SEQUENCE LISTING

<110> Regeneron Pharmaceuticals, Inc.

<120> ANTI-SARS-COV-2-SPIKE GLYCOPROTEIN ANTIBODIES AND ANTIGEN-BINDING FRAGMENTS

<130> 10753WO01

<160> 850

<170> PatentIn version 3.5

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ccagggaagg ggctggagtg ggtttcatac attactagta gtggtagtac catgtactac 180

gcagactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctcactgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgttt attactgtgc gagagacggc 300

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn 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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Gly Phe Thr Phe Arg Asn Tyr Glu
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Ile Thr Ser Ser Gly Ser Thr Met
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Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
35 40 45

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

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

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

Ser Val Gly Arg Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu
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Ser Ser Asn Ile Gly Asn Asn Tyr
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ccagggaagg ggctggagtg ggtttcatac attactagta gtggtagtac catgtactac 180

gcagactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctcactgtat 240

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ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 600

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaact cctgggggga 720

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccccct 780

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ctgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc 1140

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn 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 Gly Phe Tyr Tyr Tyr Tyr Ala Met Asp Val Trp Gly Gln
100 105 110

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
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Gly Lys
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ccaggaacag cccccaaact cctcatttat gacaataata agcgaccctc agggattcct 180

gaccgattct ctggctccaa gtctggcacg tcagccaccc tgggcatcac cggactccag 240

actggggacg aggccgatta ttactgcgga acatgggata gcagcctgag tgttggccga 300

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accctgttcc ccccctcctc cgaggagctg caggccaaca aggccaccct ggtgtgcctg 420

atctccgact tctaccccgg cgccgtgacc gtggcctgga aggccgactc ctcccccgtg 480

aaggccggcg tggagaccac cacccctcc aagcagtcca acaacaagta cgccgcctcc 540

tcctacctgt ccctgacccc cgagcagtgg aagtcccacc ggtcctactc ctgccaggtg 600

acccacgagg gctccaccgt ggagaagacc gtggccccca ccgagtgctc ctga 654

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Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
20 25 30

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

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

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

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

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

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe

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    130                 135                 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val
145                 150                 155                 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys
                165                 170                 175

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
            180                 185                 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
        195                 200                 205

Lys Thr Val Ala Pro Thr Glu Cys Ser
    210                 215
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ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggcagcac attctacgca 180

gactccgtga agggccgatt caccatctcc agacacaatt ccaagaacac gctgtatctt 240

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ggatactttg actactgggg ccagggaacc ctggtcaccg tctcctca 348

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<400> 22

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Val Ser Ser Asn
            20   25   30

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

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
    50   55   60

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

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

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

Thr Val Ser Ser
        115

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<212> DNA
<213> Artificial Sequence

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<400> 23
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<210> 24
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 24

Gly Phe Thr Val Ser Ser Asn Tyr

1 5

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

<220>
<223> Synthetic

<400> 25
atttatagcg gtggcagcac a 21

<210> 26
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 26

Ile Tyr Ser Gly Gly Ser Thr
1 5

<210> 27
<211> 30
<212> DNA
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<400> 27
gcgagagatc tgggggata ctttgactac 30

<210> 28
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<212> PRT
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<220>
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<400> 28

Ala Arg Asp Leu Gly Gly Tyr Phe Asp Tyr
1 5 10

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<400> 29
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gggaaagccc ctaagctcct gatctataag gcgtctagtt tagagagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240

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accaagctgg agatcaaa 318

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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Phe Ser Ser Trp
20 25 30

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

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

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

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Tyr Thr
85 90 95

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

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<211> 18
<212> DNA
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<400> 31
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<210> 32
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<212> PRT
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<400> 32

Gln Ser Phe Ser Ser Trp
1 5

<210> 33
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<400> 33
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<210> 34
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Lys Ala Ser
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<400> 35
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<210> 36
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 36

Gln Gln Tyr Asn Ser Tyr Tyr Thr
1 5

<210> 37
<211> 1341
<212> DNA
<213> Artificial Sequence

<220>
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ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggcagcac attctacgca 180

gactccgtga agggccgatt caccatctcc agacacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagacc tgaggacacg gccgtgtatt actgtgcgag agatctgggg 300

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aaaactcaca catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc 720

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ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1260

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagtccctc 1320

tccctgtctc cgggtaaatg a 1341

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<220>
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<400> 38

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Val Ser Ser Asn
20 25 30

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

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
50 55 60

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

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

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

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

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

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

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

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

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

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    210                 215                 220

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
225                 230                 235                 240

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

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

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285
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Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    290                 295                 300

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

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

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

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

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

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

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

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

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445
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<212> DNA
<213> Artificial Sequence

<220>
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gggaaagccc ctaagctcct gatctataag gcgtctagtt tagagagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240

gatgattttg caacttatta ctgccaacag tataatagtt attacacttt tggccagggg 300

accaagctgg agatcaaacg aactgtggct gcaccatctg tcttcatctt cccgccatct 360

gatgagcagt tgaaatctgg aactgcctct gttgtgtgcc tgctgaataa cttctatccc 420

agagaggcca aagtacagtg gaaggtggat aacgccctcc aatcgggtaa ctcccaggag 480

agtgtcacag agcaggacag caaggacagc acctacagcc tcagcagcac cctgacgctg 540

agcaaagcag actacgagaa acacaaagtc tacgcctgcg aagtcaccca tcagggcctg 600

agctcgcccg tcacaaagag cttcaacagg ggagagtgtt ag 642

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

<220>
<223> Synthetic

<400> 40

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Phe Ser Ser Trp
20 25 30

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

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

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

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Tyr Thr
85 90 95

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

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

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

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

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

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

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

Asn Arg Gly Glu Cys
    210

<210> 41
<211> 1341
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 41
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggagggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagg aattatgaaa tgaactgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtttcatac attactagta gtggtagtac catgtactac 180

gcagactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctcactgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgttt attactgtgc gagagacggc 300

ttttactact actacgctat ggacgtctgg ggccaaggga ccacggtcac cgtctcctca 360

gcctccacca agggcccatc ggtcttcccc ctggcgccct gctccaggag cacctccgag 420

agcacagccg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacgaagacc 600

tacacctgca acgtagatca caagcccagc aacaccaagg tggacaagag agttgagtcc 660

aaatatggtc ccccatgccc accgtgccca gcaccaggcg gtggcggacc atcagtcttc 720

ctgttccccc caaaacccaa ggacactctc atgatctccc ggacccctga ggtcacgtgc 780

gtggtggtgg acgtgagcca ggaagacccc gaggtccagt tcaactggta cgtggatggc 840

gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agttcaacag cacgtaccgt 900

gtggtcagcg tcctcaccgt cctgcaccag gactggctga acggcaagga gtacaagtgc 960

aaggtctcca acaaaggcct cccgtcctcc atcgagaaaa ccatctccaa agccaaaggg 1020

cagccccgag agccacaggt gtacaccctg cccccatccc aggaggagat gaccaagaac 1080

caggtcagcc tgacctgcct ggtcaaaggc ttctacccca gcgacatcgc cgtggagtgg 1140

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200

ggctccttct tcctctacag caggctcacc gtggacaaga gcaggtggca ggaggggaat 1260

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacaca gaagtccctc 1320

tccctgtctc tgggtaaatg a 1341

<210> 42
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 42

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 Phe Arg Asn Tyr
20 25 30

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

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

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn 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 Gly Phe Tyr Tyr Tyr Tyr Ala Met Asp Val Trp Gly Gln
            100                 105                 110

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

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

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

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

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

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

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

Pro Cys Pro Pro Cys Pro Ala Pro Gly Gly Gly Gly Pro Ser Val Phe
225                 230                 235                 240

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 43
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 43
gaggtgcagc tggtggagtc tggaggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctgggtt aatagtcagt cgcaactaca tgatctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac attctacgca 180

gactccgtga agggccgatt caccatctcc agacacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc tgaggacacg gccgtatatt actgtgcgag agatctgggt 300

acaggaggta tggacgtctg gggccaaggg accacggtca ccgtctcctc a 351

<210> 44
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 44

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 Leu Ile Val Ser Arg Asn
20 25 30

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

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
50 55 60

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

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

Arg Asp Leu Gly Thr Gly Gly Met Asp Val Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser
115

<210> 45
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 45
gggttaatag tcagtcgcaa ctac 24

<210> 46
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 46

Gly Leu Ile Val Ser Arg Asn Tyr
1 5

<210> 47
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 47
atttatagcg gtggtagcac a 21

<210> 48
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 48
gcgagagatc tgggtacagg aggtatggac gtc 33

<210> 49
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 49

Ala Arg Asp Leu Gly Thr Gly Gly Met Asp Val
1 5 10

<210> 50
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 50
gacatccagt tgacccagtc tccatccttc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgct gggccagtca gggcattagc agttatttag cctggtatca gcaaaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccactt tgcaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240

gaagattttg caacttatta ctgtcaacag cttaatagtt accctctcac tttcggcgga 300

gggaccaagg tggagatcaa a 321

<210> 51
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 51

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

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

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

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

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

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

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

<210> 52
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 52
cagggcatta gcagttat 18

<210> 53
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 53

Gln Gly Ile Ser Ser Tyr
1 5

<210> 54
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 54
gctgcatcc 9

<210> 55
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 55

Ala Ala Ser
1

<210> 56
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 56
caacagctta atagttaccc tctcact 27

<210> 57
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 57

Gln Gln Leu Asn Ser Tyr Pro Leu Thr
1 5

<210> 58
<211> 1332
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 58
gaggtgcagc tggtggagtc tggaggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctgggtt aatagtcagt cgcaactaca tgatctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac attctacgca 180

gactccgtga agggccgatt caccatctcc agacacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc tgaggacacg gccgtatatt actgtgcgag agatctgggt 300

acaggaggta tggacgtctg gggccaaggg accacggtca ccgtctcctc agcctccacc 360

aagggcccat cggtcttccc cctggcgccc tgctccagga gcacctccga gagcacagcc 420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacgaagac ctacacctgc 600

aacgtagatc acaagcccag caacaccaag gtggacaaga gagttgagtc caaatatggt 660

cccccatgcc caccgtgccc agcaccaggc ggtggcggac catcagtctt cctgttcccc 720

ccaaaaccca aggacactct catgatctcc cggacccctg aggtcacgtg cgtggtggtg 780

gacgtgagcc aggaagaccc cgaggtccag ttcaactggt acgtggatgg cgtggaggtg 840

cataatgcca agacaaagcc gcgggaggag cagttcaaca gcacgtaccg tgtggtcagc 900

gtcctcaccg tcctgcacca ggactggctg aacggcaagg agtacaagtg caaggtctcc 960

aacaaaggcc tcccgtcctc catcgagaaa accatctcca aagccaaagg gcagccccga 1020

gagccacagg tgtacaccct gcccccatcc caggaggaga tgaccaagaa ccaggtcagc 1080

ctgacctgcc tggtcaaagg cttctacccc agcgacatcg ccgtggagtg ggagagcaat 1140

gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1200

ttcctctaca gcaggctcac cgtggacaag agcaggtggc aggaggggaa tgtcttctca 1260

tgctccgtga tgcatgaggc tctgcacaac cactacacac agaagtccct ctccctgtct 1320

ctgggtaaat ga 1332

<210> 59
<211> 443
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 59

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 Leu Ile Val Ser Arg Asn
20 25 30

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

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

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

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

Arg Asp Leu Gly Thr Gly Gly Met Asp Val Trp Gly Gln Gly Thr Thr
            100                 105                 110

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

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
    130                 135                 140

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

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

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

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

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

Pro Cys Pro Ala Pro Gly Gly Gly Gly Pro Ser Val Phe Leu Phe Pro
225                 230                 235                 240

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

Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
            260                 265                 270
```

```
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
        275                 280                 285

Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
    290                 295                 300

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

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

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

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
        355                 360                 365

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
    370                 375                 380

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
385                 390                 395                 400

Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly
                405                 410                 415

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
            420                 425                 430

Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440
```

<210> 60
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 60

gacatccagt tgacccagtc tccatccttc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgct gggccagtca gggcattagc agttatttag cctggtatca gcaaaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccactt tgcaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240

gaagattttg caacttatta ctgtcaacag cttaatagtt accctctcac tttcggcgga 300

gggaccaagg tggagatcaa acgaactgtg 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 gttag 645

<210> 61
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 61

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

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

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

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

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

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

```
Thr 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> 1329
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 62

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gaggtgcagc tggtggagtc tggaggaggc ttggtccagc ctgggggtc cctgagactc       60

tcctgtgcag cctctgggtt caccgtcagt agcaactaca tgaactgggt ccgccaggct      120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggcagcac attctacgca      180

gactccgtga agggccgatt caccatctcc agacacaatt ccaagaacac gctgtatctt      240

caaatgaaca gcctgagacc tgaggacacg gccgtgtatt actgtgcgag agatctgggg      300

ggatactttg actactgggg ccagggaacc ctggtcaccg tctcctcagc ctccaccaag      360
```

ggcccatcgg tcttcccccct ggcgccctgc tccaggagca cctccgagag cacagccgcc 420

ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 480

gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc 540

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cgaagaccta cacctgcaac 600

gtagatcaca agcccagcaa caccaaggtg gacaagagag ttgagtccaa atatggtccc 660

ccatgcccac cgtgcccagc accaggcggt ggcggaccat cagtcttcct gttcccccca 720

aaacccaagg acactctcat gatctcccgg acccctgagg tcacgtgcgt ggtggtggac 780

gtgagccagg aagaccccga ggtccagttc aactggtacg tggatggcgt ggaggtgcat 840

aatgccaaga caaagccgcg ggaggagcag ttcaacagca cgtaccgtgt ggtcagcgtc 900

ctcaccgtcc tgcaccagga ctggctgaac ggcaaggagt acaagtgcaa ggtctccaac 960

aaaggcctcc cgtcctccat cgagaaaacc atctccaaag ccaaagggca gccccgagag 1020

ccacaggtgt acaccctgcc cccatcccag gaggagatga ccaagaacca ggtcagcctg 1080

acctgcctgg tcaaaggctt ctaccccagc gacatcgccg tggagtggga gagcaatggg 1140

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc 1200

ctctacagca ggctcaccgt ggacaagagc aggtggcagg aggggaatgt cttctcatgc 1260

tccgtgatgc atgaggctct gcacaaccac tacacacaga agtccctctc cctgtctctg 1320

ggtaaatga 1329

<210> 63
<211> 442
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 63

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 Val Ser Ser Asn
20 25 30

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

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

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

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

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

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

Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu
    130                 135                 140

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

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

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

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

Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro
    210                 215                 220

Cys Pro Ala Pro Gly Gly Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
225                 230                 235                 240

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

Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp
```

```
            260                 265                 270

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
        275                 280                 285

Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
    290                 295                 300

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

Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
                325                 330                 335

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu
            340                 345                 350

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
        355                 360                 365

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
    370                 375                 380

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
385                 390                 395                 400

Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn
                405                 410                 415

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
            420                 425                 430

Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440
```

<210> 64
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 64
caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cgtctggatt caccttcagt tactatggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagtt atatggtatg atggaagtaa taaattctat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc ggcagctcgg 300

ccgggctact actacggtat ggacgtctgg ggccaaggga ccacggtcac cgtctcctca 360

<210> 65
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 65

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

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Ala Ala Arg Pro Gly Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 66
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 66
ggattcacct tcagttacta tggc 24

<210> 67
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 67

Gly Phe Thr Phe Ser Tyr Tyr Gly
1 5

<210> 68
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 68
atatggtatg atggaagtaa taaa 24

<210> 69
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 69

Ile Trp Tyr Asp Gly Ser Asn Lys
1 5

<210> 70
<211> 39

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 70
gcggcagctc ggccgggcta ctactacggt atggacgtc 39

<210> 71
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 71

Ala Ala Ala Arg Pro Gly Tyr Tyr Tyr Gly Met Asp Val
1 5 10

<210> 72
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 72
gacatccaga tgacccagtc tccatcctca ctgtctgctt ctgtaggaga cagagtcacc 60

atcacttgtc gggcgagtca gggcattagc aattatttag cctggtttca gcagaaacca 120

gggaaagccc ctaattccct gatctatgct gcatccagtt tgcaacgtgg ggtcccatca 180

aagttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240

gaagattttg caacttatta ctgccaacag tataatagtt accctcggac gttcggccaa 300

gggaccaagg tggaaatcaa a 321

<210> 73
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 73

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

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

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

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

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

<210> 74
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 74
cagggcatta gcaattat 18

<210> 75
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 75

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Gln Gly Ile Ser Asn Tyr
1               5
```

<210> 76
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 76
caacagtata atagttaccc tcggacg 27

<210> 77
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 77

Gln Gln Tyr Asn Ser Tyr Pro Arg Thr
1 5

<210> 78
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 78
caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cgtctggatt caccttcagt tactatggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagtt atatggtatg atggaagtaa taaattctat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc ggcagctcgg 300

ccgggctact actacggtat ggacgtctgg ggccaaggga ccacggtcac cgtctcctca 360

gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 600

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaact cctgggggga 720

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccccct 780

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 900

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960

gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1020

aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggatgag 1080

ctgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc 1140

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200

ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg 1260

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1320

cagaagtccc tctccctgtc tccgggtaaa tga 1353

<210> 79
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 79

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

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Ala Ala Arg Pro Gly Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln
            100                 105                 110

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

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

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

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

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

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

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

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

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

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

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

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
```

```
    290                 295                 300

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

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

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

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

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

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

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

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

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

Gly Lys
    450
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<210> 80
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 80
gacatccaga tgacccagtc tccatcctca ctgtctgctt ctgtaggaga cagagtcacc 60

atcacttgtc gggcgagtca gggcattagc aattatttag cctggtttca gcagaaacca 120

gggaaagccc ctaattccct gatctatgct gcatccagtt tgcaacgtgg ggtcccatca 180

aagttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240

gaagattttg caacttatta ctgccaacag tataatagtt accctcggac gttcggccaa 300

gggaccaagg tggaaatcaa acgaactgtg 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 gttag 645

<210> 81
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

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

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

Tyr Ala Ala Ser Ser Leu Gln Arg Gly Val Pro Ser Lys 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 Tyr Asn Ser Tyr Pro Arg
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
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<210> 82
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 82
gaggtgcagc tggtggagtc tggaggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctgggat caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac attctacgca 180

gactccgtga agggccgatt caccatctcc agacacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc tgaggacacg gccgtgtatt actgtgcgag agaacgtaac 300

tttgatgctt ttgatatctg gggccaaggg acaatggtca ccgtctcttc a 351

<210> 83
<211> 117

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 83

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 Ile Thr Val Ser Ser Asn
20 25 30

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

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
50 55 60

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

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

Arg Glu Arg Asn Phe Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met
100 105 110

Val Thr Val Ser Ser
115

<210> 84
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 84
gggatcaccg tcagtagcaa ctac 24

<210> 85
<211> 8
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 85

Gly Ile Thr Val Ser Ser Asn Tyr
1 5

<210> 86
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 86
gcgagagaac gtaactttga tgcttttgat atc 33

<210> 87
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 87

Ala Arg Glu Arg Asn Phe Asp Ala Phe Asp Ile
1 5 10

<210> 88
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 88
gacatccaga tgacccagtc tccatcttcc gtgtctgcat ctgtaggaga cagagtcacc 60

atcacttgtc gggcgagtca gggtattagc agctggttag cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240

gaagattttg caacttacta ttgtcaacag gctaacagtt tccccctatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 89
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 89

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

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

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

Tyr Ala Ala Ser Ser Leu Gln 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 Ala Asn Ser Phe Pro Leu
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 90
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 90
cagggtatta gcagctgg 18

<210> 91

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

<220>
<223> Synthetic

<400> 91

Gln Gly Ile Ser Ser Trp
1 5

<210> 92
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 92
caacaggcta acagtttccc cctattcact 30

<210> 93
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 93

Gln Gln Ala Asn Ser Phe Pro Leu Phe Thr
1 5 10

<210> 94
<211> 1344
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 94
gaggtgcagc tggtggagtc tggaggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctgggat caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac attctacgca 180

gactccgtga agggccgatt caccatctcc agacacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc tgaggacacg gccgtgtatt actgtgcgag agaacgtaac 300

tttgatgctt ttgatatctg gggccaaggg acaatggtca ccgtctcttc agcctccacc 360

aagggcccat cggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 600

aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 660

gacaaaactc acacatgccc accgtgccca gcacctgaac tcctgggggg accgtcagtc 720

ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 780

tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 840

ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac 900

cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 960

tgcaaggtct ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa 1020

gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggatga gctgaccaag 1080

aaccaggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag 1140

tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 1200

gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg 1260

aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagtcc 1320

ctctccctgt ctccgggtaa atga 1344

<210> 95
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 95

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 Ile Thr Val Ser Ser Asn

```
            20                  25                  30

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

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
    50                  55                  60

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

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

Arg Glu Arg Asn Phe Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met
            100                 105                 110

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

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

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

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

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

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

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
    210                 215                 220

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 96
<211> 648
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 96
gacatccaga tgacccagtc tccatcttcc gtgtctgcat ctgtaggaga cagagtcacc 60

atcacttgtc gggcgagtca gggtattagc agctggttag cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240

gaagattttg caacttacta ttgtcaacag gctaacagtt tccccctatt cactttcggc 300

cctgggacca aagtggatat caaacgaact gtggctgcac catctgtctt catcttcccg 360

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 480

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 600

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgttag 648

<210> 97
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 97

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

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

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

Tyr Ala Ala Ser Ser Leu Gln 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 Ala Asn Ser Phe Pro Leu
                85                  90                  95


Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
            100                 105                 110


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


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


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


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


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


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


Ser Phe Asn Arg Gly Glu Cys
    210                 215


<210>  98
<211>  357
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  98
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggagggtc cctgagactc       60

tcctgtgcag cctctggatt caccttcagt atttatgaaa tgaactgggt ccgccaggct      120

ccagggaagg ggctggagtg ggtttcatac attactagta gtggtactac catatactac      180
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gcagactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctcactgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgttt attactgtgc gagtagcagc 300

tcgtccgggt actactttga ctactggggc cagggaaccc tggtcaccgt ctcctca 357

<210> 99
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 99

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 Phe Ser Ile Tyr
20 25 30

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn 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 Ser Ser Ser Ser Ser Gly Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 100
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 100
ggattcacct tcagtattta tgaa 24

<210> 101
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 101

Gly Phe Thr Phe Ser Ile Tyr Glu
1 5

<210> 102
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 102
attactagta gtggtactac cata 24

<210> 103
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 103

Ile Thr Ser Ser Gly Thr Thr Ile
1 5

<210> 104
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 104

gcgagtagca gctcgtccgg gtactacttt gactac 36

<210> 105
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 105

Ala Ser Ser Ser Ser Ser Gly Tyr Tyr Phe Asp Tyr
1 5 10

<210> 106
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 106
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtgtttta tacagctcca acaataagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aatctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtcagcaata ttatagtact 300

cctcccactt ttggccaggg gaccaagctg gagatcaaa 339

<210> 107
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 107

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

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

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

Pro Pro Asn Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50   55   60

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

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

Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
            100   105   110

Lys

<210> 108
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 108
cagagtgttt tatacagctc caacaataag aactac   36

<210> 109
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 109

Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr
1   5   10

<210> 110
<211> 9
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 110
tgggcatct 9

<210> 111
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 111

Trp Ala Ser
1

<210> 112
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 112
cagcaatatt atagtactcc tcccact 27

<210> 113
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 113

Gln Gln Tyr Tyr Ser Thr Pro Pro Thr
1 5

<210> 114
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 114
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggagggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt atttatgaaa tgaactgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtttcatac attactagta gtggtactac catatactac 180

gcagactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctcactgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgttt attactgtgc gagtagcagc 300

tcgtccgggt actactttga ctactggggc cagggaaccc tggtcaccgt ctcctcagcc 360

tccaccaagg 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 acaagaaagt 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 cctctacagc aagctcaccg tggacaagag caggtggcag 1260

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320

aagtccctct ccctgtctcc gggtaaatga 1350

<210> 115
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 115

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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 Phe Ser Ile Tyr
            20                  25                  30


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


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


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn 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 Ser Ser Ser Ser Ser Gly Tyr Tyr Phe Asp 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 Lys 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
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420 425 430

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

Lys

<210> 116
<211> 663
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 116
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtgtttta tacagctcca acaataagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aatctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtcagcaata ttatagtact 300

cctcccactt ttggccaggg gaccaagctg gagatcaaac gaactgtggc tgcaccatct 360

gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc 420

ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgccctc 480

caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 540

ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600

gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

tag 663

<210> 117
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 117

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

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

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

Pro Pro Asn Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50                  55                  60

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

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

Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
            100                 105                 110

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

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

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

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

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

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

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215                 220
```

<210> 118
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 118
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggata caccttcatt aactactata tacactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg atcaacccta acagtggtgg cacaaactat 180

gcacagaagt ttcagggcag ggtcaccatg accagggaca cgtccatcag cacagcctac 240

atggagctga gcaggctgag atctgacgac acggccgtgt attactgtgc gattattacg 300

atttttggag tggttacctg gttcgacccc tggggccagg gaaccctggt caccgtctcc 360

tca 363

<210> 119
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 119

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

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

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

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50 55 60

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

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

Ala Ile Ile Thr Ile Phe Gly Val Val Thr Trp Phe Asp Pro Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 120
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 120
ggatacacct tcattaacta ctat 24

<210> 121
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 121

Gly Tyr Thr Phe Ile Asn Tyr Tyr
1 5

<210> 122
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 122
atcaacccta acagtggtgg caca 24

<210> 123
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 123

Ile Asn Pro Asn Ser Gly Gly Thr
1   5

<210> 124
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 124
gcgattatta cgatttttgg agtggttacc tggttcgacc cc   42

<210> 125
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 125

Ala Ile Ile Thr Ile Phe Gly Val Val Thr Trp Phe Asp Pro
1   5   10

<210> 126
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 126
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc   60

atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca   120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca   180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct   240

gaagattttg caacttacta ctgtcaacag agttacagta ccccgctcac tttcggcgga   300

gggaccaagg tggagatcaa a   321

<210> 127
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 127

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 Ser Ile Ser Ser Tyr
20 25 30

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

Tyr Ala Ala Ser Ser Leu Gln 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 Tyr Ser Thr Pro Leu
85 90 95

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

<210> 128
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 128
cagagcatta gcagctat 18

<210> 129
<211> 6
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 129

Gln Ser Ile Ser Ser Tyr
1 5

<210> 130
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 130
caacagagtt acagtacccc gctcact 27

<210> 131
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 131

Gln Gln Ser Tyr Ser Thr Pro Leu Thr
1 5

<210> 132
<211> 1356
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 132
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggata caccttcatt aactactata tacactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg atcaacccta acagtggtgg cacaaactat 180

gcacagaagt ttcagggcag ggtcaccatg accagggaca cgtccatcag cacagcctac 180

atggagctga gcaggctgag atctgacgac acggccgtgt attactgtgc gattattacg 300

attttggag tggttacctg gttcgacccc tggggccagg gaaccctggt caccgtctcc 360

tcagcctcca 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 gaaagttgag 660

cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg 720

ggaccgtcag tcttcctctt cccccaaaa 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 atcccgggat 1080

gagctgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac 1140

atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1200

gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg 1260

tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1320

acgcagaagt ccctctccct gtctccgggt aaatga 1356

<210> 133
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 133

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

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

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

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
    50                  55                  60

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

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

Ala Ile Ile Thr Ile Phe Gly Val Val Thr Trp Phe Asp Pro 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 Lys 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 Asp Glu Leu 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
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<210> 134

<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 134
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacagta ccccgctcac tttcggcgga 300

gggaccaagg tggagatcaa acgaactgtg 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 gttag 645

<210> 135
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 135

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 Ser Ile Ser Ser Tyr
20 25 30

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

Tyr Ala Ala Ser Ser Leu Gln 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 Tyr Ser Thr Pro Leu
                85                  90                  95

Thr 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> 136
<211> 345
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 136
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60

acctgcactg tctctggtgg ctccatcagt agttactact ggagttggat ccggcagccc 120

ccagggaagg gactggagtg gattgggtat atctattaca gtgggagcac caactacaac 180

ccctccctca agagtcgagt caccatatca gtagacacgt ccaagaacca gttctccctg 240

aaactgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgcgag agacccgctc 300

ctcattgact actggggcca gggaaccctg gtcaccgtct cctca 345

<210> 137
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 137

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 Ile Ser Ser Tyr
20 25 30

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

Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

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

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

Arg Asp Pro Leu Leu Ile Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 138
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 138
ggtggctcca tcagtagtta ctac 24

<210> 139
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 139

Gly Gly Ser Ile Ser Ser Tyr Tyr
1 5

<210> 140
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 140
atctattaca gtgggagcac c 21

<210> 141
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 141

Ile Tyr Tyr Ser Gly Ser Thr
1 5

<210> 142
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 142
gcgagagacc cgctcctcat tgactac 27

<210> 143
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 143

Ala Arg Asp Pro Leu Leu Ile Asp Tyr
1 5

<210> 144
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 144
gaaattgtgt tgacgcagtc tccaggtacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagt agaagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgtatcca gcagggccac tggcatccca 180

gacaggttca gcggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttattgtcag cagtatggta gctcacctca gacttttggc 300

caggggacca agctggagat caaa 324

<210> 145
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 145

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

```
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Arg Ser
            20                  25                  30

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

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

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

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

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

<210> 146
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 146
cagagtgtta gtagaagcta c 21

<210> 147
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 147

```
Gln Ser Val Ser Arg Ser Tyr
1               5
```

<210> 148
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 148
ggtgtatcc 9

<210> 149
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 149

Gly Val Ser
1

<210> 150
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 150
cagcagtatg gtagctcacc tcagact 27

<210> 151
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 151

Gln Gln Tyr Gly Ser Ser Pro Gln Thr
1 5

<210> 152
<211> 1338
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 152
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60

acctgcactg tctctggtgg ctccatcagt agttactact ggagttggat ccggcagccc 120

ccagggaagg gactggagtg gattgggtat atctattaca gtgggagcac caactacaac 180

ccctccctca agagtcgagt caccatatca gtagacacgt ccaagaacca gttctccctg 240

aaactgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgcgag agacccgctc 300

ctcattgact actggggcca gggaaccctg gtcaccgtct cctcagcctc caccaagggc 360

ccatcggtct tcccccctggc accctcctcc aagagcacct ctgggggcac agcggccctg 420

ggctgcctgg tcaaggacta cttccccgaa ccggtgacgg tgtcgtggaa ctcaggcgcc 480

ctgaccagcg gcgtgcacac cttcccggct gtcctacagt cctcaggact ctactccctc 540

agcagcgtgg tgaccgtgcc ctccagcagc ttgggcaccc agacctacat ctgcaacgtg 600

aatcacaagc ccagcaacac caaggtggac aagaaagttg agcccaaatc ttgtgacaaa 660

actcacacat gcccaccgtg cccagcacct gaactcctgg ggggaccgtc agtcttcctc 720

ttccccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg 780

gtggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg 840

gaggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg 900

gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcaag 960

gtctccaaca aagccctccc agcccccatc gagaaaacca tctccaaagc caaagggcag 1020

ccccgagaac cacaggtgta caccctgccc ccatcccggg atgagctgac caagaaccag 1080

gtcagcctga cctgcctggt caaaggcttc tatcccagcg acatcgccgt ggagtgggag 1140

agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc 1200

tccttcttcc tctacagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc 1260

ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gtccctctcc 1320

ctgtctccgg gtaaatga 1338

<210> 153
<211> 445
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 153

```
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 Ile Ser Ser Tyr
            20                  25                  30

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

Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
    50                  55                  60

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

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

Arg Asp Pro Leu Leu Ile Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
            100                 105                 110

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

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
    130                 135                 140

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
145                 150                 155                 160

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

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

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

```
Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
    210                 215                 220

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
225                 230                 235                 240

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

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

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

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

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

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

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

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

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    370                 375                 380

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

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                405                 410                 415

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            420                 425                 430
```

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


<210>  154
<211>  648
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  154
gaaattgtgt tgacgcagtc tccaggtacc ctgtctttgt ctccagggga aagagccacc       60

ctctcctgca gggccagtca gagtgttagt agaagctact tagcctggta ccagcagaaa      120

cctggccagg ctcccaggct cctcatctat ggtgtatcca gcagggccac tggcatccca      180

gacaggttca gcggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag      240

cctgaagatt ttgcagtgta ttattgtcag cagtatggta gctcacctca gacttttggc      300

caggggacca agctggagat caaacgaact gtggctgcac catctgtctt catcttcccg      360

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc      420

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc      480

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg      540

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag      600

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgttag                   648


<210>  155
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  155

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


Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Arg Ser
            20                  25                  30
```

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

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

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

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

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

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

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

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

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

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

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

Ser Phe Asn Arg Gly Glu Cys
    210                 215


<210>  156
<211>  1341
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic
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<400> 156
caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cgtctggatt caccttcagt tactatggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagtt atatggtatg atggaagtaa taaattctat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc ggcagctcgg 300

ccgggctact actacggtat ggacgtctgg ggccaaggga ccacggtcac cgtctcctca 360

gcctccacca agggcccatc ggtcttcccc ctggcgccct gctccaggag cacctccgag 420

agcacagccg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacgaagacc 600

tacacctgca acgtagatca caagcccagc aacaccaagg tggacaagag agttgagtcc 660

aaatatggtc ccccatgccc accgtgccca gcaccaggcg gtggcggacc atcagtcttc 720

ctgttccccc caaaacccaa ggacactctc atgatctccc ggacccctga ggtcacgtgc 780

gtggtggtgg acgtgagcca ggaagacccc gaggtccagt tcaactggta cgtggatggc 840

gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agttcaacag cacgtaccgt 900

gtggtcagcg tcctcaccgt cctgcaccag gactggctga acggcaagga gtacaagtgc 960

aaggtctcca acaaaggcct cccgtcctcc atcgagaaaa ccatctccaa agccaaaggg 1020

cagccccgag agccacaggt gtacaccctg cccccatccc aggaggagat gaccaagaac 1080

caggtcagcc tgacctgcct ggtcaaaggc ttctacccca gcgacatcgc cgtggagtgg 1140

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200

ggctccttct tcctctacag caggctcacc gtggacaaga gcaggtggca ggaggggaat 1260

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacaca gaagtccctc 1320

tccctgtctc tgggtaaatg a 1341

<210> 157
<211> 446
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 157

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


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


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


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


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Ala Ala Arg Pro Gly Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln
            100                 105                 110


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


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


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


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


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


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

```
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
    210                 215                 220

Pro Cys Pro Pro Cys Pro Ala Pro Gly Gly Gly Gly Pro Ser Val Phe
225                 230                 235                 240

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

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

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

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

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

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

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

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

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

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

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

Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            420                 425                 430
```

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

<210> 158
<211> 1332
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 158
gaggtgcagc tggtggagtc tggaggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctgggat caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac attctacgca 180

gactccgtga agggccgatt caccatctcc agacacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc tgaggacacg gccgtgtatt actgtgcgag agaacgtaac 300

tttgatgctt ttgatatctg gggccaaggg acaatggtca ccgtctcttc agcctccacc 360

aagggcccat cggtcttccc cctggcgccc tgctccagga gcacctccga gagcacagcc 420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacgaagac ctacacctgc 600

aacgtagatc acaagcccag caacaccaag gtggacaaga gagttgagtc caaatatggt 660

cccccatgcc caccgtgccc agcaccaggc ggtggcggac catcagtctt cctgttcccc 720

ccaaaaccca aggacactct catgatctcc cggacccctg aggtcacgtg cgtggtggtg 780

gacgtgagcc aggaagaccc cgaggtccag ttcaactggt acgtggatgg cgtggaggtg 840

cataatgcca agacaaagcc gcgggaggag cagttcaaca gcacgtaccg tgtggtcagc 900

gtcctcaccg tcctgcacca ggactggctg aacggcaagg agtacaagtg caaggtctcc 960

aacaaaggcc tcccgtcctc catcgagaaa accatctcca aagccaaagg gcagccccga 1020

gagccacagg tgtacaccct gcccccatcc caggaggaga tgaccaagaa ccaggtcagc 1080

ctgacctgcc tggtcaaagg cttctacccc agcgacatcg ccgtggagtg ggagagcaat 1140

gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1200

ttcctctaca gcaggctcac cgtggacaag agcaggtggc aggaggggaa tgtcttctca 1260

tgctccgtga tgcatgaggc tctgcacaac cactacacac agaagtccct ctccctgtct 1320

ctgggtaaat ga 1332

<210> 159
<211> 443
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 159

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 Ile Thr Val Ser Ser Asn
20 25 30

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

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
50 55 60

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

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

Arg Glu Arg Asn Phe Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met
100 105 110

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

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
130 135 140

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

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

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

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

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

Pro Cys Pro Ala Pro Gly Gly Gly Gly Pro Ser Val Phe Leu Phe Pro
225                 230                 235                 240

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

Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
            260                 265                 270

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
        275                 280                 285

Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
    290                 295                 300

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

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

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

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
        355                 360                 365

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
```

```
    370                 375                 380

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
385                 390                 395                 400

Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly
                405                 410                 415

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
            420                 425                 430

Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440
```

<210> 160
<211> 1338
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 160

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gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggagggtc cctgagactc       60

tcctgtgcag cctctggatt caccttcagt atttatgaaa tgaactgggt ccgccaggct      120

ccagggaagg ggctggagtg ggtttcatac attactagta gtggtactac catatactac      180

gcagactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctcactgtat      240

ctgcaaatga acagcctgag agccgaggac acggctgttt attactgtgc gagtagcagc      300

tcgtccgggt actactttga ctactggggc cagggaaccc tggtcaccgt ctcctcagcc      360

tccaccaagg gcccatcggt cttccccctg gcgccctgct ccaggagcac ctccgagagc      420

acagccgccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg      480

aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga      540

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac gaagacctac      600

acctgcaacg tagatcacaa gcccagcaac accaaggtgg acaagagagt tgagtccaaa      660

tatggtcccc catgcccacc gtgcccagca ccaggcggtg gcggaccatc agtcttcctg      720

ttcccccaa aacccaagga cactctcatg atctcccgga cccctgaggt cacgtgcgtg      780

gtggtggacg tgagccagga agaccccgag gtccagttca actggtacgt ggatggcgtg      840
```

gaggtgcata atgccaagac aaagccgcgg gaggagcagt tcaacagcac gtaccgtgtg 900

gtcagcgtcc tcaccgtcct gcaccaggac tggctgaacg gcaaggagta caagtgcaag 960

gtctccaaca aaggcctccc gtcctccatc gagaaaacca tctccaaagc caaagggcag 1020

ccccgagagc cacaggtgta caccctgccc ccatcccagg aggagatgac caagaaccag 1080

gtcagcctga cctgcctggt caaaggcttc taccccagcg acatcgccgt ggagtgggag 1140

agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc 1200

tccttcttcc tctacagcag gctcaccgtg gacaagagca ggtggcagga ggggaatgtc 1260

ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacacagaa gtccctctcc 1320

ctgtctctgg gtaaatga 1338

<210> 161
<211> 445
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 161

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 Phe Ser Ile Tyr
20 25 30

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn 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 Ser Ser Ser Ser Ser Gly Tyr Tyr Phe Asp 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 Cys Ser Arg Ser Thr Ser Glu Ser 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 Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
        195                 200                 205

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

Cys Pro Pro Cys Pro Ala Pro Gly Gly Gly Gly Pro Ser Val Phe Leu
225                 230                 235                 240

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

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

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

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

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

```
Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
                325                 330                 335

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

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

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    370                 375                 380

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

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
                405                 410                 415

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            420                 425                 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440                 445
```

<210> 162
<211> 1344
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 162

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caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc       60

tcctgcaagg cttctggata caccttcatt aactactata tacactgggt gcgacaggcc      120

cctggacaag ggcttgagtg gatgggatgg atcaacccta acagtggtgg cacaaactat      180

gcacagaagt ttcagggcag ggtcaccatg accagggaca cgtccatcag cacagcctac      240

atggagctga gcaggctgag atctgacgac acggccgtgt attactgtgc gattattacg      300

atttttggag tggttacctg gttcgacccc tggggccagg gaaccctggt caccgtctcc      360

tcagcctcca ccaagggccc atcggtcttc cccctggcgc cctgctccag gagcacctcc      420
```

gagagcacag ccgccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480

tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacgaag 600

acctacacct gcaacgtaga tcacaagccc agcaacacca aggtggacaa gagagttgag 660

tccaaatatg gtcccccatg cccaccgtgc ccagcaccag gcggtggcgg accatcagtc 720

ttcctgttcc ccccaaaacc caaggacact ctcatgatct cccggacccc tgaggtcacg 780

tgcgtggtgg tggacgtgag ccaggaagac cccgaggtcc agttcaactg gtacgtggat 840

ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagttcaa cagcacgtac 900

cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaacggcaa ggagtacaag 960

tgcaaggtct ccaacaaagg cctcccgtcc tccatcgaga aaaccatctc caaagccaaa 1020

gggcagcccc gagagccaca ggtgtacacc ctgcccccat cccaggagga gatgaccaag 1080

aaccaggtca gcctgacctg cctggtcaaa ggcttctacc ccagcgacat cgccgtggag 1140

tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 1200

gacggctcct tcttcctcta cagcaggctc accgtggaca agagcaggtg gcaggagggg 1260

aatgtcttct catgctccgt gatgcatgag gctctgcaca accactacac acagaagtcc 1320

ctctccctgt ctctgggtaa atga 1344

<210> 163
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 163

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

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

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

```
Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
    50                  55                  60

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

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

Ala Ile Ile Thr Ile Phe Gly Val Val Thr Trp Phe Asp Pro 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 Cys Ser Arg Ser Thr Ser Glu Ser 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 Lys Thr Tyr Thr Cys Asn Val Asp His
        195                 200                 205

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

Pro Pro Cys Pro Pro Cys Pro Ala Pro Gly Gly Gly Gly Pro Ser Val
225                 230                 235                 240

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

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
            260                 265                 270
```

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

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

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

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

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

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

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

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

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

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

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

<210> 164
<211> 1326
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 164
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc   60

acctgcactg tctctggtgg ctccatcagt agttactact ggagttggat ccggcagccc 120

ccagggaagg gactggagtg gattgggtat atctattaca gtgggagcac caactacaac 180

ccctccctca agagtcgagt caccatatca gtagacacgt ccaagaacca gttctccctg 240

aaactgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgcgag agacccgctc 300

ctcattgact actggggcca gggaaccctg gtcaccgtct cctcagcctc caccaagggc 360

ccatcggtct tcccccctggc gccctgctcc aggagcacct ccgagagcac agccgccctg 420

ggctgcctgg tcaaggacta cttccccgaa ccggtgacgg tgtcgtggaa ctcaggcgcc 480

ctgaccagcg gcgtgcacac cttcccggct gtcctacagt cctcaggact ctactccctc 540

agcagcgtgg tgaccgtgcc ctccagcagc ttgggcacga agacctacac ctgcaacgta 600

gatcacaagc ccagcaacac caaggtggac aagagagttg agtccaaata tggtccccca 660

tgcccaccgt gcccagcacc aggcggtggc ggaccatcag tcttcctgtt cccccaaaa 720

cccaaggaca ctctcatgat ctcccggacc cctgaggtca cgtgcgtggt ggtggacgtg 780

agccaggaag accccgaggt ccagttcaac tggtacgtgg atggcgtgga ggtgcataat 840

gccaagacaa agccgcggga ggagcagttc aacagcacgt accgtgtggt cagcgtcctc 900

accgtcctgc accaggactg gctgaacggc aaggagtaca agtgcaaggt ctccaacaaa 960

ggcctcccgt cctccatcga gaaaaccatc tccaaagcca aagggcagcc ccgagagcca 1020

caggtgtaca ccctgccccc atcccaggag gagatgacca agaaccaggt cagcctgacc 1080

tgcctggtca aaggcttcta ccccagcgac atcgccgtgg agtgggagag caatgggcag 1140

ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc 1200

tacagcaggc tcaccgtgga caagagcagg tggcaggagg ggaatgtctt ctcatgctcc 1260

gtgatgcatg aggctctgca caaccactac acacagaagt ccctctccct gtctctgggt 1320

aaatga 1326

<210> 165
<211> 441
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 165

```
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 Ile Ser Ser Tyr
            20                  25                  30

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

Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
    50                  55                  60

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

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

Arg Asp Pro Leu Leu Ile Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
            100                 105                 110

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

Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val
    130                 135                 140

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
145                 150                 155                 160

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

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

Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys
        195                 200                 205

Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys
    210                 215                 220
```

```
Pro Ala Pro Gly Gly Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
225                 230                 235                 240


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


Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
            260                 265                 270


Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
        275                 280                 285


Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
    290                 295                 300


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


Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
                325                 330                 335


Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met
            340                 345                 350


Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
        355                 360                 365


Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
    370                 375                 380


Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
385                 390                 395                 400


Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val
                405                 410                 415


Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
            420                 425                 430


Lys Ser Leu Ser Leu Ser Leu Gly Lys
```

435 440

<210> 166
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 166
gaagtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgat gattatgcca tgtactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attagttgga atagtggtag cataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag agctgcggac acggccttgt attactgtgc aaaagataaa 300

gactggaact cgagaggtta ctactactac ggtatggacg tctggggcca agggaccacg 360

gtcaccgtct cctca 375

<210> 167
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 167

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

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

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

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

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

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

Ala Lys Asp Lys Asp Trp Asn Ser Arg Gly Tyr Tyr Tyr Tyr Gly Met
100 105 110

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

<210> 168
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 168
ggattcacct ttgatgatta tgcc 24

<210> 169
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 169

Gly Phe Thr Phe Asp Asp Tyr Ala
1 5

<210> 170
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 170
attagttgga atagtggtag cata 24

<210> 171
<211> 8
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 171

Ile Ser Trp Asn Ser Gly Ser Ile
1 5

<210> 172
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 172
gcaaaagata aagactggaa ctcgagaggt tactactact acggtatgga cgtc 54

<210> 173
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 173

Ala Lys Asp Lys Asp Trp Asn Ser Arg Gly Tyr Tyr Tyr Tyr Gly Met
1 5 10 15

Asp Val

<210> 174
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 174
gatgttgtga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacatta ctccgtacac ttttggccag 300

gggaccaagg tggagatcaa a 321

<210> 175
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 175

Asp Val Val 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 Ser Ile Ser Ser Tyr
20 25 30

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

Tyr Ala Ala Ser Ser Leu Gln 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 Tyr Ile Thr Pro Tyr
85 90 95

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

<210> 176
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 176

caacagagtt acattactcc gtacact 27

<210> 177
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 177

Gln Gln Ser Tyr Ile Thr Pro Tyr Thr
1 5

<210> 178
<211> 1368
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 178
gaagtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgat gattatgcca tgtactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attagttgga atagtggtag cataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag agctgcggac acggccttgt attactgtgc aaaagataaa 300

gactggaact cgagaggtta ctactactac ggtatggacg tctggggcca agggaccacg 360

gtcaccgtct cctcagcctc caccaagggc ccatcggtct tcccccctggc accctcctcc 420

aagagcacct ctgggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa 480

ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct 540

gtcctacagt cctcaggact ctactccctc agcagcgtgg tgaccgtgcc ctccagcagc 600

ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac 660

aagaaagttg agcccaaatc ttgtgacaaa actcacacat gcccaccgtg cccagcacct 720

gaactcctgg ggggaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 780

atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 840

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 900

gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 960

tggctgaatg gcaaggagta caagtgcaag gtctccaaca aagccctccc agcccccatc 1020

gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc 1080

ccatcccggg atgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 1140

tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag 1200

accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg 1260

gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1320

cacaaccact acacgcagaa gtccctctcc ctgtctccgg gtaaatga 1368

<210> 179
<211> 455
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 179

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

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

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

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

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

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

Ala Lys Asp Lys Asp Trp Asn Ser Arg Gly Tyr Tyr Tyr Tyr Gly Met
100 105 110

```
Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr
        115                 120                 125

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

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

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

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

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

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

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

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
                245                 250                 255

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

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

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

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

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

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

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

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
    370                 375                 380

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

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

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

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

Leu Ser Leu Ser Pro Gly Lys
    450                 455
```

<210> 180
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 180
gatgttgtga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacatta ctccgtacac ttttggccag 300

gggaccaagg tggagatcaa acgaactgtg 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 gttag 645

<210> 181
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 181

Asp Val Val 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 Ser Ile Ser Ser Tyr
20 25 30

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

Tyr Ala Ala Ser Ser Leu Gln 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 Tyr Ile Thr 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>  182
<211>  1356
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  182
gaagtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc       60

tcctgtgcag cctctggatt cacctttgat gattatgcca tgtactgggt ccggcaagct      120

ccagggaagg gcctggagtg ggtctcaggt attagttgga atagtggtag cataggctat      180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat      240

ctgcaaatga acagtctgag agctgcggac acggccttgt attactgtgc aaaagataaa      300

gactggaact cgagaggtta ctactactac ggtatggacg tctggggcca agggaccacg      360

gtcaccgtct cctcagcctc caccaagggc ccatcggtct tcccctggc gccctgctcc       420

aggagcacct ccgagagcac agccgccctg ggctgcctgg tcaaggacta cttccccgaa      480

ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct      540

gtcctacagt cctcaggact ctactccctc agcagcgtgg tgaccgtgcc ctccagcagc      600

ttgggcacga agacctacac ctgcaacgta gatcacaagc ccagcaacac caaggtggac      660

aagagagttg agtccaaata tggtccccca tgcccaccgt gcccagcacc aggcggtggc      720
```

ggaccatcag tcttcctgtt ccccccaaaa cccaaggaca ctctcatgat ctcccggacc 780

cctgaggtca cgtgcgtggt ggtggacgtg agccaggaag accccgaggt ccagttcaac 840

tggtacgtgg atggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagttc 900

aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaacggc 960

aaggagtaca agtgcaaggt ctccaacaaa ggcctcccgt cctccatcga gaaaaccatc 1020

tccaaagcca aggggcagcc ccgagagcca caggtgtaca ccctgccccc atcccaggag 1080

gagatgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta ccccagcgac 1140

atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1200

gtgctggact ccgacggctc cttcttcctc tacagcaggc tcaccgtgga caagagcagg 1260

tggcaggagg ggaatgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1320

acacagaagt ccctctccct gtctctgggt aaatga 1356

<210> 183
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 183

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

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

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

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

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

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

```
Ala Lys Asp Lys Asp Trp Asn Ser Arg Gly Tyr Tyr Tyr Tyr Gly Met
            100                 105                 110

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

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

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

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

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

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys
        195                 200                 205

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

Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Gly Gly 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 Gln
            260                 265                 270

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

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe 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 Gly Leu Pro Ser Ser 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 Gln 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 Arg Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Glu 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

Leu Gly Lys
450

<210> 184
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 184
gaggtgcagc tggtggagtc tggaggaggc ttggtccagt ctgggggtc cctgagactc 60

tcctgtgcag cctctgggct caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg gactggagtg ggtctcagtt atttatagcg gtggtagcac attctactca 180

gactccgtga agggccgatt caccatctcc agacacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc tgaggacacg gccgtgtatt actgtgcgag agcgagggga 300

gacgcttttg atatctgggg ccaagggaca atggtcaccg tctcttca 348

<210> 185
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 185

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Leu Thr Val Ser Ser Asn
20 25 30

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

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ser Asp Ser Val Lys
50 55 60

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

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

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

Thr Val Ser Ser
115

<210> 186
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 186
gggctcaccg tcagtagcaa ctac 24

<210> 187
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 187

Gly Leu Thr Val Ser Ser Asn Tyr
1 5

<210> 188
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 188
gcgagagcga ggggagacgc ttttgatatc 30

<210> 189
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 189

Ala Arg Ala Arg Gly Asp Ala Phe Asp Ile
1 5 10

<210> 190
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 190
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtgggaga cagagtcacc 60

atcacttgcc aggcgagtca gggcattagc aactatttaa attggtatca gcagaaacca 120

gggaaagccc ctaaactcct gatctccgat gcatccaatt tggaaacagg ggtcccatca 180

aggttcagtg gaagtggatc tgggacagat tttactttca ccatcagcag cctgcagcct 240

gaggatattg caacatatta ctgtcaacag tatgataatc tccgcttttt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 191
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 191

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 Gly 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

Ser 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 Tyr Cys Gln Gln Tyr Asp Asn Leu Arg Phe
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 192
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 192
cagggcatta gcaactat 18

<210> 193
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 193
gatgcatcc 9

<210> 194
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 194

Asp Ala Ser
1

<210> 195
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 195
caacagtatg ataatctccg ctttttcact 30

<210> 196
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 196

Gln Gln Tyr Asp Asn Leu Arg Phe Phe Thr
1 5 10

<210> 197
<211> 1341
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 197
gaggtgcagc tggtggagtc tggaggaggc ttggtccagt ctgggggtc cctgagactc 60

tcctgtgcag cctctgggct caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg gactggagtg ggtctcagtt atttatagcg gtggtagcac attctactca 180

gactccgtga agggccgatt caccatctcc agacacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc tgaggacacg gccgtgtatt actgtgcgag agcgagggga 300

gacgcttttg atatctgggg ccaagggaca atggtcaccg tctcttcagc ctccaccaag 360

ggcccatcgg tcttcccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 420

ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 480

gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc 540

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 600

gtgaatcaca agcccagcaa caccaaggtg gacaagaaag ttgagcccaa atcttgtgac 660

aaaactcaca catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc 720

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 780

gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 840

gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt 900

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 960

aaggtctcca acaaagccct cccagccccc atcgagaaaa ccatctccaa agccaaaggg 1020

cagccccgag aaccacaggt gtacaccctg cccccatccc gggatgagct gaccaagaac 1080

caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1140

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1260

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagtccctc 1320

tccctgtctc cgggtaaatg a 1341

<210> 198
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 198

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Leu Thr Val Ser Ser Asn
20 25 30

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

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ser Asp Ser Val Lys
50 55 60

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

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

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

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

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

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

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

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

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

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    210                 215                 220

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
225                 230                 235                 240

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

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

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

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

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

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

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

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

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

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


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


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


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


<210>  199
<211>  648
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  199
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtgggaga cagagtcacc       60

atcacttgcc aggcgagtca gggcattagc aactatttaa attggtatca gcagaaacca      120

gggaaagccc ctaaactcct gatctccgat gcatccaatt tggaaacagg ggtcccatca      180

aggttcagtg gaagtggatc tgggacagat tttactttca ccatcagcag cctgcagcct      240

gaggatattg caacatatta ctgtcaacag tatgataatc tccgcttttt cactttcggc      300

cctgggacca aagtggatat caaacgaact gtggctgcac catctgtctt catcttcccg      360

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc      420

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc      480

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg      540

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag      600

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgttag                  648


<210>  200
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
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<223> Synthetic

<400> 200

```
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 Gly 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


Ser 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 Tyr Cys Gln Gln Tyr Asp Asn Leu Arg Phe
                85                  90                  95


Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
            100                 105                 110


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


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


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


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


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


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

Ser Phe Asn Arg Gly Glu Cys
    210   215

<210> 201
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 201
caggtgcagc tggtggagtc tgggggaggc ttggtcaagc ctggagggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt gactactaca tgagctggat ccgccaggct 120

ccagggaagg ggctggagtg ggtttcatac attacttata gtggtagtac catatactac 180

gcagactctg tgaagggccg attcaccatc tccagggaca acgccaagag ctcactgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gagagatcgc 300

ggtacaacta tggtcccctt tgactactgg ggccagggaa ccctggtcac cgtctcctca 360

<210> 202
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 202

Gln Val Gln Leu Val 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 Asp Tyr
            20   25   30

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Ser 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 Thr Thr Met Val Pro Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 203
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 203
ggattcacct tcagtgacta ctac 24

<210> 204
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 204

Gly Phe Thr Phe Ser Asp Tyr Tyr
1 5

<210> 205
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 205
attacttata gtggtagtac cata 24

<210> 206
<211> 8
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 206

Ile Thr Tyr Ser Gly Ser Thr Ile
1 5

<210> 207
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 207
gcgagagatc gcggtacaac tatggtcccc tttgactac 39

<210> 208
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 208

Ala Arg Asp Arg Gly Thr Thr Met Val Pro Phe Asp Tyr
1 5 10

<210> 209
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 209
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc aggcgagtca ggacattacc aactatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctacgct gcatccaatt tggaaacagg ggtcccatca 180

aggttcagtg gaagtggatc tgggacagat tttactttca ccatcagcgg cctgcagcct 240

gaagatattg caacatatta ctgtcaacag tatgataatc tccctctcac tttcggcgga 300

gggaccaagg tggagatcaa a 321

<210> 210
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 210

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 Thr 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 Ala 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 Gly Leu Gln Pro
65 70 75 80

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

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

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

<220>
<223> Synthetic

<400> 211
caggacatta ccaactat 18

<210> 212

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

<220>
<223> Synthetic

<400> 212

Gln Asp Ile Thr Asn Tyr
1 5

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

<220>
<223> Synthetic

<400> 213
caacagtatg ataatctccc tctcact 27

<210> 214
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 214

Gln Gln Tyr Asp Asn Leu Pro Leu Thr
1 5

<210> 215
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 215
caggtgcagc tggtggagtc tgggggaggc ttggtcaagc ctggagggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt gactactaca tgagctggat ccgccaggct 120

ccagggaagg ggctggagtg ggtttcatac attacttata gtggtagtac catatactac 180

gcagactctg tgaagggccg attcaccatc tccagggaca acgccaagag ctcactgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gagagatcgc 300

ggtacaacta tggtcccctt tgactactgg ggccagggaa ccctggtcac cgtctcctca 360

gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 600

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaact cctgggggga 720

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct 780

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 900

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960

gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1020

aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgccccatc ccgggatgag 1080

ctgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc 1140

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200

ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg 1260

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1320

cagaagtccc tctccctgtc tccgggtaaa tga 1353

<210> 216
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 216

Gln Val Gln Leu Val 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 Asp Tyr

```
            20                  25                  30

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Ser 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 Thr Thr Met Val Pro Phe Asp Tyr Trp Gly Gln
            100                 105                 110

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Lys
    450
```

<210> 217
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 217
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc aggcgagtca ggacattacc aactatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctacgct gcatccaatt tggaaacagg ggtcccatca 180

aggttcagtg gaagtggatc tgggacagat tttactttca ccatcagcgg cctgcagcct 240

gaagatattg caacatatta ctgtcaacag tatgataatc tccctctcac tttcggcgga 300

gggaccaagg tggagatcaa acgaactgtg 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 gttag 645

<210> 218
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 218

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 Thr 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 Ala 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 Gly Leu Gln Pro
65                  70                  75                  80

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

Thr 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> 219
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 219
gaggtgcagc tggtggagtc tgggggaggc ttggtaaagc ctgggggtc ccttagactc 60

tcctgtgcag cctctggaat cactttcagt aacgcctgga tgagttgggt ccgccaggct 120

ccagggaagg ggctggagtg ggttggccgt attaaaagca aaactgatgg tgggacaaca 180

gactacgccg cacccgtgaa aggcagattc accatctcaa gagatgattc aaaaaacacg 240

ctgtatctac aaatgaacag cctgaaaacc gaggacacag ccgtgtatta ctgtaccaca 300

gcgaggtggg actggtactt cgatctctgg ggccgtggca ccctggtcac tgtctcctca 360

<210> 220
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 220

Glu Val Gln Leu Val 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 Ile Thr Phe Ser Asn Ala
20 25 30

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

Gly Arg Ile Lys Ser Lys Thr Asp Gly Gly Thr Thr Asp Tyr Ala Ala
50 55 60

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

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

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 221
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 221
ggaatcactt tcagtaacgc ctgg 24

<210> 222
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 222

Gly Ile Thr Phe Ser Asn Ala Trp
1 5

<210> 223
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 223
attaaaagca aaactgatgg tgggacaaca 30

<210> 224
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 224

Ile Lys Ser Lys Thr Asp Gly Gly Thr Thr
1 5 10

<210> 225
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 225
accacagcga ggtgggactg gtacttcgat ctc   33

<210> 226
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 226

Thr Thr Ala Arg Trp Asp Trp Tyr Phe Asp Leu
1   5   10

<210> 227
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 227
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc   60

atcacttgcc aggcgagtca ggacatttgg aattatataa attggtatca gcagaaacca   120

gggaaggccc ctaagctcct gatctacgat gcatccaatt tgaaaacagg ggtcccatca   180

aggttcagtg gaagtggatc tgggacagat tttactttca ccatcagcag cctgcagcct   240

gaagatattg caacatatta ctgtcaacag catgatgatc tccctccgac cttcggccaa   300

gggaccaagg tggaaatcaa a   321

<210> 228
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 228

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 Trp Asn Tyr
            20                  25                  30

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

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

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

<210> 229
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 229
caggacattt ggaattat 18

<210> 230
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 230

```
Gln Asp Ile Trp Asn Tyr
1               5
```

<210> 231
<211> 27
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 231
caacagcatg atgatctccc tccgacc 27

<210> 232
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 232

Gln Gln His Asp Asp Leu Pro Pro Thr
1 5

<210> 233
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 233
gaggtgcagc tggtggagtc tgggggaggc ttggtaaagc ctgggggGTC ccttagactc 60

tcctgtgcag cctctggaat cactttcagt aacgcctgga tgagttgggt ccgccaggct 120

ccagggaagg ggctggagtg ggttggccgt attaaaagca aaactgatgg tgggacaaca 180

gactacgccg cacccgtgaa aggcagattc accatctcaa gagatgattc aaaaaacacg 240

ctgtatctac aaatgaacag cctgaaaacc gaggacacag ccgtgtatta ctgtaccaca 300

gcgaggtggg actggtactt cgatctctgg ggccgtggca ccctggtcac tgtctcctca 360

gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 600

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaact cctgggggga 720

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct 780

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 900

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960

gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1020

aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggatgag 1080

ctgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc 1140

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200

ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg 1260

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1320

cagaagtccc tctccctgtc tccgggtaaa tga 1353

<210> 234
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 234

Glu Val Gln Leu Val 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 Ile Thr Phe Ser Asn Ala
20 25 30

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

Gly Arg Ile Lys Ser Lys Thr Asp Gly Gly Thr Thr Asp Tyr Ala Ala
50 55 60

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

Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr

```
                85                  90                  95

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

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

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

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

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

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

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

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

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

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

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

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

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

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


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


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


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


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


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


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


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


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


Gly Lys
    450
```

<210> 235
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 235
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc aggcgagtca ggacatttgg aattatataa attggtatca gcagaaacca 120

gggaaggccc ctaagctcct gatctacgat gcatccaatt tgaaaacagg ggtcccatca 180

aggttcagtg gaagtggatc tgggacagat tttactttca ccatcagcag cctgcagcct 240

gaagatattg caacatatta ctgtcaacag catgatgatc tccctccgac cttcggccaa 300

gggaccaagg tggaaatcaa acgaactgtg 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 gttag 645

<210> 236
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 236

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 Trp Asn Tyr
20 25 30

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

Tyr Asp Ala Ser Asn Leu Lys 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 Tyr Cys Gln Gln His Asp Asp Leu Pro Pro
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>  237
<211>  360
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  237
gaggtgcagc tggtggagtc tggaggaggc ttggtccagc ctgggggtc cctgagactc       60

tcctgtgcag cctctgggtt caccgtcagt agcaactaca tgagctgggt ccgccaggct      120

ccagggaagg ggctggagtg ggtctcactt atttatagcg gtggtagcac atactatgca      180

gactccgtga agggccgatt caccatctcc agacacaatt ccaagaacac gctgtatctt      240

caaatgaaca gcctgagatc tgaggacacg gccgtgtatt actgtgcgag agtccccctg      300

ggggattact actacggtat ggacgtctgg ggccaaggga ccacggtcac cgtctcctca      360


<210>  238
<211>  120
<212>  PRT
<213>  Artificial Sequence
```

<220>
<223> Synthetic

<400> 238

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 Val Ser Ser Asn
            20   25   30

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

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

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

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

Arg Val Pro Leu Gly Asp Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln
            100   105   110

Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 239
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 239
gcgagagtcc ccctggggga ttactactac ggtatggacg tc   42

<210> 240
<211> 14
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 240

Ala Arg Val Pro Leu Gly Asp Tyr Tyr Tyr Gly Met Asp Val
1 5 10

<210> 241
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 241
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc aggcgagtca ggacattaac aagtatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctacgat gcatccaatt tggaaacagg ggtcccatca 180

aggttcagtg gaagtggatc tgggacagat tttactttca ccatcagcag cctgcagcct 240

gaagatattg caacatatta ctgtcaacag tctgataatc tccctctcac tttcggcgga 300

gggaccaagg tggagatcaa a 321

<210> 242
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 242

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 Asn Lys 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 Tyr Cys Gln Gln Ser Asp Asn Leu Pro Leu
85 90 95

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

<210> 243
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 243
caggacatta acaagtat 18

<210> 244
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 244

Gln Asp Ile Asn Lys Tyr
1 5

<210> 245
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 245
caacagtctg ataatctccc tctcact 27

<210> 246
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 246

Gln Gln Ser Asp Asn Leu Pro Leu Thr
1   5

<210> 247
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 247
gaggtgcagc tggtggagtc tggaggaggc ttggtccagc ctgggggtc cctgagactc   60

tcctgtgcag cctctgggtt caccgtcagt agcaactaca tgagctgggt ccgccaggct   120

ccagggaagg ggctggagtg ggtctcactt atttatagcg gtggtagcac atactatgca   180

gactccgtga agggccgatt caccatctcc agacacaatt ccaagaacac gctgtatctt   240

caaatgaaca gcctgagatc tgaggacacg gccgtgtatt actgtgcgag agtccccctg   300

ggggattact actacggtat ggacgtctgg ggccaaggga ccacggtcac cgtctcctca   360

gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg   420

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg   480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca   540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc   600

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc   660

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaact cctgggggga   720

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct   780

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg   840

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac   900

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag   960

gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc   1020

aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggatgag   1080

ctgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc 1140

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200

ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg 1260

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1320

cagaagtccc tctccctgtc tccgggtaaa tga 1353

<210> 248
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 248

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 Val Ser Ser Asn
20 25 30

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

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

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

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

Arg Val Pro Leu Gly Asp Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln
100 105 110

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

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

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


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


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


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


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


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


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


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


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


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


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


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


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


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

```
        355                 360                 365

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

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

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

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

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

Gly Lys
    450
```

<210> 249
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 249
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc aggcgagtca ggacattaac aagtatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctacgat gcatccaatt tggaaacagg ggtcccatca 180

aggttcagtg gaagtggatc tgggacagat tttactttca ccatcagcag cctgcagcct 240

gaagatattg caacatatta ctgtcaacag tctgataatc tccctctcac tttcggcgga 300

gggaccaagg tggagatcaa acgaactgtg 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 gttag 645

<210> 250
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 250

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 Asn Lys 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 Tyr Cys Gln Gln Ser Asp Asn Leu Pro Leu
85 90 95

Thr 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> 251
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 251

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caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc       60

tcctgtgcag cgtctggatt caccttcaga aactatggca tgcactgggt ccgccaggct      120

ccaggcaagg ggctggagtg ggtgtcagtt atatggtatg atggaagtaa tagatactat      180

gcagactccg tgaagggccg attcaccatc tccagagaca cttccaagaa cacgctgtat      240

ctgcaaatga acagcctgag agccgaagac acggctgtgt attactgtgc gagagatcct      300

cctataactg gaacgacggg gggcgatgct tttgatatct ggggccaagg gacaatggtc      360

accgtctctt ca                                                          372
```

<210> 252
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 252

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

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

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


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


Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr 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 Pro Pro Ile Thr Gly Thr Thr Gly Gly Asp Ala Phe Asp
            100                 105                 110


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


<210>  253
<211>  24
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  253
ggattcacct tcagaaacta tggc                                              24


<210>  254
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  254

Gly Phe Thr Phe Arg Asn Tyr Gly
1               5


<210>  255
<211>  24
<212>  DNA
```

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 255
atatggtatg atggaagtaa taga 24

<210> 256
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 256

Ile Trp Tyr Asp Gly Ser Asn Arg
1 5

<210> 257
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 257
gcgagagatc ctcctataac tggaacgacg gggggcgatg cttttgatat c 51

<210> 258
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 258

Ala Arg Asp Pro Pro Ile Thr Gly Thr Thr Gly Gly Asp Ala Phe Asp
1 5 10 15

Ile

<210> 259
<211> 321

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 259
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120

gggaaagccc ctcacctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacagta ctccttacac ttttggccag 300

gggaccaagc tggagatcaa a 321

<210> 260
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 260

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 Ser Ile Ser Ser Tyr
20 25 30

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

Tyr Ala Ala Ser Ser Leu Gln 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 Tyr Ser Thr Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys

100 105

<210> 261
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 261
caacagagtt acagtactcc ttacact 27

<210> 262
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 262

Gln Gln Ser Tyr Ser Thr Pro Tyr Thr
1 5

<210> 263
<211> 1365
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 263
caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cgtctggatt caccttcaga aactatggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtgtcagtt atatggtatg atggaagtaa tagatactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca cttccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaagac acggctgtgt attactgtgc gagagatcct 300

cctataactg gaacgacggg gggcgatgct tttgatatct ggggccaagg gacaatggtc 360

accgtctctt cagcctccac caagggccca tcggtcttcc ccctggcacc ctcctccaag 420

agcacctctg ggggcacagc ggccctgggc tgcctggtca aggactactt ccccgaaccg 480

gtgacggtgt cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc 540

ctacagtcct caggactcta ctccctcagc agcgtggtga ccgtgccctc cagcagcttg 600

ggcacccaga cctacatctg caacgtgaat cacaagccca gcaacaccaa ggtggacaag 660

aaagttgagc ccaaatcttg tgacaaaact cacacatgcc caccgtgccc agcacctgaa 720

ctcctggggg gaccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgatc 780

tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc 840

aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag 900

gagcagtaca acagcacgta ccgtgtggtc agcgtcctca ccgtcctgca ccaggactgg 960

ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc ccccatcgag 1020

aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca 1080

tcccgggatg agctgaccaa gaaccaggtc agcctgacct gcctggtcaa aggcttctat 1140

cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1200

acgcctcccg tgctggactc cgacggctcc ttcttcctct acagcaagct caccgtggac 1260

aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 1320

aaccactaca cgcagaagtc cctctccctg tctccgggta aatga 1365

<210> 264
<211> 454
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 264

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

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

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

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

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr 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 Pro Pro Ile Thr Gly Thr Thr Gly Gly Asp Ala Phe Asp
            100                 105                 110

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Leu Ser Pro Gly Lys
    450
```

<210> 265
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 265

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120

gggaaagccc ctcacctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacagta ctccttacac ttttggccag 300

gggaccaagc tggagatcaa acgaactgtg 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 gttag 645

<210> 266
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 266

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 Ser Ile Ser Ser Tyr
20 25 30

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

Tyr Ala Ala Ser Ser Leu Gln 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 Tyr Ser Thr Pro Tyr
85 90 95

```
Thr Phe Gly Gln Gly Thr Lys Leu 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> 267
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 267

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cagatcacct tgaaggagtc tggtcctacg ctggtgaaac ccacacagac cctcacgctg       60

acctgcacct tctctgggtt ctcactcagc actaatgtag tgggtgtggg ctggatccgt      120

cagcccccag gaaaggccct ggagtggctt gcactcattt attggaatga tgataagcgc      180

tacagcccat ctctgaagag caggctcacc atcaccaagg acacctccaa aaaccaggtg      240

gtccttacaa tgaccaacat ggaccctgtg gacacagcca catattactg tgcacacggc      300

ccaactgggg actactttga ctactggggc cagggaaccc tggtcaccgt ctcctca         357
```

<210> 268
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 268

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

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Asn
20 25 30

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

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

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

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala His Gly Pro Thr Gly Asp Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 269
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 269
gggttctcac tcagcactaa tgtagtgggt 30

<210> 270
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 270

Gly Phe Ser Leu Ser Thr Asn Val Val Gly
1 5 10

<210> 271
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 271
atttattgga atgatgataa g 21

<210> 272
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 272

Ile Tyr Trp Asn Asp Asp Lys
1 5

<210> 273
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 273
gcacacggcc caactgggga ctactttgac tac 33

<210> 274
<211> 11
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 274

Ala His Gly Pro Thr Gly Asp Tyr Phe Asp Tyr
1 5 10

<210> 275
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 275
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tacaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag acttacagta ccctcatgta cacttttggc 300

caggggacca agctggagat caaa 324

<210> 276
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 276

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 Ser Ile Ser Ser Tyr
20 25 30

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

Tyr Ala Ala Ser Ser Leu Gln 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 Thr Tyr Ser Thr Leu Met
                85   90   95

Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100   105

<210> 277
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 277
caacagactt acagtaccct catgtacact   30

<210> 278
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 278

Gln Gln Thr Tyr Ser Thr Leu Met Tyr Thr
1   5   10

<210> 279
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 279
cagatcacct tgaaggagtc tggtcctacg ctggtgaaac ccacacagac cctcacgctg   60

acctgcacct tctctgggtt ctcactcagc actaatgtag tgggtgtggg ctggatccgt   120

cagcccccag gaaaggccct ggagtggctt gcactcattt attggaatga tgataagcgc 180

tacagcccat ctctgaagag caggctcacc atcaccaagg acacctccaa aaaccaggtg 240

gtccttacaa tgaccaacat ggaccctgtg gacacagcca catattactg tgcacacggc 300

ccaactgggg actactttga ctactggggc cagggaaccc tggtcaccgt ctcctcagcc 360

tccaccaagg 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 acaagaaagt 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 cctctacagc aagctcaccg tggacaagag caggtggcag 1260

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320

aagtccctct ccctgtctcc gggtaaatga 1350

<210> 280
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 280

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

```
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Asn
            20                  25                  30

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

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

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

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
                85                  90                  95

Cys Ala His Gly Pro Thr Gly Asp Tyr Phe Asp 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 Lys 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
```

