SEQUENCE LISTING

<110> SystImmune, Inc.

<120> BISPECIFIC TETRAVALENT ANTIBODIES AND METHODS OF MAKIING AND USING THEREOF

<130> EM01.0003PCT1

<150> US 62095348
<151> 2014-12-22

<160> 138

<170> PatentIn version 3.5

<210> 1
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<212> DNA
<213> artificial sequence

<220>
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cacccaggca aagcccccaa actcatgatc tatgatgtca gtgatcggcc ctcaggggtg 180

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caggctgacg acgaggctga ttattactgc agctcatatg ggagcagcag cactcatgtg 300

attttcggcg gagggaccaa gctgaccgtc ctacgtacgg tggctgcacc atctgtcttc 360

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aataacttct atcccagaga ggccaaagta cagtggaagg tggataacgc cctccaatcg 480

ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcagc 540

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cacccaggca aagcccccaa actcatgatc tatgatgtca gtgatcggcc ctcaggggtg 180

tctgatcgct tctccggctc caagtctggc aacacggcct ccctgatcat ctctggcctc 240

caggctgacg acgaggctga ttattactgc agctcatatg ggagcagcag cactcatgtg 300

attttcggcg gagggaccaa gctgaccgtc cta 333

<210> 3
<211> 218
<212> PRT
<213> artificial sequence

<220>
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<400> 3

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1               5                  10                  15

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
            20                  25                  30

Asn Phe Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
        35                  40                  45

Met Ile Tyr Asp Val Ser Asp Arg Pro Ser Gly Val Ser Asp Arg Phe
    50                  55                  60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Ile Ile Ser Gly Leu
65                  70                  75                  80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Gly Ser Ser
                85                  90                  95

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

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
        115                 120                 125

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
    130                 135                 140

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145                 150                 155                 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
                165                 170                 175

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
            180                 185                 190

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
        195                 200                 205

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215
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<210> 4
<211> 110
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 4

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

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
20 25 30

Asn Phe Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
35 40 45

Met Ile Tyr Asp Val Ser Asp Arg Pro Ser Gly Val Ser Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Ile Ile Ser Gly Leu
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Gly Ser Ser
85 90 95

Ser Thr His Val Ile Phe Gly Gly Gly Thr Lys Leu Thr Val
100 105 110

<210> 5
<211> 1344
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

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ccagggaagg ggctggagtg ggtggccaac ataaaccgcg atggaagtgc gagttactat 180

gtggactctg tgaagggccg attcaccatc tccagagacg acgccaagaa ctcactgtat 240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gagagatcgt 300

ggggtgggct acttcgatct ctggggccgt ggcaccctgg tcaccgtctc gagcgctagc 360

accaagggcc catcggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca 420

gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600

tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agagagttga gcccaaatct 660

tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 720

gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 780

acatgcgtgg tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840

gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 900

taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960

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aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1140

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tccgacggct ccttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag 1260

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320

agcctctccc tgtctccggg taaa 1344

<210> 6
<211> 354
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 6
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tcctgtgcag cctctggatt cacctttagt agttattgga tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtggccaac ataaaccgcg atggaagtgc gagttactat 180

gtggactctg tgaagggccg attcaccatc tccagagacg acgccaagaa ctcactgtat 240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gagagatcgt 300

ggggtgggct acttcgatct ctggggccgt ggcaccctgg tcaccgtctc gagc 354

<210> 7
<211> 448
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 7

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

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Ala Asn Ile Asn Arg Asp Gly Ser Ala Ser Tyr Tyr Val Asp Ser Val
    50                  55                  60

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

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

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

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115                 120                 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
    130                 135                 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                 150                 155                 160

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

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190

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

Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr
    210                 215                 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
225                 230                 235                 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245                 250                 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            260                 265                 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275                 280                 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
    290                 295                 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305                 310                 315                 320
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Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
340 345 350

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380

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

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

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

<210> 8
<211> 118
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 8

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ala Asn Ile Asn Arg Asp Gly Ser Ala Ser Tyr Tyr Val Asp Ser Val
50 55 60

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

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

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

Leu Val Thr Val Ser Ser
115

<210> 9
<211> 642
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 9

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

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

Gly Thr Cys Thr Gly Cys Ala Thr Cys Thr Gly Thr Ala Gly Gly Ala
35 40 45

Gly Ala Cys Ala Gly Ala Gly Thr Cys Ala Cys Cys Ala Thr Cys Ala
50 55 60

Cys Thr Thr Gly Cys Cys Ala Gly Gly Cys Gly Ala Gly Thr Cys Ala
65 70 75 80

Gly Gly Ala Cys Ala Thr Cys Ala Gly Cys Ala Ala Cys Thr Ala Thr
85 90 95

Thr Thr Ala Ala Ala Thr Thr Gly Gly Thr Ala Thr Cys Ala Gly Cys
100 105 110

Ala Gly Ala Ala Ala Cys Cys Ala Gly Gly Gly Ala Ala Ala Gly Cys
115 120 125

Cys Cys Cys Thr Ala Ala Ala Cys Thr Cys Cys Thr Gly Ala Thr Cys
130 135 140

Thr Ala Cys Gly Ala Thr Gly Cys Ala Thr Cys Cys Ala Ala Thr Thr
145 150 155 160

Thr Gly Gly Ala Ala Ala Cys Ala Gly Gly Gly Gly Thr Cys Cys Cys
165 170 175

Ala Thr Cys Ala Ala Gly Gly Thr Thr Cys Ala Gly Thr Gly Gly Ala
180 185 190

Ala Gly Thr Gly Gly Ala Thr Cys Thr Gly Gly Gly Ala Cys Ala Gly
195 200 205

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Ala Thr Thr Thr Thr Ala Cys Thr Thr Thr Cys Ala Cys Cys Ala Thr
    210                 215                 220

Cys Ala Gly Cys Ala Gly Cys Cys Thr Gly Cys Ala Gly Cys Cys Thr
225                 230                 235                 240

Gly Ala Ala Gly Ala Thr Ala Thr Thr Gly Cys Ala Ala Cys Ala Thr
                245                 250                 255

Ala Thr Thr Thr Cys Thr Gly Thr Cys Ala Ala Cys Ala Cys Thr Thr
            260                 265                 270

Thr Gly Ala Thr Cys Ala Thr Cys Thr Cys Cys Cys Gly Cys Thr Cys
        275                 280                 285

Gly Cys Thr Thr Thr Cys Gly Gly Cys Gly Gly Ala Gly Gly Gly Ala
    290                 295                 300

Cys Cys Ala Ala Gly Gly Thr Gly Gly Ala Ala Ala Thr Thr Ala Ala
305                 310                 315                 320

Ala Cys Gly Thr Ala Cys Gly Gly Thr Gly Gly Cys Thr Gly Cys Ala
                325                 330                 335

Cys Cys Ala Thr Cys Thr Gly Thr Cys Thr Thr Cys Ala Thr Cys Thr
            340                 345                 350

Thr Cys Cys Cys Gly Cys Cys Ala Thr Cys Thr Gly Ala Thr Gly Ala
        355                 360                 365

Gly Cys Ala Gly Thr Thr Gly Ala Ala Ala Thr Cys Thr Gly Gly Ala
    370                 375                 380

Ala Cys Thr Gly Cys Cys Thr Cys Thr Gly Thr Thr Gly Thr Gly Thr
385                 390                 395                 400

Gly Cys Cys Thr Gly Cys Thr Gly Ala Ala Thr Ala Ala Cys Thr Thr
                405                 410                 415

Cys Thr Ala Thr Cys Cys Cys Ala Gly Ala Gly Ala Gly Gly Cys Cys
            420                 425                 430

Ala Ala Ala Gly Thr Ala Cys Ala Gly Thr Gly Gly Ala Ala Gly Gly
        435                 440                 445

Thr Gly Gly Ala Thr Ala Ala Cys Gly Cys Cys Cys Thr Cys Cys Ala
    450                 455                 460

Ala Thr Cys Gly Gly Gly Thr Ala Ala Cys Thr Cys Cys Cys Ala Gly
465                 470                 475                 480
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Gly Ala Gly Ala Gly Thr Gly Thr Cys Ala Cys Ala Gly Ala Gly Cys
485 490 495

Ala Gly Gly Ala Cys Ala Gly Cys Ala Ala Gly Gly Ala Cys Ala Gly
500 505 510

Cys Ala Cys Cys Thr Ala Cys Ala Gly Cys Cys Thr Cys Ala Gly Cys
515 520 525

Ala Gly Cys Ala Cys Cys Cys Thr Gly Ala Cys Gly Cys Thr Gly Ala
530 535 540

Gly Cys Ala Ala Ala Gly Cys Ala Gly Ala Cys Thr Ala Cys Gly Ala
545 550 555 560

Gly Ala Ala Ala Cys Ala Cys Ala Ala Ala Gly Thr Cys Thr Ala Cys
565 570 575

Gly Cys Cys Thr Gly Cys Gly Ala Ala Gly Thr Cys Ala Cys Cys Cys
580 585 590

Ala Thr Cys Ala Gly Gly Gly Cys Cys Thr Gly Ala Gly Cys Thr Cys
595 600 605

Gly Cys Cys Cys Gly Thr Cys Ala Cys Ala Ala Ala Gly Ala Gly Cys
610 615 620

Thr Thr Cys Ala Ala Cys Ala Gly Gly Gly Gly Ala Gly Ala Gly Thr
625 630 635 640

Gly Thr

<210> 10
<211> 321
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

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atcacttgcc aggcgagtca ggacatcagc aactatttaa attggtatca gcagaaacca 120

gggaaagccc ctaaactcct gatctacgat gcatccaatt tggaaacagg ggtcccatca 180

aggttcagtg gaagtggatc tgggacagat tttactttca ccatcagcag cctgcagcct 240

gaagatattg caacatattt ctgtcaacac tttgatcatc tcccgctcgc tttcggcgga 300

gggaccaagg tggaaattaa a 321

<210> 11
<211> 214
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 11

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
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Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
            20                  25                  30

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

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

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

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

Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

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

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
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<210> 12
<211> 107

<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<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 Gln Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

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

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

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

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

Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 13
<211> 1347
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 13
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acctgcactg tctctggtgg ctccgtcagc agtggtgatt actactggac ctggatccgg 120

cagtccccag ggaagggact ggagtggatt ggacacatct attacagtgg gaacaccaat 180

tataacccct ccctcaagag ccgactcacc atatcaattg acacgtccaa gactcagttc 240

tccctgaagc tgagttctgt gaccgctgcg gacacggcca tttattactg tgtgcgagat 300

cgagtgactg gtgcttttga tatctggggc caagggacaa tggtcaccgt ctcgagcgct 360

agcaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420

acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480

aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600

atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagagagt tgagcccaaa 660

tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 720

tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780

gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840

gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900

acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960

tacaagtgca aggtctccaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1020

gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggaggagatg 1080

accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200

gactccgacg gctccttctt cctctatagc aagctcaccg tggacaagag caggtggcag 1260

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320

aagagcctct ccctgtctcc gggtaaa 1347

<210> 14
<211> 357
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 14
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acctgcactg tctctggtgg ctccgtcagc agtggtgatt actactggac ctggatccgg 120

cagtccccag ggaagggact ggagtggatt ggacacatct attacagtgg gaacaccaat 180

tataacccct ccctcaagag ccgactcacc atatcaattg acacgtccaa gactcagttc 240

tccctgaagc tgagttctgt gaccgctgcg gacacggcca tttattactg tgtgcgagat 300

cgagtgactg gtgcttttga tatctggggc caagggacaa tggtcaccgt ctcgagc 357

<210> 15
<211> 449
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 15

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Val Ser Ser Gly
20 25 30

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

```
Trp Ile Gly His Ile Tyr Tyr Ser Gly Asn Thr Asn Tyr Asn Pro Ser
    50                  55                  60

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

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Ile Tyr Tyr
                85                  90                  95

Cys Val Arg Asp Arg Val Thr Gly Ala Phe Asp Ile Trp Gly Gln Gly
            100                 105                 110

Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190

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

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
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Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
325 330 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
340 345 350

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385 390 395 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445

Lys

<210> 16
<211> 119
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 16

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Val Ser Ser Gly
20 25 30

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

Trp Ile Gly His Ile Tyr Tyr Ser Gly Asn Thr Asn Tyr Asn Pro Ser
50 55 60

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

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Ile Tyr Tyr
85 90 95

Cys Val Arg Asp Arg Val Thr Gly Ala Phe Asp Ile Trp Gly Gln Gly
100 105 110

Thr Met Val Thr Val Ser Ser
115

<210> 17
<211> 642
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 17
gatatccaga tgacccagtc cccgagctcc ctgtccgcct ctgtgggcga tagggtcacc 60

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ggaaaagctc cgaagcttct gatttactcg gcatccttcc tctactctgg agtcccttct 180

cgcttctctg gtagcggttc cgggacggat ttcactctga ccatcagcag tctgcagccg 240

gaagacttcg caacttatta ctgtcagcaa agtgagccgg agccgtacac gttcggacag 300

ggtaccaagg tggagatcaa acgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 18
<211> 321
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 18
gatatccaga tgacccagtc cccgagctcc ctgtccgcct ctgtgggcga tagggtcacc 60

atcacctgcc gtgccagtca gaatattgct actgatgtag cctggtatca acagaaacca 120

ggaaaagctc cgaagcttct gatttactcg gcatccttcc tctactctgg agtcccttct 180

cgcttctctg gtagcggttc cgggacggat ttcactctga ccatcagcag tctgcagccg 240

gaagacttcg caacttatta ctgtcagcaa agtgagccgg agccgtacac gttcggacag 300

ggtaccaagg tggagatcaa a 321

<210> 19
<211> 214
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 19

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 Asn Ile Ala Thr Asp
20 25 30

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

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

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 20
<211> 107
<212> PRT
<213> artificial sequence

<220>

<223> Synthesized

<400> 20

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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 Asn Ile Ala Thr Asp
            20                  25                  30

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105
```

