SEQUENCE LISTING

<110> Micreos Human Health B.V.

<120> Combination treatment for atopic dermatitis

<130> P6045048PCT

<160> 100

<170> PatentIn version 3.3

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<211> 1461
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<213> Staphylococcus bacteriophage 2638A

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caaggtgtgg tcatccacaa tgattatggt agtatgacac ctagtcaata cttaccatgg 660

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<213> Staphylococcus bacteriophage 2638A

<400> 2

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            20                  25                  30

Asn Tyr His Glu Asn Gly Ile Asn Tyr Asp Glu Phe Cys Gly Gly Tyr
        35                  40                  45

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

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

Gly Thr Phe Val Ile Arg Asp Ala Asn Asp Asn Asp Trp Ile Tyr Gly
                85                  90                  95

His Leu Gln Arg Gly Ser Met Arg Phe Val Val Gly Asp Lys Val Asn
            100                 105                 110

Gln Gly Asp Ile Ile Gly Leu Gln Gly Asn Ser Asn Tyr Tyr Asp Asn
        115                 120                 125

Pro Met Ser Val His Leu His Leu Gln Leu Arg Pro Lys Asp Ala Lys
    130                 135                 140

Lys Asp Glu Lys Ser Gln Val Cys Ser Gly Leu Ala Met Glu Lys Tyr
145                 150                 155                 160

Asp Ile Thr Asn Leu Asn Ala Lys Gln Asp Lys Ser Lys Asn Gly Ser
                165                 170                 175

Val Lys Glu Leu Lys His Ile Tyr Ser Asn His Ile Lys Gly Asn Lys
            180                 185                 190

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

Tyr Gly Ser Met Thr Pro Ser Gln Tyr Leu Pro Trp Leu Tyr Ala Arg
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Glu Asn Asn Gly Thr His Val Asn Gly Trp Ala Ser Val Tyr Ala Asn
225                 230                 235                 240
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Arg Asn Glu Val Leu Trp Tyr His Pro Thr Asp Tyr Val Glu Trp His
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Cys Gly Asn Gln Trp Ala Asn Ala Asn Leu Ile Gly Phe Glu Val Cys
            260                 265                 270

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

Glu Ala Thr Leu Lys Val Ala Ala Asp Val Met Lys Ser Tyr Gly Leu
    290                 295                 300

Pro Val Asn Arg Asn Thr Val Arg Leu His Asn Glu Phe Phe Gly Thr
305                 310                 315                 320

Ser Cys Pro His Arg Ser Trp Asp Leu His Val Gly Lys Gly Glu Pro
                325                 330                 335

Tyr Thr Thr Thr Asn Ile Asn Lys Met Lys Asp Tyr Phe Ile Lys Arg
            340                 345                 350

Ile Lys His Tyr Tyr Asp Gly Gly Lys Leu Glu Val Ser Lys Ala Ala
        355                 360                 365

Thr Ile Lys Gln Ser Asp Val Lys Gln Glu Val Lys Lys Gln Glu Ala
    370                 375                 380

Lys Gln Ile Val Lys Ala Thr Asp Trp Lys Gln Asn Lys Asp Gly Ile
385                 390                 395                 400

Trp Tyr Lys Ala Glu His Ala Ser Phe Thr Val Thr Ala Pro Glu Gly
                405                 410                 415

Ile Ile Thr Arg Tyr Lys Gly Pro Trp Thr Gly His Pro Gln Ala Gly
            420                 425                 430

Val Leu Gln Lys Gly Gln Thr Ile Lys Tyr Asp Glu Val Gln Lys Phe
        435                 440                 445

Asp Gly His Val Trp Val Ser Trp Glu Thr Phe Glu Gly Glu Thr Val
    450                 455                 460

Tyr Met Pro Val Arg Thr Trp Asp Ala Lys Thr Gly Lys Val Gly Lys
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Leu Trp Gly Glu Ile Lys
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<211> 279
<212> DNA
<213> Staphylococcus simulans

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aaagcaggtc aaacaattca ttatgatgaa gtgatgaaac aagacggtca tgtttgggta 180

ggttatacag gtaacagtgg ccaacgtatt tacttgcctg taagaacatg gaataaatct 240

actaatactt taggtgttct ttggggaact ataaagtga 279

<210> 4
<211> 92
<212> PRT
<213> Staphylococcus simulans

<400> 4

Trp Lys Thr Asn Lys Tyr Gly Thr Leu Tyr Lys Ser Glu Ser Ala Ser
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Phe Thr Pro Asn Thr Asp Ile Ile Thr Arg Thr Thr Gly Pro Phe Arg
20 25 30

Ser Met Pro Gln Ser Gly Val Leu Lys Ala Gly Gln Thr Ile His Tyr
35 40 45

Asp Glu Val Met Lys Gln Asp Gly His Val Trp Val Gly Tyr Thr Gly
50 55 60

Asn Ser Gly Gln Arg Ile Tyr Leu Pro Val Arg Thr Trp Asn Lys Ser
65 70 75 80

Thr Asn Thr Leu Gly Val Leu Trp Gly Thr Ile Lys
85 90

<210> 5
<211> 285
<212> DNA
<213> Staphylococcus bacteriophage 2638A

<400> 5
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gcaccagagg gaattatcac aagatacaaa ggtccttgga ctggtcaccc acaagctggt 120

gtattacaaa aaggtcaaac gattaaatat gatgaggttc aaaaatttga cggtcatgtt 180

tgggtatcgt gggaaacgtt tgagggcgaa actgtataca tgccggtacg cacatgggac 240

gctaaaactg gtaaagttgg taagttgtgg ggcgaaatta aataa 285

<210> 6
<211> 94
<212> PRT
<213> Staphylococcus bacteriophage 2638A

<400> 6

Trp Lys Gln Asn Lys Asp Gly Ile Trp Tyr Lys Ala Glu His Ala Ser
1 5 10 15

Phe Thr Val Thr Ala Pro Glu Gly Ile Ile Thr Arg Tyr Lys Gly Pro
20 25 30

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

Lys Tyr Asp Glu Val Gln Lys Phe Asp Gly His Val Trp Val Ser Trp
50 55 60

Glu Thr Phe Glu Gly Glu Thr Val Tyr Met Pro Val Arg Thr Trp Asp
65 70 75 80

Ala Lys Thr Gly Lys Val Gly Lys Leu Trp Gly Glu Ile Lys
85 90

<210> 7
<211> 282
<212> DNA
<213> Staphylococcus bacteriophage phiNM3

<400> 7
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aaaggtgctt attttaatgc gaaaatcgac ggcttaggtg ctacttcagc cactagatac 120

ggtgataatc gtactaacta tagattcgat gttggacagg ctgtatacgc gcctggaaca 180

ttaatatatg tgtttgaaat tatagatggt tggtgtcgca tttattggaa caatcataat 240

gagtggatat ggcatgagag attgattgtg aaagaagtgt tt 282

<210> 8
<211> 94
<212> PRT
<213> Staphylococcus bacteriophage phiNM3

<400> 8

Gly Lys Ser Ala Ser Lys Ile Thr Val Gly Ser Lys Ala Pro Tyr Asn
1 5 10 15

Leu Lys Trp Ser Lys Gly Ala Tyr Phe Asn Ala Lys Ile Asp Gly Leu
20 25 30

Gly Ala Thr Ser Ala Thr Arg Tyr Gly Asp Asn Arg Thr Asn Tyr Arg
35 40 45

Phe Asp Val Gly Gln Ala Val Tyr Ala Pro Gly Thr Leu Ile Tyr Val
50 55 60

Phe Glu Ile Ile Asp Gly Trp Cys Arg Ile Tyr Trp Asn Asn His Asn
65 70 75 80

Glu Trp Ile Trp His Glu Arg Leu Ile Val Lys Glu Val Phe
85 90

<210> 9
<211> 585
<212> DNA
<213> Staphylococcus bacteriophage K

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gatagccctt acagagttaa aaaagctaca agttatgacc catcatttgg tgtaatggaa 120

gcaggagcca ttgatgcaga tggttactat cacgctcagt gtcaagacct tattacagac 180

tatgttttat ggttaacaga taataaagtt agaacttggg gtaatgctaa agaccaaatt 240

aaacagagtt atggtactgg atttaaaata catgaaaata aaccttctac tgtacctaaa 300

aaaggttgga ttgcggtatt tacatccggt agttatgaac agtggggtca cataggtatt 360

gtatatgatg gaggtaatac ttctacattt actattttag agcaaaactg gaatggttat 420

gctaataaaa aacctacaaa acgtgtagat aattattacg gattaactca cttcattgaa 480

atacctgtaa aagcaggaac tactgttaaa aaagaaacag ctaagaaaag cgcaagtaaa 540

acgcctgcac ctaaaaagaa agcaacacta aaagtttcta agaat 585

<210> 10
<211> 195
<212> PRT
<213> Staphylococcus bacteriophage K

<400> 10

Met Ala Lys Thr Gln Ala Glu Ile Asn Lys Arg Leu Asp Ala Tyr Ala
1 5 10 15

Lys Gly Thr Val Asp Ser Pro Tyr Arg Val Lys Lys Ala Thr Ser Tyr
20 25 30

Asp Pro Ser Phe Gly Val Met Glu Ala Gly Ala Ile Asp Ala Asp Gly
35 40 45

Tyr Tyr His Ala Gln Cys Gln Asp Leu Ile Thr Asp Tyr Val Leu Trp
50 55 60

Leu Thr Asp Asn Lys Val Arg Thr Trp Gly Asn Ala Lys Asp Gln Ile
65 70 75 80

Lys Gln Ser Tyr Gly Thr Gly Phe Lys Ile His Glu Asn Lys Pro Ser
85 90 95

Thr Val Pro Lys Lys Gly Trp Ile Ala Val Phe Thr Ser Gly Ser Tyr
100 105 110

Glu Gln Trp Gly His Ile Gly Ile Val Tyr Asp Gly Gly Asn Thr Ser
115 120 125

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Thr Phe Thr Ile Leu Glu Gln Asn Trp Asn Gly Tyr Ala Asn Lys Lys
    130                 135                 140

Pro Thr Lys Arg Val Asp Asn Tyr Tyr Gly Leu Thr His Phe Ile Glu
145                 150                 155                 160

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

Ser Ala Ser Lys Thr Pro Ala Pro Lys Lys Lys Ala Thr Leu Lys Val
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Ser Lys Asn
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<210> 11
<211> 420
<212> DNA
<213> Staphylococcus bacteriophage Twort

<400> 11

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acagatggta aaataagaat gtggggtaat gctaaggatg cgataaataa ctcttttggt    180

ggtactgcta cggtatataa aaactaccct gcttttagac ctaagtacgg tgatgtagtc    240

gtatggacta ctggtaattt tgcaacttat ggtcatatcg caatagttac taaccctgac    300

ccttatggag accttcaata tgttacagtt cttgaacaaa actggaacgg taacgggatt    360

tataaaaccg agttagctac aatcagaaca cacgattaca caggaattac acattttatt    420
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<210> 12
<211> 140
<212> PRT
<213> Staphylococcus bacteriophage Twort

<400> 12

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Thr Gly Thr Asp Phe Asp Gly Leu Tyr Gly Tyr Gln Cys Met Asp Leu
            20                  25                  30

Ala Val Asp Tyr Ile Tyr His Val Thr Asp Gly Lys Ile Arg Met Trp
        35                  40                  45

Gly Asn Ala Lys Asp Ala Ile Asn Asn Ser Phe Gly Gly Thr Ala Thr
    50                  55                  60

Val Tyr Lys Asn Tyr Pro Ala Phe Arg Pro Lys Tyr Gly Asp Val Val
65                  70                  75                  80
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Val Trp Thr Thr Gly Asn Phe Ala Thr Tyr Gly His Ile Ala Ile Val
85 90 95

Thr Asn Pro Asp Pro Tyr Gly Asp Leu Gln Tyr Val Thr Val Leu Glu
100 105 110

Gln Asn Trp Asn Gly Asn Gly Ile Tyr Lys Thr Glu Leu Ala Thr Ile
115 120 125

Arg Thr His Asp Tyr Thr Gly Ile Thr His Phe Ile
130 135 140

<210> 13
<211> 438
<212> DNA
<213> Staphylococcus bacteriophage 2638A

<400> 13
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gacgtgcctg ctgttactag cggaacagtt attgaagcaa acgattacgg taattttggt 240

ggtacattcg ttattagaga cgctaacgat aacgattgga tatatgggca tctacaacgt 300

ggctcaatgc gatttgttgt aggcgacaaa gtcaatcaag gtgacattat tggtttacaa 360

ggtaatagca actattacga caatcctatg agtgtacatt tacatttaca attacgccct 420

aaagacgcaa agaaagat 438

<210> 14
<211> 146
<212> PRT
<213> Staphylococcus bacteriophage 2638A

<400> 14

Met Leu Thr Ala Ile Asp Tyr Leu Thr Lys Lys Gly Trp Lys Ile Ser
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Ser Asp Pro Arg Thr Tyr Asp Gly Tyr Pro Lys Asn Tyr Gly Tyr Arg
20 25 30

Asn Tyr His Glu Asn Gly Ile Asn Tyr Asp Glu Phe Cys Gly Gly Tyr
35 40 45

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

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

Gly Thr Phe Val Ile Arg Asp Ala Asn Asp Asn Asp Trp Ile Tyr Gly
85 90 95

His Leu Gln Arg Gly Ser Met Arg Phe Val Val Gly Asp Lys Val Asn
100 105 110

Gln Gly Asp Ile Ile Gly Leu Gln Gly Asn Ser Asn Tyr Tyr Asp Asn
115 120 125

Pro Met Ser Val His Leu His Leu Gln Leu Arg Pro Lys Asp Ala Lys
130 135 140

Lys Asp
145

<210> 15
<211> 420
<212> DNA
<213> Staphylococcus simulans

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attggaacac cagtaaaagc tatttcaagc ggaaaaatag ttgaagctgg ttggagtaat 180

tacggaggag gtaatcaaat aggtcttatt gaaaatgatg gagtgcatag acaatggtat 240

atgcatctaa gtaaatataa tgttaaagta ggagattatg tcaaagctgg tcaaataatc 300

ggttggtctg gaagcactgg ttattctaca gcaccacatt tacacttcca aagaatggtt 360

aattcatttt caaattcaac tgcccaagat ccaatgcctt tcttaaagag cgcaggatat 420

<210> 16
<211> 140
<212> PRT
<213> Staphylococcus simulans

<400> 16

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1 5 10 15

Gly Tyr Gly Tyr Gly Pro Tyr Pro Leu Gly Ile Asn Gly Gly Met His
20 25 30

Tyr Gly Val Asp Phe Phe Met Asn Ile Gly Thr Pro Val Lys Ala Ile
35 40 45

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

Asn Gln Ile Gly Leu Ile Glu Asn Asp Gly Val His Arg Gln Trp Tyr
65 70 75 80

Met His Leu Ser Lys Tyr Asn Val Lys Val Gly Asp Tyr Val Lys Ala
85 90 95

Gly Gln Ile Ile Gly Trp Ser Gly Ser Thr Gly Tyr Ser Thr Ala Pro
100 105 110

His Leu His Phe Gln Arg Met Val Asn Ser Phe Ser Asn Ser Thr Ala
115 120 125

Gln Asp Pro Met Pro Phe Leu Lys Ser Ala Gly Tyr
130 135 140

<210> 17
<211> 510
<212> DNA
<213> Staphylococcus bacteriophage 2638A

<400> 17
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cacgttaacg gttgggctag tgtttatgca aatagaaacg aagtgctttg gtatcatccg 180

acagactacg tagagtggca ttgtggtaat caatgggcaa atgctaactt aatcggattt 240

gaagtgtgtg agtcgtatcc tggtagaatc tcggacaaat tattcttaga aaatgaagaa 300

gcgacattga aagtagctgc ggatgtgatg aagtcgtacg gattaccagt taatcgcaac 360

actgtacgtc tgcataacga attcttcgga acttcttgtc cacatcgttc gtgggacttg 420

catgttggca aaggtgagcc ttacacaact actaatatta ataaaatgaa agactacttc 480

atcaaacgca tcaaacatta ttatgacggt 510

<210> 18
<211> 169
<212> PRT
<213> Staphylococcus bacteriophage 2638A

<400> 18

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1 5 10 15

Asn Asp Tyr Gly Ser Met Thr Pro Ser Gln Tyr Leu Pro Trp Leu Tyr
20 25 30

Ala Arg Glu Asn Asn Gly Thr His Val Asn Gly Trp Ala Ser Val Tyr
35 40 45

Ala Asn Arg Asn Glu Val Leu Trp Tyr His Pro Thr Asp Tyr Val Glu
50 55 60

Trp His Cys Gly Asn Gln Trp Ala Asn Ala Asn Leu Ile Gly Phe Glu
65 70 75 80

Val Cys Glu Ser Tyr Pro Gly Arg Ile Ser Asp Lys Leu Phe Leu Glu
85 90 95

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

Gly Leu Pro Val Asn Arg Asn Thr Val Arg Leu His Asn Glu Phe Phe
115 120 125

Gly Thr Ser Cys Pro His Arg Ser Trp Asp Leu His Val Gly Lys Gly
130 135 140

Glu Pro Tyr Thr Thr Thr Asn Ile Asn Lys Met Lys Asp Tyr Phe Ile
145 150 155 160

Lys Arg Ile Lys His Tyr Tyr Asp Gly
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<210> 19
<211> 1407
<212> DNA
<213> artificial

<220>
<223> artificial construct

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gatagccctt acagagttaa aaaagctaca agttatgacc catcatttgg tgtaatggaa 120

gcaggagcca ttgatgcaga tggttactat cacgctcagt gtcaagacct tattacagac 180

tatgttttat ggttaacaga taataaagtt agaacttggg gtaatgctaa agaccaaatt 240

aaacagagtt atggtactgg atttaaaata catgaaaata aaccttctac tgtacctaaa 300

aaaggttgga ttgcggtatt tacatccggt agttatgaac agtggggtca cataggtatt 360

gtatatgatg gaggtaatac ttctacattt actattttag agcaaaactg gaatggttat 420

gctaataaaa aacctacaaa acgtgtagat aattattacg gattaactca cttcattgaa 480

atacctgtaa aagcaggaac tactgttaaa aaagaaacag ctaagaaaag cgcaagtaaa 540

acgcctgcac ctaaaaagaa agcaacacta aaagtttcta agaatgagct catggctaag 600

actcaagcag aaataaataa acgtttagat gcttatgcaa aaggaacagt agatagccct 660

tacagagtta aaaaagctac aagttatgac ccatcatttg gtgtaatgga agcaggagcc 720

attgatgcag atggttacta tcacgctcag tgtcaagacc ttattacaga ctatgtttta 780

tggttaacag ataataaagt tagaacttgg ggtaatgcta aagaccaaat taaacagagt 840

tatggtactg gatttaaaat acatgaaaat aaaccttcta ctgtacctaa aaaaggttgg 900

attgcggtat ttacatccgg tagttatgaa cagtggggtc acataggtat tgtatatgat 960

ggaggtaata cttctacatt tactatttta gagcaaaact ggaatggtta tgctaataaa 1020

aaacctacaa aacgtgtaga taattattac ggattaactc acttcattga aatacctgta 1080

aaagcaggaa aagcaggtgg tacagtaact ccaacgccga atacaggttg gaaaacaaac 1140

aaatatggca cactatataa atcagagtca gctagcttca cacctaatac agatataata 1200

acaagaacga ctggtccatt tagaagcatg ccgcagtcag gagtcttaaa agcaggtcaa 1260

acaattcatt atgatgaagt gatgaaacaa gacggtcatg tttgggtagg ttatacaggt 1320

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<210> 20
<211> 468
<212> PRT
<213> artificial

<220>
<223> artificial construct

<400> 20

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Lys Gly Thr Val Asp Ser Pro Tyr Arg Val Lys Lys Ala Thr Ser Tyr
20 25 30

Asp Pro Ser Phe Gly Val Met Glu Ala Gly Ala Ile Asp Ala Asp Gly
35 40 45

Tyr Tyr His Ala Gln Cys Gln Asp Leu Ile Thr Asp Tyr Val Leu Trp
50 55 60

Leu Thr Asp Asn Lys Val Arg Thr Trp Gly Asn Ala Lys Asp Gln Ile
65 70 75 80

Lys Gln Ser Tyr Gly Thr Gly Phe Lys Ile His Glu Asn Lys Pro Ser
85 90 95

Thr Val Pro Lys Lys Gly Trp Ile Ala Val Phe Thr Ser Gly Ser Tyr
100 105 110

Glu Gln Trp Gly His Ile Gly Ile Val Tyr Asp Gly Gly Asn Thr Ser
115 120 125

Thr Phe Thr Ile Leu Glu Gln Asn Trp Asn Gly Tyr Ala Asn Lys Lys
130 135 140

Pro Thr Lys Arg Val Asp Asn Tyr Tyr Gly Leu Thr His Phe Ile Glu
145 150 155 160

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

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Ser Ala Ser Lys Thr Pro Ala Pro Lys Lys Lys Ala Thr Leu Lys Val
            180                 185                 190

Ser Lys Asn Glu Leu Met Ala Lys Thr Gln Ala Glu Ile Asn Lys Arg
        195                 200                 205

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

Lys Ala Thr Ser Tyr Asp Pro Ser Phe Gly Val Met Glu Ala Gly Ala
225                 230                 235                 240

Ile Asp Ala Asp Gly Tyr Tyr His Ala Gln Cys Gln Asp Leu Ile Thr
                245                 250                 255

Asp Tyr Val Leu Trp Leu Thr Asp Asn Lys Val Arg Thr Trp Gly Asn
            260                 265                 270

Ala Lys Asp Gln Ile Lys Gln Ser Tyr Gly Thr Gly Phe Lys Ile His
        275                 280                 285

Glu Asn Lys Pro Ser Thr Val Pro Lys Lys Gly Trp Ile Ala Val Phe
    290                 295                 300

Thr Ser Gly Ser Tyr Glu Gln Trp Gly His Ile Gly Ile Val Tyr Asp
305                 310                 315                 320

Gly Gly Asn Thr Ser Thr Phe Thr Ile Leu Glu Gln Asn Trp Asn Gly
                325                 330                 335

Tyr Ala Asn Lys Lys Pro Thr Lys Arg Val Asp Asn Tyr Tyr Gly Leu
            340                 345                 350

Thr His Phe Ile Glu Ile Pro Val Lys Ala Gly Lys Ala Gly Gly Thr
        355                 360                 365

Val Thr Pro Thr Pro Asn Thr Gly Trp Lys Thr Asn Lys Tyr Gly Thr
    370                 375                 380

Leu Tyr Lys Ser Glu Ser Ala Ser Phe Thr Pro Asn Thr Asp Ile Ile
385                 390                 395                 400

Thr Arg Thr Thr Gly Pro Phe Arg Ser Met Pro Gln Ser Gly Val Leu
                405                 410                 415

Lys Ala Gly Gln Thr Ile His Tyr Asp Glu Val Met Lys Gln Asp Gly
            420                 425                 430

His Val Trp Val Gly Tyr Thr Gly Asn Ser Gly Gln Arg Ile Tyr Leu
        435                 440                 445
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Pro Val Arg Thr Trp Asn Lys Ser Thr Asn Thr Leu Gly Val Leu Trp
450 455 460

Gly Thr Ile Lys
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<210> 21
<211> 1209
<212> DNA
<213> artificial

<220>
<223> artificial construct

<400> 21
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ggtccttatc cattaggtat aaatggcggt atgcactacg gagttgattt ttttatgaat 120