Lys

<210> 281
<211> 648
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 281
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tacaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag acttacagta ccctcatgta cacttttggc 300

caggggacca agctggagat caaacgaact gtggctgcac catctgtctt catcttcccg 360

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 480

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 600

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgttag 648

<210> 282
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 282

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 Ser Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

```
        35                  40                  45

Tyr Ala Ala Ser Ser Leu Gln 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 Thr Tyr Ser Thr Leu Met
                85                  90                  95

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

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

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

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

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

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

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

Ser Phe Asn Arg Gly Glu Cys
    210                 215


<210>  283
<211>  366
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic
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<400> 283
gaagtgcagc tggtggagtc tgggggaggc ttggttcagc ctggcaggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgat gattatgcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt gttagttgga atagtggtac catagactat 180

gcggactctg tgaagggccg attcaccatt attagagaca acgctaagaa ctccctgtat 240

ctgcaaatga acagtctgag agctgaagac acggccttgt attactgttc aaaagatatg 300

gggaggctag actactactc cggtttggac gtctggggcc aagggaccac ggtcaccgtc 360

tcctca 366

<210> 284
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 284

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

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

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

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

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

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

Ser Lys Asp Met Gly Arg Leu Asp Tyr Tyr Ser Gly Leu Asp Val Trp
100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser

115 120

<210> 285
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 285
gttagttgga atagtggtac cata 24

<210> 286
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 286

Val Ser Trp Asn Ser Gly Thr Ile
1 5

<210> 287
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 287
tcaaaagata tggggaggct agactactac tccggtttgg acgtc 45

<210> 288
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 288

Ser Lys Asp Met Gly Arg Leu Asp Tyr Tyr Ser Gly Leu Asp Val
1 5 10 15

<210> 289
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 289
gaaatagtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagcgact ttgcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggtatccca 180

gacaggttca gtggcagtgg gtctgggaca gatttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccttg gacgttcggc 300

caagggacca aggtggaaat caaa 324

<210> 290
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 290

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30

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

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

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

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

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

<210> 291
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 291
cagagtgtta gcagcagcga c 21

<210> 292
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 292

Gln Ser Val Ser Ser Ser Asp
1 5

<210> 293
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 293
ggtgcatcc 9

<210> 294
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 294

Gly Ala Ser
1

<210> 295
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 295
cagcagtatg gtagctcacc ttggacg 27

<210> 296
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 296

Gln Gln Tyr Gly Ser Ser Pro Trp Thr
1 5

<210> 297
<211> 1359
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 297
gaagtgcagc tggtggagtc tgggggaggc ttggttcagc ctggcaggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgat gattatgcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt gttagttgga atagtggtac catagactat 180

gcggactctg tgaagggccg attcaccatt attagagaca acgctaagaa ctccctgtat 240

ctgcaaatga acagtctgag agctgaagac acggccttgt attactgttc aaaagatatg 300

gggaggctag actactactc cggtttggac gtctggggcc aagggaccac ggtcaccgtc 360

tcctcagcct ccaccaaggg cccatcggtc ttcccctgg caccctcctc caagagcacc 420

tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 480

gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag 540

tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 600

cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt 660

gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 720

gggggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 780

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 840

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 900

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 960

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc 1020

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1080

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 1140

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1200

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 1260

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1320

tacacgcaga agtccctctc cctgtctccg ggtaaatga 1359

<210> 298
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 298

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

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

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

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

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

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

Ser Lys Asp Met Gly Arg Leu Asp Tyr Tyr Ser Gly Leu Asp Val Trp
            100                 105                 110

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys
450

<210> 299
<211> 648
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 299
gaaatagtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagcgact ttgcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggtatccca 180

gacaggttca gtggcagtgg gtctgggaca gatttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccttg gacgttcggc 300

caagggacca aggtggaaat caaacgaact gtggctgcac catctgtctt catcttcccg 360

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 480

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 600

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgttag 648

<210> 300
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 300

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30

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

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

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

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

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


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


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


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


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


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


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


Ser Phe Asn Arg Gly Glu Cys
    210                 215


<210>  301
<211>  354
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  301
gaggtgcagc tggtggagtc tggaggaggc ttggtccagc ctgggggtc cctgagactc       60

tcctgtgcag tctctgggtt caccgtcagt agcaactaca tgagctgggt ccgccaggct      120

ccagggaagg gactggaatg ggtctcactt atttatagcg gtggtagcac attctacgca      180

gactccgtga agggccgatt caccatctcc agacacaatt ccaagaacac gctgtatctt      240

caaatgaaca gcctgagagc tgaggacacg gccgtatatt actgtgcgag agaaggtgga      300

tacagctatg attacaacta ctggggccag ggaaccctgg tcaccgtctc ctca            354
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<210> 302
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 302

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 Val Ser Gly Phe Thr Val Ser Ser Asn
20 25 30

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

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

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

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

Arg Glu Gly Gly Tyr Ser Tyr Asp Tyr Asn Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 303
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 303
gcgagagaag gtggatacag ctatgattac aactac 36

<210> 304

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

<220>
<223> Synthetic

<400> 304

Ala Arg Glu Gly Gly Tyr Ser Tyr Asp Tyr Asn Tyr
1 5 10

<210> 305
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 305
gacatccaga tgacccagtc tccatcctcc ctgtccgcat ctgtaggaga cagagtcacc 60

atcacgtgcc aggcgagtca ggacattaga aactatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctacgat gcatccaatt tggaaacagg ggtcccatca 180

aggttcagtg gaattggatc tgggacagat tttactttca ccatcagcag cctgcagcct 240

gaagatattg caacatatta ctgtcaacag tatgataacc tccctatcac cttcggccaa 300

gggacacgac tggagattaa a 321

<210> 306
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 306

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 Arg 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

Ile 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 Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Ile
                85   90   95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
            100   105

<210> 307
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 307
caggacatta gaaactat   18

<210> 308
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 308

Gln Asp Ile Arg Asn Tyr
1   5

<210> 309
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 309
caacagtatg ataacctccc tatcacc   27

<210> 310
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 310

Gln Gln Tyr Asp Asn Leu Pro Ile Thr
1 5

<210> 311
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 311
gaggtgcagc tggtggagtc tggaggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag tctctgggtt caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg gactggaatg ggtctcactt atttatagcg gtggtagcac attctacgca 180

gactccgtga agggccgatt caccatctcc agacacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc tgaggacacg gccgtatatt actgtgcgag agaaggtgga 300

tacagctatg attacaacta ctggggccag ggaaccctgg tcaccgtctc ctcagcctcc 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 agaaagttga 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 tgagctgacc 1080

aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1140

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200

tccgacggct ccttcttcct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag 1260

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320

tccctctccc tgtctccggg taaatga 1347

<210> 312
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 312

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 Val Ser Gly Phe Thr Val Ser Ser Asn
20 25 30

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

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

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

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

Arg Glu Gly Gly Tyr Ser Tyr Asp Tyr Asn Tyr Trp Gly Gln 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 Lys 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 Asp Glu Leu 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> 313
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 313
gacatccaga tgacccagtc tccatcctcc ctgtccgcat ctgtaggaga cagagtcacc 60

atcacgtgcc aggcgagtca ggacattaga aactatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctacgat gcatccaatt tggaaacagg ggtcccatca 180

aggttcagtg gaattggatc tgggacagat tttactttca ccatcagcag cctgcagcct 240

gaagatattg caacatatta ctgtcaacag tatgataacc tccctatcac cttcggccaa 300

gggacacgac tggagattaa acgaactgtg 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 gttag 645

<210> 314
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 314

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 Arg 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

Ile 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 Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu 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> 315
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 315

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gaggtgcagc tggtggagtc tggaggaggc ttggtccagc cgggggggtc cctgagactc       60

tcctgtgcag cctctgggtt aaccgtcagt agcaactaca tgaactgggt ccgccaggtt      120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagtaa attctacgta      180

gactccgtga agggccgatt caccatctcc agacacaatt ccaagaacac gctgtatctt      240

caaatgaaca gcctgagacc tgaggacacg gccgtgtatt actgtacgcg agacgcgcaa      300

tactacggta tggacgtctg gggccaaggg accacggtca ccgtctcctc a               351
```

<210> 316
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 316

```
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 Leu Thr Val Ser Ser Asn
            20                  25                  30
```

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

Ser Val Ile Tyr Ser Gly Gly Ser Lys Phe Tyr Val Asp Ser Val Lys
    50   55   60

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

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

Arg Asp Ala Gln Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr
            100   105   110

Val Thr Val Ser Ser
        115

<210> 317
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 317
gggttaaccg tcagtagcaa ctac   24

<210> 318
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 318
atttatagcg gtggtagtaa a   21

<210> 319
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 319

Ile Tyr Ser Gly Gly Ser Lys
1 5

<210> 320
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 320
acgcgagacg cgcaatacta cggtatggac gtc 33

<210> 321
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 321

Thr Arg Asp Ala Gln Tyr Tyr Gly Met Asp Val
1 5 10

<210> 322
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 322
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtgggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattagc acctatttac attggtatca gcagaaacca 120

ggagaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacagta cccctccgga gatttttggc 300

caggggacca agctggagat caaa 324

<210> 323
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 323

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 Ser Ile Ser Thr Tyr
20 25 30

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

Tyr Ala Ala Ser Ser Leu Gln 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 Tyr Ser Thr Pro Pro
85 90 95

Glu Ile Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 324
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 324
cagagcatta gcacctat 18

<210> 325
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 325

Gln Ser Ile Ser Thr Tyr
1   5

<210> 326
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 326
caacagagtt acagtacccc tccggagatt   30

<210> 327
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 327

Gln Gln Ser Tyr Ser Thr Pro Pro Glu Ile
1   5   10

<210> 328
<211> 1344
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 328
gaggtgcagc tggtggagtc tggaggaggc ttggtccagc cgggggggtc cctgagactc   60

tcctgtgcag cctctgggtt aaccgtcagt agcaactaca tgaactgggt ccgccaggtt   120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagtaa attctacgta   180

gactccgtga agggccgatt caccatctcc agacacaatt ccaagaacac gctgtatctt   240

caaatgaaca gcctgagacc tgaggacacg gccgtgtatt actgtacgcg agacgcgcaa   300

tactacggta tggacgtctg gggccaaggg accacggtca ccgtctcctc agcctccacc 360

aagggcccat cggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 600

aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 660

gacaaaactc acacatgccc accgtgccca gcacctgaac tcctgggggg accgtcagtc 720

ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 780

tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 840

ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac 900

cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 960

tgcaaggtct ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa 1020

gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggatga gctgaccaag 1080

aaccaggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag 1140

tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 1200

gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg 1260

aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagtcc 1320

ctctccctgt ctccgggtaa atga 1344

<210> 329
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 329

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 Leu Thr Val Ser Ser Asn
20 25 30

```
Tyr Met Asn Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Val Ile Tyr Ser Gly Gly Ser Lys Phe Tyr Val Asp Ser Val Lys
    50                  55                  60

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

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

Arg Asp Ala Gln Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr
            100                 105                 110

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

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

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

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

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

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

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
    210                 215                 220

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 330
<211> 648
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 330
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtgggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattagc acctatttac attggtatca gcagaaacca 120

ggagaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacagta cccctccgga gatttttggc 300

caggggacca agctggagat caaacgaact gtggctgcac catctgtctt catcttcccg 360

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 480

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 600

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgttag 648

<210> 331
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 331

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 Ser Ile Ser Thr Tyr
20 25 30

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

Tyr Ala Ala Ser Ser Leu Gln 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 Tyr Ser Thr Pro Pro
                85                  90                  95

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

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

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

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

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

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

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

Ser Phe Asn Arg Gly Glu Cys
    210                 215
```

<210> 332
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 332
gaggtgcagc tggtggagtc tggaggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctgggat caccgtcagt agcaattaca tgacctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac attctacgca 180

gactccgtga agggccgatt caccatctcc agacacaatt ccaagaacac gctgtatctt 240

caaatgaaca acctgagagc tgaggacacg gccgtgtatt actgtgtgag agatctagag 300

gttcggggcg gtatggacgt ctggggccaa gggaccacgg tcaccgtctc ctca 354

<210> 333
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 333

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 Ile Thr Val Ser Ser Asn
20 25 30

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

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
50 55 60

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

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

Arg Asp Leu Glu Val Arg Gly Gly Met Asp Val Trp Gly Gln Gly Thr
100 105 110

Thr Val Thr Val Ser Ser
115

<210> 334
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 334

gggatcaccg tcagtagcaa ttac 24

<210> 335
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 335
gtgagagatc tagaggttcg gggcggtatg gacgtc 36

<210> 336
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 336

Val Arg Asp Leu Glu Val Arg Gly Gly Met Asp Val
1 5 10

<210> 337
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 337
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagttttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccttg gacgttcggc 300

caagggacca aggtggaaat caaa 324

<210> 338
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 338

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Phe Ser Ser Ser
            20   25   30

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

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

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

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

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

<210> 339
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 339
cagagtttta gcagcagcta c   21

<210> 340
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 340

Gln Ser Phe Ser Ser Ser Tyr
1 5

<210> 341
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 341
gaggtgcagc tggtggagtc tggaggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctgggat caccgtcagt agcaattaca tgacctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac attctacgca 180

gactccgtga agggccgatt caccatctcc agacacaatt ccaagaacac gctgtatctt 240

caaatgaaca acctgagagc tgaggacacg gccgtgtatt actgtgtgag agatctagag 300

gttcggggcg gtatggacgt ctggggccaa gggaccacgg tcaccgtctc ctcagcctcc 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 agaaagttga 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 tgagctgacc 1080

aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1140

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200

tccgacggct ccttcttcct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag 1260

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320

tccctctccc tgtctccggg taaatga 1347

<210> 342
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 342

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 Ile Thr Val Ser Ser Asn
20 25 30

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

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
50 55 60

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

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

Arg Asp Leu Glu Val Arg Gly Gly Met Asp Val Trp Gly Gln Gly Thr
100 105 110

Thr 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 Lys 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 Asp Glu Leu 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> 343
<211> 648
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 343
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagttttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccttg gacgttcggc 300

caagggacca aggtggaaat caaacgaact gtggctgcac catctgtctt catcttcccg 360

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 480

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 600

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgttag 648

<210> 344
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 344

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Phe Ser Ser Ser
            20   25   30

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

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

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

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

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

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

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

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

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

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

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

Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 345
<211> 1329
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 345
gaggtgcagc tggtggagtc tggaggaggc ttggtccagt ctgggggtc cctgagactc 60

tcctgtgcag cctctgggct caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg gactggagtg ggtctcagtt atttatagcg gtggtagcac attctactca 180

gactccgtga agggccgatt caccatctcc agacacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc tgaggacacg gccgtgtatt actgtgcgag agcgagggga 300

gacgcttttg atatctgggg ccaagggaca atggtcaccg tctcttcagc ctccaccaag 360

ggcccatcgg tcttcccccc ggcgccctgc tccaggagca cctccgagag cacagccgcc 420

ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 480

gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc 540

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cgaagaccta cacctgcaac 600

gtagatcaca agcccagcaa caccaaggtg gacaagagag ttgagtccaa atatggtccc 660

ccatgcccac cgtgcccagc accaggcggt ggcggaccat cagtcttcct gttcccccca 720

aaacccaagg acactctcat gatctcccgg acccctgagg tcacgtgcgt ggtggtggac 780

gtgagccagg aagaccccga ggtccagttc aactggtacg tggatggcgt ggaggtgcat 840

aatgccaaga caaagccgcg ggaggagcag ttcaacagca cgtaccgtgt ggtcagcgtc 900

ctcaccgtcc tgcaccagga ctggctgaac ggcaaggagt acaagtgcaa ggtctccaac 960

aaaggcctcc cgtcctccat cgagaaaacc atctccaaag ccaaagggca gccccgagag 1020

ccacaggtgt acaccctgcc cccatcccag gaggagatga ccaagaacca ggtcagcctg 1080

acctgcctgg tcaaaggctt ctaccccagc gacatcgccg tggagtggga gagcaatggg 1140

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc 1200

ctctacagca ggctcaccgt ggacaagagc aggtggcagg aggggaatgt cttctcatgc 1260

tccgtgatgc atgaggctct gcacaaccac tacacacaga agtccctctc cctgtctctg 1320

ggtaaatga 1329

<210> 346
<211> 442
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 346

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Leu Thr Val Ser Ser Asn
20 25 30

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

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ser Asp Ser Val Lys
50 55 60

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

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

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

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

Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu
130 135 140

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

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

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

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

Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro
    210                 215                 220

Cys Pro Ala Pro Gly Gly Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
225                 230                 235                 240

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

Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp
            260                 265                 270

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
        275                 280                 285

Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
    290                 295                 300

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

Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
                325                 330                 335

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu
            340                 345                 350

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
        355                 360                 365

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
```

```
    370                 375                 380

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
385                 390                 395                 400

Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn
                405                 410                 415

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
            420                 425                 430

Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440
```

<210> 347
<211> 1341
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 347

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caggtgcagc tggtggagtc tgggggaggc ttggtcaagc ctggagggtc cctgagactc       60

tcctgtgcag cctctggatt caccttcagt gactactaca tgagctggat ccgccaggct      120

ccagggaagg ggctggagtg ggtttcatac attacttata gtggtagtac catatactac      180

gcagactctg tgaagggccg attcaccatc tccagggaca acgccaagag ctcactgtat      240

ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gagagatcgc      300

ggtacaacta tggtcccctt tgactactgg ggccagggaa ccctggtcac cgtctcctca      360

gcctccacca agggcccatc ggtcttcccc ctggcgccct gctccaggag cacctccgag      420

agcacagccg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg      480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca      540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacgaagacc      600

tacacctgca acgtagatca caagcccagc aacaccaagg tggacaagag agttgagtcc      660

aaatatggtc ccccatgccc accgtgccca gcaccaggcg gtggcggacc atcagtcttc      720

ctgttccccc caaaacccaa ggacactctc atgatctccc ggacccctga ggtcacgtgc      780

gtggtggtgg acgtgagcca ggaagacccc gaggtccagt tcaactggta cgtggatggc      840
```

gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agttcaacag cacgtaccgt 900

gtggtcagcg tcctcaccgt cctgcaccag gactggctga acggcaagga gtacaagtgc 960

aaggtctcca acaaaggcct cccgtcctcc atcgagaaaa ccatctccaa agccaaaggg 1020

cagccccgag agccacaggt gtacaccctg cccccatccc aggaggagat gaccaagaac 1080

caggtcagcc tgacctgcct ggtcaaaggc ttctacccca gcgacatcgc cgtggagtgg 1140

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200

ggctccttct tcctctacag caggctcacc gtggacaaga gcaggtggca ggaggggaat 1260

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacaca gaagtccctc 1320

tccctgtctc tgggtaaatg a 1341

<210> 348
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 348

Gln Val Gln Leu Val 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 Asp Tyr
20 25 30

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

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

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

```
            100                 105                 110

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

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

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

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

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

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

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

Pro Cys Pro Pro Cys Pro Ala Pro Gly Gly Gly Gly Pro Ser Val Phe
225                 230                 235                 240

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

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

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

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

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

```
Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
                325                 330                 335

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

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

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

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

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

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

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

<210> 349
<211> 1341
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 349
gaggtgcagc tggtggagtc tgggggaggc ttggtaaagc ctgggggtc ccttagactc 60

tcctgtgcag cctctggaat cactttcagt aacgcctgga tgagttgggt ccgccaggct 120

ccagggaagg ggctggagtg ggttggccgt attaaaagca aaactgatgg tgggacaaca 180

gactacgccg cacccgtgaa aggcagattc accatctcaa gagatgattc aaaaaacacg 240

ctgtatctac aaatgaacag cctgaaaacc gaggacacag ccgtgtatta ctgtaccaca 300

gcgaggtggg actggtactt cgatctctgg ggccgtggca ccctggtcac tgtctcctca 360

gcctccacca agggcccatc ggtcttcccc ctggcgccct gctccaggag cacctccgag 420

agcacagccg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacgaagacc 600

tacacctgca acgtagatca caagcccagc aacaccaagg tggacaagag agttgagtcc 660

aaatatggtc ccccatgccc accgtgccca gcaccaggcg gtggcggacc atcagtcttc 720

ctgttccccc caaaacccaa ggacactctc atgatctccc ggacccctga ggtcacgtgc 780

gtggtggtgg acgtgagcca ggaagacccc gaggtccagt tcaactggta cgtggatggc 840

gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agttcaacag cacgtaccgt 900

gtggtcagcg tcctcaccgt cctgcaccag gactggctga acggcaagga gtacaagtgc 960

aaggtctcca acaaaggcct cccgtcctcc atcgagaaaa ccatctccaa agccaaaggg 1020

cagccccgag agccacaggt gtacaccctg cccccatccc aggaggagat gaccaagaac 1080

caggtcagcc tgacctgcct ggtcaaaggc ttctacccca gcgacatcgc cgtggagtgg 1140

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200

ggctccttct tcctctacag caggctcacc gtggacaaga gcaggtggca ggaggggaat 1260

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacaca gaagtccctc 1320

tccctgtctc tgggtaaatg a 1341

<210> 350
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 350

Glu Val Gln Leu Val 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 Ile Thr Phe Ser Asn Ala
20 25 30

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

```
Gly Arg Ile Lys Ser Lys Thr Asp Gly Gly Thr Thr Asp Tyr Ala Ala
    50                  55                  60

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

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

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

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

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

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

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

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

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

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

Pro Cys Pro Pro Cys Pro Ala Pro Gly Gly Gly Gly Pro Ser Val Phe
225                 230                 235                 240

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

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
            260                 265                 270
```

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

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

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

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

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

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

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

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

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

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

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


<210>  351
<211>  1341
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  351
gaggtgcagc tggtggagtc tggaggaggc ttggtccagc ctgggggtc cctgagactc       60
```

tcctgtgcag cctctgggtt caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcactt atttatagcg gtggtagcac atactatgca 180

gactccgtga agggccgatt caccatctcc agacacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagatc tgaggacacg gccgtgtatt actgtgcgag agtccccctg 300

ggggattact actacggtat ggacgtctgg ggccaaggga ccacggtcac cgtctcctca 360

gcctccacca agggcccatc ggtcttcccc ctggcgccct gctccaggag cacctccgag 420

agcacagccg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacgaagacc 600

tacacctgca acgtagatca caagcccagc aacaccaagg tggacaagag agttgagtcc 660

aaatatggtc ccccatgccc accgtgccca gcaccaggcg gtggcggacc atcagtcttc 720

ctgttccccc caaaacccaa ggacactctc atgatctccc ggacccctga ggtcacgtgc 780

gtggtggtgg acgtgagcca ggaagacccc gaggtccagt tcaactggta cgtggatggc 840

gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agttcaacag cacgtaccgt 900

gtggtcagcg tcctcaccgt cctgcaccag gactggctga acggcaagga gtacaagtgc 960

aaggtctcca acaaaggcct cccgtcctcc atcgagaaaa ccatctccaa agccaaaggg 1020

cagccccgag agccacaggt gtacaccctg cccccatccc aggaggagat gaccaagaac 1080

caggtcagcc tgacctgcct ggtcaaaggc ttctacccca gcgacatcgc cgtggagtgg 1140

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200

ggctccttct tcctctacag caggctcacc gtggacaaga gcaggtggca ggaggggaat 1260

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacaca gaagtccctc 1320

tccctgtctc tgggtaaatg a 1341

<210> 352
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 352

```
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 Val Ser Ser Asn
            20                  25                  30

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

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

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

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

Arg Val Pro Leu Gly Asp Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln
            100                 105                 110

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

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

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

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

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

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

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
    210                 215                 220
```

```
Pro Cys Pro Pro Cys Pro Ala Pro Gly Gly Gly Gly Pro Ser Val Phe
225                 230                 235                 240

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

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

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

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

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

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

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

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

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

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

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

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

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
```

435 440 445

<210> 353
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 353
caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cgtctggatt caccttcaga aactatggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtgtcagtt atatggtatg atggaagtaa tagatactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca cttccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaagac acggctgtgt attactgtgc gagagatcct 300

cctataactg gaacgacggg gggcgatgct tttgatatct ggggccaagg gacaatggtc 360

accgtctctt cagcctccac caagggccca tcggtcttcc ccctggcgcc ctgctccagg 420

agcacctccg agagcacagc cgccctgggc tgcctggtca aggactactt ccccgaaccg 480

gtgacggtgt cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc 540

ctacagtcct caggactcta ctccctcagc agcgtggtga ccgtgccctc cagcagcttg 600

ggcacgaaga cctacacctg caacgtagat cacaagccca gcaacaccaa ggtggacaag 660

agagttgagt ccaaatatgg tcccccatgc ccaccgtgcc cagcaccagg cggtggcgga 720

ccatcagtct tcctgttccc cccaaaaccc aaggacactc tcatgatctc ccggacccct 780

gaggtcacgt gcgtggtggt ggacgtgagc caggaagacc ccgaggtcca gttcaactgg 840

tacgtggatg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagttcaac 900

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaacggcaag 960

gagtacaagt gcaaggtctc caacaaaggc ctcccgtcct ccatcgagaa aaccatctcc 1020

aaagccaaag ggcagccccg agagccacag gtgtacaccc tgcccccatc ccaggaggag 1080

atgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctaccc cagcgacatc 1140

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200

ctggactccg acggctcctt cttcctctac agcaggctca ccgtggacaa gagcaggtgg 1260

caggagggga atgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacaca 1320

cagaagtccc tctccctgtc tctgggtaaa tga 1353

<210> 354
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 354

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

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr 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 Pro Pro Ile Thr Gly Thr Thr Gly Gly Asp Ala Phe Asp
100 105 110

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

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

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

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr

```
                165                 170                 175

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

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

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

Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Gly Gly Gly Gly
225                 230                 235                 240

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Lys
    450
```

<210> 355
<211> 1338
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 355

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cagatcacct tgaaggagtc tggtcctacg ctggtgaaac ccacacagac cctcacgctg       60

acctgcacct tctctgggtt ctcactcagc actaatgtag tgggtgtggg ctggatccgt      120

cagcccccag gaaaggccct ggagtggctt gcactcattt attggaatga tgataagcgc      180

tacagcccat ctctgaagag caggctcacc atcaccaagg acacctccaa aaaccaggtg      240

gtccttacaa tgaccaacat ggaccctgtg gacacagcca catattactg tgcacacggc      300

ccaactgggg actactttga ctactggggc cagggaaccc tggtcaccgt ctcctcagcc      360

tccaccaagg gcccatcggt cttccccctg gcgccctgct ccaggagcac ctccgagagc      420

acagccgccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg      480

aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga      540

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac gaagacctac      600

acctgcaacg tagatcacaa gcccagcaac accaaggtgg acaagagagt tgagtccaaa      660

tatggtcccc catgcccacc gtgcccagca ccaggcggtg gcggaccatc agtcttcctg      720

ttcccccaa aacccaagga cactctcatg atctcccgga cccctgaggt cacgtgcgtg      780
```

gtggtggacg tgagccagga agaccccgag gtccagttca actggtacgt ggatggcgtg 840

gaggtgcata atgccaagac aaagccgcgg gaggagcagt tcaacagcac gtaccgtgtg 900

gtcagcgtcc tcaccgtcct gcaccaggac tggctgaacg gcaaggagta caagtgcaag 960

gtctccaaca aaggcctccc gtcctccatc gagaaaacca tctccaaagc caaagggcag 1020

ccccgagagc cacaggtgta caccctgccc ccatcccagg aggagatgac caagaaccag 1080

gtcagcctga cctgcctggt caaaggcttc taccccagcg acatcgccgt ggagtgggag 1140

agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc 1200

tccttcttcc tctacagcag gctcaccgtg gacaagagca ggtggcagga ggggaatgtc 1260

ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacacagaa gtccctctcc 1320

ctgtctctgg gtaaatga 1338

<210> 356
<211> 445
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 356

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

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Asn
20 25 30

Val Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Leu Ile Tyr Trp Asn Asp Asp Lys Arg Tyr Ser Pro Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Asn Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

```
Cys Ala His Gly Pro Thr Gly Asp Tyr Phe Asp 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 Cys Ser Arg Ser Thr Ser Glu Ser 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 Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
        195                 200                 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
    210                 215                 220

Cys Pro Pro Cys Pro Ala Pro Gly Gly Gly Gly Pro Ser Val Phe Leu
225                 230                 235                 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                245                 250                 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
            260                 265                 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        275                 280                 285

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    290                 295                 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305                 310                 315                 320
```

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
325 330 335

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
340 345 350

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
370 375 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385 390 395 400

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
405 410 415

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 357
<211> 1335
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 357
gaggtgcagc tggtggagtc tggaggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag tctctgggtt caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg gactggaatg ggtctcactt atttatagcg gtggtagcac attctacgca 180

gactccgtga agggccgatt caccatctcc agacacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc tgaggacacg gccgtatatt actgtgcgag agaaggtgga 300

tacagctatg attacaacta ctggggccag ggaaccctgg tcaccgtctc ctcagcctcc 360

accaagggcc catcggtctt ccccctggcg ccctgctcca ggagcacctc cgagagcaca 420

gccgccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcacgaa gacctacacc 600

tgcaacgtag atcacaagcc cagcaacacc aaggtggaca agagagttga gtccaaatat 660

ggtcccccat gcccaccgtg cccagcacca ggcggtggcg gaccatcagt cttcctgttc 720

cccccaaaac ccaaggacac tctcatgatc tcccggaccc ctgaggtcac gtgcgtggtg 780

gtggacgtga gccaggaaga ccccgaggtc agttcaact ggtacgtgga tggcgtggag 840

gtgcataatg ccaagacaaa gccgcgggag gagcagttca acagcacgta ccgtgtggtc 900

agcgtcctca ccgtcctgca ccaggactgg ctgaacggca aggagtacaa gtgcaaggtc 960

tccaacaaag gcctcccgtc ctccatcgag aaaaccatct ccaaagccaa agggcagccc 1020

cgagagccac aggtgtacac cctgccccca tcccaggagg agatgaccaa gaaccaggtc 1080

agcctgacct gcctggtcaa aggcttctac cccagcgaca tcgccgtgga gtgggagagc 1140

aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc 1200

ttcttcctct acagcaggct caccgtggac aagagcaggt ggcaggaggg gaatgtcttc 1260

tcatgctccg tgatgcatga ggctctgcac aaccactaca cacagaagtc cctctccctg 1320

tctctgggta aatga 1335

<210> 358
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 358

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 Val Ser Gly Phe Thr Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

```
Ser Leu Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
    50                  55                  60

Gly Arg Phe Thr Ile Ser Arg His Asn Ser Lys Asn Thr Leu Tyr Leu
65                  70                  75                  80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Glu Gly Gly Tyr Ser Tyr Asp Tyr Asn Tyr Trp Gly Gln 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 Cys Ser Arg Ser Thr Ser Glu Ser 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 Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
    210                 215                 220

Pro Pro Cys Pro Ala Pro Gly Gly Gly Gly Pro Ser Val Phe Leu Phe
225                 230                 235                 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
                245                 250                 255

Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
            260                 265                 270
```

```
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
        275                 280                 285

Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
    290                 295                 300

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305                 310                 315                 320

Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
                325                 330                 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln
            340                 345                 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
        355                 360                 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
    370                 375                 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
385                 390                 395                 400

Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu
                405                 410                 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
            420                 425                 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440
```

<210> 359
<211> 1332
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 359

gaggtgcagc tggtggagtc tggaggaggc ttggtccagc cgggggggtc cctgagactc 60

tcctgtgcag cctctgggtt aaccgtcagt agcaactaca tgaactgggt ccgccaggtt 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagtaa attctacgta 180

gactccgtga agggccgatt caccatctcc agacacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagacc tgaggacacg gccgtgtatt actgtacgcg agacgcgcaa 300

tactacggta tggacgtctg gggccaaggg accacggtca ccgtctcctc agcctccacc 360

aagggcccat cggtcttccc cctggcgccc tgctccagga gcacctccga gagcacagcc 420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacgaagac ctacacctgc 600

aacgtagatc acaagcccag caacaccaag gtggacaaga gagttgagtc caaatatggt 660

cccccatgcc caccgtgccc agcaccaggc ggtggcggac catcagtctt cctgttcccc 720

ccaaaaccca aggacactct catgatctcc cggacccctg aggtcacgtg cgtggtggtg 780

gacgtgagcc aggaagaccc cgaggtccag ttcaactggt acgtggatgg cgtggaggtg 840

cataatgcca agacaaagcc gcgggaggag cagttcaaca gcacgtaccg tgtggtcagc 900

gtcctcaccg tcctgcacca ggactggctg aacggcaagg agtacaagtg caaggtctcc 960

aacaaaggcc tcccgtcctc catcgagaaa accatctcca aagccaaagg gcagccccga 1020

gagccacagg tgtacaccct gcccccatcc caggaggaga tgaccaagaa ccaggtcagc 1080

ctgacctgcc tggtcaaagg cttctacccc agcgacatcg ccgtggagtg ggagagcaat 1140

gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1200

ttcctctaca gcaggctcac cgtggacaag agcaggtggc aggaggggaa tgtcttctca 1260

tgctccgtga tgcatgaggc tctgcacaac cactacacac agaagtccct ctccctgtct 1320

ctgggtaaat ga 1332

<210> 360
<211> 443
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 360

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 Leu Thr Val Ser Ser Asn
20 25 30

Tyr Met Asn Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Lys Phe Tyr Val Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg His Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr
85 90 95

Arg Asp Ala Gln Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
115 120 125

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
180 185 190

Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
195 200 205

Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro

```
    210                 215                 220

Pro Cys Pro Ala Pro Gly Gly Gly Gly Pro Ser Val Phe Leu Phe Pro
225                 230                 235                 240

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
                245                 250                 255

Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
            260                 265                 270

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
        275                 280                 285

Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
    290                 295                 300

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
305                 310                 315                 320

Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
                325                 330                 335

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu
            340                 345                 350

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
        355                 360                 365

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
    370                 375                 380

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
385                 390                 395                 400

Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly
                405                 410                 415

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
            420                 425                 430
```

Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440

<210> 361
<211> 1335
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 361
gaggtgcagc tggtggagtc tggaggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctgggat caccgtcagt agcaattaca tgacctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac attctacgca 180

gactccgtga agggccgatt caccatctcc agacacaatt ccaagaacac gctgtatctt 240

caaatgaaca acctgagagc tgaggacacg gccgtgtatt actgtgtgag agatctagag 300

gttcggggcg gtatggacgt ctggggccaa gggaccacgg tcaccgtctc ctcagcctcc 360

accaagggcc catcggtctt ccccctggcg ccctgctcca ggagcacctc cgagagcaca 420

gccgccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcacgaa gacctacacc 600

tgcaacgtag atcacaagcc cagcaacacc aaggtggaca agagagttga gtccaaatat 660

ggtccccat gcccaccgtg cccagcacca ggcggtggcg gaccatcagt cttcctgttc 720

cccccaaaac ccaaggacac tctcatgatc tcccggaccc ctgaggtcac gtgcgtggtg 780

gtggacgtga gccaggaaga ccccgaggtc agttcaact ggtacgtgga tggcgtggag 840

gtgcataatg ccaagacaaa gccgcgggag gagcagttca acagcacgta ccgtgtggtc 900

agcgtcctca ccgtcctgca ccaggactgg ctgaacggca aggagtacaa gtgcaaggtc 960

tccaacaaag gcctcccgtc ctccatcgag aaaaccatct ccaaagccaa agggcagccc 1020

cgagagccac aggtgtacac cctgccccca tcccaggagg agatgaccaa gaaccaggtc 1080

agcctgacct gcctggtcaa aggcttctac cccagcgaca tcgccgtgga gtgggagagc 1140

aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc 1200

ttcttcctct acagcaggct caccgtggac aagagcaggt ggcaggaggg gaatgtcttc 1260

tcatgctccg tgatgcatga ggctctgcac aaccactaca cacagaagtc cctctccctg 1320

tctctgggta aatga 1335

<210> 362
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 362

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 Ile Thr Val Ser Ser Asn
20 25 30

Tyr Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg His Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Asn Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Val
85 90 95

Arg Asp Leu Glu Val Arg Gly Gly Met Asp Val Trp Gly Gln Gly Thr
100 105 110

Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser 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 Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
    210                 215                 220

Pro Pro Cys Pro Ala Pro Gly Gly Gly Gly Pro Ser Val Phe Leu Phe
225                 230                 235                 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
                245                 250                 255

Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
            260                 265                 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
        275                 280                 285

Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
    290                 295                 300

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305                 310                 315                 320

Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
                325                 330                 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln
            340                 345                 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
        355                 360                 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
    370                 375                 380
```

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Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
385                 390                 395                 400


Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu
                405                 410                 415


Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
            420                 425                 430


Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440


<210>  363
<211>  1347
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  363
gaagtgcagc tggtggagtc tgggggaggc ttggttcagc ctggcaggtc cctgagactc       60

tcctgtgcag cctctggatt cacctttgat gattatgcca tgcactgggt ccggcaagct      120

ccagggaagg gcctggagtg ggtctcaggt gttagttgga atagtggtac catagactat      180

gcggactctg tgaagggccg attcaccatt attagagaca acgctaagaa ctccctgtat      240

ctgcaaatga acagtctgag agctgaagac acggccttgt attactgttc aaaagatatg      300

gggaggctag actactactc cggtttggac gtctggggcc aagggaccac ggtcaccgtc      360

tcctcagcct ccaccaaggg cccatcggtc ttcccctgg cgccctgctc caggagcacc       420

tccgagagca cagccgccct gggctgcctg gtcaaggact acttccccga accggtgacg      480

gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag      540

tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacg      600

aagacctaca cctgcaacgt agatcacaag cccagcaaca ccaaggtgga caagagagtt      660

gagtccaaat atggtccccc atgcccaccg tgcccagcac caggcggtgg cggaccatca      720

gtcttcctgt tccccccaaa acccaaggac actctcatga tctcccggac ccctgaggtc      780

acgtgcgtgg tggtggacgt gagccaggaa gaccccgagg tccagttcaa ctggtacgtg      840

gatggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagtt caacagcacg      900
```

taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaacgg caaggagtac 960

aagtgcaagg tctccaacaa aggcctcccg tcctccatcg agaaaaccat ctccaaagcc 1020

aaagggcagc cccgagagcc acaggtgtac accctgcccc catcccagga ggagatgacc 1080

aagaaccagg tcagcctgac ctgcctggtc aaaggcttct accccagcga catcgccgtg 1140

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200

tccgacggct ccttcttcct ctacagcagg ctcaccgtgg acaagagcag gtggcaggag 1260

gggaatgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacacagaag 1320

tccctctccc tgtctctggg taaatga 1347

<210> 364
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 364

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Val Ser Trp Asn Ser Gly Thr Ile Asp Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ile Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ser Lys Asp Met Gly Arg Leu Asp Tyr Tyr Ser Gly Leu Asp Val Trp
100 105 110

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Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
        115                 120                 125

Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr
    130                 135                 140

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145                 150                 155                 160

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
                165                 170                 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
            180                 185                 190

Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp
        195                 200                 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr
    210                 215                 220

Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Gly Gly 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 Gln Glu Asp Pro
            260                 265                 270

Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275                 280                 285

Lys Thr Lys Pro Arg Glu Glu Gln Phe 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 Gly Leu Pro Ser Ser Ile Glu Lys Thr
                325                 330                 335
```

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Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
            340                 345                 350

Pro Pro Ser Gln 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 Arg Leu Thr Val Asp Lys Ser
                405                 410                 415

Arg Trp Gln Glu 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 Leu Gly Lys
        435                 440                 445
```

