctctctggtg tctaaactgg actctggagt ccctgacagg 660

ttcactggca gtggatcagg gacagatttc acactgagaa tcagcagagt ggaggctgag 720

gatttgggaa tttattattg ctggcaaggt acacattttc ctgggacgtt cggtggaggg 780

accaagctgg agataaaagc tagcaccacg acgccagcgc cgcgaccacc aacaccggcg 840

cccaccatcg cgtcgcagcc cctgtccctg cgcccagagg cgtgccggcc agcggcgggg 900

ggcgcagtgc acacgagggg gctggacttc gcctgtgata tctacatctg ggcgcccttg 960

gccgggactt gtggggtcct tctcctgtca ctggttatca ccctttactg caaacggggc 1020

agaaagaaac tcctgtatat attcaaacaa ccatttatga gaccagtaca aactactcaa 1080

gaggaagatg gctgtagctg ccgatttcca gaagaagaag aaggaggatg tgaactgaga 1140

gtgaagttca gcaggagcgc agacgccccc gcgtacaagc agggccagaa ccagctctat 1200

aacgagctca atctaggacg aagagaggag tacgatgttt tggacaagag acgtggccgg 1260

gaccctgaga tgggggggaaa gccgagaagg aagaaccctc aggaaggcct gtacaatgaa 1320

ctgcagaaag ataagatggc ggaggcctac agtgagattg ggatgaaagg cgagcgccgg 1380

aggggcaagg ggcacgatgg cctttaccag ggtctcagta cagccaccaa ggacacctac 1440

gacgcccttc acatgcaggc cctgcccccc cgc 1473

<210> 20
<211> 1465
<212> DNA
<213> Artificial Sequence

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

<400> 20
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgggatccg acatccagat gacccagagc cctagcagcc tgagcgccag cgtgggcgac 120

agagtgacca tcacctgtcg ggccagccag ggcatcagaa acaacctggc ctggtatcag 180

cagaagcccg gcaaggcccc caagagactg atctacgctg ccagcaatct gcagagcggc 240

gtgcccagca gattcaccgg aagcggctcc ggcaccgagt tcaccctgat cgtgtccagc 300

ctgcagcccg aggacttcgc cacctactac tgcctgcagc accacagcta ccctctgacc 360

agcggcggag gcaccaaggt ggagatcaag cggaccggca gcaccagcgg cagcggcaag 420

cctggcagcg gcgagggaag cgaggtccag gtgctggaat ctggcggcgg actggtgcag 480

cctggcggca gcctgagact gagctgtgcc gccagcggct tcaccttcag cagctacgcc 540

atgtcttggg tccggcaggc tcctggaaag ggcctggaat gggtgtccgc catcagcggc 600

tctggcggct ccaccaacta cgccgacagc gtgaagggcc ggttcaccat cagccgggac 660

aacagcaaga acaccctgta tctgcagatg aacagcctga gagccgagga caccgccgtg 720

tactactgtg ccggcagcag cgggtggagc gagtactggg gccagggcac actggtcaca 780

gtgtctagcg ctagcaccac gacgccagcg ccgcgaccac caacaccggc gcccaccatc 840

gcgtcgcagc ccctgtccct gcgcccagag gcgtgccggc cagcggcggg gggcgcagtg 900

cacacgaggg ggctggactt cgcctgtgat atctacatct gggcgccctt ggccgggact 960

tgtggggtcc ttctcctgtc actggttatc acccтttact gcaaacgggg cagaaagaaa 1020

ctcctgtata tattcaaaca accatttatg agaccagtac aaactactca agaggaagat 1080

ggctgtagct gccgatttcc agaagaagaa gaaggaggat gtgaactgag agtgaagttc 1140

agcaggagcg cagacgcccc cgcgtacaag cagggccaga accagctcta taacgagctc 1200

aatctaggac gaagagagga gtacgatgtt ttggacaaga gacgtggccg ggaccctgag 1260

atgggggaa agccgagaag gaagaaccct caggaaggcc tgtacaatga actgcagaaa 1320

gataagatgg cggaggccta cagtgagatt gggatgaaag gcgagcgccg gaggggcaag 1380

gggcacgatg gcctttacca gggtctcagt acagccacca aggacaccta cgacgccctt 1440

cacatgcagg ccctgccccc tcgct 1465

<210> 21
<211> 114
<212> PRT
<213> Artificial Sequence

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

<400> 21
Glu Ile Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Thr Gly Ser Gly Phe Asn Ile Glu Asp Tyr
20 25 30

Tyr Ile His Trp Val Lys Gln Arg Thr Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Arg Ile Asp Pro Glu Asn Asp Glu Thr Lys Tyr Gly Pro Ile Phe
50 55 60

Gln Gly Arg Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Val Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Phe Arg Gly Gly Val Tyr Trp Gly Pro Gly Thr Thr Leu Thr Val
100 105 110

Ser Ser

<210> 22
<211> 5
<212> PRT
<213> Artificial Sequence

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

<400> 22
Asp Tyr Tyr Ile His
1 5

<210> 23
<211> 17
<212> PRT
<213> Artificial Sequence

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

<400> 23
Arg Ile Asp Pro Glu Asn Asp Glu Thr Lys Tyr Gly Pro Ile Phe Gln
1 5 10 15

Gly

<210> 24
<211> 5
<212> PRT
<213> Artificial Sequence

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

<400> 24
Arg Gly Gly Val Tyr
1 5

<210> 25
<211> 112
<212> PRT
<213> Artificial Sequence

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

polypeptide"

<400> 25
Asp Val Val Met Thr Gln Ser Pro Leu Thr Leu Ser Val Ala Ile Gly
1 5 10 15

Gln Ser Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

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

Pro Lys Arg Leu Ile Ser Leu Val Ser Lys Leu Asp Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Leu Gly Ile Tyr Tyr Cys Trp Gln Gly
85 90 95

Thr His Phe Pro Gly Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 26
<211> 16
<212> PRT
<213> Artificial Sequence

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

<400> 26
Lys Ser Ser Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn
1 5 10 15

<210> 27
<211> 7

<212> PRT
<213> Artificial Sequence

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

<400> 27
Leu Val Ser Lys Leu Asp Ser
1 5

<210> 28
<211> 9
<212> PRT
<213> Artificial Sequence

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

<400> 28
Trp Gln Gly Thr His Phe Pro Gly Thr
1 5

<210> 29
<211> 114
<212> PRT
<213> Artificial Sequence

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

<400> 29
Glu Ile Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Thr Gly Ser Gly Phe Asn Ile Glu Asp Tyr
20 25 30

Tyr Ile His Trp Val Lys Gln Arg Thr Glu Gln Gly Leu Glu Trp Ile

_SL
35 40 45

Gly Arg Ile Asp Pro Glu Asn Asp Glu Thr Lys Tyr Gly Pro Ile Phe
50 55 60

Gln Gly Arg Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Val Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Phe Arg Gly Gly Val Tyr Trp Gly Pro Gly Thr Thr Leu Thr Val
100 105 110

Ser Ser

<210> 30
<211> 7
<212> PRT
<213> Artificial Sequence

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

<400> 30
Gly Phe Asn Ile Glu Asp Tyr
1 5

<210> 31
<211> 6
<212> PRT
<213> Artificial Sequence

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

<400> 31
Asp Pro Glu Asn Asp Glu
1 5

<210> 32
<211> 5
<212> PRT
<213> Artificial Sequence

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

<400> 32
Arg Gly Gly Val Tyr
1 5

<210> 33
<211> 112
<212> PRT
<213> Artificial Sequence

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

<400> 33
Asp Val Val Met Thr Gln Ser Pro Leu Thr Leu Ser Val Ala Ile Gly
1 5 10 15

Gln Ser Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

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

Pro Lys Arg Leu Ile Ser Leu Val Ser Lys Leu Asp Ser Gly Val Pro
50 55 60

Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Arg Ile

_SL
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Leu Gly Ile Tyr Tyr Cys Trp Gln Gly
85 90 95

Thr His Phe Pro Gly Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 34
<211> 12
<212> PRT
<213> Artificial Sequence

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

<400> 34
Ser Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr
1 5 10

<210> 35
<211> 3
<212> PRT
<213> Artificial Sequence

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

<400> 35
Leu Val Ser
1

<210> 36
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 36
Gly Thr His Phe Pro Gly
1 5

<210> 37
<211> 5
<212> PRT
<213> Artificial Sequence

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

<400> 37
Gly Gly Gly Gly Ser
1 5

<210> 38
<211> 246
<212> PRT
<213> Artificial Sequence

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

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

Thr Val Lys Ile Ser Cys Lys Gly Ser Gly Phe Asn Ile Glu Asp Tyr
20 25 30

Tyr Ile His Trp Val Gln Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Arg Ile Asp Pro Glu Asn Asp Glu Thr Lys Tyr Gly Pro Ile Phe
50 55 60

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Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Asn Thr Val Tyr
65                  70                  75                  80

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

Ala Phe Arg Gly Gly Val Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
            100                 105                 110

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

Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln Ser Pro Asp Ser
    130                 135                 140

Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser
145                 150                 155                 160

Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Gln
                165                 170                 175

Gln Lys Pro Gly Gln Pro Pro Lys Arg Leu Ile Ser Leu Val Ser Lys
            180                 185                 190

Leu Asp Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val
    210                 215                 220

Tyr Tyr Cys Trp Gln Gly Thr His Phe Pro Gly Thr Phe Gly Gly Gly
225                 230                 235                 240