<210> 21
<211> 1353
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 21

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gaggtgcagc tggtcgagtc tggcggcgga ctggtgcagc ccggtggctc tctgcgactg       60

tcttgtgccg cctctggctt caccctcagt ggcgattgga tccactgggt gcgacaggct      120

cccggaaagg gcctggagtg ggtgggtgag atctctgctg ccggtggcta caccgattac      180

gccgactctg tgaagggccg attcaccatc tctgccgaca cctctaagaa caccgcctac      240

ctgcagatga actctctgcg agccgaggac accgctgtgt actactgtgc acgagaaagt      300

agagtttcct tcgaagccgc catggactac tggggccagg gcaccctggt gaccgtgtcc      360

tctgctagca ccaagggccc atcggtcttc cccctggcac cctcctccaa gagcacctct      420

gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg      480

tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc      540

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag      600

acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gagagttgag      660

cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg      720

ggaccgtcag tcttcctctt ccccccaaaa cccaaggaca ccctcatgat ctcccggacc      780

cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac      840
```

tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 900

aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960

aaggagtaca agtgcaaggt ctccaacaaa gccctcccag cccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc atcccgggag 1080

gagatgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac 1140

atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1200

gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg 1260

tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1320

acgcagaaga gcctctccct gtctccgggt aaa 1353

<210> 22
<211> 363
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 22

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

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

Gly Gly Thr Gly Cys Ala Gly Cys Cys Cys Gly Gly Thr Gly Gly Cys
35 40 45

Thr Cys Thr Cys Thr Gly Cys Gly Ala Cys Thr Gly Thr Cys Thr Thr
50 55 60

Gly Thr Gly Cys Cys Gly Cys Cys Thr Cys Thr Gly Gly Cys Thr Thr
65 70 75 80

Cys Ala Cys Cys Cys Thr Cys Ala Gly Thr Gly Gly Cys Gly Ala Thr
85 90 95

Thr Gly Gly Ala Thr Cys Cys Ala Cys Thr Gly Gly Gly Thr Gly Cys
100 105 110

Gly Ala Cys Ala Gly Gly Cys Thr Cys Cys Cys Gly Gly Ala Ala Ala
115 120 125

Gly Gly Gly Cys Cys Thr Gly Gly Ala Gly Thr Gly Gly Gly Thr Gly
130 135 140

Gly Gly Thr Gly Ala Gly Ala Thr Cys Thr Cys Thr Gly Cys Thr Gly
145 150 155 160

```
Cys Cys Gly Gly Thr Gly Gly Cys Thr Ala Cys Ala Cys Cys Gly Ala
                165                 170                 175

Thr Thr Ala Cys Gly Cys Cys Gly Ala Cys Thr Cys Thr Gly Thr Gly
            180                 185                 190

Ala Ala Gly Gly Gly Cys Cys Gly Ala Thr Thr Cys Ala Cys Cys Ala
        195                 200                 205

Thr Cys Thr Cys Thr Gly Cys Cys Gly Ala Cys Ala Cys Cys Thr Cys
    210                 215                 220

Thr Ala Ala Gly Ala Ala Cys Ala Cys Cys Gly Cys Cys Thr Ala Cys
225                 230                 235                 240

Cys Thr Gly Cys Ala Gly Ala Thr Gly Ala Ala Cys Thr Cys Thr Cys
                245                 250                 255

Thr Gly Cys Gly Ala Gly Cys Cys Gly Ala Gly Gly Ala Cys Ala Cys
            260                 265                 270

Cys Gly Cys Thr Gly Thr Gly Thr Ala Cys Thr Ala Cys Thr Gly Thr
        275                 280                 285

Gly Cys Ala Cys Gly Ala Gly Ala Ala Ala Gly Thr Ala Gly Ala Gly
    290                 295                 300

Thr Thr Thr Cys Cys Thr Thr Cys Gly Ala Ala Gly Cys Cys Gly Cys
305                 310                 315                 320

Cys Ala Thr Gly Gly Ala Cys Thr Ala Cys Thr Gly Gly Gly Gly Cys
                325                 330                 335

Cys Ala Gly Gly Gly Cys Ala Cys Cys Cys Thr Gly Gly Thr Gly Ala
            340                 345                 350

Cys Cys Gly Thr Gly Thr Cys Cys Thr Cys Thr
        355                 360
```

<210> 23
<211> 451
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 23

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

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser Gly Asp
            20                  25                  30

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

Gly Glu Ile Ser Ala Ala Gly Gly Tyr Thr Asp Tyr Ala Asp Ser Val
    50                  55                  60

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

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

Ala Arg Glu Ser Arg Val Ser Phe Glu Ala Ala Met Asp Tyr Trp Gly
            100                 105                 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
        115                 120                 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
    130                 135                 140

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

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225                 230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285
```

```
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
                325                 330                 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                405                 410                 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445

Pro Gly Lys
    450
```

<210> 24
<211> 121
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 24

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

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

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

Gly Glu Ile Ser Ala Ala Gly Gly Tyr Thr Asp Tyr Ala Asp Ser Val
    50                  55                  60
```

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

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

Ala Arg Glu Ser Arg Val Ser Phe Glu Ala Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 25
<211> 657
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 25
gatattcaaa tgactcaatc tccttcttct ctttctgctt ctgttggtga tcgtgttact 60

attacttgtc gttcttctca aaatattgtt cattctaatg gtaatactta tcttgattgg 120

tatcaacaaa ctcctggtaa agctcctaaa cttcttattt ataaagtttc taatcgtttt 180

tctggtgttc cttctcgttt ttctggttct ggttctggta ctgattttac ttttactatt 240

tcttctcttc aacctgaaga tattgctact tattattgtt ttcaatattc tcatgttcct 300

tggacttttg gtcaaggtac taaacttcaa attactcgta cggtggctgc accatctgtc 360

ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg 420

ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa 480

tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc 540

agcagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 600

gtcacccatc agggcctgag ctcgcccgtc acaaagagct tcaacagggg agagtgt 657

<210> 26
<211> 336
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 26
gatattcaaa tgactcaatc tccttcttct ctttctgctt ctgttggtga tcgtgttact 60

attacttgtc gttcttctca aaatattgtt cattctaatg gtaatactta tcttgattgg 120

tatcaacaaa ctcctggtaa agctcctaaa cttcttattt ataaagtttc taatcgtttt 180

tctggtgttc cttctcgttt ttctggttct ggttctggta ctgattttac ttttactatt 240

tcttctcttc aacctgaaga tattgctact tattattgtt ttcaatattc tcatgttcct 300

tggacttttg gtcaaggtac taaacttcaa attact 336

<210> 27
<211> 219
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 27

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 Ser Ser Gln Asn Ile Val His Ser
20 25 30

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

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

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

Ser His Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Leu Gln Ile Thr
100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
130 135 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
180 185 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 28
<211> 112
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 28

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 Ser Ser Gln Asn Ile Val His Ser
20 25 30

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

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

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

Ser His Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Leu Gln Ile Thr
100 105 110

<210> 29
<211> 1359
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 29
caagttcaac ttcaacaatc tggtgctgaa gttaaaaaac ctggttcttc tgttaaagtt 60

tcttgtaaag cctctggtta tacttttact aattattata tttattgggt tcgtcaagct 120

cctggtcaag gtcttgaatg gattggtggt attaatccta cttctggtgg ttctaatttt 180

aatgaaaaat ttaaaactcg tgttactatt actgttgatg aatctacgaa cactgcttat 240

atggaacttt cttctcttcg ttctgaagat actgcttttt atttttgtgc gcgtcaaggt 300

ctttggtttg attctgatgg tcgtggtttt gatttttggg gtcaaggttc cactgttact 360

gtctcgagcg ctagcaccaa gggcccatcg gtcttccccc tggcaccctc ctccaagagc 420

acctctgggg gcacagcggc cctgggctgc ctggtcaagg actacttccc cgaaccggtg 480

acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta 540

cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc 600

acccagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaga 660

gttgagccca aatcttgtga caaaactcac acatgcccac cgtgcccagc acctgaactc 720

ctgggggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 780

cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 840

ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 900

cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 960

aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1020

accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gcccccatcc 1080

cgggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatccc 1140

agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1200

cctcccgtgc tggactccga cggctccttc ttcctctata gcaagctcac cgtggacaag 1260

agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1320

cactacacgc agaagagcct ctccctgtct ccgggtaaa 1359

<210> 30
<211> 369
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 30
caagttcaac ttcaacaatc tggtgctgaa gttaaaaaac ctggttcttc tgttaaagtt 60

tcttgtaaag cctctggtta tacttttact aattattata tttattgggt tcgtcaagct 120

cctggtcaag gtcttgaatg gattggtggt attaatccta cttctggtgg ttctaatttt 180

aatgaaaaat ttaaaactcg tgttactatt actgttgatg aatctacgaa cactgcttat 240

atggaacttt cttctcttcg ttctgaagat actgcttttt atttttgtgc gcgtcaaggt 300

ctttggtttg attctgatgg tcgtggtttt gatttttggg gtcaaggttc cactgttact 360

gtctcgagc 369

<210> 31
<211> 453
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 31

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

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

Gly Gly Ile Asn Pro Thr Ser Gly Gly Ser Asn Phe Asn Glu Lys Phe
    50                  55                  60

Lys Thr Arg Val Thr Ile Thr Val Asp Glu Ser Thr Asn Thr Ala Tyr
65                  70                  75                  80

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

Ala Arg Gln Gly Leu Trp Phe Asp Ser Asp Gly Arg Gly Phe Asp Phe
            100                 105                 110

Trp Gly Gln Gly Ser Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

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

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

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

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
225                 230                 235                 240

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

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300
```

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305 310 315 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
325 330 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
340 345 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
355 360 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
370 375 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385 390 395 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
405 410 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
420 425 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
435 440 445

Leu Ser Pro Gly Lys
450

<210> 32
<211> 123
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 32

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

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

Gly Gly Ile Asn Pro Thr Ser Gly Gly Ser Asn Phe Asn Glu Lys Phe
50 55 60

Lys Thr Arg Val Thr Ile Thr Val Asp Glu Ser Thr Asn Thr Ala Tyr
65 70 75 80

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

Ala Arg Gln Gly Leu Trp Phe Asp Ser Asp Gly Arg Gly Phe Asp Phe
100 105 110

Trp Gly Gln Gly Ser Thr Val Thr Val Ser Ser
115 120

<210> 33
<211> 657
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 33
gatattcaaa tgactcaatc tccttcttct ctttctgctt ctgttggtga tcgtgttact 60

attacttgtc gttcttctca aaatattgtt cattctaatg gtaatactta tcttgattgg 120

tatcaacaaa ctcctggtaa agctcctaaa cttcttattt ataaagtttc taatcgtttt 180

tctggtgttc cttctcgttt ttctggttct ggttctggta ctgattttac ttttactatt 240

tcttctcttc aacctgaaga tattgctact tattattgtt ttcaatattc tcatgttcct 300

tggacttttg gtcaaggtac taaacttcaa attactcgta cggtggctgc accatctgtc 360

ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg 420

ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa 480

tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc 540

agcagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 600

gtcacccatc agggcctgag ctcgcccgtc acaaagagct tcaacagggg agagtgt 657

<210> 34
<211> 336
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 34
gatattcaaa tgactcaatc tccttcttct ctttctgctt ctgttggtga tcgtgttact 60

attacttgtc gttcttctca aaatattgtt cattctaatg gtaatactta tcttgattgg 120

tatcaacaaa ctcctggtaa agctcctaaa cttcttattt ataaagtttc taatcgtttt 180

tctggtgttc cttctcgttt ttctggttct ggttctggta ctgattttac ttttactatt 240

tcttctcttc aacctgaaga tattgctact tattattgtt ttcaatattc tcatgttcct 300

tggacttttg gtcaaggtac taaacttcaa attact 336

<210> 35
<211> 218
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 35

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

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
20 25 30

Asn Phe Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
35 40 45

Met Ile Tyr Asp Val Ser Asp Arg Pro Ser Gly Val Ser Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Ile Ile Ser Gly Leu
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Gly Ser Ser
85 90 95

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

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
115 120 125

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
180 185 190

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
195 200 205

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 36
<211> 111
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 36

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

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
20 25 30

Asn Phe Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
35 40 45

Met Ile Tyr Asp Val Ser Asp Arg Pro Ser Gly Val Ser Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Ile Ile Ser Gly Leu
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Gly Ser Ser
85 90 95