attggaacac cagtaaaagc tatttcaagc ggaaaaatag ttgaagctgg ttggagtaat 180

tacggaggag gtaatcaaat aggtcttatt gaaaatgatg gagtgcatag acaatggtat 240

atgcatctaa gtaaatataa tgttaaagta ggagattatg tcaaagctgg tcaaataatc 300

ggttggtctg gaagcactgg ttattctaca gcaccacatt tacacttcca aagaatggtt 360

aattcatttt caaattcaac tgcccaagat ccaatgcctt tcttaaagag cgcaggatat 420

ggaaaagcag gtggtacagt aactccaacg ccgaatacag gtgagctcgc tgcaacacat 480

gaacattcag cacaatggtt gaataattac aaaaaaggat atggttacgg tccttatcca 540

ttaggtataa atggcggtat gcactacgga gttgattttt ttatgaatat tggaacacca 600

gtaaaagcta tttcaagcgg aaaaatagtt gaagctggtt ggagtaatta cggaggaggt 660

aatcaaatag gtcttattga aaatgatgga gtgcatagac aatggtatat gcatctaagt 720

aaatataatg ttaaagtagg agattatgtc aaagctggtc aaataatcgg ttggtctgga 780

agcactggtt attctacagc accacattta cacttccaaa gaatggttaa ttcattttca 840

aattcaactg cccaagatcc aatgcctttc ttaaagagcg caggatatgg aaaagcaggt 900

ggtacagtaa ctccaacgcc gaatacaggt tggaaaacaa acaaatatgg cacactatat 960

aaatcagagt cagctagctt cacacctaat acagatataa taacaagaac gactggtcca 1020

tttagaagca tgccgcagtc aggagtctta aaagcaggtc aaacaattca ttatgatgaa 1080

gtgatgaaac aagacggtca tgtttgggta ggttatacag gtaacagtgg ccaacgtatt 1140

tacttgcctg taagaacatg gaataaatct actaatactt taggtgttct ttggggaact 1200

ataaagtaa 1209

<210> 22
<211> 402
<212> PRT
<213> artificial

<220>
<223> artificial construct

<400> 22

Ala Ala Thr His Glu His Ser Ala Gln Trp Leu Asn Asn Tyr Lys Lys
1 5 10 15

Gly Tyr Gly Tyr Gly Pro Tyr Pro Leu Gly Ile Asn Gly Gly Met His
20 25 30

Tyr Gly Val Asp Phe Phe Met Asn Ile Gly Thr Pro Val Lys Ala Ile
35 40 45

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

Asn Gln Ile Gly Leu Ile Glu Asn Asp Gly Val His Arg Gln Trp Tyr
65 70 75 80

Met His Leu Ser Lys Tyr Asn Val Lys Val Gly Asp Tyr Val Lys Ala
85 90 95

Gly Gln Ile Ile Gly Trp Ser Gly Ser Thr Gly Tyr Ser Thr Ala Pro
100 105 110

His Leu His Phe Gln Arg Met Val Asn Ser Phe Ser Asn Ser Thr Ala
115 120 125

Gln Asp Pro Met Pro Phe Leu Lys Ser Ala Gly Tyr Gly Lys Ala Gly
130 135 140

Gly Thr Val Thr Pro Thr Pro Asn Thr Gly Glu Leu Ala Ala Thr His
145 150 155 160

Glu His Ser Ala Gln Trp Leu Asn Asn Tyr Lys Lys Gly Tyr Gly Tyr
165 170 175

Gly Pro Tyr Pro Leu Gly Ile Asn Gly Gly Met His Tyr Gly Val Asp
180 185 190

Phe Phe Met Asn Ile Gly Thr Pro Val Lys Ala Ile Ser Ser Gly Lys
195 200 205

Ile Val Glu Ala Gly Trp Ser Asn Tyr Gly Gly Gly Asn Gln Ile Gly
210 215 220

Leu Ile Glu Asn Asp Gly Val His Arg Gln Trp Tyr Met His Leu Ser
225 230 235 240

Lys Tyr Asn Val Lys Val Gly Asp Tyr Val Lys Ala Gly Gln Ile Ile
245 250 255

Gly Trp Ser Gly Ser Thr Gly Tyr Ser Thr Ala Pro His Leu His Phe
260 265 270

Gln Arg Met Val Asn Ser Phe Ser Asn Ser Thr Ala Gln Asp Pro Met
275 280 285

Pro Phe Leu Lys Ser Ala Gly Tyr Gly Lys Ala Gly Gly Thr Val Thr
290 295 300

Pro Thr Pro Asn Thr Gly Trp Lys Thr Asn Lys Tyr Gly Thr Leu Tyr
305 310 315 320

Lys Ser Glu Ser Ala Ser Phe Thr Pro Asn Thr Asp Ile Ile Thr Arg
325 330 335

Thr Thr Gly Pro Phe Arg Ser Met Pro Gln Ser Gly Val Leu Lys Ala
340 345 350

Gly Gln Thr Ile His Tyr Asp Glu Val Met Lys Gln Asp Gly His Val
355 360 365

Trp Val Gly Tyr Thr Gly Asn Ser Gly Gln Arg Ile Tyr Leu Pro Val
370 375 380

Arg Thr Trp Asn Lys Ser Thr Asn Thr Leu Gly Val Leu Trp Gly Thr
385 390 395 400

Ile Lys

<210> 23
<211> 1686
<212> DNA
<213> artificial

<220>
<223> artificial construct

<400> 23
gcaaagaaag atgaaaaatc acaagtatgt agtggtttgg ctatggaaaa atatgacatt 60

acaaatttaa atgctaaaca agataaatca aagaatggga gcgtgaaaga gttgaaacat 120

atctattcaa accatattaa aggtaacaag attacagcac caaaacctag tattcaaggt 180

gtggtcatcc acaatgatta tggtagtatg acacctagtc aatacttacc atggttatat 240

gcacgtgaga ataacggtac acacgttaac ggttgggcta gtgtttatgc aaatagaaac 300

gaagtgcttt ggtatcatcc gacagactac gtagagtggc attgtggtaa tcaatgggca 360

aatgctaact taatcggatt tgaagtgtgt gagtcgtatc ctggtagaat ctcggacaaa 420

ttattcttag aaaatgaaga agcgacattg aaagtagctg cggatgtgat gaagtcgtac 480

ggattaccag ttaatcgcaa cactgtacgt ctgcataacg aattcttcgg aacttcttgt 540

ccacatcgtt cgtgggactt gcatgttggc aaaggtgagc cttacacaac tactaatatt 600

aataaaatga aagactactt catcaaacgc atcaaacatt attatgacgg tgagctcgca 660

aagaaagatg aaaaatcaca agtatgtagt ggtttggcta tggaaaaata tgacattaca 720

aatttaaatg ctaaacaaga taaatcaaag aatgggagcg tgaaagagtt gaaacatatc 780

tattcaaacc atattaaagg taacaagatt acagcaccaa aacctagtat tcaaggtgtg 840

gtcatccaca atgattatgg tagtatgaca cctagtcaat acttaccatg gttatatgca 900

cgtgagaata acggtacaca cgttaacggt tgggctagtg tttatgcaaa tagaaacgaa 960

gtgctttggt atcatccgac agactacgta gagtggcatt gtggtaatca atgggcaaat 1020

gctaacttaa tcggatttga agtgtgtgag tcgtatcctg gtagaatctc ggacaaatta 1080

ttcttagaaa atgaagaagc gacattgaaa gtagctgcgg atgtgatgaa gtcgtacgga 1140

ttaccagtta atcgcaacac tgtacgtctg cataacgaat tcttcggaac ttcttgtcca 1200

catcgttcgt gggacttgca tgttggcaaa ggtgagcctt acacaactac taatattaat 1260

aaaatgaaag actacttcat caaacgcatc aaacattatt atgacggtgg aaagctagaa 1320

gtaagcaaag cagcaactat caaacaatct gacgttaagc aagaagttaa aaagcaagaa 1380

gcaaaacaaa ttgtgaaagc aacagattgg aaaacaaaca aatatggcac actatataaa 1440

tcagagtcag ctagcttcac acctaataca gatataataa caagaacgac tggtccattt 1500

agaagcatgc cgcagtcagg agtcttaaaa gcaggtcaaa caattcatta tgatgaagtg 1560

atgaaacaag acggtcatgt ttgggtaggt tatacaggta acagtggcca acgtatttac 1620

ttgcctgtaa gaacatggaa taaatctact aatactttag gtgttctttg gggaactata 1680

aagtaa 1686

<210> 24
<211> 561
<212> PRT
<213> artificial

<220>
<223> artificial construct

<400> 24

Ala Lys Lys Asp Glu Lys Ser Gln Val Cys Ser Gly Leu Ala Met Glu
1 5 10 15

Lys Tyr Asp Ile Thr Asn Leu Asn Ala Lys Gln Asp Lys Ser Lys Asn
20 25 30

Gly Ser Val Lys Glu Leu Lys His Ile Tyr Ser Asn His Ile Lys Gly
35 40 45

Asn Lys Ile Thr Ala Pro Lys Pro Ser Ile Gln Gly Val Val Ile His
50 55 60

Asn Asp Tyr Gly Ser Met Thr Pro Ser Gln Tyr Leu Pro Trp Leu Tyr
65 70 75 80

```
Ala Arg Glu Asn Asn Gly Thr His Val Asn Gly Trp Ala Ser Val Tyr
                85                  90                  95

Ala Asn Arg Asn Glu Val Leu Trp Tyr His Pro Thr Asp Tyr Val Glu
            100                 105                 110

Trp His Cys Gly Asn Gln Trp Ala Asn Ala Asn Leu Ile Gly Phe Glu
        115                 120                 125

Val Cys Glu Ser Tyr Pro Gly Arg Ile Ser Asp Lys Leu Phe Leu Glu
    130                 135                 140

Asn Glu Glu Ala Thr Leu Lys Val Ala Ala Asp Val Met Lys Ser Tyr
145                 150                 155                 160

Gly Leu Pro Val Asn Arg Asn Thr Val Arg Leu His Asn Glu Phe Phe
                165                 170                 175

Gly Thr Ser Cys Pro His Arg Ser Trp Asp Leu His Val Gly Lys Gly
            180                 185                 190

Glu Pro Tyr Thr Thr Thr Asn Ile Asn Lys Met Lys Asp Tyr Phe Ile
        195                 200                 205

Lys Arg Ile Lys His Tyr Tyr Asp Gly Glu Leu Ala Lys Lys Asp Glu
    210                 215                 220

Lys Ser Gln Val Cys Ser Gly Leu Ala Met Glu Lys Tyr Asp Ile Thr
225                 230                 235                 240

Asn Leu Asn Ala Lys Gln Asp Lys Ser Lys Asn Gly Ser Val Lys Glu
                245                 250                 255

Leu Lys His Ile Tyr Ser Asn His Ile Lys Gly Asn Lys Ile Thr Ala
            260                 265                 270

Pro Lys Pro Ser Ile Gln Gly Val Val Ile His Asn Asp Tyr Gly Ser
        275                 280                 285

Met Thr Pro Ser Gln Tyr Leu Pro Trp Leu Tyr Ala Arg Glu Asn Asn
    290                 295                 300

Gly Thr His Val Asn Gly Trp Ala Ser Val Tyr Ala Asn Arg Asn Glu
305                 310                 315                 320

Val Leu Trp Tyr His Pro Thr Asp Tyr Val Glu Trp His Cys Gly Asn
                325                 330                 335

Gln Trp Ala Asn Ala Asn Leu Ile Gly Phe Glu Val Cys Glu Ser Tyr
            340                 345                 350
```

Pro Gly Arg Ile Ser Asp Lys Leu Phe Leu Glu Asn Glu Glu Ala Thr
355 360 365

Leu Lys Val Ala Ala Asp Val Met Lys Ser Tyr Gly Leu Pro Val Asn
370 375 380

Arg Asn Thr Val Arg Leu His Asn Glu Phe Phe Gly Thr Ser Cys Pro
385 390 395 400

His Arg Ser Trp Asp Leu His Val Gly Lys Gly Glu Pro Tyr Thr Thr
405 410 415

Thr Asn Ile Asn Lys Met Lys Asp Tyr Phe Ile Lys Arg Ile Lys His
420 425 430

Tyr Tyr Asp Gly Gly Lys Leu Glu Val Ser Lys Ala Ala Thr Ile Lys
435 440 445

Gln Ser Asp Val Lys Gln Glu Val Lys Lys Gln Glu Ala Lys Gln Ile
450 455 460

Val Lys Ala Thr Asp Trp Lys Thr Asn Lys Tyr Gly Thr Leu Tyr Lys
465 470 475 480

Ser Glu Ser Ala Ser Phe Thr Pro Asn Thr Asp Ile Ile Thr Arg Thr
485 490 495

Thr Gly Pro Phe Arg Ser Met Pro Gln Ser Gly Val Leu Lys Ala Gly
500 505 510

Gln Thr Ile His Tyr Asp Glu Val Met Lys Gln Asp Gly His Val Trp
515 520 525

Val Gly Tyr Thr Gly Asn Ser Gly Gln Arg Ile Tyr Leu Pro Val Arg
530 535 540

Thr Trp Asn Lys Ser Thr Asn Thr Leu Gly Val Leu Trp Gly Thr Ile
545 550 555 560

Lys

<210> 25
<211> 1131
<212> DNA
<213> artificial

<220>
<223> artificial construct

<400> 25
atgagaggat cgcatcacca tcaccatcac ggatctggct ctggatctgg tatcgaggga 60

aggccttata atggaactgg atccgcatgc gagctcgcaa agaaagatga aaaatcacaa 120

gtatgtagtg gtttggctat ggaaaaatat gacattacaa atttaaatgc taaacaagat 180

aaatcaaaga atgggagcgt gaaagagttg aaacatatct attcaaacca tattaaaggt 240

aacaagatta cagcaccaaa acctagtatt caaggtgtgg tcatccacaa tgattatggt 300

agtatgacac ctagtcaata cttaccatgg ttatatgcac gtgagaataa cggtacacac 360

gttaacggtt gggctagtgt ttatgcaaat agaaacgaag tgctttggta tcatccgaca 420

gactacgtag agtggcattg tggtaatcaa tgggcaaatg ctaacttaat cggatttgaa 480

gtgtgtgagt cgtatcctgg tagaatctcg gacaaattat tcttagaaaa tgaagaagcg 540

acattgaaag tagctgcgga tgtgatgaag tcgtacggat taccagttaa tcgcaacact 600

gtacgtctgc ataacgaatt cttcggaact tcttgtccac atcgttcgtg ggacttgcat 660

gttggcaaag gtgagcctta cacaactact aatattaata aaatgaaaga ctacttcatc 720

aaacgcatca aacattatta tgacggtgga aagctagaag taagcaaagc agcaactatc 780

aaacaatctg acgttaagca agaagttaaa aagcaagaag caaaacaaat tgtgaaagca 840

acagattgga aacagaataa agatggcatt tggtataaag ctgaacatgc ttcgttcaca 900

gtgacagcac cagagggaat tatcacaaga tacaaaggtc cttggactgg tcacccacaa 960

gctggtgtat tacaaaaagg tcaaacgatt aaatatgatg aggttcaaaa atttgacggt 1020

catgtttggg tatcgtggga aacgtttgag ggcgaaactg tatacatgcc ggtacgcaca 1080

tgggacgcta aaactggtaa agttggtaag ttgtggggcg aaattaaata a 1131

<210> 26
<211> 376
<212> PRT
<213> artificial

<220>
<223> artificial construct

<400> 26

Met Arg Gly Ser His His His His His His Gly Ser Gly Ser Gly Ser
1 5 10 15

Gly Ile Glu Gly Arg Pro Tyr Asn Gly Thr Gly Ser Ala Cys Glu Leu
20 25 30

Ala Lys Lys Asp Glu Lys Ser Gln Val Cys Ser Gly Leu Ala Met Glu
35 40 45

Lys Tyr Asp Ile Thr Asn Leu Asn Ala Lys Gln Asp Lys Ser Lys Asn
50 55 60

Gly Ser Val Lys Glu Leu Lys His Ile Tyr Ser Asn His Ile Lys Gly
65 70 75 80

Asn Lys Ile Thr Ala Pro Lys Pro Ser Ile Gln Gly Val Val Ile His
85 90 95

```
Asn Asp Tyr Gly Ser Met Thr Pro Ser Gln Tyr Leu Pro Trp Leu Tyr
            100                 105                 110

Ala Arg Glu Asn Asn Gly Thr His Val Asn Gly Trp Ala Ser Val Tyr
        115                 120                 125

Ala Asn Arg Asn Glu Val Leu Trp Tyr His Pro Thr Asp Tyr Val Glu
    130                 135                 140

Trp His Cys Gly Asn Gln Trp Ala Asn Ala Asn Leu Ile Gly Phe Glu
145                 150                 155                 160

Val Cys Glu Ser Tyr Pro Gly Arg Ile Ser Asp Lys Leu Phe Leu Glu
                165                 170                 175

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

Gly Leu Pro Val Asn Arg Asn Thr Val Arg Leu His Asn Glu Phe Phe
        195                 200                 205

Gly Thr Ser Cys Pro His Arg Ser Trp Asp Leu His Val Gly Lys Gly
    210                 215                 220

Glu Pro Tyr Thr Thr Thr Asn Ile Asn Lys Met Lys Asp Tyr Phe Ile
225                 230                 235                 240

Lys Arg Ile Lys His Tyr Tyr Asp Gly Gly Lys Leu Glu Val Ser Lys
                245                 250                 255

Ala Ala Thr Ile Lys Gln Ser Asp Val Lys Gln Glu Val Lys Lys Gln
            260                 265                 270

Glu Ala Lys Gln Ile Val Lys Ala Thr Asp Trp Lys Gln Asn Lys Asp
        275                 280                 285

Gly Ile Trp Tyr Lys Ala Glu His Ala Ser Phe Thr Val Thr Ala Pro
    290                 295                 300

Glu Gly Ile Ile Thr Arg Tyr Lys Gly Pro Trp Thr Gly His Pro Gln
305                 310                 315                 320

Ala Gly Val Leu Gln Lys Gly Gln Thr Ile Lys Tyr Asp Glu Val Gln
                325                 330                 335

Lys Phe Asp Gly His Val Trp Val Ser Trp Glu Thr Phe Glu Gly Glu
            340                 345                 350

Thr Val Tyr Met Pro Val Arg Thr Trp Asp Ala Lys Thr Gly Lys Val
        355                 360                 365
```

Gly Lys Leu Trp Gly Glu Ile Lys
370 375

<210> 27
<211> 1125
<212> DNA
<213> artificial

<220>
<223> artificial construct

<400> 27
atgagaggat cgcatcacca tcaccatcac ggatctggct ctggatctgg tatcgaggga 60

aggccttata atggaactgg atccgcatgc gagctcgcaa agaaagatga aaaatcacaa 120

gtatgtagtg gtttggctat ggaaaaatat gacattacaa atttaaatgc taaacaagat 180

aaatcaaaga atgggagcgt gaaagagttg aaacatatct attcaaacca tattaaaggt 240

aacaagatta cagcaccaaa acctagtatt caaggtgtgg tcatccacaa tgattatggt 300

agtatgacac ctagtcaata cttaccatgg ttatatgcac gtgagaataa cggtacacac 360

gttaacggtt gggctagtgt ttatgcaaat agaaacgaag tgctttggta tcatccgaca 420

gactacgtag agtggcattg tggtaatcaa tgggcaaatg ctaacttaat cggatttgaa 480

gtgtgtgagt cgtatcctgg tagaatctcg gacaaattat tcttagaaaa tgaagaagcg 540

acattgaaag tagctgcgga tgtgatgaag tcgtacggat taccagttaa tcgcaacact 600

gtacgtctgc ataacgaatt cttcggaact tcttgtccac atcgttcgtg ggacttgcat 660

gttggcaaag gtgagcctta cacaactact aatattaata aaatgaaaga ctacttcatc 720

aaacgcatca aacattatta tgacggtgga aagctagaag taagcaaagc agcaactatc 780

aaacaatctg acgttaagca agaagttaaa aagcaagaag caaaacaaat tgtgaaagca 840

acagattgga aaacaaacaa atatggcaca ctatataaat cagagtcagc tagcttcaca 900

cctaatacag atataataac aagaacgact ggtccattta gaagcatgcc gcagtcagga 960

gtcttaaaag caggtcaaac aattcattat gatgaagtga tgaaacaaga cggtcatgtt 1020

tgggtaggtt atacaggtaa cagtggccaa cgtatttact tgcctgtaag aacatggaat 1080

aaatctacta atactttagg tgttctttgg ggaactataa agtaa 1125

<210> 28
<211> 374
<212> PRT
<213> artificial

<220>
<223> artificial construct

<400> 28

Met Arg Gly Ser His His His His His His Gly Ser Gly Ser Gly Ser
1 5 10 15

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Gly Ile Glu Gly Arg Pro Tyr Asn Gly Thr Gly Ser Ala Cys Glu Leu
            20                  25                  30

Ala Lys Lys Asp Glu Lys Ser Gln Val Cys Ser Gly Leu Ala Met Glu
        35                  40                  45

Lys Tyr Asp Ile Thr Asn Leu Asn Ala Lys Gln Asp Lys Ser Lys Asn
    50                  55                  60

Gly Ser Val Lys Glu Leu Lys His Ile Tyr Ser Asn His Ile Lys Gly
65                  70                  75                  80

Asn Lys Ile Thr Ala Pro Lys Pro Ser Ile Gln Gly Val Val Ile His
                85                  90                  95

Asn Asp Tyr Gly Ser Met Thr Pro Ser Gln Tyr Leu Pro Trp Leu Tyr
            100                 105                 110

Ala Arg Glu Asn Asn Gly Thr His Val Asn Gly Trp Ala Ser Val Tyr
        115                 120                 125

Ala Asn Arg Asn Glu Val Leu Trp Tyr His Pro Thr Asp Tyr Val Glu
    130                 135                 140

Trp His Cys Gly Asn Gln Trp Ala Asn Ala Asn Leu Ile Gly Phe Glu
145                 150                 155                 160

Val Cys Glu Ser Tyr Pro Gly Arg Ile Ser Asp Lys Leu Phe Leu Glu
                165                 170                 175

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

Gly Leu Pro Val Asn Arg Asn Thr Val Arg Leu His Asn Glu Phe Phe
        195                 200                 205

Gly Thr Ser Cys Pro His Arg Ser Trp Asp Leu His Val Gly Lys Gly
    210                 215                 220

Glu Pro Tyr Thr Thr Thr Asn Ile Asn Lys Met Lys Asp Tyr Phe Ile
225                 230                 235                 240

Lys Arg Ile Lys His Tyr Tyr Asp Gly Gly Lys Leu Glu Val Ser Lys
                245                 250                 255

Ala Ala Thr Ile Lys Gln Ser Asp Val Lys Gln Glu Val Lys Lys Gln
            260                 265                 270

Glu Ala Lys Gln Ile Val Lys Ala Thr Asp Trp Lys Thr Asn Lys Tyr
        275                 280                 285
```

Gly Thr Leu Tyr Lys Ser Glu Ser Ala Ser Phe Thr Pro Asn Thr Asp
290 295 300

Ile Ile Thr Arg Thr Thr Gly Pro Phe Arg Ser Met Pro Gln Ser Gly
305 310 315 320

Val Leu Lys Ala Gly Gln Thr Ile His Tyr Asp Glu Val Met Lys Gln
325 330 335

Asp Gly His Val Trp Val Gly Tyr Thr Gly Asn Ser Gly Gln Arg Ile
340 345 350

Tyr Leu Pro Val Arg Thr Trp Asn Lys Ser Thr Asn Thr Leu Gly Val
355 360 365

Leu Trp Gly Thr Ile Lys
370

<210> 29
<211> 1131
<212> DNA
<213> artificial

<220>
<223> artificial construct

<400> 29
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aggccttata atggaactgg atccgcatgc gagctcgcaa agaaagatga aaaatcacaa 120

gtatgtagtg gtttggctat ggaaaaatat gacattacaa atttaaatgc taaacaagat 180

aaatcaaaga atgggagcgt gaaagagttg aaacatatct attcaaacca tattaaaggt 240

aacaagatta cagcaccaaa acctagtatt caaggtgtgg tcatccacaa tgattatggt 300

agtatgacac ctagtcaata cttaccatgg ttatatgcac gtgagaataa cggtacacac 360

gttaacggtt gggctagtgt ttatgcaaat agaaacgaag tgctttggta tcatccgaca 420

gactacgtag agtggcattg tggtaatcaa tgggcaaatg ctaacttaat cggatttgaa 480

gtgtgtgagt cgtatcctgg tagaatctcg gacaaattat tcttagaaaa tgaagaagcg 540

acattgaaag tagctgcgga tgtgatgaag tcgtacggat taccagttaa tcgcaacact 600

gtacgtctgc ataacgaatt cttcggaact tcttgtccac atcgttcgtg ggacttgcat 660

gttggcaaag gtgagcctta cacaactact aatattaata aaatgaaaga ctacttcatc 720

aaacgcatca aacattatta tgacggtgga aagctagaag taagcaaagc agcaactatc 780

aaacaatctg acgttaagca agaagttaaa aagcaagaag caaaacaaat tgtgaaagca 840

acagatggta aatctgcaag taaaataaca gttggaagta aagcgcctta taaccttaaa 900

tggtcaaaag gtgcttattt taatgcgaaa atcgacggct taggtgctac ttcagccact 960

agatacggtg ataatcgtac taactataga ttcgatgttg gacaggctgt atacgcgcct 1020

ggaacattaa tatatgtgtt tgaaattata gatggttggt gtcgcattta ttggaacaat 1080

cataatgagt ggatatggca tgagagattg attgtgaaag aagtgtttta a 1131

<210> 30
<211> 376
<212> PRT
<213> artificial

<220>
<223> artificial construct

<400> 30

Met Arg Gly Ser His His His His His His Gly Ser Gly Ser Gly Ser
1 5 10 15

Gly Ile Glu Gly Arg Pro Tyr Asn Gly Thr Gly Ser Ala Cys Glu Leu
20 25 30

Ala Lys Lys Asp Glu Lys Ser Gln Val Cys Ser Gly Leu Ala Met Glu
35 40 45

Lys Tyr Asp Ile Thr Asn Leu Asn Ala Lys Gln Asp Lys Ser Lys Asn
50 55 60

Gly Ser Val Lys Glu Leu Lys His Ile Tyr Ser Asn His Ile Lys Gly
65 70 75 80

Asn Lys Ile Thr Ala Pro Lys Pro Ser Ile Gln Gly Val Val Ile His
85 90 95

Asn Asp Tyr Gly Ser Met Thr Pro Ser Gln Tyr Leu Pro Trp Leu Tyr
100 105 110

Ala Arg Glu Asn Asn Gly Thr His Val Asn Gly Trp Ala Ser Val Tyr
115 120 125

Ala Asn Arg Asn Glu Val Leu Trp Tyr His Pro Thr Asp Tyr Val Glu
130 135 140

Trp His Cys Gly Asn Gln Trp Ala Asn Ala Asn Leu Ile Gly Phe Glu
145 150 155 160

Val Cys Glu Ser Tyr Pro Gly Arg Ile Ser Asp Lys Leu Phe Leu Glu
165 170 175

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

Gly Leu Pro Val Asn Arg Asn Thr Val Arg Leu His Asn Glu Phe Phe
195 200 205

Gly Thr Ser Cys Pro His Arg Ser Trp Asp Leu His Val Gly Lys Gly
210 215 220

```
Glu Pro Tyr Thr Thr Thr Asn Ile Asn Lys Met Lys Asp Tyr Phe Ile
225                 230                 235                 240

Lys Arg Ile Lys His Tyr Tyr Asp Gly Gly Lys Leu Glu Val Ser Lys
                245                 250                 255

Ala Ala Thr Ile Lys Gln Ser Asp Val Lys Gln Glu Val Lys Lys Gln
            260                 265                 270

Glu Ala Lys Gln Ile Val Lys Ala Thr Asp Gly Lys Ser Ala Ser Lys
        275                 280                 285

Ile Thr Val Gly Ser Lys Ala Pro Tyr Asn Leu Lys Trp Ser Lys Gly
    290                 295                 300

Ala Tyr Phe Asn Ala Lys Ile Asp Gly Leu Gly Ala Thr Ser Ala Thr
305                 310                 315                 320

Arg Tyr Gly Asp Asn Arg Thr Asn Tyr Arg Phe Asp Val Gly Gln Ala
                325                 330                 335

Val Tyr Ala Pro Gly Thr Leu Ile Tyr Val Phe Glu Ile Ile Asp Gly
            340                 345                 350

Trp Cys Arg Ile Tyr Trp Asn Asn His Asn Glu Trp Ile Trp His Glu
        355                 360                 365

Arg Leu Ile Val Lys Glu Val Phe
    370                 375
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<210> 31
<211> 975
<212> DNA
<213> artificial

<220>
<223> artificial construct

<400> 31

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aggccttata atggaactgg atccgcatgc gagctcatgg ctaagactca agcagaaata    120

aataaacgtt tagatgctta tgcaaaagga acagtagata gcccttacag agttaaaaaa    180

gctacaagtt atgacccatc atttggtgta atggaagcag gagccattga tgcagatggt    240

tactatcacg ctcagtgtca agaccttatt acagactatg ttttatggtt aacagataat    300

aaagttagaa cttggggtaa tgctaaagac caaattaaac agagttatgg tactggattt    360

aaaatacatg aaaataaacc ttctactgta cctaaaaaag gttggattgc ggtatttaca    420

tccggtagtt atgaacagtg gggtcacata ggtattgtat atgatggagg taatacttct    480

acatttacta ttttagagca aaactggaat ggttatgcta ataaaaaacc tacaaaacgt    540
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gtagataatt attacggatt aactcacttc attgaaatac ctgtaaaagc aggaaagcta 600

gaagtaagca aagcagcaac tatcaaacaa tctgacgtta agcaagaagt taaaaagcaa 660

gaagcaaaac aaattgtgaa agcaacagat tggaaacaga ataaagatgg catttggtat 720

aaagctgaac atgcttcgtt cacagtgaca gcaccagagg gaattatcac aagatacaaa 780

ggtccttgga ctggtcaccc acaagctggt gtattacaaa aaggtcaaac gattaaatat 840

gatgaggttc aaaaatttga cggtcatgtt tgggtatcgt gggaaacgtt tgagggcgaa 900

actgtataca tgccggtacg cacatgggac gctaaaactg gtaaagttgg taagttgtgg 960

ggcgaaatta aataa 975

<210> 32
<211> 324
<212> PRT
<213> artificial

<220>
<223> artificial construct

<400> 32

Met Arg Gly Ser His His His His His His Gly Ser Gly Ser Gly Ser
1 5 10 15

Gly Ile Glu Gly Arg Pro Tyr Asn Gly Thr Gly Ser Ala Cys Glu Leu
20 25 30

Met Ala Lys Thr Gln Ala Glu Ile Asn Lys Arg Leu Asp Ala Tyr Ala
35 40 45

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

Asp Pro Ser Phe Gly Val Met Glu Ala Gly Ala Ile Asp Ala Asp Gly
65 70 75 80

Tyr Tyr His Ala Gln Cys Gln Asp Leu Ile Thr Asp Tyr Val Leu Trp
85 90 95

Leu Thr Asp Asn Lys Val Arg Thr Trp Gly Asn Ala Lys Asp Gln Ile
100 105 110

Lys Gln Ser Tyr Gly Thr Gly Phe Lys Ile His Glu Asn Lys Pro Ser
115 120 125

Thr Val Pro Lys Lys Gly Trp Ile Ala Val Phe Thr Ser Gly Ser Tyr
130 135 140

Glu Gln Trp Gly His Ile Gly Ile Val Tyr Asp Gly Gly Asn Thr Ser
145 150 155 160

Thr Phe Thr Ile Leu Glu Gln Asn Trp Asn Gly Tyr Ala Asn Lys Lys
165 170 175

Pro Thr Lys Arg Val Asp Asn Tyr Tyr Gly Leu Thr His Phe Ile Glu
180 185 190

Ile Pro Val Lys Ala Gly Lys Leu Glu Val Ser Lys Ala Ala Thr Ile
195 200 205

Lys Gln Ser Asp Val Lys Gln Glu Val Lys Lys Gln Glu Ala Lys Gln
210 215 220

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

Lys Ala Glu His Ala Ser Phe Thr Val Thr Ala Pro Glu Gly Ile Ile
245 250 255

Thr Arg Tyr Lys Gly Pro Trp Thr Gly His Pro Gln Ala Gly Val Leu
260 265 270

Gln Lys Gly Gln Thr Ile Lys Tyr Asp Glu Val Gln Lys Phe Asp Gly
275 280 285

His Val Trp Val Ser Trp Glu Thr Phe Glu Gly Glu Thr Val Tyr Met
290 295 300

Pro Val Arg Thr Trp Asp Ala Lys Thr Gly Lys Val Gly Lys Leu Trp
305 310 315 320

Gly Glu Ile Lys

<210> 33
<211> 912
<212> DNA
<213> artificial

<220>
<223> artificial construct

<400> 33
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aggccttata atggaactgg atccgcatgc gagctcatgg ctaagactca agcagaaata 120

aataaacgtt tagatgctta tgcaaaagga acagtagata gcccttacag agttaaaaaa 180

gctacaagtt atgacccatc atttggtgta atggaagcag gagccattga tgcagatggt 240

tactatcacg ctcagtgtca agaccttatt acagactatg ttttatggtt aacagataat 300

aaagttagaa cttggggtaa tgctaaagac caaattaaac agagttatgg tactggattt 360

aaaatacatg aaaataaacc ttctactgta cctaaaaaag gttggattgc ggtatttaca 420

tccggtagtt atgaacagtg gggtcacata ggtattgtat atgatggagg taatacttct 480

acatttacta ttttagagca aaactggaat ggttatgcta ataaaaaacc tacaaaacgt 540

gtagataatt attacggatt aactcacttc attgaaatac ctgtaaaagc aggaaaagca 600

ggtggtacag taactccaac gccgaataca ggttggaaaa caaacaaata tggcacacta 660

tataaatcag agtcagctag cttcacacct aatacagata taataacaag aacgactggt 720

ccatttagaa gcatgccgca gtcaggagtc ttaaaagcag gtcaaacaat tcattatgat 780

gaagtgatga aacaagacgg tcatgtttgg gtaggttata caggtaacag tggccaacgt 840

atttacttgc ctgtaagaac atggaataaa tctactaata ctttaggtgt tctttgggga 900

actataaagt aa 912

<210> 34
<211> 303
<212> PRT
<213> artificial

<220>
<223> artificial construct

<400> 34

Met Arg Gly Ser His His His His His His Gly Ser Gly Ser Gly Ser
1 5 10 15

Gly Ile Glu Gly Arg Pro Tyr Asn Gly Thr Gly Ser Ala Cys Glu Leu
20 25 30

Met Ala Lys Thr Gln Ala Glu Ile Asn Lys Arg Leu Asp Ala Tyr Ala
35 40 45

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

Asp Pro Ser Phe Gly Val Met Glu Ala Gly Ala Ile Asp Ala Asp Gly
65 70 75 80

Tyr Tyr His Ala Gln Cys Gln Asp Leu Ile Thr Asp Tyr Val Leu Trp
85 90 95

Leu Thr Asp Asn Lys Val Arg Thr Trp Gly Asn Ala Lys Asp Gln Ile
100 105 110

Lys Gln Ser Tyr Gly Thr Gly Phe Lys Ile His Glu Asn Lys Pro Ser
115 120 125

Thr Val Pro Lys Lys Gly Trp Ile Ala Val Phe Thr Ser Gly Ser Tyr
130 135 140

Glu Gln Trp Gly His Ile Gly Ile Val Tyr Asp Gly Gly Asn Thr Ser
145 150 155 160

Thr Phe Thr Ile Leu Glu Gln Asn Trp Asn Gly Tyr Ala Asn Lys Lys
165 170 175

Pro Thr Lys Arg Val Asp Asn Tyr Tyr Gly Leu Thr His Phe Ile Glu
180 185 190

Ile Pro Val Lys Ala Gly Lys Ala Gly Gly Thr Val Thr Pro Thr Pro
195 200 205

Asn Thr Gly Trp Lys Thr Asn Lys Tyr Gly Thr Leu Tyr Lys Ser Glu
210 215 220

Ser Ala Ser Phe Thr Pro Asn Thr Asp Ile Ile Thr Arg Thr Thr Gly
225 230 235 240

Pro Phe Arg Ser Met Pro Gln Ser Gly Val Leu Lys Ala Gly Gln Thr
245 250 255

Ile His Tyr Asp Glu Val Met Lys Gln Asp Gly His Val Trp Val Gly
260 265 270

Tyr Thr Gly Asn Ser Gly Gln Arg Ile Tyr Leu Pro Val Arg Thr Trp
275 280 285

Asn Lys Ser Thr Asn Thr Leu Gly Val Leu Trp Gly Thr Ile Lys
290 295 300

<210> 35
<211> 966
<212> DNA
<213> artificial

<220>
<223> artificial construct

<400> 35
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aggccttata atggaactgg atccgcatgc gagctcatgg ctaagactca agcagaaata 120