Thr Lys Val Glu Ile Lys
                245
```

<210> 39
<211> 738
<212> DNA
<213> Artificial Sequence

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

<400> 39
gaaatccagc tggtccaatc gggagctgag gtcaagaagc cgggagccac cgtcaagatc 60

tcatgcaagg ggtcgggatt caacatcgag gactactaca ttcactgggt gcagcaagct 120

ccgggaaaag gcctggaatg gatgggcaga atcgacccag aaaacgacga aactaagtac 180

ggaccgattt tccaaggaag agtgactatc accgccgata cttcaaccaa taccgtctac 240

atggaactga gctcgctccg gtccgaagat actgcagtgt attactgtgc ctttcgcgga 300

ggggtgtact ggggccaagg aactactgtc actgtctcgt caggaggcgg agggtcggga 360

ggaggcggga gcggaggcgg tggctcgggt ggcggaggaa gcgacgtggt gatgacccag 420

tccccggact ccctcgccgt gagcctcgga gagagggcga ctatcaattg caagtcgtcc 480

cagtcacttc tggattccga tggtaaaacg tacctcaact ggctgcagca aaagccaggg 540

cagccaccca aacggttgat ctcccttgtg tccaaactgg atagcggagt gcctgaccgc 600

ttctcgggtt ccggtagcgg gaccgacttc accctgacga tcagctcact gcaggcggag 660

gacgtggcag tgtactactg ctggcaggga acccacttcc ctggcacctt tggaggtggc 720

accaaggtgg agatcaag 738

<210> 40
<211> 831
<212> DNA
<213> Artificial Sequence

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

polynucleotide"

<400> 40
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60

cccgaaatcc agctggtcca atcgggagct gaggtcaaga agccgggagc caccgtcaag 120

atctcatgca aggggtcggg attcaacatc gaggactact acattcactg ggtgcagcaa 180

gctccgggaa aaggcctgga atggatgggc agaatcgacc cagaaaacga cgaaactaag 240

tacggaccga ttttccaagg aagagtgact atcaccgccg atacttcaac caataccgtc 300

tacatggaac tgagctcgct ccggtccgaa gatactgcag tgtattactg tgcctttcgc 360

ggaggggtgt actggggcca aggaactact gtcactgtct cgtcaggagg cggagggtcg 420

ggaggaggcg ggagcggagg cggtggctcg ggtggcggag gaagcgacgt ggtgatgacc 480

cagtccccgg actccctcgc cgtgagcctc ggagagaggg cgactatcaa ttgcaagtcg 540

tcccagtcac ttctggattc cgatggtaaa acgtacctca actggctgca gcaaaagcca 600

gggcagccac ccaaacggtt gatctccctt gtgtccaaac tggatagcgg agtgcctgac 660

cgcttctcgg gttccggtag cgggaccgac ttcaccctga cgatcagctc actgcaggcg 720

gaggacgtgg cagtgtacta ctgctggcag ggaacccact tccctggcac ctttggaggt 780

ggcaccaagg tggagatcaa gggatcgcac caccatcacc atcatcatca c 831

<210> 41
<211> 277
<212> PRT
<213> Artificial Sequence

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

<400> 41
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Glu Ile Gln Leu Val Gln Ser Gly Ala Glu Val

_SL

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            20                  25                  30

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

Asn Ile Glu Asp Tyr Tyr Ile His Trp Val Gln Gln Ala Pro Gly Lys
    50                  55                  60

Gly Leu Glu Trp Met Gly Arg Ile Asp Pro Glu Asn Asp Glu Thr Lys
65                  70                  75                  80

Tyr Gly Pro Ile Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser
                85                  90                  95

Thr Asn Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
            100                 105                 110

Ala Val Tyr Tyr Cys Ala Phe Arg Gly Gly Val Tyr Trp Gly Gln Gly
        115                 120                 125

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

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr
145                 150                 155                 160

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

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

Leu Asn Trp Leu Gln Gln Lys Pro Gly Gln Pro Pro Lys Arg Leu Ile
        195                 200                 205

Ser Leu Val Ser Lys Leu Asp Ser Gly Val Pro Asp Arg Phe Ser Gly
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                                        _SL
    210                 215                 220


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


Glu Asp Val Ala Val Tyr Tyr Cys Trp Gln Gly Thr His Phe Pro Gly
                245                 250                 255


Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Ser His His His
            260                 265                 270


His His His His His
        275


<210> 42
<211> 1470
<212> DNA
<213> Artificial Sequence

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

<400> 42
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg       60

cccgagatcc agctggtgca gtcgggagct gaagtcaaaa agcctggcgc aaccgtcaag      120

atctcgtgca aaggatcagg gttcaacatc gaggactact acatccattg ggtgcaacag      180

gcacccggaa aaggcctgga gtggatgggg aggattgacc cagaaaatga cgaaaccaag      240

tacggaccga tcttccaagg acgggtgacc atcacggctg acacttccac taacaccgtc      300

tacatggaac tctcgagcct tcgctcggaa gataccgcgg tgtactactg cgcctttaga      360

ggtggagtct actggggaca agggactacc gtcaccgtgt cgtcaggtgg cggaggatca      420

ggcggaggcg gctccggtgg aggaggaagc ggaggaggtg gctccgacgt ggtgatgacg      480

cagtcaccgg actccttggc ggtgagcctg ggtgaacgcg ccactatcaa ctgcaagagc      540
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tcccagagct tgctggactc cgatggaaag acttatctca attggctgca acagaagcct 600

ggccagccgc caaagagact catctcactg gtgagcaagc tggatagcgg agtgccagat 660

cggttttcgg gatcgggctc aggcaccgac ttcaccctga ctatttcctc cctccaagcc 720

gaggatgtgg ccgtctacta ctgttggcag gggactcact tcccggggac cttcggtgga 780

ggcactaagg tggagatcaa aaccactacc ccagcaccga ggccacccac cccggctcct 840

accatcgcct cccagcctct gtccctgcgt ccggaggcat gtagacccgc agctggtggg 900

gccgtgcata cccggggtct tgacttcgcc tgcgatatct acatttgggc ccctctggct 960

ggtacttgcg gggtcctgct gctttcactc gtgatcactc tttactgtaa gcgcggtcgg 1020

aagaagctgc tgtacatctt taagcaaccc ttcatgaggc ctgtgcagac tactcaagag 1080

gaggacggct gttcatgccg gttcccagag gaggaggaag gcggctgcga actgcgcgtg 1140

aaattcagcc gcagcgcaga tgctccagcc tacaagcagg ggcagaacca gctctacaac 1200

gaactcaatc ttggtcggag agaggagtac gacgtgctgg acaagcggag aggacgggac 1260

ccagaaatgg gcgggaagcc gcgcagaaag aatccccaag agggcctgta caacgagctc 1320

caaaaggata agatggcaga agcctatagc gagattggta tgaaagggga acgcagaaga 1380

ggcaaaggcc acgacggact gtaccaggga ctcagcaccg ccaccaagga cacctatgac 1440

gctcttcaca tgcaggccct gccgcctcgg 1470

<210> 43
<211> 490
<212> PRT
<213> Artificial Sequence

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

<400> 43
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

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

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

Asn Ile Glu Asp Tyr Tyr Ile His Trp Val Gln Gln Ala Pro Gly Lys
    50                  55                  60

Gly Leu Glu Trp Met Gly Arg Ile Asp Pro Glu Asn Asp Glu Thr Lys
65                  70                  75                  80

Tyr Gly Pro Ile Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser
                85                  90                  95

Thr Asn Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
            100                 105                 110

Ala Val Tyr Tyr Cys Ala Phe Arg Gly Gly Val Tyr Trp Gly Gln Gly
        115                 120                 125

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

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr
145                 150                 155                 160

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

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

Leu Asn Trp Leu Gln Gln Lys Pro Gly Gln Pro Pro Lys Arg Leu Ile
        195                 200                 205
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                                            _SL
Ser Leu Val Ser Lys Leu Asp Ser Gly Val Pro Asp Arg Phe Ser Gly
    210                 215                 220

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

Glu Asp Val Ala Val Tyr Tyr Cys Trp Gln Gly Thr His Phe Pro Gly
                245                 250                 255

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala
            260                 265                 270

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

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

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

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
                325                 330                 335

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
            340                 345                 350

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
        355                 360                 365

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
    370                 375                 380

Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn
385                 390                 395                 400
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_SL
Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
405 410 415

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
420 425 430

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
435 440 445

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
450 455 460

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
465 470 475 480

Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 44
<211> 246
<212> PRT
<213> Artificial Sequence

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

<400> 44
Asp Val Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Leu Gln Gln Lys Pro Gly Gln Pro
35 40 45

Pro Lys Arg Leu Ile Ser Leu Val Ser Lys Leu Asp Ser Gly Val Pro

_SL

50 55 60

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

Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Trp Gln Gly
85 90 95

Thr His Phe Pro Gly Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

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

Gly Gly Gly Ser Glu Ile Gln Leu Val Gln Ser Gly Ala Glu Val Lys
130 135 140

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

Ile Glu Asp Tyr Tyr Ile His Trp Val Gln Gln Ala Pro Gly Lys Gly
165 170 175

Leu Glu Trp Met Gly Arg Ile Asp Pro Glu Asn Asp Glu Thr Lys Tyr
180 185 190

Gly Pro Ile Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr
195 200 205

Asn Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
210 215 220

Val Tyr Tyr Cys Ala Phe Arg Gly Gly Val Tyr Trp Gly Gln Gly Thr
225 230 235 240

Thr Val Thr Val Ser Ser

<210> 45
<211> 738
<212> DNA
<213> Artificial Sequence

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

<400> 45
gatgtcgtga tgacccagtc cccagactcc ctcgcagtgt ccttgggaga acgggccacc 60

atcaactgca aatcgagcca gtcactgctg gactcagacg gaaagaccta cctcaactgg 120

ctgcagcaga agcctggcca gccaccgaag cgcctgatct ccctggtgtc caagctggac 180

tcgggcgtcc cggacaggtt tagcggtagc ggctcgggaa ccgacttcac tctgaccatt 240

agctcgctcc aagctgaaga tgtggcggtc tactactgct ggcaggggac ccacttcccc 300

gggacctttg gcggaggaac taaagtcgaa atcaaaggag gaggcggatc aggtggagga 360

ggcagcggag gaggagggag cggcggtggc ggctccgaaa ttcaacttgt gcaatccggt 420

gccgaggtga agaaacctgg tgccactgtc aagatctcgt gtaagggatc gggattcaat 480

atcgaggact actacatcca ctgggtgcaa caggcgccag gaaagggatt ggagtggatg 540

ggtcgcatcg acccggaaaa cgatgagact aagtacggac cgatcttcca aggccgggtc 600

acgatcactg cggatacctc cactaatacc gtgtatatgg agctctcgtc actgagaagc 660

gaagatacgg ccgtgtacta ctgcgcattc agaggaggtg tgtactgggg ccagggaact 720

actgtgaccg tgtcgtcg 738

<210> 46
<211> 831
<212> DNA
<213> Artificial Sequence

<220>
<221> source

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

<400> 46
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60

cccgatgtcg tgatgaccca gtccccagac tccctcgcag tgtccttggg agaacgggcc 120

accatcaact gcaaatcgag ccagtcactg ctggactcag acggaaagac ctacctcaac 180

tggctgcagc agaagcctgg ccagccaccg aagcgcctga tctccctggt gtccaagctg 240

gactcgggcg tcccggacag gtttagcggt agcggctcgg gaaccgactt cactctgacc 300

attagctcgc tccaagctga agatgtggcg gtctactact gctggcaggg gacccacttc 360

cccgggacct ttggcggagg aactaaagtc gaaatcaaag gaggaggcgg atcaggtgga 420

ggaggcagcg gaggaggagg gagcggcggt ggcggctccg aaattcaact tgtgcaatcc 480

ggtgccgagg tgaagaaacc tggtgccact gtcaagatct cgtgtaaggg atcgggattc 540

aatatcgagg actactacat ccactgggtg caacaggcgc caggaaaggg attggagtgg 600

atgggtcgca tcgacccgga aaacgatgag actaagtacg gaccgatctt ccaaggccgg 660

gtcacgatca ctgcggatac ctccactaat accgtgtata tggagctctc gtcactgaga 720

agcgaagata cggccgtgta ctactgcgca ttcagaggag gtgtgtactg gggccaggga 780

actactgtga ccgtgtcgtc ggggtcacat caccaccatc atcatcacca c 831

<210> 47
<211> 277
<212> PRT
<213> Artificial Sequence

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

<400> 47
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

```
                                        _SL
His Ala Ala Arg Pro Asp Val Val Met Thr Gln Ser Pro Asp Ser Leu
            20                  25                  30

Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln
        35                  40                  45

Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Gln Gln
    50                  55                  60

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

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

Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr
            100                 105                 110

Tyr Cys Trp Gln Gly Thr His Phe Pro Gly Thr Phe Gly Gly Gly Thr
        115                 120                 125

Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    130                 135                 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Gln Leu Val Gln Ser
145                 150                 155                 160

Gly Ala Glu Val Lys Lys Pro Gly Ala Thr Val Lys Ile Ser Cys Lys
                165                 170                 175

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

Ala Pro Gly Lys Gly Leu Glu Trp Met Gly Arg Ile Asp Pro Glu Asn
        195                 200                 205
```

```
                                        _SL
Asp Glu Thr Lys Tyr Gly Pro Ile Phe Gln Gly Arg Val Thr Ile Thr
    210                 215                 220


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


Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Phe Arg Gly Gly Val Tyr
                245                 250                 255


Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Ser His His His
            260                 265                 270


His His His His His
        275


<210> 48
<211> 1470
<212> DNA
<213> Artificial Sequence

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

<400> 48
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg       60

cccgacgtgg tcatgactca aagcccagat tccttggctg tctcccttgg agaaagagca      120

acgatcaatt gcaaaagctc gcagtccctg ttggactccg atggaaaaac ctacctcaac      180

tggctgcagc agaagccggg acaaccacca aagcggctga tttccctcgt gtccaagctg      240

gacagcggcg tgccggatcg cttctcgggc agcggctcgg gaaccgattt tactctcact      300

atttcgtcac tgcaagcgga ggacgtggcg gtgtattact gctggcaggg cactcacttc      360

ccgggtactt ttggtggagg taccaaagtc gaaatcaagg gtggaggcgg gagcggagga      420

ggcgggtcgg gaggaggagg atcgggtggc ggaggctcag aaatccagct ggtgcagtca      480

ggtgccgaag tgaagaagcc tggggccacg gtgaagatct cgtgcaaggg gagcggattc      540
```

aacatcgagg attactacat ccattgggtg caacaggccc ctggcaaagg gctggaatgg 600

atgggaagga tcgaccccga gaatgacgag actaagtacg gcccgatctt ccaaggacgg 660

gtgaccatca ctgcagacac ttcaaccaac accgtctaca tggaactctc ctcgctgcgc 720

tccgaggaca ccgccgtgta ctactgtgct ttcagaggag gagtctactg gggacaggga 780

acgaccgtga ccgtcagctc aaccactacc ccagcaccga ggccacccac cccggctcct 840

accatcgcct cccagcctct gtccctgcgt ccggaggcat gtagacccgc agctggtggg 900

gccgtgcata cccggggtct tgacttcgcc tgcgatatct acatttgggc ccctctggct 960

ggtacttgcg gggtcctgct gctttcactc gtgatcactc tttactgtaa gcgcggtcgg 1020

aagaagctgc tgtacatctt taagcaaccc ttcatgaggc ctgtgcagac tactcaagag 1080

gaggacggct gttcatgccg gttcccagag gaggaggaag gcggctgcga actgcgcgtg 1140

aaattcagcc gcagcgcaga tgctccagcc tacaagcagg ggcagaacca gctctacaac 1200

gaactcaatc ttggtcggag agaggagtac gacgtgctgg acaagcggag aggacgggac 1260

ccagaaatgg gcgggaagcc gcgcagaaag aatccccaag agggcctgta caacgagctc 1320

caaaaggata agatggcaga agcctatagc gagattggta tgaaaggggа acgcagaaga 1380

ggcaaaggcc acgacggact gtaccaggga ctcagcaccg ccaccaagga cacctatgac 1440

gctcttcaca tgcaggccct gccgcctcgg 1470

<210> 49
<211> 490
<212> PRT
<213> Artificial Sequence

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

<400> 49
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

```
His Ala Ala Arg Pro Asp Val Val Met Thr Gln Ser Pro Asp Ser Leu
            20                  25                  30

Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln
        35                  40                  45

Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Gln Gln
    50                  55                  60

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

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

Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr
            100                 105                 110

Tyr Cys Trp Gln Gly Thr His Phe Pro Gly Thr Phe Gly Gly Gly Thr
        115                 120                 125

Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    130                 135                 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Gln Leu Val Gln Ser
145                 150                 155                 160

Gly Ala Glu Val Lys Lys Pro Gly Ala Thr Val Lys Ile Ser Cys Lys
                165                 170                 175

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

Ala Pro Gly Lys Gly Leu Glu Trp Met Gly Arg Ile Asp Pro Glu Asn
        195                 200                 205
```

```
Asp Glu Thr Lys Tyr Gly Pro Ile Phe Gln Gly Arg Val Thr Ile Thr
    210                 215                 220

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

Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Phe Arg Gly Gly Val Tyr
                245                 250                 255

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Thr Thr Thr Pro Ala
            260                 265                 270

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

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

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

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
                325                 330                 335

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
            340                 345                 350

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
        355                 360                 365

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
    370                 375                 380

Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn
385                 390                 395                 400
```

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
405 410 415

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
420 425 430

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
435 440 445

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
450 455 460

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
465 470 475 480

Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 50
<211> 246
<212> PRT
<213> Artificial Sequence

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

<400> 50
Glu Ile Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Phe Asn Ile Glu Asp Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

```
                                            _SL
Gly Arg Ile Asp Pro Glu Asn Asp Glu Thr Lys Tyr Gly Pro Ile Phe
    50                  55                  60

Gln Gly His Val Thr Ile Ser Ala Asp Thr Ser Ile Asn Thr Val Tyr
65                  70                  75                  80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
                85                  90                  95

Ala Phe Arg Gly Gly Val Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
            100                 105                 110

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

Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln Ser Pro Leu Ser
    130                 135                 140

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

Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Gln
                165                 170                 175

Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Ser Leu Val Ser Lys
            180                 185                 190