<210> 365
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 365
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc actgagactc 60

tcctgtgcag cctctggaat caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcactt atttatagtg gtggtagcac atactacgca 180

gactccgtga agggcagatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagt cgaggacacg gctgtgtatt actgtgcgag agatcacggt 300

atggcagcag cggggtataa ttactggggc cagggaaccc tggtcaccgt ctcctca 357

<210> 366
<211> 119
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 366

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 Ile Thr Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Leu Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp His Gly Met Ala Ala Ala Gly Tyr Asn Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 367
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 367
ggaatcaccg tcagtagcaa ctac 24

<210> 368
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 368
atttatagtg gtggtagcac a 21

<210> 369
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 369
gcgagagatc acggtatggc agcagcgggg tataattac 39

<210> 370
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 370

Ala Arg Asp His Gly Met Ala Ala Ala Gly Tyr Asn Tyr
1 5 10

<210> 371
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 371
gacatccaga tgacccagtc tccatcctcc ctgtctgcgt ctgtaggaga cagagtcacc 60

atcacttgcc aggcgagtca ggacattaac aaatatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctacgat gcatccaatt tggaaacagg ggtcccatca 180

aggttcagtg gaagtggatc tgggacagat tttactttca ccatcaacag cctgcagcct 240

gaagattttg caacatattt ctgtcaacag tatgataatc tccctccagc gttcggccaa 300

gggaccaagg tggaaatcaa a 321

<210> 372
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 372

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 Asn Lys 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 Asn Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Tyr Asp Asn Leu Pro Pro
85 90 95

Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 373
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 373
caggacatta acaaatat 18

<210> 374
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 374
caacagtatg ataatctccc tccagcg 27

<210> 375
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 375

Gln Gln Tyr Asp Asn Leu Pro Pro Ala
1 5

<210> 376
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 376
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggGtc actgagactc 60

tcctgtgcag cctctggaat caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcactt atttatagtg gtggtagcac atactacgca 180

gactccgtga agggcagatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagt cgaggacacg gctgtgtatt actgtgcgag agatcacggt 300

atggcagcag cggggtataa ttactggggc cagggaaccc tggtcaccgt ctcctcagcc 360

tccaccaagg 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 acaagaaagt 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 cctctacagc aagctcaccg tggacaagag caggtggcag 1260

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320

aagtccctct ccctgtctcc gggtaaatga 1350

<210> 377
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 377

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 Ile Thr Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Leu Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

```
Arg Asp His Gly Met Ala Ala Ala Gly Tyr Asn 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 Lys 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

Lys

<210> 378
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 378
gacatccaga tgacccagtc tccatcctcc ctgtctgcgt ctgtaggaga cagagtcacc 60

atcacttgcc aggcgagtca ggacattaac aaatatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctacgat gcatccaatt tggaaacagg ggtcccatca 180

aggttcagtg gaagtggatc tgggacagat tttactttca ccatcaacag cctgcagcct 240

gaagattttg caacatattt ctgtcaacag tatgataatc tccctccagc gttcggccaa 300

gggaccaagg tggaaatcaa acgaactgtg 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 gttag 645

<210> 379
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 379

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 Asn Lys 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 Asn Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Tyr Asp Asn Leu Pro Pro
85 90 95

Ala 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> 380
<211> 345
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 380
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagagtc 60

tcctgtgcag cctctggatt caccgtcagt aggaactaca tgagttgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac attctacgca 180

gactccgtga agggcagatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc cgaggacacg gctatatatt actgtgcgag atacattcct 300

aggttcgacc cctggggcca gggaaccctg gtcaccgtct cctca 345

<210> 381
<211> 115
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 381

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Val Ser Cys Ala Ala Ser Gly Phe Thr Val Ser Arg Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys Ala
85 90 95

Arg Tyr Ile Pro Arg Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 382
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 382
ggattcaccg tcagtaggaa ctac 24

<210> 383
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 383

Gly Phe Thr Val Ser Arg Asn Tyr
1 5

<210> 384
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 384
gcgagataca ttcctaggtt cgacccc 27

<210> 385
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 385

Ala Arg Tyr Ile Pro Arg Phe Asp Pro
1 5

<210> 386
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 386
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc aggcgagtca ggacattagc aactatttaa attggtttca gcagaaacca 120

gggagagccc ctaagctcct catctacgat gcatccaatt tggaaacagg ggtcccatca 180

aggttcagtg gaagtggatc tgggacagat tttactttca ccatcagcag cctgcagcct 240

gaagatattg caacatatta ctgtcaacag tatgataatc tcccgatcac cttcggccaa 300

gggacacgac tggagattaa a 321

<210> 387
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 387

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 Phe Gln Gln Lys Pro Gly Arg 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 Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 388
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 388
caggacatta gcaactat 18

<210> 389
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 389

Gln Asp Ile Ser Asn Tyr
1   5

<210> 390
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 390
caacagtatg ataatctccc gatcacc   27

<210> 391
<211> 1338
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 391
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagagtc   60

tcctgtgcag cctctggatt caccgtcagt aggaactaca tgagttgggt ccgccaggct   120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac attctacgca   180

gactccgtga agggcagatt caccatctcc agagacaatt ccaagaacac gctgtatctt   240

caaatgaaca gcctgagagc cgaggacacg gctatatatt actgtgcgag atacattcct   300

aggttcgacc cctggggcca gggaaccctg gtcaccgtct cctcagcctc caccaagggc   360

ccatcggtct tcccctggc accctcctcc aagagcacct ctgggggcac agcggccctg   420

ggctgcctgg tcaaggacta cttccccgaa ccggtgacgg tgtcgtggaa ctcaggcgcc   480

ctgaccagcg gcgtgcacac cttcccggct gtcctacagt cctcaggact ctactccctc   540

agcagcgtgg tgaccgtgcc ctccagcagc ttgggcaccc agacctacat ctgcaacgtg   600

aatcacaagc ccagcaacac caaggtggac aagaaagttg agcccaaatc ttgtgacaaa   660

actcacacat gcccaccgtg cccagcacct gaactcctgg ggggaccgtc agtcttcctc   720

ttccccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg   780

gtggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg 840

gaggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg 900

gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcaag 960

gtctccaaca aagccctccc agcccccatc gagaaaacca tctccaaagc caaagggcag 1020

ccccgagaac cacaggtgta caccctgccc ccatcccggg atgagctgac caagaaccag 1080

gtcagcctga cctgcctggt caaaggcttc tatcccagcg acatcgccgt ggagtgggag 1140

agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc 1200

tccttcttcc tctacagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc 1260

ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gtccctctcc 1320

ctgtctccgg gtaaatga 1338

<210> 392
<211> 445
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 392

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Val Ser Cys Ala Ala Ser Gly Phe Thr Val Ser Arg Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys Ala
85 90 95

```
Arg Tyr Ile Pro Arg Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr
            100                 105                 110

Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
        115                 120                 125

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
    130                 135                 140

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
145                 150                 155                 160

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
                165                 170                 175

Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
            180                 185                 190

Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
        195                 200                 205

Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
    210                 215                 220

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
225                 230                 235                 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                245                 250                 255

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
            260                 265                 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        275                 280                 285

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    290                 295                 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305                 310                 315                 320
```

```
Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                325                 330                 335

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            340                 345                 350

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        355                 360                 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    370                 375                 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385                 390                 395                 400

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                405                 410                 415

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            420                 425                 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445


<210>  393
<211>  645
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  393
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc       60

atcacttgcc aggcgagtca ggacattagc aactatttaa attggtttca gcagaaacca      120

gggagagccc ctaagctcct catctacgat gcatccaatt tggaaacagg ggtcccatca      180

aggttcagtg gaagtggatc tgggacagat tttactttca ccatcagcag cctgcagcct      240

gaagatattg caacatatta ctgtcaacag tatgataatc tcccgatcac cttcggccaa      300

gggacacgac tggagattaa acgaactgtg gctgcaccat ctgtcttcat cttcccgcca      360
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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 gttag 645

<210> 394
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 394

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 Phe Gln Gln Lys Pro Gly Arg 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 Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu 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>  395
<211>  351
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  395
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc       60

tcctgtgcag cctccggact caccgtcagt agcaactaca tgagctgggt ccgccaggct      120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac attctacgca      180

gactccgtga agggccgatt caccatctcc agagacaatt ccaagaacac gctgtatctt      240

caaatgaaca gcctgagagc tgaggacacg gctgtgtatt actgtgcgag agatcttatc      300

aaatacggta tggacgtctg gggccaaggg accacggtca ccgtctcctc a               351


<210>  396
<211>  117
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  396

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 Leu Thr Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Leu Ile Lys Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser
115

<210> 397
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 397
ggactcaccg tcagtagcaa ctac 24

<210> 398
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 398
gcgagagatc ttatcaaata cggtatggac gtc 33

<210> 399
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 399

Ala Arg Asp Leu Ile Lys Tyr Gly Met Asp Val
1 5 10

<210> 400
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 400
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc aggcgagtca ggacattagc aactatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctacgat gcatccaatt tggaaacagg ggtcccatca 180

aggttcagtg gaagtggatc tgggacagat tttactttca ccatcagcag cctgcagcct 240

gaagatattg caacatatta ctgtcaacag tatgataatc tccctcccca tttcggccct 300

gggaccaaag tggatatcaa a 321

<210> 401
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 401

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 Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Pro
85 90 95

His Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 402
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 402
caacagtatg ataatctccc tccccat 27

<210> 403
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 403

Gln Gln Tyr Asp Asn Leu Pro Pro His
1 5

<210> 404
<211> 1344
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 404
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctccggact caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac attctacgca 180

gactccgtga agggccgatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc tgaggacacg gctgtgtatt actgtgcgag agatcttatc 300

aaatacggta tggacgtctg gggccaaggg accacggtca ccgtctcctc agcctccacc 360

aagggcccat cggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 600

aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 660

gacaaaactc acacatgccc accgtgccca gcacctgaac tcctgggggg accgtcagtc 720

ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 780

tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 840

ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac 900

cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 960

tgcaaggtct ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa 1020

gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggatga gctgaccaag 1080

aaccaggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag 1140

tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 1200

gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg 1260

aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagtcc 1320

ctctccctgt ctccgggtaa atga 1344

<210> 405
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 405

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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 Leu Thr Val Ser Ser Asn
            20                  25                  30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
    50                  55                  60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65                  70                  75                  80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Leu Ile Lys Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr
            100                 105                 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
        115                 120                 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
    130                 135                 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145                 150                 155                 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
                165                 170                 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
            180                 185                 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
        195                 200                 205

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
    210                 215                 220
```

```
Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
225                 230                 235                 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
                245                 250                 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
            260                 265                 270

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
        275                 280                 285

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
    290                 295                 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305                 310                 315                 320

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
                325                 330                 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
            340                 345                 350

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
        355                 360                 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
    370                 375                 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385                 390                 395                 400

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
                405                 410                 415

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
            420                 425                 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
```

435 440 445

<210> 406
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 406
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc aggcgagtca ggacattagc aactatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctacgat gcatccaatt tggaaacagg ggtcccatca 180

aggttcagtg gaagtggatc tgggacagat tttactttca ccatcagcag cctgcagcct 240

gaagatattg caacatatta ctgtcaacag tatgataatc tccctcccca tttcggccct 300

gggaccaaag tggatatcaa acgaactgtg 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 gttag 645

<210> 407
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 407

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 Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Pro
                85                  90                  95

His Phe Gly Pro Gly Thr Lys Val Asp 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> 408
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 408

gaggtgcagc tggtggagtc tggaggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggggt caccgtcagt agcaactata tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagtac attctacgca 180

gactccgtga agggccgatt taccatctcc agagacaact ccaagaacac gctgtttctt 240

caaatgaaca gcctgagaat tgaggacacg gccgtgtatt attgtgcgag agatttaggt 300

ccttacggta tggacgtctg gggccaaggg accacggtca ccgtctcctc a 351

<210> 409
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 409

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 Val Thr Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ile Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Leu Gly Pro Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser
115

<210> 410
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 410
ggggtcaccg tcagtagcaa ctat 24

<210> 411
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 411

Gly Val Thr Val Ser Ser Asn Tyr
1 5

<210> 412
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 412
atttatagcg gtggtagtac a 21

<210> 413
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 413
gcgagagatt taggtcctta cggtatggac gtc 33

<210> 414
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 414

Ala Arg Asp Leu Gly Pro Tyr Gly Met Asp Val
1   5   10

<210> 415
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 415
gacatccagt tgacccagtc tccatccttc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggccagtca gggcattagc agttatttag cctggtatca gcaaaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccactt tgcaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacacaa ttcattctca caatcagcag cctgcagcct 240

gaagattttg caacttatta ctgtcaacag cttaatagtt accccggatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 416
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 416

Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1   5   10   15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Tyr
            20   25   30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Thr Gln Phe Ile Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Asn Ser Tyr Pro Gly
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 417
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 417
caacagctta atagttaccc cggattcact 30

<210> 418
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 418

Gln Gln Leu Asn Ser Tyr Pro Gly Phe Thr
1 5 10

<210> 419
<211> 1344
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 419
gaggtgcagc tggtggagtc tggaggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggggt caccgtcagt agcaactata tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagtac attctacgca 180

gactccgtga agggccgatt taccatctcc agagacaact ccaagaacac gctgtttctt 240

caaatgaaca gcctgagaat tgaggacacg gccgtgtatt attgtgcgag agatttaggt 300

ccttacggta tggacgtctg gggccaaggg accacggtca ccgtctcctc agcctccacc 360

aagggcccat cggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 600

aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 660

gacaaaactc acacatgccc accgtgccca gcacctgaac tcctgggggg accgtcagtc 720

ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 780

tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 840

ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac 900

cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 960

tgcaaggtct ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa 1020

gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggatga gctgaccaag 1080

aaccaggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag 1140

tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 1200

gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg 1260

aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagtcc 1320

ctctccctgt ctccgggtaa atga 1344

<210> 420
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 420

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 Val Thr Val Ser Ser Asn
            20                  25                  30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
    50                  55                  60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe Leu
65                  70                  75                  80

Gln Met Asn Ser Leu Arg Ile Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Leu Gly Pro Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr
            100                 105                 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
        115                 120                 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
    130                 135                 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145                 150                 155                 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
                165                 170                 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
            180                 185                 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
        195                 200                 205

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
    210                 215                 220

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
225                 230                 235                 240
```

```
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
                245                 250                 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
            260                 265                 270

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
        275                 280                 285

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
    290                 295                 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305                 310                 315                 320

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
                325                 330                 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
            340                 345                 350

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
        355                 360                 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
    370                 375                 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385                 390                 395                 400

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
                405                 410                 415

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
            420                 425                 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445
```

<210> 421
<211> 648

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 421
gacatccagt tgacccagtc tccatccttc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggccagtca gggcattagc agttatttag cctggtatca gcaaaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccactt tgcaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacacaa ttcattctca caatcagcag cctgcagcct 240

gaagattttg caacttatta ctgtcaacag cttaatagtt accccggatt cactttcggc 300

cctgggacca aagtggatat caaacgaact gtggctgcac catctgtctt catcttcccg 360

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 480

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 600

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgttag 648

<210> 422
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 422

Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

```
Ser Gly Ser Gly Thr Gln Phe Ile Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Asn Ser Tyr Pro Gly
                85                  90                  95


Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
            100                 105                 110


Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115                 120                 125


Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    130                 135                 140


Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160


Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
                165                 170                 175


Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
            180                 185                 190


Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
        195                 200                 205


Ser Phe Asn Arg Gly Glu Cys
    210                 215


<210>  423
<211>  1338
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  423
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc actgagactc       60

tcctgtgcag cctctggaat caccgtcagt agcaactaca tgagctgggt ccgccaggct      120

ccagggaagg ggctggagtg ggtctcactt atttatagtg gtggtagcac atactacgca      180
```

gactccgtga agggcagatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagt cgaggacacg gctgtgtatt actgtgcgag agatcacggt 300

atggcagcag cggggtataa ttactggggc cagggaaccc tggtcaccgt ctcctcagcc 360

tccaccaagg gcccatcggt cttccccctg gcgccctgct ccaggagcac ctccgagagc 420

acagccgccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480

aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac gaagacctac 600

acctgcaacg tagatcacaa gcccagcaac accaaggtgg acaagagagt tgagtccaaa 660

tatggtcccc catgcccacc gtgcccagca ccaggcggtg gcggaccatc agtcttcctg 720

ttcccccaa aacccaagga cactctcatg atctcccgga cccctgaggt cacgtgcgtg 780

gtggtggacg tgagccagga agaccccgag gtccagttca actggtacgt ggatggcgtg 840

gaggtgcata atgccaagac aaagccgcgg gaggagcagt tcaacagcac gtaccgtgtg 900

gtcagcgtcc tcaccgtcct gcaccaggac tggctgaacg gcaaggagta caagtgcaag 960

gtctccaaca aaggcctccc gtcctccatc gagaaaacca tctccaaagc caaagggcag 1020

ccccgagagc cacaggtgta caccctgccc ccatcccagg aggagatgac caagaaccag 1080

gtcagcctga cctgcctggt caaaggcttc taccccagcg acatcgccgt ggagtgggag 1140

agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc 1200

tccttcttcc tctacagcag gctcaccgtg gacaagagca ggtggcagga ggggaatgtc 1260

ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacacagaa gtccctctcc 1320

ctgtctctgg gtaaatga 1338

<210> 424
<211> 445
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 424

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 Ile Thr Val Ser Ser Asn
            20                  25                  30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Leu Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
    50                  55                  60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65                  70                  75                  80

Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp His Gly Met Ala Ala Ala Gly Tyr Asn 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 Cys Ser Arg Ser Thr Ser Glu Ser 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 Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
        195                 200                 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
    210                 215                 220

Cys Pro Pro Cys Pro Ala Pro Gly Gly Gly Gly Pro Ser Val Phe Leu
225                 230                 235                 240
```

```
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                245                 250                 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
            260                 265                 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        275                 280                 285

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    290                 295                 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305                 310                 315                 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
                325                 330                 335

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            340                 345                 350

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        355                 360                 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    370                 375                 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385                 390                 395                 400

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
                405                 410                 415

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            420                 425                 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440                 445
```

<210> 425

<211> 1326
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 425
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggGtc cctgagagtc 60

tcctgtgcag cctctggatt caccgtcagt aggaactaca tgagttgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac attctacgca 180

gactccgtga agggcagatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc cgaggacacg gctatatatt actgtgcgag atacattcct 300

aggttcgacc cctggggcca gggaaccctg gtcaccgtct cctcagcctc caccaagggc 360

ccatcggtct tcccCctggc gccctgctcc aggagcacct ccgagagcac agccgccctg 420

ggctgcctgg tcaaggacta cttccccgaa ccggtgacgg tgtcgtggaa ctcaggcgcc 480

ctgaccagcg gcgtgcacac cttcccggct gtcctacagt cctcaggact ctactccctc 540

agcagcgtgg tgaccgtgcc ctccagcagc ttgggcacga agacctacac ctgcaacgta 600

gatcacaagc ccagcaacac caaggtggac aagagagttg agtccaaata tggtccccca 660

tgcccaccgt gcccagcacc aggcggtggc ggaccatcag tcttcctgtt cccccCaaaa 720

cccaaggaca ctctcatgat ctcccggacc cctgaggtca cgtgcgtggt ggtggacgtg 780

agccaggaag accccgaggt ccagttcaac tggtacgtgg atggcgtgga ggtgcataat 840

gccaagacaa agccgcggga ggagcagttc aacagcacgt accgtgtggt cagcgtcctc 900

accgtcctgc accaggactg gctgaacggc aaggagtaca agtgcaaggt ctccaacaaa 960

ggcctcccgt cctccatcga gaaaaccatc tccaaagcca aagggcagcc ccgagagcca 1020

caggtgtaca ccctgccccc atcccaggag gagatgacca agaaccaggt cagcctgacc 1080

tgcctggtca aaggcttcta ccccagcgac atcgccgtgg agtgggagag caatgggcag 1140

ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc 1200

tacagcaggc tcaccgtgga caagagcagg tggcaggagg ggaatgtctt ctcatgctcc 1260

gtgatgcatg aggctctgca caaccactac acacagaagt ccctctccct gtctctgggt 1320

aaatga 1326

<210> 426
<211> 441
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 426

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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Val Ser Cys Ala Ala Ser Gly Phe Thr Val Ser Arg Asn
            20                  25                  30


Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
    50                  55                  60


Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65                  70                  75                  80


Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys Ala
                85                  90                  95


Arg Tyr Ile Pro Arg Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr
            100                 105                 110


Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
        115                 120                 125


Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val
    130                 135                 140


Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
145                 150                 155                 160


Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
                165                 170                 175


Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
```

```
            180                 185                 190

Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys
        195                 200                 205

Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys
    210                 215                 220

Pro Ala Pro Gly Gly Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
225                 230                 235                 240

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
                245                 250                 255

Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
            260                 265                 270

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
        275                 280                 285

Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
    290                 295                 300

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
305                 310                 315                 320

Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
                325                 330                 335

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met
            340                 345                 350

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
        355                 360                 365

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
    370                 375                 380

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
385                 390                 395                 400
```

```
Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val
                405                 410                 415


Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
            420                 425                 430


Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440


<210>  427
<211>  1332
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  427
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc       60

tcctgtgcag cctccggact caccgtcagt agcaactaca tgagctgggt ccgccaggct      120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac attctacgca      180

gactccgtga agggccgatt caccatctcc agagacaatt ccaagaacac gctgtatctt      240

caaatgaaca gcctgagagc tgaggacacg gctgtgtatt actgtgcgag agatcttatc      300

aaatacggta tggacgtctg gggccaaggg accacggtca ccgtctcctc agcctccacc      360

aagggcccat cggtcttccc cctggcgccc tgctccagga gcacctccga gagcacagcc      420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca      480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac      540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacgaagac ctacacctgc      600

aacgtagatc acaagcccag caacaccaag gtggacaaga gagttgagtc caaatatggt      660

cccccatgcc caccgtgccc agcaccaggc ggtggcggac catcagtctt cctgttcccc      720

ccaaaaccca aggacactct catgatctcc cggacccctg aggtcacgtg cgtggtggtg      780

gacgtgagcc aggaagaccc cgaggtccag ttcaactggt acgtggatgg cgtggaggtg      840

cataatgcca agacaaagcc gcgggaggag cagttcaaca gcacgtaccg tgtggtcagc      900

gtcctcaccg tcctgcacca ggactggctg aacggcaagg agtacaagtg caaggtctcc      960

aacaaaggcc tcccgtcctc catcgagaaa accatctcca aagccaaagg gcagccccga     1020
```

gagccacagg tgtacaccct gcccccatcc caggaggaga tgaccaagaa ccaggtcagc 1080

ctgacctgcc tggtcaaagg cttctacccc agcgacatcg ccgtggagtg ggagagcaat 1140

gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1200

ttcctctaca gcaggctcac cgtggacaag agcaggtggc aggaggggaa tgtcttctca 1260

tgctccgtga tgcatgaggc tctgcacaac cactacacac agaagtccct ctccctgtct 1320

ctgggtaaat ga 1332

<210> 428
<211> 443
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 428

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 Leu Thr Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Leu Ile Lys Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
115 120 125

```
Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
    130                 135                 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145                 150                 155                 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
                165                 170                 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
            180                 185                 190

Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
        195                 200                 205

Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro
    210                 215                 220

Pro Cys Pro Ala Pro Gly Gly Gly Gly Pro Ser Val Phe Leu Phe Pro
225                 230                 235                 240

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
                245                 250                 255

Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
            260                 265                 270

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
        275                 280                 285

Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
    290                 295                 300

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
305                 310                 315                 320

Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
                325                 330                 335

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu
            340                 345                 350
```

```
Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
        355                 360                 365

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
    370                 375                 380

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
385                 390                 395                 400

Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly
                405                 410                 415

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
            420                 425                 430

Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440
```

<210> 429
<211> 1332
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 429

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gaggtgcagc tggtggagtc tggaggaggc ttggtccagc ctgggggtc cctgagactc       60

tcctgtgcag cctctggggt caccgtcagt agcaactata tgagctgggt ccgccaggct      120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagtac attctacgca      180

gactccgtga agggccgatt taccatctcc agagacaact ccaagaacac gctgtttctt      240

caaatgaaca gcctgagaat tgaggacacg gccgtgtatt attgtgcgag agatttaggt      300

ccttacggta tggacgtctg gggccaaggg accacggtca ccgtctcctc agcctccacc      360

aagggcccat cggtcttccc cctggcgccc tgctccagga gcacctccga gagcacagcc      420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca      480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac      540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacgaagac ctacacctgc      600

aacgtagatc acaagcccag caacaccaag gtggacaaga gagttgagtc caaatatggt      660
```

```
cccccatgcc caccgtgccc agcaccaggc ggtggcggac catcagtctt cctgttcccc      720

ccaaaaccca aggacactct catgatctcc cggacccctg aggtcacgtg cgtggtggtg      780

gacgtgagcc aggaagaccc cgaggtccag ttcaactggt acgtggatgg cgtggaggtg      840

cataatgcca agacaaagcc gcgggaggag cagttcaaca gcacgtaccg tgtggtcagc      900

gtcctcaccg tcctgcacca ggactggctg aacggcaagg agtacaagtg caaggtctcc      960

aacaaaggcc tcccgtcctc catcgagaaa accatctcca aagccaaagg gcagccccga     1020

gagccacagg tgtacaccct gcccccatcc caggaggaga tgaccaagaa ccaggtcagc     1080

ctgacctgcc tggtcaaagg cttctacccc agcgacatcg ccgtggagtg ggagagcaat     1140

gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc     1200

ttcctctaca gcaggctcac cgtggacaag agcaggtggc aggaggggaa tgtcttctca     1260

tgctccgtga tgcatgaggc tctgcacaac cactacacac agaagtccct ctccctgtct     1320

ctgggtaaat ga                                                         1332
```

<210> 430
<211> 443
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 430

```
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 Val Thr Val Ser Ser Asn
            20                  25                  30


Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
    50                  55                  60


Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe Leu
65                  70                  75                  80
```

```
Gln Met Asn Ser Leu Arg Ile Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Leu Gly Pro Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr
            100                 105                 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
        115                 120                 125

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
    130                 135                 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145                 150                 155                 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
                165                 170                 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
            180                 185                 190

Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
        195                 200                 205

Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro
    210                 215                 220

Pro Cys Pro Ala Pro Gly Gly Gly Gly Pro Ser Val Phe Leu Phe Pro
225                 230                 235                 240

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
                245                 250                 255

Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
            260                 265                 270

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
        275                 280                 285

Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
    290                 295                 300
```

```
Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
305                 310                 315                 320

Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
                325                 330                 335

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu
            340                 345                 350

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
        355                 360                 365

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
    370                 375                 380

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
385                 390                 395                 400

Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly
                405                 410                 415

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
            420                 425                 430

Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440
```

<210> 431
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 431
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60

acctgcactg tctctggtgg ctccatcaat aattactact ggatctggat ccggcagccc 120

ccagggaagg gactggagtg gattgggtat atctatcaca gtgggagcac caactacaac 180

ccctccctca agagtcgagt caccatatca gtagacacgt ccaagaacca attctccctg 240

aaggtgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgcgaa tatggttcgg 300

ggagtttatg aagatgacta ctggggccag ggaaccctgg tcaccgtctc ctca 354

<210> 432
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 432

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 Ile Asn Asn Tyr
20 25 30

Tyr Trp Ile Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Tyr His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

Lys Val Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Asn Met Val Arg Gly Val Tyr Glu Asp Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 433
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 433
ggtggctcca tcaataatta ctac 24

<210> 434
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 434

Gly Gly Ser Ile Asn Asn Tyr Tyr
1 5

<210> 435
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 435
atctatcaca gtgggagcac c 21

<210> 436
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 436

Ile Tyr His Ser Gly Ser Thr
1 5

<210> 437
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 437
gcgaatatgg ttcggggagt ttatgaagat gactac 36

<210> 438
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 438

Ala Asn Met Val Arg Gly Val Tyr Glu Asp Asp Tyr
1 5 10

<210> 439
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 439
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattagc aactatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctttgct gcctccagtt tgcgaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaccct 240

gaagattttg caacttacta ctgtcaacag aattacaata ccccctcac tttcggccct 300

gggaccaaag tggatatcaa a 321

<210> 440
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 440

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 Ser 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

Phe Ala Ala Ser Ser Leu Arg 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 His Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asn Tyr Asn Thr Pro Leu
                85                  90                  95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
            100                 105
```

<210> 441
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 441
cagagcatta gcaactat 18

<210> 442
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 442

```
Gln Ser Ile Ser Asn Tyr
1               5
```

<210> 443
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 443

gctgcctcc 9

<210> 444
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 444
caacagaatt acaatacccc cctcact 27

<210> 445
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 445

Gln Gln Asn Tyr Asn Thr Pro Leu Thr
1 5

<210> 446
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 446
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60

acctgcactg tctctggtgg ctccatcaat aattactact ggatctggat ccggcagccc 120

ccagggaagg gactggagtg gattgggtat atctatcaca gtgggagcac caactacaac 180

ccctccctca agagtcgagt caccatatca gtagacacgt ccaagaacca attctccctg 240

aaggtgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgcgaa tatggttcgg 300

ggagtttatg aagatgacta ctggggccag ggaaccctgg tcaccgtctc ctcagcctcc 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 agaaagttga 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 tgagctgacc 1080

aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1140

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200

tccgacggct ccttcttcct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag 1260

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320

tccctctccc tgtctccggg taaatga 1347

<210> 447
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 447

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 Ile Asn Asn Tyr
20 25 30

Tyr Trp Ile Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Tyr His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

```
Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65                  70                  75                  80

Lys Val Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Asn Met Val Arg Gly Val Tyr Glu Asp Asp Tyr Trp Gly Gln 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 Lys 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 Asp Glu Leu 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>  448
<211>  645
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  448
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc       60

atcacttgcc gggcaagtca gagcattagc aactatttaa attggtatca gcagaaacca      120
```

gggaaagccc ctaagctcct gatctttgct gcctccagtt tgcgaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaccct 240

gaagattttg caacttacta ctgtcaacag aattacaata ccccccctcac tttcggccct 300

gggaccaaag tggatatcaa acgaactgtg 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 gttag 645

<210> 449
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 449

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 Ser 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

Phe Ala Ala Ser Ser Leu Arg 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 His Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asn Tyr Asn Thr Pro Leu
85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp 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> 450
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 450
gaggtgcagc tggtggagtc tggaggaggc ttgatccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctgtgtt caccgtcagt tacaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac atactacgca 180

gactccgtga agggccgatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc cgaggacacg gccgtgtatt actgtgcgag agccctcccc 300

gggtggggtg ggagcttcga gtactttgac tactggggcc agggaaccct ggtcaccgtc 360

tcctca 366

<210> 451

<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 451

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Ile Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Val Phe Thr Val Ser Tyr Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Ala Leu Pro Gly Trp Gly Gly Ser Phe Glu Tyr Phe Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 452
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 452
gtgttcaccg tcagttacaa ctac 24

<210> 453
<211> 8

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 453

Val Phe Thr Val Ser Tyr Asn Tyr
1 5

<210> 454
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 454
gcgagagccc tccccgggtg gggtgggagc ttcgagtact ttgactac 48

<210> 455
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 455

Ala Arg Ala Leu Pro Gly Trp Gly Gly Ser Phe Glu Tyr Phe Asp Tyr
1 5 10 15

<210> 456
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 456
gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggccagtca gagtattagt agttggttgg cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctataag gcatctagtt tagaaagtgg ggtctcatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240

gatgattttg caacttatta ctgccaacag tataatagtt attctgtgac gttcggccaa 300

gggaccaagg tggaaatcaa a 321

<210> 457
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 457

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Ser Leu Glu Ser Gly Val Ser Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Ser Val
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 458
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 458
cagagtatta gtagttgg 18

<210> 459
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 459

Gln Ser Ile Ser Ser Trp
1 5

<210> 460
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 460
aaggcatct 9

<210> 461
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 461
caacagtata atagttattc tgtgacg 27

<210> 462
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 462

Gln Gln Tyr Asn Ser Tyr Ser Val Thr
1 5

<210> 463
<211> 1359
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 463
gaggtgcagc tggtggagtc tggaggaggc ttgatccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctgtgtt caccgtcagt tacaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac atactacgca 180

gactccgtga agggccgatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc cgaggacacg gccgtgtatt actgtgcgag agccctcccc 300

gggtggggtg ggagcttcga gtactttgac tactggggcc agggaaccct ggtcaccgtc 360

tcctcagcct ccaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc 420

tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 480

gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag 540

tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 600

cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt 660

gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 720

gggggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 780

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 840

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 900

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 960

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc 1020

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1080

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 1140

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1200

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 1260

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1320

tacacgcaga agtccctctc cctgtctccg ggtaaatga 1359

<210> 464
<211> 452

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 464

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Ile Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Val Phe Thr Val Ser Tyr Asn
            20                  25                  30


Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
    50                  55                  60


Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65                  70                  75                  80


Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95


Arg Ala Leu Pro Gly Trp Gly Gly Ser Phe Glu Tyr Phe Asp Tyr Trp
            100                 105                 110


Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
        115                 120                 125


Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
    130                 135                 140


Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145                 150                 155                 160


Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
                165                 170                 175


Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
            180                 185                 190
```

```
Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
        195                 200                 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
    210                 215                 220

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
225                 230                 235                 240

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                245                 250                 255

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            260                 265                 270

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
        275                 280                 285

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
    290                 295                 300

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
305                 310                 315                 320

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
                325                 330                 335

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            340                 345                 350

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
        355                 360                 365

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    370                 375                 380

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
385                 390                 395                 400

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
                405                 410                 415
```

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
420 425 430

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
435 440 445

Ser Pro Gly Lys
450

<210> 465
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 465
gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggccagtca gagtattagt agttggttgg cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctataag gcatctagtt tagaaagtgg ggtctcatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240

gatgattttg caacttatta ctgccaacag tataatagtt attctgtgac gttcggccaa 300

gggaccaagg tggaaatcaa acgaactgtg 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 gttag 645

<210> 466
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 466

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1               5                  10                  15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Lys Ala Ser Ser Leu Glu Ser Gly Val Ser Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Ser Val
                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> 467
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 467
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggact caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagtac attctacgca 180

gactccgtga agggccgatt caccatctcc agagacaatt ccaagaacac gttgtatctt 240

cagatgaaca gcctgagacc tgaggacacg gctgtgtatt actgtgcgag agagggccgt 300

atagcagcaa ctggctacgg tatggacgtc tggggccaag ggaccacggt caccgtctcc 360

tca 363

<210> 468
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 468

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 Leu Thr Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

```
Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95


Arg Glu Gly Arg Ile Ala Ala Thr Gly Tyr Gly Met Asp Val Trp Gly
            100                 105                 110


Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210>  469
<211>  45
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  469
gcgagagagg gccgtatagc agcaactggc tacggtatgg acgtc                          45


<210>  470
<211>  15
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  470

Ala Arg Glu Gly Arg Ile Ala Ala Thr Gly Tyr Gly Met Asp Val
1               5                   10                  15


<210>  471
<211>  321
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  471
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc       60

atcacttgcc aggcgagtca ggacattagc aactatttaa attggtatca gcagaaacca      120

gggaaagccc ctaagctcct gatctacgat gcatccaatt tgggaacagg ggtcccatca      180

aggttcagtg gaagtagatc tgggacagat tttactttca ccatcagcag cctgcagcct      240
```

gaagatattg cgacatatta ctgtcatcag tatgataatc tccctcaaac tttcggccct 300

gggaccaaag tggatatcaa a 321

<210> 472
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 472

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 Gly Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Arg Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys His Gln Tyr Asp Asn Leu Pro Gln
85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 473
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 473
catcagtatg ataatctccc tcaaact 27

<210> 474
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 474

His Gln Tyr Asp Asn Leu Pro Gln Thr
1 5

<210> 475
<211> 1356
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 475
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggact caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagtac attctacgca 180

gactccgtga agggccgatt caccatctcc agagacaatt ccaagaacac gttgtatctt 240

cagatgaaca gcctgagacc tgaggacacg gctgtgtatt actgtgcgag agagggccgt 300

atagcagcaa ctggctacgg tatggacgtc tggggccaag ggaccacggt caccgtctcc 360

tcagcctcca 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 gaaagttgag 660

cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg 720

ggaccgtcag tcttcctctt cccccaaaa 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 aggggcagcc ccgagaacca caggtgtaca ccctgccccc atcccgggat 1080

gagctgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac 1140

atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1200

gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg 1260

tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1320

acgcagaagt ccctctccct gtctccgggt aaatga 1356

<210> 476
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 476

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 Leu Thr Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Glu Gly Arg Ile Ala Ala Thr Gly Tyr Gly Met Asp Val Trp Gly
100 105 110

Gln Gly Thr Thr 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 Lys 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 Asp Glu Leu 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> 477
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 477
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc aggcgagtca ggacattagc aactatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctacgat gcatccaatt tgggaacagg ggtcccatca 180

aggttcagtg gaagtagatc tgggacagat tttactttca ccatcagcag cctgcagcct 240

gaagatattg cgacatatta ctgtcatcag tatgataatc tccctcaaac tttcggccct 300

gggaccaaag tggatatcaa acgaactgtg 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 gttag 645

<210> 478
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 478

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 Gly Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Arg Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys His Gln Tyr Asp Asn Leu Pro Gln
85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp 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>  479
<211>  342
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  479
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc       60

tcctgtgcag cctctggatt caccgtcagt agcaactaca tgagctgggt ccgccaggct      120

ccagggaagg ggctggagtg ggtctcagtt atttatcccg gtggtagtac attctacgca      180

gactccgtga agggcagatt caccatctcc agagacaatt ccaagaacac gctgtatctt      240

caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag agatcaacgc      300

gattttgcct ggggccaggg aaccctggtc accgtctcct ca                         342


<210>  480
<211>  114
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  480

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 Val Ser Ser Asn
            20                  25                  30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Val Ile Tyr Pro Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
    50                  55                  60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65                  70                  75                  80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Gln Arg Asp Phe Ala Trp Gly Gln Gly Thr Leu Val Thr Val
            100                 105                 110

Ser Ser
```

<210> 481
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 481
ggattcaccg tcagtagcaa ctac 24