aataaacgtt tagatgctta tgcaaaagga acagtagata gcccttacag agttaaaaaa 180

gctacaagtt atgacccatc atttggtgta atggaagcag gagccattga tgcagatggt 240

tactatcacg ctcagtgtca agaccttatt acagactatg ttttatggtt aacagataat 300

aaagttagaa cttggggtaa tgctaaagac caaattaaac agagttatgg tactggattt 360

aaaatacatg aaaataaacc ttctactgta cctaaaaaag gttggattgc ggtatttaca 420

tccggtagtt atgaacagtg gggtcacata ggtattgtat atgatggagg taatacttct 480

acatttacta ttttagagca aaactggaat ggttatgcta ataaaaaacc tacaaaacgt 540

gtagataatt attacggatt aactcacttc attgaaatac ctgtaaaagc aggaactact 600

gttaaaaaag aaacagctaa gaaaagcgca agtaaaacgc ctgcacctaa aaagaaagca 660

acactaaaag tttctaagaa tggtaaatct gcaagtaaaa taacagttgg aagtaaagcg 720

ccttataacc ttaaatggtc aaaaggtgct tattttaatg cgaaaatcga cggcttaggt 780

gctacttcag ccactagata cggtgataat cgtactaact atagattcga tgttggacag 840

gctgtatacg cgcctggaac attaatatat gtgtttgaaa ttatagatgg ttggtgtcgc 900

atttattgga acaatcataa tgagtggata tggcatgaga gattgattgt gaaagaagtg 960

ttttaa 966

<210> 36
<211> 321
<212> PRT
<213> artificial

<220>
<223> artificial construct

<400> 36

Met Arg Gly Ser His His His His His His Gly Ser Gly Ser Gly Ser
1 5 10 15

Gly Ile Glu Gly Arg Pro Tyr Asn Gly Thr Gly Ser Ala Cys Glu Leu
20 25 30

Met Ala Lys Thr Gln Ala Glu Ile Asn Lys Arg Leu Asp Ala Tyr Ala
35 40 45

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

Asp Pro Ser Phe Gly Val Met Glu Ala Gly Ala Ile Asp Ala Asp Gly
65 70 75 80

Tyr Tyr His Ala Gln Cys Gln Asp Leu Ile Thr Asp Tyr Val Leu Trp
85 90 95

Leu Thr Asp Asn Lys Val Arg Thr Trp Gly Asn Ala Lys Asp Gln Ile
100 105 110

Lys Gln Ser Tyr Gly Thr Gly Phe Lys Ile His Glu Asn Lys Pro Ser
115 120 125

Thr Val Pro Lys Lys Gly Trp Ile Ala Val Phe Thr Ser Gly Ser Tyr
130 135 140

Glu Gln Trp Gly His Ile Gly Ile Val Tyr Asp Gly Gly Asn Thr Ser
145 150 155 160

Thr Phe Thr Ile Leu Glu Gln Asn Trp Asn Gly Tyr Ala Asn Lys Lys
165 170 175

Pro Thr Lys Arg Val Asp Asn Tyr Tyr Gly Leu Thr His Phe Ile Glu
180 185 190

Ile Pro Val Lys Ala Gly Thr Thr Val Lys Lys Glu Thr Ala Lys Lys
195 200 205

Ser Ala Ser Lys Thr Pro Ala Pro Lys Lys Lys Ala Thr Leu Lys Val
210 215 220

Ser Lys Asn Gly Lys Ser Ala Ser Lys Ile Thr Val Gly Ser Lys Ala
225 230 235 240

Pro Tyr Asn Leu Lys Trp Ser Lys Gly Ala Tyr Phe Asn Ala Lys Ile
245 250 255

Asp Gly Leu Gly Ala Thr Ser Ala Thr Arg Tyr Gly Asp Asn Arg Thr
260 265 270

Asn Tyr Arg Phe Asp Val Gly Gln Ala Val Tyr Ala Pro Gly Thr Leu
275 280 285

Ile Tyr Val Phe Glu Ile Ile Asp Gly Trp Cys Arg Ile Tyr Trp Asn
290 295 300

Asn His Asn Glu Trp Ile Trp His Glu Arg Leu Ile Val Lys Glu Val
305 310 315 320

Phe

<210> 37
<211> 927
<212> DNA
<213> artificial

<220>
<223> artificial construct

<400> 37
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aggccttata atggaactgg atccgcatgc gagctcatga aaaccctgaa acaagcagag 120

tcctacatta agagtaaagt aaatacagga actgattttg atggtttata tgggtatcag 180

tgtatggact tagcagtaga ttatatttac catgtaacag atggtaaaat aagaatgtgg 240

ggtaatgcta aggatgcgat aaataactct tttggtggta ctgctacggt atataaaaac 300

taccctgctt ttagacctaa gtacggtgat gtagtcgtat ggactactgg taattttgca 360

acttatggtc atatcgcaat agttactaac cctgaccctt atggagacct tcaatatgtt 420

acagttcttg aacaaaactg gaacggtaac gggatttata aaaccgagtt agctacaatc 480

agaacacacg attacacagg aattacacat tttattagac ctaactttgc tactgaatca 540

agtgtaaaaa agaaagatac aaagaaaaaa ccaaaaccat caaatagaga tggaataaat 600

aaagataaaa ttgtatatga tagaactaat attaattaca attggaaaca gaataaagat 660

ggcatttggt ataaagctga acatgcttcg ttcacagtga cagcaccaga gggaattatc 720

acaagataca aaggtccttg gactggtcac ccacaagctg gtgtattaca aaaaggtcaa 780

acgattaaat atgatgaggt tcaaaaattt gacggtcatg tttgggtatc gtgggaaacg 840

tttgagggcg aaactgtata catgccggta cgcacatggg acgctaaaac tggtaaagtt 900

ggtaagttgt ggggcgaaat taaataa 927

<210> 38
<211> 308
<212> PRT
<213> artificial

<220>
<223> artificial construct

<400> 38

Met Arg Gly Ser His His His His His His Gly Ser Gly Ser Gly Ser
1 5 10 15

Gly Ile Glu Gly Arg Pro Tyr Asn Gly Thr Gly Ser Ala Cys Glu Leu
20 25 30

Met Lys Thr Leu Lys Gln Ala Glu Ser Tyr Ile Lys Ser Lys Val Asn
35 40 45

Thr Gly Thr Asp Phe Asp Gly Leu Tyr Gly Tyr Gln Cys Met Asp Leu
50 55 60

Ala Val Asp Tyr Ile Tyr His Val Thr Asp Gly Lys Ile Arg Met Trp
65 70 75 80

Gly Asn Ala Lys Asp Ala Ile Asn Asn Ser Phe Gly Gly Thr Ala Thr
85 90 95

Val Tyr Lys Asn Tyr Pro Ala Phe Arg Pro Lys Tyr Gly Asp Val Val
100 105 110

Val Trp Thr Thr Gly Asn Phe Ala Thr Tyr Gly His Ile Ala Ile Val
115 120 125

Thr Asn Pro Asp Pro Tyr Gly Asp Leu Gln Tyr Val Thr Val Leu Glu
130 135 140

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

Arg Thr His Asp Tyr Thr Gly Ile Thr His Phe Ile Arg Pro Asn Phe
165 170 175

Ala Thr Glu Ser Ser Val Lys Lys Lys Asp Thr Lys Lys Lys Pro Lys
180 185 190

Pro Ser Asn Arg Asp Gly Ile Asn Lys Asp Lys Ile Val Tyr Asp Arg
195 200 205

Thr Asn Ile Asn Tyr Asn Trp Lys Gln Asn Lys Asp Gly Ile Trp Tyr
210 215 220

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

Thr Arg Tyr Lys Gly Pro Trp Thr Gly His Pro Gln Ala Gly Val Leu
245 250 255

Gln Lys Gly Gln Thr Ile Lys Tyr Asp Glu Val Gln Lys Phe Asp Gly
260 265 270

His Val Trp Val Ser Trp Glu Thr Phe Glu Gly Glu Thr Val Tyr Met
275 280 285

Pro Val Arg Thr Trp Asp Ala Lys Thr Gly Lys Val Gly Lys Leu Trp
290 295 300

Gly Glu Ile Lys
305

<210> 39
<211> 921
<212> DNA
<213> artificial

<220>
<223> artificial construct

<400> 39
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aggccttata atggaactgg atccgcatgc gagctcatga aaaccctgaa acaagcagag 120

tcctacatta agagtaaagt aaatacagga actgattttg atggtttata tgggtatcag 180

tgtatggact tagcagtaga ttatatttac catgtaacag atggtaaaat aagaatgtgg 240

ggtaatgcta aggatgcgat aaataactct tttggtggta ctgctacggt atataaaaac 300

taccctgctt ttagacctaa gtacggtgat gtagtcgtat ggactactgg taattttgca 360

acttatggtc atatcgcaat agttactaac cctgaccctt atggagacct tcaatatgtt 420

acagttcttg aacaaaactg gaacggtaac gggatttata aaaccgagtt agctacaatc 480

agaacacacg attacacagg aattacacat tttattagac ctaactttgc tactgaatca 540

agtgtaaaaa agaaagatac aaagaaaaaa ccaaaaccat caaatagaga tggaataaat 600

aaagataaaa ttgtatatga tagaactaat attaattaca attggaaaac aaacaaatat 660

ggcacactat ataaatcaga gtcagctagc ttcacaccta atacagatat aataacaaga 720

acgactggtc catttagaag catgccgcag tcaggagtct taaaagcagg tcaaacaatt 780

cattatgatg aagtgatgaa acaagacggt catgtttggg taggttatac aggtaacagt 840

ggccaacgta tttacttgcc tgtaagaaca tggaataaat ctactaatac tttaggtgtt 900

ctttggggaa ctataaagta a 921

<210> 40
<211> 306
<212> PRT
<213> artificial

<220>
<223> artificial construct

<400> 40

Met Arg Gly Ser His His His His His His Gly Ser Gly Ser Gly Ser
1 5 10 15

Gly Ile Glu Gly Arg Pro Tyr Asn Gly Thr Gly Ser Ala Cys Glu Leu
20 25 30

Met Lys Thr Leu Lys Gln Ala Glu Ser Tyr Ile Lys Ser Lys Val Asn
35 40 45

Thr Gly Thr Asp Phe Asp Gly Leu Tyr Gly Tyr Gln Cys Met Asp Leu
50 55 60

Ala Val Asp Tyr Ile Tyr His Val Thr Asp Gly Lys Ile Arg Met Trp
65 70 75 80

Gly Asn Ala Lys Asp Ala Ile Asn Asn Ser Phe Gly Gly Thr Ala Thr
85 90 95

Val Tyr Lys Asn Tyr Pro Ala Phe Arg Pro Lys Tyr Gly Asp Val Val
100 105 110

Val Trp Thr Thr Gly Asn Phe Ala Thr Tyr Gly His Ile Ala Ile Val
115 120 125

Thr Asn Pro Asp Pro Tyr Gly Asp Leu Gln Tyr Val Thr Val Leu Glu
130 135 140

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

Arg Thr His Asp Tyr Thr Gly Ile Thr His Phe Ile Arg Pro Asn Phe
165 170 175

Ala Thr Glu Ser Ser Val Lys Lys Lys Asp Thr Lys Lys Lys Pro Lys
180 185 190

Pro Ser Asn Arg Asp Gly Ile Asn Lys Asp Lys Ile Val Tyr Asp Arg
195 200 205

Thr Asn Ile Asn Tyr Asn Trp Lys Thr Asn Lys Tyr Gly Thr Leu Tyr
210 215 220

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

Thr Thr Gly Pro Phe Arg Ser Met Pro Gln Ser Gly Val Leu Lys Ala
245 250 255

Gly Gln Thr Ile His Tyr Asp Glu Val Met Lys Gln Asp Gly His Val
260 265 270

Trp Val Gly Tyr Thr Gly Asn Ser Gly Gln Arg Ile Tyr Leu Pro Val
275 280 285

Arg Thr Trp Asn Lys Ser Thr Asn Thr Leu Gly Val Leu Trp Gly Thr
290 295 300

Ile Lys
305

<210> 41
<211> 927
<212> DNA
<213> artificial

<220>
<223> artificial construct

<400> 41
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aggccttata atggaactgg atccgcatgc gagctcatga aaaccctgaa acaagcagag 120

tcctacatta agagtaaagt aaatacagga actgattttg atggtttata tgggtatcag 180

tgtatggact tagcagtaga ttatatttac catgtaacag atggtaaaat aagaatgtgg 240

ggtaatgcta aggatgcgat aaataactct tttggtggta ctgctacggt atataaaaac 300

taccctgctt ttagacctaa gtacggtgat gtagtcgtat ggactactgg taattttgca 360

acttatggtc atatcgcaat agttactaac cctgaccctt atggagacct tcaatatgtt 420

acagttcttg aacaaaactg gaacggtaac gggatttata aaaccgagtt agctacaatc 480

agaacacacg attacacagg aattacacat tttattagac ctaactttgc tactgaatca 540

agtgtaaaaa agaaagatac aaagaaaaaa ccaaaaccat caaatagaga tggaataaat 600

aaagataaaa ttgtatatga tagaactaat attaattaca atggtaaatc tgcaagtaaa 660

ataacagttg gaagtaaagc gccttataac cttaaatggt caaaaggtgc ttattttaat 720

gcgaaaatcg acggcttagg tgctacttca gccactagat acggtgataa tcgtactaac 780

tatagattcg atgttggaca ggctgtatac gcgcctggaa cattaatata tgtgtttgaa 840

attatagatg gttggtgtcg catttattgg aacaatcata atgagtggat atggcatgag 900

agattgattg tgaaagaagt gttttaa 927

<210> 42
<211> 308
<212> PRT
<213> artificial

<220>
<223> artificial construct

<400> 42

Met Arg Gly Ser His His His His His His Gly Ser Gly Ser Gly Ser
1 5 10 15

Gly Ile Glu Gly Arg Pro Tyr Asn Gly Thr Gly Ser Ala Cys Glu Leu
20 25 30

Met Lys Thr Leu Lys Gln Ala Glu Ser Tyr Ile Lys Ser Lys Val Asn
35 40 45

Thr Gly Thr Asp Phe Asp Gly Leu Tyr Gly Tyr Gln Cys Met Asp Leu
50 55 60

Ala Val Asp Tyr Ile Tyr His Val Thr Asp Gly Lys Ile Arg Met Trp
65 70 75 80

Gly Asn Ala Lys Asp Ala Ile Asn Asn Ser Phe Gly Gly Thr Ala Thr
85 90 95

Val Tyr Lys Asn Tyr Pro Ala Phe Arg Pro Lys Tyr Gly Asp Val Val
100 105 110

Val Trp Thr Thr Gly Asn Phe Ala Thr Tyr Gly His Ile Ala Ile Val
115 120 125

Thr Asn Pro Asp Pro Tyr Gly Asp Leu Gln Tyr Val Thr Val Leu Glu
130 135 140

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

Arg Thr His Asp Tyr Thr Gly Ile Thr His Phe Ile Arg Pro Asn Phe
165 170 175

Ala Thr Glu Ser Ser Val Lys Lys Lys Asp Thr Lys Lys Lys Pro Lys
180 185 190

Pro Ser Asn Arg Asp Gly Ile Asn Lys Asp Lys Ile Val Tyr Asp Arg
195 200 205

Thr Asn Ile Asn Tyr Asn Gly Lys Ser Ala Ser Lys Ile Thr Val Gly
210 215 220

Ser Lys Ala Pro Tyr Asn Leu Lys Trp Ser Lys Gly Ala Tyr Phe Asn
225 230 235 240

Ala Lys Ile Asp Gly Leu Gly Ala Thr Ser Ala Thr Arg Tyr Gly Asp
245 250 255

Asn Arg Thr Asn Tyr Arg Phe Asp Val Gly Gln Ala Val Tyr Ala Pro
260 265 270

Gly Thr Leu Ile Tyr Val Phe Glu Ile Ile Asp Gly Trp Cys Arg Ile
275 280 285

Tyr Trp Asn Asn His Asn Glu Trp Ile Trp His Glu Arg Leu Ile Val
290 295 300

Lys Glu Val Phe
305

<210> 43
<211> 843
<212> DNA
<213> artificial

<220>
<223> artificial construct

<400> 43
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aggccttata atggaactgg atccgcatgc gagctcgctg caacacatga acattcagca 120

caatggttga ataattacaa aaaaggatat ggttacggtc cttatccatt aggtataaat 180

ggcggtatgc actacggagt tgatttttt atgaatattg gaacaccagt aaaagctatt 240

tcaagcggaa aaatagttga agctggttgg agtaattacg gaggaggtaa tcaaataggt 300

cttattgaaa atgatggagt gcatagacaa tggtatatgc atctaagtaa atataatgtt 360

aaagtaggag attatgtcaa agctggtcaa ataatcggtt ggtctggaag cactggttat 420

tctacagcac cacatttaca cttccaaaga atggttaatt cattttcaaa ttcaactgcc 480

caagatccaa tgcctttctt aaagagcgca ggatatggaa aagcaggtgg tacagtaact 540

ccaacgccga atacaggttg gaaacagaat aaagatggca tttggtataa agctgaacat 600

gcttcgttca cagtgacagc accagaggga attatcacaa gatacaaagg tccttggact 660

ggtcacccac aagctggtgt attacaaaaa ggtcaaacga ttaaatatga tgaggttcaa 720

aaatttgacg gtcatgtttg ggtatcgtgg gaaacgtttg agggcgaaac tgtatacatg 780

ccggtacgca catgggacgc taaaactggt aaagttggta agttgtgggg cgaaattaaa 840

taa 843

<210> 44
<211> 280

<212> PRT
<213> artificial

<220>
<223> artificial construct

<400> 44

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Met Arg Gly Ser His His His His His His Gly Ser Gly Ser Gly Ser
1               5                  10                  15

Gly Ile Glu Gly Arg Pro Tyr Asn Gly Thr Gly Ser Ala Cys Glu Leu
            20                  25                  30

Ala Ala Thr His Glu His Ser Ala Gln Trp Leu Asn Asn Tyr Lys Lys
        35                  40                  45

Gly Tyr Gly Tyr Gly Pro Tyr Pro Leu Gly Ile Asn Gly Gly Met His
    50                  55                  60

Tyr Gly Val Asp Phe Phe Met Asn Ile Gly Thr Pro Val Lys Ala Ile
65                  70                  75                  80

Ser Ser Gly Lys Ile Val Glu Ala Gly Trp Ser Asn Tyr Gly Gly Gly
                85                  90                  95

Asn Gln Ile Gly Leu Ile Glu Asn Asp Gly Val His Arg Gln Trp Tyr
            100                 105                 110

Met His Leu Ser Lys Tyr Asn Val Lys Val Gly Asp Tyr Val Lys Ala
        115                 120                 125

Gly Gln Ile Ile Gly Trp Ser Gly Ser Thr Gly Tyr Ser Thr Ala Pro
    130                 135                 140

His Leu His Phe Gln Arg Met Val Asn Ser Phe Ser Asn Ser Thr Ala
145                 150                 155                 160

Gln Asp Pro Met Pro Phe Leu Lys Ser Ala Gly Tyr Gly Lys Ala Gly
                165                 170                 175

Gly Thr Val Thr Pro Thr Pro Asn Thr Gly Trp Lys Gln Asn Lys Asp
            180                 185                 190

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

Glu Gly Ile Ile Thr Arg Tyr Lys Gly Pro Trp Thr Gly His Pro Gln
    210                 215                 220

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

Thr Val Tyr Met Pro Val Arg Thr Trp Asp Ala Lys Thr Gly Lys Val
260 265 270

Gly Lys Leu Trp Gly Glu Ile Lys
275 280

<210> 45
<211> 837
<212> DNA
<213> artificial

<220>
<223> artificial construct

<400> 45
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aggccttata atggaactgg atccgcatgc gagctcgctg caacacatga acattcagca 120

caatggttga ataattacaa aaaaggatat ggttacggtc cttatccatt aggtataaat 180

ggcggtatgc actacggagt tgatttttt atgaatattg gaacaccagt aaaagctatt 240

tcaagcggaa aaatagttga agctggttgg agtaattacg gaggaggtaa tcaaataggt 300

cttattgaaa atgatggagt gcatagacaa tggtatatgc atctaagtaa atataatgtt 360

aaagtaggag attatgtcaa agctggtcaa ataatcggtt ggtctggaag cactggttat 420

tctacagcac cacatttaca cttccaaaga atggttaatt cattttcaaa ttcaactgcc 480

caagatccaa tgcctttctt aaagagcgca ggatatggaa aagcaggtgg tacagtaact 540

ccaacgccga atacaggttg gaaaacaaac aaatatggca cactatataa atcagagtca 600

gctagcttca cacctaatac agatataata acaagaacga ctggtccatt tagaagcatg 660

ccgcagtcag gagtcttaaa agcaggtcaa acaattcatt atgatgaagt gatgaaacaa 720

gacggtcatg tttgggtagg ttatacaggt aacagtggcc aacgtattta cttgcctgta 780

agaacatgga ataaatctac taatacttta ggtgttcttt ggggaactat aaagtaa 837

<210> 46
<211> 278
<212> PRT
<213> artificial

<220>
<223> artificial construct

<400> 46

Met Arg Gly Ser His His His His His His Gly Ser Gly Ser Gly Ser
1 5 10 15

Gly Ile Glu Gly Arg Pro Tyr Asn Gly Thr Gly Ser Ala Cys Glu Leu
20 25 30

```
Ala Ala Thr His Glu His Ser Ala Gln Trp Leu Asn Asn Tyr Lys Lys
        35                  40                  45

Gly Tyr Gly Tyr Gly Pro Tyr Pro Leu Gly Ile Asn Gly Gly Met His
    50                  55                  60

Tyr Gly Val Asp Phe Phe Met Asn Ile Gly Thr Pro Val Lys Ala Ile
65                  70                  75                  80

Ser Ser Gly Lys Ile Val Glu Ala Gly Trp Ser Asn Tyr Gly Gly Gly
                85                  90                  95

Asn Gln Ile Gly Leu Ile Glu Asn Asp Gly Val His Arg Gln Trp Tyr
            100                 105                 110

Met His Leu Ser Lys Tyr Asn Val Lys Val Gly Asp Tyr Val Lys Ala
        115                 120                 125

Gly Gln Ile Ile Gly Trp Ser Gly Ser Thr Gly Tyr Ser Thr Ala Pro
    130                 135                 140

His Leu His Phe Gln Arg Met Val Asn Ser Phe Ser Asn Ser Thr Ala
145                 150                 155                 160

Gln Asp Pro Met Pro Phe Leu Lys Ser Ala Gly Tyr Gly Lys Ala Gly
                165                 170                 175

Gly Thr Val Thr Pro Thr Pro Asn Thr Gly Trp Lys Thr Asn Lys Tyr
            180                 185                 190

Gly Thr Leu Tyr Lys Ser Glu Ser Ala Ser Phe Thr Pro Asn Thr Asp
        195                 200                 205

Ile Ile Thr Arg Thr Thr Gly Pro Phe Arg Ser Met Pro Gln Ser Gly
    210                 215                 220

Val Leu Lys Ala Gly Gln Thr Ile His Tyr Asp Glu Val Met Lys Gln
225                 230                 235                 240

Asp Gly His Val Trp Val Gly Tyr Thr Gly Asn Ser Gly Gln Arg Ile
                245                 250                 255

Tyr Leu Pro Val Arg Thr Trp Asn Lys Ser Thr Asn Thr Leu Gly Val
            260                 265                 270

Leu Trp Gly Thr Ile Lys
        275
```

<210> 47
<211> 843
<212> DNA
<213> artificial

<220>
<223> artificial construct

<400> 47
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aggccttata atggaactgg atccgcatgc gagctcgctg caacacatga acattcagca 120

caatggttga ataattacaa aaaaggatat ggttacggtc cttatccatt aggtataaat 180

ggcggtatgc actacggagt tgatttttt atgaatattg gaacaccagt aaaagctatt 240

tcaagcggaa aaatagttga agctggttgg agtaattacg gaggaggtaa tcaaataggt 300

cttattgaaa atgatggagt gcatagacaa tggtatatgc atctaagtaa atataatgtt 360

aaagtaggag attatgtcaa agctggtcaa ataatcggtt ggtctggaag cactggttat 420

tctacagcac cacatttaca cttccaaaga atggttaatt cattttcaaa ttcaactgcc 480

caagatccaa tgcctttctt aaagagcgca ggatatggaa aagcaggtgg tacagtaact 540

ccaacgccga atacaggtgg taaatctgca agtaaaataa cagttggaag taaagcgcct 600

tataacctta aatggtcaaa aggtgcttat tttaatgcga aaatcgacgg cttaggtgct 660

acttcagcca ctagatacgg tgataatcgt actaactata gattcgatgt tggacaggct 720

gtatacgcgc ctggaacatt aatatatgtg tttgaaatta tagatggttg gtgtcgcatt 780

tattggaaca atcataatga gtggatatgg catgagagat tgattgtgaa agaagtgttt 840

taa 843

<210> 48
<211> 280
<212> PRT
<213> artificial

<220>
<223> artificial construct

<400> 48

Met Arg Gly Ser His His His His His His Gly Ser Gly Ser Gly Ser
1 5 10 15

Gly Ile Glu Gly Arg Pro Tyr Asn Gly Thr Gly Ser Ala Cys Glu Leu
20 25 30

Ala Ala Thr His Glu His Ser Ala Gln Trp Leu Asn Asn Tyr Lys Lys
35 40 45

Gly Tyr Gly Tyr Gly Pro Tyr Pro Leu Gly Ile Asn Gly Gly Met His
50 55 60

Tyr Gly Val Asp Phe Phe Met Asn Ile Gly Thr Pro Val Lys Ala Ile
65 70 75 80

Ser Ser Gly Lys Ile Val Glu Ala Gly Trp Ser Asn Tyr Gly Gly Gly
85 90 95

```
Asn Gln Ile Gly Leu Ile Glu Asn Asp Gly Val His Arg Gln Trp Tyr
            100                 105                 110

Met His Leu Ser Lys Tyr Asn Val Lys Val Gly Asp Tyr Val Lys Ala
        115                 120                 125

Gly Gln Ile Ile Gly Trp Ser Gly Ser Thr Gly Tyr Ser Thr Ala Pro
    130                 135                 140

His Leu His Phe Gln Arg Met Val Asn Ser Phe Ser Asn Ser Thr Ala
145                 150                 155                 160

Gln Asp Pro Met Pro Phe Leu Lys Ser Ala Gly Tyr Gly Lys Ala Gly
                165                 170                 175

Gly Thr Val Thr Pro Thr Pro Asn Thr Gly Gly Lys Ser Ala Ser Lys
            180                 185                 190

Ile Thr Val Gly Ser Lys Ala Pro Tyr Asn Leu Lys Trp Ser Lys Gly
        195                 200                 205

Ala Tyr Phe Asn Ala Lys Ile Asp Gly Leu Gly Ala Thr Ser Ala Thr
    210                 215                 220

Arg Tyr Gly Asp Asn Arg Thr Asn Tyr Arg Phe Asp Val Gly Gln Ala
225                 230                 235                 240

Val Tyr Ala Pro Gly Thr Leu Ile Tyr Val Phe Glu Ile Ile Asp Gly
                245                 250                 255

Trp Cys Arg Ile Tyr Trp Asn Asn His Asn Glu Trp Ile Trp His Glu
            260                 265                 270

Arg Leu Ile Val Lys Glu Val Phe
        275                 280


<210>  49
<211>  1755
<212>  DNA
<213>  artificial

<220>
<223>  artificial construct

<400>  49
atgagaggat cgcatcacca tcaccatcac ggatctggct ctggatctgg tatcgaggga     60

agggcaaaga aagatgaaaa atcacaagta tgtagtggtt tggctatgga aaaatatgac    120

attacaaatt taaatgctaa acaagataaa tcaaagaatg ggagcgtgaa agagttgaaa    180

catatctatt caaaccatat taaaggtaac aagattacag caccaaaacc tagtattcaa    240

ggtgtggtca tccacaatga ttatggtagt atgacaccta gtcaatactt accatggtta    300
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tatgcacgtg agaataacgg tacacacgtt aacggttggg ctagtgttta tgcaaataga 360

aacgaagtgc tttggtatca tccgacagac tacgtagagt ggcattgtgg taatcaatgg 420

gcaaatgcta acttaatcgg atttgaagtg tgtgagtcgt atcctggtag aatctcggac 480

aaattattct tagaaaatga agaagcgaca ttgaaagtag ctgcggatgt gatgaagtcg 540

tacggattac cagttaatcg caacactgta cgtctgcata acgaattctt cggaacttct 600

tgtccacatc gttcgtggga cttgcatgtt ggcaaaggtg agccttacac aactactaat 660

attaataaaa tgaaagacta cttcatcaaa cgcatcaaac attattatga cggtgagctc 720

gcaaagaaag atgaaaaatc acaagtatgt agtggtttgg ctatggaaaa atatgacatt 780

acaaatttaa atgctaaaca agataaatca aagaatggga gcgtgaaaga gttgaaacat 840

atctattcaa accatattaa aggtaacaag attacagcac caaaacctag tattcaaggt 900

gtggtcatcc acaatgatta tggtagtatg acacctagtc aatacttacc atggttatat 960

gcacgtgaga ataacggtac acacgttaac ggttgggcta gtgtttatgc aaatagaaac 1020

gaagtgcttt ggtatcatcc gacagactac gtagagtggc attgtggtaa tcaatgggca 1080

aatgctaact taatcggatt tgaagtgtgt gagtcgtatc ctggtagaat ctcggacaaa 1140

ttattcttag aaaatgaaga agcgacattg aaagtagctg cggatgtgat gaagtcgtac 1200

ggattaccag ttaatcgcaa cactgtacgt ctgcataacg aattcttcgg aacttcttgt 1260

ccacatcgtt cgtgggactt gcatgttggc aaaggtgagc cttacacaac tactaatatt 1320

aataaaatga aagactactt catcaaacgc atcaaacatt attatgacgg tggaaagcta 1380

gaagtaagca aagcagcaac tatcaaacaa tctgacgtta agcaagaagt taaaaagcaa 1440

gaagcaaaac aaattgtgaa agcaacagat tggaaacaga ataaagatgg catttggtat 1500

aaagctgaac atgcttcgtt cacagtgaca gcaccagagg gaattatcac aagatacaaa 1560

ggtccttgga ctggtcaccc acaagctggt gtattacaaa aaggtcaaac gattaaatat 1620

gatgaggttc aaaaatttga cggtcatgtt tgggtatcgt gggaaacgtt tgagggcgaa 1680

actgtataca tgccggtacg cacatgggac gctaaaactg gtaaagttgg taagttgtgg 1740

ggcgaaatta aataa 1755

<210> 50
<211> 584
<212> PRT
<213> artificial

<220>
<223> artificial construct

<400> 50

Met Arg Gly Ser His His His His His His Gly Ser Gly Ser Gly Ser
1 5 10 15

Gly Ile Glu Gly Arg Ala Lys Lys Asp Glu Lys Ser Gln Val Cys Ser
20 25 30