Leu Asp Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205

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

Tyr Tyr Cys Trp Gln Gly Thr His Phe Pro Gly Thr Phe Gly Gly Gly
225                 230                 235                 240
```

Thr Lys Val Glu Ile Lys
245

<210> 51
<211> 738
<212> DNA
<213> Artificial Sequence

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

<400> 51
gagattcagc tggtccaaag cggcgcagaa gtgaaaaagc caggggaatc gttgcgcatc 60

agctgtaaag gttccggctt caacatcgag gactattaca tccattgggt gcggcagatg 120

ccaggaaagg ggctggaatg gatgggacgg attgacccgg agaacgacga aaccaagtac 180

ggaccgatct ttcaaggaca cgtgactatc tccgccgaca ccagcatcaa tacggtgtac 240

ctccaatggt cctcactcaa ggcctcggat accgcgatgt actactgcgc gttcagagga 300

ggcgtctact ggggacaagg gactactgtg actgtctcat caggaggtgg aggaagcgga 360

ggaggtggct cgggcggagg tggatcggga ggaggagggt ccgatgtggt gatgacccag 420

tccccactgt cgctcccggt gaccctcgga cagcctgcta gcatctcgtg caaatcctcg 480

caatccctgc tggactcgga cggaaaaacg tacctcaatt ggctgcagca gcgccctggc 540

cagagcccga gaaggcttat ctcgctggtg tcaaagctgg atagcggtgt gcccgaccgg 600

ttcagcggct cagggtcagg aaccgatttc accttgaaga tctcccgcgt ggaagccgaa 660

gatgtcggag tctactactg ctggcagggt actcacttcc cggggacctt tggtggcggc 720

actaaggtcg agattaag 738

<210> 52
<211> 831
<212> DNA
<213> Artificial Sequence

<220>

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

<400> 52
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60

cccgagattc agctggtcca aagcggcgca gaagtgaaaa agccagggga atcgttgcgc 120

atcagctgta aaggttccgg cttcaacatc gaggactatt acatccattg ggtgcggcag 180

atgccaggaa aggggctgga atggatggga cggattgacc cggagaacga cgaaaccaag 240

tacggaccga tctttcaagg acacgtgact atctccgccg acaccagcat caatacggtg 300

tacctccaat ggtcctcact caaggcctcg gataccgcga tgtactactg cgcgttcaga 360

ggaggcgtct actggggaca agggactact gtgactgtct catcaggagg tggaggaagc 420

ggaggaggtg gctcgggcgg aggtggatcg ggaggaggag ggtccgatgt ggtgatgacc 480

cagtccccac tgtcgctccc ggtgaccctc ggacagcctg ctagcatctc gtgcaaatcc 540

tcgcaatccc tgctggactc ggacggaaaa acgtacctca attggctgca gcagcgccct 600

ggccagagcc cgagaaggct tatctcgctg gtgtcaaagc tggatagcgg tgtgcccgac 660

cggttcagcg gctcagggtc aggaaccgat ttcaccttga agatctcccg cgtggaagcc 720

gaagatgtcg gagtctacta ctgctggcag ggtactcact tcccggggac ctttggtggc 780

ggcactaagg tcgagattaa gggctcacac catcatcacc atcaccacca c 831

<210> 53
<211> 277
<212> PRT
<213> Artificial Sequence

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

<400> 53
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

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

Lys Lys Pro Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Phe
        35                  40                  45

Asn Ile Glu Asp Tyr Tyr Ile His Trp Val Arg Gln Met Pro Gly Lys
    50                  55                  60

Gly Leu Glu Trp Met Gly Arg Ile Asp Pro Glu Asn Asp Glu Thr Lys
65                  70                  75                  80

Tyr Gly Pro Ile Phe Gln Gly His Val Thr Ile Ser Ala Asp Thr Ser
                85                  90                  95

Ile Asn Thr Val Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr
            100                 105                 110

Ala Met Tyr Tyr Cys Ala Phe Arg Gly Gly Val Tyr Trp Gly Gln Gly
        115                 120                 125

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

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr
145                 150                 155                 160

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

Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr
            180                 185                 190

Leu Asn Trp Leu Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile
        195                 200                 205
```

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
225 230 235 240

Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly Thr His Phe Pro Gly
245 250 255

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Ser His His His
260 265 270

His His His His His
275

<210> 54
<211> 1470
<212> DNA
<213> Artificial Sequence

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

<400> 54
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60

cccgaaatcc agctggtgca aagcggagcc gaggtgaaga agcccggaga atccctgcgc 120

atctcgtgta agggttccgg ctttaacatc gaggattact acatccactg ggtgagacag 180

atgccgggca aaggtctgga atggatgggc cgcatcgacc cggagaacga cgaaaccaaa 240

tacggaccaa tcttccaagg acatgtgact atttccgcgg atacctccat caacactgtc 300

tacttgcagt ggagctcgct caaggcgtcg gataccgcca tgtactactg cgcattcaga 360

ggaggtgtgt actggggcca gggcactacg gtcaccgtgt cctcgggagg tggagggtca 420

ggaggcggag gctcgggcgg tggaggatca ggcggaggag gaagcgatgt ggtcatgact 480

caatccccac tgtcactgcc tgtcactctg gggcaaccgg cttccatctc atgcaagtca 540

agccaatcgc tgctcgactc cgacggaaaa acctacctca attggcttca gcagcgccca 600

ggccagtcgc ctcggaggct gatctcactc gtgtcgaagc ttgactccgg ggtgccggat 660

cggtttagcg gaagcggatc ggggaccgac ttcacgttga agattagccg ggtggaagcc 720

gaggacgtgg gagtctatta ctgctggcag gggacccact tcccggggac tttcggagga 780

ggcaccaaag tcgagattaa gaccactacc ccagcaccga ggccacccac cccggctcct 840

accatcgcct cccagcctct gtccctgcgt ccggaggcat gtagacccgc agctggtggg 900

gccgtgcata cccggggtct tgacttcgcc tgcgatatct acatttgggc ccctctggct 960

ggtacttgcg gggtcctgct gctttcactc gtgatcactc tttactgtaa gcgcggtcgg 1020

aagaagctgc tgtacatctt taagcaaccc ttcatgaggc ctgtgcagac tactcaagag 1080

gaggacggct gttcatgccg gttcccagag gaggaggaag gcggctgcga actgcgcgtg 1140

aaattcagcc gcagcgcaga tgctccagcc tacaagcagg ggcagaacca gctctacaac 1200

gaactcaatc ttggtcggag agaggagtac gacgtgctgg acaagcggag aggacgggac 1260

ccagaaatgg gcgggaagcc gcgcagaaag aatccccaag agggcctgta caacgagctc 1320

caaaaggata agatggcaga agcctatagc gagattggta tgaaagggga acgcagaaga 1380

ggcaaaggcc acgacggact gtaccaggga ctcagcaccg ccaccaagga cacctatgac 1440

gctcttcaca tgcaggccct gccgcctcgg 1470

<210> 55
<211> 490
<212> PRT
<213> Artificial Sequence

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

<400> 55
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

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

Lys Lys Pro Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Phe
        35                  40                  45

Asn Ile Glu Asp Tyr Tyr Ile His Trp Val Arg Gln Met Pro Gly Lys
    50                  55                  60

Gly Leu Glu Trp Met Gly Arg Ile Asp Pro Glu Asn Asp Glu Thr Lys
65                  70                  75                  80

Tyr Gly Pro Ile Phe Gln Gly His Val Thr Ile Ser Ala Asp Thr Ser
                85                  90                  95

Ile Asn Thr Val Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr
            100                 105                 110

Ala Met Tyr Tyr Cys Ala Phe Arg Gly Gly Val Tyr Trp Gly Gln Gly
        115                 120                 125

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

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr
145                 150                 155                 160

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

Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr
            180                 185                 190

Leu Asn Trp Leu Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile
        195                 200                 205
```

```
Ser Leu Val Ser Lys Leu Asp Ser Gly Val Pro Asp Arg Phe Ser Gly
    210                 215                 220

Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
225                 230                 235                 240

Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly Thr His Phe Pro Gly
                245                 250                 255

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala
            260                 265                 270

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

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

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

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
                325                 330                 335

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
            340                 345                 350

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
        355                 360                 365

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
    370                 375                 380

Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn
385                 390                 395                 400
```

```
Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
                405                 410                 415


Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
            420                 425                 430


Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
        435                 440                 445


Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
    450                 455                 460


Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
465                 470                 475                 480


Ala Leu His Met Gln Ala Leu Pro Pro Arg
                485                 490


<210> 56
<211> 246
<212> PRT
<213> Artificial Sequence

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

<400> 56
Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1               5                   10                  15


Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
            20                  25                  30


Asp Gly Lys Thr Tyr Leu Asn Trp Leu Gln Gln Arg Pro Gly Gln Ser
        35                  40                  45
```

```
Pro Arg Arg Leu Ile Ser Leu Val Ser Lys Leu Asp Ser Gly Val Pro
    50                  55                  60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly
                85                  90                  95

Thr His Phe Pro Gly Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110

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

Gly Gly Gly Ser Glu Ile Gln Leu Val Gln Ser Gly Ala Glu Val Lys
    130                 135                 140

Lys Pro Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Phe Asn
145                 150                 155                 160

Ile Glu Asp Tyr Tyr Ile His Trp Val Arg Gln Met Pro Gly Lys Gly
                165                 170                 175

Leu Glu Trp Met Gly Arg Ile Asp Pro Glu Asn Asp Glu Thr Lys Tyr
            180                 185                 190

Gly Pro Ile Phe Gln Gly His Val Thr Ile Ser Ala Asp Thr Ser Ile
        195                 200                 205

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

Met Tyr Tyr Cys Ala Phe Arg Gly Gly Val Tyr Trp Gly Gln Gly Thr
225                 230                 235                 240
```

Thr Val Thr Val Ser Ser
245

<210> 57
<211> 738
<212> DNA
<213> Artificial Sequence

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

<400> 57
gacgtcgtca tgacccagag cccgctgtca ctgcctgtga ccctgggcca gccggcgtcc 60

attagctgca aatcctcgca atccctgctc gactcagacg gaaaaacgta cttgaactgg 120

ctccaacagc gccctgggca atccccaagg cggcttatct cactcgtcag caagctcgat 180

agcggtgtcc cagacagatt ttcgggctcg ggatcgggca ctgatttcac tctgaagatc 240

tcgcgggtgg aagccgagga tgtgggagtg tactattgct ggcagggcac tcacttcccc 300

gggacgtttg gcggaggaac taaggtcgag atcaaaggag gaggtggatc aggcggaggt 360

gggagcggag gaggaggaag cggtggtgga ggttccgaaa tccagctggt gcaatcagga 420

gccgaggtga agaagccggg agaatccctg cgcatctcgt gcaagggctc gggcttcaac 480

atcgaggatt actacatcca ctgggtgcgg cagatgccgg gaaaggggtt ggaatggatg 540

ggacgcattg acccggaaaa tgatgaaacc aaatacgggc caatcttcca aggccacgtg 600

accattagcg ctgacacttc catcaacacc gtgtaccttc agtggtcctc actgaaggcg 660

tcggacactg ccatgtacta ctgtgcattc agaggagggg tctactgggg acagggcacc 720

accgtgaccg tgagctcc 738

<210> 58
<211> 831
<212> DNA
<213> Artificial Sequence

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

<400> 58
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60

cccgacgtcg tcatgaccca gagcccgctg tcactgcctg tgaccctggg ccagccggcg 120

tccattagct gcaaatcctc gcaatccctg ctcgactcag acggaaaaac gtacttgaac 180

tggctccaac agcgccctgg gcaatcccca aggcggctta tctcactcgt cagcaagctc 240

gatagcggtg tcccagacag attttcgggc tcgggatcgg gcactgattt cactctgaag 300

atctcgcggg tggaagccga ggatgtggga gtgtactatt gctggcaggg cactcacttc 360

cccgggacgt ttggcggagg aactaaggtc gagatcaaag gaggaggtgg atcaggcgga 420

ggtgggagcg gaggaggagg aagcggtggt ggaggttccg aaatccagct ggtgcaatca 480

ggagccgagg tgaagaagcc gggagaatcc ctgcgcatct cgtgcaaggg ctcgggcttc 540

aacatcgagg attactacat ccactgggtg cggcagatgc cgggaaaggg gttggaatgg 600

atgggacgca ttgacccgga aaatgatgaa accaaatacg ggccaatctt ccaaggccac 660

gtgaccatta gcgctgacac ttccatcaac accgtgtacc ttcagtggtc ctcactgaag 720

gcgtcggaca ctgccatgta ctactgtgca ttcagaggag gggtctactg gggacagggc 780

accaccgtga ccgtgagctc cggctcgcat caccatcatc accaccatca c 831

<210> 59
<211> 277
<212> PRT
<213> Artificial Sequence

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

<400> 59
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

```
His Ala Ala Arg Pro Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu
            20                  25                  30

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

Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Gln Gln
    50                  55                  60

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

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

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

Tyr Cys Trp Gln Gly Thr His Phe Pro Gly Thr Phe Gly Gly Gly Thr
        115                 120                 125

Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    130                 135                 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Gln Leu Val Gln Ser
145                 150                 155                 160

Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Arg Ile Ser Cys Lys
                165                 170                 175

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

Met Pro Gly Lys Gly Leu Glu Trp Met Gly Arg Ile Asp Pro Glu Asn
        195                 200                 205
```

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

Ala Asp Thr Ser Ile Asn Thr Val Tyr Leu Gln Trp Ser Ser Leu Lys
225 230 235 240

Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Phe Arg Gly Gly Val Tyr
245 250 255

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Ser His His His
260 265 270

His His His His His
275

<210> 60
<211> 1470
<212> DNA
<213> Artificial Sequence

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

<400> 60
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60

cccgacgtcg tcatgaccca atcccctctc tccctgccgg tcaccctggg tcagccggcg 120

tcgatctcat gcaaaagctc acagtccctg ctggattcgg acggaaaaac ctacttgaac 180

tggctccaac agaggccggg tcagtcccct cgcagactga tctcgctggt gagcaagctc 240

gactcgggtg tgccggatcg gttctccggg tcaggatcgg gcaccgactt tacgctcaag 300

atttcgagag tggaggccga ggatgtggga gtgtactatt gctggcaggg cacgcatttc 360

cccgggacct ttggaggcgg gactaaggtg gaaatcaagg gaggtggcgg atcaggcgga 420

ggaggcagcg gcggaggtgg atcaggaggc ggagggtcag agatccagct ggtccaaagc 480

ggagcagagg tgaagaagcc aggcgagtcc cttcgcattt cgtgcaaagg gagcggcttc 540

aacattgaag attactacat ccactgggtg cggcaaatgc caggaaaggg tctggaatgg 600

atgggacgga tcgacccaga aaatgatgaa actaagtacg gaccgatctt ccaaggacac 660

gtcactatct ccgcggacac ttcgatcaac accgtgtacc tccagtggag cagcttgaaa 720

gcctccgaca ccgctatgta ctactgtgcc ttccgcggag gagtctactg gggacagggg 780

actactgtga ccgtgtcgtc caccactacc ccagcaccga ggccacccac cccggctcct 840

accatcgcct cccagcctct gtccctgcgt ccggaggcat gtagacccgc agctggtggg 900

gccgtgcata cccggggtct tgacttcgcc tgcgatatct acatttgggc ccctctggct 960

ggtacttgcg gggtcctgct gctttcactc gtgatcactc tttactgtaa gcgcggtcgg 1020

aagaagctgc tgtacatctt taagcaaccc ttcatgaggc ctgtgcagac tactcaagag 1080

gaggacggct gttcatgccg gttcccagag gaggaggaag gcggctgcga actgcgcgtg 1140

aaattcagcc gcagcgcaga tgctccagcc tacaagcagg ggcagaacca gctctacaac 1200

gaactcaatc ttggtcggag agaggagtac gacgtgctgg acaagcggag aggacgggac 1260

ccagaaatgg gcgggaagcc gcgcagaaag aatccccaag agggcctgta caacgagctc 1320

caaaaggata agatggcaga agcctatagc gagattggta tgaaaggggа acgcagaaga 1380

ggcaaaggcc acgacggact gtaccaggga ctcagcaccg ccaccaagga cacctatgac 1440

gctcttcaca tgcaggccct gccgcctcgg 1470

<210> 61
<211> 490
<212> PRT
<213> Artificial Sequence

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

<400> 61
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu

```
                                        _SL
1               5                   10                  15

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

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

Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Gln Gln
    50                  55                  60

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

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

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

Tyr Cys Trp Gln Gly Thr His Phe Pro Gly Thr Phe Gly Gly Gly Thr
        115                 120                 125

Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    130                 135                 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Gln Leu Val Gln Ser
145                 150                 155                 160

Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Arg Ile Ser Cys Lys
                165                 170                 175

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

Met Pro Gly Lys Gly Leu Glu Trp Met Gly Arg Ile Asp Pro Glu Asn
```

```
                                        _SL
        195                 200                 205

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

Ala Asp Thr Ser Ile Asn Thr Val Tyr Leu Gln Trp Ser Ser Leu Lys
225                 230                 235                 240

Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Phe Arg Gly Gly Val Tyr
                245                 250                 255

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Thr Thr Thr Pro Ala
            260                 265                 270

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

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

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

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
                325                 330                 335

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
            340                 345                 350

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
        355                 360                 365

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
    370                 375                 380

Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn
```

_SL
385 390 395 400

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
405 410 415

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
420 425 430

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
435 440 445

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
450 455 460

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
465 470 475 480

Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 62
<211> 246
<212> PRT
<213> Artificial Sequence

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

<400> 62
Glu Ile Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Thr Val Lys Ile Ser Cys Lys Gly Ser Gly Phe Asn Ile Glu Asp Tyr
20 25 30

Tyr Ile His Trp Val Gln Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

```
Gly Arg Ile Asp Pro Glu Asn Asp Glu Thr Lys Tyr Gly Pro Ile Phe
    50                  55                  60

Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Asn Thr Val Tyr
65                  70                  75                  80

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

Ala Phe Arg Gly Gly Val Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
            100                 105                 110

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

Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln Ser Pro Leu Ser
    130                 135                 140

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

Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Gln
                165                 170                 175

Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Ser Leu Val Ser Lys
            180                 185                 190

Leu Asp Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205

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

Tyr Tyr Cys Trp Gln Gly Thr His Phe Pro Gly Thr Phe Gly Gly Gly
225                 230                 235                 240
```

Thr Lys Val Glu Ile Lys
245

<210> 63
<211> 738
<212> DNA
<213> Artificial Sequence

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

<400> 63
gaaatccagc tcgtgcagag cggagccgag gtcaagaaac cgggtgctac cgtgaagatt 60

tcatgcaagg gatcgggctt caacatcgag gattactaca tccactgggt gcagcaggca 120

ccaggaaaag gacttgaatg gatgggccgg atcgacccgg aaaatgacga gactaagtac 180

ggccctatct tccaaggacg ggtgacgatc accgcagaca ctagcaccaa caccgtctat 240

atggaactct cgtccctgag gtccgaagat actgccgtgt actactgtgc gtttcgcgga 300

ggtgtgtact ggggacaggg taccaccgtc accgtgtcat cgggcggtgg aggctccggt 360

ggaggagggt caggaggcgg tggaagcgga ggaggcggca gcgacgtggt catgactcaa 420

tcgccgctgt cgctgcccgt cactctggga caacccgcgt ccatcagctg caaatcctcg 480

cagtcactgc ttgactccga tggaaagacc tacctcaact ggctgcagca acgcccaggc 540

caatccccaa gacgcctgat ctcgttggtg tcaaagctgg actcaggggt gccggaccgg 600

ttctccggga gcgggtcggg cacggatttc actctcaaga tctccagagt ggaagccgag 660

gatgtgggag tctactactg ctggcaggga acccatttcc ctggaacttt tggcggagga 720

actaaggtcg agattaaa 738

<210> 64
<211> 831
<212> DNA
<213> Artificial Sequence

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

<400> 64
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60

cccgaaatcc agctcgtgca gagcggagcc gaggtcaaga aaccgggtgc taccgtgaag 120

atttcatgca agggatcggg cttcaacatc gaggattact acatccactg ggtgcagcag 180

gcaccaggaa aaggacttga atggatgggc cggatcgacc cggaaaatga cgagactaag 240

tacggcccta tcttccaagg acgggtgacg atcaccgcag acactagcac caacaccgtc 300

tatatggaac tctcgtccct gaggtccgaa gatactgccg tgtactactg tgcgtttcgc 360

ggaggtgtgt actggggaca gggtaccacc gtcaccgtgt catcgggcgg tggaggctcc 420

ggtggaggag ggtcaggagg cggtggaagc ggaggaggcg gcagcgacgt ggtcatgact 480

caatcgccgc tgtcgctgcc cgtcactctg ggacaacccg cgtccatcag ctgcaaatcc 540

tcgcagtcac tgcttgactc cgatggaaag acctacctca actggctgca gcaacgccca 600

ggccaatccc caagacgcct gatctcgttg gtgtcaaagc tggactcagg ggtgccggac 660

cggttctccg ggagcgggtc gggcacggat ttcactctca agatctccag agtggaagcc 720

gaggatgtgg gagtctacta ctgctggcag ggaacccatt tccctggaac ttttggcgga 780

ggaactaagg tcgagattaa agggagccac catcatcatc accaccacca c 831

<210> 65
<211> 277
<212> PRT
<213> Artificial Sequence

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

<400> 65
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu

```
                                        _SL
1               5                   10                  15

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

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

Asn Ile Glu Asp Tyr Tyr Ile His Trp Val Gln Gln Ala Pro Gly Lys
    50                  55                  60

Gly Leu Glu Trp Met Gly Arg Ile Asp Pro Glu Asn Asp Glu Thr Lys
65                  70                  75                  80

Tyr Gly Pro Ile Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser
                85                  90                  95

Thr Asn Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
            100                 105                 110

Ala Val Tyr Tyr Cys Ala Phe Arg Gly Gly Val Tyr Trp Gly Gln Gly
        115                 120                 125

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

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr
145                 150                 155                 160

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

Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr
            180                 185                 190

Leu Asn Trp Leu Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile
```

```
                                        _SL
        195                 200                 205


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


Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
225                 230                 235                 240


Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly Thr His Phe Pro Gly
                245                 250                 255


Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Ser His His His
            260                 265                 270


His His His His His
        275


<210> 66
<211> 1470
<212> DNA
<213> Artificial Sequence

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

<400> 66
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg       60

cccgaaatcc agctcgtgca gagcggagcc gaggtcaaga aaccgggtgc taccgtgaag      120

atttcatgca agggatcggg cttcaacatc gaggattact acatccactg ggtgcagcag      180

gcaccaggaa aaggacttga atggatgggc cggatcgacc cggaaaatga cgagactaag      240

tacggcccta tcttccaagg acgggtgacg atcaccgcag acactagcac caacaccgtc      300

tatatggaac tctcgtccct gaggtccgaa gatactgccg tgtactactg tgcgtttcgc      360

ggaggtgtgt actggggaca gggtaccacc gtcaccgtgt catcgggcgg tggaggctcc      420
```

ggtggaggag ggtcaggagg cggtggaagc ggaggaggcg gcagcgacgt ggtcatgact 480

caatcgccgc tgtcgctgcc cgtcactctg ggacaacccg cgtccatcag ctgcaaatcc 540

tcgcagtcac tgcttgactc cgatggaaag acctacctca actggctgca gcaacgccca 600

ggccaatccc caagacgcct gatctcgttg gtgtcaaagc tggactcagg ggtgccggac 660

cggttctccg ggagcgggtc gggcacggat ttcactctca agatctccag agtggaagcc 720

gaggatgtgg gagtctacta ctgctggcag ggaacccatt tccctggaac ttttggcgga 780

ggaactaagg tcgagattaa aaccactacc ccagcaccga ggccacccac cccggctcct 840

accatcgcct cccagcctct gtccctgcgt ccggaggcat gtagacccgc agctggtggg 900

gccgtgcata cccggggtct tgacttcgcc tgcgatatct acatttgggc ccctctggct 960

ggtacttgcg gggtcctgct gctttcactc gtgatcactc tttactgtaa gcgcggtcgg 1020

aagaagctgc tgtacatctt taagcaaccc ttcatgaggc ctgtgcagac tactcaagag 1080

gaggacggct gttcatgccg gttcccagag gaggaggaag gcggctgcga actgcgcgtg 1140

aaattcagcc gcagcgcaga tgctccagcc tacaagcagg ggcagaacca gctctacaac 1200

gaactcaatc ttggtcggag agaggagtac gacgtgctgg acaagcggag aggacgggac 1260

ccagaaatgg gcgggaagcc gcgcagaaag aatccccaag agggcctgta caacgagctc 1320

caaaaggata agatggcaga agcctatagc gagattggta tgaaagggga acgcagaaga 1380

ggcaaaggcc acgacggact gtaccaggga ctcagcaccg ccaccaagga cacctatgac 1440

gctcttcaca tgcaggccct gccgcctcgg 1470

<210> 67
<211> 490
<212> PRT
<213> Artificial Sequence

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

<400> 67

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


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


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


Asn Ile Glu Asp Tyr Tyr Ile His Trp Val Gln Gln Ala Pro Gly Lys
    50                  55                  60


Gly Leu Glu Trp Met Gly Arg Ile Asp Pro Glu Asn Asp Glu Thr Lys
65                  70                  75                  80


Tyr Gly Pro Ile Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser
                85                  90                  95


Thr Asn Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
            100                 105                 110


Ala Val Tyr Tyr Cys Ala Phe Arg Gly Gly Val Tyr Trp Gly Gln Gly
        115                 120                 125


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


Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr
145                 150                 155                 160


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


Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr
            180                 185                 190
```

```
                                        _SL
Leu Asn Trp Leu Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile
        195                 200                 205

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
225                 230                 235                 240

Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly Thr His Phe Pro Gly
                245                 250                 255

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala
            260                 265                 270

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

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

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

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
                325                 330                 335

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
            340                 345                 350

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
        355                 360                 365

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
    370                 375                 380
```

_SL
Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn
385 390 395 400

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
405 410 415

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
420 425 430

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
435 440 445

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
450 455 460

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
465 470 475 480

Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 68
<211> 246
<212> PRT
<213> Artificial Sequence

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

<400> 68
Glu Ile Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Phe Asn Ile Glu Asp Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met

_SL
35 40 45

Gly Arg Ile Asp Pro Glu Asn Asp Glu Thr Lys Tyr Gly Pro Ile Phe
50 55 60

Gln Gly His Val Thr Ile Ser Ala Asp Thr Ser Ile Asn Thr Val Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Phe Arg Gly Gly Val Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
100 105 110

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

Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln Ser Pro Asp Ser
130 135 140

Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser
145 150 155 160

Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Gln
165 170 175

Gln Lys Pro Gly Gln Pro Pro Lys Arg Leu Ile Ser Leu Val Ser Lys
180 185 190

Leu Asp Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val
210 215 220

Tyr Tyr Cys Trp Gln Gly Thr His Phe Pro Gly Thr Phe Gly Gly Gly

_SL
225 230 235 240

Thr Lys Val Glu Ile Lys
245

<210> 69
<211> 738
<212> DNA
<213> Artificial Sequence

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

<400> 69
gaaatccagc tggtgcagtc aggcgccgag gtcaagaagc cgggagagtc gctgagaatc 60

tcgtgcaagg gctcggggtt caacatcgag gactactaca ttcactgggt caggcagatg 120

ccgggaaagg gactggaatg gatgggccgg atcgacccag aaaatgacga aaccaaatac 180

gggccgattt ttcaaggcca cgtgactatc agcgcagaca cgagcatcaa cactgtctac 240

ctccagtggt cctcgcttaa ggccagcgat accgctatgt actactgcgc attcagaggc 300

ggggtgtact ggggacaagg aaccactgtg accgtgagca gcggaggtgg cggctcggga 360

ggaggtggga gcggaggagg aggttccggc ggtggaggat cagatgtcgt gatgacccag 420

tccccggact ccctcgctgt ctcactgggc gagcgcgcga ccatcaactg caaatcgagc 480

cagtcgctgt tggactccga tggaaagact tatctgaatt ggctgcaaca gaaaccagga 540

caacctccca agcggctcat ctcgcttgtg tcaaaactcg attcgggagt gccagaccgc 600

ttctcggggt ccgggagcgg aactgacttt actttgacca tttcctcact gcaagcggag 660

gatgtggccg tgtattactg ttggcagggc acgcatttcc ctggaacctt cggtggcgga 720

actaaggtgg aaatcaag 738

<210> 70
<211> 834
<212> DNA

<213> Artificial Sequence

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

<400> 70
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60

cccgaaatcc agctggtgca gtcaggcgcc gaggtcaaga agccgggaga gtcgctgaga 120

atctcgtgca agggctcggg gttcaacatc gaggactact acattcactg ggtcaggcag 180

atgccgggaa agggactgga atggatgggc cggatcgacc cagaaaatga cgaaaccaaa 240

tacgggccga tttttcaagg ccacgtgact atcagcgcag acacgagcat caacactgtc 300

tacctccagt ggtcctcgct taaggccagc gataccgcta tgtactactg cgcattcaga 360

ggcggggtgt actggggaca aggaaccact gtgaccgtga gcagcggagg tggcggctcg 420

ggaggaggtg ggagcggagg aggaggttcc ggcggtggag gatcagatgt cgtgatgacc 480

cagtccccgg actccctcgc tgtctcactg ggcgagcgcg cgaccatcaa ctgcaaatcg 540

agccagtcgc tgttggactc cgatggaaag acttatctga attggctgca acagaaacca 600

ggacaacctc ccaagcggct catctcgctt gtgtcaaaac tcgattcggg agtgccagac 660

cgcttctcgg ggtccgggag cggaactgac tttactttga ccatttcctc actgcaagcg 720

gaggatgtgg ccgtgtatta ctgttggcag ggcacgcatt tccctggaac cttcggtggc 780

ggaactaagg tggaaatcaa gggatcacac caccatcatc accatcacca ccat 834

<210> 71
<211> 278
<212> PRT
<213> Artificial Sequence

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

<400> 71

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


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


Lys Lys Pro Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Phe
        35                  40                  45


Asn Ile Glu Asp Tyr Tyr Ile His Trp Val Arg Gln Met Pro Gly Lys
    50                  55                  60


Gly Leu Glu Trp Met Gly Arg Ile Asp Pro Glu Asn Asp Glu Thr Lys
65                  70                  75                  80


Tyr Gly Pro Ile Phe Gln Gly His Val Thr Ile Ser Ala Asp Thr Ser
                85                  90                  95


Ile Asn Thr Val Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr
            100                 105                 110


Ala Met Tyr Tyr Cys Ala Phe Arg Gly Gly Val Tyr Trp Gly Gln Gly
        115                 120                 125


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


Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr
145                 150                 155                 160


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


Asn Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr
            180                 185                 190
```

```
                                        _SL
Leu Asn Trp Leu Gln Gln Lys Pro Gly Gln Pro Pro Lys Arg Leu Ile
        195                 200                 205


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


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


Glu Asp Val Ala Val Tyr Tyr Cys Trp Gln Gly Thr His Phe Pro Gly
                245                 250                 255


Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Ser His His His
            260                 265                 270