Ser Thr His Val Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 37
<211> 1356
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 37
caggtgcagc tgcagcagag cggcgccgag gtgaagaagc ccggcagcag cgtgaaggtg 60

agctgcaagg ccagcggcta caccttcacc aactactaca tctactgggt gcggcaggcc 120

cccggccagg gcctggagtg gatcggcggc atcaacccca ccagcggcgg cagcaacttc 180

aacgagaagt tcaagacccg ggtgaccatc accgccgacg agagcagcac caccgcctac 240

atggagctga gcagcctgcg gagcgaggac accgccttct acttctgcac ccggcagggc 300

ctgtggttcg acagcgacgg ccggggcttc gacttctggg gccagggcac caccgtgacc 360

gtgagcagcg ctagcaccaa gggcccatcg gtcttccccc tggcaccctc ctccaagagc 420

acctctgggg gcacagcggc cctgggctgc ctggtcaagg actacttccc cgaaccggtg 480

acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta 540

cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc 600

acccagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaga 660

gttgagccca aatcttgtga caaaactcac acatgcccac cgtgcccagc acctgaactc 720

ctggggggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 780

cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 840

ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 900

cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 960

aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1020

accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gcccccatcc 1080

cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatccc 1140

agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1200

cctcccgtgc tggactccga cggctccttc ttcctctata gcaagctcac cgtggacaag 1260

agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1320

cactacacgc agaagagcct ctccctgtct ccgggt 1356

<210> 38
<211> 369
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 38
caggtgcagc tgcagcagag cggcgccgag gtgaagaagc ccggcagcag cgtgaaggtg 60

agctgcaagg ccagcggcta caccttcacc aactactaca tctactgggt gcggcaggcc 120

cccggccagg gcctggagtg gatcggcggc atcaacccca ccagcggcgg cagcaacttc 180

aacgagaagt tcaagacccg ggtgaccatc accgccgacg agagcagcac caccgcctac 240

atggagctga gcagcctgcg gagcgaggac accgccttct acttctgcac ccggcagggc 300

ctgtggttcg acagcgacgg ccggggcttc gacttctggg gccagggcac caccgtgacc 360

gtgagcagc 369

<210> 39
<211> 452
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 39

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

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

Gly Gly Ile Asn Pro Thr Ser Gly Gly Ser Asn Phe Asn Glu Lys Phe
    50                  55                  60

Lys Thr Arg Val Thr Ile Thr Ala Asp Glu Ser Ser Thr Thr Ala Tyr
65                  70                  75                  80

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

Thr Arg Gln Gly Leu Trp Phe Asp Ser Asp Gly Arg Gly Phe Asp Phe
            100                 105                 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

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

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

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

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
225                 230                 235                 240

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

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300
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Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305 310 315 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
325 330 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
340 345 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
355 360 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
370 375 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385 390 395 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
405 410 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
420 425 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
435 440 445

Leu Ser Pro Gly
450

<210> 40
<211> 123
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 40

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

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

Gly Gly Ile Asn Pro Thr Ser Gly Gly Ser Asn Phe Asn Glu Lys Phe
50 55 60

Lys Thr Arg Val Thr Ile Thr Ala Asp Glu Ser Ser Thr Thr Ala Tyr
65 70 75 80

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

Thr Arg Gln Gly Leu Trp Phe Asp Ser Asp Gly Arg Gly Phe Asp Phe
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 41
<211> 642
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 41
gacatcttgc tgactcagtc tccagtcatc ctgtctgtga gtccaggaga aagagtcagt 60

ttctcctgca gggccagtca gagtattggc acaaacatac actggtatca gcaaagaaca 120

aatggttctc caaggcttct cataaagtat gcttctgagt ctatctctgg gattccttcc 180

aggtttagtg gcagtggatc agggacagat tttactctta gcatcaacag tgtggagtct 240

gaagatattg cagattatta ctgtcaacaa aataataact ggccaaccac gttcggtgct 300

gggaccaagc tggagctgaa acgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 42
<211> 321
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 42
gacatcttgc tgactcagtc tccagtcatc ctgtctgtga gtccaggaga aagagtcagt 60

ttctcctgca gggccagtca gagtattggc acaaacatac actggtatca gcaaagaaca 120

aatggttctc caaggcttct cataaagtat gcttctgagt ctatctctgg gattccttcc 180

aggtttagtg gcagtggatc agggacagat tttactctta gcatcaacag tgtggagtct 240

gaagatattg cagattatta ctgtcaacaa aataataact ggccaaccac gttcggtgct 300

gggaccaagc tggagctgaa a 321

<210> 43
<211> 214
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 43

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

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

Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
35 40 45

Lys Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Ser Val Glu Ser
65 70 75 80

Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
85 90 95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Val Ala Ala
100 105 110

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

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 44
<211> 107

<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 44

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

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

Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
35 40 45

Lys Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Ser Val Glu Ser
65 70 75 80

Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
85 90 95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105

<210> 45
<211> 1347
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 45
caggtgcagc tgaagcagtc aggacctggc ctagtgcagc cctcacagag cctgtccatc 60

acctgcacag tctctggttt ctcattaact aactatggtg tacactgggt tcgccagtct 120

ccaggaaagg gtctggagtg gctgggagtg atatggagtg gtggaaacac agactataat 180

acacctttca catccagact gagcatcaac aaggacaatt ccaagagcca agttttcttt 240

aaaatgaaca gtctgcaatc taatgacaca gccatatatt actgtgccag agccctcacc 300

tactatgatt acgagtttgc ttactggggc caagggactc tggtcactgt ctctagcgct 360

agcaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420

acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480

aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600

atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagagagt tgagcccaaa 660

tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 720

tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780

gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840

gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900

acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960

tacaagtgca aggtctccaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1020

gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggaggagatg 1080

accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200

gactccgacg gctccttctt cctctatagc aagctcaccg tggacaagag caggtggcag 1260

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320

aagagcctct ccctgtctcc gggtaaa 1347

<210> 46
<211> 357
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 46
caggtgcagc tgaagcagtc aggacctggc ctagtgcagc cctcacagag cctgtccatc 60

acctgcacag tctctggttt ctcattaact aactatggtg tacactgggt tcgccagtct 120

ccaggaaagg gtctggagtg gctgggagtg atatggagtg gtggaaacac agactataat 180

acacctttca catccagact gagcatcaac aaggacaatt ccaagagcca agttttcttt 240

aaaatgaaca gtctgcaatc taatgacaca gccatatatt actgtgccag agccctcacc 300

tactatgatt acgagtttgc ttactggggc caagggactc tggtcactgt ctctagc 357

<210> 47
<211> 449
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 47

Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
1 5 10 15

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

Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

```
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50                  55                  60

Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65                  70                  75                  80

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

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

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190

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

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
```

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
325 330 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
340 345 350

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385 390 395 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445

Lys

<210> 48
<211> 119
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 48

Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
1 5 10 15

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

Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
50 55 60

Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65 70 75 80

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

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

Thr Leu Val Thr Val Ser Ser
115

<210> 49
<211> 654
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 49
cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc gatcaccatc 60

tcctgcactg gaaccagcag tgacgttggt ggttataact ttgtctcctg gtaccaacaa 120

cacccaggca aagcccccaa actcatgatc tatgatgtca gtgatcggcc ctcaggggtg 180

tctgatcgct tctccggctc caagtctggc aacacggcct ccctgatcat ctctggcctc 240

caggctgacg acgaggctga ttattactgc agctcatatg ggagcagcag cactcatgtg 300

attttcggcg gagggaccaa gctgaccgtc ctacgtacgg tggctgcacc atctgtcttc 360

atcttcccgc catctgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgctg 420

aataacttct atcccagaga ggccaaagta cagtggaagg tggataacgc cctccaatcg 480

ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcagc 540

agcaccctga cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc 600

acccatcagg gcctgagctc gcccgtcaca aagagcttca acaggggaga gtgt 654

<210> 50
<211> 333
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 50
cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc gatcaccatc 60

tcctgcactg gaaccagcag tgacgttggt ggttataact ttgtctcctg gtaccaacaa 120

cacccaggca aagcccccaa actcatgatc tatgatgtca gtgatcggcc ctcaggggtg 180

tctgatcgct tctccggctc caagtctggc aacacggcct ccctgatcat ctctggcctc 240

caggctgacg acgaggctga ttattactgc agctcatatg ggagcagcag cactcatgtg 300

attttcggcg gagggaccaa gctgaccgtc cta 333

<210> 51
<211> 218
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 51

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

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
20 25 30

Asn Phe Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
35 40 45

Met Ile Tyr Asp Val Ser Asp Arg Pro Ser Gly Val Ser Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Ile Ile Ser Gly Leu
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Gly Ser Ser
85 90 95

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

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
115 120 125

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
180 185 190

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
195 200 205

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 52
<211> 111
<212> PRT
<213> artificial sequence

<220>

<223> Synthesized

<400> 52

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

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
20 25 30

Asn Phe Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
35 40 45

Met Ile Tyr Asp Val Ser Asp Arg Pro Ser Gly Val Ser Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Ile Ile Ser Gly Leu
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Gly Ser Ser
85 90 95

Ser Thr His Val Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 53
<211> 2100
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 53
caggtgcagc tgcaggagtc ggggggaggc ctggtcaagc ctggagggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagt agttattgga tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtggccaac ataaaccgcg atggaagtgc gagttactat 180

gtggactctg tgaagggccg attcaccatc tccagagacg acgccaagaa ctcactgtat 240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gagagatcgt 300

ggggtgggct acttcgatct ctggggccgt ggcaccctgg tcaccgtctc gagcgctagc 360

accaagggcc catcggtctt cccctggca ccctcctcca agagcacctc tgggggcaca 420

gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600

tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agagagttga gcccaaatct 660

tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 720

gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 780

acatgcgtgg tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840

gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 900

taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960

aagtgcaagg tctccaacaa agccctccca gcccccatcg agaaaaccat ctccaaagcc 1020

aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc 1080

aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1140

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200

tccgacggct ccttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag 1260

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320

agcctctccc tgtctccggg taaaggcggt ggaggatccg gcggtggtgg atcacaggtg 1380

cagctgcagg agtcgggccc aggactggtg aagccttcgg agaccctgtc cctcacctgc 1440

actgtctctg gtggctccgt cagcagtggt gattactact ggacctggat acggcagtcc 1500

ccagggaagg gactggagtg gattggacac atctattaca gtgggaacac caattataac 1560

ccctccctca agagccgact caccatatca attgacacgt ccaagactca gttctccctg 1620

aagctgagtt ctgtgaccgc tgcggacacg gccatttatt actgtgtgcg agatcgagtg 1680

actggtgctt ttgatatctg gggccaaggg acaatggtca ccgtctcgag cggtggaggc 1740

ggttcaggcg gaggtggttc cggcggtggc ggctccgaca tccagatgac ccagtctcca 1800

tcctccctgt ctgcatctgt aggagacaga gtcaccatca cttgccaggc gagtcaggac 1860

atcagcaact atttaaattg gtatcagcag aaaccaggga aagcccctaa actcctgatc 1920

tacgatgcat ccaatttgga aacaggggtc ccatcaaggt tcagtggaag tggatctggg 1980

acagatttta ctttcaccat cagcagcctg cagcctgaag atattgcaac atatttctgt 2040

caacactttg atcatctccc gctcgctttc ggcggaggga ccaaggtgga aattaaacgt 2100

<210> 54
<211> 354
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 54
caggtgcagc tgcaggagtc ggggggaggc ctggtcaagc ctggagggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagt agttattgga tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtggccaac ataaaccgcg atggaagtgc gagttactat 180

gtggactctg tgaagggccg attcaccatc tccagagacg acgccaagaa ctcactgtat 240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gagagatcgt 300

ggggtgggct acttcgatct ctggggccgt ggcaccctgg tcaccgtctc gagc 354

<210> 55
<211> 726

<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 55
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60

acctgcactg tctctggtgg ctccgtcagc agtggtgatt actactggac ctggatacgg 120

cagtccccag ggaagggact ggagtggatt ggacacatct attacagtgg gaacaccaat 180

tataacccct ccctcaagag ccgactcacc atatcaattg acacgtccaa gactcagttc 240

tccctgaagc tgagttctgt gaccgctgcg gacacggcca tttattactg tgtgcgagat 300

cgagtgactg gtgcttttga tatctggggc caagggacaa tggtcaccgt ctcgagcggt 360

ggaggcggtt caggcggagg tggttccggc ggtggcggct ccgacatcca gatgacccag 420

tctccatcct ccctgtctgc atctgtagga gacagagtca ccatcacttg ccaggcgagt 480

caggacatca gcaactattt aaattggtat cagcagaaac cagggaaagc ccctaaactc 540

ctgatctacg atgcatccaa tttggaaaca ggggtcccat caaggttcag tggaagtgga 600

tctgggacag attttacttt caccatcagc agcctgcagc ctgaagatat tgcaacatat 660

ttctgtcaac actttgatca tctcccgctc gctttcggcg gagggaccaa ggtggaaatt 720

aaacgt 726

<210> 56
<211> 700
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 56

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ala Asn Ile Asn Arg Asp Gly Ser Ala Ser Tyr Tyr Val Asp Ser Val
50 55 60

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

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

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

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115                 120                 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
    130                 135                 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                 150                 155                 160

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

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190

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

Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr
    210                 215                 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
225                 230                 235                 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245                 250                 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            260                 265                 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275                 280                 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
    290                 295                 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305                 310                 315                 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
                325                 330                 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
            340                 345                 350

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

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

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
                405                 410                 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            420                 425                 430

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

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu
    450                 455                 460

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

Thr Val Ser Gly Gly Ser Val Ser Ser Gly Asp Tyr Tyr Trp Thr Trp
                485                 490                 495

Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile Gly His Ile Tyr
            500                 505                 510

Tyr Ser Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr
        515                 520                 525

Ile Ser Ile Asp Thr Ser Lys Thr Gln Phe Ser Leu Lys Leu Ser Ser
    530                 535                 540

Val Thr Ala Ala Asp Thr Ala Ile Tyr Tyr Cys Val Arg Asp Arg Val
545                 550                 555                 560

Thr Gly Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser
                565                 570                 575

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            580                 585                 590

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

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
    610                 615                 620

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
625                 630                 635                 640
```

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
645 650 655

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
660 665 670

Glu Asp Ile Ala Thr Tyr Phe Cys Gln His Phe Asp His Leu Pro Leu
675 680 685

Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
690 695 700

<210> 57
<211> 118
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 57

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ala Asn Ile Asn Arg Asp Gly Ser Ala Ser Tyr Tyr Val Asp Ser Val
50 55 60

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

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

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

Leu Val Thr Val Ser Ser
115

<210> 58
<211> 242
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 58

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Val Ser Ser Gly
            20                  25                  30

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

Trp Ile Gly His Ile Tyr Tyr Ser Gly Asn Thr Asn Tyr Asn Pro Ser
    50                  55                  60

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

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Ile Tyr Tyr
                85                  90                  95

Cys Val Arg Asp Arg Val Thr Gly Ala Phe Asp Ile Trp Gly Gln Gly
            100                 105                 110

Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125

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

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ala Ser
145                 150                 155                 160

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

Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val
            180                 185                 190

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

Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln His
    210                 215                 220

Phe Asp His Leu Pro Leu Ala Phe Gly Gly Gly Thr Lys Val Glu Ile
225                 230                 235                 240

Lys Arg
```

<210> 59
<211> 642
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 59
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc aggcgagtca ggacatcagc aactatttaa attggtatca gcagaaacca 120

gggaaagccc ctaaactcct gatctacgat gcatccaatt tggaaacagg ggtcccatca 180

aggttcagtg gaagtggatc tgggacagat tttactttca ccatcagcag cctgcagcct 240

gaagatattg caacatattt ctgtcaacac tttgatcatc tcccgctcgc tttcggcgga 300

gggaccaagg tggaaattaa acgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 60
<211> 321
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 60
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc aggcgagtca ggacatcagc aactatttaa attggtatca gcagaaacca 120

gggaaagccc ctaaactcct gatctacgat gcatccaatt tggaaacagg ggtcccatca 180

aggttcagtg gaagtggatc tgggacagat tttactttca ccatcagcag cctgcagcct 240

gaagatattg caacatattt ctgtcaacac tttgatcatc tcccgctcgc tttcggcgga 300

gggaccaagg tggaaattaa a 321

<210> 61
<211> 214
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 61

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 Gln Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

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

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

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

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

Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

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

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 62
<211> 107
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 62

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 Gln Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

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

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

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

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

Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 63
<211> 2109
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 63
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60

acctgcactg tctctggtgg ctccgtcagc agtggtgatt actactggac ctggatccgg 120

cagtccccag ggaagggact ggagtggatt ggacacatct attacagtgg gaacaccaat 180

tataacccct ccctcaagag ccgactcacc atatcaattg acacgtccaa gactcagttc 240

tccctgaagc tgagttctgt gaccgctgcg gacacggcca tttattactg tgtgcgagat 300

cgagtgactg gtgcttttga tatctggggc caagggacaa tggtcaccgt ctcgagcgct 360

agcaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420

acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480

aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600

atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagagagt tgagcccaaa 660

tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 720

tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780

gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840

gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900

acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960

tacaagtgca aggtctccaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1020

gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggaggagatg 1080

accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200

gactccgacg gctccttctt cctctatagc aagctcaccg tggacaagag caggtggcag 1260

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320

aagagcctct ccctgtctcc gggtaaaggc ggtggaggat ccggcggtgg tggatcacag 1380

gtgcagctgc aggagtcggg gggaggcctg gtcaagcctg gagggtccct gagactctcc 1440

tgtgcagcct ctggattcac ctttagtagt tattggatga gctgggtccg ccaggctcca 1500

gggaaggggc tggagtgggt ggccaacata aaccgcgatg gaagtgcgag ttactatgtg 1560

gactctgtga agggccgatt caccatctcc agagacgacg ccaagaactc actgtatctg 1620

caaatgaaca gcctgagagc tgaggacacg gctgtgtatt actgtgcgag agatcgtggg 1680

gtgggctact tcgatctctg gggccgtggc accctggtca ccgtctcgag cggtggaggc 1740

ggttcaggcg gaggtggttc cggcggtggc ggctcccagt ctgccctgac tcagcctgcc 1800

tccgtgtctg ggtctcctgg acagtcgatc accatctcct gcactggaac cagcagtgac 1860

gttggtggtt ataactttgt ctcctggtac caacaacacc caggcaaagc ccccaaactc 1920

atgatctatg atgtcagtga tcggccctca ggggtgtctg atcgcttctc cggctccaag 1980

tctggcaaca cggcctccct gatcatctct ggcctccagg ctgacgacga ggctgattat 2040

tactgcagct catatgggag cagcagcact catgtgattt tcggcggagg gaccaaggtg 2100

accgtccta 2109

<210> 64
<211> 357
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 64
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60

acctgcactg tctctggtgg ctccgtcagc agtggtgatt actactggac ctggatccgg 120

cagtccccag ggaagggact ggagtggatt ggacacatct attacagtgg gaacaccaat 180

tataacccct ccctcaagag ccgactcacc atatcaattg acacgtccaa gactcagttc 240

tccctgaagc tgagttctgt gaccgctgcg gacacggcca tttattactg tgtgcgagat 300

cgagtgactg gtgcttttga tatctggggc caagggacaa tggtcaccgt ctcgagc 357

<210> 65
<211> 732
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 65
caggtgcagc tgcaggagtc ggggggaggc ctggtcaagc ctggagggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagt agttattgga tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtggccaac ataaaccgcg atggaagtgc gagttactat 180

gtggactctg tgaagggccg attcaccatc tccagagacg acgccaagaa ctcactgtat 240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gagagatcgt 300

ggggtgggct acttcgatct ctggggccgt ggcaccctgg tcaccgtctc gagcggtgga 360

ggcggttcag gcggaggtgg ttccggcggt ggcggctccc agtctgccct gactcagcct 420

gcctccgtgt ctgggtctcc tggacagtcg atcaccatct cctgcactgg aaccagcagt 480

gacgttggtg gttataactt tgtctcctgg taccaacaac acccaggcaa agcccccaaa 540

ctcatgatct atgatgtcag tgatcggccc tcaggggtgt ctgatcgctt ctccggctcc 600

aagtctggca acacggcctc cctgatcatc tctggcctcc aggctgacga cgaggctgat 660

tattactgca gctcatatgg gagcagcagc actcatgtga ttttcggcgg agggaccaag 720

gtgaccgtcc ta 732

<210> 66
<211> 703
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 66

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Val Ser Ser Gly
20 25 30

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

Trp Ile Gly His Ile Tyr Tyr Ser Gly Asn Thr Asn Tyr Asn Pro Ser
50 55 60

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

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Ile Tyr Tyr
85 90 95

Cys Val Arg Asp Arg Val Thr Gly Ala Phe Asp Ile Trp Gly Gln Gly
100 105 110

Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
130 135 140

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Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190

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

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415
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Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445

Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
    450                 455                 460

Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly Ser Leu Arg Leu Ser
465                 470                 475                 480

Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Trp Met Ser Trp Val
                485                 490                 495

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Asn Ile Asn Arg
            500                 505                 510

Asp Gly Ser Ala Ser Tyr Tyr Val Asp Ser Val Lys Gly Arg Phe Thr
        515                 520                 525

Ile Ser Arg Asp Asp Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser
    530                 535                 540

Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Arg Gly
545                 550                 555                 560

Val Gly Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val Thr Val Ser
                565                 570                 575

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            580                 585                 590

Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
        595                 600                 605

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
    610                 615                 620

Asn Phe Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
625                 630                 635                 640

Met Ile Tyr Asp Val Ser Asp Arg Pro Ser Gly Val Ser Asp Arg Phe
                645                 650                 655

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Ile Ile Ser Gly Leu
            660                 665                 670

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Gly Ser Ser
        675                 680                 685
```

Ser Thr His Val Ile Phe Gly Gly Gly Thr Lys Val Thr Val Leu
690 695 700

<210> 67
<211> 119
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 67

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Val Ser Ser Gly
20 25 30

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

Trp Ile Gly His Ile Tyr Tyr Ser Gly Asn Thr Asn Tyr Asn Pro Ser
50 55 60

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

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Ile Tyr Tyr
85 90 95

Cys Val Arg Asp Arg Val Thr Gly Ala Phe Asp Ile Trp Gly Gln Gly
100 105 110

Thr Met Val Thr Val Ser Ser
115

<210> 68
<211> 243
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 68

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ala Asn Ile Asn Arg Asp Gly Ser Ala Ser Tyr Tyr Val Asp Ser Val
50 55 60

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

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

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

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

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

Gly Ser Pro Gly Gln Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser
145 150 155 160

Asp Val Gly Gly Tyr Asn Phe Val Ser Trp Tyr Gln Gln His Pro Gly
165 170 175

Lys Ala Pro Lys Leu Met Ile Tyr Asp Val Ser Asp Arg Pro Ser Gly
180 185 190

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

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

Ser Tyr Gly Ser Ser Ser Thr His Val Ile Phe Gly Gly Gly Thr Lys
225 230 235 240

Val Thr Val

<210> 69
<211> 654
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 69
cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc gatcaccatc 60

tcctgcactg gaaccagcag tgacgttggt ggttataact ttgtctcctg gtaccaacaa 120

cacccaggca aagcccccaa actcatgatc tatgatgtca gtgatcggcc ctcaggggtg 180

tctgatcgct tctccggctc caagtctggc aacacggcct ccctgatcat ctctggcctc 240

caggctgacg acgaggctga ttattactgc agctcatatg ggagcagcag cactcatgtg 300

attttcggcg gagggaccaa gctgaccgtc ctacgtacgg tggctgcacc atctgtcttc 360

atcttcccgc catctgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgctg 420

aataacttct atcccagaga ggccaaagta cagtggaagg tggataacgc cctccaatcg 480

ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcagc 540

agcaccctga cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc 600

acccatcagg gcctgagctc gcccgtcaca aagagcttca acaggggaga gtgt 654

<210> 70
<211> 333
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 70
cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc gatcaccatc 60

tcctgcactg gaaccagcag tgacgttggt ggttataact ttgtctcctg gtaccaacaa 120

cacccaggca aagcccccaa actcatgatc tatgatgtca gtgatcggcc ctcaggggtg 180

tctgatcgct tctccggctc caagtctggc aacacggcct ccctgatcat ctctggcctc 240

caggctgacg acgaggctga ttattactgc agctcatatg ggagcagcag cactcatgtg 300

attttcggcg gagggaccaa gctgaccgtc cta 333

<210> 71
<211> 218
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 71

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

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
20 25 30

Asn Phe Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
35 40 45

Met Ile Tyr Asp Val Ser Asp Arg Pro Ser Gly Val Ser Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Ile Ile Ser Gly Leu
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Gly Ser Ser
85 90 95

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

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
115 120 125

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
180 185 190

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
195 200 205

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 72
<211> 111
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 72

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

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
20 25 30

Asn Phe Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
35 40 45

Met Ile Tyr Asp Val Ser Asp Arg Pro Ser Gly Val Ser Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Ile Ile Ser Gly Leu
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Gly Ser Ser
85 90 95

Ser Thr His Val Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 73
<211> 2127
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 73
caggtgcagc tgcaggagtc gggggggaggc ctggtcaagc ctggagggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagt agttattgga tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtggccaac ataaaccgcg atggaagtgc gagttactat 180

gtggactctg tgaagggccg attcaccatc tccagagacg acgccaagaa ctcactgtat 240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gagagatcgt 300

ggggtgggct acttcgatct ctggggccgt ggcaccctgg tcaccgtctc gagcgctagc 360

accaagggcc catcggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca 420

gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600

tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agagagttga gcccaaatct 660

tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 720

gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 780

acatgcgtgg tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840

gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 900

taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960

aagtgcaagg tctccaacaa agccctccca gcccccatcg agaaaaccat ctccaaagcc 1020

aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc 1080

aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1140

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200

tccgacggct ccttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag 1260

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320

agcctctccc tgtctccggg taaaggcggt ggaggatccg gcggtggtgg atcacaagtt 1380

caacttcaac aatctggtgc tgaagttaaa aaacctggtt cttctgttaa agtttcttgt 1440

aaagcctctg gttatacttt tactaattat tatatttatt gggttcgtca agctcctggt 1500

caaggtcttg aatggattgg tggtattaat cctacttctg gtggttctaa ttttaatgaa 1560

aaatttaaaa ctcgtgttac tattactgtt gatgaatcta cgaacactgc ttatatggaa 1620

ctttcttctc ttcgttctga agatactgct ttttattttt gtgcgcgtca aggtctttgg 1680

tttgattctg atggtcgtgg ttttgatttt tggggtcaag gttccactgt tactgtctcg 1740

agcggtggag gcggttcagg cggaggtggt tccggcggtg gcggctccga tattcaaatg 1800

actcaatctc cttcttctct ttctgcttct gttggtgatc gtgttactat tacttgtcgt 1860

tcttctcaaa atattgttca ttctaatggt aatacttatc ttgattggta tcaacaaact 1920

cctggtaaag ctcctaaact tcttatttat aaagtttcta atcgtttttc tggtgttcct 1980

tctcgttttt ctggttctgg ttctggtact gattttactt ttactatttc ttctcttcaa 2040

cctgaagata ttgctactta ttattgtttt caatattctc atgttccttg gacttttggt 2100

caaggtacta aacttcaaat tactcgt 2127

<210> 74
<211> 354
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 74
caggtgcagc tgcaggagtc ggggggaggc ctggtcaagc ctggagggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagt agttattgga tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtggccaac ataaaccgcg atggaagtgc gagttactat 180

gtggactctg tgaagggccg attcaccatc tccagagacg acgccaagaa ctcactgtat 240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gagagatcgt 300

ggggtgggct acttcgatct ctggggccgt ggcaccctgg tcaccgtctc gagc 354

<210> 75
<211> 753
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 75
caagttcaac ttcaacaatc tggtgctgaa gttaaaaaac ctggttcttc tgttaaagtt 60

tcttgtaaag cctctggtta tacttttact aattattata tttattgggt tcgtcaagct 120

cctggtcaag gtcttgaatg gattggtggt attaatccta cttctggtgg ttctaatttt 180

aatgaaaaat ttaaaactcg tgttactatt actgttgatg aatctacgaa cactgcttat 240

atggaacttt cttctcttcg ttctgaagat actgcttttt atttttgtgc gcgtcaaggt 300

ctttggtttg attctgatgg tcgtggtttt gatttttggg gtcaaggttc cactgttact 360

gtctcgagcg gtggaggcgg ttcaggcgga ggtggttccg gcggtggcgg ctccgatatt 420

caaatgactc aatctccttc ttctctttct gcttctgttg gtgatcgtgt tactattact 480

tgtcgttctt ctcaaaatat tgttcattct aatggtaata cttatcttga ttggtatcaa 540

caaactcctg gtaaagctcc taaacttctt atttataaag tttctaatcg tttttctggt 600

gttccttctc gtttttctgg ttctggttct ggtactgatt ttacttttac tatttcttct 660

cttcaacctg aagatattgc tacttattat tgttttcaat attctcatgt tccttggact 720

tttggtcaag gtactaaact tcaaattact cgt 753

<210> 76
<211> 709
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 76

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ala Asn Ile Asn Arg Asp Gly Ser Ala Ser Tyr Tyr Val Asp Ser Val
50 55 60

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

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

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

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

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

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

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

Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr
    210                 215                 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
225                 230                 235                 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245                 250                 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            260                 265                 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275                 280                 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
    290                 295                 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305                 310                 315                 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
                325                 330                 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
            340                 345                 350

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
        355                 360                 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
    370                 375                 380

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

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
                405                 410                 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            420                 425                 430

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

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln
    450                 455                 460
```

Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys
465 470 475 480

Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Tyr Ile Tyr Trp Val Arg
485 490 495

Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Gly Ile Asn Pro Thr
500 505 510

Ser Gly Gly Ser Asn Phe Asn Glu Lys Phe Lys Thr Arg Val Thr Ile
515 520 525

Thr Val Asp Glu Ser Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu
530 535 540

Arg Ser Glu Asp Thr Ala Phe Tyr Phe Cys Ala Arg Gln Gly Leu Trp
545 550 555 560

Phe Asp Ser Asp Gly Arg Gly Phe Asp Phe Trp Gly Gln Gly Ser Thr
565 570 575

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
580 585 590

Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
595 600 605

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ser Ser Gln Asn
610 615 620

Ile Val His Ser Asn Gly Asn Thr Tyr Leu Asp Trp Tyr Gln Gln Thr
625 630 635 640

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe
645 650 655

Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
660 665 670

Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr
675 680 685

Cys Phe Gln Tyr Ser His Val Pro Trp Thr Phe Gly Gln Gly Thr Lys
690 695 700

Leu Gln Ile Thr Arg
705

<210> 77
<211> 118
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 77

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ala Asn Ile Asn Arg Asp Gly Ser Ala Ser Tyr Tyr Val Asp Ser Val
50 55 60

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

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

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

Leu Val Thr Val Ser Ser
115

<210> 78
<211> 251
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 78

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

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

Gly Gly Ile Asn Pro Thr Ser Gly Gly Ser Asn Phe Asn Glu Lys Phe
50 55 60

Lys Thr Arg Val Thr Ile Thr Val Asp Glu Ser Thr Asn Thr Ala Tyr
65 70 75 80

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

Ala Arg Gln Gly Leu Trp Phe Asp Ser Asp Gly Arg Gly Phe Asp Phe
100 105 110

Trp Gly Gln Gly Ser Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln
130 135 140

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

Cys Arg Ser Ser Gln Asn Ile Val His Ser Asn Gly Asn Thr Tyr Leu
165 170 175

Asp Trp Tyr Gln Gln Thr Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
180 185 190

Lys Val Ser Asn Arg Phe Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
195 200 205

Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu
210 215 220

Asp Ile Ala Thr Tyr Tyr Cys Phe Gln Tyr Ser His Val Pro Trp Thr
225 230 235 240

Phe Gly Gln Gly Thr Lys Leu Gln Ile Thr Arg
245 250

<210> 79
<211> 657
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 79
gatattcaaa tgactcaatc tccttcttct ctttctgctt ctgttggtga tcgtgttact 60

attacttgtc gttcttctca aaatattgtt cattctaatg gtaatactta tcttgattgg 120

tatcaacaaa ctcctggtaa agctcctaaa cttcttattt ataaagtttc taatcgtttt 180

tctggtgttc cttctcgttt ttctggttct ggttctggta ctgattttac ttttactatt 240

tcttctcttc aacctgaaga tattgctact tattattgtt ttcaatattc tcatgttcct 300

tggacttttg gtcaaggtac taaacttcaa attactcgta cggtggctgc accatctgtc 360

ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg 420

ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa 480

tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc 540

agcagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 600

gtcacccatc agggcctgag ctcgcccgtc acaaagagct tcaacagggg agagtgt 657

<210> 80
<211> 336
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 80
gatattcaaa tgactcaatc tccttcttct ctttctgctt ctgttggtga tcgtgttact 60

attacttgtc gttcttctca aaatattgtt cattctaatg gtaatactta tcttgattgg 120

tatcaacaaa ctcctggtaa agctcctaaa cttcttattt ataaagtttc taatcgtttt 180

tctggtgttc cttctcgttt ttctggttct ggttctggta ctgattttac ttttactatt 240

tcttctcttc aacctgaaga tattgctact tattattgtt ttcaatattc tcatgttcct 300

tggacttttg gtcaaggtac taaacttcaa attact 336

<210> 81
<211> 219
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 81

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 Ser Ser Gln Asn Ile Val His Ser
20 25 30

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

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

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

Ser His Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Leu Gln Ile Thr
100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
130 135 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
180 185 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 82
<211> 112
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 82

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 Ser Ser Gln Asn Ile Val His Ser
20 25 30

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

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

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

Ser His Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Leu Gln Ile Thr
100 105 110

<210> 83
<211> 2121

<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 83
caagttcaac ttcaacaatc tggtgctgaa gttaaaaaac ctggttcttc tgttaaagtt 60

tcttgtaaag cctctggtta tacttttact aattattata tttattgggt tcgtcaagct 120

cctggtcaag gtcttgaatg gattggtggt attaatccta cttctggtgg ttctaatttt 180

aatgaaaaat ttaaaactcg tgttactatt actgttgatg aatctacgaa cactgcttat 240

atggaacttt cttctcttcg ttctgaagat actgcttttt atttttgtgc gcgtcaaggt 300

ctttggtttg attctgatgg tcgtggtttt gatttttggg gtcaaggttc cactgttact 360

gtctcgagcg ctagcaccaa gggcccatcg gtcttccccc tggcaccctc ctccaagagc 420

acctctgggg gcacagcggc cctgggctgc ctggtcaagg actacttccc cgaaccggtg 480

acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta 540

cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc 600

acccagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaga 660

gttgagccca aatcttgtga caaaactcac acatgcccac cgtgcccagc acctgaactc 720

ctgggggggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 780

cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 840

ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 900

cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 960

aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1020

accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gcccccatcc 1080

cgggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatccc 1140

agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1200

cctcccgtgc tggactccga cggctccttc ttcctctata gcaagctcac cgtggacaag 1260

agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1320

cactacacgc agaagagcct ctccctgtct ccgggtaaag gcggtggagg atccggcggt 1380

ggtggatcac aggtgcagct gcaggagtcg gggggaggcc tggtcaagcc tggagggtcc 1440

ctgagactct cctgtgcagc ctctggattc acctttagta gttattggat gagctgggtc 1500

cgccaggctc cagggaaggg gctggagtgg gtggccaaca taaaccgcga tggaagtgcg 1560

agttactatg tggactctgt gaagggccga ttcaccatct ccagagacga cgccaagaac 1620

tcactgtatc tgcaaatgaa cagcctgaga gctgaggaca cggctgtgta ttactgtgcg 1680

agagatcgtg gggtgggcta cttcgatctc tggggccgtg gcaccctggt caccgtctcg 1740

agcggtggag gcggttcagg cggaggtggt tccggcggtg gcggctccca gtctgccctg 1800

actcagcctg cctccgtgtc tgggtctcct ggacagtcga tcaccatctc ctgcactgga 1860

accagcagtg acgttggtgg ttataacttt gtctcctggt accaacaaca cccaggcaaa 1920

gcccccaaac tcatgatcta tgatgtcagt gatcggccct caggggtgtc tgatcgcttc 1980

tccggctcca agtctggcaa cacggcctcc ctgatcatct ctggcctcca ggctgacgac 2040

gaggctgatt attactgcag ctcatatggg agcagcagca ctcatgtgat tttcggcgga 2100

gggaccaagg tgaccgtcct a 2121

<210> 84
<211> 369
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 84
caagttcaac ttcaacaatc tggtgctgaa gttaaaaaac ctggttcttc tgttaaagtt 60

tcttgtaaag cctctggtta tacttttact aattattata tttattgggt tcgtcaagct 120

cctggtcaag gtcttgaatg gattggtggt attaatccta cttctggtgg ttctaatttt 180

aatgaaaaat ttaaaactcg tgttactatt actgttgatg aatctacgaa cactgcttat 240

atggaacttt cttctcttcg ttctgaagat actgcttttt atttttgtgc gcgtcaaggt 300

ctttggtttg attctgatgg tcgtggtttt gatttttggg gtcaaggttc cactgttact 360

gtctcgagc 369

<210> 85
<211> 732
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 85
caggtgcagc tgcaggagtc gggggggaggc ctggtcaagc ctggagggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagt agttattgga tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtggccaac ataaaccgcg atggaagtgc gagttactat 180

gtggactctg tgaagggccg attcaccatc tccagagacg acgccaagaa ctcactgtat 240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gagagatcgt 300

ggggtgggct acttcgatct ctggggccgt ggcaccctgg tcaccgtctc gagcggtgga 360

ggcggttcag gcggaggtgg ttccggcggt ggcggctccc agtctgccct gactcagcct 420

gcctccgtgt ctgggtctcc tggacagtcg atcaccatct cctgcactgg aaccagcagt 480

gacgttggtg gttataactt tgtctcctgg taccaacaac acccaggcaa agcccccaaa 540

ctcatgatct atgatgtcag tgatcggccc tcaggggtgt ctgatcgctt ctccggctcc 600

aagtctggca acacggcctc cctgatcatc tctggcctcc aggctgacga cgaggctgat 660

tattactgca gctcatatgg gagcagcagc actcatgtga ttttcggcgg agggaccaag 720

gtgaccgtcc ta 732

<210> 86
<211> 707
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 86

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

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

Gly Gly Ile Asn Pro Thr Ser Gly Gly Ser Asn Phe Asn Glu Lys Phe
50 55 60

Lys Thr Arg Val Thr Ile Thr Val Asp Glu Ser Thr Asn Thr Ala Tyr
65 70 75 80

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

Ala Arg Gln Gly Leu Trp Phe Asp Ser Asp Gly Arg Gly Phe Asp Phe
100 105 110

Trp Gly Gln Gly Ser Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
130 135 140

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

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
165 170 175

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

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
195 200 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
210 215 220

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Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
225                 230                 235                 240

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

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445

Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
    450                 455                 460

Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly Ser
465                 470                 475                 480

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Trp
                485                 490                 495
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Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
500 505 510

Asn Ile Asn Arg Asp Gly Ser Ala Ser Tyr Tyr Val Asp Ser Val Lys
515 520 525

Gly Arg Phe Thr Ile Ser Arg Asp Asp Ala Lys Asn Ser Leu Tyr Leu
530 535 540

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
545 550 555 560

Arg Asp Arg Gly Val Gly Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu
565 570 575

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
580 585 590

Gly Gly Gly Ser Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly
595 600 605

Ser Pro Gly Gln Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp
610 615 620

Val Gly Gly Tyr Asn Phe Val Ser Trp Tyr Gln Gln His Pro Gly Lys
625 630 635 640

Ala Pro Lys Leu Met Ile Tyr Asp Val Ser Asp Arg Pro Ser Gly Val
645 650 655

Ser Asp Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Ile
660 665 670

Ile Ser Gly Leu Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ser Ser
675 680 685