<210> 482
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 482
atttatcccg gtggtagtac a 21

<210> 483
<211> 7

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 483

Ile Tyr Pro Gly Gly Ser Thr
1 5

<210> 484
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 484
gcgagagatc aacgcgattt tgcc 24

<210> 485
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 485

Ala Arg Asp Gln Arg Asp Phe Ala
1 5

<210> 486
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 486
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc aggcgagtca ggacattagc aactatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctacgat gcatccaatt tggaaacagg ggtcccatca 180

aggttcagtg gaagtggatc tgggacagat tttactttca ccatcagcgg cctgcagcct 240

gaagatattg caacatatta ctgtcaacag tatgataatc tccctccgac cttcggccaa 300

gggacacgac tggagattaa a 321

<210> 487
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 487

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 Gly Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 488
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 488
caacagtatg ataatctccc tccgacc 27

<210> 489
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 489

Gln Gln Tyr Asp Asn Leu Pro Pro Thr
1 5

<210> 490
<211> 1335
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 490
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatcccg gtggtagtac attctacgca 180

gactccgtga agggcagatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag agatcaacgc 300

gattttgcct ggggccaggg aaccctggtc accgtctcct cagcctccac caagggccca 360

tcggtcttcc ccctggcacc ctcctccaag agcacctctg ggggcacagc ggccctgggc 420

tgcctggtca aggactactt ccccgaaccg gtgacggtgt cgtggaactc aggcgccctg 480

accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcagc 540

agcgtggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat 600

cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaatcttg tgacaaaact 660

cacacatgcc caccgtgccc agcacctgaa ctcctggggg gaccgtcagt cttcctcttc 720

cccccaaaac ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg 780

gtggacgtga gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag 840

gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtggtc 900

agcgtcctca ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc 960

tccaacaaag ccctcccagc ccccatcgag aaaaccatct ccaaagccaa agggcagccc 1020

cgagaaccac aggtgtacac cctgccccca tcccgggatg agctgaccaa gaaccaggtc 1080

agcctgacct gcctggtcaa aggcttctat cccagcgaca tcgccgtgga gtgggagagc 1140

aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc 1200

ttcttcctct acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc 1260

tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagtc cctctccctg 1320

tctccgggta aatga 1335

<210> 491
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 491

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 Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Pro Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Gln Arg Asp Phe Ala Trp Gly Gln Gly Thr Leu Val Thr Val
100 105 110

Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
115 120 125

```
Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
    130                 135                 140

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
145                 150                 155                 160

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
                165                 170                 175

Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
            180                 185                 190

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
        195                 200                 205

Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
    210                 215                 220

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
225                 230                 235                 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
                245                 250                 255

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
            260                 265                 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
        275                 280                 285

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
    290                 295                 300

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305                 310                 315                 320

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
                325                 330                 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
```

```
            340                 345                 350

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
        355                 360                 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
    370                 375                 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
385                 390                 395                 400

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
                405                 410                 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
            420                 425                 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440
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<210> 492
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 492
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc aggcgagtca ggacattagc aactatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctacgat gcatccaatt tggaaacagg ggtcccatca 180

aggttcagtg gaagtggatc tgggacagat tttactttca ccatcagcgg cctgcagcct 240

gaagatattg caacatatta ctgtcaacag tatgataatc tccctccgac cttcggccaa 300

gggacacgac tggagattaa acgaactgtg 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 gttag 645

<210> 493
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 493

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 Gly Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu 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> 494
<211> 381
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 494
caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt agctatgcta tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagtaa taaatactac 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gagagacggc 300

cggactatta ctatggttcg gggagttatt gatgatgctt ttgatatctg gggccaaggg 360

acaatggtca ccgtctcttc a 381

<210> 495
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 495

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

```
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Gly Arg Thr Ile Thr Met Val Arg Gly Val Ile Asp Asp
            100                 105                 110


Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120                 125


<210>  496
<211>  24
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  496
ggattcacct tcagtagcta tgct                                              24


<210>  497
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  497

Gly Phe Thr Phe Ser Ser Tyr Ala
1               5


<210>  498
<211>  24
<212>  DNA
```

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 498
atatcatatg atggaagtaa taaa 24

<210> 499
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 499

Ile Ser Tyr Asp Gly Ser Asn Lys
1 5

<210> 500
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 500
gcgagagacg gccggactat tactatggtt cggggagtta ttgatgatgc ttttgatatc 60

<210> 501
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 501

Ala Arg Asp Gly Arg Thr Ile Thr Met Val Arg Gly Val Ile Asp Asp
1 5 10 15

Ala Phe Asp Ile
20

<210> 502
<211> 321

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 502
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc aggcgagtca ggacattagc aactatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctacgat gcatccaatt tggaaacagg ggtcccatca 180

aggttcagtg gaagtggatc tgggacagat tttactttca ccatcagcag cctgcagcct 240

gaagatattg caacatatta ctgtcaacag tatgataatc tccccctcac cttcggccaa 300

gggacacgac tggagattaa a 321

<210> 503
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 503

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 Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys

100 105

<210> 504
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 504
caacagtatg ataatctccc cctcacc 27

<210> 505
<211> 1374
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 505
caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt agctatgcta tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagtaa taaatactac 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gagagacggc 300

cggactatta ctatggttcg gggagttatt gatgatgctt ttgatatctg gggccaaggg 360

acaatggtca ccgtctcttc agcctccacc aagggcccat cggtcttccc cctggcaccc 420

tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctggtcaa ggactacttc 480

cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 540

ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc 600

agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 660

gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca 720

gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 900

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1320

gctctgcaca accactacac gcagaagtcc ctctccctgt ctccgggtaa atga 1374

<210> 506
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 506

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Gly Arg Thr Ile Thr Met Val Arg Gly Val Ile Asp Asp
100 105 110

Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala

```
        115                 120                 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
    130                 135                 140

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145                 150                 155                 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
                165                 170                 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
            180                 185                 190

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
        195                 200                 205

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
    210                 215                 220

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
225                 230                 235                 240

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335
```

```
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                405                 410                 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        435                 440                 445

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455
```

<210> 507
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 507

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gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc       60

atcacttgcc aggcgagtca ggacattagc aactatttaa attggtatca gcagaaacca      120

gggaaagccc ctaagctcct gatctacgat gcatccaatt tggaaacagg ggtcccatca      180

aggttcagtg gaagtggatc tgggacagat tttactttca ccatcagcag cctgcagcct      240

gaagatattg caacatatta ctgtcaacag tatgataatc tccccctcac cttcggccaa      300

gggacacgac tggagattaa acgaactgtg 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 gttag 645

<210> 508
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 508

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 Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu 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>  509
<211>  360
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  509
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc       60

tcctgtgcag cctctggatt caccgtcagt agcaactaca tgagctgggt ccgccaggct      120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagtac atactacgca      180

gactccgtga agggccgatt caccatctcc agagacaatt ccaagaacac gctgtatctt      240

caaatgaaca gactgagagc tgacgacacg gctgtctatt actgtgtgag agatccggtg      300

gggcgctact actacggtat ggacgtctgg ggccaaggga ccacggtcac cgtctcctca      360


<210>  510
<211>  120
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  510

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 Val Ser Ser Asn
            20   25   30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
    50   55   60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65   70   75   80

Gln Met Asn Arg Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Cys Val
                85   90   95

Arg Asp Pro Val Gly Arg Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln
            100   105   110

Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 511
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 511
gtgagagatc cggtggggcg ctactactac ggtatggacg tc   42

<210> 512
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 512

Val Arg Asp Pro Val Gly Arg Tyr Tyr Tyr Gly Met Asp Val
1   5   10

<210> 513
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 513
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc aggcgagtca ggacattaac aactatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctacgat gcatccaatt tggaaacagg ggtcccatca 180

aggttcagtg gaagtggatc tgggacagat tttactttca ccatcagcag cctgcagcct 240

gaagatattg caacatatta ttgtcaacag tatgataatc tccctcgcac tttcggcgga 300

gggaccaagg tggagatcaa a 321

<210> 514
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 514

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 Asn 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 Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Arg
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 515
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 515
caggacatta acaactat 18

<210> 516
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 516

Gln Asp Ile Asn Asn Tyr
1 5

<210> 517
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 517
caacagtatg ataatctccc tcgcact 27

<210> 518
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 518

Gln Gln Tyr Asp Asn Leu Pro Arg Thr
1 5

<210> 519
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 519
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagtac atactacgca 180

gactccgtga agggccgatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240

caaatgaaca gactgagagc tgacgacacg gctgtctatt actgtgtgag agatccggtg 300

gggcgctact actacggtat ggacgtctgg ggccaaggga ccacggtcac cgtctcctca 360

gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 600

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaact cctgggggga 720

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct 780

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 900

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960

gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1020

aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggatgag 1080

ctgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc 1140

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200

ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg 1260

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1320

cagaagtccc tctccctgtc tccgggtaaa tga 1353

<210> 520
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 520

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 Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Arg Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Cys Val
85 90 95

Arg Asp Pro Val Gly Arg Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

```
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
        355                 360                 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
```

385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gly Lys
450

<210> 521
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 521
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc aggcgagtca ggacattaac aactatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctacgat gcatccaatt tggaaacagg ggtcccatca 180

aggttcagtg gaagtggatc tgggacagat tttactttca ccatcagcag cctgcagcct 240

gaagatattg caacatatta ttgtcaacag tatgataatc tccctcgcac tttcggcgga 300

gggaccaagg tggagatcaa acgaactgtg 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 gttag 645

<210> 522
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 522

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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 Gln Ala Ser Gln Asp Ile Asn 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 Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Arg
                85                  90                  95


Thr 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> 523
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 523
gaggtgcagc tggtggagtc tggaggaggc ttgatccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggggt caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtc atttatagcg gcggtagcac attctactca 180

gactccgtga agggccgatt cagcatctcc agagacaatt ccaagaacac actgtatctt 240

caaatgaaca gcctgagagc cgaggacacg gccgtgtatt actgtgcgag agacctctac 300

tactacggta tggacgtctg gggccaaggg accacggtca ccgtctcctc a 351

<210> 524
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 524

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Ile Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Thr Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ser Asp Ser Val Lys
50 55 60

```
Gly Arg Phe Ser Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65                  70                  75                  80


Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95


Arg Asp Leu Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr
            100                 105                 110


Val Thr Val Ser Ser
        115


<210>  525
<211>  24
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  525
ggggtcaccg tcagtagcaa ctac                                          24


<210>  526
<211>  21
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  526
atttatagcg gcggtagcac a                                             21


<210>  527
<211>  33
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  527
gcgagagacc tctactacta cggtatggac gtc                                 33


<210>  528
<211>  11
<212>  PRT
```

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 528

Ala Arg Asp Leu Tyr Tyr Tyr Gly Met Asp Val
1 5 10

<210> 529
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 529
gacatccagt tgacccagtc tccatccttc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggccagtca gggcattagc acttatttag cctggtatca gcaaaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccactt tgcaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240

gaagattttg caacttatta ctgtcaacag cttgatagtt accctgggct cactttcggc 300

ggagggacca aggtggagat caaa 324

<210> 530
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 530

Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Thr Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Asp Ser Tyr Pro Gly
                85   90   95

Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 531
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 531
cagggcatta gcacttat   18

<210> 532
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 532

Gln Gly Ile Ser Thr Tyr
1   5

<210> 533
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 533
caacagcttg atagttaccc tgggctcact   30

<210> 534

<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 534

Gln Gln Leu Asp Ser Tyr Pro Gly Leu Thr
1 5 10

<210> 535
<211> 1344
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 535
gaggtgcagc tggtggagtc tggaggaggc ttgatccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggggt caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtc atttatagcg gcggtagcac attctactca 180

gactccgtga agggccgatt cagcatctcc agagacaatt ccaagaacac actgtatctt 240

caaatgaaca gcctgagagc cgaggacacg gccgtgtatt actgtgcgag agacctctac 300

tactacggta tggacgtctg gggccaaggg accacggtca ccgtctcctc agcctccacc 360

aagggcccat cggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 600

aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 660

gacaaaactc acacatgccc accgtgccca gcacctgaac tcctgggggg accgtcagtc 720

ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 780

tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 840

ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac 900

cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 960

tgcaaggtct ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa 1020

gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggatga gctgaccaag 1080

aaccaggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag 1140

tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 1200

gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg 1260

aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagtcc 1320

ctctccctgt ctccgggtaa atga 1344

<210> 536
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 536

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Ile Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Thr Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ser Asp Ser Val Lys
50 55 60

Gly Arg Phe Ser Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Leu Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
115 120 125

```
Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
    130                 135                 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145                 150                 155                 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
                165                 170                 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
            180                 185                 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
        195                 200                 205

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
    210                 215                 220

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
225                 230                 235                 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
                245                 250                 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
            260                 265                 270

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
        275                 280                 285

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
    290                 295                 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305                 310                 315                 320

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
                325                 330                 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
            340                 345                 350
```

```
Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
        355                 360                 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
    370                 375                 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385                 390                 395                 400

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
                405                 410                 415

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
            420                 425                 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445
```

<210> 537
<211> 648
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 537
gacatccagt tgacccagtc tccatccttc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggccagtca gggcattagc acttatttag cctggtatca gcaaaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccactt tgcaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240

gaagattttg caacttatta ctgtcaacag cttgatagtt accctgggct cactttcggc 300

ggagggacca aggtggagat caaacgaact gtggctgcac catctgtctt catcttcccg 360

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 480

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 600

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgttag 648

<210> 538
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 538

Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Thr Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Asp Ser Tyr Pro Gly
85 90 95

Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
195 200 205

Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 539
<211> 1335
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 539
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60

acctgcactg tctctggtgg ctccatcaat aattactact ggatctggat ccggcagccc 120

ccagggaagg gactggagtg gattgggtat atctatcaca gtgggagcac caactacaac 180

ccctccctca agagtcgagt caccatatca gtagacacgt ccaagaacca attctccctg 240

aaggtgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgcgaa tatggttcgg 300

ggagtttatg aagatgacta ctggggccag ggaaccctgg tcaccgtctc ctcagcctcc 360

accaagggcc catcggtctt ccccctggcg ccctgctcca ggagcacctc cgagagcaca 420

gccgccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcacgaa gacctacacc 600

tgcaacgtag atcacaagcc cagcaacacc aaggtggaca agagagttga gtccaaatat 660

ggtccccat gcccaccgtg cccagcacca ggcggtggcg gaccatcagt cttcctgttc 720

cccccaaaac ccaaggacac tctcatgatc tcccggaccc ctgaggtcac gtgcgtggtg 780

gtggacgtga gccaggaaga ccccgaggtc cagttcaact ggtacgtgga tggcgtggag 840

gtgcataatg ccaagacaaa gccgcgggag gagcagttca acagcacgta ccgtgtggtc 900

agcgtcctca ccgtcctgca ccaggactgg ctgaacggca aggagtacaa gtgcaaggtc 960

tccaacaaag gcctcccgtc ctccatcgag aaaaccatct ccaaagccaa agggcagccc 1020

cgagagccac aggtgtacac cctgccccca tcccaggagg agatgaccaa gaaccaggtc 1080

agcctgacct gcctggtcaa aggcttctac cccagcgaca tcgccgtgga gtgggagagc 1140

aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc 1200

ttcttcctct acagcaggct caccgtggac aagagcaggt ggcaggaggg gaatgtcttc 1260

tcatgctccg tgatgcatga ggctctgcac aaccactaca cacagaagtc cctctccctg 1320

tctctgggta aatga 1335

<210> 540
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 540

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 Ile Asn Asn Tyr
20 25 30

Tyr Trp Ile Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Tyr His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

Lys Val Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Asn Met Val Arg Gly Val Tyr Glu Asp Asp Tyr Trp Gly Gln 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 Cys Ser Arg Ser Thr Ser Glu Ser 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 Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
    210                 215                 220

Pro Pro Cys Pro Ala Pro Gly Gly Gly Gly Pro Ser Val Phe Leu Phe
225                 230                 235                 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
                245                 250                 255

Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
            260                 265                 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
        275                 280                 285

Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
    290                 295                 300

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305                 310                 315                 320

Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
                325                 330                 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln
```

```
            340                 345                 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
        355                 360                 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
    370                 375                 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
385                 390                 395                 400

Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu
                405                 410                 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
            420                 425                 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440
```

<210> 541
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 541

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gaggtgcagc tggtggagtc tggaggaggc ttgatccagc ctgggggtc cctgagactc       60

tcctgtgcag cctctgtgtt caccgtcagt tacaactaca tgagctgggt ccgccaggct      120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac atactacgca      180

gactccgtga agggccgatt caccatctcc agagacaatt ccaagaacac gctgtatctt      240

caaatgaaca gcctgagagc cgaggacacg gccgtgtatt actgtgcgag agccctcccc      300

gggtggggtg ggagcttcga gtactttgac tactggggcc agggaaccct ggtcaccgtc      360

tcctcagcct ccaccaaggg cccatcggtc ttcccctgg cgccctgctc caggagcacc      420

tccgagagca cagccgccct gggctgcctg gtcaaggact acttccccga accggtgacg      480

gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag      540

tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacg      600
```

aagacctaca cctgcaacgt agatcacaag cccagcaaca ccaaggtgga caagagagtt 660

gagtccaaat atggtccccc atgcccaccg tgcccagcac caggcggtgg cggaccatca 720

gtcttcctgt tccccccaaa acccaaggac actctcatga tctcccggac ccctgaggtc 780

acgtgcgtgg tggtggacgt gagccaggaa gaccccgagg tccagttcaa ctggtacgtg 840

gatggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagtt caacagcacg 900

taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaacgg caaggagtac 960

aagtgcaagg tctccaacaa aggcctcccg tcctccatcg agaaaaccat ctccaaagcc 1020

aaagggcagc cccgagagcc acaggtgtac accctgcccc catcccagga ggagatgacc 1080

aagaaccagg tcagcctgac ctgcctggtc aaaggcttct accccagcga catcgccgtg 1140

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200

tccgacggct ccttcttcct ctacagcagg ctcaccgtgg acaagagcag gtggcaggag 1260

gggaatgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacacagaag 1320

tccctctccc tgtctctggg taaatga 1347

<210> 542
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 542

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Ile Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Val Phe Thr Val Ser Tyr Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu

```
65                  70                  75                  80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Ala Leu Pro Gly Trp Gly Gly Ser Phe Glu Tyr Phe Asp Tyr Trp
            100                 105                 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
        115                 120                 125

Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr
    130                 135                 140

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145                 150                 155                 160

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
                165                 170                 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
            180                 185                 190

Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp
        195                 200                 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr
    210                 215                 220

Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Gly Gly 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 Gln Glu Asp Pro
            260                 265                 270

Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275                 280                 285
```

```
Lys Thr Lys Pro Arg Glu Glu Gln Phe 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 Gly Leu Pro Ser Ser 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 Gln 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 Arg Leu Thr Val Asp Lys Ser
                405                 410                 415

Arg Trp Gln Glu 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 Leu Gly Lys
        435                 440                 445
```

<210> 543
<211> 1344
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 543
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggact caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagtac attctacgca 180

gactccgtga agggccgatt caccatctcc agagacaatt ccaagaacac gttgtatctt 240

cagatgaaca gcctgagacc tgaggacacg gctgtgtatt actgtgcgag agagggccgt 300

atagcagcaa ctggctacgg tatggacgtc tggggccaag ggaccacggt caccgtctcc 360

tcagcctcca ccaagggccc atcggtcttc cccctggcgc cctgctccag gagcacctcc 420

gagagcacag ccgccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480

tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacgaag 600

acctacacct gcaacgtaga tcacaagccc agcaacacca aggtggacaa gagagttgag 660

tccaaatatg gtcccccatg cccaccgtgc ccagcaccag gcggtggcgg accatcagtc 720

ttcctgttcc ccccaaaacc caaggacact ctcatgatct cccggacccc tgaggtcacg 780

tgcgtggtgg tggacgtgag ccaggaagac cccgaggtcc agttcaactg gtacgtggat 840

ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagttcaa cagcacgtac 900

cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaacggcaa ggagtacaag 960

tgcaaggtct ccaacaaagg cctcccgtcc tccatcgaga aaaccatctc caaagccaaa 1020

gggcagcccc gagagccaca ggtgtacacc ctgcccccat cccaggagga gatgaccaag 1080

aaccaggtca gcctgacctg cctggtcaaa ggcttctacc ccagcgacat cgccgtggag 1140

tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 1200

gacggctcct tcttcctcta cagcaggctc accgtggaca agagcaggtg gcaggagggg 1260

aatgtcttct catgctccgt gatgcatgag gctctgcaca accactacac acagaagtcc 1320

ctctccctgt ctctgggtaa atga 1344

<210> 544
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 544

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 Leu Thr Val Ser Ser Asn
            20                  25                  30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
    50                  55                  60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65                  70                  75                  80

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Glu Gly Arg Ile Ala Ala Thr Gly Tyr Gly Met Asp Val Trp Gly
            100                 105                 110

Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
        115                 120                 125

Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser 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 Lys Thr Tyr Thr Cys Asn Val Asp His
        195                 200                 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly
    210                 215                 220

Pro Pro Cys Pro Pro Cys Pro Ala Pro Gly Gly Gly Gly Pro Ser Val
225                 230                 235                 240
```

```
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
                245                 250                 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
            260                 265                 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
        275                 280                 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
    290                 295                 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305                 310                 315                 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
                325                 330                 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
            340                 345                 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
        355                 360                 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
    370                 375                 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385                 390                 395                 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
                405                 410                 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
            420                 425                 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440                 445
```

<210> 545
<211> 1323

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 545
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatcccg gtggtagtac attctacgca 180

gactccgtga agggcagatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag agatcaacgc 300

gattttgcct ggggccaggg aaccctggtc accgtctcct cagcctccac caagggccca 360

tcggtcttcc ccctggcgcc ctgctccagg agcacctccg agagcacagc cgccctgggc 420

tgcctggtca aggactactt ccccgaaccg gtgacggtgt cgtggaactc aggcgccctg 480

accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcagc 540

agcgtggtga ccgtgccctc cagcagcttg ggcacgaaga cctacacctg caacgtagat 600

cacaagccca gcaacaccaa ggtggacaag agagttgagt ccaaatatgg tcccccatgc 660

ccaccgtgcc cagcaccagg cggtggcgga ccatcagtct tcctgttccc cccaaaaccc 720

aaggacactc tcatgatctc ccggacccct gaggtcacgt gcgtggtggt ggacgtgagc 780

caggaagacc ccgaggtcca gttcaactgg tacgtggatg gcgtggaggt gcataatgcc 840

aagacaaagc cgcgggagga gcagttcaac agcacgtacc gtgtggtcag cgtcctcacc 900

gtcctgcacc aggactggct gaacggcaag gagtacaagt gcaaggtctc caacaaaggc 960

ctcccgtcct ccatcgagaa aaccatctcc aaagccaaag ggcagccccg agagccacag 1020

gtgtacaccc tgcccccatc ccaggaggag atgaccaaga accaggtcag cctgacctgc 1080

ctggtcaaag gcttctaccc cagcgacatc gccgtggagt gggagagcaa tgggcagccg 1140

gagaacaact acaagaccac gcctcccgtg ctggactccg acggctcctt cttcctctac 1200

agcaggctca ccgtggacaa gagcaggtgg caggagggga atgtcttctc atgctccgtg 1260

atgcatgagg ctctgcacaa ccactacaca cagaagtccc tctccctgtc tctgggtaaa 1320

tga 1323

<210> 546

<211> 440
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 546

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 Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Pro Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Gln Arg Asp Phe Ala Trp Gly Gln Gly Thr Leu Val Thr Val
100 105 110

Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys
115 120 125

Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys
130 135 140

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
145 150 155 160

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
165 170 175

Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
180 185 190

```
Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val
        195                 200                 205

Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro
    210                 215                 220

Ala Pro Gly Gly Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
225                 230                 235                 240

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
                245                 250                 255

Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val
            260                 265                 270

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
        275                 280                 285

Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
    290                 295                 300

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly
305                 310                 315                 320

Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
                325                 330                 335

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr
            340                 345                 350

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
        355                 360                 365

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
    370                 375                 380

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
385                 390                 395                 400

Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe
```

405 410 415

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
420 425 430

Ser Leu Ser Leu Ser Leu Gly Lys
435 440

<210> 547
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 547
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cttctggagg caccttcagc agctatgcta tcacctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaagg atcatcccta tgtttggtat agcaaactac 180

gcacagaagt tccagggcag agtcacgatt accgcggaca aatccacgag cacagcctac 240

atggaggtga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaacaccg 300

ttttactatg atagtagtgg ttattacctt gactactggg gccagggaac cctggtcacc 360

gtctcctca 369

<210> 548
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 548

Gln Val Gln Leu Val 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 Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Arg Ile Ile Pro Met Phe Gly Ile Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Val Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Thr Pro Phe Tyr Tyr Asp Ser Ser Gly Tyr Tyr Leu Asp Tyr
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 549
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 549
ggaggcacct tcagcagcta tgct 24

<210> 550
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 550

Gly Gly Thr Phe Ser Ser Tyr Ala
1 5

<210> 551
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 551
atcatcccta tgtttggtat agca 24

<210> 552
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 552

Ile Ile Pro Met Phe Gly Ile Ala
1 5

<210> 553
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 553
gcgagaacac cgttttacta tgatagtagt ggttattacc ttgactac 48

<210> 554
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 554

Ala Arg Thr Pro Phe Tyr Tyr Asp Ser Ser Gly Tyr Tyr Leu Asp Tyr
1 5 10 15

<210> 555
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 555
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcttgca gggccagtca gagtgttagc agcaactact tagcctggta ccagcagagt 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagttta ttactgtcag cagtatgtta ggtcaccccg gacgttcggc 300

caagggacca aggtggaaat caaa 324

<210> 556
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 556

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Ser Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Val Arg Ser Pro
85 90 95

Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 557
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 557
cagagtgtta gcagcaacta c 21

<210> 558
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 558

Gln Ser Val Ser Ser Asn Tyr
1 5

<210> 559
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 559
cagcagtatg ttaggtcacc ccggacg 27

<210> 560
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 560

Gln Gln Tyr Val Arg Ser Pro Arg Thr
1 5

<210> 561
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 561
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cttctggagg caccttcagc agctatgcta tcacctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaagg atcatcccta tgtttggtat agcaaactac 180

gcacagaagt tccagggcag agtcacgatt accgcggaca aatccacgag cacagcctac 240

atggaggtga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaacaccg 300

ttttactatg atagtagtgg ttattacctt gactactggg gccagggaac cctggtcacc 360

gtctcctcag cctccaccaa 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 ggacaagaaa 660

gttgagccca aatcttgtga caaaactcac acatgcccac cgtgcccagc acctgaactc 720

ctgggggggac 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 ttcctctaca gcaagctcac cgtggacaag 1260

agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1320

cactacacgc agaagtccct ctccctgtct ccgggtaaat ga 1362

<210> 562
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 562

```
Gln Val Gln Leu Val 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 Gly Thr Phe Ser Ser Tyr
            20                  25                  30

Ala Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Arg Ile Ile Pro Met Phe Gly Ile Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Val Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Thr Pro Phe Tyr Tyr Asp Ser Ser Gly Tyr Tyr Leu Asp Tyr
            100                 105                 110

Trp Gly Gln Gly Thr Leu 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 Lys 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 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 Lys
450

<210> 563
<211> 648
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 563
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcttgca gggccagtca gagtgttagc agcaactact tagcctggta ccagcagagt 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagttta ttactgtcag cagtatgtta ggtcaccccg gacgttcggc 300

caagggacca aggtggaaat caaacgaact gtggctgcac catctgtctt catcttcccg 360

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 480

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 600

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgttag 648

<210> 564
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 564

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

```
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
            20                  25                  30

Tyr Leu Ala Trp Tyr Gln Gln Ser Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Val Arg Ser Pro
                85                  90                  95

Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
            100                 105                 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115                 120                 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    130                 135                 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
                165                 170                 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
            180                 185                 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
        195                 200                 205

Ser Phe Asn Arg Gly Glu Cys
    210                 215
```

<210> 565
<211> 1362
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 565
caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt agctatgcta tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagtaa taaatactac 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gagagacggc 300

cggactatta ctatggttcg gggagttatt gatgatgctt ttgatatctg gggccaaggg 360

acaatggtca ccgtctcttc agcctccacc aagggcccat cggtcttccc cctggcgccc 420

tgctccagga gcacctccga gagcacagcc gccctgggct gcctggtcaa ggactacttc 480

cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 540

ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc 600

agcagcttgg gcacgaagac ctacacctgc aacgtagatc acaagcccag caacaccaag 660

gtggacaaga gagttgagtc caaatatggt cccccatgcc caccgtgccc agcaccaggc 720

ggtggcggac catcagtctt cctgttcccc ccaaaaccca aggacactct catgatctcc 780

cggacccctg aggtcacgtg cgtggtggtg gacgtgagcc aggaagaccc cgaggtccag 840

ttcaactggt acgtggatgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 900

cagttcaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 960

aacggcaagg agtacaagtg caaggtctcc aacaaaggcc tcccgtcctc catcgagaaa 1020

accatctcca aagccaaagg gcagccccga gagccacagg tgtacaccct gcccccatcc 1080

caggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctacccc 1140

agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1200

cctcccgtgc tggactccga cggctccttc ttcctctaca gcaggctcac cgtggacaag 1260

agcaggtggc aggaggggaa tgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1320

cactacacac agaagtccct ctccctgtct ctgggtaaat ga 1362

<210> 566
<211> 453

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 566

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Gly Arg Thr Ile Thr Met Val Arg Gly Val Ile Asp Asp
100 105 110

Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala
115 120 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser
130 135 140

Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145 150 155 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
165 170 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
180 185 190

```
Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr
        195                 200                 205

Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg
    210                 215                 220

Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Gly
225                 230                 235                 240

Gly 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 Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe 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 Gly Leu Pro Ser
                325                 330                 335

Ser 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 Gln 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 Arg Leu
                405                 410                 415
```

Thr Val Asp Lys Ser Arg Trp Gln Glu 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 Leu Gly Lys
450

<210> 567
<211> 1341
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 567
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagtac atactacgca 180

gactccgtga agggccgatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240

caaatgaaca gactgagagc tgacgacacg gctgtctatt actgtgtgag agatccggtg 300

gggcgctact actacggtat ggacgtctgg ggccaaggga ccacggtcac cgtctcctca 360

gcctccacca agggcccatc ggtcttcccc ctggcgccct gctccaggag cacctccgag 420

agcacagccg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacgaagacc 600

tacacctgca acgtagatca caagcccagc aacaccaagg tggacaagag agttgagtcc 660

aaatatggtc ccccatgccc accgtgccca gcaccaggcg gtggcggacc atcagtcttc 720

ctgttccccc caaaacccaa ggacactctc atgatctccc ggacccctga ggtcacgtgc 780

gtggtggtgg acgtgagcca ggaagacccc gaggtccagt tcaactggta cgtggatggc 840

gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agttcaacag cacgtaccgt 900

gtggtcagcg tcctcaccgt cctgcaccag gactggctga acggcaagga gtacaagtgc 960

aaggtctcca acaaaggcct cccgtcctcc atcgagaaaa ccatctccaa agccaaaggg 1020

cagccccgag agccacaggt gtacaccctg cccccatccc aggaggagat gaccaagaac 1080

caggtcagcc tgacctgcct ggtcaaaggc ttctacccca gcgacatcgc cgtggagtgg 1140

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200

ggctccttct tcctctacag caggctcacc gtggacaaga gcaggtggca ggaggggaat 1260

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacaca gaagtccctc 1320

tccctgtctc tgggtaaatg a 1341

<210> 568
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 568

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 Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Arg Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Cys Val
85 90 95

Arg Asp Pro Val Gly Arg Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

```
Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
    210                 215                 220

Pro Cys Pro Pro Cys Pro Ala Pro Gly Gly Gly Gly Pro Ser Val Phe
225                 230                 235                 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                245                 250                 255

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
            260                 265                 270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
    290                 295                 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305                 310                 315                 320

Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
                325                 330                 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
```

```
            340                 345                 350

Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
        355                 360                 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    370                 375                 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385                 390                 395                 400

Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
                405                 410                 415

Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            420                 425                 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440                 445
```

<210> 569
<211> 1332
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 569

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gaggtgcagc tggtggagtc tggaggaggc ttgatccagc ctgggggtc cctgagactc       60

tcctgtgcag cctctggggt caccgtcagt agcaactaca tgagctgggt ccgccaggct      120

ccagggaagg ggctggagtg ggtctcagtc atttatagcg gcggtagcac attctactca      180

gactccgtga agggccgatt cagcatctcc agagacaatt ccaagaacac actgtatctt      240

caaatgaaca gcctgagagc cgaggacacg gccgtgtatt actgtgcgag agacctctac      300

tactacggta tggacgtctg gggccaaggg accacggtca ccgtctcctc agcctccacc      360

aagggcccat cggtcttccc cctggcgccc tgctccagga gcacctccga gagcacagcc      420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca      480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac      540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacgaagac ctacacctgc      600
```

aacgtagatc acaagcccag caacaccaag gtggacaaga gagttgagtc caaatatggt 660

cccccatgcc caccgtgccc agcaccaggc ggtggcggac catcagtctt cctgttcccc 720

ccaaaaccca aggacactct catgatctcc cggacccctg aggtcacgtg cgtggtggtg 780

gacgtgagcc aggaagaccc cgaggtccag ttcaactggt acgtggatgg cgtggaggtg 840

cataatgcca agacaaagcc gcgggaggag cagttcaaca gcacgtaccg tgtggtcagc 900

gtcctcaccg tcctgcacca ggactggctg aacggcaagg agtacaagtg caaggtctcc 960

aacaaaggcc tcccgtcctc catcgagaaa accatctcca aagccaaagg gcagccccga 1020

gagccacagg tgtacaccct gcccccatcc caggaggaga tgaccaagaa ccaggtcagc 1080

ctgacctgcc tggtcaaagg cttctacccc agcgacatcg ccgtggagtg ggagagcaat 1140

gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1200

ttcctctaca gcaggctcac cgtggacaag agcaggtggc aggaggggaa tgtcttctca 1260

tgctccgtga tgcatgaggc tctgcacaac cactacacac agaagtccct ctccctgtct 1320

ctgggtaaat ga 1332

<210> 570
<211> 443
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 570

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Ile Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Thr Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ser Asp Ser Val Lys
50 55 60

Gly Arg Phe Ser Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu

```
65                  70                  75                  80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Leu Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr
            100                 105                 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
        115                 120                 125

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
    130                 135                 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145                 150                 155                 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
                165                 170                 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
            180                 185                 190

Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
        195                 200                 205

Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro
    210                 215                 220

Pro Cys Pro Ala Pro Gly Gly Gly Gly Pro Ser Val Phe Leu Phe Pro
225                 230                 235                 240

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
                245                 250                 255

Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
            260                 265                 270

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
        275                 280                 285
```

```
Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
    290                 295                 300

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
305                 310                 315                 320

Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
                325                 330                 335

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu
            340                 345                 350

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
        355                 360                 365

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
    370                 375                 380

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
385                 390                 395                 400

Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly
                405                 410                 415

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
            420                 425                 430

Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440


<210>  571
<211>  1350
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  571
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc       60

tcctgcaagg cttctggagg caccttcagc agctatgcta tcacctgggt gcgacaggcc      120

cctggacaag ggcttgagtg gatgggaagg atcatcccta tgtttggtat agcaaactac      180
```

gcacagaagt tccagggcag agtcacgatt accgcggaca aatccacgag cacagcctac 240

atggaggtga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaacaccg 300

ttttactatg atagtagtgg ttattacctt gactactggg gccagggaac cctggtcacc 360

gtctcctcag cctccaccaa gggcccatcg gtcttccccc tggcgccctg ctccaggagc 420

acctccgaga gcacagccgc cctgggctgc ctggtcaagg actacttccc cgaaccggtg 480

acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta 540

cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc 600

acgaagacct acacctgcaa cgtagatcac aagcccagca acaccaaggt ggacaagaga 660

gttgagtcca aatatggtcc cccatgccca ccgtgcccag caccaggcgg tggcggacca 720

tcagtcttcc tgttcccccc aaaacccaag gacactctca tgatctcccg gacccctgag 780

gtcacgtgcg tggtggtgga cgtgagccag gaagaccccg aggtccagtt caactggtac 840

gtggatggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gttcaacagc 900

acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa cggcaaggag 960

tacaagtgca aggtctccaa caaaggcctc ccgtcctcca tcgagaaaac catctccaaa 1020

gccaaagggc agccccgaga gccacaggtg tacaccctgc ccccatccca ggaggagatg 1080

accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctaccccag cgacatcgcc 1140

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200

gactccgacg gctccttctt cctctacagc aggctcaccg tggacaagag caggtggcag 1260

gaggggaatg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacacag 1320

aagtccctct ccctgtctct gggtaaatga 1350

<210> 572
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 572

Gln Val Gln Leu Val 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 Gly Thr Phe Ser Ser Tyr
            20                  25                  30

Ala Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Arg Ile Ile Pro Met Phe Gly Ile Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Val Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Thr Pro Phe Tyr Tyr Asp Ser Ser Gly Tyr Tyr Leu Asp Tyr
            100                 105                 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser
    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 Lys Thr Tyr Thr Cys Asn Val
        195                 200                 205

Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys
    210                 215                 220

Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Gly Gly 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 Gln Glu Asp
            260                 265                 270

Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe 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 Gly Leu Pro Ser Ser 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 Gln 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 Arg Leu Thr Val Asp Lys
                405                 410                 415

Ser Arg Trp Gln Glu 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 Leu Gly
        435                 440                 445