His His His His His His
        275


<210> 72
<211> 1470
<212> DNA
<213> Artificial Sequence

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

<400> 72
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg       60

cccgagattc agctcgtgca atcgggagcg gaagtcaaga agccaggaga gtccttgcgg      120

atctcatgca agggtagcgg ctttaacatc gaggattact acatccactg ggtgaggcag      180

atgccgggga agggactcga atggatggga cggatcgacc cagaaaacga cgaaactaag      240

tacggtccga tcttccaagg ccatgtgact attagcgccg atacttcaat caataccgtg      300

tatctgcaat ggtcctcatt gaaagcctca gataccgcga tgtactactg tgctttcaga      360

ggaggggtct actggggaca gggaactacc gtgactgtct cgtccggcgg aggcgggtca      420
```

ggaggtggcg gcagcggagg aggagggtcc ggcggaggtg ggtccgacgt cgtgatgacc 480

cagagccctg acagcctggc agtgagcctg ggcgaaagag ctaccattaa ctgcaaatcg 540

tcgcagagcc tgctggactc ggacggaaaa acgtacctca attggctgca gcaaaagcct 600

ggccagccac cgaagcgcct tatctcactg gtgtcgaagc tggattcggg agtgcccgat 660

cgcttctccg gctcgggatc gggtactgac ttcaccctca ctatctcctc gcttcaagca 720

gaggacgtgg ccgtctacta ctgctggcag ggaacccact ttccgggaac cttcggcgga 780

gggacgaaag tggagatcaa gaccactacc ccagcaccga ggccacccac cccggctcct 840

accatcgcct cccagcctct gtccctgcgt ccggaggcat gtagacccgc agctggtggg 900

gccgtgcata cccggggtct tgacttcgcc tgcgatatct acatttgggc ccctctggct 960

ggtacttgcg gggtcctgct gctttcactc gtgatcactc tttactgtaa gcgcggtcgg 1020

aagaagctgc tgtacatctt taagcaaccc ttcatgaggc ctgtgcagac tactcaagag 1080

gaggacggct gttcatgccg gttcccagag gaggaggaag gcggctgcga actgcgcgtg 1140

aaattcagcc gcagcgcaga tgctccagcc tacaagcagg ggcagaacca gctctacaac 1200

gaactcaatc ttggtcggag agaggagtac gacgtgctgg acaagcggag aggacgggac 1260

ccagaaatgg gcgggaagcc gcgcagaaag aatccccaag agggcctgta caacgagctc 1320

caaaaggata agatggcaga agcctatagc gagattggta tgaaaggggа acgcagaaga 1380

ggcaaaggcc acgacggact gtaccaggga ctcagcaccg ccaccaagga cacctatgac 1440

gctcttcaca tgcaggccct gccgcctcgg 1470

<210> 73
<211> 490
<212> PRT
<213> Artificial Sequence

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

_SL

<400> 73

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

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

Lys Lys Pro Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Phe
        35                  40                  45

Asn Ile Glu Asp Tyr Tyr Ile His Trp Val Arg Gln Met Pro Gly Lys
    50                  55                  60

Gly Leu Glu Trp Met Gly Arg Ile Asp Pro Glu Asn Asp Glu Thr Lys
65                  70                  75                  80

Tyr Gly Pro Ile Phe Gln Gly His Val Thr Ile Ser Ala Asp Thr Ser
                85                  90                  95

Ile Asn Thr Val Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr
            100                 105                 110

Ala Met Tyr Tyr Cys Ala Phe Arg Gly Gly Val Tyr Trp Gly Gln Gly
        115                 120                 125

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

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr
145                 150                 155                 160

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

Asn Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr
            180                 185                 190
```

```
Leu Asn Trp Leu Gln Gln Lys Pro Gly Gln Pro Pro Lys Arg Leu Ile
        195                 200                 205

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

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

Glu Asp Val Ala Val Tyr Tyr Cys Trp Gln Gly Thr His Phe Pro Gly
                245                 250                 255

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala
            260                 265                 270

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

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

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

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
                325                 330                 335

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
            340                 345                 350

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
        355                 360                 365

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
    370                 375                 380
```

```
Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn
385                 390                 395                 400


Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
                405                 410                 415


Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
            420                 425                 430


Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
        435                 440                 445


Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
    450                 455                 460


Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
465                 470                 475                 480


Ala Leu His Met Gln Ala Leu Pro Pro Arg
                485                 490


<210> 74
<211> 246
<212> PRT
<213> Artificial Sequence

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

<400> 74
Asp Val Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15


Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
            20                  25                  30
```

```
                                        _SL
Asp Gly Lys Thr Tyr Leu Asn Trp Leu Gln Gln Lys Pro Gly Gln Pro
        35                  40                  45

Pro Lys Arg Leu Ile Ser Leu Val Ser Lys Leu Asp Ser Gly Val Pro
    50                  55                  60

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

Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Trp Gln Gly
                85                  90                  95

Thr His Phe Pro Gly Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110

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

Gly Gly Gly Ser Glu Ile Gln Leu Val Gln Ser Gly Ala Glu Val Lys
    130                 135                 140

Lys Pro Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Phe Asn
145                 150                 155                 160

Ile Glu Asp Tyr Tyr Ile His Trp Val Arg Gln Met Pro Gly Lys Gly
                165                 170                 175

Leu Glu Trp Met Gly Arg Ile Asp Pro Glu Asn Asp Glu Thr Lys Tyr
            180                 185                 190

Gly Pro Ile Phe Gln Gly His Val Thr Ile Ser Ala Asp Thr Ser Ile
        195                 200                 205

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

_SL
Met Tyr Tyr Cys Ala Phe Arg Gly Gly Val Tyr Trp Gly Gln Gly Thr
225 230 235 240

Thr Val Thr Val Ser Ser
245

<210> 75
<211> 738
<212> DNA
<213> Artificial Sequence

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

<400> 75
gacgtggtga tgacccaatc gccagattcc ctggcagtgt ccctgggcga acgcgccact 60

attaactgca aatcgtcaca gtccttgctt gattccgacg gaaagaccta cctcaattgg 120

ctccagcaga agccaggaca accgccaaag agactgatct ccctggtgtc aaagctggac 180

tcgggagtgc ctgatcggtt ctcgggtagc gggagcggca ccgacttcac tctgaccatc 240

tcgtcactcc aggctgagga cgtggccgtg tattactgtt ggcagggtac tcactttccg 300

ggcactttcg gaggcggcac caaggtggag attaaaggag gaggcggaag cggaggtgga 360

ggatcgggag gtggtgggag cggcggagga gggagcgaga tccagctcgt ccaatcggga 420

gcggaagtga agaagcccgg agagtcactt agaatctcat gcaaggggtc gggcttcaac 480

atcgaggatt actacatcca ttgggtccgc cagatgcctg gtaaaggact ggaatggatg 540

gggaggattg acccggaaaa cgacgaaact aagtacggac cgatctttca agggcacgtg 600

actatctccg ctgatacctc aatcaatact gtctacctcc agtggtcctc gctgaaagca 660

agcgacaccg cgatgtacta ctgcgccttc cggggaggag tgtactgggg ccaaggcacc 720

acggtcacgg tcagctcc 738

<210> 76
<211> 834

<212> DNA
<213> Artificial Sequence

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

<400> 76
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60

cccgacgtgg tgatgaccca atcgccagat tccctggcag tgtccctggg cgaacgcgcc 120

actattaact gcaaatcgtc acagtccttg cttgattccg acggaaagac ctacctcaat 180

tggctccagc agaagccagg acaaccgcca aagagactga tctccctggt gtcaaagctg 240

gactcgggag tgcctgatcg gttctcgggt agcgggagcg gcaccgactt cactctgacc 300

atctcgtcac tccaggctga ggacgtggcc gtgtattact gttggcaggg tactcacttt 360

ccgggcactt tcggaggcgg caccaaggtg gagattaaag gaggaggcgg aagcggaggt 420

ggaggatcgg gaggtggtgg gagcggcgga ggagggagcg agatccagct cgtccaatcg 480

ggagcggaag tgaagaagcc cggagagtca cttagaatct catgcaaggg gtcgggcttc 540

aacatcgagg attactacat ccattgggtc cgccagatgc ctggtaaagg actggaatgg 600

atggggagga ttgacccgga aaacgacgaa actaagtacg gaccgatctt tcaagggcac 660

gtgactatct ccgctgatac ctcaatcaat actgtctacc tccagtggtc ctcgctgaaa 720

gcaagcgaca ccgcgatgta ctactgcgcc ttccggggag gagtgtactg gggccaaggc 780

accacggtca cggtcagctc cggctcccat caccaccacc atcaccatca tcac 834

<210> 77
<211> 278
<212> PRT
<213> Artificial Sequence

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

_SL

<400> 77

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

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

Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln
        35                  40                  45

Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Gln Gln
    50                  55                  60

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

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

Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr
            100                 105                 110

Tyr Cys Trp Gln Gly Thr His Phe Pro Gly Thr Phe Gly Gly Gly Thr
        115                 120                 125

Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    130                 135                 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Gln Leu Val Gln Ser
145                 150                 155                 160

Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Arg Ile Ser Cys Lys
                165                 170                 175

Gly Ser Gly Phe Asn Ile Glu Asp Tyr Tyr Ile His Trp Val Arg Gln
            180                 185                 190
```

```
Met Pro Gly Lys Gly Leu Glu Trp Met Gly Arg Ile Asp Pro Glu Asn
        195                 200                 205


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


Ala Asp Thr Ser Ile Asn Thr Val Tyr Leu Gln Trp Ser Ser Leu Lys
225                 230                 235                 240


Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Phe Arg Gly Gly Val Tyr
                245                 250                 255


Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Ser His His His
            260                 265                 270


His His His His His His
        275
```

<210> 78
<211> 1470
<212> DNA
<213> Artificial Sequence

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

<400> 78

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atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg       60

cccgacgtgg tgatgactca gtcgcctgac tcgctggctg tgtcccttgg agagcgggcc      120

actatcaatt gcaagtcatc ccagtcgctg ctggattccg acgggaaaac ctacctcaat      180

tggctgcagc aaaaaccggg acagcctcca aagcggctca tcagcctggt gtccaagttg      240

gacagcggcg tgccagaccg cttctccggt tcgggaagcg gtactgattt cacgctgacc      300

atctcatccc tccaagcgga ggatgtggca gtctactact gttggcaggg cacgcatttt      360
```

ccgggcactt ttggaggagg gaccaaggtc gaaatcaagg gaggaggtgg ctcgggcgga 420

ggaggctcgg gaggaggagg atcaggaggc ggtggaagcg agattcaact ggtccagagc 480

ggcgcagaag tcaagaagcc gggtgaatcg ctcagaatct cgtgcaaagg atcgggattc 540

aacatcgagg actactacat tcactgggtc agacaaatgc cgggcaaagg gctggaatgg 600

atggggagga tcgaccccga aaacgatgaa accaagtacg gaccaatctt ccaagggcac 660

gtgaccattt cggcggacac ctcaatcaac actgtgtacc tccagtggag ctcacttaag 720

gccagcgata ccgccatgta ctattgcgct ttccgcggag gggtgtactg gggacagggc 780

actactgtga ccgtgtcatc caccactacc ccagcaccga ggccacccac cccggctcct 840

accatcgcct cccagcctct gtccctgcgt ccggaggcat gtagacccgc agctggtggg 900

gccgtgcata cccggggtct tgacttcgcc tgcgatatct acatttgggc ccctctggct 960

ggtacttgcg gggtcctgct gctttcactc gtgatcactc tttactgtaa gcgcggtcgg 1020

aagaagctgc tgtacatctt taagcaaccc ttcatgaggc ctgtgcagac tactcaagag 1080

gaggacggct gttcatgccg gttcccagag gaggaggaag gcggctgcga actgcgcgtg 1140

aaattcagcc gcagcgcaga tgctccagcc tacaagcagg ggcagaacca gctctacaac 1200

gaactcaatc ttggtcggag agaggagtac gacgtgctgg acaagcggag aggacgggac 1260

ccagaaatgg gcgggaagcc gcgcagaaag aatccccaag agggcctgta caacgagctc 1320

caaaaggata agatggcaga agcctatagc gagattggta tgaaagggga acgcagaaga 1380

ggcaaaggcc acgacggact gtaccaggga ctcagcaccg ccaccaagga cacctatgac 1440

gctcttcaca tgcaggccct gccgcctcgg 1470

<210> 79
<211> 490
<212> PRT
<213> Artificial Sequence

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

<400> 79
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1   5   10   15

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

Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln
        35   40   45

Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Gln Gln
    50   55   60

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

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

Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr
            100   105   110

Tyr Cys Trp Gln Gly Thr His Phe Pro Gly Thr Phe Gly Gly Gly Thr
        115   120   125

Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    130   135   140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Gln Leu Val Gln Ser
145   150   155   160

Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Arg Ile Ser Cys Lys
                165   170   175

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

```
Met Pro Gly Lys Gly Leu Glu Trp Met Gly Arg Ile Asp Pro Glu Asn
        195                 200                 205

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

Ala Asp Thr Ser Ile Asn Thr Val Tyr Leu Gln Trp Ser Ser Leu Lys
225                 230                 235                 240

Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Phe Arg Gly Gly Val Tyr
                245                 250                 255

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Thr Thr Thr Pro Ala
            260                 265                 270

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

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

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

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
                325                 330                 335

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
            340                 345                 350

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
        355                 360                 365

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
    370                 375                 380
```

```
Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn
385                 390                 395                 400


Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
                405                 410                 415


Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
            420                 425                 430


Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
        435                 440                 445


Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
    450                 455                 460


Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
465                 470                 475                 480


Ala Leu His Met Gln Ala Leu Pro Pro Arg
                485                 490


<210> 80
<211> 246
<212> PRT
<213> Artificial Sequence

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

<400> 80
Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1               5                   10                  15


Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
            20                  25                  30
```

```
Asp Gly Lys Thr Tyr Leu Asn Trp Leu Gln Gln Arg Pro Gly Gln Ser
        35                  40                  45

Pro Arg Arg Leu Ile Ser Leu Val Ser Lys Leu Asp Ser Gly Val Pro
    50                  55                  60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly
                85                  90                  95

Thr His Phe Pro Gly Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110

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

Gly Gly Gly Ser Glu Ile Gln Leu Val Gln Ser Gly Ala Glu Val Lys
    130                 135                 140

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

Ile Glu Asp Tyr Tyr Ile His Trp Val Gln Gln Ala Pro Gly Lys Gly
                165                 170                 175

Leu Glu Trp Met Gly Arg Ile Asp Pro Glu Asn Asp Glu Thr Lys Tyr
            180                 185                 190

Gly Pro Ile Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr
        195                 200                 205