```
Gly Leu Ala Met Glu Lys Tyr Asp Ile Thr Asn Leu Asn Ala Lys Gln
        35                  40                  45

Asp Lys Ser Lys Asn Gly Ser Val Lys Glu Leu Lys His Ile Tyr Ser
    50                  55                  60

Asn His Ile Lys Gly Asn Lys Ile Thr Ala Pro Lys Pro Ser Ile Gln
65                  70                  75                  80

Gly Val Val Ile His Asn Asp Tyr Gly Ser Met Thr Pro Ser Gln Tyr
                85                  90                  95

Leu Pro Trp Leu Tyr Ala Arg Glu Asn Asn Gly Thr His Val Asn Gly
            100                 105                 110

Trp Ala Ser Val Tyr Ala Asn Arg Asn Glu Val Leu Trp Tyr His Pro
        115                 120                 125

Thr Asp Tyr Val Glu Trp His Cys Gly Asn Gln Trp Ala Asn Ala Asn
    130                 135                 140

Leu Ile Gly Phe Glu Val Cys Glu Ser Tyr Pro Gly Arg Ile Ser Asp
145                 150                 155                 160

Lys Leu Phe Leu Glu Asn Glu Glu Ala Thr Leu Lys Val Ala Ala Asp
                165                 170                 175

Val Met Lys Ser Tyr Gly Leu Pro Val Asn Arg Asn Thr Val Arg Leu
            180                 185                 190

His Asn Glu Phe Phe Gly Thr Ser Cys Pro His Arg Ser Trp Asp Leu
        195                 200                 205

His Val Gly Lys Gly Glu Pro Tyr Thr Thr Thr Asn Ile Asn Lys Met
    210                 215                 220

Lys Asp Tyr Phe Ile Lys Arg Ile Lys His Tyr Tyr Asp Gly Glu Leu
225                 230                 235                 240

Ala Lys Lys Asp Glu Lys Ser Gln Val Cys Ser Gly Leu Ala Met Glu
                245                 250                 255

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

Gly Ser Val Lys Glu Leu Lys His Ile Tyr Ser Asn His Ile Lys Gly
        275                 280                 285

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

Ala Arg Glu Asn Asn Gly Thr His Val Asn Gly Trp Ala Ser Val Tyr
                325                 330                 335

Ala Asn Arg Asn Glu Val Leu Trp Tyr His Pro Thr Asp Tyr Val Glu
            340                 345                 350

Trp His Cys Gly Asn Gln Trp Ala Asn Ala Asn Leu Ile Gly Phe Glu
        355                 360                 365

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

Asn Glu Glu Ala Thr Leu Lys Val Ala Ala Asp Val Met Lys Ser Tyr
385                 390                 395                 400

Gly Leu Pro Val Asn Arg Asn Thr Val Arg Leu His Asn Glu Phe Phe
                405                 410                 415

Gly Thr Ser Cys Pro His Arg Ser Trp Asp Leu His Val Gly Lys Gly
            420                 425                 430

Glu Pro Tyr Thr Thr Thr Asn Ile Asn Lys Met Lys Asp Tyr Phe Ile
        435                 440                 445

Lys Arg Ile Lys His Tyr Tyr Asp Gly Gly Lys Leu Glu Val Ser Lys
    450                 455                 460

Ala Ala Thr Ile Lys Gln Ser Asp Val Lys Gln Glu Val Lys Lys Gln
465                 470                 475                 480

Glu Ala Lys Gln Ile Val Lys Ala Thr Asp Trp Lys Gln Asn Lys Asp
                485                 490                 495

Gly Ile Trp Tyr Lys Ala Glu His Ala Ser Phe Thr Val Thr Ala Pro
            500                 505                 510

Glu Gly Ile Ile Thr Arg Tyr Lys Gly Pro Trp Thr Gly His Pro Gln
        515                 520                 525

Ala Gly Val Leu Gln Lys Gly Gln Thr Ile Lys Tyr Asp Glu Val Gln
    530                 535                 540

Lys Phe Asp Gly His Val Trp Val Ser Trp Glu Thr Phe Glu Gly Glu
545                 550                 555                 560

Thr Val Tyr Met Pro Val Arg Thr Trp Asp Ala Lys Thr Gly Lys Val
                565                 570                 575
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Gly Lys Leu Trp Gly Glu Ile Lys
580

<210> 51
<211> 1749
<212> DNA
<213> artificial

<220>
<223> artificial construct

<400> 51
atgagaggat cgcatcacca tcaccatcac ggatctggct ctggatctgg tatcgaggga 60

agggcaaaga aagatgaaaa atcacaagta tgtagtggtt tggctatgga aaaatatgac 120

attacaaatt taaatgctaa acaagataaa tcaaagaatg ggagcgtgaa agagttgaaa 180

catatctatt caaaccatat taaaggtaac aagattacag caccaaaacc tagtattcaa 240

ggtgtggtca tccacaatga ttatggtagt atgacaccta gtcaatactt accatggtta 300

tatgcacgtg agaataacgg tacacacgtt aacggttggg ctagtgttta tgcaaataga 360

aacgaagtgc tttggtatca tccgacagac tacgtagagt ggcattgtgg taatcaatgg 420

gcaaatgcta acttaatcgg atttgaagtg tgtgagtcgt atcctggtag aatctcggac 480

aaattattct tagaaaatga agaagcgaca ttgaaagtag ctgcggatgt gatgaagtcg 540

tacggattac cagttaatcg caacactgta cgtctgcata acgaattctt cggaacttct 600

tgtccacatc gttcgtggga cttgcatgtt ggcaaaggtg agccttacac aactactaat 660

attaataaaa tgaaagacta cttcatcaaa cgcatcaaac attattatga cggtgagctc 720

gcaaagaaag atgaaaaatc acaagtatgt agtggtttgg ctatggaaaa atatgacatt 780

acaaatttaa atgctaaaca agataaatca aagaatggga gcgtgaaaga gttgaaacat 840

atctattcaa accatattaa aggtaacaag attacagcac caaaacctag tattcaaggt 900

gtggtcatcc acaatgatta tggtagtatg acacctagtc aatacttacc atggttatat 960

gcacgtgaga ataacggtac acacgttaac ggttgggcta gtgtttatgc aaatagaaac 1020

gaagtgcttt ggtatcatcc gacagactac gtagagtggc attgtggtaa tcaatgggca 1080

aatgctaact taatcggatt tgaagtgtgt gagtcgtatc ctggtagaat ctcggacaaa 1140

ttattcttag aaaatgaaga agcgacattg aaagtagctg cggatgtgat gaagtcgtac 1200

ggattaccag ttaatcgcaa cactgtacgt ctgcataacg aattcttcgg aacttcttgt 1260

ccacatcgtt cgtgggactt gcatgttggc aaaggtgagc cttacacaac tactaatatt 1320

aataaaatga aagactactt catcaaacgc atcaaacatt attatgacgg tggaaagcta 1380

gaagtaagca aagcagcaac tatcaaacaa tctgacgtta agcaagaagt taaaaagcaa 1440

gaagcaaaac aaattgtgaa agcaacagat tggaaaacaa acaaatatgg cacactatat 1500

aaatcagagt cagctagctt cacacctaat acagatataa taacaagaac gactggtcca 1560

tttagaagca tgccgcagtc aggagtctta aaagcaggtc aaacaattca ttatgatgaa 1620

gtgatgaaac aagacggtca tgtttgggta ggttatacag gtaacagtgg ccaacgtatt 1680

tacttgcctg taagaacatg gaataaatct actaatactt taggtgttct ttggggaact 1740

ataaagtaa 1749

<210> 52
<211> 582
<212> PRT
<213> artificial

<220>
<223> artificial construct

<400> 52

Met Arg Gly Ser His His His His His His Gly Ser Gly Ser Gly Ser
1 5 10 15

Gly Ile Glu Gly Arg Ala Lys Lys Asp Glu Lys Ser Gln Val Cys Ser
20 25 30

Gly Leu Ala Met Glu Lys Tyr Asp Ile Thr Asn Leu Asn Ala Lys Gln
35 40 45

Asp Lys Ser Lys Asn Gly Ser Val Lys Glu Leu Lys His Ile Tyr Ser
50 55 60

Asn His Ile Lys Gly Asn Lys Ile Thr Ala Pro Lys Pro Ser Ile Gln
65 70 75 80

Gly Val Val Ile His Asn Asp Tyr Gly Ser Met Thr Pro Ser Gln Tyr
85 90 95

Leu Pro Trp Leu Tyr Ala Arg Glu Asn Asn Gly Thr His Val Asn Gly
100 105 110

Trp Ala Ser Val Tyr Ala Asn Arg Asn Glu Val Leu Trp Tyr His Pro
115 120 125

Thr Asp Tyr Val Glu Trp His Cys Gly Asn Gln Trp Ala Asn Ala Asn
130 135 140

Leu Ile Gly Phe Glu Val Cys Glu Ser Tyr Pro Gly Arg Ile Ser Asp
145 150 155 160

Lys Leu Phe Leu Glu Asn Glu Glu Ala Thr Leu Lys Val Ala Ala Asp
165 170 175

Val Met Lys Ser Tyr Gly Leu Pro Val Asn Arg Asn Thr Val Arg Leu
180 185 190

His Asn Glu Phe Phe Gly Thr Ser Cys Pro His Arg Ser Trp Asp Leu
195 200 205

```
His Val Gly Lys Gly Glu Pro Tyr Thr Thr Thr Asn Ile Asn Lys Met
    210                 215                 220

Lys Asp Tyr Phe Ile Lys Arg Ile Lys His Tyr Tyr Asp Gly Glu Leu
225                 230                 235                 240

Ala Lys Lys Asp Glu Lys Ser Gln Val Cys Ser Gly Leu Ala Met Glu
                245                 250                 255

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

Gly Ser Val Lys Glu Leu Lys His Ile Tyr Ser Asn His Ile Lys Gly
        275                 280                 285

Asn Lys Ile Thr Ala Pro Lys Pro Ser Ile Gln Gly Val Val Ile His
    290                 295                 300

Asn Asp Tyr Gly Ser Met Thr Pro Ser Gln Tyr Leu Pro Trp Leu Tyr
305                 310                 315                 320

Ala Arg Glu Asn Asn Gly Thr His Val Asn Gly Trp Ala Ser Val Tyr
                325                 330                 335

Ala Asn Arg Asn Glu Val Leu Trp Tyr His Pro Thr Asp Tyr Val Glu
            340                 345                 350

Trp His Cys Gly Asn Gln Trp Ala Asn Ala Asn Leu Ile Gly Phe Glu
        355                 360                 365

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

Asn Glu Glu Ala Thr Leu Lys Val Ala Ala Asp Val Met Lys Ser Tyr
385                 390                 395                 400

Gly Leu Pro Val Asn Arg Asn Thr Val Arg Leu His Asn Glu Phe Phe
                405                 410                 415

Gly Thr Ser Cys Pro His Arg Ser Trp Asp Leu His Val Gly Lys Gly
            420                 425                 430

Glu Pro Tyr Thr Thr Thr Asn Ile Asn Lys Met Lys Asp Tyr Phe Ile
        435                 440                 445

Lys Arg Ile Lys His Tyr Tyr Asp Gly Gly Lys Leu Glu Val Ser Lys
    450                 455                 460

Ala Ala Thr Ile Lys Gln Ser Asp Val Lys Gln Glu Val Lys Lys Gln
465                 470                 475                 480
```

Glu Ala Lys Gln Ile Val Lys Ala Thr Asp Trp Lys Thr Asn Lys Tyr
485 490 495

Gly Thr Leu Tyr Lys Ser Glu Ser Ala Ser Phe Thr Pro Asn Thr Asp
500 505 510

Ile Ile Thr Arg Thr Thr Gly Pro Phe Arg Ser Met Pro Gln Ser Gly
515 520 525

Val Leu Lys Ala Gly Gln Thr Ile His Tyr Asp Glu Val Met Lys Gln
530 535 540

Asp Gly His Val Trp Val Gly Tyr Thr Gly Asn Ser Gly Gln Arg Ile
545 550 555 560

Tyr Leu Pro Val Arg Thr Trp Asn Lys Ser Thr Asn Thr Leu Gly Val
565 570 575

Leu Trp Gly Thr Ile Lys
580

<210> 53
<211> 1755
<212> DNA
<213> artificial

<220>
<223> artificial construct

<400> 53
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agggcaaaga aagatgaaaa atcacaagta tgtagtggtt tggctatgga aaaatatgac 120

attacaaatt taaatgctaa acaagataaa tcaaagaatg ggagcgtgaa agagttgaaa 180

catatctatt caaaccatat taaaggtaac aagattacag caccaaaacc tagtattcaa 240

ggtgtggtca tccacaatga ttatggtagt atgacaccta gtcaatactt accatggtta 300

tatgcacgtg agaataacgg tacacacgtt aacggttggg ctagtgttta tgcaaataga 360

aacgaagtgc tttggtatca tccgacagac tacgtagagt ggcattgtgg taatcaatgg 420

gcaaatgcta acttaatcgg atttgaagtg tgtgagtcgt atcctggtag aatctcggac 480

aaattattct tagaaaatga agaagcgaca ttgaaagtag ctgcggatgt gatgaagtcg 540

tacggattac cagttaatcg caacactgta cgtctgcata acgaattctt cggaacttct 600

tgtccacatc gttcgtggga cttgcatgtt ggcaaaggtg agccttacac aactactaat 660

attaataaaa tgaaagacta cttcatcaaa cgcatcaaac attattatga cggtgagctc 720

gcaaagaaag atgaaaaatc acaagtatgt agtggtttgg ctatggaaaa atatgacatt 780

acaaatttaa atgctaaaca agataaatca aagaatggga gcgtgaaaga gttgaaacat 840

atctattcaa accatattaa aggtaacaag attacagcac caaaacctag tattcaaggt 900

gtggtcatcc acaatgatta tggtagtatg acacctagtc aatacttacc atggttatat 960

gcacgtgaga ataacggtac acacgttaac ggttgggcta gtgtttatgc aaatagaaac 1020

gaagtgcttt ggtatcatcc gacagactac gtagagtggc attgtggtaa tcaatgggca 1080

aatgctaact taatcggatt tgaagtgtgt gagtcgtatc ctggtagaat ctcggacaaa 1140

ttattcttag aaaatgaaga agcgacattg aaagtagctg cggatgtgat gaagtcgtac 1200

ggattaccag ttaatcgcaa cactgtacgt ctgcataacg aattcttcgg aacttcttgt 1260

ccacatcgtt cgtgggactt gcatgttggc aaaggtgagc cttacacaac tactaatatt 1320

aataaaatga aagactactt catcaaacgc atcaaacatt attatgacgg tggaaagcta 1380

gaagtaagca aagcagcaac tatcaaacaa tctgacgtta agcaagaagt taaaaagcaa 1440

gaagcaaaac aaattgtgaa agcaacagat ggtaaatctg caagtaaaat aacagttgga 1500

agtaaagcgc cttataacct taaatggtca aaaggtgctt attttaatgc gaaaatcgac 1560

ggcttaggtg ctacttcagc cactagatac ggtgataatc gtactaacta tagattcgat 1620

gttggacagg ctgtatacgc gcctggaaca ttaatatatg tgtttgaaat tatagatggt 1680

tggtgtcgca tttattggaa caatcataat gagtggatat ggcatgagag attgattgtg 1740

aaagaagtgt tttaa 1755

<210> 54
<211> 584
<212> PRT
<213> artificial

<220>
<223> artificial construct

<400> 54

Met Arg Gly Ser His His His His His His Gly Ser Gly Ser Gly Ser
1 5 10 15

Gly Ile Glu Gly Arg Ala Lys Lys Asp Glu Lys Ser Gln Val Cys Ser
20 25 30

Gly Leu Ala Met Glu Lys Tyr Asp Ile Thr Asn Leu Asn Ala Lys Gln
35 40 45

Asp Lys Ser Lys Asn Gly Ser Val Lys Glu Leu Lys His Ile Tyr Ser
50 55 60

Asn His Ile Lys Gly Asn Lys Ile Thr Ala Pro Lys Pro Ser Ile Gln
65 70 75 80

Gly Val Val Ile His Asn Asp Tyr Gly Ser Met Thr Pro Ser Gln Tyr
85 90 95

Leu Pro Trp Leu Tyr Ala Arg Glu Asn Asn Gly Thr His Val Asn Gly
100 105 110

```
Trp Ala Ser Val Tyr Ala Asn Arg Asn Glu Val Leu Trp Tyr His Pro
        115                 120                 125

Thr Asp Tyr Val Glu Trp His Cys Gly Asn Gln Trp Ala Asn Ala Asn
    130                 135                 140

Leu Ile Gly Phe Glu Val Cys Glu Ser Tyr Pro Gly Arg Ile Ser Asp
145                 150                 155                 160

Lys Leu Phe Leu Glu Asn Glu Glu Ala Thr Leu Lys Val Ala Ala Asp
                165                 170                 175

Val Met Lys Ser Tyr Gly Leu Pro Val Asn Arg Asn Thr Val Arg Leu
            180                 185                 190

His Asn Glu Phe Phe Gly Thr Ser Cys Pro His Arg Ser Trp Asp Leu
        195                 200                 205

His Val Gly Lys Gly Glu Pro Tyr Thr Thr Thr Asn Ile Asn Lys Met
    210                 215                 220

Lys Asp Tyr Phe Ile Lys Arg Ile Lys His Tyr Tyr Asp Gly Glu Leu
225                 230                 235                 240

Ala Lys Lys Asp Glu Lys Ser Gln Val Cys Ser Gly Leu Ala Met Glu
                245                 250                 255

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

Gly Ser Val Lys Glu Leu Lys His Ile Tyr Ser Asn His Ile Lys Gly
        275                 280                 285

Asn Lys Ile Thr Ala Pro Lys Pro Ser Ile Gln Gly Val Val Ile His
    290                 295                 300

Asn Asp Tyr Gly Ser Met Thr Pro Ser Gln Tyr Leu Pro Trp Leu Tyr
305                 310                 315                 320

Ala Arg Glu Asn Asn Gly Thr His Val Asn Gly Trp Ala Ser Val Tyr
                325                 330                 335

Ala Asn Arg Asn Glu Val Leu Trp Tyr His Pro Thr Asp Tyr Val Glu
            340                 345                 350

Trp His Cys Gly Asn Gln Trp Ala Asn Ala Asn Leu Ile Gly Phe Glu
        355                 360                 365

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

Asn Glu Glu Ala Thr Leu Lys Val Ala Ala Asp Val Met Lys Ser Tyr
385 390 395 400

Gly Leu Pro Val Asn Arg Asn Thr Val Arg Leu His Asn Glu Phe Phe
405 410 415

Gly Thr Ser Cys Pro His Arg Ser Trp Asp Leu His Val Gly Lys Gly
420 425 430

Glu Pro Tyr Thr Thr Thr Asn Ile Asn Lys Met Lys Asp Tyr Phe Ile
435 440 445

Lys Arg Ile Lys His Tyr Tyr Asp Gly Gly Lys Leu Glu Val Ser Lys
450 455 460

Ala Ala Thr Ile Lys Gln Ser Asp Val Lys Gln Glu Val Lys Lys Gln
465 470 475 480

Glu Ala Lys Gln Ile Val Lys Ala Thr Asp Gly Lys Ser Ala Ser Lys
485 490 495

Ile Thr Val Gly Ser Lys Ala Pro Tyr Asn Leu Lys Trp Ser Lys Gly
500 505 510

Ala Tyr Phe Asn Ala Lys Ile Asp Gly Leu Gly Ala Thr Ser Ala Thr
515 520 525

Arg Tyr Gly Asp Asn Arg Thr Asn Tyr Arg Phe Asp Val Gly Gln Ala
530 535 540

Val Tyr Ala Pro Gly Thr Leu Ile Tyr Val Phe Glu Ile Ile Asp Gly
545 550 555 560

Trp Cys Arg Ile Tyr Trp Asn Asn His Asn Glu Trp Ile Trp His Glu
565 570 575

Arg Leu Ile Val Lys Glu Val Phe
580

<210> 55
<211> 1533
<212> DNA
<213> artificial

<220>
<223> artificial construct

<400> 55
atgagaggat cgcatcacca tcaccatcac ggatctggct ctggatctgg tatcgaggga 60

aggatggcta agactcaagc agaaataaat aaacgtttag atgcttatgc aaaaggaaca 120

gtagatagcc cttacagagt taaaaaagct acaagttatg acccatcatt tggtgtaatg 180

gaagcaggag ccattgatgc agatggttac tatcacgctc agtgtcaaga ccttattaca 240

gactatgttt tatggttaac agataataaa gttagaactt ggggtaatgc taaagaccaa 300

attaaacaga gttatggtac tggatttaaa atacatgaaa ataaaccttc tactgtacct 360

aaaaaaggtt ggattgcggt atttacatcc ggtagttatg aacagtgggg tcacataggt 420

attgtatatg atggaggtaa tacttctaca tttactattt tagagcaaaa ctggaatggt 480

tatgctaata aaaaacctac aaaacgtgta gataattatt acggattaac tcacttcatt 540

gaaatacctg taaaagcagg aactactgtt aaaaaagaaa cagctaagaa aagcgcaagt 600

aaaacgcctg cacctaaaaa gaaagcaaca ctaaaagttt ctaagaatga gctcatggct 660

aagactcaag cagaaataaa taaacgttta gatgcttatg caaaaggaac agtagatagc 720

ccttacagag ttaaaaaagc tacaagttat gacccatcat ttggtgtaat ggaagcagga 780

gccattgatg cagatggtta ctatcacgct cagtgtcaag accttattac agactatgtt 840

ttatggttaa cagataataa agttagaact tggggtaatg ctaaagacca aattaaacag 900

agttatggta ctggatttaa aatacatgaa aataaacctt ctactgtacc taaaaaaggt 960

tggattgcgg tatttacatc cggtagttat gaacagtggg gtcacatagg tattgtatat 1020

gatggaggta atacttctac atttactatt ttagagcaaa actggaatgg ttatgctaat 1080

aaaaaaccta caaaacgtgt agataattat tacggattaa ctcacttcat tgaaatacct 1140

gtaaaagcag gaaagctaga agtaagcaaa gcagcaacta tcaaacaatc tgacgttaag 1200

caagaagtta aaaagcaaga agcaaaacaa attgtgaaag caacagattg gaaacagaat 1260

aaagatggca tttggtataa agctgaacat gcttcgttca cagtgacagc accagaggga 1320

attatcacaa gatacaaagg tccttggact ggtcacccac aagctggtgt attacaaaaa 1380

ggtcaaacga ttaaatatga tgaggttcaa aaatttgacg gtcatgtttg ggtatcgtgg 1440

gaaacgtttg agggcgaaac tgtatacatg ccggtacgca catgggacgc taaaactggt 1500

aaagttggta agttgtgggg cgaaattaaa taa 1533

<210> 56
<211> 510
<212> PRT
<213> artificial

<220>
<223> artificial construct

<400> 56

Met Arg Gly Ser His His His His His His Gly Ser Gly Ser Gly Ser
1 5 10 15

Gly Ile Glu Gly Arg Met Ala Lys Thr Gln Ala Glu Ile Asn Lys Arg
20 25 30

Leu Asp Ala Tyr Ala Lys Gly Thr Val Asp Ser Pro Tyr Arg Val Lys
35 40 45

```
Lys Ala Thr Ser Tyr Asp Pro Ser Phe Gly Val Met Glu Ala Gly Ala
    50                  55                  60

Ile Asp Ala Asp Gly Tyr Tyr His Ala Gln Cys Gln Asp Leu Ile Thr
65                  70                  75                  80

Asp Tyr Val Leu Trp Leu Thr Asp Asn Lys Val Arg Thr Trp Gly Asn
                85                  90                  95

Ala Lys Asp Gln Ile Lys Gln Ser Tyr Gly Thr Gly Phe Lys Ile His
            100                 105                 110

Glu Asn Lys Pro Ser Thr Val Pro Lys Lys Gly Trp Ile Ala Val Phe
        115                 120                 125

Thr Ser Gly Ser Tyr Glu Gln Trp Gly His Ile Gly Ile Val Tyr Asp
    130                 135                 140

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

Tyr Ala Asn Lys Lys Pro Thr Lys Arg Val Asp Asn Tyr Tyr Gly Leu
                165                 170                 175

Thr His Phe Ile Glu Ile Pro Val Lys Ala Gly Thr Thr Val Lys Lys
            180                 185                 190

Glu Thr Ala Lys Lys Ser Ala Ser Lys Thr Pro Ala Pro Lys Lys Lys
        195                 200                 205

Ala Thr Leu Lys Val Ser Lys Asn Glu Leu Met Ala Lys Thr Gln Ala
    210                 215                 220

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

Pro Tyr Arg Val Lys Lys Ala Thr Ser Tyr Asp Pro Ser Phe Gly Val
                245                 250                 255

Met Glu Ala Gly Ala Ile Asp Ala Asp Gly Tyr Tyr His Ala Gln Cys
            260                 265                 270

Gln Asp Leu Ile Thr Asp Tyr Val Leu Trp Leu Thr Asp Asn Lys Val
        275                 280                 285

Arg Thr Trp Gly Asn Ala Lys Asp Gln Ile Lys Gln Ser Tyr Gly Thr
    290                 295                 300

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

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

Gln Asn Trp Asn Gly Tyr Ala Asn Lys Lys Pro Thr Lys Arg Val Asp
        355                 360                 365

Asn Tyr Tyr Gly Leu Thr His Phe Ile Glu Ile Pro Val Lys Ala Gly
    370                 375                 380

Lys Leu Glu Val Ser Lys Ala Ala Thr Ile Lys Gln Ser Asp Val Lys
385                 390                 395                 400

Gln Glu Val Lys Lys Gln Glu Ala Lys Gln Ile Val Lys Ala Thr Asp
                405                 410                 415