Tyr Gly Ser Ser Ser Thr His Val Ile Phe Gly Gly Gly Thr Lys Val
690 695 700

Thr Val Leu
705

<210> 87
<211> 123
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 87

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

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

Gly Gly Ile Asn Pro Thr Ser Gly Gly Ser Asn Phe Asn Glu Lys Phe
50 55 60

Lys Thr Arg Val Thr Ile Thr Val Asp Glu Ser Thr Asn Thr Ala Tyr
65 70 75 80

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

Ala Arg Gln Gly Leu Trp Phe Asp Ser Asp Gly Arg Gly Phe Asp Phe
100 105 110

Trp Gly Gln Gly Ser Thr Val Thr Val Ser Ser
115 120

<210> 88
<211> 244
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 88

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ala Asn Ile Asn Arg Asp Gly Ser Ala Ser Tyr Tyr Val Asp Ser Val
50 55 60

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

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

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

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

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

Gly Ser Pro Gly Gln Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser
145 150 155 160

Asp Val Gly Gly Tyr Asn Phe Val Ser Trp Tyr Gln Gln His Pro Gly
165 170 175

Lys Ala Pro Lys Leu Met Ile Tyr Asp Val Ser Asp Arg Pro Ser Gly
180 185 190

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

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

Ser Tyr Gly Ser Ser Ser Thr His Val Ile Phe Gly Gly Gly Thr Lys
225 230 235 240

Val Thr Val Leu

<210> 89
<211> 657
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 89
gatattcaaa tgactcaatc tccttcttct ctttctgctt ctgttggtga tcgtgttact 60

attacttgtc gttcttctca aaatattgtt cattctaatg gtaatactta tcttgattgg 120

tatcaacaaa ctcctggtaa agctcctaaa cttcttattt ataaagtttc taatcgtttt 180

tctggtgttc cttctcgttt ttctggttct ggttctggta ctgattttac ttttactatt 240

tcttctcttc aacctgaaga tattgctact tattattgtt ttcaatattc tcatgttcct 300

tggacttttg gtcaaggtac taaacttcaa attactcgta cggtggctgc accatctgtc 360

ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg 420

ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa 480

tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc 540

agcagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 600

gtcacccatc agggcctgag ctcgcccgtc acaaagagct tcaacagggg agagtgt 657

<210> 90
<211> 336
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 90
gatattcaaa tgactcaatc tccttcttct ctttctgctt ctgttggtga tcgtgttact 60

attacttgtc gttcttctca aaatattgtt cattctaatg gtaatactta tcttgattgg 120

tatcaacaaa ctcctggtaa agctcctaaa cttcttattt ataaagtttc taatcgtttt 180

tctggtgttc cttctcgttt ttctggttct ggttctggta ctgattttac ttttactatt 240

tcttctcttc aacctgaaga tattgctact tattattgtt ttcaatattc tcatgttcct 300

tggacttttg gtcaaggtac taaacttcaa attact 336

<210> 91
<211> 336
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 91
gacatccaga tgacccagtc cccttccagc ctgtccgctt ccgtgggcga cagggtgacc 60

atcacctgca ggtcctccca gaacatcgtg cactccaacg gcaataccta cctggactgg 120

taccagcaga cccccggcaa ggcccctaag ctgctgatct acaaggtgag caaccggttc 180

agcggcgtgc cttcccggtt ttccggatcc ggctccggca cagacttcac cttcaccatc 240

tcctccctgc aacccgagga catcgccacc tactactgct tccagtactc ccatgtgccc 300

tggaccttcg gccagggcac caagctgcag atcacc 336

<210> 92
<211> 218
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 92

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

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
20 25 30

Asn Phe Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
35 40 45

Met Ile Tyr Asp Val Ser Asp Arg Pro Ser Gly Val Ser Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Ile Ile Ser Gly Leu
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Gly Ser Ser
85 90 95

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

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
115 120 125

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
180 185 190

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
195 200 205

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 93
<211> 111
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 93

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

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
20 25 30

Asn Phe Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
35 40 45

Met Ile Tyr Asp Val Ser Asp Arg Pro Ser Gly Val Ser Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Ile Ile Ser Gly Leu
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Gly Ser Ser
85 90 95

Ser Thr His Val Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 94
<211> 2118
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 94
caggtgcagc tgcagcagag cggcgccgag gtgaagaagc ccggcagcag cgtgaaggtg 60

agctgcaagg ccagcggcta caccttcacc aactactaca tctactgggt gcggcaggcc 120

cccggccagg gcctggagtg gatcggcggc atcaacccca ccagcggcgg cagcaacttc 180

aacgagaagt tcaagacccg ggtgaccatc accgccgacg agagcagcac caccgcctac 240

atggagctga gcagcctgcg gagcgaggac accgccttct acttctgcac ccggcagggc 300

ctgtggttcg acagcgacgg ccggggcttc gacttctggg gccagggcac caccgtgacc 360

gtgagcagcg ctagcaccaa gggcccatcg gtcttccccc tggcaccctc ctccaagagc 420

acctctgggg gcacagcggc cctgggctgc ctggtcaagg actacttccc cgaaccggtg 480

acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta 540

cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc 600

acccagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaga 660

gttgagccca aatcttgtga caaaactcac acatgcccac cgtgcccagc acctgaactc 720

ctgggggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 780

cggaccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 840

ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 900

cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 960

aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1020

accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gcccccatcc 1080

cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatccc 1140

agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1200

cctcccgtgc tggactccga cggctccttc ttcctctata gcaagctcac cgtggacaag 1260

agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1320

cactacacgc agaagagcct ctccctgtct ccgggtggcg gtggagggtc cggcggtggt 1380

ggatcacagg tgcaattgca ggagtcgggg ggaggcctgg tcaagcctgg agggtccctg 1440

agactctcct gtgcagcctc tggattcacc tttagtagtt attggatgag ctgggtccgc 1500

caggctccag ggaaggggct ggagtgggtg gccaacataa accgcgatgg aagtgcgagt 1560

tactatgtgg actctgtgaa gggccgattc accatctcca gagacgacgc caagaactca 1620

ctgtatctgc aaatgaacag cctgagagct gaggacacgg ctgtgtatta ctgtgcgaga 1680

gatcgtgggg tgggctactt cgatctctgg ggccgtggca ccctggtcac cgtctcgagc 1740

ggtggaggcg gttcaggcgg aggtggttcc ggcggtggcg gctcccagtc tgccctgact 1800

cagcctgcct ccgtgtctgg gtctcctgga cagtcgatca ccatctcctg cactggaacc 1860

agcagtgacg ttggtggtta taactttgtc tcctggtacc aacaacaccc aggcaaagcc 1920

cccaaactca tgatctatga tgtcagtgat cggccctcag gggtgtctga tcgcttctcc 1980

ggctccaagt ctggcaacac ggcctccctg atcatctctg gcctccaggc tgacgacgag 2040

gctgattatt actgcagctc atatgggagc agcagcactc atgtgatttt cggcggaggg 2100

accaaggtga ccgtccta 2118

<210> 95
<211> 369
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 95
caggtgcagc tgcagcagag cggcgccgag gtgaagaagc ccggcagcag cgtgaaggtg 60

agctgcaagg ccagcggcta caccttcacc aactactaca tctactgggt gcggcaggcc 120

cccggccagg gcctggagtg gatcggcggc atcaacccca ccagcggcgg cagcaacttc 180

aacgagaagt tcaagacccg ggtgaccatc accgccgacg agagcagcac caccgcctac 240

atggagctga gcagcctgcg gagcgaggac accgccttct acttctgcac ccggcagggc 300

ctgtggttcg acagcgacgg ccggggcttc gacttctggg gccagggcac caccgtgacc 360

gtgagcagc 369

<210> 96
<211> 369
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 96
caggtgcagc tgcagcaatc cggcgccgag gtgaagaagc ctggctccag cgtgaaggtg 60

tcctgcaagg cctccggcta caccttcacc aactactaca tctactgggt gaggcaggct 120

cctggccagg gactggagtg gatcggcggc atcaacccta cctccggcgg ctccaacttc 180

aacgagaagt tcaagacccg ggtgaccatc accgccgatg agagctccac caccgcctac 240

atggagctgt cctccctgag gtccgaggac accgcctttt acttctgcac caggcaggga 300

ctgtggttcg actccgacgg ccggggcttc gatttttggg gccagggcac cacagtgacc 360

gtgtcctcc 369

<210> 97
<211> 732
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 97
caggtgcaat tgcaggagtc gggggggaggc ctggtcaagc ctggagggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagt agttattgga tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtggccaac ataaaccgcg atggaagtgc gagttactat 180

gtggactctg tgaagggccg attcaccatc tccagagacg acgccaagaa ctcactgtat 240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gagagatcgt 300

ggggtgggct acttcgatct ctggggccgt ggcaccctgg tcaccgtctc gagcggtgga 360

ggcggttcag gcggaggtgg ttccggcggt ggcggctccc agtctgccct gactcagcct 420

gcctccgtgt ctgggtctcc tggacagtcg atcaccatct cctgcactgg aaccagcagt 480

gacgttggtg gttataactt tgtctcctgg taccaacaac acccaggcaa agcccccaaa 540

ctcatgatct atgatgtcag tgatcggccc tcaggggtgt ctgatcgctt ctccggctcc 600

aagtctggca acacggcctc cctgatcatc tctggcctcc aggctgacga cgaggctgat 660

tattactgca gctcatatgg gagcagcagc actcatgtga ttttcggcgg agggaccaag 720

gtgaccgtcc ta 732

<210> 98
<211> 706
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 98

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

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

Gly Gly Ile Asn Pro Thr Ser Gly Gly Ser Asn Phe Asn Glu Lys Phe
50 55 60

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Lys Thr Arg Val Thr Ile Thr Ala Asp Glu Ser Ser Thr Thr Ala Tyr
65                  70                  75                  80

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

Thr Arg Gln Gly Leu Trp Phe Asp Ser Asp Gly Arg Gly Phe Asp Phe
            100                 105                 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

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

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

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

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
225                 230                 235                 240

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

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335
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Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445

Leu Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
    450                 455                 460

Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly Ser Leu
465                 470                 475                 480

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Trp Met
                485                 490                 495

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Asn
            500                 505                 510

Ile Asn Arg Asp Gly Ser Ala Ser Tyr Tyr Val Asp Ser Val Lys Gly
        515                 520                 525

Arg Phe Thr Ile Ser Arg Asp Asp Ala Lys Asn Ser Leu Tyr Leu Gln
    530                 535                 540

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
545                 550                 555                 560

Asp Arg Gly Val Gly Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val
                565                 570                 575

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
            580                 585                 590