Asn Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
    210                 215                 220
```

Val Tyr Tyr Cys Ala Phe Arg Gly Gly Val Tyr Trp Gly Gln Gly Thr
225 230 235 240

Thr Val Thr Val Ser Ser
245

<210> 81
<211> 738
<212> DNA
<213> Artificial Sequence

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

<400> 81
gatgtggtca tgacgcagtc accactgtcc ctccccgtga cccttggaca gccagcgtcg 60

attagctgca agtcatccca atccctgctc gattcggatg gaaagaccta tctcaactgg 120

ctgcagcaaa gacccggtca gagccctagg agactcatct cgttggtgtc aaagctggac 180

agcggagtgc cggaccggtt ttccggttcg ggatcgggga cggacttcac tctgaagatt 240

tcacgggtgg aagctgagga tgtgggagtg tactactgct ggcagggaac ccatttccct 300

ggcacttttg gcggaggaac taaggtcgaa atcaagggag gaggtggctc gggaggaggc 360

ggatcgggcg gaggcgggag cggcggagga gggtccgaaa tccaacttgt ccagtcagga 420

gccgaagtga agaaaccggg agccaccgtc aaaatcagct gtaagggatc gggattcaat 480

atcgaggact actacatcca ctgggtgcag caagctccgg gcaaaggact ggagtggatg 540

gggcgcatcg acccagagaa cgacgaaacc aaatacggcc cgatcttcca agggcgggtg 600

accatcaccg cggacacctc aactaacact gtgtacatgg agctgagctc cctgcgctcc 660

gaagatactg cagtctacta ctgcgccttc cgcggtggtg tgtactgggg acagggcacc 720

actgtgactg tcagctcg 738

<210> 82

<211> 831
<212> DNA
<213> Artificial Sequence

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

<400> 82
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60

cccgatgtgg tcatgacgca gtcaccactg tccctccccg tgacccttgg acagccagcg 120

tcgattagct gcaagtcatc ccaatccctg ctcgattcgg atggaaagac ctatctcaac 180

tggctgcagc aaagacccgg tcagagccct aggagactca tctcgttggt gtcaaagctg 240

gacagcggag tgccggaccg gttttccggt tcgggatcgg ggacggactt cactctgaag 300

atttcacggg tggaagctga ggatgtggga gtgtactact gctggcaggg aacccatttc 360

cctggcactt ttggcggagg aactaaggtc gaaatcaagg gaggaggtgg ctcgggagga 420

ggcggatcgg gcggaggcgg gagcggcgga ggagggtccg aaatccaact tgtccagtca 480

ggagccgaag tgaagaaacc gggagccacc gtcaaaatca gctgtaaggg atcgggattc 540

aatatcgagg actactacat ccactgggtg cagcaagctc cgggcaaagg actggagtgg 600

atggggcgca tcgacccaga gaacgacgaa accaaatacg gcccgatctt ccaagggcgg 660

gtgaccatca ccgcggacac ctcaactaac actgtgtaca tggagctgag ctccctgcgc 720

tccgaagata ctgcagtcta ctactgcgcc ttccgcggtg gtgtgtactg gggacagggc 780

accactgtga ctgtcagctc ggggtcccac catcatcacc accaccatca c 831

<210> 83
<211> 277
<212> PRT
<213> Artificial Sequence

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

<400> 83
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1   5   10   15

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

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

Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Gln Gln
    50   55   60

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

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

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

Tyr Cys Trp Gln Gly Thr His Phe Pro Gly Thr Phe Gly Gly Gly Thr
        115   120   125

Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    130   135   140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Gln Leu Val Gln Ser
145   150   155   160

Gly Ala Glu Val Lys Lys Pro Gly Ala Thr Val Lys Ile Ser Cys Lys
                165   170   175

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

```
Ala Pro Gly Lys Gly Leu Glu Trp Met Gly Arg Ile Asp Pro Glu Asn
        195                 200                 205


Asp Glu Thr Lys Tyr Gly Pro Ile Phe Gln Gly Arg Val Thr Ile Thr
    210                 215                 220


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


Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Phe Arg Gly Gly Val Tyr
                245                 250                 255


Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Ser His His His
            260                 265                 270


His His His His His
        275


<210> 84
<211> 1470
<212> DNA
<213> Artificial Sequence

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

<400> 84
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg       60

cccgatgtgg tcatgacgca gtcaccactg tccctccccg tgacccttgg acagccagcg      120

tcgattagct gcaagtcatc ccaatccctg ctcgattcgg atggaaagac ctatctcaac      180

tggctgcagc aaagacccgg tcagagccct aggagactca tctcgttggt gtcaaagctg      240

gacagcggag tgccggaccg gttttccggt tcgggatcgg ggacggactt cactctgaag      300

atttcacggg tggaagctga ggatgtggga gtgtactact gctggcaggg aacccatttc      360
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cctggcactt ttggcggagg aactaaggtc gaaatcaagg gaggaggtgg ctcgggagga 420

ggcggatcgg gcggaggcgg gagcggcgga ggagggtccg aaatccaact tgtccagtca 480

ggagccgaag tgaagaaacc gggagccacc gtcaaaatca gctgtaaggg atcgggattc 540

aatatcgagg actactacat ccactgggtg cagcaagctc cgggcaaagg actggagtgg 600

atggggcgca tcgacccaga gaacgacgaa accaaatacg gcccgatctt ccaagggcgg 660

gtgaccatca ccgcggacac ctcaactaac actgtgtaca tggagctgag ctccctgcgc 720

tccgaagata ctgcagtcta ctactgcgcc ttccgcggtg gtgtgtactg gggacagggc 780

accactgtga ctgtcagctc gaccactacc ccagcaccga ggccacccac cccggctcct 840

accatcgcct cccagcctct gtccctgcgt ccggaggcat gtagacccgc agctggtggg 900

gccgtgcata cccggggtct tgacttcgcc tgcgatatct acatttgggc ccctctggct 960

ggtacttgcg gggtcctgct gctttcactc gtgatcactc tttactgtaa gcgcggtcgg 1020

aagaagctgc tgtacatctt taagcaaccc ttcatgaggc ctgtgcagac tactcaagag 1080

gaggacggct gttcatgccg gttcccagag gaggaggaag gcggctgcga actgcgcgtg 1140

aaattcagcc gcagcgcaga tgctccagcc tacaagcagg ggcagaacca gctctacaac 1200

gaactcaatc ttggtcggag agaggagtac gacgtgctgg acaagcggag aggacgggac 1260

ccagaaatgg gcgggaagcc gcgcagaaag aatccccaag agggcctgta caacgagctc 1320

caaaaggata agatggcaga agcctatagc gagattggta tgaaagggga acgcagaaga 1380

ggcaaaggcc acgacggact gtaccaggga ctcagcaccg ccaccaagga cacctatgac 1440

gctcttcaca tgcaggccct gccgcctcgg 1470

<210> 85
<211> 490
<212> PRT
<213> Artificial Sequence

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

_SL
polypeptide"

<400> 85
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1   5   10   15

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

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

Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Gln Gln
    50   55   60

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

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

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

Tyr Cys Trp Gln Gly Thr His Phe Pro Gly Thr Phe Gly Gly Gly Thr
        115   120   125

Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    130   135   140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Gln Leu Val Gln Ser
145   150   155   160

Gly Ala Glu Val Lys Lys Pro Gly Ala Thr Val Lys Ile Ser Cys Lys
                165   170   175

Gly Ser Gly Phe Asn Ile Glu Asp Tyr Tyr Ile His Trp Val Gln Gln

_SL

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            180                 185                 190

Ala Pro Gly Lys Gly Leu Glu Trp Met Gly Arg Ile Asp Pro Glu Asn
        195                 200                 205

Asp Glu Thr Lys Tyr Gly Pro Ile Phe Gln Gly Arg Val Thr Ile Thr
    210                 215                 220

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

Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Phe Arg Gly Gly Val Tyr
                245                 250                 255

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Thr Thr Thr Pro Ala
            260                 265                 270

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

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

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

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
                325                 330                 335

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
            340                 345                 350

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
        355                 360                 365

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
```

_SL
370 375 380

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

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
405 410 415

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
420 425 430

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
435 440 445

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
450 455 460

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
465 470 475 480

Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 86
<211> 243
<212> PRT
<213> Artificial Sequence

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

<400> 86
Glu Ile Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Thr Gly Ser Gly Phe Asn Ile Glu Asp Tyr
20 25 30

```
Tyr Ile His Trp Val Lys Gln Arg Thr Glu Gln Gly Leu Glu Trp Ile
        35                  40                  45

Gly Arg Ile Asp Pro Glu Asn Asp Glu Thr Lys Tyr Gly Pro Ile Phe
    50                  55                  60

Gln Gly Arg Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Val Tyr
65                  70                  75                  80

Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Phe Arg Gly Gly Val Tyr Trp Gly Pro Gly Thr Thr Leu Thr Val
            100                 105                 110

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

Ser His Met Asp Val Val Met Thr Gln Ser Pro Leu Thr Leu Ser Val
    130                 135                 140

Ala Ile Gly Gln Ser Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu
145                 150                 155                 160

Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro
                165                 170                 175

Gly Gln Ser Pro Lys Arg Leu Ile Ser Leu Val Ser Lys Leu Asp Ser
            180                 185                 190

Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Ile Tyr Tyr Cys
    210                 215                 220
```

Trp Gln Gly Thr His Phe Pro Gly Thr Phe Gly Gly Gly Thr Lys Leu
225 230 235 240

Glu Ile Lys

<210> 87
<211> 822
<212> DNA
<213> Artificial Sequence

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

<400> 87
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60

cccgagatcc agctccaaca gagcggagcc gaactggtca aaccgggagc gtcggtgaag 120

ttgtcatgca ctggatcggg cttcaacatc gaggattact acatccactg ggtcaagcaa 180

cgcaccgagc aggggctgga atggatcgga cggatcgacc ccgaaaacga tgaaaccaag 240

tacgggccta tcttccaagg acgggccacc attacggctg acacgtcaag caataccgtc 300

tacctccagc tttccagcct gacctccgag gacactgccg tgtactactg cgccttcaga 360

ggaggcgtgt actggggacc aggaaccact ttgaccgtgt ccagcggagg cggtggatca 420

ggaggaggag gctcaggcgg tggcggctcg cacatggacg tggtcatgac tcagtccccg 480

ctgaccctgt cggtggcaat tggacagagc gcatccatct cgtgcaagag ctcacagtcg 540

ctgctggatt ccgacggaaa gacttatctg aactggctgc tccaaagacc agggcaatca 600

ccgaaacgcc ttatctccct ggtgtcgaaa ctcgactcgg gtgtgccgga tcggtttacc 660

ggtagcgggt ccggcacgga cttcactctc cgcatttcga gggtggaagc ggaggatctc 720

gggatctact actgttggca gggaacccac ttccctggga cttttggagg cggaactaag 780

ctggaaatca agggtagcca tcaccatcac caccaccatc at 822

<210> 88
<211> 274
<212> PRT
<213> Artificial Sequence

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

<400> 88
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

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

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

Asn Ile Glu Asp Tyr Tyr Ile His Trp Val Lys Gln Arg Thr Glu Gln
50 55 60

Gly Leu Glu Trp Ile Gly Arg Ile Asp Pro Glu Asn Asp Glu Thr Lys
65 70 75 80

Tyr Gly Pro Ile Phe Gln Gly Arg Ala Thr Ile Thr Ala Asp Thr Ser
85 90 95

Ser Asn Thr Val Tyr Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Ala Phe Arg Gly Gly Val Tyr Trp Gly Pro Gly
115 120 125

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

```
Ser Gly Gly Gly Gly Ser His Met Asp Val Val Met Thr Gln Ser Pro
145                 150                 155                 160


Leu Thr Leu Ser Val Ala Ile Gly Gln Ser Ala Ser Ile Ser Cys Lys
                165                 170                 175


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


Leu Leu Gln Arg Pro Gly Gln Ser Pro Lys Arg Leu Ile Ser Leu Val
        195                 200                 205


Ser Lys Leu Asp Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser
    210                 215                 220


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


Gly Ile Tyr Tyr Cys Trp Gln Gly Thr His Phe Pro Gly Thr Phe Gly
                245                 250                 255


Gly Gly Thr Lys Leu Glu Ile Lys Gly Ser His His His His His His
            260                 265                 270


His His
```

<210> 89
<211> 1461
<212> DNA
<213> Artificial Sequence

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

<400> 89

atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60

cccgagatcc agctccaaca gagcggagcc gaactggtca aaccgggagc gtcggtgaag 120

ttgtcatgca ctggatcggg cttcaacatc gaggattact acatccactg ggtcaagcaa 180

cgcaccgagc aggggctgga atggatcgga cggatcgacc ccgaaaacga tgaaaccaag 240

tacgggccta tcttccaagg acgggccacc attacggctg acacgtcaag caataccgtc 300

tacctccagc tttccagcct gacctccgag gacactgccg tgtactactg cgccttcaga 360

ggaggcgtgt actggggacc aggaaccact ttgaccgtgt ccagcggagg cggtggatca 420

ggaggaggag gctcaggcgg tggcggctcg cacatggacg tggtcatgac tcagtccccg 480

ctgaccctgt cggtggcaat tggacagagc gcatccatct cgtgcaagag ctcacagtcg 540

ctgctggatt ccgacggaaa gacttatctg aactggctgc tccaaagacc agggcaatca 600

ccgaaacgcc ttatctccct ggtgtcgaaa ctcgactcgg gtgtgccgga tcggtttacc 660

ggtagcgggt ccggcacgga cttcactctc cgcatttcga gggtggaagc ggaggatctc 720

gggatctact actgttggca gggaacccac ttccctggga cttttggagg cggaactaag 780

ctggaaatca agaccactac cccagcaccg aggccaccca ccccggctcc taccatcgcc 840

tcccagcctc tgtccctgcg tccggaggca tgtagacccg cagctggtgg ggccgtgcat 900

acccggggtc ttgacttcgc ctgcgatatc tacatttggg cccctctggc tggtacttgc 960

ggggtcctgc tgctttcact cgtgatcact ctttactgta agcgcggtcg gaagaagctg 1020

ctgtacatct ttaagcaacc cttcatgagg cctgtgcaga ctactcaaga ggaggacggc 1080

tgttcatgcc ggttcccaga ggaggaggaa ggcggctgcg aactgcgcgt gaaattcagc 1140

cgcagcgcag atgctccagc ctacaagcag gggcagaacc agctctacaa cgaactcaat 1200

cttggtcgga gagaggagta cgacgtgctg gacaagcgga gaggacggga cccagaaatg 1260

ggcgggaagc cgcgcagaaa gaatccccaa gagggcctgt acaacgagct ccaaaaggat 1320

aagatggcag aagcctatag cgagattggt atgaaagggg aacgcagaag aggcaaaggc 1380

cacgacggac tgtaccaggg actcagcacc gccaccaagg acacctatga cgctcttcac 1440

atgcaggccc tgccgcctcg g 1461

<210> 90
<211> 487
<212> PRT
<213> Artificial Sequence

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

<400> 90
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

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

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

Asn Ile Glu Asp Tyr Tyr Ile His Trp Val Lys Gln Arg Thr Glu Gln
50 55 60

Gly Leu Glu Trp Ile Gly Arg Ile Asp Pro Glu Asn Asp Glu Thr Lys
65 70 75 80

Tyr Gly Pro Ile Phe Gln Gly Arg Ala Thr Ile Thr Ala Asp Thr Ser
85 90 95

Ser Asn Thr Val Tyr Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Ala Phe Arg Gly Gly Val Tyr Trp Gly Pro Gly
115 120 125

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