Trp Lys Gln Asn Lys Asp Gly Ile Trp Tyr Lys Ala Glu His Ala Ser
            420                 425                 430

Phe Thr Val Thr Ala Pro Glu Gly Ile Ile Thr Arg Tyr Lys Gly Pro
        435                 440                 445

Trp Thr Gly His Pro Gln Ala Gly Val Leu Gln Lys Gly Gln Thr Ile
    450                 455                 460

Lys Tyr Asp Glu Val Gln Lys Phe Asp Gly His Val Trp Val Ser Trp
465                 470                 475                 480

Glu Thr Phe Glu Gly Glu Thr Val Tyr Met Pro Val Arg Thr Trp Asp
                485                 490                 495

Ala Lys Thr Gly Lys Val Gly Lys Leu Trp Gly Glu Ile Lys
            500                 505                 510
```

<210> 57
<211> 1470
<212> DNA
<213> artificial

<220>
<223> artificial construct

<400> 57
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aggatggcta agactcaagc agaaataaat aaacgtttag atgcttatgc aaaaggaaca 120

gtagatagcc cttacagagt taaaaaagct acaagttatg acccatcatt tggtgtaatg 180

gaagcaggag ccattgatgc agatggttac tatcacgctc agtgtcaaga ccttattaca 240

gactatgttt tatggttaac agataataaa gttagaactt ggggtaatgc taaagaccaa 300

attaaacaga gttatggtac tggatttaaa atacatgaaa ataaaccttc tactgtacct 360

aaaaaaggtt ggattgcggt atttacatcc ggtagttatg aacagtgggg tcacataggt 420

attgtatatg atggaggtaa tacttctaca tttactattt tagagcaaaa ctggaatggt 480

tatgctaata aaaaacctac aaaacgtgta gataattatt acggattaac tcacttcatt 540

gaaatacctg taaaagcagg aactactgtt aaaaaagaaa cagctaagaa aagcgcaagt 600

aaaacgcctg cacctaaaaa gaaagcaaca ctaaaagttt ctaagaatga gctcatggct 660

aagactcaag cagaaataaa taaacgttta gatgcttatg caaaaggaac agtagatagc 720

ccttacagag ttaaaaaagc tacaagttat gacccatcat ttggtgtaat ggaagcagga 780

gccattgatg cagatggtta ctatcacgct cagtgtcaag accttattac agactatgtt 840

ttatggttaa cagataataa agttagaact tggggtaatg ctaaagacca aattaaacag 900

agttatggta ctggatttaa aatacatgaa aataaacctt ctactgtacc taaaaaaggt 960

tggattgcgg tatttacatc cggtagttat gaacagtggg gtcacatagg tattgtatat 1020

gatggaggta atacttctac atttactatt ttagagcaaa actggaatgg ttatgctaat 1080

aaaaaaccta caaaacgtgt agataattat tacggattaa ctcacttcat tgaaatacct 1140

gtaaaagcag gaaaagcagg tggtacagta actccaacgc cgaatacagg ttggaaaaca 1200

aacaaatatg gcacactata taaatcagag tcagctagct tcacacctaa tacagatata 1260

ataacaagaa cgactggtcc atttagaagc atgccgcagt caggagtctt aaaagcaggt 1320

caaacaattc attatgatga agtgatgaaa caagacggtc atgtttgggt aggttataca 1380

ggtaacagtg gccaacgtat ttacttgcct gtaagaacat ggaataaatc tactaatact 1440

ttaggtgttc tttggggaac tataaagtaa 1470

<210> 58
<211> 489
<212> PRT
<213> artificial

<220>
<223> artificial construct

<400> 58

Met Arg Gly Ser His His His His His His Gly Ser Gly Ser Gly Ser
1 5 10 15

Gly Ile Glu Gly Arg Met Ala Lys Thr Gln Ala Glu Ile Asn Lys Arg
20 25 30

Leu Asp Ala Tyr Ala Lys Gly Thr Val Asp Ser Pro Tyr Arg Val Lys
35 40 45

Lys Ala Thr Ser Tyr Asp Pro Ser Phe Gly Val Met Glu Ala Gly Ala
50 55 60

```
Ile Asp Ala Asp Gly Tyr Tyr His Ala Gln Cys Gln Asp Leu Ile Thr
65                  70                  75                  80

Asp Tyr Val Leu Trp Leu Thr Asp Asn Lys Val Arg Thr Trp Gly Asn
                85                  90                  95

Ala Lys Asp Gln Ile Lys Gln Ser Tyr Gly Thr Gly Phe Lys Ile His
            100                 105                 110

Glu Asn Lys Pro Ser Thr Val Pro Lys Lys Gly Trp Ile Ala Val Phe
        115                 120                 125

Thr Ser Gly Ser Tyr Glu Gln Trp Gly His Ile Gly Ile Val Tyr Asp
    130                 135                 140

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

Tyr Ala Asn Lys Lys Pro Thr Lys Arg Val Asp Asn Tyr Tyr Gly Leu
                165                 170                 175

Thr His Phe Ile Glu Ile Pro Val Lys Ala Gly Thr Thr Val Lys Lys
            180                 185                 190

Glu Thr Ala Lys Lys Ser Ala Ser Lys Thr Pro Ala Pro Lys Lys Lys
        195                 200                 205

Ala Thr Leu Lys Val Ser Lys Asn Glu Leu Met Ala Lys Thr Gln Ala
    210                 215                 220

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

Pro Tyr Arg Val Lys Lys Ala Thr Ser Tyr Asp Pro Ser Phe Gly Val
                245                 250                 255

Met Glu Ala Gly Ala Ile Asp Ala Asp Gly Tyr Tyr His Ala Gln Cys
            260                 265                 270

Gln Asp Leu Ile Thr Asp Tyr Val Leu Trp Leu Thr Asp Asn Lys Val
        275                 280                 285

Arg Thr Trp Gly Asn Ala Lys Asp Gln Ile Lys Gln Ser Tyr Gly Thr
    290                 295                 300

Gly Phe Lys Ile His Glu Asn Lys Pro Ser Thr Val Pro Lys Lys Gly
305                 310                 315                 320

Trp Ile Ala Val Phe Thr Ser Gly Ser Tyr Glu Gln Trp Gly His Ile
                325                 330                 335
```

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

Gln Asn Trp Asn Gly Tyr Ala Asn Lys Lys Pro Thr Lys Arg Val Asp
        355                 360                 365

Asn Tyr Tyr Gly Leu Thr His Phe Ile Glu Ile Pro Val Lys Ala Gly
    370                 375                 380

Lys Ala Gly Gly Thr Val Thr Pro Thr Pro Asn Thr Gly Trp Lys Thr
385                 390                 395                 400

Asn Lys Tyr Gly Thr Leu Tyr Lys Ser Glu Ser Ala Ser Phe Thr Pro
                405                 410                 415

Asn Thr Asp Ile Ile Thr Arg Thr Thr Gly Pro Phe Arg Ser Met Pro
            420                 425                 430

Gln Ser Gly Val Leu Lys Ala Gly Gln Thr Ile His Tyr Asp Glu Val
        435                 440                 445

Met Lys Gln Asp Gly His Val Trp Val Gly Tyr Thr Gly Asn Ser Gly
    450                 455                 460

Gln Arg Ile Tyr Leu Pro Val Arg Thr Trp Asn Lys Ser Thr Asn Thr
465                 470                 475                 480

Leu Gly Val Leu Trp Gly Thr Ile Lys
                485
```

<210> 59
<211> 1524
<212> DNA
<213> artificial

<220>
<223> artificial construct

<400> 59

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atgagaggat cgcatcacca tcaccatcac ggatctggct ctggatctgg tatcgaggga     60

aggatggcta agactcaagc agaaataaat aaacgtttag atgcttatgc aaaaggaaca    120

gtagatagcc cttacagagt taaaaaagct acaagttatg acccatcatt tggtgtaatg    180

gaagcaggag ccattgatgc agatggttac tatcacgctc agtgtcaaga ccttattaca    240

gactatgttt tatggttaac agataataaa gttagaactt ggggtaatgc taaagaccaa    300

attaaacaga gttatggtac tggatttaaa atacatgaaa ataaaccttc tactgtacct    360

aaaaaaggtt ggattgcggt atttacatcc ggtagttatg aacagtgggg tcacataggt    420

attgtatatg atggaggtaa tacttctaca tttactattt tagagcaaaa ctggaatggt    480

tatgctaata aaaaacctac aaaacgtgta gataattatt acggattaac tcacttcatt    540

gaaatacctg taaaagcagg aactactgtt aaaaaagaaa cagctaagaa aagcgcaagt    600
```

aaaacgcctg cacctaaaaa gaaagcaaca ctaaaagttt ctaagaatga gctcatggct 660

aagactcaag cagaaataaa taaacgttta gatgcttatg caaaaggaac agtagatagc 720

ccttacagag ttaaaaaagc tacaagttat gacccatcat ttggtgtaat ggaagcagga 780

gccattgatg cagatggtta ctatcacgct cagtgtcaag accttattac agactatgtt 840

ttatggttaa cagataataa agttagaact tggggtaatg ctaaagacca aattaaacag 900

agttatggta ctggatttaa aatacatgaa aataaacctt ctactgtacc taaaaaaggt 960

tggattgcgg tatttacatc cggtagttat gaacagtggg gtcacatagg tattgtatat 1020

gatggaggta atacttctac atttactatt ttagagcaaa actggaatgg ttatgctaat 1080

aaaaaaccta caaaacgtgt agataattat tacggattaa ctcacttcat tgaaatacct 1140

gtaaaagcag gaactactgt taaaaaagaa acagctaaga aaagcgcaag taaaacgcct 1200

gcacctaaaa agaaagcaac actaaaagtt tctaagaatg gtaaatctgc aagtaaaata 1260

acagttggaa gtaaagcgcc ttataacctt aaatggtcaa aaggtgctta ttttaatgcg 1320

aaaatcgacg gcttaggtgc tacttcagcc actagatacg gtgataatcg tactaactat 1380

agattcgatg ttggacaggc tgtatacgcg cctggaacat taatatatgt gtttgaaatt 1440

atagatggtt ggtgtcgcat ttattggaac aatcataatg agtggatatg gcatgagaga 1500

ttgattgtga aagaagtgtt ttaa 1524

<210> 60
<211> 507
<212> PRT
<213> artificial

<220>
<223> artificial construct

<400> 60

Met Arg Gly Ser His His His His His His Gly Ser Gly Ser Gly Ser
1 5 10 15

Gly Ile Glu Gly Arg Met Ala Lys Thr Gln Ala Glu Ile Asn Lys Arg
20 25 30

Leu Asp Ala Tyr Ala Lys Gly Thr Val Asp Ser Pro Tyr Arg Val Lys
35 40 45

Lys Ala Thr Ser Tyr Asp Pro Ser Phe Gly Val Met Glu Ala Gly Ala
50 55 60

Ile Asp Ala Asp Gly Tyr Tyr His Ala Gln Cys Gln Asp Leu Ile Thr
65 70 75 80

Asp Tyr Val Leu Trp Leu Thr Asp Asn Lys Val Arg Thr Trp Gly Asn
85 90 95

```
Ala Lys Asp Gln Ile Lys Gln Ser Tyr Gly Thr Gly Phe Lys Ile His
            100                 105                 110

Glu Asn Lys Pro Ser Thr Val Pro Lys Lys Gly Trp Ile Ala Val Phe
        115                 120                 125

Thr Ser Gly Ser Tyr Glu Gln Trp Gly His Ile Gly Ile Val Tyr Asp
    130                 135                 140

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

Tyr Ala Asn Lys Lys Pro Thr Lys Arg Val Asp Asn Tyr Tyr Gly Leu
                165                 170                 175

Thr His Phe Ile Glu Ile Pro Val Lys Ala Gly Thr Thr Val Lys Lys
            180                 185                 190

Glu Thr Ala Lys Lys Ser Ala Ser Lys Thr Pro Ala Pro Lys Lys Lys
        195                 200                 205

Ala Thr Leu Lys Val Ser Lys Asn Glu Leu Met Ala Lys Thr Gln Ala
    210                 215                 220

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

Pro Tyr Arg Val Lys Lys Ala Thr Ser Tyr Asp Pro Ser Phe Gly Val
                245                 250                 255

Met Glu Ala Gly Ala Ile Asp Ala Asp Gly Tyr Tyr His Ala Gln Cys
            260                 265                 270

Gln Asp Leu Ile Thr Asp Tyr Val Leu Trp Leu Thr Asp Asn Lys Val
        275                 280                 285

Arg Thr Trp Gly Asn Ala Lys Asp Gln Ile Lys Gln Ser Tyr Gly Thr
    290                 295                 300

Gly Phe Lys Ile His Glu Asn Lys Pro Ser Thr Val Pro Lys Lys Gly
305                 310                 315                 320

Trp Ile Ala Val Phe Thr Ser Gly Ser Tyr Glu Gln Trp Gly His Ile
                325                 330                 335

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

Gln Asn Trp Asn Gly Tyr Ala Asn Lys Lys Pro Thr Lys Arg Val Asp
        355                 360                 365
```

Asn Tyr Tyr Gly Leu Thr His Phe Ile Glu Ile Pro Val Lys Ala Gly
370 375 380

Thr Thr Val Lys Lys Glu Thr Ala Lys Lys Ser Ala Ser Lys Thr Pro
385 390 395 400

Ala Pro Lys Lys Lys Ala Thr Leu Lys Val Ser Lys Asn Gly Lys Ser
405 410 415

Ala Ser Lys Ile Thr Val Gly Ser Lys Ala Pro Tyr Asn Leu Lys Trp
420 425 430

Ser Lys Gly Ala Tyr Phe Asn Ala Lys Ile Asp Gly Leu Gly Ala Thr
435 440 445

Ser Ala Thr Arg Tyr Gly Asp Asn Arg Thr Asn Tyr Arg Phe Asp Val
450 455 460

Gly Gln Ala Val Tyr Ala Pro Gly Thr Leu Ile Tyr Val Phe Glu Ile
465 470 475 480

Ile Asp Gly Trp Cys Arg Ile Tyr Trp Asn Asn His Asn Glu Trp Ile
485 490 495

Trp His Glu Arg Leu Ile Val Lys Glu Val Phe
500 505

<210> 61
<211> 1446
<212> DNA
<213> artificial

<220>
<223> artificial construct

<400> 61
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aggatgaaaa ccctgaaaca agcagagtcc tacattaaga gtaaagtaaa tacaggaact 120

gattttgatg gtttatatgg gtatcagtgt atggacttag cagtagatta tatttaccat 180

gtaacagatg gtaaaataag aatgtggggt aatgctaagg atgcgataaa taactctttt 240

ggtggtactg ctacggtata taaaaactac cctgctttta gacctaagta cggtgatgta 300

gtcgtatgga ctactggtaa ttttgcaact tatggtcata tcgcaatagt tactaaccct 360

gacccttatg gagaccttca atatgttaca gttcttgaac aaaactggaa cggtaacggg 420

atttataaaa ccgagttagc tacaatcaga acacacgatt acacaggaat tacacatttt 480

attagaccta actttgctac tgaatcaagt gtaaaaaaga aagatacaaa gaaaaaacca 540

aaaccatcaa atagagatgg aataaataaa gataaaattg tatatgatag aactaatatt 600

aattacaatg agctcatgaa aaccctgaaa caagcagagt cctacattaa gagtaaagta 660

aatacaggaa ctgattttga tggtttatat gggtatcagt gtatggactt agcagtagat 720

tatatttacc atgtaacaga tggtaaaata agaatgtggg gtaatgctaa ggatgcgata 780

aataactctt ttggtggtac tgctacggta tataaaaact accctgcttt tagacctaag 840

tacggtgatg tagtcgtatg gactactggt aattttgcaa cttatggtca tatcgcaata 900

gttactaacc ctgaccctta tggagacctt caatatgtta cagttcttga acaaaactgg 960

aacggtaacg ggatttataa aaccgagtta gctacaatca gaacacacga ttacacagga 1020

attacacatt ttattagacc taactttgct actgaatcaa gtgtaaaaaa gaaagataca 1080

aagaaaaaac caaaaccatc aaatagagat ggaataaata aagataaaat tgtatatgat 1140

agaactaata ttaattacaa ttggaaacag aataaagatg gcatttggta taaagctgaa 1200

catgcttcgt tcacagtgac agcaccagag ggaattatca caagatacaa aggtccttgg 1260

actggtcacc cacaagctgg tgtattacaa aaaggtcaaa cgattaaata tgatgaggtt 1320

caaaaatttg acggtcatgt ttgggtatcg tgggaaacgt ttgagggcga aactgtatac 1380

atgccggtac gcacatggga cgctaaaact ggtaaagttg gtaagttgtg gggcgaaatt 1440

aaataa 1446

<210> 62
<211> 481
<212> PRT
<213> artificial

<220>
<223> artificial construct

<400> 62

Met Arg Gly Ser His His His His His His Gly Ser Gly Ser Gly Ser
1 5 10 15

Gly Ile Glu Gly Arg Met Lys Thr Leu Lys Gln Ala Glu Ser Tyr Ile
20 25 30

Lys Ser Lys Val Asn Thr Gly Thr Asp Phe Asp Gly Leu Tyr Gly Tyr
35 40 45

Gln Cys Met Asp Leu Ala Val Asp Tyr Ile Tyr His Val Thr Asp Gly
50 55 60

Lys Ile Arg Met Trp Gly Asn Ala Lys Asp Ala Ile Asn Asn Ser Phe
65 70 75 80

Gly Gly Thr Ala Thr Val Tyr Lys Asn Tyr Pro Ala Phe Arg Pro Lys
85 90 95

Tyr Gly Asp Val Val Val Trp Thr Thr Gly Asn Phe Ala Thr Tyr Gly
100 105 110

His Ile Ala Ile Val Thr Asn Pro Asp Pro Tyr Gly Asp Leu Gln Tyr
115 120 125

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Val Thr Val Leu Glu Gln Asn Trp Asn Gly Asn Gly Ile Tyr Lys Thr
    130                 135                 140

Glu Leu Ala Thr Ile Arg Thr His Asp Tyr Thr Gly Ile Thr His Phe
145                 150                 155                 160

Ile Arg Pro Asn Phe Ala Thr Glu Ser Ser Val Lys Lys Lys Asp Thr
                165                 170                 175

Lys Lys Lys Pro Lys Pro Ser Asn Arg Asp Gly Ile Asn Lys Asp Lys
            180                 185                 190

Ile Val Tyr Asp Arg Thr Asn Ile Asn Tyr Asn Glu Leu Met Lys Thr
        195                 200                 205

Leu Lys Gln Ala Glu Ser Tyr Ile Lys Ser Lys Val Asn Thr Gly Thr
    210                 215                 220

Asp Phe Asp Gly Leu Tyr Gly Tyr Gln Cys Met Asp Leu Ala Val Asp
225                 230                 235                 240

Tyr Ile Tyr His Val Thr Asp Gly Lys Ile Arg Met Trp Gly Asn Ala
                245                 250                 255

Lys Asp Ala Ile Asn Asn Ser Phe Gly Gly Thr Ala Thr Val Tyr Lys
            260                 265                 270

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

Thr Gly Asn Phe Ala Thr Tyr Gly His Ile Ala Ile Val Thr Asn Pro
    290                 295                 300

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

Asn Gly Asn Gly Ile Tyr Lys Thr Glu Leu Ala Thr Ile Arg Thr His
                325                 330                 335

Asp Tyr Thr Gly Ile Thr His Phe Ile Arg Pro Asn Phe Ala Thr Glu
            340                 345                 350

Ser Ser Val Lys Lys Lys Asp Thr Lys Lys Lys Pro Lys Pro Ser Asn
        355                 360                 365

Arg Asp Gly Ile Asn Lys Asp Lys Ile Val Tyr Asp Arg Thr Asn Ile
    370                 375                 380

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

Lys Gly Pro Trp Thr Gly His Pro Gln Ala Gly Val Leu Gln Lys Gly
420 425 430

Gln Thr Ile Lys Tyr Asp Glu Val Gln Lys Phe Asp Gly His Val Trp
435 440 445

Val Ser Trp Glu Thr Phe Glu Gly Glu Thr Val Tyr Met Pro Val Arg
450 455 460

Thr Trp Asp Ala Lys Thr Gly Lys Val Gly Lys Leu Trp Gly Glu Ile
465 470 475 480

Lys

<210> 63
<211> 1440
<212> DNA
<213> artificial

<220>
<223> artificial construct

<400> 63
atgagaggat cgcatcacca tcaccatcac ggatctggct ctggatctgg tatcgaggga 60

aggatgaaaa ccctgaaaca agcagagtcc tacattaaga gtaaagtaaa tacaggaact 120

gattttgatg gtttatatgg gtatcagtgt atggacttag cagtagatta tatttaccat 180

gtaacagatg gtaaaataag aatgtggggt aatgctaagg atgcgataaa taactctttt 240

ggtggtactg ctacggtata taaaaactac cctgctttta gacctaagta cggtgatgta 300

gtcgtatgga ctactggtaa ttttgcaact tatggtcata tcgcaatagt tactaaccct 360

gacccttatg gagaccttca atatgttaca gttcttgaac aaaactggaa cggtaacggg 420

atttataaaa ccgagttagc tacaatcaga acacacgatt acacaggaat tacacatttt 480

attagaccta actttgctac tgaatcaagt gtaaaaaaga aagatacaaa gaaaaaacca 540

aaaccatcaa atagagatgg aataaataaa gataaaattg tatatgatag aactaatatt 600

aattacaatg agctcatgaa aaccctgaaa caagcagagt cctacattaa gagtaaagta 660

aatacaggaa ctgattttga tggtttatat gggtatcagt gtatggactt agcagtagat 720

tatatttacc atgtaacaga tggtaaaata agaatgtggg gtaatgctaa ggatgcgata 780

aataactctt ttggtggtac tgctacggta tataaaaact accctgcttt tagacctaag 840

tacggtgatg tagtcgtatg gactactggt aattttgcaa cttatggtca tatcgcaata 900

gttactaacc ctgaccctta tggagacctt caatatgtta cagttcttga acaaaactgg 960

aacggtaacg ggatttataa aaccgagtta gctacaatca gaacacacga ttacacagga 1020

attacacatt ttattagacc taactttgct actgaatcaa gtgtaaaaaa gaaagataca 1080

aagaaaaaac caaaaccatc aaatagagat ggaataaata aagataaaat tgtatatgat 1140

agaactaata ttaattacaa ttggaaaaca aacaaatatg gcacactata taaatcagag 1200

tcagctagct tcacacctaa tacagatata ataacaagaa cgactggtcc atttagaagc 1260

atgccgcagt caggagtctt aaaagcaggt caaacaattc attatgatga agtgatgaaa 1320

caagacggtc atgtttgggt aggttataca ggtaacagtg gccaacgtat ttacttgcct 1380

gtaagaacat ggaataaatc tactaatact ttaggtgttc tttggggaac tataaagtaa 1440

<210> 64
<211> 479
<212> PRT
<213> artificial

<220>
<223> artificial construct

<400> 64

Met Arg Gly Ser His His His His His His Gly Ser Gly Ser Gly Ser
1 5 10 15

Gly Ile Glu Gly Arg Met Lys Thr Leu Lys Gln Ala Glu Ser Tyr Ile
20 25 30

Lys Ser Lys Val Asn Thr Gly Thr Asp Phe Asp Gly Leu Tyr Gly Tyr
35 40 45

Gln Cys Met Asp Leu Ala Val Asp Tyr Ile Tyr His Val Thr Asp Gly
50 55 60

Lys Ile Arg Met Trp Gly Asn Ala Lys Asp Ala Ile Asn Asn Ser Phe
65 70 75 80

Gly Gly Thr Ala Thr Val Tyr Lys Asn Tyr Pro Ala Phe Arg Pro Lys
85 90 95

Tyr Gly Asp Val Val Val Trp Thr Thr Gly Asn Phe Ala Thr Tyr Gly
100 105 110

His Ile Ala Ile Val Thr Asn Pro Asp Pro Tyr Gly Asp Leu Gln Tyr
115 120 125

Val Thr Val Leu Glu Gln Asn Trp Asn Gly Asn Gly Ile Tyr Lys Thr
130 135 140

Glu Leu Ala Thr Ile Arg Thr His Asp Tyr Thr Gly Ile Thr His Phe
145 150 155 160

Ile Arg Pro Asn Phe Ala Thr Glu Ser Ser Val Lys Lys Lys Asp Thr
165 170 175

```
Lys Lys Lys Pro Lys Pro Ser Asn Arg Asp Gly Ile Asn Lys Asp Lys
            180                 185                 190

Ile Val Tyr Asp Arg Thr Asn Ile Asn Tyr Asn Glu Leu Met Lys Thr
        195                 200                 205

Leu Lys Gln Ala Glu Ser Tyr Ile Lys Ser Lys Val Asn Thr Gly Thr
    210                 215                 220

Asp Phe Asp Gly Leu Tyr Gly Tyr Gln Cys Met Asp Leu Ala Val Asp
225                 230                 235                 240

Tyr Ile Tyr His Val Thr Asp Gly Lys Ile Arg Met Trp Gly Asn Ala
                245                 250                 255

Lys Asp Ala Ile Asn Asn Ser Phe Gly Gly Thr Ala Thr Val Tyr Lys
            260                 265                 270

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

Thr Gly Asn Phe Ala Thr Tyr Gly His Ile Ala Ile Val Thr Asn Pro
    290                 295                 300

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

Asn Gly Asn Gly Ile Tyr Lys Thr Glu Leu Ala Thr Ile Arg Thr His
                325                 330                 335

Asp Tyr Thr Gly Ile Thr His Phe Ile Arg Pro Asn Phe Ala Thr Glu
            340                 345                 350

Ser Ser Val Lys Lys Lys Asp Thr Lys Lys Lys Pro Lys Pro Ser Asn
        355                 360                 365

Arg Asp Gly Ile Asn Lys Asp Lys Ile Val Tyr Asp Arg Thr Asn Ile
    370                 375                 380

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

Ser Ala Ser Phe Thr Pro Asn Thr Asp Ile Ile Thr Arg Thr Thr Gly
                405                 410                 415

Pro Phe Arg Ser Met Pro Gln Ser Gly Val Leu Lys Ala Gly Gln Thr
            420                 425                 430

Ile His Tyr Asp Glu Val Met Lys Gln Asp Gly His Val Trp Val Gly
        435                 440                 445
```

Tyr Thr Gly Asn Ser Gly Gln Arg Ile Tyr Leu Pro Val Arg Thr Trp
450 455 460

Asn Lys Ser Thr Asn Thr Leu Gly Val Leu Trp Gly Thr Ile Lys
465 470 475

<210> 65
<211> 1446
<212> DNA
<213> artificial

<220>
<223> artificial construct

<400> 65
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aggatgaaaa ccctgaaaca agcagagtcc tacattaaga gtaaagtaaa tacaggaact 120

gattttgatg gtttatatgg gtatcagtgt atggacttag cagtagatta tatttaccat 180

gtaacagatg gtaaaataag aatgtggggt aatgctaagg atgcgataaa taactctttt 240

ggtggtactg ctacggtata taaaaactac cctgctttta gacctaagta cggtgatgta 300

gtcgtatgga ctactggtaa ttttgcaact tatggtcata tcgcaatagt tactaaccct 360

gacccttatg gagaccttca atatgttaca gttcttgaac aaaactggaa cggtaacggg 420

atttataaaa ccgagttagc tacaatcaga acacacgatt acacaggaat tacacatttt 480

attagaccta actttgctac tgaatcaagt gtaaaaaaga aagatacaaa gaaaaaacca 540

aaaccatcaa atagagatgg aataaataaa gataaaattg tatatgatag aactaatatt 600

aattacaatg agctcatgaa aaccctgaaa caagcagagt cctacattaa gagtaaagta 660

aatacaggaa ctgattttga tggtttatat gggtatcagt gtatggactt agcagtagat 720

tatatttacc atgtaacaga tggtaaaata agaatgtggg gtaatgctaa ggatgcgata 780

aataactctt ttggtggtac tgctacggta tataaaaact accctgcttt tagacctaag 840

tacggtgatg tagtcgtatg gactactggt aattttgcaa cttatggtca tatcgcaata 900

gttactaacc ctgaccctta tggagacctt caatatgtta cagttcttga acaaaactgg 960

aacggtaacg ggatttataa aaccgagtta gctacaatca gaacacacga ttacacagga 1020

attacacatt ttattagacc taactttgct actgaatcaa gtgtaaaaaa gaaagataca 1080

aagaaaaaac caaaaccatc aaatagagat ggaataaata aagataaaat tgtatatgat 1140

agaactaata ttaattacaa tggtaaatct gcaagtaaaa taacagttgg aagtaaagcg 1200

ccttataacc ttaaatggtc aaaaggtgct tattttaatg cgaaaatcga cggcttaggt 1260

gctacttcag ccactagata cggtgataat cgtactaact atagattcga tgttggacag 1320

gctgtatacg cgcctggaac attaatatat gtgtttgaaa ttatagatgg ttggtgtcgc 1380

atttattgga acaatcataa tgagtggata tggcatgaga gattgattgt gaaagaagtg 1440

ttttaa 1446

<210> 66
<211> 481
<212> PRT
<213> artificial

<220>
<223> artificial construct

<400> 66

Met Arg Gly Ser His His His His His His Gly Ser Gly Ser Gly Ser
1 5 10 15

Gly Ile Glu Gly Arg Met Lys Thr Leu Lys Gln Ala Glu Ser Tyr Ile
20 25 30

Lys Ser Lys Val Asn Thr Gly Thr Asp Phe Asp Gly Leu Tyr Gly Tyr
35 40 45

Gln Cys Met Asp Leu Ala Val Asp Tyr Ile Tyr His Val Thr Asp Gly
50 55 60

Lys Ile Arg Met Trp Gly Asn Ala Lys Asp Ala Ile Asn Asn Ser Phe
65 70 75 80

Gly Gly Thr Ala Thr Val Tyr Lys Asn Tyr Pro Ala Phe Arg Pro Lys
85 90 95

Tyr Gly Asp Val Val Val Trp Thr Thr Gly Asn Phe Ala Thr Tyr Gly
100 105 110

His Ile Ala Ile Val Thr Asn Pro Asp Pro Tyr Gly Asp Leu Gln Tyr
115 120 125

Val Thr Val Leu Glu Gln Asn Trp Asn Gly Asn Gly Ile Tyr Lys Thr
130 135 140

Glu Leu Ala Thr Ile Arg Thr His Asp Tyr Thr Gly Ile Thr His Phe
145 150 155 160

Ile Arg Pro Asn Phe Ala Thr Glu Ser Ser Val Lys Lys Lys Asp Thr
165 170 175

Lys Lys Lys Pro Lys Pro Ser Asn Arg Asp Gly Ile Asn Lys Asp Lys
180 185 190

Ile Val Tyr Asp Arg Thr Asn Ile Asn Tyr Asn Glu Leu Met Lys Thr
195 200 205

Leu Lys Gln Ala Glu Ser Tyr Ile Lys Ser Lys Val Asn Thr Gly Thr
210 215 220