Gly Gly Ser Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser
        595                 600                 605
```

Pro Gly Gln Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val
610 615 620

Gly Gly Tyr Asn Phe Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala
625 630 635 640

Pro Lys Leu Met Ile Tyr Asp Val Ser Asp Arg Pro Ser Gly Val Ser
645 650 655

Asp Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Ile Ile
660 665 670

Ser Gly Leu Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr
675 680 685

Gly Ser Ser Ser Thr His Val Ile Phe Gly Gly Gly Thr Lys Val Thr
690 695 700

Val Leu
705

<210> 99
<211> 123
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 99

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

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

Gly Gly Ile Asn Pro Thr Ser Gly Gly Ser Asn Phe Asn Glu Lys Phe
50 55 60

Lys Thr Arg Val Thr Ile Thr Ala Asp Glu Ser Ser Thr Thr Ala Tyr
65 70 75 80

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

Thr Arg Gln Gly Leu Trp Phe Asp Ser Asp Gly Arg Gly Phe Asp Phe
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 100
<211> 244
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 100

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ala Asn Ile Asn Arg Asp Gly Ser Ala Ser Tyr Tyr Val Asp Ser Val
50 55 60

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

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

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

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

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

Gly Ser Pro Gly Gln Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser
145 150 155 160

Asp Val Gly Gly Tyr Asn Phe Val Ser Trp Tyr Gln Gln His Pro Gly
165 170 175

Lys Ala Pro Lys Leu Met Ile Tyr Asp Val Ser Asp Arg Pro Ser Gly
180 185 190

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

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

Ser Tyr Gly Ser Ser Ser Thr His Val Ile Phe Gly Gly Gly Thr Lys
225 230 235 240

Val Thr Val Leu

<210> 101
<211> 654
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 101
cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc gatcaccatc 60

tcctgcactg gaaccagcag tgacgttggt ggttataact ttgtctcctg gtaccaacaa 120

cacccaggca aagcccccaa actcatgatc tatgatgtca gtgatcggcc ctcaggggtg 180

tctgatcgct tctccggctc caagtctggc aacacggcct ccctgatcat ctctggcctc 240

caggctgacg acgaggctga ttattactgc agctcatatg ggagcagcag cactcatgtg 300

attttcggcg gagggaccaa gctgaccgtc ctacgtacgg tggctgcacc atctgtcttc 360

atcttcccgc catctgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgctg 420

aataacttct atcccagaga ggccaaagta cagtggaagg tggataacgc cctccaatcg 480

ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcagc 540

agcaccctga cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc 600

acccatcagg gcctgagctc gcccgtcaca aagagcttca acaggggaga gtgt 654

<210> 102
<211> 333
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 102
cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc gatcaccatc 60

tcctgcactg gaaccagcag tgacgttggt ggttataact ttgtctcctg gtaccaacaa 120

cacccaggca aagcccccaa actcatgatc tatgatgtca gtgatcggcc ctcaggggtg 180

tctgatcgct tctccggctc caagtctggc aacacggcct ccctgatcat ctctggcctc 240

caggctgacg acgaggctga ttattactgc agctcatatg ggagcagcag cactcatgtg 300

attttcggcg gagggaccaa gctgaccgtc cta 333

<210> 103
<211> 218
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 103

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

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
20 25 30

Asn Phe Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
35 40 45

Met Ile Tyr Asp Val Ser Asp Arg Pro Ser Gly Val Ser Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Ile Ile Ser Gly Leu
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Gly Ser Ser
85 90 95

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

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
115 120 125

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
180 185 190

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
195 200 205

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 104
<211> 111
<212> PRT
<213> artificial sequence

<220>

<223> Synthesized

<400> 104

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

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
20 25 30

Asn Phe Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
35 40 45

Met Ile Tyr Asp Val Ser Asp Arg Pro Ser Gly Val Ser Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Ile Ile Ser Gly Leu
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Gly Ser Ser
85 90 95

Ser Thr His Val Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 105
<211> 2100
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 105
caggtgcagc tgcaggagtc ggggggaggc ctggtcaagc ctggagggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagt agttattgga tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtggccaac ataaaccgcg atggaagtgc gagttactat 180

gtggactctg tgaagggccg attcaccatc tccagagacg acgccaagaa ctcactgtat 240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gagagatcgt 300

ggggtgggct acttcgatct ctggggccgt ggcaccctgg tcaccgtctc gagcgctagc 360

accaagggcc catcggtctt cccctggca ccctcctcca agagcacctc tgggggcaca 420

gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600

tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agagagttga gcccaaatct 660

tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 720

gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 780

acatgcgtgg tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840

gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 900

taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960

aagtgcaagg tctccaacaa agccctccca gcccccatcg agaaaaccat ctccaaagcc 1020

aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc 1080

aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1140

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200

tccgacggct ccttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag 1260

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320

agcctctccc tgtctccggg taaaggcggt ggaggatccg gcggtggtgg atcacaggtg 1380

cagctgaagc agtcaggacc tggcctagtg cagccctcac agagcctgtc catcacctgc 1440

acagtctctg gtttctcatt aactaactat ggtgtacact gggttcgcca gtctccagga 1500

aagggtctgg agtggctggg agtgatatgg agtggtggaa acacagacta taatacacct 1560

ttcacatcca gactgagcat caacaaggac aattccaaga gccaagtttt ctttaaaatg 1620

aacagtctgc aatctaatga cacagccata tattactgtg ccagagccct cacctactat 1680

gattacgagt ttgcttactg gggccaaggg actctggtca ctgtctctag cggtggaggc 1740

ggttcaggcg gaggtggttc cggcggtggc ggctccgaca tcttgctgac tcagtctcca 1800

gtcatcctgt ctgtgagtcc aggagaaaga gtcagtttct cctgcagggc cagtcagagt 1860

attggcacaa acatacactg gtatcagcaa agaacaaatg gttctccaag gcttctcata 1920

aagtatgctt ctgagtctat ctctgggatt ccttccaggt ttagtggcag tggatcaggg 1980

acagatttta ctcttagcat caacagtgtg gagtctgaag atattgcaga ttattactgt 2040

caacaaaata ataactggcc aaccacgttc ggtgctggga ccaagctgga gctgaaacgt 2100

<210> 106
<211> 354
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 106
caggtgcagc tgcaggagtc ggggggaggc ctggtcaagc ctggagggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagt agttattgga tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtggccaac ataaaccgcg atggaagtgc gagttactat 180

gtggactctg tgaagggccg attcaccatc tccagagacg acgccaagaa ctcactgtat 240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gagagatcgt 300

ggggtgggct acttcgatct ctggggccgt ggcaccctgg tcaccgtctc gagc 354

<210> 107
<211> 726

<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 107
caggtgcagc tgaagcagtc aggacctggc ctagtgcagc cctcacagag cctgtccatc 60

acctgcacag tctctggttt ctcattaact aactatggtg tacactgggt tcgccagtct 120

ccaggaaagg gtctggagtg gctgggagtg atatggagtg gtggaaacac agactataat 180

acacctttca catccagact gagcatcaac aaggacaatt ccaagagcca agttttcttt 240

aaaatgaaca gtctgcaatc taatgacaca gccatatatt actgtgccag agccctcacc 300

tactatgatt acgagtttgc ttactggggc caagggactc tggtcactgt ctctagcggt 360

ggaggcggtt caggcggagg tggttccggc ggtggcggct ccgacatctt gctgactcag 420

tctccagtca tcctgtctgt gagtccagga gaaagagtca gtttctcctg cagggccagt 480

cagagtattg gcacaaacat acactggtat cagcaaagaa caaatggttc tccaaggctt 540

ctcataaagt atgcttctga gtctatctct gggattcctt ccaggtttag tggcagtgga 600

tcagggacag attttactct tagcatcaac agtgtggagt ctgaagatat tgcagattat 660

tactgtcaac aaaataataa ctggccaacc acgttcggtg ctgggaccaa gctggagctg 720

aaacgt 726

<210> 108
<211> 700
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 108

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ala Asn Ile Asn Arg Asp Gly Ser Ala Ser Tyr Tyr Val Asp Ser Val
50 55 60

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

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

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

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115                 120                 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
    130                 135                 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                 150                 155                 160

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

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190

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

Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr
    210                 215                 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
225                 230                 235                 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245                 250                 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            260                 265                 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275                 280                 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
    290                 295                 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305                 310                 315                 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
                325                 330                 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
            340                 345                 350

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

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

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
                405                 410                 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            420                 425                 430

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

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Lys Gln
    450                 455                 460

Ser Gly Pro Gly Leu Val Gln Pro Ser Gln Ser Leu Ser Ile Thr Cys
465                 470                 475                 480

Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr Gly Val His Trp Val Arg
                485                 490                 495

Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Ser Gly
            500                 505                 510

Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr Ser Arg Leu Ser Ile Asn
        515                 520                 525

Lys Asp Asn Ser Lys Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln
    530                 535                 540

Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala Arg Ala Leu Thr Tyr Tyr
545                 550                 555                 560

Asp Tyr Glu Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
                565                 570                 575

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            580                 585                 590

Asp Ile Leu Leu Thr Gln Ser Pro Val Ile Leu Ser Val Ser Pro Gly
        595                 600                 605

Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
    610                 615                 620

Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
625                 630                 635                 640
```

Lys Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
645 650 655

Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Ser Val Glu Ser
660 665 670

Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
675 680 685

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
690 695 700

<210> 109
<211> 118
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 109

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ala Asn Ile Asn Arg Asp Gly Ser Ala Ser Tyr Tyr Val Asp Ser Val
50 55 60

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

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

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

Leu Val Thr Val Ser Ser
115

<210> 110
<211> 242
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 110

```
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
1               5                   10                  15

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

Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45

Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50                  55                  60

Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65                  70                  75                  80

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

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

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125

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

Leu Ser Val Ser Pro Gly Glu Arg Val Ser Phe Ser Cys Arg Ala Ser
145                 150                 155                 160

Gln Ser Ile Gly Thr Asn Ile His Trp Tyr Gln Gln Arg Thr Asn Gly
                165                 170                 175

Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser Glu Ser Ile Ser Gly Ile
            180                 185                 190

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

Ile Asn Ser Val Glu Ser Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln
    210                 215                 220

Asn Asn Asn Trp Pro Thr Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
225                 230                 235                 240

Lys Arg
```

<210> 111
<211> 642
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 111
gacatcttgc tgactcagtc tccagtcatc ctgtctgtga gtccaggaga aagagtcagt 60

ttctcctgca gggccagtca gagtattggc acaaacatac actggtatca gcaaagaaca 120

aatggttctc caaggcttct cataaagtat gcttctgagt ctatctctgg gattccttcc 180

aggtttagtg gcagtggatc agggacagat tttactctta gcatcaacag tgtggagtct 240

gaagatattg cagattatta ctgtcaacaa aataataact ggccaaccac gttcggtgct 300

gggaccaagc tggagctgaa acgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 112
<211> 321
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 112
gacatcttgc tgactcagtc tccagtcatc ctgtctgtga gtccaggaga aagagtcagt 60

ttctcctgca gggccagtca gagtattggc acaaacatac actggtatca gcaaagaaca 120

aatggttctc caaggcttct cataaagtat gcttctgagt ctatctctgg gattccttcc 180

aggtttagtg gcagtggatc agggacagat tttactctta gcatcaacag tgtggagtct 240

gaagatattg cagattatta ctgtcaacaa aataataact ggccaaccac gttcggtgct 300

gggaccaagc tggagctgaa a 321

<210> 113
<211> 214
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 113

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

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

```
Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
        35                  40                  45

Lys Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Ser Val Glu Ser
65                  70                  75                  80

Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
                85                  90                  95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Val Ala Ala
            100                 105                 110

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

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210


<210>  114
<211>  107
<212>  PRT
<213>  artificial sequence

<220>
<223>  Synthesized

<400>  114

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

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

Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
        35                  40                  45
```

Lys Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Ser Val Glu Ser
65 70 75 80

Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
85 90 95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105

<210> 115
<211> 2109
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 115
caggtgcagc tgaagcagtc aggacctggc ctagtgcagc cctcacagag cctgtccatc 60

acctgcacag tctctggttt ctcattaact aactatggtg tacactgggt tcgccagtct 120

ccaggaaagg gtctggagtg gctgggagtg atatggagtg gtggaaacac agactataat 180

acacctttca catccagact gagcatcaac aaggacaatt ccaagagcca agttttcttt 240

aaaatgaaca gtctgcaatc taatgacaca gccatatatt actgtgccag agccctcacc 300

tactatgatt acgagtttgc ttactggggc caagggactc tggtcactgt ctctagcgct 360

agcaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420

acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480

aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600

atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagagagt tgagcccaaa 660

tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 720

tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780

gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840

gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900

acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960

tacaagtgca aggtctccaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1020

gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggaggagatg 1080

accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200

gactccgacg gctccttctt cctctatagc aagctcaccg tggacaagag caggtggcag 1260

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320

aagagcctct ccctgtctcc gggtaaaggc ggtggaggat ccggcggtgg tggatcacag 1380

gtgcagctgc aggagtcggg gggaggcctg gtcaagcctg gagggtccct gagactctcc 1440

tgtgcagcct ctggattcac ctttagtagt tattggatga gctgggtccg ccaggctcca 1500

gggaaggggc tggagtgggt ggccaacata aaccgcgatg gaagtgcgag ttactatgtg 1560

gactctgtga agggccgatt caccatctcc agagacgacg ccaagaactc actgtatctg 1620

caaatgaaca gcctgagagc tgaggacacg gctgtgtatt actgtgcgag agatcgtggg 1680

gtgggctact tcgatctctg gggccgtggc accctggtca ccgtctcgag cggtggaggc 1740

ggttcaggcg gaggtggttc cggcggtggc ggctcccagt ctgccctgac tcagcctgcc 1800

tccgtgtctg ggtctcctgg acagtcgatc accatctcct gcactggaac cagcagtgac 1860

gttggtggtt ataactttgt ctcctggtac caacaacacc caggcaaagc ccccaaactc 1920

atgatctatg atgtcagtga tcggccctca ggggtgtctg atcgcttctc cggctccaag 1980

tctggcaaca cggcctccct gatcatctct ggcctccagg ctgacgacga ggctgattat 2040

tactgcagct catatgggag cagcagcact catgtgattt tcggcggagg gaccaaggtg 2100

accgtccta 2109

<210> 116
<211> 357
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 116
caggtgcagc tgaagcagtc aggacctggc ctagtgcagc cctcacagag cctgtccatc 60

acctgcacag tctctggttt ctcattaact aactatggtg tacactgggt tcgccagtct 120

ccaggaaagg gtctggagtg gctgggagtg atatggagtg gtggaaacac agactataat 180

acacctttca catccagact gagcatcaac aaggacaatt ccaagagcca agttttcttt 240

aaaatgaaca gtctgcaatc taatgacaca gccatatatt actgtgccag agccctcacc 300

tactatgatt acgagtttgc ttactggggc caagggactc tggtcactgt ctctagc 357

<210> 117
<211> 732
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 117
caggtgcagc tgcaggagtc gggggggaggc ctggtcaagc ctggagggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagt agttattgga tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtggccaac ataaaccgcg atggaagtgc gagttactat 180

gtggactctg tgaagggccg attcaccatc tccagagacg acgccaagaa ctcactgtat 240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gagagatcgt 300

ggggtgggct acttcgatct ctggggccgt ggcaccctgg tcaccgtctc gagcggtgga 360

ggcggttcag gcggaggtgg ttccggcggt ggcggctccc agtctgccct gactcagcct 420

gcctccgtgt ctgggtctcc tggacagtcg atcaccatct cctgcactgg aaccagcagt 480

gacgttggtg gttataactt tgtctcctgg taccaacaac acccaggcaa agcccccaaa 540

ctcatgatct atgatgtcag tgatcggccc tcaggggtgt ctgatcgctt ctccggctcc 600

aagtctggca acacggcctc cctgatcatc tctggcctcc aggctgacga cgaggctgat 660

tattactgca gctcatatgg gagcagcagc actcatgtga ttttcggcgg agggaccaag 720

gtgaccgtcc ta 732

<210> 118
<211> 703
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 118

Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
1 5 10 15

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

Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
50 55 60

Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65 70 75 80

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

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

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
130 135 140

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Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190