```
Ser Gly Gly Gly Gly Ser His Met Asp Val Val Met Thr Gln Ser Pro
145                 150                 155                 160

Leu Thr Leu Ser Val Ala Ile Gly Gln Ser Ala Ser Ile Ser Cys Lys
                165                 170                 175

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

Leu Leu Gln Arg Pro Gly Gln Ser Pro Lys Arg Leu Ile Ser Leu Val
        195                 200                 205

Ser Lys Leu Asp Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser
    210                 215                 220

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

Gly Ile Tyr Tyr Cys Trp Gln Gly Thr His Phe Pro Gly Thr Phe Gly
                245                 250                 255

Gly Gly Thr Lys Leu Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro
            260                 265                 270

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

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

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

Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly
                325                 330                 335
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Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val
            340                 345                 350

Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu
        355                 360                 365

Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp
    370                 375                 380

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

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
                405                 410                 415

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
            420                 425                 430

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
        435                 440                 445

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
    450                 455                 460

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
465                 470                 475                 480

Met Gln Ala Leu Pro Pro Arg
                485
```

<210> 91
<211> 240
<212> PRT
<213> Artificial Sequence

<220>

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

<400> 91

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asn
            20                  25                  30

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

Tyr Ala Ala Ser Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Thr Gly
    50                  55                  60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His His Ser Tyr Pro Leu
                85                  90                  95

Thr Ser Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Gly Ser Thr
            100                 105                 110

Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Glu Val Gln Val
        115                 120                 125

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

Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met Ser Trp
145                 150                 155                 160

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

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

Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn
195 200 205

Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Gly Ser Ser
210 215 220

Gly Trp Ser Glu Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
225 230 235 240

<210> 92
<211> 720
<212> DNA
<213> Artificial Sequence

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

<400> 92
gatatccaaa tgactcagag cccttcatcc ctgagcgcca gcgtcggaga cagggtgacc 60

atcacgtgcc gggcatccca aggcattaga aataacttgg cgtggtatca gcaaaaacca 120

ggaaaggccc cgaagcgcct gatctacgcg gcctccaacc ttcagtcagg agtgccctcg 180

cgcttcaccg ggagcggtag cggaactgag tttaccctta tcgtgtcgtc cctgcagcca 240

gaggacttcg cgacctacta ctgcctccag catcactcgt acccgttgac ttcgggaggc 300

ggaaccaagg tcgaaatcaa acgcactggc tcgacgtcag ggtccggtaa accgggatcg 360

ggagaaggat cggaagtcca agtgctggag agcggaggcg gactcgtgca acctggcggg 420

tcgctgcggc tcagctgtgc cgcgtcgggt tttactttca gctcgtacgc tatgtcatgg 480

gtgcggcagg ctccgggaaa ggggctggaa tgggtgtccg ctatttccgg ctcgggtgga 540

agcaccaatt acgccgactc cgtgaaggga cgcttcacca tctcacggga taactccaag 600

aatactctgt acctccagat gaactcgctg agagccgagg acaccgcagt gtactactgc 660

gcagggtcaa gcggctggtc cgaatactgg ggacagggca ccctcgtcac tgtcagctcc 720

<210> 93
<211> 807
<212> DNA
<213> Artificial Sequence

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

<400> 93
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg 60

cccgatatcc aaatgactca gagcccttca tccctgagcg ccagcgtcgg agacagggtg 120

accatcacgt gccgggcatc ccaaggcatt agaaataact tggcgtggta tcagcaaaaa 180

ccaggaaagg ccccgaagcg cctgatctac gcggcctcca accttcagtc aggagtgccc 240

tcgcgcttca ccgggagcgg tagcggaact gagtttaccc ttatcgtgtc gtccctgcag 300

ccagaggact tcgcgaccta ctactgcctc cagcatcact cgtacccgtt gacttcggga 360

ggcggaacca aggtcgaaat caaacgcact ggctcgacgt cagggtccgg taaaccggga 420

tcgggagaag gatcggaagt ccaagtgctg gagagcggag gcggactcgt gcaacctggc 480

gggtcgctgc ggctcagctg tgccgcgtcg ggttttactt tcagctcgta cgctatgtca 540

tgggtgcggc aggctccggg aaaggggctg gaatgggtgt ccgctatttc cggctcgggt 600

ggaagcacca attacgccga ctccgtgaag ggacgcttca ccatctcacg ggataactcc 660

aagaatactc tgtacctcca gatgaactcg ctgagagccg aggacaccgc agtgtactac 720

tgcgcagggt caagcggctg gtccgaatac tggggacagg gcaccctcgt cactgtcagc 780

tcccatcacc atcaccacca ccatcac 807

<210> 94
<211> 269
<212> PRT

<213> Artificial Sequence

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

<400> 94
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

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

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

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

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

Ser Arg Phe Thr Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Ile Val
85 90 95

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

His Ser Tyr Pro Leu Thr Ser Gly Gly Gly Thr Lys Val Glu Ile Lys
115 120 125

Arg Thr Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly
130 135 140

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

                                        _SL
Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser
                165   170   175

Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
            180   185   190

Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Asn Tyr Ala Asp Ser
        195   200   205

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
    210   215   220

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
225   230   235   240

Cys Ala Gly Ser Ser Gly Trp Ser Glu Tyr Trp Gly Gln Gly Thr Leu
                245   250   255

Val Thr Val Ser Ser His His His His His His His His
            260   265

<210> 95
<211> 1452
<212> DNA
<213> Artificial Sequence

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

<400> 95
atggccctcc ctgtcaccgc cctgctgctt ccgctggctc ttctgctcca cgccgctcgg   60

cccgatatcc aaatgactca gagcccttca tccctgagcg ccagcgtcgg agacagggtg   120

accatcacgt gccgggcatc ccaaggcatt agaaataact tggcgtggta tcagcaaaaa   180

ccaggaaagg ccccgaagcg cctgatctac gcggcctcca accttcagtc aggagtgccc   240

tcgcgcttca ccgggagcgg tagcggaact gagtttaccc ttatcgtgtc gtccctgcag   300

ccagaggact tcgcgaccta ctactgcctc cagcatcact cgtacccgtt gacttcggga 360

ggcggaacca aggtcgaaat caaacgcact ggctcgacgt cagggtccgg taaaccggga 420

tcgggagaag gatcggaagt ccaagtgctg gagagcggag gcggactcgt gcaacctggc 480

gggtcgctgc ggctcagctg tgccgcgtcg ggttttactt tcagctcgta cgctatgtca 540

tgggtgcggc aggctccggg aaaggggctg gaatgggtgt ccgctatttc cggctcgggt 600

ggaagcacca attacgccga ctccgtgaag ggacgcttca ccatctcacg ggataactcc 660

aagaatactc tgtacctcca gatgaactcg ctgagagccg aggacaccgc agtgtactac 720

tgcgcagggt caagcggctg gtccgaatac tggggacagg gcaccctcgt cactgtcagc 780

tccaccacta ccccagcacc gaggccaccc accccggctc ctaccatcgc ctcccagcct 840

ctgtccctgc gtccggaggc atgtagaccc gcagctggtg gggccgtgca tacccggggt 900

cttgacttcg cctgcgatat ctacatttgg gcccctctgg ctggtacttg cggggtcctg 960

ctgctttcac tcgtgatcac tctttactgt aagcgcggtc ggaagaagct gctgtacatc 1020

tttaagcaac ccttcatgag gcctgtgcag actactcaag aggaggacgg ctgttcatgc 1080

cggttcccag aggaggagga aggcggctgc gaactgcgcg tgaaattcag ccgcagcgca 1140

gatgctccag cctacaagca ggggcagaac cagctctaca acgaactcaa tcttggtcgg 1200

agagaggagt acgacgtgct ggacaagcgg agaggacggg acccagaaat gggcgggaag 1260

ccgcgcagaa agaatcccca agagggcctg tacaacgagc tccaaaagga taagatggca 1320

gaagcctata gcgagattgg tatgaaaggg gaacgcagaa gaggcaaagg ccacgacgga 1380

ctgtaccagg gactcagcac cgccaccaag gacacctatg acgctcttca catgcaggcc 1440

ctgccgcctc gg 1452

<210> 96
<211> 484
<212> PRT
<213> Artificial Sequence

<220>

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

<400> 96

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

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

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

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

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

Ser Arg Phe Thr Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Ile Val
                85                  90                  95

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

His Ser Tyr Pro Leu Thr Ser Gly Gly Gly Thr Lys Val Glu Ile Lys
        115                 120                 125

Arg Thr Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly
    130                 135                 140

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

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser
                165                 170                 175
```

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Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
            180                 185                 190

Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Asn Tyr Ala Asp Ser
        195                 200                 205

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
    210                 215                 220

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
225                 230                 235                 240

Cys Ala Gly Ser Ser Gly Trp Ser Glu Tyr Trp Gly Gln Gly Thr Leu
                245                 250                 255

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

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

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

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

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

Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr
            340                 345                 350

Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly
        355                 360                 365
```

Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala
370 375 380

Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
385 390 395 400

Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
405 410 415

Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
420 425 430

Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
435 440 445

Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
450 455 460

Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
465 470 475 480

Leu Pro Pro Arg

<210> 97
<211> 1183
<212> DNA
<213> Artificial Sequence

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

<400> 97
gtgaggctcc ggtgcccgtc agtgggcaga gcgcacatcg cccacagtcc ccgagaagtt 60

gggggggaggg gtcggcaatt gaaccggtgc ctagagaagg tggcgcgggg taaactggga 120

aagtgatgtc gtgtactggc tccgcctttt tcccgagggt gggggagaac cgtatataag 180

tgcagtagtc gccgtgaacg ttctttttcg caacgggttt gccgccagaa cacaggtaag 240

tgccgtgtgt ggttcccgcg ggcctggcct ctttacgggt tatggccctt gcgtgccttg 300

aattacttcc acctggctgc agtacgtgat tcttgatccc gagcttcggg ttggaagtgg 360

gtgggagagt tcgaggcctt gcgcttaagg agcccttcg cctcgtgctt gagttgaggc 420

ctggcctggg cgctggggcc gccgcgtgcg aatctggtgg caccttcgcg cctgtctcgc 480

tgctttcgat aagtctctag ccatttaaaa tttttgatga cctgctgcga cgcttttttt 540

ctggcaagat agtcttgtaa atgcgggcca agatctgcac actggtattt cggttttgg 600

ggccgcgggc ggcgacgggg cccgtgcgtc ccagcgcaca tgttcggcga ggcggggcct 660

gcgagcgcgg ccaccgagaa tcggacgggg gtagtctcaa gctggccggc ctgctctggt 720

gcctggcctc gcgccgccgt gtatcgcccc gccctgggcg gcaaggctgg cccggtcggc 780

accagttgcg tgagcggaaa gatggccgct tcccggccct gctgcaggga gctcaaaatg 840

gaggacgcgg cgctcgggag agcgggcggg tgagtcaccc acacaaagga aaagggcctt 900

tccgtcctca gccgtcgctt catgtgactc cacggagtac cgggcgccgt ccaggcacct 960

cgattagttc tcgagctttt ggagtacgtc gtctttaggt tgggggggagg ggttttatgc 1020

gatggagttt ccccacactg agtgggtgga gactgaagtt aggccagctt ggcacttgat 1080

gtaattctcc ttggaatttg ccctttttga gtttggatct tggttcattc tcaagcctca 1140

gacagtggtt caaagttttt ttcttccatt tcaggtgtcg tga 1183

<210> 98
<211> 729
<212> DNA
<213> Artificial Sequence

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

<400> 98

gagatccagc tccaacagag cggagccgaa ctggtcaaac cgggagcgtc ggtgaagttg 60

tcatgcactg gatcgggctt caacatcgag gattactaca tccactgggt caagcaacgc 120

accgagcagg ggctggaatg gatcggacgg atcgaccccg aaaacgatga aaccaagtac 180

gggcctatct tccaaggacg ggccaccatt acggctgaca cgtcaagcaa taccgtctac 240

ctccagcttt ccagcctgac ctccgaggac actgccgtgt actactgcgc cttcagagga 300

ggcgtgtact ggggaccagg aaccactttg accgtgtcca gcggaggcgg tggatcagga 360

ggaggaggct caggcggtgg cggctcgcac atggacgtgg tcatgactca gtccccgctg 420

accctgtcgg tggcaattgg acagagcgca tccatctcgt gcaagagctc acagtcgctg 480

ctggattccg acggaaagac ttatctgaac tggctgctcc aaagaccagg gcaatcaccg 540

aaacgcctta tctccctggt gtcgaaactc gactcgggtg tgccggatcg gtttaccggt 600

agcgggtccg gcacggactt cactctccgc atttcgaggg tggaagcgga ggatctcggg 660

atctactact gttggcaggg aacccacttc cctgggactt ttggaggcgg aactaagctg 720

gaaatcaag 729

<210> 99
<211> 112
<212> PRT
<213> Homo sapiens

<400> 99
Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
1 5 10 15

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

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
35 40 45

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

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

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

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

<210> 100
<211> 336
<212> DNA
<213> Homo sapiens

<400> 100
agagtgaagt tcagcaggag cgcagacgcc cccgcgtacc agcagggcca gaaccagctc 60

tataacgagc tcaatctagg acgaagagag gagtacgatg ttttggacaa gagacgtggc 120

cgggaccctg agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgtacaat 180

gaactgcaga aagataagat ggcggaggcc tacagtgaga ttgggatgaa aggcgagcgc 240

cggaggggca aggggcacga tggcctttac cagggtctca gtacagccac caaggacacc 300

tacgacgccc ttcacatgca ggccctgccc cctcgc 336

<210> 101
<211> 14
<212> PRT
<213> Artificial Sequence

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

<400> 101
Leu Glu Glu Lys Lys Gly Asn Tyr Val Val Thr Asp His Cys
1 5 10

<210> 102

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

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

<400> 102
Gln Arg Arg Lys Tyr Arg Ser Asn Lys Gly Glu Ser Pro Val Glu Pro
1 5 10 15

Ala Glu Pro Cys Arg Tyr Ser Cys Pro Arg Glu Glu Glu Gly Ser Thr
20 25 30

Ile Pro Ile Gln Glu Asp Tyr Arg Lys Pro Glu Pro Ala Cys Ser Pro
35 40 45

<210> 103
<211> 123
<212> DNA
<213> Artificial Sequence

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

<400> 103
aggagtaaga ggagcaggct cctgcacagt gactacatga acatgactcc ccgccgcccc 60

gggcccaccc gcaagcatta ccagccctat gccccaccac gcgacttcgc agcctatcgc 120

tcc 123

<210> 104
<211> 230
<212> PRT
<213> Artificial Sequence

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

_SL

polypeptide"

<400> 104

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe
1 5 10 15

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
20 25 30

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
35 40 45

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
50 55 60

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
65 70 75 80

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
85 90 95

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
100 105 110

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
115 120 125

Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
130 135 140

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
145 150 155 160

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
165 170 175

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu

_SL
180 185 190

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
195 200 205

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
210 215 220

Leu Ser Leu Gly Lys Met
225 230

<210> 105
<211> 690
<212> DNA
<213> Artificial Sequence

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

<400> 105
gagagcaagt acggccctcc ctgcccccct tgccctgccc ccgagttcct gggcggaccc 60

agcgtgttcc tgttcccccc caagcccaag gacaccctga tgatcagccg gacccccgag 120

gtgacctgtg tggtggtgga cgtgtcccag gaggaccccg aggtccagtt caactggtac 180

gtggacggcg tggaggtgca caacgccaag accaagcccc gggaggagca gttcaatagc 240

acctaccggg tggtgtccgt gctgaccgtg ctgcaccagg actggctgaa cggcaaggaa 300

tacaagtgta aggtgtccaa caagggcctg cccagcagca tcgagaaaac catcagcaag 360

gccaagggcc agcctcggga gccccaggtg tacaccctgc cccctagcca agaggagatg 420

accaagaacc aggtgtccct gacctgcctg gtgaagggct tctaccccag cgacatcgcc 480

gtggagtggg agagcaacgg ccagcccgag aacaactaca agaccacccc ccctgtgctg 540

gacagcgacg gcagcttctt cctgtacagc cggctgaccg tggacaagag ccggtggcag 600

gagggcaacg tctttagctg ctccgtgatg cacgaggccc tgcacaacca ctacacccag 660

aagagcctga gcctgtccct gggcaagatg 690

<210> 106
<211> 282
<212> PRT
<213> Artificial Sequence

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

<400> 106
Arg Trp Pro Glu Ser Pro Lys Ala Gln Ala Ser Ser Val Pro Thr Ala
1 5 10 15

Gln Pro Gln Ala Glu Gly Ser Leu Ala Lys Ala Thr Thr Ala Pro Ala
20 25 30

Thr Thr Arg Asn Thr Gly Arg Gly Gly Glu Glu Lys Lys Lys Glu Lys
35 40 45

Glu Lys Glu Glu Gln Glu Glu Arg Glu Thr Lys Thr Pro Glu Cys Pro
50 55 60

Ser His Thr Gln Pro Leu Gly Val Tyr Leu Leu Thr Pro Ala Val Gln
65 70 75 80

Asp Leu Trp Leu Arg Asp Lys Ala Thr Phe Thr Cys Phe Val Val Gly
85 90 95

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

Pro Thr Gly Gly Val Glu Glu Gly Leu Leu Glu Arg His Ser Asn Gly
115 120 125

Ser Gln Ser Gln His Ser Arg Leu Thr Leu Pro Arg Ser Leu Trp Asn
130 135 140

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

Gln Arg Leu Met Ala Leu Arg Glu Pro Ala Ala Gln Ala Pro Val Lys
                165                 170                 175

Leu Ser Leu Asn Leu Leu Ala Ser Ser Asp Pro Pro Glu Ala Ala Ser
            180                 185                 190

Trp Leu Leu Cys Glu Val Ser Gly Phe Ser Pro Pro Asn Ile Leu Leu
        195                 200                 205

Met Trp Leu Glu Asp Gln Arg Glu Val Asn Thr Ser Gly Phe Ala Pro
    210                 215                 220

Ala Arg Pro Pro Pro Gln Pro Gly Ser Thr Thr Phe Trp Ala Trp Ser
225                 230                 235                 240

Val Leu Arg Val Pro Ala Pro Pro Ser Pro Gln Pro Ala Thr Tyr Thr
                245                 250                 255

Cys Val Val Ser His Glu Asp Ser Arg Thr Leu Leu Asn Ala Ser Arg
            260                 265                 270

Ser Leu Glu Val Ser Tyr Val Thr Asp His
        275                 280
```