```
Asp Phe Asp Gly Leu Tyr Gly Tyr Gln Cys Met Asp Leu Ala Val Asp
225                 230                 235                 240

Tyr Ile Tyr His Val Thr Asp Gly Lys Ile Arg Met Trp Gly Asn Ala
                245                 250                 255

Lys Asp Ala Ile Asn Asn Ser Phe Gly Gly Thr Ala Thr Val Tyr Lys
            260                 265                 270

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

Thr Gly Asn Phe Ala Thr Tyr Gly His Ile Ala Ile Val Thr Asn Pro
    290                 295                 300

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

Asn Gly Asn Gly Ile Tyr Lys Thr Glu Leu Ala Thr Ile Arg Thr His
                325                 330                 335

Asp Tyr Thr Gly Ile Thr His Phe Ile Arg Pro Asn Phe Ala Thr Glu
            340                 345                 350

Ser Ser Val Lys Lys Lys Asp Thr Lys Lys Lys Pro Lys Pro Ser Asn
        355                 360                 365

Arg Asp Gly Ile Asn Lys Asp Lys Ile Val Tyr Asp Arg Thr Asn Ile
    370                 375                 380

Asn Tyr Asn Gly Lys Ser Ala Ser Lys Ile Thr Val Gly Ser Lys Ala
385                 390                 395                 400

Pro Tyr Asn Leu Lys Trp Ser Lys Gly Ala Tyr Phe Asn Ala Lys Ile
                405                 410                 415

Asp Gly Leu Gly Ala Thr Ser Ala Thr Arg Tyr Gly Asp Asn Arg Thr
            420                 425                 430

Asn Tyr Arg Phe Asp Val Gly Gln Ala Val Tyr Ala Pro Gly Thr Leu
        435                 440                 445

Ile Tyr Val Phe Glu Ile Ile Asp Gly Trp Cys Arg Ile Tyr Trp Asn
    450                 455                 460

Asn His Asn Glu Trp Ile Trp His Glu Arg Leu Ile Val Lys Glu Val
465                 470                 475                 480

Phe
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<210> 67
<211> 1278
<212> DNA
<213> artificial

<220>
<223> artificial construct

<400> 67
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agggctgcaa cacatgaaca ttcagcacaa tggttgaata attacaaaaa aggatatggt 120

tacggtcctt atccattagg tataaatggc ggtatgcact acggagttga ttttttttatg 180

aatattggaa caccagtaaa agctatttca agcggaaaaa tagttgaagc tggttggagt 240

aattacggag gaggtaatca aataggtctt attgaaaatg atggagtgca tagacaatgg 300

tatatgcatc taagtaaata taatgttaaa gtaggagatt atgtcaaagc tggtcaaata 360

atcggttggt ctggaagcac tggttattct acagcaccac atttacactt ccaaagaatg 420

gttaattcat tttcaaattc aactgcccaa gatccaatgc ctttcttaaa gagcgcagga 480

tatggaaaag caggtggtac agtaactcca acgccgaata caggtgagct cgctgcaaca 540

catgaacatt cagcacaatg gttgaataat tacaaaaaag gatatggtta cggtccttat 600

ccattaggta taaatggcgg tatgcactac ggagttgatt tttttatgaa tattggaaca 660

ccagtaaaag ctatttcaag cggaaaaata gttgaagctg gttggagtaa ttacggagga 720

ggtaatcaaa taggtcttat tgaaaatgat ggagtgcata gacaatggta tatgcatcta 780

agtaaatata atgttaaagt aggagattat gtcaaagctg gtcaaataat cggttggtct 840

ggaagcactg gttattctac agcaccacat ttacacttcc aaagaatggt taattcattt 900

tcaaattcaa ctgcccaaga tccaatgcct ttcttaaaga gcgcaggata tggaaaagca 960

ggtggtacag taactccaac gccgaataca ggttggaaac agaataaaga tggcatttgg 1020

tataaagctg aacatgcttc gttcacagtg acagcaccag agggaattat cacaagatac 1080

aaaggtcctt ggactggtca cccacaagct ggtgtattac aaaaaggtca aacgattaaa 1140

tatgatgagg ttcaaaaatt tgacggtcat gtttgggtat cgtgggaaac gtttgagggc 1200

gaaactgtat acatgccggt acgcacatgg gacgctaaaa ctggtaaagt tggtaagttg 1260

tggggcgaaa ttaaataa 1278

<210> 68
<211> 425
<212> PRT
<213> artificial

<220>
<223> artificial construct

<400> 68

Met Arg Gly Ser His His His His His His Gly Ser Gly Ser Gly Ser
1 5 10 15

```
Gly Ile Glu Gly Arg Ala Ala Thr His Glu His Ser Ala Gln Trp Leu
            20                  25                  30

Asn Asn Tyr Lys Lys Gly Tyr Gly Tyr Gly Pro Tyr Pro Leu Gly Ile
        35                  40                  45

Asn Gly Gly Met His Tyr Gly Val Asp Phe Phe Met Asn Ile Gly Thr
    50                  55                  60

Pro Val Lys Ala Ile Ser Ser Gly Lys Ile Val Glu Ala Gly Trp Ser
65                  70                  75                  80

Asn Tyr Gly Gly Gly Asn Gln Ile Gly Leu Ile Glu Asn Asp Gly Val
                85                  90                  95

His Arg Gln Trp Tyr Met His Leu Ser Lys Tyr Asn Val Lys Val Gly
            100                 105                 110

Asp Tyr Val Lys Ala Gly Gln Ile Ile Gly Trp Ser Gly Ser Thr Gly
        115                 120                 125

Tyr Ser Thr Ala Pro His Leu His Phe Gln Arg Met Val Asn Ser Phe
    130                 135                 140

Ser Asn Ser Thr Ala Gln Asp Pro Met Pro Phe Leu Lys Ser Ala Gly
145                 150                 155                 160

Tyr Gly Lys Ala Gly Gly Thr Val Thr Pro Thr Pro Asn Thr Gly Glu
                165                 170                 175

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

Lys Gly Tyr Gly Tyr Gly Pro Tyr Pro Leu Gly Ile Asn Gly Gly Met
        195                 200                 205

His Tyr Gly Val Asp Phe Phe Met Asn Ile Gly Thr Pro Val Lys Ala
    210                 215                 220

Ile Ser Ser Gly Lys Ile Val Glu Ala Gly Trp Ser Asn Tyr Gly Gly
225                 230                 235                 240

Gly Asn Gln Ile Gly Leu Ile Glu Asn Asp Gly Val His Arg Gln Trp
                245                 250                 255

Tyr Met His Leu Ser Lys Tyr Asn Val Lys Val Gly Asp Tyr Val Lys
            260                 265                 270

Ala Gly Gln Ile Ile Gly Trp Ser Gly Ser Thr Gly Tyr Ser Thr Ala
        275                 280                 285
```

```
Pro His Leu His Phe Gln Arg Met Val Asn Ser Phe Ser Asn Ser Thr
    290                 295                 300

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

Gly Gly Thr Val Thr Pro Thr Pro Asn Thr Gly Trp Lys Gln Asn Lys
                325                 330                 335

Asp Gly Ile Trp Tyr Lys Ala Glu His Ala Ser Phe Thr Val Thr Ala
            340                 345                 350

Pro Glu Gly Ile Ile Thr Arg Tyr Lys Gly Pro Trp Thr Gly His Pro
        355                 360                 365

Gln Ala Gly Val Leu Gln Lys Gly Gln Thr Ile Lys Tyr Asp Glu Val
    370                 375                 380

Gln Lys Phe Asp Gly His Val Trp Val Ser Trp Glu Thr Phe Glu Gly
385                 390                 395                 400

Glu Thr Val Tyr Met Pro Val Arg Thr Trp Asp Ala Lys Thr Gly Lys
                405                 410                 415

Val Gly Lys Leu Trp Gly Glu Ile Lys
            420                 425
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<210> 69
<211> 1272
<212> DNA
<213> artificial

<220>
<223> artificial construct

<400> 69

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agggctgcaa cacatgaaca ttcagcacaa tggttgaata attacaaaaa aggatatggt    120

tacggtcctt atccattagg tataaatggc ggtatgcact acggagttga ttttttttatg    180

aatattggaa caccagtaaa agctatttca agcggaaaaa tagttgaagc tggttggagt    240

aattacggag gaggtaatca aataggtctt attgaaaatg atggagtgca tagacaatgg    300

tatatgcatc taagtaaata taatgttaaa gtaggagatt atgtcaaagc tggtcaaata    360

atcggttggt ctggaagcac tggttattct acagcaccac atttacactt ccaaagaatg    420

gttaattcat tttcaaattc aactgcccaa gatccaatgc ctttcttaaa gagcgcagga    480

tatggaaaag caggtggtac agtaactcca acgccgaata caggtgagct cgctgcaaca    540

catgaacatt cagcacaatg gttgaataat tacaaaaaag gatatggtta cggtccttat    600

ccattaggta taaatggcgg tatgcactac ggagttgatt tttttatgaa tattggaaca    660

ccagtaaaag ctatttcaag cggaaaaata gttgaagctg gttggagtaa ttacggagga    720
```

ggtaatcaaa taggtcttat tgaaaatgat ggagtgcata gacaatggta tatgcatcta 780

agtaaatata atgttaaagt aggagattat gtcaaagctg gtcaaataat cggttggtct 840

ggaagcactg gttattctac agcaccacat ttacacttcc aaagaatggt taattcattt 900

tcaaattcaa ctgcccaaga tccaatgcct ttcttaaaga gcgcaggata tggaaaagca 960

ggtggtacag taactccaac gccgaataca ggttggaaaa caaacaaata tggcacacta 1020

tataaatcag agtcagctag cttcacacct aatacagata taataacaag aacgactggt 1080

ccatttagaa gcatgccgca gtcaggagtc ttaaaagcag gtcaaacaat tcattatgat 1140

gaagtgatga aacaagacgg tcatgtttgg gtaggttata caggtaacag tggccaacgt 1200

atttacttgc ctgtaagaac atggaataaa tctactaata ctttaggtgt tctttgggga 1260

actataaagt aa 1272

<210> 70
<211> 423
<212> PRT
<213> artificial

<220>
<223> artificial construct

<400> 70

Met Arg Gly Ser His His His His His His Gly Ser Gly Ser Gly Ser
1 5 10 15

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

Asn Asn Tyr Lys Lys Gly Tyr Gly Tyr Gly Pro Tyr Pro Leu Gly Ile
35 40 45

Asn Gly Gly Met His Tyr Gly Val Asp Phe Phe Met Asn Ile Gly Thr
50 55 60

Pro Val Lys Ala Ile Ser Ser Gly Lys Ile Val Glu Ala Gly Trp Ser
65 70 75 80

Asn Tyr Gly Gly Gly Asn Gln Ile Gly Leu Ile Glu Asn Asp Gly Val
85 90 95

His Arg Gln Trp Tyr Met His Leu Ser Lys Tyr Asn Val Lys Val Gly
100 105 110

Asp Tyr Val Lys Ala Gly Gln Ile Ile Gly Trp Ser Gly Ser Thr Gly
115 120 125

Tyr Ser Thr Ala Pro His Leu His Phe Gln Arg Met Val Asn Ser Phe
130 135 140

```
Ser Asn Ser Thr Ala Gln Asp Pro Met Pro Phe Leu Lys Ser Ala Gly
145                 150                 155                 160

Tyr Gly Lys Ala Gly Gly Thr Val Thr Pro Thr Pro Asn Thr Gly Glu
                165                 170                 175

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

Lys Gly Tyr Gly Tyr Gly Pro Tyr Pro Leu Gly Ile Asn Gly Gly Met
        195                 200                 205

His Tyr Gly Val Asp Phe Phe Met Asn Ile Gly Thr Pro Val Lys Ala
    210                 215                 220

Ile Ser Ser Gly Lys Ile Val Glu Ala Gly Trp Ser Asn Tyr Gly Gly
225                 230                 235                 240

Gly Asn Gln Ile Gly Leu Ile Glu Asn Asp Gly Val His Arg Gln Trp
                245                 250                 255

Tyr Met His Leu Ser Lys Tyr Asn Val Lys Val Gly Asp Tyr Val Lys
            260                 265                 270

Ala Gly Gln Ile Ile Gly Trp Ser Gly Ser Thr Gly Tyr Ser Thr Ala
        275                 280                 285

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

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

Gly Gly Thr Val Thr Pro Thr Pro Asn Thr Gly Trp Lys Thr Asn Lys
                325                 330                 335

Tyr Gly Thr Leu Tyr Lys Ser Glu Ser Ala Ser Phe Thr Pro Asn Thr
            340                 345                 350

Asp Ile Ile Thr Arg Thr Thr Gly Pro Phe Arg Ser Met Pro Gln Ser
        355                 360                 365

Gly Val Leu Lys Ala Gly Gln Thr Ile His Tyr Asp Glu Val Met Lys
    370                 375                 380

Gln Asp Gly His Val Trp Val Gly Tyr Thr Gly Asn Ser Gly Gln Arg
385                 390                 395                 400

Ile Tyr Leu Pro Val Arg Thr Trp Asn Lys Ser Thr Asn Thr Leu Gly
                405                 410                 415
```

Val Leu Trp Gly Thr Ile Lys
420

<210> 71
<211> 1278
<212> DNA
<213> artificial

<220>
<223> artificial construct

<400> 71
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agggctgcaa cacatgaaca ttcagcacaa tggttgaata attacaaaaa aggatatggt 120

tacggtcctt atccattagg tataaatggc ggtatgcact acggagttga ttttttttatg 180

aatattggaa caccagtaaa agctatttca agcggaaaaa tagttgaagc tggttggagt 240

aattacggag gaggtaatca aataggtctt attgaaaatg atggagtgca tagacaatgg 300

tatatgcatc taagtaaata taatgttaaa gtaggagatt atgtcaaagc tggtcaaata 360

atcggttggt ctggaagcac tggttattct acagcaccac atttacactt ccaaagaatg 420

gttaattcat tttcaaattc aactgcccaa gatccaatgc ctttcttaaa gagcgcagga 480

tatggaaaag caggtggtac agtaactcca acgccgaata caggtgagct cgctgcaaca 540

catgaacatt cagcacaatg gttgaataat tacaaaaaag gatatggtta cggtccttat 600

ccattaggta taaatggcgg tatgcactac ggagttgatt tttttatgaa tattggaaca 660

ccagtaaaag ctatttcaag cggaaaaata gttgaagctg gttggagtaa ttacggagga 720

ggtaatcaaa taggtcttat tgaaaatgat ggagtgcata gacaatggta tatgcatcta 780

agtaaatata atgttaaagt aggagattat gtcaaagctg gtcaaataat cggttggtct 840

ggaagcactg gttattctac agcaccacat ttacacttcc aaagaatggt taattcattt 900

tcaaattcaa ctgcccaaga tccaatgcct ttcttaaaga gcgcaggata tggaaaagca 960

ggtggtacag taactccaac gccgaataca ggtggtaaat ctgcaagtaa aataacagtt 1020

ggaagtaaag cgccttataa ccttaaatgg tcaaaaggtg cttattttaa tgcgaaaatc 1080

gacggcttag gtgctacttc agccactaga tacggtgata atcgtactaa ctatagattc 1140

gatgttggac aggctgtata cgcgcctgga acattaatat atgtgtttga aattatagat 1200

ggttggtgtc gcatttattg gaacaatcat aatgagtgga tatggcatga gagattgatt 1260

gtgaaagaag tgttttaa 1278

<210> 72
<211> 425
<212> PRT
<213> artificial

<220>
<223> artificial construct

<400> 72

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Met Arg Gly Ser His His His His His His Gly Ser Gly Ser Gly Ser
1               5                  10                  15

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

Asn Asn Tyr Lys Lys Gly Tyr Gly Tyr Gly Pro Tyr Pro Leu Gly Ile
        35                  40                  45

Asn Gly Gly Met His Tyr Gly Val Asp Phe Phe Met Asn Ile Gly Thr
    50                  55                  60

Pro Val Lys Ala Ile Ser Ser Gly Lys Ile Val Glu Ala Gly Trp Ser
65                  70                  75                  80

Asn Tyr Gly Gly Gly Asn Gln Ile Gly Leu Ile Glu Asn Asp Gly Val
                85                  90                  95

His Arg Gln Trp Tyr Met His Leu Ser Lys Tyr Asn Val Lys Val Gly
            100                 105                 110

Asp Tyr Val Lys Ala Gly Gln Ile Ile Gly Trp Ser Gly Ser Thr Gly
        115                 120                 125

Tyr Ser Thr Ala Pro His Leu His Phe Gln Arg Met Val Asn Ser Phe
    130                 135                 140

Ser Asn Ser Thr Ala Gln Asp Pro Met Pro Phe Leu Lys Ser Ala Gly
145                 150                 155                 160

Tyr Gly Lys Ala Gly Gly Thr Val Thr Pro Thr Pro Asn Thr Gly Glu
                165                 170                 175

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

Lys Gly Tyr Gly Tyr Gly Pro Tyr Pro Leu Gly Ile Asn Gly Gly Met
        195                 200                 205

His Tyr Gly Val Asp Phe Phe Met Asn Ile Gly Thr Pro Val Lys Ala
    210                 215                 220

Ile Ser Ser Gly Lys Ile Val Glu Ala Gly Trp Ser Asn Tyr Gly Gly
225                 230                 235                 240

Gly Asn Gln Ile Gly Leu Ile Glu Asn Asp Gly Val His Arg Gln Trp
                245                 250                 255

Tyr Met His Leu Ser Lys Tyr Asn Val Lys Val Gly Asp Tyr Val Lys
            260                 265                 270
```

```
Ala Gly Gln Ile Ile Gly Trp Ser Gly Ser Thr Gly Tyr Ser Thr Ala
        275                 280                 285


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


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


Gly Gly Thr Val Thr Pro Thr Pro Asn Thr Gly Gly Lys Ser Ala Ser
                325                 330                 335


Lys Ile Thr Val Gly Ser Lys Ala Pro Tyr Asn Leu Lys Trp Ser Lys
            340                 345                 350


Gly Ala Tyr Phe Asn Ala Lys Ile Asp Gly Leu Gly Ala Thr Ser Ala
        355                 360                 365


Thr Arg Tyr Gly Asp Asn Arg Thr Asn Tyr Arg Phe Asp Val Gly Gln
    370                 375                 380


Ala Val Tyr Ala Pro Gly Thr Leu Ile Tyr Val Phe Glu Ile Ile Asp
385                 390                 395                 400


Gly Trp Cys Arg Ile Tyr Trp Asn Asn His Asn Glu Trp Ile Trp His
                405                 410                 415


Glu Arg Leu Ile Val Lys Glu Val Phe
            420                 425


<210>  73
<211>  63
<212>  DNA
<213>  artificial

<220>
<223>  artificial his-tag

<400>  73
atgagaggat cgcatcacca tcaccatcac ggatctggct ctggatctgg tatcgaggga     60

agg                                                                   63


<210>  74
<211>  21
<212>  PRT
<213>  artificial

<220>
<223>  artificial Hist-tag

<400>  74

Met Arg Gly Ser His His His His His His Gly Ser Gly Ser Gly Ser
1               5                   10                  15
```

Gly Ile Glu Gly Arg
            20

<210> 75
<211> 741
<212> DNA
<213> Staphylococcus simulans

<400> 75
gctgcaacac atgaacattc agcacaatgg ttgaataatt acaaaaaagg atatggttac 60

ggtccttatc cattaggtat aaatggcggt atgcactacg gagttgattt ttttatgaat 120

attggaacac cagtaaaagc tatttcaagc ggaaaaatag ttgaagctgg ttggagtaat 180

tacggaggag gtaatcaaat aggtcttatt gaaaatgatg gagtgcatag acaatggtat 240

atgcatctaa gtaaatataa tgttaaagta ggagattatg tcaaagctgg tcaaataatc 300

ggttggtctg gaagcactgg ttattctaca gcaccacatt tacacttcca aagaatggtt 360

aattcatttt caaattcaac tgcccaagat ccaatgcctt tcttaaagag cgcaggatat 420

ggaaaagcag gtggtacagt aactccaacg ccgaatacag gttggaaaac aaacaaatat 480

ggcacactat ataaatcaga gtcagctagc ttcacaccta atacagatat aataacaaga 540

acgactggtc catttagaag catgccgcag tcaggagtct taaaagcagg tcaaacaatt 600

cattatgatg aagtgatgaa acaagacggt catgtttggg taggttatac aggtaacagt 660

ggccaacgta tttacttgcc tgtaagaaca tggaataaat ctactaatac tttaggtgtt 720

ctttggggaa ctataaagtg a 741

<210> 76
<211> 246
<212> PRT
<213> Staphylococcus simulans

<400> 76

Ala Ala Thr His Glu His Ser Ala Gln Trp Leu Asn Asn Tyr Lys Lys
1   5   10   15

Gly Tyr Gly Tyr Gly Pro Tyr Pro Leu Gly Ile Asn Gly Gly Met His
            20   25   30

Tyr Gly Val Asp Phe Phe Met Asn Ile Gly Thr Pro Val Lys Ala Ile
        35   40   45

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

Asn Gln Ile Gly Leu Ile Glu Asn Asp Gly Val His Arg Gln Trp Tyr
65   70   75   80

Met His Leu Ser Lys Tyr Asn Val Lys Val Gly Asp Tyr Val Lys Ala
                85   90   95

Gly Gln Ile Ile Gly Trp Ser Gly Ser Thr Gly Tyr Ser Thr Ala Pro
100 105 110

His Leu His Phe Gln Arg Met Val Asn Ser Phe Ser Asn Ser Thr Ala
115 120 125

Gln Asp Pro Met Pro Phe Leu Lys Ser Ala Gly Tyr Gly Lys Ala Gly
130 135 140

Gly Thr Val Thr Pro Thr Pro Asn Thr Gly Trp Lys Thr Asn Lys Tyr
145 150 155 160

Gly Thr Leu Tyr Lys Ser Glu Ser Ala Ser Phe Thr Pro Asn Thr Asp
165 170 175

Ile Ile Thr Arg Thr Thr Gly Pro Phe Arg Ser Met Pro Gln Ser Gly
180 185 190

Val Leu Lys Ala Gly Gln Thr Ile His Tyr Asp Glu Val Met Lys Gln
195 200 205

Asp Gly His Val Trp Val Gly Tyr Thr Gly Asn Ser Gly Gln Arg Ile
210 215 220

Tyr Leu Pro Val Arg Thr Trp Asn Lys Ser Thr Asn Thr Leu Gly Val
225 230 235 240

Leu Trp Gly Thr Ile Lys
245

<210> 77
<211> 2019
<212> DNA
<213> artificial

<220>
<223> artificial construct

<400> 77
atgagaggat cgcatcacca tcaccatcac ggatccatgc aagcaaaatt aactaaaaat 60

gagtttatag agtggttgaa aacttctgag ggaaaacaat tcaatgtgga cttatggtat 120

ggatttcaat gctttgatta tgccaatgct ggttggaaag ttttgtttgg attacttcta 180

aaaggtttag gtgcaaaaga tattccgttc gctaacaact tcgacggatt agctactgta 240

taccaaaata caccggactt cttagcacaa cctggcgaca tggtggtatt cggtagcaac 300

tacggtgctg gatatggtca cgttgcatgg gtaattgaag caactttaga ttacatcatt 360

gtatatgagc agaattggct aggcggtggc tggactgacg gaatcgaaca acccggctgg 420

ggttgggaaa aagttacaag acgacaacat gcttatgatt tccctatgtg gtttatccgt 480

ccgaatttta aaagtgagac agcgccacga tcagttcaat ctcctacaca agcacctaaa 540

aaagaaacag ctggatccat gctaactgct attgactatc ttacgaaaaa aggttggaaa 600

atatcatctg accctcgcac ttacgatggt taccctaaaa actacggcta cagaaattac 660

catgaaaacg gcattaatta tgatgagttt tgtggtggtt atcatagagc ttttgatgtt 720

tacagtaacg aaactaacga cgtgcctgct gttactagcg gaacagttat tgaagcaaac 780

gattacggta attttggtgg tacattcgtt attagagacg ctaacgataa cgattggata 840

tatgggcatc tacaacgtgg ctcaatgcga tttgttgtag gcgacaaagt caatcaaggt 900

gacattattg gtttacaagg taatagcaac tattacgaca atcctatgag tgtacattta 960

catttacaat tacgccctaa agacgcaaag aaagatgaaa aatcacaagt atgtagtggt 1020

ttggctatgg aaaaatatga cattacaaat ttaaatgcta aacaagataa atcaaagaat 1080

gggagcgtga aagagttgaa acatatctat tcaaaccata ttaaaggtaa caagattaca 1140

gcaccaaaac ctagtattca aggtgtggtc atccacaatg attatggtag tatgacacct 1200

agtcaatact taccatggtt atatgcacgt gagaataacg gtacacacgt taacggttgg 1260

gctagtgttt atgcaaatag aaacgaagtg ctttggtatc atccgacaga ctacgtagag 1320

tggcattgtg gtaatcaatg ggcaaatgct aacttaatcg gatttgaagt gtgtgagtcg 1380

tatcctggta gaatctcgga caaattattc ttagaaaatg aagaagcgac attgaaagta 1440

gctgcggatg tgatgaagtc gtacggatta ccagttaatc gcaacactgt acgtctgcat 1500

aacgaattct tcggaacttc ttgtccacat cgttcgtggg acttgcatgt tggcaaaggt 1560

gagccttaca caactactaa tattaataaa atgaaagact acttcatcaa acgcatcaaa 1620

cattattatg acggtggaaa gctagaagta agcaaagcag caactatcaa acaatctgac 1680

gttaagcaag aagttaaaaa gcaagaagca aaacaaattg tgaaagcaac agattggaaa 1740

cagaataaag atggcatttg gtataaagct gaacatgctt cgttcacagt gacagcacca 1800

gagggaatta tcacaagata caaaggtcct tggactggtc acccacaagc tggtgtatta 1860

caaaaaggtc aaacgattaa atatgatgag gttcaaaaat ttgacggtca tgtttgggta 1920

tcgtgggaaa cgtttgaggg cgaaactgta tacatgccgg tacgcacatg ggacgctaaa 1980

actggtaaag ttggtaagtt gtggggcgaa attaaataa 2019

<210> 78
<211> 672
<212> PRT
<213> artificial

<220>
<223> artificial construct

<400> 78

Met Arg Gly Ser His His His His His His Gly Ser Met Gln Ala Lys
1 5 10 15

Leu Thr Lys Asn Glu Phe Ile Glu Trp Leu Lys Thr Ser Glu Gly Lys
20 25 30

```
Gln Phe Asn Val Asp Leu Trp Tyr Gly Phe Gln Cys Phe Asp Tyr Ala
        35                  40                  45

Asn Ala Gly Trp Lys Val Leu Phe Gly Leu Leu Leu Lys Gly Leu Gly
    50                  55                  60

Ala Lys Asp Ile Pro Phe Ala Asn Asn Phe Asp Gly Leu Ala Thr Val
65                  70                  75                  80

Tyr Gln Asn Thr Pro Asp Phe Leu Ala Gln Pro Gly Asp Met Val Val
                85                  90                  95

Phe Gly Ser Asn Tyr Gly Ala Gly Tyr Gly His Val Ala Trp Val Ile
            100                 105                 110

Glu Ala Thr Leu Asp Tyr Ile Ile Val Tyr Glu Gln Asn Trp Leu Gly
        115                 120                 125

Gly Gly Trp Thr Asp Gly Ile Glu Gln Pro Gly Trp Gly Trp Glu Lys
    130                 135                 140

Val Thr Arg Arg Gln His Ala Tyr Asp Phe Pro Met Trp Phe Ile Arg
145                 150                 155                 160