Lys
```

<210> 573
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 573
gaggtgcagc tggtggagtc tggaggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctgggct caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg gactggagtg ggtctcagtt atttatagcg gaggtaccac atactacgca 180

gactccgtga agggccgatt caccatctcc agacacaatt ccaagaacac gctgtctctt 240

caaatgaaca gcctgagagc tgaggacacg gccgtgtatt actgtgcgcg aggggagggg 300

gccaactact acggtatgga cgtctggggc caagggacca cggtcaccgt ctcctca 357

<210> 574
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 574

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 Leu Thr Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Thr Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg His Asn Ser Lys Asn Thr Leu Ser Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala

85 90 95

Arg Gly Glu Gly Ala Asn Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

<210> 575
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 575
atttatagcg gaggtaccac a 21

<210> 576
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 576

Ile Tyr Ser Gly Gly Thr Thr
1 5

<210> 577
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 577
gcgcgagggg agggggccaa ctactacggt atggacgtc 39

<210> 578
<211> 13
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 578

Ala Arg Gly Glu Gly Ala Asn Tyr Tyr Gly Met Asp Val
1 5 10

<210> 579
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 579
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60

tcctgcactg ggagcagctc caacatcggg acaggttatg atgtacactg gtaccagcag 120

cttccaggaa cagcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc 180

cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240

caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttat 300

gtggtattcg gcggagggac caagctgacc gtccta 336

<210> 580
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 580

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Thr Gly
20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
35 40 45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
85 90 95

Leu Ser Gly Tyr Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 581
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 581
agctccaaca tcgggacagg ttatgat 27

<210> 582
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 582

Ser Ser Asn Ile Gly Thr Gly Tyr Asp
1 5

<210> 583
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 583
ggtaacagc 9

<210> 584
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 584

Gly Asn Ser
1

<210> 585
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 585
cagtcctatg acagcagcct gagtggttat gtggta   36

<210> 586
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 586

Gln Ser Tyr Asp Ser Ser Leu Ser Gly Tyr Val Val
1   5   10

<210> 587
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 587
gaggtgcagc tggtggagtc tggaggaggc ttggtccagc ctgggggtc cctgagactc   60

tcctgtgcag cctctgggct caccgtcagt agcaactaca tgagctgggt ccgccaggct   120

ccagggaagg gactggagtg ggtctcagtt atttatagcg gaggtaccac atactacgca   180

gactccgtga agggccgatt caccatctcc agacacaatt ccaagaacac gctgtctctt   240

caaatgaaca gcctgagagc tgaggacacg gccgtgtatt actgtgcgcg aggggagggg   300

gccaactact acggtatgga cgtctggggc caagggacca cggtcaccgt ctcctcagcc 360

tccaccaagg 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 acaagaaagt 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 cctctacagc aagctcaccg tggacaagag caggtggcag 1260

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320

aagtccctct ccctgtctcc gggtaaatga 1350

<210> 588
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 588

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 Leu Thr Val Ser Ser Asn
20 25 30

```
Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Val Ile Tyr Ser Gly Gly Thr Thr Tyr Tyr Ala Asp Ser Val Lys
    50                  55                  60

Gly Arg Phe Thr Ile Ser Arg His Asn Ser Lys Asn Thr Leu Ser Leu
65                  70                  75                  80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Gly Glu Gly Ala Asn Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly
            100                 105                 110

Thr Thr 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 Lys 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

Lys
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<210> 589
<211> 657

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 589
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60

tcctgcactg ggagcagctc caacatcggg acaggttatg atgtacactg gtaccagcag 120

cttccaggaa cagcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc 180

cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240

caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttat 300

gtggtattcg gcggagggac caagctgacc gtcctaggcc agcccaaggc cgccccctcc 360

gtgaccctgt tccccccctc ctccgaggag ctgcaggcca acaaggccac cctggtgtgc 420

ctgatctccg acttctaccc cggcgccgtg accgtggcct ggaaggccga ctcctccccc 480

gtgaaggccg gcgtggagac caccaccccc tccaagcagt ccaacaacaa gtacgccgcc 540

tcctcctacc tgtccctgac ccccgagcag tggaagtccc accggtccta ctcctgccag 600

gtgacccacg agggctccac cgtggagaag accgtggccc ccaccgagtg ctcctga 657

<210> 590
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 590

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Thr Gly
20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
35 40 45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
50 55 60

```
Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80


Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
                85                  90                  95


Leu Ser Gly Tyr Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105                 110


Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser
        115                 120                 125


Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp
    130                 135                 140


Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro
145                 150                 155                 160


Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn
                165                 170                 175


Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
            180                 185                 190


Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val
        195                 200                 205


Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
    210                 215


<210>  591
<211>  1338
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  591
gaggtgcagc tggtggagtc tggaggaggc ttggtccagc ctgggggtc cctgagactc       60

tcctgtgcag cctctgggct caccgtcagt agcaactaca tgagctgggt ccgccaggct      120

ccagggaagg gactggagtg ggtctcagtt atttatagcg gaggtaccac atactacgca      180
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gactccgtga agggccgatt caccatctcc agacacaatt ccaagaacac gctgtctctt 240

caaatgaaca gcctgagagc tgaggacacg gccgtgtatt actgtgcgcg aggggagggg 300

gccaactact acggtatgga cgtctggggc caagggacca cggtcaccgt ctcctcagcc 360

tccaccaagg gcccatcggt cttccccctg gcgccctgct ccaggagcac ctccgagagc 420

acagccgccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480

aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac gaagacctac 600

acctgcaacg tagatcacaa gcccagcaac accaaggtgg acaagagagt tgagtccaaa 660

tatggtcccc catgcccacc gtgcccagca ccaggcggtg gcggaccatc agtcttcctg 720

ttcccccaa aacccaagga cactctcatg atctcccgga cccctgaggt cacgtgcgtg 780

gtggtggacg tgagccagga agaccccgag gtccagttca actggtacgt ggatggcgtg 840

gaggtgcata atgccaagac aaagccgcgg gaggagcagt tcaacagcac gtaccgtgtg 900

gtcagcgtcc tcaccgtcct gcaccaggac tggctgaacg gcaaggagta caagtgcaag 960

gtctccaaca aaggcctccc gtcctccatc gagaaaacca tctccaaagc caaagggcag 1020

ccccgagagc cacaggtgta caccctgccc ccatcccagg aggagatgac caagaaccag 1080

gtcagcctga cctgcctggt caaaggcttc taccccagcg acatcgccgt ggagtgggag 1140

agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc 1200

tccttcttcc tctacagcag gctcaccgtg gacaagagca ggtggcagga ggggaatgtc 1260

ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacacagaa gtccctctcc 1320

ctgtctctgg gtaaatga 1338

<210> 592
<211> 445
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 592

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 Leu Thr Val Ser Ser Asn
            20                  25                  30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Val Ile Tyr Ser Gly Gly Thr Thr Tyr Tyr Ala Asp Ser Val Lys
    50                  55                  60

Gly Arg Phe Thr Ile Ser Arg His Asn Ser Lys Asn Thr Leu Ser Leu
65                  70                  75                  80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Gly Glu Gly Ala Asn Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly
            100                 105                 110

Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser 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 Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
        195                 200                 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
    210                 215                 220

Cys Pro Pro Cys Pro Ala Pro Gly Gly Gly Gly Pro Ser Val Phe Leu
225                 230                 235                 240
```

```
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                245                 250                 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
            260                 265                 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        275                 280                 285

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    290                 295                 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305                 310                 315                 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
                325                 330                 335

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            340                 345                 350

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        355                 360                 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    370                 375                 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385                 390                 395                 400

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
                405                 410                 415

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            420                 425                 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440                 445
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<210> 593

<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 593
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggact caccgtcaat cgcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcactt atttatagcg gtggtagcac atactacgca 180

gactccgtta agggccgatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagact tgaggacacg gctgtgtatt actgtgcgag aggtgaactg 300

gggatcccct acggtatgga cgtctggggc caagggacca cggtcaccgt ctcctca 357

<210> 594
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 594

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 Leu Thr Val Asn Arg Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Leu Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Leu Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Gly Glu Leu Gly Ile Pro Tyr Gly Met Asp Val Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

<210> 595
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 595
ggactcaccg tcaatcgcaa ctac 24

<210> 596
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 596

Gly Leu Thr Val Asn Arg Asn Tyr
1 5

<210> 597
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 597
gcgagaggtg aactggggat cccctacggt atggacgtc 39

<210> 598
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 598

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Ala Arg Gly Glu Leu Gly Ile Pro Tyr Gly Met Asp Val
1               5                   10


<210>  599
<211>  330
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  599
cagtctgtgt tgacgcagcc gccctcagtg tctgcggccc caggacagaa ggtcaccatc       60

tcctgctctg gaagcagctc caacattggg aataattatg tatcctggta ccagcagctc      120

ccaggaacag cccccaaact cctcatttat gacaataata agcgaccctc agggattcct      180

gaccgcttct ctggctccaa gtctggcacg tcagccaccc tgggcatcac cggactccag      240

actggggacg aggccgatta ttactgcgga acatgggata gcagcctgag tgctggggtg      300

ttcggcggag ggaccaagct gaccgtccta                                       330


<210>  600
<211>  110
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  600

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Ala Ala Pro Gly Gln
1               5                   10                  15


Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
            20                  25                  30


Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
        35                  40                  45


Ile Tyr Asp Asn Asn Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Lys Ser Gly Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln
65                  70                  75                  80
```

Thr Gly Asp Glu Ala Asp Tyr Tyr Cys Gly Thr Trp Asp Ser Ser Leu
85 90 95

Ser Ala Gly Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 601
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 601
ggaacatggg atagcagcct gagtgctggg gtg 33

<210> 602
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 602

Gly Thr Trp Asp Ser Ser Leu Ser Ala Gly Val
1 5 10

<210> 603
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 603
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggact caccgtcaat cgcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcactt atttatagcg gtggtagcac atactacgca 180

gactccgtta agggccgatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagact tgaggacacg gctgtgtatt actgtgcgag aggtgaactg 300

gggatcccct acggtatgga cgtctggggc caagggacca cggtcaccgt ctcctcagcc 360

tccaccaagg 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 acaagaaagt 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 cctctacagc aagctcaccg tggacaagag caggtggcag 1260

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320

aagtccctct ccctgtctcc gggtaaatga 1350

<210> 604
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 604

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 Leu Thr Val Asn Arg Asn
20 25 30

```
Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Leu Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
    50                  55                  60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65                  70                  75                  80

Gln Met Asn Ser Leu Arg Leu Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Gly Glu Leu Gly Ile Pro Tyr Gly Met Asp Val Trp Gly Gln Gly
            100                 105                 110

Thr Thr 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 Lys 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

Lys
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<210> 605
<211> 651

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 605
cagtctgtgt tgacgcagcc gccctcagtg tctgcggccc caggacagaa ggtcaccatc 60

tcctgctctg gaagcagctc caacattggg aataattatg tatcctggta ccagcagctc 120

ccaggaacag cccccaaact cctcatttat gacaataata agcgaccctc agggattcct 180

gaccgcttct ctggctccaa gtctggcacg tcagccaccc tgggcatcac cggactccag 240

actggggacg aggccgatta ttactgcgga acatgggata gcagcctgag tgctggggtg 300

ttcggcggag ggaccaagct gaccgtccta ggccagccca aggccgcccc ctccgtgacc 360

ctgttccccc cctcctccga ggagctgcag gccaacaagg ccaccctggt gtgcctgatc 420

tccgacttct accccggcgc cgtgaccgtg gcctggaagg ccgactcctc ccccgtgaag 480

gccggcgtgg agaccaccac cccctccaag cagtccaaca acaagtacgc cgcctcctcc 540

tacctgtccc tgaccccga gcagtggaag tcccaccggt cctactcctg ccaggtgacc 600

cacgagggct ccaccgtgga gaagaccgtg gcccccaccg agtgctcctg a 651

<210> 606
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 606

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Ala Ala Pro Gly Gln
1 5 10 15

Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
20 25 30

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
35 40 45

Ile Tyr Asp Asn Asn Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser
50 55 60

```
Gly Ser Lys Ser Gly Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln
65                  70                  75                  80


Thr Gly Asp Glu Ala Asp Tyr Tyr Cys Gly Thr Trp Asp Ser Ser Leu
                85                  90                  95


Ser Ala Gly Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
            100                 105                 110


Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
        115                 120                 125


Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
    130                 135                 140


Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
145                 150                 155                 160


Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
                165                 170                 175


Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
            180                 185                 190


Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
        195                 200                 205


Thr Val Ala Pro Thr Glu Cys Ser
    210                 215
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<210> 607
<211> 384
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 607
gaagtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgat gattatgcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attagttgga ataggggtag cataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga gcagtctgag agctgaggac acggccttgt attactgcgc aaaagatggc 300

gagagatggg atagtgtagt agtaccatct gctaggaacg gtatggacgt ctggggccaa 360

gggaccacgg tcaccgtctc ctca 384

<210> 608
<211> 128
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 608

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Ser Trp Asn Arg Gly Ser Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Ser Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Asp Gly Glu Arg Trp Asp Ser Val Val Val Pro Ser Ala Arg
100 105 110

Asn Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 609
<211> 24
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 609
attagttgga ataggggtag cata 24

<210> 610
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 610

Ile Ser Trp Asn Arg Gly Ser Ile
1 5

<210> 611
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 611
gcaaaagatg gcgagagatg ggatagtgta gtagtaccat ctgctaggaa cggtatggac 60

gtc 63

<210> 612
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 612

Ala Lys Asp Gly Glu Arg Trp Asp Ser Val Val Val Pro Ser Ala Arg
1 5 10 15

Asn Gly Met Asp Val
20

<210> 613
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 613
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60

tcctgcactg ggagcagctc caacatcggg gcaggttatg atgtacattg gtaccagcag 120

cttccaggaa cagccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc 180

cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240

caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggctct 300

tatgtcttcg gaactgggac caaggtcacc gtccta 336

<210> 614
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 614

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
35 40 45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
85 90 95

Leu Ser Gly Ser Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu
100 105 110

<210> 615
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 615
agctccaaca tcggggcagg ttatgat 27

<210> 616
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 616

Ser Ser Asn Ile Gly Ala Gly Tyr Asp
1 5

<210> 617
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 617
cagtcctatg acagcagcct gagtggctct tatgtc 36

<210> 618
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 618

Gln Ser Tyr Asp Ser Ser Leu Ser Gly Ser Tyr Val
1 5 10

<210> 619
<211> 1377
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 619
gaagtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgat gattatgcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attagttgga ataggggtag cataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga gcagtctgag agctgaggac acggccttgt attactgcgc aaaagatggc 300

gagagatggg atagtgtagt agtaccatct gctaggaacg gtatggacgt ctggggccaa 360

gggaccacgg tcaccgtctc ctcagcctcc accaagggcc catcggtctt cccctggca 420

ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 480

ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 540

ttcccggctg tcctacagtc ctcaggactc tactccctca gcagcgtggt gaccgtgccc 600

tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 660

aaggtggaca agaaagttga gcccaaatct tgtgacaaaa ctcacacatg cccaccgtgc 720

ccagcacctg aactcctggg gggaccgtca gtcttcctct tccccccaaa acccaaggac 780

accctcatga tctcccggac ccctgaggtc acatgcgtgg tggtggacgt gagccacgaa 840

gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca 900

aagccgcggg aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg 960

caccaggact ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctccca 1020

gcccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac 1080

accctgcccc catcccggga tgagctgacc aagaaccagg tcagcctgac ctgcctggtc 1140

aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac 1200

aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctacagcaag 1260

ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat 1320

gaggctctgc acaaccacta cacgcagaag tccctctccc tgtctccggg taaatga 1377

<210> 620
<211> 458
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 620

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Ser Trp Asn Arg Gly Ser Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Ser Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Asp Gly Glu Arg Trp Asp Ser Val Val Val Pro Ser Ala Arg
100 105 110

Asn Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
130 135 140

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
145 150 155 160

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
165 170 175

```
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
            180                 185                 190

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
        195                 200                 205

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
    210                 215                 220

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
225                 230                 235                 240

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
                245                 250                 255

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
            260                 265                 270

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
        275                 280                 285

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
    290                 295                 300

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
305                 310                 315                 320

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
                325                 330                 335

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
            340                 345                 350

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
        355                 360                 365

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
    370                 375                 380

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
```

385 390 395 400

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
405 410 415

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
420 425 430

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
435 440 445

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455

<210> 621
<211> 657
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 621
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc agggcagag ggtcaccatc 60

tcctgcactg ggagcagctc caacatcggg gcaggttatg atgtacattg gtaccagcag 120

cttccaggaa cagccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc 180

cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240

caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggctct 300

tatgtcttcg gaactgggac caaggtcacc gtcctaggcc agcccaaggc cgccccctcc 360

gtgaccctgt tccccccctc ctccgaggag ctgcaggcca acaaggccac cctggtgtgc 420

ctgatctccg acttctaccc cggcgccgtg accgtggcct ggaaggccga ctcctccccc 480

gtgaaggccg gcgtggagac caccaccccc tccaagcagt ccaacaacaa gtacgccgcc 540

tcctcctacc tgtccctgac ccccgagcag tggaagtccc accggtccta ctcctgccag 600

gtgacccacg agggctccac cgtggagaag accgtggccc ccaccgagtg ctcctga 657

<210> 622
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 622

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1   5   10   15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
            20   25   30

Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35   40   45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50   55   60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65   70   75   80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
                85   90   95

Leu Ser Gly Ser Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu
            100   105   110

Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser
        115   120   125

Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp
    130   135   140

Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro
145   150   155   160

Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn
                165   170   175

Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
            180   185   190

Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val

195 200 205

Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 623
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 623
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctgaatt caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctagagtg ggtctcagtt atttatagcg gtggtagcac attttacgca 180

gactccgtga agggcagatt caccatctcc agagacaatt ccaagaacac gttgtatctt 240

caaatgaaca gtctgagagc cgaggacacg gctgtatatt actgtgcgag agctcttccc 300

tacggtgact tgcattttga ctactggggc cagggaaccc tggtcaccgt ctcctca 357

<210> 624
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 624

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 Glu Phe Thr Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Ala Leu Pro Tyr Gly Asp Leu His Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 625
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 625
gaattcaccg tcagtagcaa ctac 24

<210> 626
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 626

Glu Phe Thr Val Ser Ser Asn Tyr
1 5

<210> 627
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 627
gcgagagctc ttccctacgg tgacttgcat tttgactac 39

<210> 628

<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 628

Ala Arg Ala Leu Pro Tyr Gly Asp Leu His Phe Asp Tyr
1 5 10

<210> 629
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 629
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60

tcctgcactg ggagcagctc caacatcggg acaggttatg atgtacactg gtaccagcag 120

cttccaggaa cagcccccaa actcctcatc tatggtaaca ccaatcggcc ctcaggggtc 180

cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240

caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtgactct 300

tatgtcttcg gaactgggac caaggtcacc gtccta 336

<210> 630
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 630

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Thr Gly
20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
35 40 45

Leu Ile Tyr Gly Asn Thr Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
85 90 95

Leu Ser Asp Ser Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu
100 105 110

<210> 631
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 631
ggtaacacc 9

<210> 632
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 632

Gly Asn Thr
1

<210> 633
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 633
cagtcctatg acagcagcct gagtgactct tatgtc 36

<210> 634
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 634

Gln Ser Tyr Asp Ser Ser Leu Ser Asp Ser Tyr Val
1 5 10

<210> 635
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 635
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctgaatt caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctagagtg ggtctcagtt atttatagcg gtggtagcac attttacgca 180

gactccgtga agggcagatt caccatctcc agagacaatt ccaagaacac gttgtatctt 240

caaatgaaca gtctgagagc cgaggacacg gctgtatatt actgtgcgag agctcttccc 300

tacggtgact tgcattttga ctactggggc cagggaaccc tggtcaccgt ctcctcagcc 360

tccaccaagg 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 acaagaaagt 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 cctctacagc aagctcaccg tggacaagag caggtggcag 1260

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320

aagtccctct ccctgtctcc gggtaaatga 1350

<210> 636
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 636

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 Glu Phe Thr Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Ala Leu Pro Tyr Gly Asp Leu His Phe Asp 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 Lys 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

Lys
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<210> 637
<211> 657
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 637
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tcctgcactg ggagcagctc caacatcggg acaggttatg atgtacactg gtaccagcag 120

cttccaggaa cagccccaa actcctcatc tatggtaaca ccaatcggcc ctcaggggtc 180

cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240

caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtgactct 300

tatgtcttcg gaactgggac caaggtcacc gtcctaggcc agcccaaggc cgccccctcc 360

gtgaccctgt tccccccctc ctccgaggag ctgcaggcca acaaggccac cctggtgtgc 420

ctgatctccg acttctaccc cggcgccgtg accgtggcct ggaaggccga ctcctccccc 480

gtgaaggccg gcgtggagac caccaccccc tccaagcagt ccaacaacaa gtacgccgcc 540

tcctcctacc tgtccctgac ccccgagcag tggaagtccc accggtccta ctcctgccag 600

gtgacccacg agggctccac cgtggagaag accgtggccc ccaccgagtg ctcctga 657

<210> 638
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 638

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Thr Gly
20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
35 40 45

Leu Ile Tyr Gly Asn Thr Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
85 90 95

Leu Ser Asp Ser Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu
100 105 110

Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser
115 120 125

Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp
130 135 140

```
Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro
145                 150                 155                 160


Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn
                165                 170                 175


Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
            180                 185                 190


Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val
        195                 200                 205


Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
    210                 215


<210>  639
<211>  360
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  639
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tcctgtgcag cctctggatt caccttcagt aactatgcta tgtactgggt ccgccaggct      120

ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagtaa taaatactat      180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgag aactgaggac acggctgtgt attactgtgc gagtggctcc      300

gactacggtg actacttatt ggtttactgg ggccagggaa ccctggtcac cgtctcctca      360


<210>  640
<211>  120
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  640

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                   10                  15
```

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
            20   25   30

Ala Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Ser Gly Ser Asp Tyr Gly Asp Tyr Leu Leu Val Tyr Trp Gly Gln
            100   105   110

Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 641
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 641
ggattcacct tcagtaacta tgct   24

<210> 642
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 642

Gly Phe Thr Phe Ser Asn Tyr Ala
1   5

<210> 643
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 643
gcgagtggct ccgactacgg tgactactta ttggtttac 39

<210> 644
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 644

Ala Ser Gly Ser Asp Tyr Gly Asp Tyr Leu Leu Val Tyr
1 5 10

<210> 645
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 645
cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc gatcaccatc 60

tcctgcactg gaaccagcag tgacgttggt ggttataact atgtctcctg gtaccaacaa 120

cacccaggca aagcccccaa actcatgatt tatgatgtca gtaagcggcc ctcaggggtt 180

tctaatcgct tctctggctc caagtctggc aacacggcct ccctgaccat ctctgggctc 240

cagtctgagg acgaggctga ttattactgc aactctttga caagcatcag cacttgggtg 300

ttcggcggag ggaccaagct gaccgtccta 330

<210> 646
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 646

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 Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
35 40 45

Met Ile Tyr Asp Val Ser Lys Arg Pro Ser Gly Val Ser Asn Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Leu Thr Ser Ile
85 90 95

Ser Thr Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 647
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 647
agcagtgacg ttggtggtta taactat 27

<210> 648
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 648

Ser Ser Asp Val Gly Gly Tyr Asn Tyr
1 5

<210> 649
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 649
gatgtcagt 9

<210> 650
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 650

Asp Val Ser
1

<210> 651
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 651
aactctttga caagcatcag cacttgggtg 30

<210> 652
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 652

Asn Ser Leu Thr Ser Ile Ser Thr Trp Val
1 5 10

<210> 653

<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 653
caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt aactatgcta tgtactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagtaa taaatactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag aactgaggac acggctgtgt attactgtgc gagtggctcc 300

gactacggtg actacttatt ggtttactgg ggccagggaa ccctggtcac cgtctcctca 360

gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 600

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaact cctgggggga 720

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccccct 780

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 900

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960

gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1020

aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggatgag 1080

ctgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc 1140

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200

ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg 1260

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1320

cagaagtccc tctccctgtc tccgggtaaa tga 1353

<210> 654
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 654

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Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
            20                  25                  30


Ala Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Ser Gly Ser Asp Tyr Gly Asp Tyr Leu Leu Val Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125


Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140


Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160


Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175


Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
```

```
            180                 185                 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
        355                 360                 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400
```

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gly Lys
450

<210> 655
<211> 651
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 655
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tcctgcactg gaaccagcag tgacgttggt ggttataact atgtctcctg gtaccaacaa 120

cacccaggca aagcccccaa actcatgatt tatgatgtca gtaagcggcc ctcaggggtt 180

tctaatcgct tctctggctc caagtctggc aacacggcct ccctgaccat ctctgggctc 240

cagtctgagg acgaggctga ttattactgc aactctttga caagcatcag cacttgggtg 300

ttcggcggag ggaccaagct gaccgtccta ggccagccca aggccgcccc ctccgtgacc 360

ctgttccccc cctcctccga ggagctgcag gccaacaagg ccaccctggt gtgcctgatc 420

tccgacttct accccggcgc cgtgaccgtg gcctggaagg ccgactcctc ccccgtgaag 480

gccggcgtgg agaccaccac cccctccaag cagtccaaca acaagtacgc cgcctcctcc 540

tacctgtccc tgaccccga gcagtggaag tcccaccggt cctactcctg ccaggtgacc 600

cacgagggct ccaccgtgga gaagaccgtg gcccccaccg agtgctcctg a 651

<210> 656
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 656

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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 Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
        35                  40                  45

Met Ile Tyr Asp Val Ser Lys Arg Pro Ser Gly Val Ser Asn Arg Phe
    50                  55                  60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65                  70                  75                  80

Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Leu Thr Ser Ile
                85                  90                  95

Ser Thr Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
            100                 105                 110

Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
        115                 120                 125

Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
    130                 135                 140

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
145                 150                 155                 160

Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
                165                 170                 175

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
            180                 185                 190

Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
        195                 200                 205
```

Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 657
<211> 381
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 657
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggagggtc cctgagactc 60

tcctgtacag cctctggatt caccttcagt aattatgaaa tgaactgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtttcatac attagtagta ggagtggtag taccctacac 180

tacgcagact ctgtgaaggg ccgattcacc atctccagag acaacgccaa gaactcactg 240

tatctgcaaa tgaacagcct gagagccgag gacacggctg tttattactg tgcgagaagg 300

ggcgatggta ccagctccct aatccaccac tactactaca tggacgtctg gggcaaaggg 360

accacggtca ccgtctcctc a 381

<210> 658
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 658

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 Thr Ala Ser Gly Phe Thr Phe Ser Asn Tyr
20 25 30

Glu Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Tyr Ile Ser Ser Arg Ser Gly Ser Thr Leu His Tyr Ala Asp Ser
50 55 60

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu

65 70 75 80

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Arg Gly Asp Gly Thr Ser Ser Leu Ile His His Tyr Tyr
100 105 110

Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 659
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 659
ggattcacct tcagtaatta tgaa 24

<210> 660
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 660

Gly Phe Thr Phe Ser Asn Tyr Glu
1 5

<210> 661
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 661
attagtagta ggagtggtag tacccta 27

<210> 662
<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 662

Ile Ser Ser Arg Ser Gly Ser Thr Leu
1 5

<210> 663
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 663
gcgagaaggg gcgatggtac cagctcccta atccaccact actactacat ggacgtc 57

<210> 664
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 664

Ala Arg Arg Gly Asp Gly Thr Ser Ser Leu Ile His His Tyr Tyr Tyr
1 5 10 15

Met Asp Val

<210> 665
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 665
cagtctgtgc tgactcagcc accctcagcg tctgggaccc ccgggcagag ggtcaccatc 60

tcttgttctg gaagcagctc caacatcgga agtaatactg taaactggta ccaacagctc 120

ccaggaacgg cccccaaact cctcatctat agtaataatc agcggccctc aggggtccct 180

gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccag 240

tctgaggatg aggctgatta ttactgtgca gcatgggatg acagcctgaa tggtccggta 300

ttcggcggag ggaccaagct gaccgtccta 330

<210> 666
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 666

Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
20 25 30

Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
35 40 45

Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
85 90 95

Asn Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 667
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 667
agctccaaca tcggaagtaa tact 24

<210> 668
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 668

Ser Ser Asn Ile Gly Ser Asn Thr
1 5

<210> 669
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 669
agtaataat 9

<210> 670
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 670

Ser Asn Asn
1

<210> 671
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 671
gcagcatggg atgacagcct gaatggtccg gta 33

<210> 672
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 672

Ala Ala Trp Asp Asp Ser Leu Asn Gly Pro Val
1 5 10

<210> 673
<211> 1374
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 673
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tcctgtacag cctctggatt caccttcagt aattatgaaa tgaactgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtttcatac attagtagta ggagtggtag taccctacac 180

tacgcagact ctgtgaaggg ccgattcacc atctccagag acaacgccaa gaactcactg 240

tatctgcaaa tgaacagcct gagagccgag gacacggctg tttattactg tgcgagaagg 300

ggcgatggta ccagctccct aatccaccac tactactaca tggacgtctg gggcaaaggg 360

accacggtca ccgtctcctc agcctccacc aagggcccat cggtcttccc cctggcaccc 420

tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctggtcaa ggactacttc 480

cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 540

ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc 600

agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 660

gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca 720

gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 780

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 840

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 900

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 960

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1020

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1080

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1140

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1200

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1260

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1320

gctctgcaca accactacac gcagaagtcc ctctccctgt ctccgggtaa atga 1374

<210> 674
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 674

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 Thr Ala Ser Gly Phe Thr Phe Ser Asn Tyr
20 25 30

Glu Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Tyr Ile Ser Ser Arg Ser Gly Ser Thr Leu His Tyr Ala Asp Ser
50 55 60

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu
65 70 75 80

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Arg Gly Asp Gly Thr Ser Ser Leu Ile His His Tyr Tyr
100 105 110

Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Ala

```
        115                 120                 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
    130                 135                 140

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145                 150                 155                 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
                165                 170                 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
            180                 185                 190

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
        195                 200                 205

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
    210                 215                 220

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
225                 230                 235                 240

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        275                 280                 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305                 310                 315                 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335
```

```
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            340                 345                 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        355                 360                 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                405                 410                 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        435                 440                 445

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455
```

<210> 675
<211> 651
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 675
cagtctgtgc tgactcagcc accctcagcg tctgggaccc ccgggcagag ggtcaccatc 60

tcttgttctg gaagcagctc caacatcgga agtaatactg taaactggta ccaacagctc 120

ccaggaacgg cccccaaact cctcatctat agtaataatc agcggccctc aggggtccct 180

gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccag 240

tctgaggatg aggctgatta ttactgtgca gcatgggatg acagcctgaa tggtccggta 300

ttcggcggag ggaccaagct gaccgtccta ggccagccca aggccgcccc ctccgtgacc 360

ctgttccccc cctcctccga ggagctgcag gccaacaagg ccaccctggt gtgcctgatc 420

tccgacttct accccggcgc cgtgaccgtg gcctggaagg ccgactcctc ccccgtgaag 480

gccggcgtgg agaccaccac cccctccaag cagtccaaca acaagtacgc cgcctcctcc 540

tacctgtccc tgaccccga gcagtggaag tcccaccggt cctactcctg ccaggtgacc 600

cacgagggct ccaccgtgga gaagaccgtg gcccccaccg agtgctcctg a 651

<210> 676
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 676

Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
20 25 30

Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
35 40 45

Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
85 90 95

Asn Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
100 105 110

Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
115 120 125

Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
130 135 140

```
Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
145                 150                 155                 160


Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
                165                 170                 175


Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
            180                 185                 190


Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
        195                 200                 205


Thr Val Ala Pro Thr Glu Cys Ser
    210                 215


<210>  677
<211>  369
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  677
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc       60

tcctgcaagg cttctggata catcttcacc ggctactata tgcactgggt gcgacaggcc      120

cctggacagg ggcttgagtg gatgggatgg atcaacccta acagtggtgg cgcaaactat      180

gcacagaagt ttcagggcag ggtcaccctg accagggaca cgtccatcac cacagtctac      240

atggaactga gcaggctgag atttgacgac acggccgtgt attactgtgc gagaggatcc      300

cggtatgact ggaaccagaa caactggttc gacccctggg gccagggaac cctggtcacc      360

gtctcctca                                                              369


<210>  678
<211>  123
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  678

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
```

1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Gly Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Thr Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Phe Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Ser Arg Tyr Asp Trp Asn Gln Asn Asn Trp Phe Asp Pro
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 679
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 679
ggatacatct tcaccggcta ctat 24

<210> 680
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 680

Gly Tyr Ile Phe Thr Gly Tyr Tyr
1 5

<210> 681
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 681
atcaacccta acagtggtgg cgca 24

<210> 682
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 682

Ile Asn Pro Asn Ser Gly Gly Ala
1 5

<210> 683
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 683
gcgagaggat cccggtatga ctggaaccag aacaactggt tcgacccc 48

<210> 684
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 684

Ala Arg Gly Ser Arg Tyr Asp Trp Asn Gln Asn Asn Trp Phe Asp Pro
1 5 10 15

<210> 685

<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 685
cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc gatcaccatc 60

tcctgcactg gaaccagcag tgacgttggt acttataact atgtctcctg gtaccaacaa 120

cacccaggca aagcccccaa actcatgatt tttgatgtca gtaatcggcc ctcaggggtt 180

tctgatcgct tctctggctc caagtctggc aacacggcct ccctgaccat ctctgggctc 240

caggctgagg acgaggctga ttattactgc agctcattta caaccagcag cactgtggtt 300

ttcggcggag ggaccaagct gaccgtccta 330

<210> 686
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 686

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 Thr Tyr
20 25 30

Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
35 40 45

Met Ile Phe Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Phe Thr Thr Ser
85 90 95

Ser Thr Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 687
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 687
agcagtgacg ttggtactta taactat 27

<210> 688
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 688

Ser Ser Asp Val Gly Thr Tyr Asn Tyr
1 5

<210> 689
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 689
agctcattta caaccagcag cactgtggtt 30

<210> 690
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 690

Ser Ser Phe Thr Thr Ser Ser Thr Val Val
1 5 10

<210> 691
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 691
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggata catcttcacc ggctactata tgcactgggt gcgacaggcc 120

cctggacagg ggcttgagtg gatgggatgg atcaacccta acagtggtgg cgcaaactat 180

gcacagaagt ttcagggcag ggtcaccctg accagggaca cgtccatcac cacagtctac 240

atggaactga gcaggctgag atttgacgac acggccgtgt attactgtgc gagaggatcc 300

cggtatgact ggaaccagaa caactggttc gacccctggg gccagggaac cctggtcacc 360

gtctcctcag cctccaccaa 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 ggacaagaaa 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 ttcctctaca gcaagctcac cgtggacaag 1260

agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1320

cactacacgc agaagtccct ctccctgtct ccgggtaaat ga 1362

<210> 692
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 692

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Gly Tyr
            20                  25                  30


Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Trp Ile Asn Pro Asn Ser Gly Gly Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Thr Thr Val Tyr
65                  70                  75                  80


Met Glu Leu Ser Arg Leu Arg Phe Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Gly Ser Arg Tyr Asp Trp Asn Gln Asn Asn Trp Phe Asp Pro
            100                 105                 110


Trp Gly Gln Gly Thr Leu 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 Lys 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 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 Lys
    450
```

<210> 693
<211> 651
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 693

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cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc gatcaccatc       60

tcctgcactg gaaccagcag tgacgttggt acttataact atgtctcctg gtaccaacaa      120

cacccaggca aagcccccaa actcatgatt tttgatgtca gtaatcggcc ctcaggggtt      180

tctgatcgct tctctggctc caagtctggc aacacggcct ccctgaccat ctctgggctc      240

caggctgagg acgaggctga ttattactgc agctcattta caaccagcag cactgtggtt      300

ttcggcggag ggaccaagct gaccgtccta ggccagccca aggccgcccc ctccgtgacc      360

ctgttccccc cctcctccga ggagctgcag gccaacaagg ccaccctggt gtgcctgatc      420

tccgacttct accccggcgc cgtgaccgtg gcctggaagg ccgactcctc ccccgtgaag      480

gccggcgtgg agaccaccac cccctccaag cagtccaaca acaagtacgc cgcctcctcc      540

tacctgtccc tgaccccga gcagtggaag tcccaccggt cctactcctg ccaggtgacc      600

cacgagggct ccaccgtgga gaagaccgtg gcccccaccg agtgctcctg a               651
```

<210> 694
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 694

```
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 Thr Tyr
            20                  25                  30


Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
        35                  40                  45


Met Ile Phe Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asp Arg Phe
    50                  55                  60


Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65                  70                  75                  80


Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Phe Thr Thr Ser
                85                  90                  95


Ser Thr Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
            100                 105                 110


Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
        115                 120                 125


Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
    130                 135                 140


Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
145                 150                 155                 160


Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
                165                 170                 175


Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
            180                 185                 190


Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
        195                 200                 205
```

Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 695
<211> 1338
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 695
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggact caccgtcaat cgcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcactt atttatagcg gtggtagcac atactacgca 180

gactccgtta agggccgatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagact tgaggacacg gctgtgtatt actgtgcgag aggtgaactg 300

gggatcccct acggtatgga cgtctggggc caagggacca cggtcaccgt ctcctcagcc 360

tccaccaagg gcccatcggt cttccccctg gcgccctgct ccaggagcac ctccgagagc 420

acagccgccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480

aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac gaagacctac 600

acctgcaacg tagatcacaa gcccagcaac accaaggtgg acaagagagt tgagtccaaa 660

tatggtcccc catgcccacc gtgcccagca ccaggcggtg gcggaccatc agtcttcctg 720

ttcccccaa aacccaagga cactctcatg atctcccgga cccctgaggt cacgtgcgtg 780

gtggtggacg tgagccagga agaccccgag gtccagttca actggtacgt ggatggcgtg 840

gaggtgcata atgccaagac aaagccgcgg gaggagcagt tcaacagcac gtaccgtgtg 900

gtcagcgtcc tcaccgtcct gcaccaggac tggctgaacg gcaaggagta caagtgcaag 960

gtctccaaca aaggcctccc gtcctccatc gagaaaacca tctccaaagc caaagggcag 1020

ccccgagagc cacaggtgta caccctgccc ccatcccagg aggagatgac caagaaccag 1080

gtcagcctga cctgcctggt caaaggcttc taccccagcg acatcgccgt ggagtgggag 1140

agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc 1200

tccttcttcc tctacagcag gctcaccgtg gacaagagca ggtggcagga ggggaatgtc 1260

ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacacagaa gtccctctcc 1320

ctgtctctgg gtaaatga 1338

<210> 696
<211> 445
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 696

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 Leu Thr Val Asn Arg Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Leu Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Leu Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Gly Glu Leu Gly Ile Pro Tyr Gly Met Asp Val Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser 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 Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
        195                 200                 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
    210                 215                 220