<210> 107
<211> 847
<212> DNA
<213> Artificial Sequence

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

<400> 107
aggtggcccg aaagtcccaa ggcccaggca tctagtgttc ctactgcaca gccccaggca 60

gaaggcagcc tagccaaagc tactactgca cctgccacta cgcgcaatac tggccgtggc 120

ggggaggaga agaaaaagga gaaagagaaa gaagaacagg aagagaggga gaccaagacc 180

cctgaatgtc catcccatac ccagccgctg ggcgtctatc tcttgactcc cgcagtacag 240

gacttgtggc ttagagataa ggccaccttt acatgtttcg tcgtgggctc tgacctgaag 300

gatgcccatt tgacttggga ggttgccgga aaggtaccca ggggggggt tgaggaaggg 360

ttgctggagc gccattccaa tggctctcag agccagcact caagactcac ccttccgaga 420

tccctgtgga acgccgggac ctctgtcaca tgtactctaa atcatcctag cctgccccca 480

cagcgtctga tggcccttag agagccagcc gcccaggcac cagttaagct tagcctgaat 540

ctgctcgcca gtagtgatcc cccagaggcc gccagctggc tcttatgcga agtgtccggc 600

tttagcccgc ccaacatctt gctcatgtgg ctggaggacc agcgagaagt gaacaccagc 660

ggcttcgctc cagcccggcc cccaccccag ccgggttcta ccacattctg ggcctggagt 720

gtcttaaggg tcccagcacc acctagcccc cagccagcca catacacctg tgttgtgtcc 780

catgaagata gcaggaccct gctaaatgct tctaggagtc tggaggtttc ctacgtgact 840

gaccatt 847

<210> 108
<211> 10
<212> PRT
<213> Artificial Sequence

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

<400> 108
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 109

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

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

<400> 109
ggtggcggag gttctggagg tggaggttcc 30

<210> 110
<211> 30
<212> PRT
<213> Artificial Sequence

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

<220>
<221> misc_feature
<222> (1)..(30)
<223> /note="This sequence may encompass 1, 2, 3, 4, 5, or 6
'Gly Gly Gly Gly Ser' repeating units"

<220>
<221> VARIANT
<222> (6)..(30)
<223> /replace=" "

<220>
<221> misc_feature
<222> (1)..(30)
<223> /note="Variant residues given in the sequence have no
preference with respect to those in the annotations
for variant positions"

<220>
<221> misc_feature
<222> (1)..(30)
<223> /note="See specification as filed for detailed description of
substitutions and preferred embodiments"

<400> 110
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1   5   10   15

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            20   25   30

<210> 111
<211> 150
<212> DNA
<213> Artificial Sequence

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

<400> 111
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 60

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 120

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa   150

<210> 112
<211> 4
<212> PRT
<213> Artificial Sequence

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

<400> 112
Gly Gly Gly Ser
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<210> 113
<211> 20
<212> PRT
<213> Artificial Sequence

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

<400> 113
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser
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<210> 114
<211> 15
<212> PRT
<213> Artificial Sequence

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

<400> 114
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 115
<211> 5000
<212> DNA
<213> Artificial Sequence

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

<220>
<221> misc_feature
<222> (1)..(5000)
<223> /note="This sequence may encompass between 50 and 5,000 nucleotides"

<220>
<221> variation
<222> (51)..(5000)

<223> /replace=" "

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<221> misc_feature
<222> (1)..(5000)
<223> /note="Variant bases given in the sequence have no
preference with respect to those in the annotations
for variant positions"

<220>
<221> misc_feature
<222> (1)..(5000)
<223> /note="See specification as filed for detailed description of
substitutions and preferred embodiments"

<400> 115
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 420

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 480

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 540

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 600

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 660

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 720

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 780

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 840

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<210> 116
<211> 2000
<212> DNA
<213> Artificial Sequence

<220>
<221> source

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

<220>
<221> misc_feature
<222> (1)..(2000)
<223> /note="This sequence may encompass between 50 and 2,000
nucleotides"

<220>
<221> variation
<222> (51)..(2000)
<223> /replace=" "

<220>
<221> misc_feature
<222> (1)..(2000)
<223> /note="Variant bases given in the sequence have no
preference with respect to those in the annotations
for variant positions"

<400> 116
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<210> 117
<211> 100
<212> DNA
<213> Artificial Sequence

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

<400> 117
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<210> 118
<211> 5000
<212> DNA
<213> Artificial Sequence

<220>
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polynucleotide"

<220>
<221> misc_feature
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<223> /note="This sequence may encompass between 50 and 5,000
nucleotides"

<220>
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<222> (51)..(5000)
<223> /replace=" "

<220>
<221> misc_feature
<222> (1)..(5000)
<223> /note="Variant bases given in the sequence have no
preference with respect to those in the annotations
for variant positions"

<400> 118
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<210> 119
<211> 5000
<212> DNA
<213> Artificial Sequence

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

<220>
<221> misc_feature
<222> (1)..(5000)
<223> /note="This sequence may encompass between 100 and 5,000
nucleotides"

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<220>
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<223> /note="Variant bases given in the sequence have no
preference with respect to those in the annotations
for variant positions"

<400> 119

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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3960

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4020

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4080

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4140

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4200

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4260

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4320

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4380

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4440

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4500

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4560

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4620

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4680

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4740

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4800

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4860

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aaaaaaaaaa aaaaaaaaaa 5000

<210> 120
<211> 400
<212> DNA
<213> Artificial Sequence

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

<220>
<221> misc_feature
<222> (1)..(400)
<223> /note="This sequence may encompass between 100 and 400
nucleotides"

<220>
<221> variation
<222> (101)..(400)
<223> /replace=" "

<220>
<221> misc_feature
<222> (1)..(400)
<223> /note="Variant bases given in the sequence have no
preference with respect to those in the annotations
for variant positions"

<220>
<221> misc_feature
<222> (1)..(400)
<223> /note="See specification as filed for detailed description of
substitutions and preferred embodiments"

<400> 120
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 60

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 120

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 180

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 240

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 300

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 360

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 400

<210> 121
<211> 487
<212> PRT
<213> Artificial Sequence

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

<400> 121
Met Val Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
1 5 10 15

Ala Phe Leu Ile Ile Pro Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
20 25 30

```
                                            _SL
Leu Ser Ala Ser Val Gly Asp Arg Val Ile Ile Ile Cys Arg Ala Ser
        35                  40                  45


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


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


Pro Ser Arg Phe Thr Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Ile
                85                  90                  95


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


His His Ser Tyr Pro Leu Thr Ser Gly Gly Gly Thr Lys Val Glu Ile
        115                 120                 125


Lys Phe Thr Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu
    130                 135                 140


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


Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
                165                 170                 175


Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
            180                 185                 190


Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Asn Tyr Ala Asp
        195                 200                 205


Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
    210                 215                 220
```

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                                            _SL
Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
225                 230                 235                 240


Tyr Cys Ala Gly Ser Ser Gly Trp Ser Glu Tyr Trp Gly Gln Gly Thr
                245                 250                 255


Leu Val Thr Val Ser Ser Ala Ser Thr Thr Thr Pro Ala Pro Arg Pro
            260                 265                 270


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


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


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


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


Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val
            340                 345                 350


Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu
        355                 360                 365


Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp
    370                 375                 380


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


Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
                405                 410                 415
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```
                                            _SL
Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
            420                 425                 430


Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
        435                 440                 445


Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
    450                 455                 460


Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
465                 470                 475                 480


Met Gln Ala Leu Pro Pro Arg
                485


<210> 122
<211> 114
<212> PRT
<213> Mus musculus

<400> 122
Glu Ile Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Leu Ser Cys Thr Gly Ser Gly Phe Asn Ile Glu Asp Tyr
            20                  25                  30


Tyr Ile His Trp Val Lys Gln Arg Thr Glu Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Arg Ile Asp Pro Glu Asn Asp Glu Thr Lys Tyr Gly Pro Ile Phe
    50                  55                  60


Gln Gly Arg Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Val Tyr
65                  70                  75                  80


Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
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Ala Phe Arg Gly Gly Val Tyr Trp Gly Pro Gly Thr Thr Leu Thr Val
100 105 110

Ser Ser

<210> 123
<211> 114
<212> PRT
<213> Artificial Sequence

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

<400> 123
Glu Ile Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Thr Val Lys Ile Ser Cys Lys Gly Ser Gly Phe Asn Ile Glu Asp Tyr
20 25 30

Tyr Ile His Trp Val Gln Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Arg Ile Asp Pro Glu Asn Asp Glu Thr Lys Tyr Gly Pro Ile Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

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

Ala Phe Arg Gly Gly Val Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
100 105 110

Ser Ser

<210> 124
<211> 114
<212> PRT
<213> Artificial Sequence

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

<400> 124
Glu Ile Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Phe Asn Ile Glu Asp Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Arg Ile Asp Pro Glu Asn Asp Glu Thr Lys Tyr Gly Pro Ile Phe
50 55 60

Gln Gly His Val Thr Ile Ser Ala Asp Thr Ser Ile Asn Thr Val Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Phe Arg Gly Gly Val Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
100 105 110

Ser Ser

<210> 125
<211> 112
<212> PRT
<213> Mus musculus

<400> 125
Asp Val Val Met Thr Gln Ser Pro Leu Thr Leu Ser Val Ala Ile Gly
1 5 10 15

Gln Ser Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

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

Pro Lys Arg Leu Ile Ser Leu Val Ser Lys Leu Asp Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Leu Gly Ile Tyr Tyr Cys Trp Gln Gly
85 90 95

Thr His Phe Pro Gly Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 126
<211> 112
<212> PRT
<213> Artificial Sequence

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

<400> 126
Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
            20   25   30

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

Pro Arg Arg Leu Ile Ser Leu Val Ser Lys Leu Asp Ser Gly Val Pro
    50   55   60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly
                85   90   95

Thr His Phe Pro Gly Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 127
<211> 112
<212> PRT
<213> Artificial Sequence

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

<400> 127
Asp Val Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1   5   10   15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
            20   25   30

Asp Gly Lys Thr Tyr Leu Asn Trp Leu Gln Gln Lys Pro Gly Gln Pro
        35   40   45

```
                                        _SL
Pro Lys Arg Leu Ile Ser Leu Val Ser Lys Leu Asp Ser Gly Val Pro
    50                  55                  60


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


Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Trp Gln Gly
                85                  90                  95


Thr His Phe Pro Gly Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110
```