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

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415
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Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445

Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
    450                 455                 460

Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly Ser Leu Arg Leu Ser
465                 470                 475                 480

Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Trp Met Ser Trp Val
                485                 490                 495

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Asn Ile Asn Arg
            500                 505                 510

Asp Gly Ser Ala Ser Tyr Tyr Val Asp Ser Val Lys Gly Arg Phe Thr
        515                 520                 525

Ile Ser Arg Asp Asp Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser
    530                 535                 540

Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Arg Gly
545                 550                 555                 560

Val Gly Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val Thr Val Ser
                565                 570                 575

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            580                 585                 590

Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
        595                 600                 605

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
    610                 615                 620

Asn Phe Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
625                 630                 635                 640

Met Ile Tyr Asp Val Ser Asp Arg Pro Ser Gly Val Ser Asp Arg Phe
                645                 650                 655

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Ile Ile Ser Gly Leu
            660                 665                 670

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Gly Ser Ser
        675                 680                 685
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Ser Thr His Val Ile Phe Gly Gly Gly Thr Lys Val Thr Val Leu
690 695 700

<210> 119
<211> 119
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 119

Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
1 5 10 15

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

Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
50 55 60

Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65 70 75 80

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

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

Thr Leu Val Thr Val Ser Ser
115

<210> 120
<211> 244
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 120

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ala Asn Ile Asn Arg Asp Gly Ser Ala Ser Tyr Tyr Val Asp Ser Val
50 55 60

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

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

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

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

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

Gly Ser Pro Gly Gln Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser
145 150 155 160

Asp Val Gly Gly Tyr Asn Phe Val Ser Trp Tyr Gln Gln His Pro Gly
165 170 175

Lys Ala Pro Lys Leu Met Ile Tyr Asp Val Ser Asp Arg Pro Ser Gly
180 185 190

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

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

Ser Tyr Gly Ser Ser Ser Thr His Val Ile Phe Gly Gly Gly Thr Lys
225 230 235 240

Val Thr Val Leu

<210> 121
<211> 642
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 121
gacatcttgc tgactcagtc tccagtcatc ctgtctgtga gtccaggaga aagagtcagt 60

ttctcctgca gggccagtca gagtattggc acaaacatac actggtatca gcaaagaaca 120

aatggttctc caaggcttct cataaagtat gcttctgagt ctatctctgg gattccttcc 180

aggtttagtg gcagtggatc agggacagat tttactctta gcatcaacag tgtggagtct 240

gaagatattg cagattatta ctgtcaacaa aataataact ggccaaccac gttcggtgct 300

gggaccaagc tggagctgaa acgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 122
<211> 321
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 122
gacatcttgc tgactcagtc tccagtcatc ctgtctgtga gtccaggaga aagagtcagt 60

ttctcctgca gggccagtca gagtattggc acaaacatac actggtatca gcaaagaaca 120

aatggttctc caaggcttct cataaagtat gcttctgagt ctatctctgg gattccttcc 180

aggtttagtg gcagtggatc agggacagat tttactctta gcatcaacag tgtggagtct 240

gaagatattg cagattatta ctgtcaacaa aataataact ggccaaccac gttcggtgct 300

gggaccaagc tggagctgaa a 321

<210> 123
<211> 214
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 123

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

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

Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
35 40 45

Lys Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Ser Val Glu Ser
65 70 75 80

Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
85 90 95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Val Ala Ala
100 105 110

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

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 124
<211> 107
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 124

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

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

Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
35 40 45

Lys Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Ser Val Glu Ser
65 70 75 80

Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
85 90 95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105

<210> 125
<211> 1344
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 125
caggtgcagc tgaagcagtc aggacctggc ctagtgcagc cctcacagag cctgtccatc 60

acctgcacag tctctggttt ctcattaact aactatggtg tacactgggt tcgccagtct 120

ccaggaaagg gtctggagtg gctgggagtg atatggagtg gtggaaacac agactataat 180

acacctttca catccagact gagcatcaac aaggacaatt ccaagagcca agttttcttt 240

aaaatgaaca gtctgcaatc taatgacaca gccatatatt actgtgccag agccctcacc 300

tactatgatt acgagtttgc ttactggggc caagggactc tggtcactgt ctctagcgct 360

agcaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420

acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480

aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600

atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagagagt tgagcccaaa 660

tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 720

tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780

gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840

gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900

acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960

tacaagtgca aggtctccaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1020

gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1080

accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200

gactccgacg gctccttctt cctctatagc aagctcaccg tggacaagag caggtggcag 1260

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320

aagagcctct ccctgtctcc gggt 1344

<210> 126
<211> 357
<212> DNA
<213> artificial sequence

<220>

<223> Synthesized

<400> 126
caggtgcagc tgaagcagtc aggacctggc ctagtgcagc cctcacagag cctgtccatc 60

acctgcacag tctctggttt ctcattaact aactatggtg tacactgggt tcgccagtct 120

ccaggaaagg gtctggagtg gctgggagtg atatggagtg gtggaaacac agactataat 180

acacctttca catccagact gagcatcaac aaggacaatt ccaagagcca agttttcttt 240

aaaatgaaca gtctgcaatc taatgacaca gccatatatt actgtgccag agccctcacc 300

tactatgatt acgagtttgc ttactggggc caagggactc tggtcactgt ctctagc 357

<210> 127
<211> 448
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 127

Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
1 5 10 15

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

Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
50 55 60

Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65 70 75 80

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

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

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

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Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190

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

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
```

<210> 128
<211> 119
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 128

Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
1 5 10 15

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

Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
50 55 60

Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65 70 75 80

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

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

Thr Leu Val Thr Val Ser Ser
115

<210> 129
<211> 642
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 129
gacatcttgc tgactcagtc tccagtcatc ctgtctgtga gtccaggaga aagagtcagt 60

ttctcctgca gggccagtca gagtattggc acaaacatac actggtatca gcaaagaaca 120

aatggttctc caaggcttct cataaagtat gcttctgagt ctatctctgg gattccttcc 180

aggtttagtg gcagtggatc agggacagat tttactctta gcatcaacag tgtggagtct 240

gaagatattg cagattatta ctgtcaacaa aataataact ggccaaccac gttcggtgct 300

gggaccaagc tggagctgaa acgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 130
<211> 321
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 130
gacatcttgc tgactcagtc tccagtcatc ctgtctgtga gtccaggaga aagagtcagt 60

ttctcctgca gggccagtca gagtattggc acaaacatac actggtatca gcaaagaaca 120

aatggttctc caaggcttct cataaagtat gcttctgagt ctatctctgg gattccttcc 180

aggtttagtg gcagtggatc agggacagat tttactctta gcatcaacag tgtggagtct 240

gaagatattg cagattatta ctgtcaacaa aataataact ggccaaccac gttcggtgct 300

gggaccaagc tggagctgaa a 321

<210> 131
<211> 214
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 131

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

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

Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
35 40 45

Lys Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Ser Val Glu Ser
65 70 75 80

Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
85 90 95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Val Ala Ala
100 105 110

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

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 132
<211> 107
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 132

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

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

Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
35 40 45

Lys Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Ser Val Glu Ser
65 70 75 80

Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
85 90 95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105

<210> 133
<211> 2106

<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 133
caggtgcagc tgaagcagtc aggacctggc ctagtgcagc cctcacagag cctgtccatc 60

acctgcacag tctctggttt ctcattaact aactatggtg tacactgggt tcgccagtct 120

ccaggaaagg gtctggagtg gctgggagtg atatggagtg gtggaaacac agactataat 180

acacctttca catccagact gagcatcaac aaggacaatt ccaagagcca agttttcttt 240

aaaatgaaca gtctgcaatc taatgacaca gccatatatt actgtgccag agccctcacc 300

tactatgatt acgagtttgc ttactggggc caagggactc tggtcactgt ctctagcgct 360

agcaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420

acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480

aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600

atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagagagt tgagcccaaa 660

tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 720

tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780

gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840

gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900

acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960

tacaagtgca aggtctccaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1020

gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1080

accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200

gactccgacg gctccttctt cctctatagc aagctcaccg tggacaagag caggtggcag 1260

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320

aagagcctct ccctgtctcc gggtggcggt ggagggtccg gcggtggtgg atcacaggtg 1380

caattgcagg agtcgggggg aggcctggtc aagcctggag ggtccctgag actctcctgt 1440

gcagcctctg gattcacctt tagtagttat tggatgagct gggtccgcca ggctccaggg 1500

aaggggctgg agtgggtggc caacataaac cgcgatggaa gtgcgagtta ctatgtggac 1560

tctgtgaagg gccgattcac catctccaga gacgacgcca agaactcact gtatctgcaa 1620

atgaacagcc tgagagctga ggacacggct gtgtattact gtgcgagaga tcgtggggtg 1680

ggctacttcg atctctgggg ccgtggcacc ctggtcaccg tctcgagcgg tggaggcggt 1740

tcaggcggag gtggttccgg cggtggcggc tcccagtctg ccctgactca gcctgcctcc 1800

gtgtctgggt ctcctggaca gtcgatcacc atctcctgca ctggaaccag cagtgacgtt 1860

ggtggttata actttgtctc ctggtaccaa caacacccag gcaaagcccc caaactcatg 1920

atctatgatg tcagtgatcg gccctcaggg gtgtctgatc gcttctccgg ctccaagtct 1980

ggcaacacgg cctccctgat catctctggc ctccaggctg acgacgaggc tgattattac 2040

tgcagctcat atgggagcag cagcactcat gtgattttcg gcggagggac caaggtgacc 2100

gtccta 2106

<210> 134
<211> 357
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 134
caggtgcagc tgaagcagtc aggacctggc ctagtgcagc cctcacagag cctgtccatc 60

acctgcacag tctctggttt ctcattaact aactatggtg tacactgggt tcgccagtct 120

ccaggaaagg gtctggagtg gctgggagtg atatggagtg gtggaaacac agactataat 180

acacctttca catccagact gagcatcaac aaggacaatt ccaagagcca agttttcttt 240

aaaatgaaca gtctgcaatc taatgacaca gccatatatt actgtgccag agccctcacc 300

tactatgatt acgagtttgc ttactggggc caagggactc tggtcactgt ctctagc 357

<210> 135
<211> 732
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized

<400> 135
caggtgcagc tgcaggagtc ggggggaggc ctggtcaagc ctggagggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagt agttattgga tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtggccaac ataaaccgcg atggaagtgc gagttactat 180

gtggactctg tgaagggccg attcaccatc tccagagacg acgccaagaa ctcactgtat 240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gagagatcgt 300

ggggtgggct acttcgatct ctggggccgt ggcaccctgg tcaccgtctc gagcggtgga 360

ggcggttcag gcggaggtgg ttccggcggt ggcggctccc agtctgccct gactcagcct 420

gcctccgtgt ctgggtctcc tggacagtcg atcaccatct cctgcactgg aaccagcagt 480

gacgttggtg gttataactt tgtctcctgg taccaacaac acccaggcaa agcccccaaa 540

ctcatgatct atgatgtcag tgatcggccc tcaggggtgt ctgatcgctt ctccggctcc 600

aagtctggca acacggcctc cctgatcatc tctggcctcc aggctgacga cgaggctgat 660

tattactgca gctcatatgg gagcagcagc actcatgtga ttttcggcgg agggaccaag 720

gtgaccgtcc ta 732

<210> 136
<211> 702
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 136

Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
1 5 10 15

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

Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
50 55 60

Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65 70 75 80

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

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

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

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

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys
210 215 220

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Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu
    450                 455                 460

Ser Gly Gly Gly Leu Val Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys
465                 470                 475                 480

Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Trp Met Ser Trp Val Arg
                485                 490                 495
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Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Asn Ile Asn Arg Asp
500 505 510

Gly Ser Ala Ser Tyr Tyr Val Asp Ser Val Lys Gly Arg Phe Thr Ile
515 520 525

Ser Arg Asp Asp Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu
530 535 540

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Arg Gly Val
545 550 555 560

Gly Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser
565 570 575

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
580 585 590

Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln Ser
595 600 605

Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr Asn
610 615 620

Phe Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu Met
625 630 635 640

Ile Tyr Asp Val Ser Asp Arg Pro Ser Gly Val Ser Asp Arg Phe Ser
645 650 655

Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Ile Ile Ser Gly Leu Gln
660 665 670

Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Gly Ser Ser Ser
675 680 685

Thr His Val Ile Phe Gly Gly Gly Thr Lys Val Thr Val Leu
690 695 700

<210> 137
<211> 119
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 137

Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
1 5 10 15

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

Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
50 55 60

Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65 70 75 80

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

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

Thr Leu Val Thr Val Ser Ser
115

<210> 138
<211> 244
<212> PRT
<213> artificial sequence

<220>
<223> Synthesized

<400> 138

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ala Asn Ile Asn Arg Asp Gly Ser Ala Ser Tyr Tyr Val Asp Ser Val
50 55 60

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

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

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

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

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

Gly Ser Pro Gly Gln Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser
145                 150                 155                 160

Asp Val Gly Gly Tyr Asn Phe Val Ser Trp Tyr Gln Gln His Pro Gly
                165                 170                 175

Lys Ala Pro Lys Leu Met Ile Tyr Asp Val Ser Asp Arg Pro Ser Gly
            180                 185                 190

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

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

Ser Tyr Gly Ser Ser Ser Thr His Val Ile Phe Gly Gly Gly Thr Lys
225                 230                 235                 240

Val Thr Val Leu
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