Cys Pro Pro Cys Pro Ala Pro Gly Gly Gly Gly Pro Ser Val Phe Leu
225                 230                 235                 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                245                 250                 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
            260                 265                 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        275                 280                 285

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    290                 295                 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305                 310                 315                 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
                325                 330                 335

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            340                 345                 350

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        355                 360                 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
```

```
    370                 375                 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385                 390                 395                 400

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
                405                 410                 415

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            420                 425                 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440                 445
```

<210> 697
<211> 1365
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 697

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tcctgtgcag cctctggatt cacctttgat gattatgcca tgcactgggt ccggcaagct      120

ccagggaagg gcctggagtg ggtctcaggt attagttgga ataggggtag cataggctat      180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat      240

ctgcaaatga gcagtctgag agctgaggac acggccttgt attactgcgc aaaagatggc      300

gagagatggg atagtgtagt agtaccatct gctaggaacg gtatggacgt ctggggccaa      360

gggaccacgg tcaccgtctc ctcagcctcc accaagggcc catcggtctt ccccctggcg      420

ccctgctcca ggagcacctc cgagagcaca gccgccctgg gctgcctggt caaggactac      480

ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc      540

ttcccggctg tcctacagtc ctcaggactc tactccctca gcagcgtggt gaccgtgccc      600

tccagcagct tgggcacgaa gacctacacc tgcaacgtag atcacaagcc cagcaacacc      660

aaggtggaca agagagttga gtccaaatat ggtcccccat gcccaccgtg cccagcacca      720

ggcggtggcg gaccatcagt cttcctgttc cccccaaaac ccaaggacac tctcatgatc      780

tcccggaccc ctgaggtcac gtgcgtggtg gtggacgtga gccaggaaga ccccgaggtc      840
```

cagttcaact ggtacgtgga tggcgtggag gtgcataatg ccaagacaaa gccgcgggag 900

gagcagttca acagcacgta ccgtgtggtc agcgtcctca ccgtcctgca ccaggactgg 960

ctgaacggca aggagtacaa gtgcaaggtc tccaacaaag gcctcccgtc ctccatcgag 1020

aaaaccatct ccaaagccaa agggcagccc cgagagccac aggtgtacac cctgccccca 1080

tcccaggagg agatgaccaa gaaccaggtc agcctgacct gcctggtcaa aggcttctac 1140

cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1200

acgcctcccg tgctggactc cgacggctcc ttcttcctct acagcaggct caccgtggac 1260

aagagcaggt ggcaggaggg gaatgtcttc tcatgctccg tgatgcatga ggctctgcac 1320

aaccactaca cacagaagtc cctctccctg tctctgggta aatga 1365

<210> 698
<211> 454
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 698

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Ser Trp Asn Arg Gly Ser Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Ser Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Asp Gly Glu Arg Trp Asp Ser Val Val Val Pro Ser Ala Arg

```
            100                 105                 110

Asn Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120                 125

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
    130                 135                 140

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
145                 150                 155                 160

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
                165                 170                 175

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
            180                 185                 190

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
        195                 200                 205

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
    210                 215                 220

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
225                 230                 235                 240

Gly Gly Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
                245                 250                 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
            260                 265                 270

Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
        275                 280                 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
    290                 295                 300

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
305                 310                 315                 320
```

```
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
                325                 330                 335

Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
            340                 345                 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn
        355                 360                 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
    370                 375                 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
385                 390                 395                 400

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg
                405                 410                 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys
            420                 425                 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
        435                 440                 445

Ser Leu Ser Leu Gly Lys
    450
```

<210> 699
<211> 1338
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 699
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tcctgtgcag cctctgaatt caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctagagtg ggtctcagtt atttatagcg gtggtagcac attttacgca 180

gactccgtga agggcagatt caccatctcc agagacaatt ccaagaacac gttgtatctt 240

caaatgaaca gtctgagagc cgaggacacg gctgtatatt actgtgcgag agctcttccc 300

tacggtgact tgcattttga ctactggggc cagggaaccc tggtcaccgt ctcctcagcc 360

tccaccaagg gcccatcggt cttccccctg gcgccctgct ccaggagcac ctccgagagc 420

acagccgccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480

aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac gaagacctac 600

acctgcaacg tagatcacaa gcccagcaac accaaggtgg acaagagagt tgagtccaaa 660

tatggtcccc catgcccacc gtgcccagca ccaggcggtg gcggaccatc agtcttcctg 720

ttcccccaa aacccaagga cactctcatg atctcccgga cccctgaggt cacgtgcgtg 780

gtggtggacg tgagccagga agaccccgag gtccagttca actggtacgt ggatggcgtg 840

gaggtgcata atgccaagac aaagccgcgg gaggagcagt tcaacagcac gtaccgtgtg 900

gtcagcgtcc tcaccgtcct gcaccaggac tggctgaacg gcaaggagta caagtgcaag 960

gtctccaaca aaggcctccc gtcctccatc gagaaaacca tctccaaagc caaagggcag 1020

ccccgagagc cacaggtgta caccctgccc ccatcccagg aggagatgac caagaaccag 1080

gtcagcctga cctgcctggt caaaggcttc taccccagcg acatcgccgt ggagtgggag 1140

agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc 1200

tccttcttcc tctacagcag gctcaccgtg gacaagagca ggtggcagga ggggaatgtc 1260

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ctgtctctgg gtaaatga 1338

<210> 700
<211> 445
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 700

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 Glu Phe Thr Val Ser Ser Asn
20 25 30

```
Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
    50                  55                  60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65                  70                  75                  80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Ala Leu Pro Tyr Gly Asp Leu His Phe Asp 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 Cys Ser Arg Ser Thr Ser Glu Ser 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 Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
        195                 200                 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
    210                 215                 220

Cys Pro Pro Cys Pro Ala Pro Gly Gly Gly Gly Pro Ser Val Phe Leu
225                 230                 235                 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                245                 250                 255
```

```
Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
            260                 265                 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        275                 280                 285

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    290                 295                 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305                 310                 315                 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
                325                 330                 335

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            340                 345                 350

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        355                 360                 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    370                 375                 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385                 390                 395                 400

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
                405                 410                 415

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            420                 425                 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440                 445
```

<210> 701
<211> 1341
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 701
caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt aactatgcta tgtactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagtaa taaatactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag aactgaggac acggctgtgt attactgtgc gagtggctcc 300

gactacggtg actacttatt ggtttactgg ggccagggaa ccctggtcac cgtctcctca 360

gcctccacca agggcccatc ggtcttcccc ctggcgccct gctccaggag cacctccgag 420

agcacagccg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacgaagacc 600

tacacctgca acgtagatca caagcccagc aacaccaagg tggacaagag agttgagtcc 660

aaatatggtc ccccatgccc accgtgccca gcaccaggcg gtggcggacc atcagtcttc 720

ctgttccccc caaaacccaa ggacactctc atgatctccc ggacccctga ggtcacgtgc 780

gtggtggtgg acgtgagcca ggaagacccc gaggtccagt tcaactggta cgtggatggc 840

gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agttcaacag cacgtaccgt 900

gtggtcagcg tcctcaccgt cctgcaccag gactggctga acggcaagga gtacaagtgc 960

aaggtctcca acaaaggcct cccgtcctcc atcgagaaaa ccatctccaa agccaaaggg 1020

cagccccgag agccacaggt gtacaccctg cccccatccc aggaggagat gaccaagaac 1080

caggtcagcc tgacctgcct ggtcaaaggc ttctacccca gcgacatcgc cgtggagtgg 1140

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200

ggctccttct tcctctacag caggctcacc gtggacaaga gcaggtggca ggaggggaat 1260

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacaca gaagtccctc 1320

tccctgtctc tgggtaaatg a 1341

<210> 702
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 702

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
            20   25   30

Ala Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Ser Gly Ser Asp Tyr Gly Asp Tyr Leu Leu Val Tyr Trp Gly Gln
            100   105   110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115   120   125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
    130   135   140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145   150   155   160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165   170   175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180   185   190

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
        195   200   205

```
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
    210                 215                 220

Pro Cys Pro Pro Cys Pro Ala Pro Gly Gly Gly Gly Pro Ser Val Phe
225                 230                 235                 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                245                 250                 255

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
            260                 265                 270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
    290                 295                 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305                 310                 315                 320

Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
                325                 330                 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            340                 345                 350

Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
        355                 360                 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    370                 375                 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385                 390                 395                 400

Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
                405                 410                 415

Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
```

420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 703
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 703
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tcctgtacag cctctggatt caccttcagt aattatgaaa tgaactgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtttcatac attagtagta ggagtggtag taccctacac 180

tacgcagact ctgtgaaggg ccgattcacc atctccagag acaacgccaa gaactcactg 240

tatctgcaaa tgaacagcct gagagccgag gacacggctg tttattactg tgcgagaagg 300

ggcgatggta ccagctccct aatccaccac tactactaca tggacgtctg gggcaaaggg 360

accacggtca ccgtctcctc agcctccacc aagggcccat cggtcttccc cctggcgccc 420

tgctccagga gcacctccga gagcacagcc gccctgggct gcctggtcaa ggactacttc 480

cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 540

ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc 600

agcagcttgg gcacgaagac ctacacctgc aacgtagatc acaagcccag caacaccaag 660

gtggacaaga gagttgagtc caaatatggt cccccatgcc caccgtgccc agcaccaggc 720

ggtggcggac catcagtctt cctgttcccc ccaaaaccca aggacactct catgatctcc 780

cggacccctg aggtcacgtg cgtggtggtg gacgtgagcc aggaagaccc cgaggtccag 840

ttcaactggt acgtggatgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 900

cagttcaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 960

aacggcaagg agtacaagtg caaggtctcc aacaaaggcc tcccgtcctc catcgagaaa 1020

accatctcca aagccaaagg gcagccccga gagccacagg tgtacaccct gcccccatcc 1080

caggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctacccc 1140

agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1200

cctcccgtgc tggactccga cggctccttc ttcctctaca gcaggctcac cgtggacaag 1260

agcaggtggc aggaggggaa tgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1320

cactacacac agaagtccct ctccctgtct ctgggtaaat ga 1362

<210> 704
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 704

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 Thr Ala Ser Gly Phe Thr Phe Ser Asn Tyr
20 25 30

Glu Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Tyr Ile Ser Ser Arg Ser Gly Ser Thr Leu His Tyr Ala Asp Ser
50 55 60

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu
65 70 75 80

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Arg Gly Asp Gly Thr Ser Ser Leu Ile His His Tyr Tyr
100 105 110

Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Ala
115 120 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser
130 135 140

Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe

```
145                 150                 155                 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
                165                 170                 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
            180                 185                 190

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr
        195                 200                 205

Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg
    210                 215                 220

Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Gly
225                 230                 235                 240

Gly 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 Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe 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 Gly Leu Pro Ser
                325                 330                 335

Ser 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 Gln 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 Arg Leu
                405                 410                 415

Thr Val Asp Lys Ser Arg Trp Gln Glu 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 Leu Gly Lys
    450
```

<210> 705
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 705

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cctggacagg ggcttgagtg gatgggatgg atcaacccta acagtggtgg cgcaaactat      180

gcacagaagt ttcagggcag ggtcaccctg accagggaca cgtccatcac cacagtctac      240

atggaactga gcaggctgag atttgacgac acggccgtgt attactgtgc gagaggatcc      300

cggtatgact ggaaccagaa caactggttc gacccctggg gccagggaac cctggtcacc      360

gtctcctcag cctccaccaa gggcccatcg gtcttccccc tggcgccctg ctccaggagc      420

acctccgaga gcacagccgc cctgggctgc ctggtcaagg actacttccc cgaaccggtg      480

acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta      540

cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc      600

acgaagacct acacctgcaa cgtagatcac aagcccagca acaccaaggt ggacaagaga      660
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gttgagtcca aatatggtcc cccatgccca ccgtgcccag caccaggcgg tggcggacca 720

tcagtcttcc tgttcccccc aaaacccaag gacactctca tgatctcccg gacccctgag 780

gtcacgtgcg tggtggtgga cgtgagccag gaagaccccg aggtccagtt caactggtac 840

gtggatggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gttcaacagc 900

acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa cggcaaggag 960

tacaagtgca aggtctccaa caaaggcctc ccgtcctcca tcgagaaaac catctccaaa 1020

gccaaagggc agccccgaga gccacaggtg tacaccctgc ccccatccca ggaggagatg 1080

accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctaccccag cgacatcgcc 1140

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200

gactccgacg gctccttctt cctctacagc aggctcaccg tggacaagag caggtggcag 1260

gaggggaatg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacacag 1320

aagtccctct ccctgtctct gggtaaatga 1350

<210> 706
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 706

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Gly Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Thr Thr Val Tyr
65 70 75 80

```
Met Glu Leu Ser Arg Leu Arg Phe Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Ser Arg Tyr Asp Trp Asn Gln Asn Asn Trp Phe Asp Pro
            100                 105                 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser
    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 Lys Thr Tyr Thr Cys Asn Val
        195                 200                 205

Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys
    210                 215                 220

Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Gly Gly 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 Gln Glu Asp
            260                 265                 270

Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe 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 Gly Leu Pro Ser Ser 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 Gln 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 Arg Leu Thr Val Asp Lys
                405                 410                 415


Ser Arg Trp Gln Glu 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 Leu Gly
        435                 440                 445


Lys
```

<210> 707
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 707
gaggtgcaga tggtggagtc tggaggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctgggtt caccgtcagt agtaactaca tgacctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac atactacgca 180

gactccgtga agggccgatt caccatctcc agacacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc tgaggacacg gccgtgtatt actgtgcgag agatggggta 300

tcctacggta tggacgtctg gggccaaggg accacggtca ccgtctcctc a 351

<210> 708
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 708

Glu Val Gln Met 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 Val Ser Ser Asn
20 25 30

Tyr Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg His Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Gly Val Ser Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser
115

<210> 709
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 709
gggttcaccg tcagtagtaa ctac 24

<210> 710
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 710
gcgagagatg gggtatccta cggtatggac gtc 33

<210> 711
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 711

Ala Arg Asp Gly Val Ser Tyr Gly Met Asp Val
1 5 10

<210> 712
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 712
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccgtca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacagta cccctccgat caccttcggc 300

caagggacac gactggagat taaa 324

<210> 713
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 713

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 Ser Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln 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 Tyr Ser Thr Pro Pro
85 90 95

Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 714
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 714
caacagagtt acagtacccc tccgatcacc 30

<210> 715
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 715

Gln Gln Ser Tyr Ser Thr Pro Pro Ile Thr
1 5 10

<210> 716
<211> 1344
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 716
gaggtgcaga tggtggagtc tggaggaggc ttggtccagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctgggtt caccgtcagt agtaactaca tgacctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac atactacgca 180

gactccgtga agggccgatt caccatctcc agacacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc tgaggacacg gccgtgtatt actgtgcgag agatggggta 300

tcctacggta tggacgtctg gggccaaggg accacggtca ccgtctcctc agcctccacc 360

aagggcccat cggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 600

aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 660

gacaaaactc acacatgccc accgtgccca gcacctgaac tcctgggggg accgtcagtc 720

ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 780

tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 840

ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac 900

cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 960

tgcaaggtct ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa 1020

gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggatga gctgaccaag 1080

aaccaggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag 1140

tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 1200

gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg 1260

aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagtcc 1320

ctctccctgt ctccgggtaa atga 1344

<210> 717
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 717

Glu Val Gln Met 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 Val Ser Ser Asn
20 25 30

Tyr Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg His Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Gly Val Ser Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
115 120 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
130 135 140

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Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145                 150                 155                 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
                165                 170                 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
            180                 185                 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
        195                 200                 205

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
    210                 215                 220

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
225                 230                 235                 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
                245                 250                 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
            260                 265                 270

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
        275                 280                 285

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
    290                 295                 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305                 310                 315                 320

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
                325                 330                 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
            340                 345                 350

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
        355                 360                 365
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Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
    370                 375                 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385                 390                 395                 400

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
                405                 410                 415

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
            420                 425                 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445
```

<210> 718
<211> 648
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 718
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccgtca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacagta cccctccgat caccttcggc 300

caagggacac gactggagat taaacgaact gtggctgcac catctgtctt catcttcccg 360

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 480

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 600

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgttag 648

<210> 719

<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 719

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 Ser Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln 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 Tyr Ser Thr Pro Pro
85 90 95

Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
195 200 205

Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 720
<211> 1332
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 720
gaggtgcaga tggtggagtc tggaggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctgggtt caccgtcagt agtaactaca tgacctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac atactacgca 180

gactccgtga agggccgatt caccatctcc agacacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc tgaggacacg gccgtgtatt actgtgcgag agatggggta 300

tcctacggta tggacgtctg gggccaaggg accacggtca ccgtctcctc agcctccacc 360

aagggcccat cggtcttccc cctggcgccc tgctccagga gcacctccga gagcacagcc 420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacgaagac ctacacctgc 600

aacgtagatc acaagcccag caacaccaag gtggacaaga gagttgagtc caaatatggt 660

cccccatgcc caccgtgccc agcaccaggc ggtggcggac catcagtctt cctgttcccc 720

ccaaaaccca aggacactct catgatctcc cggacccctg aggtcacgtg cgtggtggtg 780

gacgtgagcc aggaagaccc cgaggtccag ttcaactggt acgtggatgg cgtggaggtg 840

cataatgcca agacaaagcc gcgggaggag cagttcaaca gcacgtaccg tgtggtcagc 900

gtcctcaccg tcctgcacca ggactggctg aacggcaagg agtacaagtg caaggtctcc 960

aacaaaggcc tcccgtcctc catcgagaaa accatctcca aagccaaagg gcagccccga 1020

gagccacagg tgtacaccct gcccccatcc caggaggaga tgaccaagaa ccaggtcagc 1080

ctgacctgcc tggtcaaagg cttctacccc agcgacatcg ccgtggagtg ggagagcaat 1140

gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1200

ttcctctaca gcaggctcac cgtggacaag agcaggtggc aggaggggaa tgtcttctca 1260

tgctccgtga tgcatgaggc tctgcacaac cactacacac agaagtccct ctccctgtct 1320

ctgggtaaat ga 1332

<210> 721
<211> 443
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 721

Glu Val Gln Met 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 Val Ser Ser Asn
20 25 30

Tyr Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg His Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Gly Val Ser Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
115 120 125

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
130 135 140

```
Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145                 150                 155                 160


Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
                165                 170                 175


Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
            180                 185                 190


Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
        195                 200                 205


Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro
    210                 215                 220


Pro Cys Pro Ala Pro Gly Gly Gly Gly Pro Ser Val Phe Leu Phe Pro
225                 230                 235                 240


Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
                245                 250                 255


Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
            260                 265                 270


Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
        275                 280                 285


Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
    290                 295                 300


Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
305                 310                 315                 320


Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
                325                 330                 335


Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu
            340                 345                 350


Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
```

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        355                 360                 365

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
    370                 375                 380

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
385                 390                 395                 400

Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly
                405                 410                 415

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
            420                 425                 430

Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440
```

<210> 722
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 722
gaggtgcagc tggtggagtc tggaggaggc ttggtccacc ctgggggtc cctgagactc 60

tcctgtgcag cctctgggct caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac atactacgca 180

gactccgtga agggccgatt caccatctcc agacacaatt ccaagaacac gctgtttctt 240

caaatgaaca gcctgagagc tgaggacacg gccgtgtatt actgtgcgag agatcggcca 300

ataactggaa ccactttgga cgtctggggc caagggacca cggtcaccgt ctcctca 357

<210> 723
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 723

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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val His Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Leu Thr Val Ser Ser Asn
            20                  25                  30


Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
    50                  55                  60


Gly Arg Phe Thr Ile Ser Arg His Asn Ser Lys Asn Thr Leu Phe Leu
65                  70                  75                  80


Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95


Arg Asp Arg Pro Ile Thr Gly Thr Thr Leu Asp Val Trp Gly Gln Gly
            100                 105                 110


Thr Thr Val Thr Val Ser Ser
        115


<210>  724
<211>  39
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  724
gcgagagatc ggccaataac tggaaccact ttggacgtc                              39


<210>  725
<211>  13
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  725

Ala Arg Asp Arg Pro Ile Thr Gly Thr Thr Leu Asp Val
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1 5 10

<210> 726
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 726
gacatccaga tgacccagtc tccatcctcc ctgtttgcat ctgtagggga cagagtcacc 60

atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg cattttacta ctgtcaacag acttacagta cccctccgat caccttcggc 300

caagggacac gactggagat taaa 324

<210> 727
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 727

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Phe Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln 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 Phe Tyr Tyr Cys Gln Gln Thr Tyr Ser Thr Pro Pro
85 90 95

Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 728
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 728
caacagactt acagtacccc tccgatcacc 30

<210> 729
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 729

Gln Gln Thr Tyr Ser Thr Pro Pro Ile Thr
1 5 10

<210> 730
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 730
gaggtgcagc tggtggagtc tggaggaggc ttggtccacc ctgggggtc cctgagactc 60

tcctgtgcag cctctgggct caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac atactacgca 180

gactccgtga agggccgatt caccatctcc agacacaatt ccaagaacac gctgtttctt 240

caaatgaaca gcctgagagc tgaggacacg gccgtgtatt actgtgcgag agatcggcca 300

ataactggaa ccactttgga cgtctggggc caagggacca cggtcaccgt ctcctcagcc 360

tccaccaagg 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 acaagaaagt 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 cctctacagc aagctcaccg tggacaagag caggtggcag 1260

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320

aagtccctct ccctgtctcc gggtaaatga 1350

<210> 731
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 731

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val His Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Leu Thr Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

```
Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
    50                  55                  60

Gly Arg Phe Thr Ile Ser Arg His Asn Ser Lys Asn Thr Leu Phe Leu
65                  70                  75                  80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Arg Pro Ile Thr Gly Thr Thr Leu Asp Val Trp Gly Gln Gly
            100                 105                 110

Thr Thr 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 Lys 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

Lys

<210> 732
<211> 648
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 732
gacatccaga tgacccagtc tccatcctcc ctgtttgcat ctgtagggga cagagtcacc 60

atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg cattttacta ctgtcaacag acttacagta cccctccgat caccttcggc 300

caagggacac gactggagat taaacgaact gtggctgcac catctgtctt catcttcccg 360

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 480

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 600

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgttag 648

<210> 733
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 733

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Phe Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
            20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35 40 45

Tyr Ala Ala Ser Ser Leu Gln 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 Phe Tyr Tyr Cys Gln Gln Thr Tyr Ser Thr Pro Pro
85 90 95

Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
195 200 205

Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 734
<211> 1338
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 734
gaggtgcagc tggtggagtc tggaggaggc ttggtccacc ctgggggtc cctgagactc 60

tcctgtgcag cctctgggct caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac atactacgca 180

gactccgtga agggccgatt caccatctcc agacacaatt ccaagaacac gctgtttctt 240

caaatgaaca gcctgagagc tgaggacacg gccgtgtatt actgtgcgag agatcggcca 300

ataactggaa ccactttgga cgtctggggc caagggacca cggtcaccgt ctcctcagcc 360

tccaccaagg gcccatcggt cttccccctg gcgccctgct ccaggagcac ctccgagagc 420

acagccgccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480

aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac gaagacctac 600

acctgcaacg tagatcacaa gcccagcaac accaaggtgg acaagagagt tgagtccaaa 660

tatggtcccc catgcccacc gtgcccagca ccaggcggtg gcggaccatc agtcttcctg 720

ttcccccaa aacccaagga cactctcatg atctcccgga cccctgaggt cacgtgcgtg 780

gtggtggacg tgagccagga agaccccgag gtccagttca actggtacgt ggatggcgtg 840

gaggtgcata atgccaagac aaagccgcgg gaggagcagt tcaacagcac gtaccgtgtg 900

gtcagcgtcc tcaccgtcct gcaccaggac tggctgaacg gcaaggagta caagtgcaag 960

gtctccaaca aaggcctccc gtcctccatc gagaaaacca tctccaaagc caaagggcag 1020

ccccgagagc cacaggtgta caccctgccc ccatcccagg aggagatgac caagaaccag 1080

gtcagcctga cctgcctggt caaaggcttc taccccagcg acatcgccgt ggagtgggag 1140

agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc 1200

tccttcttcc tctacagcag gctcaccgtg gacaagagca ggtggcagga ggggaatgtc 1260

ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacacagaa gtccctctcc 1320

ctgtctctgg gtaaatga 1338

<210> 735
<211> 445
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 735

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val His Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Leu Thr Val Ser Ser Asn

```
            20                  25                  30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
    50                  55                  60

Gly Arg Phe Thr Ile Ser Arg His Asn Ser Lys Asn Thr Leu Phe Leu
65                  70                  75                  80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Arg Pro Ile Thr Gly Thr Thr Leu Asp Val Trp Gly Gln Gly
            100                 105                 110

Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser 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 Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
        195                 200                 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
    210                 215                 220

Cys Pro Pro Cys Pro Ala Pro Gly Gly Gly Gly Pro Ser Val Phe Leu
225                 230                 235                 240
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Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                245                 250                 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
            260                 265                 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        275                 280                 285

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    290                 295                 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305                 310                 315                 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
                325                 330                 335

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            340                 345                 350

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        355                 360                 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    370                 375                 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385                 390                 395                 400

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
                405                 410                 415

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            420                 425                 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440                 445
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<210> 736
<211> 351
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 736
gaggtgcagc tggtggagtc tggaggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctgggtt caccgtcagt agcaactaca tgaactgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac attctacgca 180

gactccgtga ggggccgatt caccatctcc agacacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc tgaggacacg gccgtgtatt actgtgcgag agatgggagc 300

gcctacggta tggacgtctg gggccaaggg accacggtca ccgtctcctc a 351

<210> 737
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 737

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 Val Ser Ser Asn
20 25 30

Tyr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Arg
50 55 60

Gly Arg Phe Thr Ile Ser Arg His Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Gly Ser Ala Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser
        115

<210> 738
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 738
gcgagagatg ggagcgccta cggtatggac gtc   33

<210> 739
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 739

Ala Arg Asp Gly Ser Ala Tyr Gly Met Asp Val
1   5   10

<210> 740
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 740
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc   60

atcacttgcc gggcaagtca gagcattagt agtttttaa attggtatca gcagaaacca   120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca   180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct   240

gaagattttg caacttacta ctgtcaacag agttacagta gtcctccgat caccttcggc   300

caagggacac gactggagat taaa   324

<210> 741

<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 741

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 Ser Ile Ser Ser Phe
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln 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 Tyr Ser Ser Pro Pro
85 90 95

Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 742
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 742
cagagcatta gtagtttt 18

<210> 743
<211> 6
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 743

Gln Ser Ile Ser Ser Phe
1 5

<210> 744
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 744
caacagagtt acagtagtcc tccgatcacc 30

<210> 745
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 745

Gln Gln Ser Tyr Ser Ser Pro Pro Ile Thr
1 5 10

<210> 746
<211> 1344
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 746
gaggtgcagc tggtggagtc tggaggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctgggtt caccgtcagt agcaactaca tgaactgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac attctacgca 180

gactccgtga ggggccgatt caccatctcc agacacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc tgaggacacg gccgtgtatt actgtgcgag agatgggagc 300

gcctacggta tggacgtctg gggccaaggg accacggtca ccgtctcctc agcctccacc 360

aagggcccat cggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 600

aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 660

gacaaaactc acacatgccc accgtgccca gcacctgaac tcctgggggg accgtcagtc 720

ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 780

tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 840

ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac 900

cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 960

tgcaaggtct ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa 1020

gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggatga gctgaccaag 1080

aaccaggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag 1140

tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 1200

gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg 1260

aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagtcc 1320

ctctccctgt ctccgggtaa atga 1344

<210> 747
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 747

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 Val Ser Ser Asn
20 25 30

Tyr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

```
Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Arg
    50                  55                  60

Gly Arg Phe Thr Ile Ser Arg His Asn Ser Lys Asn Thr Leu Tyr Leu
65                  70                  75                  80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Gly Ser Ala Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr
            100                 105                 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
        115                 120                 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
    130                 135                 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145                 150                 155                 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
                165                 170                 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
            180                 185                 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
        195                 200                 205

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
    210                 215                 220

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
225                 230                 235                 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
                245                 250                 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
```

```
            260                 265                 270

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
        275                 280                 285

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
    290                 295                 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305                 310                 315                 320

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
                325                 330                 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
            340                 345                 350

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
        355                 360                 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
    370                 375                 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385                 390                 395                 400

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
                405                 410                 415

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
            420                 425                 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445


<210>  748
<211>  648
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic
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<400> 748
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattagt agtttttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacagta gtcctccgat caccttcggc 300

caagggacac gactggagat taaacgaact gtggctgcac catctgtctt catcttcccg 360

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 480

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 600

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgttag 648

<210> 749
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 749

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 Ser Ile Ser Ser Phe
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln 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 Tyr Ser Ser Pro Pro

85 90 95

Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
195 200 205

Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 750
<211> 1332
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 750
gaggtgcagc tggtggagtc tggaggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctgggtt caccgtcagt agcaactaca tgaactgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac attctacgca 180

gactccgtga ggggccgatt caccatctcc agacacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc tgaggacacg gccgtgtatt actgtgcgag agatgggagc 300

gcctacggta tggacgtctg gggccaaggg accacggtca ccgtctcctc agcctccacc 360

aagggcccat cggtcttccc cctggcgccc tgctccagga gcacctccga gagcacagcc 420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacgaagac ctacacctgc 600

aacgtagatc acaagcccag caacaccaag gtggacaaga gagttgagtc caaatatggt 660

cccccatgcc caccgtgccc agcaccaggc ggtggcggac catcagtctt cctgttcccc 720

ccaaaaccca aggacactct catgatctcc cggacccctg aggtcacgtg cgtggtggtg 780

gacgtgagcc aggaagaccc cgaggtccag ttcaactggt acgtggatgg cgtggaggtg 840

cataatgcca agacaaagcc gcgggaggag cagttcaaca gcacgtaccg tgtggtcagc 900

gtcctcaccg tcctgcacca ggactggctg aacggcaagg agtacaagtg caaggtctcc 960

aacaaaggcc tcccgtcctc catcgagaaa accatctcca aagccaaagg gcagccccga 1020

gagccacagg tgtacaccct gcccccatcc caggaggaga tgaccaagaa ccaggtcagc 1080

ctgacctgcc tggtcaaagg cttctacccc agcgacatcg ccgtggagtg ggagagcaat 1140

gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1200

ttcctctaca gcaggctcac cgtggacaag agcaggtggc aggaggggaa tgtcttctca 1260

tgctccgtga tgcatgaggc tctgcacaac cactacacac agaagtccct ctccctgtct 1320

ctgggtaaat ga 1332

<210> 751
<211> 443
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 751

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 Val Ser Ser Asn
20 25 30

Tyr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

```
        35                  40                  45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Arg
    50                  55                  60

Gly Arg Phe Thr Ile Ser Arg His Asn Ser Lys Asn Thr Leu Tyr Leu
65                  70                  75                  80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Gly Ser Ala Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr
            100                 105                 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
        115                 120                 125

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
    130                 135                 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145                 150                 155                 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
                165                 170                 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
            180                 185                 190

Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
        195                 200                 205

Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro
    210                 215                 220

Pro Cys Pro Ala Pro Gly Gly Gly Gly Pro Ser Val Phe Leu Phe Pro
225                 230                 235                 240

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
                245                 250                 255
```

```
Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
            260                 265                 270

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
        275                 280                 285

Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
    290                 295                 300

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
305                 310                 315                 320

Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
                325                 330                 335

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu
            340                 345                 350

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
        355                 360                 365

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
    370                 375                 380

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
385                 390                 395                 400

Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly
                405                 410                 415

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
            420                 425                 430

Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440
```

<210> 752
<211> 345
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 752
gaggtgcagc tggtggagtc tggaggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctgggtt caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac attctacgca 180

gactccgtga agggccgatt caccatctcc agacacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc tgaggacacg gccgtgtatt actgtgcgag agagggctac 300

ggtatggacg tctggggcca agggaccacg gtcaccgtct cctca 345

<210> 753
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 753

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 Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg His Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Glu Gly Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr
100 105 110

Val Ser Ser
115

<210> 754
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 754
gcgagagagg gctacggtat ggacgtc 27

<210> 755
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 755

Ala Arg Glu Gly Tyr Gly Met Asp Val
1 5

<210> 756
<211> 1338
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 756
gaggtgcagc tggtggagtc tggaggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctgggtt caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac attctacgca 180

gactccgtga agggccgatt caccatctcc agacacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc tgaggacacg gccgtgtatt actgtgcgag agagggctac 300

ggtatggacg tctggggcca agggaccacg gtcaccgtct cctcagcctc caccaagggc 360

ccatcggtct tcccctggc accctcctcc aagagcacct ctgggggcac agcggccctg 420

ggctgcctgg tcaaggacta cttccccgaa ccggtgacgg tgtcgtggaa ctcaggcgcc 480

ctgaccagcg gcgtgcacac cttcccggct gtcctacagt cctcaggact ctactccctc 540

agcagcgtgg tgaccgtgcc ctccagcagc ttgggcaccc agacctacat ctgcaacgtg 600

aatcacaagc ccagcaacac caaggtggac aagaaagttg agcccaaatc ttgtgacaaa 660

actcacacat gcccaccgtg cccagcacct gaactcctgg ggggaccgtc agtcttcctc 720

ttcccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg 780

gtggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg 840

gaggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg 900

gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcaag 960

gtctccaaca aagccctccc agcccccatc gagaaaacca tctccaaagc caaagggcag 1020

ccccgagaac cacaggtgta caccctgccc ccatcccggg atgagctgac caagaaccag 1080

gtcagcctga cctgcctggt caaaggcttc tatcccagcg acatcgccgt ggagtgggag 1140

agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc 1200

tccttcttcc tctacagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc 1260

ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gtccctctcc 1320

ctgtctccgg gtaaatga 1338

<210> 757
<211> 445
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 757

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 Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
50 55 60

```
Gly Arg Phe Thr Ile Ser Arg His Asn Ser Lys Asn Thr Leu Tyr Leu
65                  70                  75                  80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Glu Gly Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr
            100                 105                 110

Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
        115                 120                 125

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
    130                 135                 140

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
145                 150                 155                 160

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
                165                 170                 175

Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
            180                 185                 190

Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
        195                 200                 205

Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
    210                 215                 220

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
225                 230                 235                 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                245                 250                 255

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
            260                 265                 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        275                 280                 285
```

```
Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    290                 295                 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305                 310                 315                 320

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                325                 330                 335

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            340                 345                 350

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        355                 360                 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    370                 375                 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385                 390                 395                 400

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                405                 410                 415

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            420                 425                 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445
```

<210> 758
<211> 1326
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 758
gaggtgcagc tggtggagtc tggaggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctgggtt caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac attctacgca 180

gactccgtga agggccgatt caccatctcc agacacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc tgaggacacg gccgtgtatt actgtgcgag agagggctac 300

ggtatggacg tctggggcca agggaccacg gtcaccgtct cctcagcctc caccaagggc 360

ccatcggtct tccccctggc gccctgctcc aggagcacct ccgagagcac agccgccctg 420

ggctgcctgg tcaaggacta cttccccgaa ccggtgacgg tgtcgtggaa ctcaggcgcc 480

ctgaccagcg gcgtgcacac cttcccggct gtcctacagt cctcaggact ctactccctc 540

agcagcgtgg tgaccgtgcc ctccagcagc ttgggcacga agacctacac ctgcaacgta 600

gatcacaagc ccagcaacac caaggtggac aagagagttg agtccaaata tggtccccca 660

tgcccaccgt gcccagcacc aggcggtggc ggaccatcag tcttcctgtt cccccaaaa 720

cccaaggaca ctctcatgat ctcccggacc cctgaggtca cgtgcgtggt ggtggacgtg 780

agccaggaag accccgaggt ccagttcaac tggtacgtgg atggcgtgga ggtgcataat 840

gccaagacaa agccgcggga ggagcagttc aacagcacgt accgtgtggt cagcgtcctc 900

accgtcctgc accaggactg gctgaacggc aaggagtaca agtgcaaggt ctccaacaaa 960

ggcctcccgt cctccatcga gaaaaccatc tccaaagcca aagggcagcc ccgagagcca 1020

caggtgtaca ccctgccccc atcccaggag gagatgacca agaaccaggt cagcctgacc 1080

tgcctggtca aaggcttcta ccccagcgac atcgccgtgg agtgggagag caatgggcag 1140

ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc 1200

tacagcaggc tcaccgtgga caagagcagg tggcaggagg ggaatgtctt ctcatgctcc 1260

gtgatgcatg aggctctgca caaccactac acacagaagt ccctctccct gtctctgggt 1320

aaatga 1326

<210> 759
<211> 441
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 759

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 Val Ser Ser Asn
            20                  25                  30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
    50                  55                  60

Gly Arg Phe Thr Ile Ser Arg His Asn Ser Lys Asn Thr Leu Tyr Leu
65                  70                  75                  80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Glu Gly Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr
            100                 105                 110

Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
        115                 120                 125

Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val
    130                 135                 140

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
145                 150                 155                 160

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
                165                 170                 175

Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
            180                 185                 190

Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys
        195                 200                 205

Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys
    210                 215                 220

Pro Ala Pro Gly Gly Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
225                 230                 235                 240
```

```
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
                245                 250                 255

Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
            260                 265                 270

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
        275                 280                 285

Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
    290                 295                 300

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
305                 310                 315                 320

Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
                325                 330                 335

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met
            340                 345                 350

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
        355                 360                 365

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
    370                 375                 380

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
385                 390                 395                 400

Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val
                405                 410                 415

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
            420                 425                 430

Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440
```