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

Gln Ala Pro Lys Lys Glu Thr Ala Gly Ser Met Leu Thr Ala Ile Asp
            180                 185                 190

Tyr Leu Thr Lys Lys Gly Trp Lys Ile Ser Ser Asp Pro Arg Thr Tyr
        195                 200                 205

Asp Gly Tyr Pro Lys Asn Tyr Gly Tyr Arg Asn Tyr His Glu Asn Gly
    210                 215                 220

Ile Asn Tyr Asp Glu Phe Cys Gly Gly Tyr His Arg Ala Phe Asp Val
225                 230                 235                 240

Tyr Ser Asn Glu Thr Asn Asp Val Pro Ala Val Thr Ser Gly Thr Val
                245                 250                 255

Ile Glu Ala Asn Asp Tyr Gly Asn Phe Gly Gly Thr Phe Val Ile Arg
            260                 265                 270

Asp Ala Asn Asp Asn Asp Trp Ile Tyr Gly His Leu Gln Arg Gly Ser
        275                 280                 285

Met Arg Phe Val Val Gly Asp Lys Val Asn Gln Gly Asp Ile Ile Gly
    290                 295                 300
```

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Leu Gln Gly Asn Ser Asn Tyr Tyr Asp Asn Pro Met Ser Val His Leu
305                 310                 315                 320

His Leu Gln Leu Arg Pro Lys Asp Ala Lys Lys Asp Glu Lys Ser Gln
                325                 330                 335

Val Cys Ser Gly Leu Ala Met Glu Lys Tyr Asp Ile Thr Asn Leu Asn
            340                 345                 350

Ala Lys Gln Asp Lys Ser Lys Asn Gly Ser Val Lys Glu Leu Lys His
        355                 360                 365

Ile Tyr Ser Asn His Ile Lys Gly Asn Lys Ile Thr Ala Pro Lys Pro
    370                 375                 380

Ser Ile Gln Gly Val Val Ile His Asn Asp Tyr Gly Ser Met Thr Pro
385                 390                 395                 400

Ser Gln Tyr Leu Pro Trp Leu Tyr Ala Arg Glu Asn Asn Gly Thr His
                405                 410                 415

Val Asn Gly Trp Ala Ser Val Tyr Ala Asn Arg Asn Glu Val Leu Trp
            420                 425                 430

Tyr His Pro Thr Asp Tyr Val Glu Trp His Cys Gly Asn Gln Trp Ala
        435                 440                 445

Asn Ala Asn Leu Ile Gly Phe Glu Val Cys Glu Ser Tyr Pro Gly Arg
    450                 455                 460

Ile Ser Asp Lys Leu Phe Leu Glu Asn Glu Glu Ala Thr Leu Lys Val
465                 470                 475                 480

Ala Ala Asp Val Met Lys Ser Tyr Gly Leu Pro Val Asn Arg Asn Thr
                485                 490                 495

Val Arg Leu His Asn Glu Phe Phe Gly Thr Ser Cys Pro His Arg Ser
            500                 505                 510

Trp Asp Leu His Val Gly Lys Gly Glu Pro Tyr Thr Thr Thr Asn Ile
        515                 520                 525

Asn Lys Met Lys Asp Tyr Phe Ile Lys Arg Ile Lys His Tyr Tyr Asp
    530                 535                 540

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

Val Lys Gln Glu Val Lys Lys Gln Glu Ala Lys Gln Ile Val Lys Ala
                565                 570                 575
```

Thr Asp Trp Lys Gln Asn Lys Asp Gly Ile Trp Tyr Lys Ala Glu His
580 585 590

Ala Ser Phe Thr Val Thr Ala Pro Glu Gly Ile Ile Thr Arg Tyr Lys
595 600 605

Gly Pro Trp Thr Gly His Pro Gln Ala Gly Val Leu Gln Lys Gly Gln
610 615 620

Thr Ile Lys Tyr Asp Glu Val Gln Lys Phe Asp Gly His Val Trp Val
625 630 635 640

Ser Trp Glu Thr Phe Glu Gly Glu Thr Val Tyr Met Pro Val Arg Thr
645 650 655

Trp Asp Ala Lys Thr Gly Lys Val Gly Lys Leu Trp Gly Glu Ile Lys
660 665 670

<210> 79
<211> 2145
<212> DNA
<213> artificial

<220>
<223> artificial construct

<400> 79
atgagaggat cgcatcacca tcaccatcac ggatccaagc cacaacctaa agcagtagaa 60

cttaaaatca tcaaagatgt ggttaaaggt tatgacctac ctaagcgtgg tagtaaccct 120

aaaggtatag ttatacacaa cgacgcaggg agcaaagggg cgactgctga agcatatcgt 180

aacggattag taaatgcacc tttatcaaga ttagaagcgg gcattgcgca tagttacgta 240

tcaggcaaca cagtttggca agccttagat gaatcacaag taggttggca taccgctaat 300

caaataggta ataaatatta ttacggtatt gaagtatgtc aatcaatggg cgcagataac 360

gcgacattct taaaaaatga acaggcaact ttccaagaat gcgctagatt gttgaaaaaa 420

tggggattac cagcaaacag aaatacaatc agattgcaca atgaatttac ttcaacatca 480

tgccctcata gaagttcggt tttacacact ggttttgacc cagtaactcg cggtctattg 540

ccagaagaca agcggttgca acttaaagac tactttatca agcagattag ggcgtacatg 600

gatggtaaaa taccggttgc cactgtctct aatgagtcaa gcgcttcaag taatacagtt 660

aaaccagttg caagtgcagg atccatgcta actgctattg actatcttac gaaaaaaggt 720

tggaaaatat catctgaccc tcgcacttac gatggttacc ctaaaaacta cggctacaga 780

aattaccatg aaaacggcat taattatgat gagttttgtg gtggttatca tagagctttt 840

gatgtttaca gtaacgaaac taacgacgtg cctgctgtta ctagcggaac agttattgaa 900

gcaaacgatt acggtaattt tggtggtaca ttcgttatta gagacgctaa cgataacgat 960

tggatatatg ggcatctaca acgtggctca atgcgatttg ttgtaggcga caaagtcaat 1020

caaggtgaca ttattggttt acaaggtaat agcaactatt acgacaatcc tatgagtgta 1080

catttacatt tacaattacg ccctaaagac gcaaagaaag atgaaaaatc acaagtatgt 1140

agtggtttgg ctatggaaaa atatgacatt acaaatttaa atgctaaaca agataaatca 1200

aagaatggga gcgtgaaaga gttgaaacat atctattcaa accatattaa aggtaacaag 1260

attacagcac caaaacctag tattcaaggt gtggtcatcc acaatgatta tggtagtatg 1320

acacctagtc aatacttacc atggttatat gcacgtgaga ataacggtac acacgttaac 1380

ggttgggcta gtgtttatgc aaatagaaac gaagtgcttt ggtatcatcc gacagactac 1440

gtagagtggc attgtggtaa tcaatgggca aatgctaact taatcggatt tgaagtgtgt 1500

gagtcgtatc ctggtagaat ctcggacaaa ttattcttag aaaatgaaga agcgacattg 1560

aaagtagctg cggatgtgat gaagtcgtac ggattaccag ttaatcgcaa cactgtacgt 1620

ctgcataacg aattcttcgg aacttcttgt ccacatcgtt cgtgggactt gcatgttggc 1680

aaaggtgagc cttacacaac tactaatatt aataaaatga aagactactt catcaaacgc 1740

atcaaacatt attatgacgg tggaaagcta gaagtaagca aagcagcaac tatcaaacaa 1800

tctgacgtta agcaagaagt taaaaagcaa gaagcaaaac aaattgtgaa agcaacagat 1860

tggaaacaga ataaagatgg catttggtat aaagctgaac atgcttcgtt cacagtgaca 1920

gcaccagagg gaattatcac aagatacaaa ggtccttgga ctggtcaccc acaagctggt 1980

gtattacaaa aaggtcaaac gattaaatat gatgaggttc aaaaatttga cggtcatgtt 2040

tgggtatcgt gggaaacgtt tgagggcgaa actgtataca tgccggtacg cacatgggac 2100

gctaaaactg gtaaagttgg taagttgtgg ggcgaaatta aataa 2145

<210> 80
<211> 714
<212> PRT
<213> artificial

<220>
<223> artificial construct

<400> 80

Met Arg Gly Ser His His His His His His Gly Ser Lys Pro Gln Pro
1 5 10 15

Lys Ala Val Glu Leu Lys Ile Ile Lys Asp Val Val Lys Gly Tyr Asp
20 25 30

Leu Pro Lys Arg Gly Ser Asn Pro Lys Gly Ile Val Ile His Asn Asp
35 40 45

Ala Gly Ser Lys Gly Ala Thr Ala Glu Ala Tyr Arg Asn Gly Leu Val
50 55 60

Asn Ala Pro Leu Ser Arg Leu Glu Ala Gly Ile Ala His Ser Tyr Val
65 70 75 80

```
Ser Gly Asn Thr Val Trp Gln Ala Leu Asp Glu Ser Gln Val Gly Trp
                85                  90                  95

His Thr Ala Asn Gln Ile Gly Asn Lys Tyr Tyr Tyr Gly Ile Glu Val
            100                 105                 110

Cys Gln Ser Met Gly Ala Asp Asn Ala Thr Phe Leu Lys Asn Glu Gln
        115                 120                 125

Ala Thr Phe Gln Glu Cys Ala Arg Leu Leu Lys Lys Trp Gly Leu Pro
    130                 135                 140

Ala Asn Arg Asn Thr Ile Arg Leu His Asn Glu Phe Thr Ser Thr Ser
145                 150                 155                 160

Cys Pro His Arg Ser Ser Val Leu His Thr Gly Phe Asp Pro Val Thr
                165                 170                 175

Arg Gly Leu Leu Pro Glu Asp Lys Arg Leu Gln Leu Lys Asp Tyr Phe
            180                 185                 190

Ile Lys Gln Ile Arg Ala Tyr Met Asp Gly Lys Ile Pro Val Ala Thr
        195                 200                 205

Val Ser Asn Glu Ser Ser Ala Ser Ser Asn Thr Val Lys Pro Val Ala
    210                 215                 220

Ser Ala Gly Ser Met Leu Thr Ala Ile Asp Tyr Leu Thr Lys Lys Gly
225                 230                 235                 240

Trp Lys Ile Ser Ser Asp Pro Arg Thr Tyr Asp Gly Tyr Pro Lys Asn
                245                 250                 255

Tyr Gly Tyr Arg Asn Tyr His Glu Asn Gly Ile Asn Tyr Asp Glu Phe
            260                 265                 270

Cys Gly Gly Tyr His Arg Ala Phe Asp Val Tyr Ser Asn Glu Thr Asn
        275                 280                 285

Asp Val Pro Ala Val Thr Ser Gly Thr Val Ile Glu Ala Asn Asp Tyr
    290                 295                 300

Gly Asn Phe Gly Gly Thr Phe Val Ile Arg Asp Ala Asn Asp Asn Asp
305                 310                 315                 320

Trp Ile Tyr Gly His Leu Gln Arg Gly Ser Met Arg Phe Val Val Gly
                325                 330                 335

Asp Lys Val Asn Gln Gly Asp Ile Ile Gly Leu Gln Gly Asn Ser Asn
            340                 345                 350
```

```
Tyr Tyr Asp Asn Pro Met Ser Val His Leu His Leu Gln Leu Arg Pro
        355                 360                 365

Lys Asp Ala Lys Lys Asp Glu Lys Ser Gln Val Cys Ser Gly Leu Ala
    370                 375                 380

Met Glu Lys Tyr Asp Ile Thr Asn Leu Asn Ala Lys Gln Asp Lys Ser
385                 390                 395                 400

Lys Asn Gly Ser Val Lys Glu Leu Lys His Ile Tyr Ser Asn His Ile
                405                 410                 415

Lys Gly Asn Lys Ile Thr Ala Pro Lys Pro Ser Ile Gln Gly Val Val
            420                 425                 430

Ile His Asn Asp Tyr Gly Ser Met Thr Pro Ser Gln Tyr Leu Pro Trp
        435                 440                 445

Leu Tyr Ala Arg Glu Asn Asn Gly Thr His Val Asn Gly Trp Ala Ser
    450                 455                 460

Val Tyr Ala Asn Arg Asn Glu Val Leu Trp Tyr His Pro Thr Asp Tyr
465                 470                 475                 480

Val Glu Trp His Cys Gly Asn Gln Trp Ala Asn Ala Asn Leu Ile Gly
                485                 490                 495

Phe Glu Val Cys Glu Ser Tyr Pro Gly Arg Ile Ser Asp Lys Leu Phe
            500                 505                 510

Leu Glu Asn Glu Glu Ala Thr Leu Lys Val Ala Ala Asp Val Met Lys
        515                 520                 525

Ser Tyr Gly Leu Pro Val Asn Arg Asn Thr Val Arg Leu His Asn Glu
    530                 535                 540

Phe Phe Gly Thr Ser Cys Pro His Arg Ser Trp Asp Leu His Val Gly
545                 550                 555                 560

Lys Gly Glu Pro Tyr Thr Thr Thr Asn Ile Asn Lys Met Lys Asp Tyr
                565                 570                 575

Phe Ile Lys Arg Ile Lys His Tyr Tyr Asp Gly Gly Lys Leu Glu Val
            580                 585                 590

Ser Lys Ala Ala Thr Ile Lys Gln Ser Asp Val Lys Gln Glu Val Lys
        595                 600                 605

Lys Gln Glu Ala Lys Gln Ile Val Lys Ala Thr Asp Trp Lys Gln Asn
    610                 615                 620
```

Lys Asp Gly Ile Trp Tyr Lys Ala Glu His Ala Ser Phe Thr Val Thr
625 630 635 640

Ala Pro Glu Gly Ile Ile Thr Arg Tyr Lys Gly Pro Trp Thr Gly His
645 650 655

Pro Gln Ala Gly Val Leu Gln Lys Gly Gln Thr Ile Lys Tyr Asp Glu
660 665 670

Val Gln Lys Phe Asp Gly His Val Trp Val Ser Trp Glu Thr Phe Glu
675 680 685

Gly Glu Thr Val Tyr Met Pro Val Arg Thr Trp Asp Ala Lys Thr Gly
690 695 700

Lys Val Gly Lys Leu Trp Gly Glu Ile Lys
705 710

<210> 81
<211> 1959
<212> DNA
<213> artificial

<220>
<223> artificial construct

<400> 81
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tcctacatta agagtaaagt aaatacagga actgattttg atggtttata tgggtatcag 120

tgtatggact tagcagtaga ttatatttac catgtaacag atggtaaaat aagaatgtgg 180

ggtaatgcta aggatgcgat aaataactct tttggtggta ctgctacggt atataaaaac 240

taccctgctt ttagacctaa gtacggtgat gtagtcgtat ggactactgg taattttgca 300

acttatggtc atatcgcaat agttactaac cctgaccctt atggagacct tcaatatgtt 360

acagttcttg aacaaaactg gaacggtaac gggatttata aaaccgagtt agctacaatc 420

agaacacacg attacacagg aattacacat tttattaaag acgcaaagaa agatgaaaaa 480

tcacaagtat gtagtggttt ggctatggaa aaatatgaca ttacaaattt aaatgctaaa 540

caagataaat caaagaatgg gagcgtgaaa gagttgaaac atatctattc aaaccatatt 600

aaaggtaaca agattacagc accaaaacct agtattcaag gtgtggtcat ccacaatgat 660

tatggtagta tgacacctag tcaatactta ccatggttat atgcacgtga gaataacggt 720

acacacgtta acggttgggc tagtgtttat gcaaatagaa acgaagtgct ttggtatcat 780

ccgacagact acgtagagtg gcattgtggt aatcaatggg caaatgctaa cttaatcgga 840

tttgaagtgt gtgagtcgta tcctggtaga atctcggaca aattattctt agaaaatgaa 900

gaagcgacat tgaaagtagc tgcggatgtg atgaagtcgt acggattacc agttaatcgc 960

aacactgtac gtctgcataa cgaattcttc ggaacttctt gtccacatcg ttcgtgggac 1020

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ttcatcaaac gcatcaaaca ttattatgac ggtggaaagc tagaagtaag caaagcagca 1140

actatcaaac aatctgacgt taagcaagaa gttaaaaagc aagaagcaaa acaaattgtg 1200

aaagcaacag atgctgcaac acatgaacat tcagcacaat ggttgaataa ttacaaaaaa 1260

ggatatggtt acggtcctta tccattaggt ataaatggcg gtatgcacta cggagttgat 1320

ttttttatga atattggaac accagtaaaa gctatttcaa gcggaaaaat agttgaagct 1380

ggttggagta attacggagg aggtaatcaa ataggtctta ttgaaaatga tggagtgcat 1440

agacaatggt atatgcatct aagtaaatat aatgttaaag taggagatta tgtcaaagct 1500

ggtcaaataa tcggttggtc tggaagcact ggttattcta cagcaccaca tttacacttc 1560

caaagaatgg ttaattcatt ttcaaattca actgcccaag atccaatgcc tttcttaaag 1620

agcgcaggat atggaaaagc aggtggtaca gtaactccaa cgccgaatac aggttggaaa 1680

cagaataaag atggcatttg gtataaagct gaacatgctt cgttcacagt gacagcacca 1740

gagggaatta tcacaagata caaaggtcct tggactggtc acccacaagc tggtgtatta 1800

caaaaaggtc aaacgattaa atatgatgag gttcaaaaat ttgacggtca tgtttgggta 1860

tcgtgggaaa cgtttgaggg cgaaactgta tacatgccgg tacgcacatg ggacgctaaa 1920

actggtaaag ttggtaagtt gtggggcgaa attaaataa 1959

<210> 82
<211> 652
<212> PRT
<213> artificial

<220>
<223> artificial construct

<400> 82

Met Arg Gly Ser His His His His His His Gly Ser Met Lys Thr Leu
1 5 10 15

Lys Gln Ala Glu Ser Tyr Ile Lys Ser Lys Val Asn Thr Gly Thr Asp
20 25 30

Phe Asp Gly Leu Tyr Gly Tyr Gln Cys Met Asp Leu Ala Val Asp Tyr
35 40 45

Ile Tyr His Val Thr Asp Gly Lys Ile Arg Met Trp Gly Asn Ala Lys
50 55 60

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

Tyr Pro Ala Phe Arg Pro Lys Tyr Gly Asp Val Val Val Trp Thr Thr
85 90 95

Gly Asn Phe Ala Thr Tyr Gly His Ile Ala Ile Val Thr Asn Pro Asp
100 105 110

```
Pro Tyr Gly Asp Leu Gln Tyr Val Thr Val Leu Glu Gln Asn Trp Asn
        115                 120                 125

Gly Asn Gly Ile Tyr Lys Thr Glu Leu Ala Thr Ile Arg Thr His Asp
    130                 135                 140

Tyr Thr Gly Ile Thr His Phe Ile Lys Asp Ala Lys Lys Asp Glu Lys
145                 150                 155                 160

Ser Gln Val Cys Ser Gly Leu Ala Met Glu Lys Tyr Asp Ile Thr Asn
                165                 170                 175

Leu Asn Ala Lys Gln Asp Lys Ser Lys Asn Gly Ser Val Lys Glu Leu
            180                 185                 190

Lys His Ile Tyr Ser Asn His Ile Lys Gly Asn Lys Ile Thr Ala Pro
        195                 200                 205

Lys Pro Ser Ile Gln Gly Val Val Ile His Asn Asp Tyr Gly Ser Met
    210                 215                 220

Thr Pro Ser Gln Tyr Leu Pro Trp Leu Tyr Ala Arg Glu Asn Asn Gly
225                 230                 235                 240

Thr His Val Asn Gly Trp Ala Ser Val Tyr Ala Asn Arg Asn Glu Val
                245                 250                 255

Leu Trp Tyr His Pro Thr Asp Tyr Val Glu Trp His Cys Gly Asn Gln
            260                 265                 270

Trp Ala Asn Ala Asn Leu Ile Gly Phe Glu Val Cys Glu Ser Tyr Pro
        275                 280                 285

Gly Arg Ile Ser Asp Lys Leu Phe Leu Glu Asn Glu Glu Ala Thr Leu
    290                 295                 300

Lys Val Ala Ala Asp Val Met Lys Ser Tyr Gly Leu Pro Val Asn Arg
305                 310                 315                 320

Asn Thr Val Arg Leu His Asn Glu Phe Phe Gly Thr Ser Cys Pro His
                325                 330                 335

Arg Ser Trp Asp Leu His Val Gly Lys Gly Glu Pro Tyr Thr Thr Thr
            340                 345                 350

Asn Ile Asn Lys Met Lys Asp Tyr Phe Ile Lys Arg Ile Lys His Tyr
        355                 360                 365

Tyr Asp Gly Gly Lys Leu Glu Val Ser Lys Ala Ala Thr Ile Lys Gln
    370                 375                 380
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Ser Asp Val Lys Gln Glu Val Lys Lys Gln Glu Ala Lys Gln Ile Val
385                 390                 395                 400

Lys Ala Thr Asp Ala Ala Thr His Glu His Ser Ala Gln Trp Leu Asn
                405                 410                 415

Asn Tyr Lys Lys Gly Tyr Gly Tyr Gly Pro Tyr Pro Leu Gly Ile Asn
            420                 425                 430

Gly Gly Met His Tyr Gly Val Asp Phe Phe Met Asn Ile Gly Thr Pro
        435                 440                 445

Val Lys Ala Ile Ser Ser Gly Lys Ile Val Glu Ala Gly Trp Ser Asn
    450                 455                 460

Tyr Gly Gly Gly Asn Gln Ile Gly Leu Ile Glu Asn Asp Gly Val His
465                 470                 475                 480

Arg Gln Trp Tyr Met His Leu Ser Lys Tyr Asn Val Lys Val Gly Asp
                485                 490                 495

Tyr Val Lys Ala Gly Gln Ile Ile Gly Trp Ser Gly Ser Thr Gly Tyr
            500                 505                 510

Ser Thr Ala Pro His Leu His Phe Gln Arg Met Val Asn Ser Phe Ser
        515                 520                 525

Asn Ser Thr Ala Gln Asp Pro Met Pro Phe Leu Lys Ser Ala Gly Tyr
    530                 535                 540

Gly Lys Ala Gly Gly Thr Val Thr Pro Thr Pro Asn Thr Gly Trp Lys
545                 550                 555                 560

Gln Asn Lys Asp Gly Ile Trp Tyr Lys Ala Glu His Ala Ser Phe Thr
                565                 570                 575

Val Thr Ala Pro Glu Gly Ile Ile Thr Arg Tyr Lys Gly Pro Trp Thr
            580                 585                 590

Gly His Pro Gln Ala Gly Val Leu Gln Lys Gly Gln Thr Ile Lys Tyr
        595                 600                 605

Asp Glu Val Gln Lys Phe Asp Gly His Val Trp Val Ser Trp Glu Thr
    610                 615                 620

Phe Glu Gly Glu Thr Val Tyr Met Pro Val Arg Thr Trp Asp Ala Lys
625                 630                 635                 640

Thr Gly Lys Val Gly Lys Leu Trp Gly Glu Ile Lys
                645                 650
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<210> 83
<211> 1554
<212> DNA
<213> artificial

<220>
<223> artificial construct

<400> 83
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caatggttga ataattacaa aaaaggatat ggttacggtc cttatccatt aggtataaat 120

ggcggtatgc actacggagt tgatttttt atgaatattg gaacaccagt aaaagctatt 180

tcaagcggaa aaatagttga agctggttgg agtaattacg gaggaggtaa tcaaataggt 240

cttattgaaa atgatggagt gcatagacaa tggtatatgc atctaagtaa atataatgtt 300

aaagtaggag attatgtcaa agctggtcaa ataatcggtt ggtctggaag cactggttat 360

tctacagcac cacatttaca cttccaaaga atggttaatt cattttcaaa ttcaactgcc 420

caagatccaa tgcctttctt aaagagcgca ggatatggaa aagcaggtgg tacagtaact 480

ccaacgccga atacaggtga gctcttacgc cctaaagacg caaagaaaga tgaaaaatca 540

caagtatgta gtggtttggc tatggaaaaa tatgacatta caaatttaaa tgctaaacaa 600

gataaatcaa agaatgggag cgtgaaagag ttgaaacata tctattcaaa ccatattaaa 660

ggtaacaaga ttacagcacc aaaacctagt attcaaggtg tggtcatcca caatgattat 720

ggtagtatga cacctagtca atacttacca tggttatatg cacgtgagaa taacggtaca 780

cacgttaacg gttgggctag tgtttatgca aatagaaacg aagtgctttg gtatcatccg 840

acagactacg tagagtggca ttgtggtaat caatgggcaa atgctaactt aatcggattt 900

gaagtgtgtg agtcgtatcc tggtagaatc tcggacaaat tattcttaga aaatgaagaa 960

gcgacattga aagtagctgc ggatgtgatg aagtcgtacg gattaccagt taatcgcaac 1020

actgtacgtc tgcataacga attcttcgga acttcttgtc cacatcgttc gtgggacttg 1080

catgttggca aaggtgagcc ttacacaact actaatatta ataaaatgaa agactacttc 1140

atcaaacgca tcaaacatta ttatgacggt ggaaagctag aagtaagcaa agcagcaact 1200

atcaaacaat ctgacgttaa gcaagaagtt aaaaagcaag aagcaaaaca aattgtgaaa 1260

gcaacagatt ggaaacagaa taaagatggc atttggtata aagctgaaca tgcttcgttc 1320

acagtgacag caccagaggg aattatcaca agatacaaag gtccttggac tggtcaccca 1380

caagctggtg tattacaaaa aggtcaaacg attaaatatg atgaggttca aaaatttgac 1440

ggtcatgttt gggtatcgtg ggaaacgttt gagggcgaaa ctgtatacat gccggtacgc 1500

acatgggacg ctaaaactgg taaagttggt aagttgtggg gcgaaattaa ataa 1554

<210> 84
<211> 517
<212> PRT
<213> artificial

<220>
<223> artificial construct

<400> 84

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Met Arg Gly Ser His His His His His His Gly Ser Ala Ala Thr His
1               5                  10                  15

Glu His Ser Ala Gln Trp Leu Asn Asn Tyr Lys Lys Gly Tyr Gly Tyr
            20                  25                  30

Gly Pro Tyr Pro Leu Gly Ile Asn Gly Gly Met His Tyr Gly Val Asp
        35                  40                  45

Phe Phe Met Asn Ile Gly Thr Pro Val Lys Ala Ile Ser Ser Gly Lys
    50                  55                  60

Ile Val Glu Ala Gly Trp Ser Asn Tyr Gly Gly Gly Asn Gln Ile Gly
65                  70                  75                  80

Leu Ile Glu Asn Asp Gly Val His Arg Gln Trp Tyr Met His Leu Ser
                85                  90                  95

Lys Tyr Asn Val Lys Val Gly Asp Tyr Val Lys Ala Gly Gln Ile Ile
            100                 105                 110

Gly Trp Ser Gly Ser Thr Gly Tyr Ser Thr Ala Pro His Leu His Phe
        115                 120                 125

Gln Arg Met Val Asn Ser Phe Ser Asn Ser Thr Ala Gln Asp Pro Met
    130                 135                 140

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

Pro Thr Pro Asn Thr Gly Glu Leu Leu Arg Pro Lys Asp Ala Lys Lys
                165                 170                 175

Asp Glu Lys Ser Gln Val Cys Ser Gly Leu Ala Met Glu Lys Tyr Asp
            180                 185                 190

Ile Thr Asn Leu Asn Ala Lys Gln Asp Lys Ser Lys Asn Gly Ser Val
        195                 200                 205

Lys Glu Leu Lys His Ile Tyr Ser Asn His Ile Lys Gly Asn Lys Ile
    210                 215                 220

Thr Ala Pro Lys Pro Ser Ile Gln Gly Val Val Ile His Asn Asp Tyr
225                 230                 235                 240

Gly Ser Met Thr Pro Ser Gln Tyr Leu Pro Trp Leu Tyr Ala Arg Glu
                245                 250                 255
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Asn Asn Gly Thr His Val Asn Gly Trp Ala Ser Val Tyr Ala Asn Arg
            260                 265                 270

Asn Glu Val Leu Trp Tyr His Pro Thr Asp Tyr Val Glu Trp His Cys
        275                 280                 285

Gly Asn Gln Trp Ala Asn Ala Asn Leu Ile Gly Phe Glu Val Cys Glu
    290                 295                 300

Ser Tyr Pro Gly Arg Ile Ser Asp Lys Leu Phe Leu Glu Asn Glu Glu
305                 310                 315                 320

Ala Thr Leu Lys Val Ala Ala Asp Val Met Lys Ser Tyr Gly Leu Pro
                325                 330                 335

Val Asn Arg Asn Thr Val Arg Leu His Asn Glu Phe Phe Gly Thr Ser
            340                 345                 350

Cys Pro His Arg Ser Trp Asp Leu His Val Gly Lys Gly Glu Pro Tyr
        355                 360                 365

Thr Thr Thr Asn Ile Asn Lys Met Lys Asp Tyr Phe Ile Lys Arg Ile
    370                 375                 380

Lys His Tyr Tyr Asp Gly Gly Lys Leu Glu Val Ser Lys Ala Ala Thr
385                 390                 395                 400

Ile Lys Gln Ser Asp Val Lys Gln Glu Val Lys Lys Gln Glu Ala Lys
                405                 410                 415

Gln Ile Val Lys Ala Thr Asp Trp Lys Gln Asn Lys Asp Gly Ile Trp
            420                 425                 430

Tyr Lys Ala Glu His Ala Ser Phe Thr Val Thr Ala Pro Glu Gly Ile
        435                 440                 445

Ile Thr Arg Tyr Lys Gly Pro Trp Thr Gly His Pro Gln Ala Gly Val
    450                 455                 460

Leu Gln Lys Gly Gln Thr Ile Lys Tyr Asp Glu Val Gln Lys Phe Asp
465                 470                 475                 480

Gly His Val Trp Val Ser Trp Glu Thr Phe Glu Gly Glu Thr Val Tyr
                485                 490                 495

Met Pro Val Arg Thr Trp Asp Ala Lys Thr Gly Lys Val Gly Lys Leu
            500                 505                 510

Trp Gly Glu Ile Lys
        515
```