<210> 760

<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 760
gaggtgcagc tggtggagtc tggaggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctgggtt aatagtcagt cgcaactaca tgatctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac attctacgca 180

gactccgtga agggccgatt caccatctcc agacacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagggc tgaggacacg gccgtatatt actgtgcgag agatctgggt 300

acaggaggta tggacgtctg gggccaaggg accacggtca ccgtctcctc a 351

<210> 761
<211> 1344
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 761
gaggtgcagc tggtggagtc tggaggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctgggtt aatagtcagt cgcaactaca tgatctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac attctacgca 180

gactccgtga agggccgatt caccatctcc agacacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagggc tgaggacacg gccgtatatt actgtgcgag agatctgggt 300

acaggaggta tggacgtctg gggccaaggg accacggtca ccgtctcctc agcctccacc 360

aagggcccat cggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 600

aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 660

gacaaaactc acacatgccc accgtgccca gcacctgaac tcctgggggg accgtcagtc 720

ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 780

tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 840

ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac 900

cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 960

tgcaaggtct ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa 1020

gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggatga gctgaccaag 1080

aaccaggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag 1140

tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 1200

gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg 1260

aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagtcc 1320

ctctccctgt ctccgggtaa atga 1344

<210> 762
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 762

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 Leu Ile Val Ser Arg Asn
20 25 30

Tyr Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg His Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

```
Arg Asp Leu Gly Thr Gly Gly Met Asp Val Trp Gly Gln Gly Thr Thr
            100                 105                 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
        115                 120                 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
    130                 135                 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145                 150                 155                 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
                165                 170                 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
            180                 185                 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
        195                 200                 205

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
    210                 215                 220

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
225                 230                 235                 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
                245                 250                 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
            260                 265                 270

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
        275                 280                 285

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
    290                 295                 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305                 310                 315                 320
```

```
Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
                325                 330                 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
            340                 345                 350

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
        355                 360                 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
    370                 375                 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385                 390                 395                 400

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
                405                 410                 415

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
            420                 425                 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445
```

<210> 763
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 763

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caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc       60

tcctgtgtag cctctggatt caccttcagt atttatggca tggactgggt ccgccaggct      120

ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagtaa taaatactat      180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgag acctgaggac acggctgtgt attactgtgc gaaagatagg      300

gaggcagctg cggatgcttt tgatatctgg ggccaaggga caatggtcac cgtctcttca      360
```

<210> 764
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 764

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Ile Tyr
20 25 30

Gly Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Asp Arg Glu Ala Ala Ala Asp Ala Phe Asp Ile Trp Gly Gln
100 105 110

Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 765
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 765
ggattcacct tcagtattta tggc 24

<210> 766
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 766

Gly Phe Thr Phe Ser Ile Tyr Gly
1 5

<210> 767
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 767
gcgaaagata gggaggcagc tgcggatgct tttgatatc 39

<210> 768
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 768

Ala Lys Asp Arg Glu Ala Ala Ala Asp Ala Phe Asp Ile
1 5 10

<210> 769
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 769
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atcacttgtc gggcgagtca gggtattagc agctggttag cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcacagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240

gaagattttg caacttacta ttgtcaacag gctaacagtt tccgtctcac tttcggcgga 300

gggaccaagg tggagatcaa a 321

<210> 770
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 770

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu His 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 Ala Asn Ser Phe Arg Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 771
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 771
caacaggcta acagtttccg tctcact 27

<210> 772
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 772

Gln Gln Ala Asn Ser Phe Arg Leu Thr
1 5

<210> 773
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 773
caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgtag cctctggatt caccttcagt atttatggca tggactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagtaa taaatactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag acctgaggac acggctgtgt attactgtgc gaaagatagg 300

gaggcagctg cggatgcttt tgatatctgg ggccaaggga caatggtcac cgtctcttca 360

gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 600

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaact cctgggggga 720

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct 780

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 900

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960

gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1020

aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggatgag 1080

ctgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc 1140

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200

ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg 1260

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1320

cagaagtccc tctccctgtc tccgggtaaa tga 1353

<210> 774
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 774

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Ile Tyr
20 25 30

Gly Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Asp Arg Glu Ala Ala Ala Asp Ala Phe Asp Ile Trp Gly Gln
100 105 110

```
Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335
```

```
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
        355                 360                 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445

Gly Lys
    450
```

<210> 775
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 775

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gacatccaga tgacccagtc tccatcttcc gtgtctgcat ctgtaggaga cagagtcacc       60

atcacttgtc gggcgagtca gggtattagc agctggttag cctggtatca gcagaaacca      120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcacagtgg ggtcccatca      180

aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct      240

gaagattttg caacttacta ttgtcaacag gctaacagtt tccgtctcac tttcggcgga      300

gggaccaagg tggagatcaa acgaactgtg gctgcaccat ctgtcttcat cttcccgcca      360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat      420
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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 gttag 645

<210> 776
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 776

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu His 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 Ala Asn Ser Phe Arg Leu
85 90 95

Thr 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>  777
<211>  1341
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  777
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tcctgtgtag cctctggatt caccttcagt atttatggca tggactgggt ccgccaggct      120

ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagtaa taaatactat      180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgag acctgaggac acggctgtgt attactgtgc gaaagatagg      300

gaggcagctg cggatgcttt tgatatctgg ggccaaggga caatggtcac cgtctcttca      360

gcctccacca agggcccatc ggtcttcccc ctggcgccct gctccaggag cacctccgag      420

agcacagccg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg      480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca      540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacgaagacc      600

tacacctgca acgtagatca caagcccagc aacaccaagg tggacaagag agttgagtcc      660

aaatatggtc ccccatgccc accgtgccca gcaccaggcg gtggcggacc atcagtcttc      720

ctgttccccc caaaacccaa ggacactctc atgatctccc ggaccctga ggtcacgtgc      780
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gtggtggtgg acgtgagcca ggaagacccc gaggtccagt tcaactggta cgtggatggc 840

gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agttcaacag cacgtaccgt 900

gtggtcagcg tcctcaccgt cctgcaccag gactggctga acggcaagga gtacaagtgc 960

aaggtctcca acaaaggcct cccgtcctcc atcgagaaaa ccatctccaa agccaaaggg 1020

cagccccgag agccacaggt gtacaccctg cccccatccc aggaggagat gaccaagaac 1080

caggtcagcc tgacctgcct ggtcaaaggc ttctacccca gcgacatcgc cgtggagtgg 1140

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200

ggctccttct tcctctacag caggctcacc gtggacaaga gcaggtggca ggaggggaat 1260

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacaca gaagtccctc 1320

tccctgtctc tgggtaaatg a 1341

<210> 778
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 778

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Ile Tyr
20 25 30

Gly Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

```
Ala Lys Asp Arg Glu Ala Ala Ala Asp Ala Phe Asp Ile Trp Gly Gln
            100                 105                 110

Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
    210                 215                 220

Pro Cys Pro Pro Cys Pro Ala Pro Gly Gly Gly Gly Pro Ser Val Phe
225                 230                 235                 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                245                 250                 255

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
            260                 265                 270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
    290                 295                 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305                 310                 315                 320
```

```
Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
                325                 330                 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            340                 345                 350

Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
        355                 360                 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    370                 375                 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385                 390                 395                 400

Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
                405                 410                 415

Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            420                 425                 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440                 445
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<210> 779
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 779
gaggtgcagc tggtggagtc tggaggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctgggtt cattgtcagt aggaactaca tgagctgggt ccgccaggct 120

ccagggaagg gactggagtg ggtctcagtt atttatagcg gtggtagcac attctacgca 180

gactccgtga agggccgctt caccatctcc cgacacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgaaagc tgaggacacg gccgtgtatt actgtgcgag agagctacga 300

gggtactttg actactgggg ccagggaacc ctggtcaccg tctcctca 348

<210> 780
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 780

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 Ile Val Ser Arg Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg His Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Glu Leu Arg Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 781
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 781
gggttcattg tcagtaggaa ctac 24

<210> 782
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 782

Gly Phe Ile Val Ser Arg Asn Tyr
1 5

<210> 783
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 783
gcgagagagc tacgagggta ctttgactac 30

<210> 784
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 784

Ala Arg Glu Leu Arg Gly Tyr Phe Asp Tyr
1 5 10

<210> 785
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 785
gacatccagt tgacccagtc tccatccttc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgct gggccagtca gggcattagc agttatttag cctggtatca gcaaaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccactt tgcaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240

gaagattttg caacttatta ctgtcaactg cttaatagtt acccgtacac ttttggccag 300

gggaccaagc tggagatcaa a 321

<210> 786
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 786

Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Trp Ala Ser Gln Gly Ile Ser Ser Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Leu Leu Asn Ser Tyr Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 787
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 787
caactgctta atagttaccc gtacact 27

<210> 788
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 788

Gln Leu Leu Asn Ser Tyr Pro Tyr Thr
1 5

<210> 789
<211> 1341
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 789
gaggtgcagc tggtggagtc tggaggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctgggtt cattgtcagt aggaactaca tgagctgggt ccgccaggct 120

ccagggaagg gactggagtg ggtctcagtt atttatagcg gtggtagcac attctacgca 180

gactccgtga agggccgctt caccatctcc cgacacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgaaagc tgaggacacg gccgtgtatt actgtgcgag agagctacga 300

gggtactttg actactgggg ccagggaacc ctggtcaccg tctcctcagc ctccaccaag 360

ggcccatcgg tcttcccccc ggcaccctcc tccaagagca cctctggggg cacagcggcc 420

ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 480

gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc 540

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 600

gtgaatcaca agcccagcaa caccaaggtg gacaagaaag ttgagcccaa atcttgtgac 660

aaaactcaca catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc 720

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 780

gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 840

gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt 900

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 960

aaggtctcca acaaagccct cccagccccc atcgagaaaa ccatctccaa agccaaaggg 1020

cagccccgag aaccacaggt gtacaccctg cccccatccc gggatgagct gaccaagaac 1080

caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1140

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1260

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagtccctc 1320

tccctgtctc cgggtaaatg a 1341

<210> 790
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 790

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 Ile Val Ser Arg Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg His Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Glu Leu Arg Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

```
Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
        115                 120                 125

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
    130                 135                 140

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
145                 150                 155                 160

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
                165                 170                 175

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
            180                 185                 190

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        195                 200                 205

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    210                 215                 220

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
225                 230                 235                 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                245                 250                 255

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            260                 265                 270

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    290                 295                 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305                 310                 315                 320

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
                325                 330                 335
```

```
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            340                 345                 350

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
        355                 360                 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    370                 375                 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385                 390                 395                 400

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                405                 410                 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            420                 425                 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445
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<210> 791
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 791
gacatccagt tgacccagtc tccatccttc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgct gggccagtca gggcattagc agttatttag cctggtatca gcaaaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccactt tgcaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240

gaagattttg caacttatta ctgtcaactg cttaatagtt acccgtacac ttttggccag 300

gggaccaagc tggagatcaa acgaactgtg 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 gttag 645

<210> 792
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 792

Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Trp Ala Ser Gln Gly Ile Ser Ser Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Leu Leu Asn Ser Tyr Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu 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> 793
<211> 1329
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 793
gaggtgcagc tggtggagtc tggaggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctgggtt cattgtcagt aggaactaca tgagctgggt ccgccaggct 120

ccagggaagg gactggagtg ggtctcagtt atttatagcg gtggtagcac attctacgca 180

gactccgtga agggccgctt caccatctcc cgacacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgaaagc tgaggacacg gccgtgtatt actgtgcgag agagctacga 300

gggtactttg actactgggg ccagggaacc ctggtcaccg tctcctcagc ctccaccaag 360

ggcccatcgg tcttcccct ggcgccctgc tccaggagca cctccgagag cacagccgcc 420

ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 480

gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc 540

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cgaagaccta cacctgcaac 600

gtagatcaca agcccagcaa caccaaggtg gacaagagag ttgagtccaa atatggtccc 660

ccatgcccac cgtgcccagc accaggcggt ggcggaccat cagtcttcct gttcccccca 720

aaacccaagg acactctcat gatctcccgg acccctgagg tcacgtgcgt ggtggtggac 780

gtgagccagg aagaccccga ggtccagttc aactggtacg tggatggcgt ggaggtgcat 840

aatgccaaga caaagccgcg ggaggagcag ttcaacagca cgtaccgtgt ggtcagcgtc 900

ctcaccgtcc tgcaccagga ctggctgaac ggcaaggagt acaagtgcaa ggtctccaac 960

aaaggcctcc cgtcctccat cgagaaaacc atctccaaag ccaaagggca gccccgagag 1020

ccacaggtgt acaccctgcc cccatcccag gaggagatga ccaagaacca ggtcagcctg 1080

acctgcctgg tcaaaggctt ctaccccagc gacatcgccg tggagtggga gagcaatggg 1140

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc 1200

ctctacagca ggctcaccgt ggacaagagc aggtggcagg aggggaatgt cttctcatgc 1260

tccgtgatgc atgaggctct gcacaaccac tacacacaga agtccctctc cctgtctctg 1320

ggtaaatga 1329

<210> 794
<211> 442
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 794

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 Ile Val Ser Arg Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg His Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Glu Leu Arg Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

```
Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
        115                 120                 125

Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu
    130                 135                 140

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
145                 150                 155                 160

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
                165                 170                 175

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
            180                 185                 190

Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr
        195                 200                 205

Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro
    210                 215                 220

Cys Pro Ala Pro Gly Gly Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
225                 230                 235                 240

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
                245                 250                 255

Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp
            260                 265                 270

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
        275                 280                 285

Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
    290                 295                 300

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
305                 310                 315                 320

Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
                325                 330                 335
```

```
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu
            340                 345                 350

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
        355                 360                 365

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
    370                 375                 380

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
385                 390                 395                 400

Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn
                405                 410                 415

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
            420                 425                 430

Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440
```

<210> 795
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 795
gaggtgcagc tggtggagtc tggaggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctgggtt caccgtcagt agtaactaca tgacctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac attctacgca 180

gactccgtga agggccgatt caccatctcc agacacaatt ccgagaacac gctgtatctt 240

caaatgaaca gcctgagagc tgaggacacg gccgtgtatt actgtgcgag agatctagca 300

gcagctggta cagactactg gggccaggga gccctggtca ccgtctcctc a 351

<210> 796
<211> 117
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 796

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 Val Ser Ser Asn
20 25 30

Tyr Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg His Asn Ser Glu Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Leu Ala Ala Ala Gly Thr Asp Tyr Trp Gly Gln Gly Ala Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 797
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 797
gcgagagatc tagcagcagc tggtacagac tac 33

<210> 798
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 798

Ala Arg Asp Leu Ala Ala Ala Gly Thr Asp Tyr
1   5   10

<210> 799
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 799
gacatccagt tgacccagtc tccatccttc ctgtctgcat ctgtaggaga cagagtcacc   60

atcacttgct gggccagtca gggcattagc agttatttag cctggtatca gcaaaaacca   120

gggaaagccc ctaagctcct gatctatgct gcatccactt tgcaaagtgg ggtcccatca   180

aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct   240

gatgattttg caacttatta ctgtcaacac cttaatagtt acctgtacac ttttggccag   300

gggaccaagc tggagatcaa a   321

<210> 800
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 800

Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1   5   10   15

Asp Arg Val Thr Ile Thr Cys Trp Ala Ser Gln Gly Ile Ser Ser Tyr
            20   25   30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln His Leu Asn Ser Tyr Leu Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 801
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 801
caacacctta atagttacct gtacact 27

<210> 802
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 802

Gln His Leu Asn Ser Tyr Leu Tyr Thr
1 5

<210> 803
<211> 1344
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 803
gaggtgcagc tggtggagtc tggaggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctgggtt caccgtcagt agtaactaca tgacctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac attctacgca 180

gactccgtga agggccgatt caccatctcc agacacaatt ccgagaacac gctgtatctt 240

caaatgaaca gcctgagagc tgaggacacg gccgtgtatt actgtgcgag agatctagca 300

gcagctggta cagactactg gggccaggga gccctggtca ccgtctcctc agcctccacc 360

aagggcccat cggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 600

aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 660

gacaaaactc acacatgccc accgtgccca gcacctgaac tcctgggggg accgtcagtc 720

ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 780

tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 840

ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac 900

cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 960

tgcaaggtct ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa 1020

gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggatga gctgaccaag 1080

aaccaggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag 1140

tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 1200

gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg 1260

aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagtcc 1320

ctctccctgt ctccgggtaa atga 1344

<210> 804
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 804

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 Val Ser Ser Asn
            20                  25                  30

Tyr Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
    50                  55                  60

Gly Arg Phe Thr Ile Ser Arg His Asn Ser Glu Asn Thr Leu Tyr Leu
65                  70                  75                  80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Leu Ala Ala Ala Gly Thr Asp Tyr Trp Gly Gln Gly Ala Leu
            100                 105                 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
        115                 120                 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
    130                 135                 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145                 150                 155                 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
                165                 170                 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
            180                 185                 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
        195                 200                 205

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
    210                 215                 220

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
225                 230                 235                 240
```

```
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
                245                 250                 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
            260                 265                 270

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
        275                 280                 285

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
    290                 295                 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305                 310                 315                 320

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
                325                 330                 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
            340                 345                 350

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
        355                 360                 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
    370                 375                 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385                 390                 395                 400

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
                405                 410                 415

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
            420                 425                 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445
```

<210> 805

<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 805
gacatccagt tgacccagtc tccatccttc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgct gggccagtca gggcattagc agttatttag cctggtatca gcaaaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccactt tgcaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240

gatgattttg caacttatta ctgtcaacac cttaatagtt acctgtacac ttttggccag 300

gggaccaagc tggagatcaa acgaactgtg 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 gttag 645

<210> 806
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 806

Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Trp Ala Ser Gln Gly Ile Ser Ser Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

```
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Asp Asp Phe Ala Thr Tyr Tyr Cys Gln His Leu Asn Ser Tyr Leu Tyr
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Leu 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>  807
<211>  1332
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  807
gaggtgcagc tggtggagtc tggaggaggc ttggtccagc ctgggggtc cctgagactc       60

tcctgtgcag cctctgggtt caccgtcagt agtaactaca tgacctgggt ccgccaggct      120
```

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac attctacgca 180

gactccgtga agggccgatt caccatctcc agacacaatt ccgagaacac gctgtatctt 240

caaatgaaca gcctgagagc tgaggacacg gccgtgtatt actgtgcgag agatctagca 300

gcagctggta cagactactg gggccaggga gccctggtca ccgtctcctc agcctccacc 360

aagggcccat cggtcttccc cctggcgccc tgctccagga gcacctccga gagcacagcc 420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacgaagac ctacacctgc 600

aacgtagatc acaagcccag caacaccaag gtggacaaga gagttgagtc caaatatggt 660

cccccatgcc caccgtgccc agcaccaggc ggtggcggac catcagtctt cctgttcccc 720

ccaaaaccca aggacactct catgatctcc cggacccctg aggtcacgtg cgtggtggtg 780

gacgtgagcc aggaagaccc cgaggtccag ttcaactggt acgtggatgg cgtggaggtg 840

cataatgcca agacaaagcc gcgggaggag cagttcaaca gcacgtaccg tgtggtcagc 900

gtcctcaccg tcctgcacca ggactggctg aacggcaagg agtacaagtg caaggtctcc 960

aacaaaggcc tcccgtcctc catcgagaaa accatctcca aagccaaagg gcagccccga 1020

gagccacagg tgtacaccct gcccccatcc caggaggaga tgaccaagaa ccaggtcagc 1080

ctgacctgcc tggtcaaagg cttctacccc agcgacatcg ccgtggagtg ggagagcaat 1140

gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1200

ttcctctaca gcaggctcac cgtggacaag agcaggtggc aggaggggaa tgtcttctca 1260

tgctccgtga tgcatgaggc tctgcacaac cactacacac agaagtccct ctccctgtct 1320

ctgggtaaat ga 1332

<210> 808
<211> 443
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 808

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 Val Ser Ser Asn
            20                  25                  30

Tyr Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
    50                  55                  60

Gly Arg Phe Thr Ile Ser Arg His Asn Ser Glu Asn Thr Leu Tyr Leu
65                  70                  75                  80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Leu Ala Ala Ala Gly Thr Asp Tyr Trp Gly Gln Gly Ala Leu
            100                 105                 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
        115                 120                 125

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
    130                 135                 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145                 150                 155                 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
                165                 170                 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
            180                 185                 190

Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
        195                 200                 205

Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro
    210                 215                 220

Pro Cys Pro Ala Pro Gly Gly Gly Gly Pro Ser Val Phe Leu Phe Pro
```

```
225                 230                 235                 240

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
                245                 250                 255

Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
            260                 265                 270

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
        275                 280                 285

Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
    290                 295                 300

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
305                 310                 315                 320

Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
                325                 330                 335

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu
            340                 345                 350

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
        355                 360                 365

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
    370                 375                 380

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
385                 390                 395                 400

Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly
                405                 410                 415

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
            420                 425                 430

Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440
```

<210> 809
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 809
caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt agctatggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagtta taagtactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gatagatggg 300

gggacagtga ctacgatttt tgactactgg ggccagggaa ccctggtcac cgtctcctca 360

<210> 810
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 810

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Tyr Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Ile Asp Gly Gly Thr Val Thr Thr Ile Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 811
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 811
ggattcacct tcagtagcta tggc 24

<210> 812
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 812

Gly Phe Thr Phe Ser Ser Tyr Gly
1 5

<210> 813
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 813
atatcatatg atggaagtta taag 24

<210> 814
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 814

Ile Ser Tyr Asp Gly Ser Tyr Lys
1 5

<210> 815
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 815
gcgatagatg gggggacagt gactacgatt tttgactac 39

<210> 816
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 816

Ala Ile Asp Gly Gly Thr Val Thr Thr Ile Phe Asp Tyr
1 5 10

<210> 817
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 817
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatact gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacagta cccctccgtg gacgttcggc 300

caagggacca aggtggaaat caaa 324

<210> 818

<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 818

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 Ser Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Thr Ala Ser Ser Leu Gln 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 Tyr Ser Thr Pro Pro
85 90 95

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 819
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 819
actgcatcc 9

<210> 820
<211> 3
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 820

Thr Ala Ser
1

<210> 821
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 821
caacagagtt acagtacccc tccgtggacg 30

<210> 822
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 822

Gln Gln Ser Tyr Ser Thr Pro Pro Trp Thr
1 5 10

<210> 823
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 823
caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt agctatggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagtta taagtactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gatagatggg 300

gggacagtga ctacgatttt tgactactgg ggccagggaa ccctggtcac cgtctcctca 360

gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 600

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaact cctgggggga 720

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct 780

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 900

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960

gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1020

aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgccccatc ccgggatgag 1080

ctgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc 1140

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200

ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg 1260

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1320

cagaagtccc tctccctgtc tccgggtaaa tga 1353

<210> 824
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 824

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

```
Ala Val Ile Ser Tyr Asp Gly Ser Tyr Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Ile Asp Gly Gly Thr Val Thr Thr Ile Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
```

260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
340 345 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gly Lys
450

<210> 825
<211> 648
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 825
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatact gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacagta cccctccgtg gacgttcggc 300

caagggacca aggtggaaat caaacgaact gtggctgcac catctgtctt catcttcccg 360

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 480

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 600

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgttag 648

<210> 826
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 826

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 Ser Ile Ser Ser Tyr
            20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35 40 45

Tyr Thr Ala Ser Ser Leu Gln 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 Tyr Ser Thr Pro Pro
85 90 95

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
195 200 205

Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 827
<211> 1341
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 827
caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt agctatggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagtta taagtactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gatagatggg 300

gggacagtga ctacgatttt tgactactgg ggccagggaa ccctggtcac cgtctcctca 360

gcctccacca agggcccatc ggtcttcccc ctggcgccct gctccaggag cacctccgag 420

agcacagccg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacgaagacc 600

tacacctgca acgtagatca caagcccagc aacaccaagg tggacaagag agttgagtcc 660

aaatatggtc ccccatgccc accgtgccca gcaccaggcg gtggcggacc atcagtcttc 720

ctgttccccc caaaacccaa ggacactctc atgatctccc ggaccctga ggtcacgtgc 780

gtggtggtgg acgtgagcca ggaagacccc gaggtccagt tcaactggta cgtggatggc 840

gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agttcaacag cacgtaccgt 900

gtggtcagcg tcctcaccgt cctgcaccag gactggctga acggcaagga gtacaagtgc 960

aaggtctcca acaaaggcct cccgtcctcc atcgagaaaa ccatctccaa agccaaaggg 1020

cagccccgag agccacaggt gtacaccctg cccccatccc aggaggagat gaccaagaac 1080

caggtcagcc tgacctgcct ggtcaaaggc ttctacccca gcgacatcgc cgtggagtgg 1140

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200

ggctccttct tcctctacag caggctcacc gtggacaaga gcaggtggca ggaggggaat 1260

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacaca gaagtccctc 1320

tccctgtctc tgggtaaatg a 1341

<210> 828
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 828

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

```
            20                  25                  30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Val Ile Ser Tyr Asp Gly Ser Tyr Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Ile Asp Gly Gly Thr Val Thr Thr Ile Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
    210                 215                 220

Pro Cys Pro Pro Cys Pro Ala Pro Gly Gly Gly Gly Pro Ser Val Phe
225                 230                 235                 240
```

```
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                245                 250                 255

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
            260                 265                 270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
    290                 295                 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305                 310                 315                 320

Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
                325                 330                 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            340                 345                 350

Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
        355                 360                 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    370                 375                 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385                 390                 395                 400

Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
                405                 410                 415

Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            420                 425                 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440                 445
```

<210> 829
<211> 251
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 829

```
Arg Val Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn
 1               5                  10                  15


Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val
            20                  25                  30


Tyr Ala Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser
        35                  40                  45


Val Leu Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val
    50                  55                  60


Ser Pro Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp
65                  70                  75                  80


Ser Phe Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln
                85                  90                  95


Thr Gly Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr
            100                 105                 110


Gly Cys Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly
        115                 120                 125


Gly Asn Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys
    130                 135                 140


Pro Phe Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr
145                 150                 155                 160


Pro Cys Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser
                165                 170                 175


Tyr Gly Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val
            180                 185                 190
```

```
Val Val Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly
        195                 200                 205


Pro Lys Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Glu
    210                 215                 220


Gln Lys Leu Ile Ser Glu Glu Asp Leu Gly Gly Glu Gln Lys Leu Ile
225                 230                 235                 240


Ser Glu Glu Asp Leu His His His His His His
                245                 250


<210> 830
<211> 456
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 830

Arg Val Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn
 1               5                  10                  15


Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val
            20                  25                  30


Tyr Ala Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser
        35                  40                  45


Val Leu Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val
    50                  55                  60


Ser Pro Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp
65                  70                  75                  80


Ser Phe Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln
                85                  90                  95


Thr Gly Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr
            100                 105                 110


Gly Cys Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly
```

```
        115                 120                 125

Gly Asn Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys
    130                 135                 140

Pro Phe Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr
145                 150                 155                 160

Pro Cys Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser
                165                 170                 175

Tyr Gly Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val
            180                 185                 190

Val Val Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly
        195                 200                 205

Pro Lys Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Glu
    210                 215                 220

Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala
225                 230                 235                 240

Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile
                245                 250                 255

Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val
            260                 265                 270

Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val
        275                 280                 285

Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp
    290                 295                 300

Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln
305                 310                 315                 320

Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp
                325                 330                 335
```

```
Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val
            340                 345                 350


Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met Thr
        355                 360                 365


Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu
    370                 375                 380


Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr
385                 390                 395                 400


Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr
                405                 410                 415


Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr
            420                 425                 430


Ser Cys Ser Val Val His Glu Gly Leu His Asn His His Thr Thr Lys
        435                 440                 445


Ser Phe Ser Arg Thr Pro Gly Lys
    450                 455


<210> 831
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 831

Arg Val Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn
 1               5                  10                  15


Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val
            20                  25                  30


Tyr Ala Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser
        35                  40                  45


Val Leu Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val
```

```
    50                  55                  60

Ser Pro Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp
65                  70                  75                  80

Ser Phe Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln
                85                  90                  95

Thr Gly Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr
            100                 105                 110

Gly Cys Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly
        115                 120                 125

Gly Asn Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys
    130                 135                 140

Pro Phe Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr
145                 150                 155                 160

Pro Cys Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser
                165                 170                 175

Tyr Gly Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val
            180                 185                 190

Val Val Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly
        195                 200                 205

Pro Lys Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270
```

```
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
        355                 360                 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445

Gly Lys
    450
```

<210> 832
<211> 1273
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 832

```
Met Phe Val Phe Leu Val Leu Leu Pro Leu Val Ser Ser Gln Cys Val
 1               5                  10                  15

Asn Leu Thr Thr Arg Thr Gln Leu Pro Pro Ala Tyr Thr Asn Ser Phe
            20                  25                  30

Thr Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser Ser Val Leu
        35                  40                  45

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
    50                  55                  60

Phe His Ala Ile His Val Ser Gly Thr Asn Gly Thr Lys Arg Phe Asp
65                  70                  75                  80

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
                85                  90                  95

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
            100                 105                 110

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
        115                 120                 125

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
    130                 135                 140

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
145                 150                 155                 160

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
                165                 170                 175

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
            180                 185                 190

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
        195                 200                 205
```

```
Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
    210                 215                 220

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
225                 230                 235                 240

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
                245                 250                 255

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
            260                 265                 270

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
        275                 280                 285

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
    290                 295                 300

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
305                 310                 315                 320

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
                325                 330                 335

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
            340                 345                 350

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
        355                 360                 365

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
    370                 375                 380

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
385                 390                 395                 400

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
                405                 410                 415

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
            420                 425                 430
```

```
Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
        435                 440                 445

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
    450                 455                 460

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
465                 470                 475                 480

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
                485                 490                 495

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
            500                 505                 510

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
        515                 520                 525

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
    530                 535                 540

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
545                 550                 555                 560

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
                565                 570                 575

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
            580                 585                 590

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
        595                 600                 605

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
    610                 615                 620

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
625                 630                 635                 640

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
                645                 650                 655
```

```
Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
            660                 665                 670

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
        675                 680                 685

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
    690                 695                 700

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
705                 710                 715                 720

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
                725                 730                 735

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
            740                 745                 750

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
        755                 760                 765

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
    770                 775                 780

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
785                 790                 795                 800

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
                805                 810                 815

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
            820                 825                 830

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
        835                 840                 845

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
    850                 855                 860

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
```

```
865                 870                 875                 880

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
                885                 890                 895

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
            900                 905                 910

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
        915                 920                 925

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
    930                 935                 940

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
945                 950                 955                 960

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
                965                 970                 975

Leu Asn Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln
            980                 985                 990

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
        995                 1000                1005

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
    1010                1015                1020

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg Val
1025                1030                1035                1040

Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln Ser Ala
                1045                1050                1055

Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro Ala Gln Glu
            1060                1065                1070

Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp Gly Lys Ala His
        1075                1080                1085
```

```
Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly Thr His Trp Phe Val
    1090                1095                1100

Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile Ile Thr Thr Asp Asn Thr
1105                1110                1115                1120

Phe Val Ser Gly Asn Cys Asp Val Val Ile Gly Ile Val Asn Asn Thr
                1125                1130                1135

Val Tyr Asp Pro Leu Gln Pro Glu Leu Asp Ser Phe Lys Glu Glu Leu
            1140                1145                1150

Asp Lys Tyr Phe Lys Asn His Thr Ser Pro Asp Val Asp Leu Gly Asp
        1155                1160                1165

Ile Ser Gly Ile Asn Ala Ser Val Val Asn Ile Gln Lys Glu Ile Asp
    1170                1175                1180

Arg Leu Asn Glu Val Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu
1185                1190                1195                1200

Gln Glu Leu Gly Lys Tyr Glu Gln Tyr Ile Lys Trp Pro Trp Tyr Ile
                1205                1210                1215

Trp Leu Gly Phe Ile Ala Gly Leu Ile Ala Ile Val Met Val Thr Ile
            1220                1225                1230

Met Leu Cys Cys Met Thr Ser Cys Cys Ser Cys Leu Lys Gly Cys Cys
        1235                1240                1245

Ser Cys Gly Ser Cys Cys Lys Phe Asp Glu Asp Asp Ser Glu Pro Val
    1250                1255                1260

Leu Lys Gly Val Lys Leu His Tyr Thr
1265                1270
```

<210> 833
<211> 1196
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 833

```
Val Asn Leu Thr Thr Arg Thr Gln Leu Pro Pro Ala Tyr Thr Asn Ser
 1               5                  10                  15

Phe Thr Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser Ser Val
            20                  25                  30

Leu His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr
        35                  40                  45

Trp Phe His Ala Ile His Val Ser Gly Thr Asn Gly Thr Lys Arg Phe
    50                  55                  60

Asp Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr
65                  70                  75                  80

Glu Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp
                85                  90                  95

Ser Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val
            100                 105                 110

Ile Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val
        115                 120                 125

Tyr Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val
    130                 135                 140

Tyr Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe
145                 150                 155                 160

Leu Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu
                165                 170                 175

Phe Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His
            180                 185                 190

Thr Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu
        195                 200                 205
```

```
Glu Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln
    210                 215                 220

Thr Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser
225                 230                 235                 240

Ser Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln
                245                 250                 255

Pro Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp
            260                 265                 270

Ala Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu
        275                 280                 285

Lys Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg
    290                 295                 300

Val Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu
305                 310                 315                 320

Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr
                325                 330                 335

Ala Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val
            340                 345                 350

Leu Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser
        355                 360                 365

Pro Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser
    370                 375                 380

Phe Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr
385                 390                 395                 400

Gly Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly
                405                 410                 415

Cys Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly
            420                 425                 430
```

```
Asn Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro
        435                 440                 445

Phe Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro
    450                 455                 460

Cys Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr
465                 470                 475                 480

Gly Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val
                485                 490                 495

Val Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro
            500                 505                 510

Lys Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe
        515                 520                 525

Asn Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe
    530                 535                 540

Leu Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala
545                 550                 555                 560

Val Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser
                565                 570                 575

Phe Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln
            580                 585                 590

Val Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala
        595                 600                 605

Ile His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly
    610                 615                 620

Ser Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His
625                 630                 635                 640

Val Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys
                645                 650                 655
```

```
Ala Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val
            660                 665                 670

Ala Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn
        675                 680                 685

Ser Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr
    690                 695                 700

Ile Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser
705                 710                 715                 720

Val Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn
                725                 730                 735

Leu Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu
            740                 745                 750

Thr Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala
        755                 760                 765

Gln Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly
    770                 775                 780

Phe Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg
785                 790                 795                 800

Ser Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala
                805                 810                 815

Gly Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg
            820                 825                 830

Asp Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro
        835                 840                 845

Leu Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala
    850                 855                 860

Gly Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln
```

```
865                 870                 875                 880

Ile Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val
                885                 890                 895

Thr Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe
            900                 905                 910

Asn Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser
        915                 920                 925

Ala Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu
    930                 935                 940

Asn Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser
945                 950                 955                 960

Val Leu Asn Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val
                965                 970                 975

Gln Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr
            980                 985                 990

Val Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn
        995                 1000                1005

Leu Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg
    1010                1015                1020

Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln Ser
1025                1030                1035                1040

Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro Ala Gln
                1045                1050                1055

Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp Gly Lys Ala
            1060                1065                1070

His Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly Thr His Trp Phe
        1075                1080                1085
```

Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile Ile Thr Thr Asp Asn
    1090   1095   1100

Thr Phe Val Ser Gly Asn Cys Asp Val Val Ile Gly Ile Val Asn Asn
1105   1110   1115   1120

Thr Val Tyr Asp Pro Leu Gln Pro Glu Leu Asp Ser Phe Lys Glu Glu
                1125   1130   1135

Leu Asp Lys Tyr Phe Lys Asn His Thr Ser Pro Asp Val Asp Leu Gly
            1140   1145   1150

Asp Ile Ser Gly Ile Asn Ala Ser Val Val Asn Ile Gln Lys Glu Ile
        1155   1160   1165

Asp Arg Leu Asn Glu Val Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp
    1170   1175   1180

Leu Gln Glu Leu Gly Lys Tyr Glu Gln Tyr Ile Lys
1185   1190   1195

<210> 834
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 834

Gly Gly Gly Gly Ser
 1   5

<210> 835
<211> 47
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 835

Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys Asn Gly
1   5   10   15

Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly Phe Gln
            20   25   30

Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val Leu
        35   40   45

<210> 836
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 836

Cys Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly
1   5   10   15

Asn Tyr Asn Tyr Leu
            20

<210> 837
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 837

Asp Ile Ser Thr Glu Ile Tyr Gln
1   5

<210> 838
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 838

Cys Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr
1   5   10   15

Gly Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val
20 25 30

Val Leu

<210> 839
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 839

Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys Asn Gly
1 5 10 15

Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly Phe Gln
20 25 30

Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val
35 40

<210> 840
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 840

Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys Asn Gly Val Glu Gly Phe
1 5 10 15

<210> 841
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 841

Pro Leu Gln Ser Tyr Gly Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln
1 5 10 15

Pro Tyr Arg Val Val Val Leu Ser Phe
            20   25

<210> 842
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 842

Tyr Ala Trp Asn Arg Lys Arg Ile Ser Asn
1   5   10

<210> 843
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 843

Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys Asn Gly
1   5   10   15

Val Glu Gly Phe
            20

<210> 844
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 844

Pro Leu Gln Ser Tyr Gly Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln
1   5   10   15

Pro Tyr Arg Val Val Val Leu
            20

<210> 845
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 845

Phe Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr
1   5   10   15

Gly Lys Ile Ala Asp Tyr Asn
            20

<210> 846
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 846

Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe Glu Arg Asp Ile
1   5   10   15

Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys Asn Gly Val Glu
            20   25   30

Gly Phe

<210> 847
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 847

Phe Pro Leu Gln Ser Tyr Gly Phe Gln Pro Thr Asn Gly Val Gly Tyr
1   5   10   15

Gln Pro Tyr Arg Val Val Val Leu Ser Phe

20 25

<210> 848
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 848

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
1 5 10 15

Lys Ile Ala Asp Tyr Asn Tyr Lys
20

<210> 849
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 849

Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys Asn Gly Val Glu Gly Phe
1 5 10 15

Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly Phe Gln Pro Thr Asn Gly
20 25 30

Val Gly Tyr Gln Pro Tyr Arg Val Val Val Leu
35 40

<210> 850
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 850

Tyr Ala Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp
1 5 10