<210> 85
<211> 1887
<212> DNA
<213> artificial

<220>
<223> artificial construct

<400> 85
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acgaaaaaag gttggaaaat atcatctgac cctcgcactt acgatggtta ccctaaaaac 120

tacggctaca gaaattacca tgaaaacggc attaattatg atgagttttg tggtggttat 180

catagagctt ttgatgttta cagtaacgaa actaacgacg tgcctgctgt tactagcgga 240

acagttattg aagcaaacga ttacggtaat tttggtggta cattcgttat tagagacgct 300

aacgataacg attggatata tgggcatcta caacgtggct caatgcgatt tgttgtaggc 360

gacaaagtca atcaaggtga cattattggt ttacaaggta atagcaacta ttacgacaat 420

cctatgagtg tacatttaca tttacaatta cgccctaaag acgcaaagaa agatgaaaaa 480

tcacaagtat gtagtggttt ggctatggaa aaatatgaca ttacaaattt aaatgctaaa 540

caagataaat caaagaatgg gagcgtgaaa gagttgaaac atatctattc aaaccatatt 600

aaaggtaaca agattacagc accaaaacct agtattcaag gtgtggtcat ccacaatgat 660

tatggtagta tgacacctag tcaatactta ccatggttat atgcacgtga gaataacggt 720

acacacgtta acggttgggc tagtgtttat gcaaatagaa acgaagtgct ttggtatcat 780

ccgacagact acgtagagtg gcattgtggt aatcaatggg caaatgctaa cttaatcgga 840

tttgaagtgt gtgagtcgta tcctggtaga atctcggaca aattattctt agaaaatgaa 900

gaagcgacat tgaaagtagc tgcggatgtg atgaagtcgt acggattacc agttaatcgc 960

aacactgtac gtctgcataa cgaattcttc ggaacttctt gtccacatcg ttcgtgggac 1020

ttgcatgttg gcaaaggtga gccttacaca actactaata ttaataaaat gaaagactac 1080

ttcatcaaac gcatcaaaca ttattatgac ggtggaaagc tagaagtaag caaagcagca 1140

actatcaaac aatctgacgt taagcaagaa gttaaaaagc aagaagcaaa acaaattgtg 1200

aaagcaacag attggaaaca gaataaagat ggcatttggt ataaagctga acatgcttcg 1260

ttcacagtga cagcaccaga gggaattatc acaagataca aaggtccttg gactggtcac 1320

ccacaagctg gtgtattaca aaaaggtcaa acgattaaat atgatgaggt tcaaaaattt 1380

gacggtcatg tttgggtatc gtgggaaacg tttgagggcg aaactgtata catgccggta 1440

cgcacatggg acgctaaaac tggtaaagtt ggtaagttgt ggggcgaaat taaagagctc 1500

ggtggaaagc tagaagtaag caaagcagca actatcaaac aatctgacgt taagcaagaa 1560

gttaaaaagc aagaagcaaa acaaattgtg aaagcaacag attggaaaca gaataaagat 1620

ggcatttggt ataaagctga acatgcttcg ttcacagtga cagcaccaga gggaattatc 1680

acaagataca aaggtccttg gactggtcac ccacaagctg gtgtattaca aaaaggtcaa 1740

acgattaaat atgatgaggt tcaaaaattt gacggtcatg tttgggtatc gtgggaaacg 1800

tttgagggcg aaactgtata catgccggta cgcacatggg acgctaaaac tggtaaagtt 1860

ggtaagttgt ggggcgaaat taaataa 1887

<210> 86
<211> 628
<212> PRT
<213> artificial

<220>
<223> artificial construct

<400> 86

Met Arg Gly Ser His His His His His His Gly Ser Met Leu Thr Ala
1 5 10 15

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

Thr Tyr Asp Gly Tyr Pro Lys Asn Tyr Gly Tyr Arg Asn Tyr His Glu
35 40 45

Asn Gly Ile Asn Tyr Asp Glu Phe Cys Gly Gly Tyr His Arg Ala Phe
50 55 60

Asp Val Tyr Ser Asn Glu Thr Asn Asp Val Pro Ala Val Thr Ser Gly
65 70 75 80

Thr Val Ile Glu Ala Asn Asp Tyr Gly Asn Phe Gly Gly Thr Phe Val
85 90 95

Ile Arg Asp Ala Asn Asp Asn Asp Trp Ile Tyr Gly His Leu Gln Arg
100 105 110

Gly Ser Met Arg Phe Val Val Gly Asp Lys Val Asn Gln Gly Asp Ile
115 120 125

Ile Gly Leu Gln Gly Asn Ser Asn Tyr Tyr Asp Asn Pro Met Ser Val
130 135 140

His Leu His Leu Gln Leu Arg Pro Lys Asp Ala Lys Lys Asp Glu Lys
145 150 155 160

Ser Gln Val Cys Ser Gly Leu Ala Met Glu Lys Tyr Asp Ile Thr Asn
165 170 175

Leu Asn Ala Lys Gln Asp Lys Ser Lys Asn Gly Ser Val Lys Glu Leu
180 185 190

Lys His Ile Tyr Ser Asn His Ile Lys Gly Asn Lys Ile Thr Ala Pro
195 200 205

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Lys Pro Ser Ile Gln Gly Val Val Ile His Asn Asp Tyr Gly Ser Met
    210                 215                 220

Thr Pro Ser Gln Tyr Leu Pro Trp Leu Tyr Ala Arg Glu Asn Asn Gly
225                 230                 235                 240

Thr His Val Asn Gly Trp Ala Ser Val Tyr Ala Asn Arg Asn Glu Val
                245                 250                 255

Leu Trp Tyr His Pro Thr Asp Tyr Val Glu Trp His Cys Gly Asn Gln
            260                 265                 270

Trp Ala Asn Ala Asn Leu Ile Gly Phe Glu Val Cys Glu Ser Tyr Pro
        275                 280                 285

Gly Arg Ile Ser Asp Lys Leu Phe Leu Glu Asn Glu Glu Ala Thr Leu
    290                 295                 300

Lys Val Ala Ala Asp Val Met Lys Ser Tyr Gly Leu Pro Val Asn Arg
305                 310                 315                 320

Asn Thr Val Arg Leu His Asn Glu Phe Phe Gly Thr Ser Cys Pro His
                325                 330                 335

Arg Ser Trp Asp Leu His Val Gly Lys Gly Glu Pro Tyr Thr Thr Thr
            340                 345                 350

Asn Ile Asn Lys Met Lys Asp Tyr Phe Ile Lys Arg Ile Lys His Tyr
        355                 360                 365

Tyr Asp Gly Gly Lys Leu Glu Val Ser Lys Ala Ala Thr Ile Lys Gln
    370                 375                 380

Ser Asp Val Lys Gln Glu Val Lys Lys Gln Glu Ala Lys Gln Ile Val
385                 390                 395                 400

Lys Ala Thr Asp Trp Lys Gln Asn Lys Asp Gly Ile Trp Tyr Lys Ala
                405                 410                 415

Glu His Ala Ser Phe Thr Val Thr Ala Pro Glu Gly Ile Ile Thr Arg
            420                 425                 430

Tyr Lys Gly Pro Trp Thr Gly His Pro Gln Ala Gly Val Leu Gln Lys
        435                 440                 445

Gly Gln Thr Ile Lys Tyr Asp Glu Val Gln Lys Phe Asp Gly His Val
    450                 455                 460

Trp Val Ser Trp Glu Thr Phe Glu Gly Glu Thr Val Tyr Met Pro Val
465                 470                 475                 480
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Arg Thr Trp Asp Ala Lys Thr Gly Lys Val Gly Lys Leu Trp Gly Glu
485 490 495

Ile Lys Glu Leu Gly Gly Lys Leu Glu Val Ser Lys Ala Ala Thr Ile
500 505 510

Lys Gln Ser Asp Val Lys Gln Glu Val Lys Lys Gln Glu Ala Lys Gln
515 520 525

Ile Val Lys Ala Thr Asp Trp Lys Gln Asn Lys Asp Gly Ile Trp Tyr
530 535 540

Lys Ala Glu His Ala Ser Phe Thr Val Thr Ala Pro Glu Gly Ile Ile
545 550 555 560

Thr Arg Tyr Lys Gly Pro Trp Thr Gly His Pro Gln Ala Gly Val Leu
565 570 575

Gln Lys Gly Gln Thr Ile Lys Tyr Asp Glu Val Gln Lys Phe Asp Gly
580 585 590

His Val Trp Val Ser Trp Glu Thr Phe Glu Gly Glu Thr Val Tyr Met
595 600 605

Pro Val Arg Thr Trp Asp Ala Lys Thr Gly Lys Val Gly Lys Leu Trp
610 615 620

Gly Glu Ile Lys
625

<210> 87
<211> 1035
<212> DNA
<213> artificial

<220>
<223> artificial construct

<400> 87
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tacggctaca gaaattacca tgaaaacggc attaattatg atgagttttg tggtggttat 180

catagagctt ttgatgttta cagtaacgaa actaacgacg tgcctgctgt tactagcgga 240

acagttattg aagcaaacga ttacggtaat tttggtggta cattcgttat tagagacgct 300

aacgataacg attggatata tgggcatcta caacgtggct caatgcgatt tgttgtaggc 360

gacaaagtca atcaaggtga cattattggt ttacaaggta atagcaacta ttacgacaat 420

cctatgagtg tacatttaca tttacaatta cgccctaaag acgcaaagaa agatgaaaaa 480

tcacaagtat gtagtggttt ggctatggaa aaatatgaca ttacaaattt aaatgctaaa 540

caagataaat caaagaatgg gagcgtgaaa gagttgaaac atatctattc aaaccatatt 600

aaaggtaaca agattacagc accaaaacct agtattcaag gtgagctcgg tggaaagcta 660

gaagtaagca aagcagcaac tatcaaacaa tctgacgtta agcaagaagt taaaaagcaa 720

gaagcaaaac aaattgtgaa agcaacagat tggaaacaga ataaagatgg catttggtat 780

aaagctgaac atgcttcgtt cacagtgaca gcaccagagg gaattatcac aagatacaaa 840

ggtccttgga ctggtcaccc acaagctggt gtattacaaa aaggtcaaac gattaaatat 900

gatgaggttc aaaaatttga cggtcatgtt tgggtatcgt gggaaacgtt tgagggcgaa 960

actgtataca tgccggtacg cacatgggac gctaaaactg gtaaagttgg taagttgtgg 1020

ggcgaaatta aataa 1035

<210> 88
<211> 344
<212> PRT
<213> artificial

<220>
<223> artificial construct

<400> 88

Met Arg Gly Ser His His His His His His Gly Ser Met Leu Thr Ala
1 5 10 15

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

Thr Tyr Asp Gly Tyr Pro Lys Asn Tyr Gly Tyr Arg Asn Tyr His Glu
35 40 45

Asn Gly Ile Asn Tyr Asp Glu Phe Cys Gly Gly Tyr His Arg Ala Phe
50 55 60

Asp Val Tyr Ser Asn Glu Thr Asn Asp Val Pro Ala Val Thr Ser Gly
65 70 75 80

Thr Val Ile Glu Ala Asn Asp Tyr Gly Asn Phe Gly Gly Thr Phe Val
85 90 95

Ile Arg Asp Ala Asn Asp Asn Asp Trp Ile Tyr Gly His Leu Gln Arg
100 105 110

Gly Ser Met Arg Phe Val Val Gly Asp Lys Val Asn Gln Gly Asp Ile
115 120 125

Ile Gly Leu Gln Gly Asn Ser Asn Tyr Tyr Asp Asn Pro Met Ser Val
130 135 140

His Leu His Leu Gln Leu Arg Pro Lys Asp Ala Lys Lys Asp Glu Lys
145 150 155 160

Ser Gln Val Cys Ser Gly Leu Ala Met Glu Lys Tyr Asp Ile Thr Asn
165 170 175

Leu Asn Ala Lys Gln Asp Lys Ser Lys Asn Gly Ser Val Lys Glu Leu
180 185 190

Lys His Ile Tyr Ser Asn His Ile Lys Gly Asn Lys Ile Thr Ala Pro
195 200 205

Lys Pro Ser Ile Gln Gly Glu Leu Gly Gly Lys Leu Glu Val Ser Lys
210 215 220

Ala Ala Thr Ile Lys Gln Ser Asp Val Lys Gln Glu Val Lys Lys Gln
225 230 235 240

Glu Ala Lys Gln Ile Val Lys Ala Thr Asp Trp Lys Gln Asn Lys Asp
245 250 255

Gly Ile Trp Tyr Lys Ala Glu His Ala Ser Phe Thr Val Thr Ala Pro
260 265 270

Glu Gly Ile Ile Thr Arg Tyr Lys Gly Pro Trp Thr Gly His Pro Gln
275 280 285

Ala Gly Val Leu Gln Lys Gly Gln Thr Ile Lys Tyr Asp Glu Val Gln
290 295 300

Lys Phe Asp Gly His Val Trp Val Ser Trp Glu Thr Phe Glu Gly Glu
305 310 315 320

Thr Val Tyr Met Pro Val Arg Thr Trp Asp Ala Lys Thr Gly Lys Val
325 330 335

Gly Lys Leu Trp Gly Glu Ile Lys
340

<210> 89
<211> 2961
<212> DNA
<213> artificial

<220>
<223> artificial construct

<400> 89
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acgaaaaaag gttggaaaat atcatctgac cctcgcactt acgatggtta ccctaaaaac 120

tacggctaca gaaattacca tgaaaacggc attaattatg atgagttttg tggtggttat 180

catagagctt ttgatgttta cagtaacgaa actaacgacg tgcctgctgt tactagcgga 240

acagttattg aagcaaacga ttacggtaat tttggtggta cattcgttat tagagacgct 300

aacgataacg attggatata tgggcatcta caacgtggct caatgcgatt tgttgtaggc 360

gacaaagtca atcaaggtga cattattggt ttacaaggta atagcaacta ttacgacaat 420

cctatgagtg tacatttaca tttacaatta cgccctaaag acgcaaagaa agatgaaaaa 480

tcacaagtat gtagtggttt ggctatggaa aaatatgaca ttacaaattt aaatgctaaa 540

caagataaat caaagaatgg gagcgtgaaa gagttgaaac atatctattc aaaccatatt 600

aaaggtaaca agattacagc accaaaacct agtattcaag gtgtggtcat ccacaatgat 660

tatggtagta tgacacctag tcaatactta ccatggttat atgcacgtga gaataacggt 720

acacacgtta acggttgggc tagtgtttat gcaaatagaa acgaagtgct ttggtatcat 780

ccgacagact acgtagagtg gcattgtggt aatcaatggg caaatgctaa cttaatcgga 840

tttgaagtgt gtgagtcgta tcctggtaga atctcggaca aattattctt agaaaatgaa 900

gaagcgacat tgaaagtagc tgcggatgtg atgaagtcgt acggattacc agttaatcgc 960

aacactgtac gtctgcataa cgaattcttc ggaacttctt gtccacatcg ttcgtgggac 1020

ttgcatgttg gcaaaggtga gccttacaca actactaata ttaataaaat gaaagactac 1080

ttcatcaaac gcatcaaaca ttattatgac ggtggaaagc tagaagtaag caaagcagca 1140

actatcaaac aatctgacgt taagcaagaa gttaaaaagc aagaagcaaa acaaattgtg 1200

aaagcaacag attggaaaca gaataaagat ggcatttggt ataaagctga acatgcttcg 1260

ttcacagtga cagcaccaga gggaattatc acaagataca aaggtccttg gactggtcac 1320

ccacaagctg gtgtattaca aaaaggtcaa acgattaaat atgatgaggt tcaaaaattt 1380

gacggtcatg tttgggtatc gtgggaaacg tttgagggcg aaactgtata catgccggta 1440

cgcacatggg acgctaaaac tggtaaagtt ggtaagttgt ggggcgaaat taaagagctc 1500

atgctaactg ctattgacta tcttacgaaa aaaggttgga aaatatcatc tgaccctcgc 1560

acttacgatg gttaccctaa aaactacggc tacagaaatt accatgaaaa cggcattaat 1620

tatgatgagt tttgtggtgg ttatcataga gcttttgatg tttacagtaa cgaaactaac 1680

gacgtgcctg ctgttactag cggaacagtt attgaagcaa acgattacgg taattttggt 1740

ggtacattcg ttattagaga cgctaacgat aacgattgga tatatgggca tctacaacgt 1800

ggctcaatgc gatttgttgt aggcgacaaa gtcaatcaag gtgacattat tggtttacaa 1860

ggtaatagca actattacga caatcctatg agtgtacatt tacatttaca attacgccct 1920

aaagacgcaa agaaagatga aaaatcacaa gtatgtagtg gtttggctat ggaaaaatat 1980

gacattacaa atttaaatgc taaacaagat aaatcaaaga atgggagcgt gaaagagttg 2040

aaacatatct attcaaacca tattaaaggt aacaagatta cagcaccaaa acctagtatt 2100

caaggtgtgg tcatccacaa tgattatggt agtatgacac ctagtcaata cttaccatgg 2160

ttatatgcac gtgagaataa cggtacacac gttaacggtt gggctagtgt ttatgcaaat 2220

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tcgtacggat taccagttaa tcgcaacact gtacgtctgc ataacgaatt cttcggaact 2460

tcttgtccac atcgttcgtg ggacttgcat gttggcaaag gtgagcctta cacaactact 2520

aatattaata aaatgaaaga ctacttcatc aaacgcatca aacattatta tgacggtgga 2580

aagctagaag taagcaaagc agcaactatc aaacaatctg acgttaagca agaagttaaa 2640

aagcaagaag caaaacaaat tgtgaaagca acagattgga aacagaataa agatggcatt 2700

tggtataaag ctgaacatgc ttcgttcaca gtgacagcac cagagggaat tatcacaaga 2760

tacaaaggtc cttggactgg tcacccacaa gctggtgtat tacaaaaagg tcaaacgatt 2820

aaatatgatg aggttcaaaa atttgacggt catgtttggg tatcgtggga aacgtttgag 2880

ggcgaaactg tatacatgcc ggtacgcaca tgggacgcta aaactggtaa agttggtaag 2940

ttgtggggcg aaattaaata a 2961

<210> 90
<211> 986
<212> PRT
<213> artificial

<220>
<223> artificial construct

<400> 90

Met Arg Gly Ser His His His His His His Gly Ser Met Leu Thr Ala
1 5 10 15

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

Thr Tyr Asp Gly Tyr Pro Lys Asn Tyr Gly Tyr Arg Asn Tyr His Glu
35 40 45

Asn Gly Ile Asn Tyr Asp Glu Phe Cys Gly Gly Tyr His Arg Ala Phe
50 55 60

Asp Val Tyr Ser Asn Glu Thr Asn Asp Val Pro Ala Val Thr Ser Gly
65 70 75 80

Thr Val Ile Glu Ala Asn Asp Tyr Gly Asn Phe Gly Gly Thr Phe Val
85 90 95

Ile Arg Asp Ala Asn Asp Asn Asp Trp Ile Tyr Gly His Leu Gln Arg
100 105 110

Gly Ser Met Arg Phe Val Val Gly Asp Lys Val Asn Gln Gly Asp Ile
115 120 125

Ile Gly Leu Gln Gly Asn Ser Asn Tyr Tyr Asp Asn Pro Met Ser Val
130 135 140

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His Leu His Leu Gln Leu Arg Pro Lys Asp Ala Lys Lys Asp Glu Lys
145                 150                 155                 160

Ser Gln Val Cys Ser Gly Leu Ala Met Glu Lys Tyr Asp Ile Thr Asn
                165                 170                 175

Leu Asn Ala Lys Gln Asp Lys Ser Lys Asn Gly Ser Val Lys Glu Leu
            180                 185                 190

Lys His Ile Tyr Ser Asn His Ile Lys Gly Asn Lys Ile Thr Ala Pro
        195                 200                 205

Lys Pro Ser Ile Gln Gly Val Val Ile His Asn Asp Tyr Gly Ser Met
    210                 215                 220

Thr Pro Ser Gln Tyr Leu Pro Trp Leu Tyr Ala Arg Glu Asn Asn Gly
225                 230                 235                 240

Thr His Val Asn Gly Trp Ala Ser Val Tyr Ala Asn Arg Asn Glu Val
                245                 250                 255

Leu Trp Tyr His Pro Thr Asp Tyr Val Glu Trp His Cys Gly Asn Gln
            260                 265                 270

Trp Ala Asn Ala Asn Leu Ile Gly Phe Glu Val Cys Glu Ser Tyr Pro
        275                 280                 285

Gly Arg Ile Ser Asp Lys Leu Phe Leu Glu Asn Glu Glu Ala Thr Leu
    290                 295                 300

Lys Val Ala Ala Asp Val Met Lys Ser Tyr Gly Leu Pro Val Asn Arg
305                 310                 315                 320

Asn Thr Val Arg Leu His Asn Glu Phe Phe Gly Thr Ser Cys Pro His
                325                 330                 335

Arg Ser Trp Asp Leu His Val Gly Lys Gly Glu Pro Tyr Thr Thr Thr
            340                 345                 350

Asn Ile Asn Lys Met Lys Asp Tyr Phe Ile Lys Arg Ile Lys His Tyr
        355                 360                 365

Tyr Asp Gly Gly Lys Leu Glu Val Ser Lys Ala Ala Thr Ile Lys Gln
    370                 375                 380

Ser Asp Val Lys Gln Glu Val Lys Lys Gln Glu Ala Lys Gln Ile Val
385                 390                 395                 400

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

Tyr Lys Gly Pro Trp Thr Gly His Pro Gln Ala Gly Val Leu Gln Lys
        435                 440                 445

Gly Gln Thr Ile Lys Tyr Asp Glu Val Gln Lys Phe Asp Gly His Val
    450                 455                 460

Trp Val Ser Trp Glu Thr Phe Glu Gly Glu Thr Val Tyr Met Pro Val
465                 470                 475                 480

Arg Thr Trp Asp Ala Lys Thr Gly Lys Val Gly Lys Leu Trp Gly Glu
                485                 490                 495

Ile Lys Glu Leu Met Leu Thr Ala Ile Asp Tyr Leu Thr Lys Lys Gly
            500                 505                 510

Trp Lys Ile Ser Ser Asp Pro Arg Thr Tyr Asp Gly Tyr Pro Lys Asn
        515                 520                 525

Tyr Gly Tyr Arg Asn Tyr His Glu Asn Gly Ile Asn Tyr Asp Glu Phe
    530                 535                 540

Cys Gly Gly Tyr His Arg Ala Phe Asp Val Tyr Ser Asn Glu Thr Asn
545                 550                 555                 560

Asp Val Pro Ala Val Thr Ser Gly Thr Val Ile Glu Ala Asn Asp Tyr
                565                 570                 575

Gly Asn Phe Gly Gly Thr Phe Val Ile Arg Asp Ala Asn Asp Asn Asp
            580                 585                 590

Trp Ile Tyr Gly His Leu Gln Arg Gly Ser Met Arg Phe Val Val Gly
        595                 600                 605

Asp Lys Val Asn Gln Gly Asp Ile Ile Gly Leu Gln Gly Asn Ser Asn
    610                 615                 620

Tyr Tyr Asp Asn Pro Met Ser Val His Leu His Leu Gln Leu Arg Pro
625                 630                 635                 640

Lys Asp Ala Lys Lys Asp Glu Lys Ser Gln Val Cys Ser Gly Leu Ala
                645                 650                 655

Met Glu Lys Tyr Asp Ile Thr Asn Leu Asn Ala Lys Gln Asp Lys Ser
            660                 665                 670

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

Ile His Asn Asp Tyr Gly Ser Met Thr Pro Ser Gln Tyr Leu Pro Trp
705                 710                 715                 720

Leu Tyr Ala Arg Glu Asn Asn Gly Thr His Val Asn Gly Trp Ala Ser
                725                 730                 735

Val Tyr Ala Asn Arg Asn Glu Val Leu Trp Tyr His Pro Thr Asp Tyr
            740                 745                 750

Val Glu Trp His Cys Gly Asn Gln Trp Ala Asn Ala Asn Leu Ile Gly
        755                 760                 765

Phe Glu Val Cys Glu Ser Tyr Pro Gly Arg Ile Ser Asp Lys Leu Phe
    770                 775                 780

Leu Glu Asn Glu Glu Ala Thr Leu Lys Val Ala Ala Asp Val Met Lys
785                 790                 795                 800

Ser Tyr Gly Leu Pro Val Asn Arg Asn Thr Val Arg Leu His Asn Glu
                805                 810                 815

Phe Phe Gly Thr Ser Cys Pro His Arg Ser Trp Asp Leu His Val Gly
            820                 825                 830

Lys Gly Glu Pro Tyr Thr Thr Thr Asn Ile Asn Lys Met Lys Asp Tyr
        835                 840                 845

Phe Ile Lys Arg Ile Lys His Tyr Tyr Asp Gly Gly Lys Leu Glu Val
    850                 855                 860

Ser Lys Ala Ala Thr Ile Lys Gln Ser Asp Val Lys Gln Glu Val Lys
865                 870                 875                 880

Lys Gln Glu Ala Lys Gln Ile Val Lys Ala Thr Asp Trp Lys Gln Asn
                885                 890                 895

Lys Asp Gly Ile Trp Tyr Lys Ala Glu His Ala Ser Phe Thr Val Thr
            900                 905                 910

Ala Pro Glu Gly Ile Ile Thr Arg Tyr Lys Gly Pro Trp Thr Gly His
        915                 920                 925

Pro Gln Ala Gly Val Leu Gln Lys Gly Gln Thr Ile Lys Tyr Asp Glu
    930                 935                 940

Val Gln Lys Phe Asp Gly His Val Trp Val Ser Trp Glu Thr Phe Glu
945                 950                 955                 960
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Gly Glu Thr Val Tyr Met Pro Val Arg Thr Trp Asp Ala Lys Thr Gly
965 970 975

Lys Val Gly Lys Leu Trp Gly Glu Ile Lys
980 985

<210> 91
<211> 1953
<212> DNA
<213> artificial

<220>
<223> artificial construct

<400> 91
atgagaggat cgcatcacca tcaccatcac ggatccatga aaaccctgaa acaagcagag 60

tcctacatta agagtaaagt aaatacagga actgattttg atggtttata tgggtatcag 120

tgtatggact tagcagtaga ttatatttac catgtaacag atggtaaaat aagaatgtgg 180

ggtaatgcta aggatgcgat aaataactct tttggtggta ctgctacggt atataaaaac 240

taccctgctt ttagacctaa gtacggtgat gtagtcgtat ggactactgg taattttgca 300

acttatggtc atatcgcaat agttactaac cctgaccctt atggagacct tcaatatgtt 360

acagttcttg aacaaaactg gaacggtaac gggatttata aaaccgagtt agctacaatc 420

agaacacacg attacacagg aattacacat tttattaaag acgcaaagaa agatgaaaaa 480

tcacaagtat gtagtggttt ggctatggaa aaatatgaca ttacaaattt aaatgctaaa 540

caagataaat caaagaatgg gagcgtgaaa gagttgaaac atatctattc aaaccatatt 600

aaaggtaaca agattacagc accaaaacct agtattcaag gtgtggtcat ccacaatgat 660

tatggtagta tgacacctag tcaatactta ccatggttat atgcacgtga gaataacggt 720

acacacgtta acggttgggc tagtgtttat gcaaatagaa acgaagtgct ttggtatcat 780

ccgacagact acgtagagtg gcattgtggt aatcaatggg caaatgctaa cttaatcgga 840

tttgaagtgt gtgagtcgta tcctggtaga atctcggaca aattattctt agaaaatgaa 900

gaagcgacat tgaaagtagc tgcggatgtg atgaagtcgt acggattacc agttaatcgc 960

aacactgtac gtctgcataa cgaattcttc ggaacttctt gtccacatcg ttcgtgggac 1020

ttgcatgttg gcaaaggtga gccttacaca actactaata ttaataaaat gaaagactac 1080

ttcatcaaac gcatcaaaca ttattatgac ggtggaaagc tagaagtaag caaagcagca 1140

actatcaaac aatctgacgt taagcaagaa gttaaaaagc aagaagcaaa acaaattgtg 1200

aaagcaacag atgctgcaac acatgaacat tcagcacaat ggttgaataa ttacaaaaaa 1260

ggatatggtt acggtcctta tccattaggt ataaatggcg gtatgcacta cggagttgat 1320

ttttttatga atattggaac accagtaaaa gctatttcaa gcggaaaaat agttgaagct 1380

ggttggagta attacggagg aggtaatcaa ataggtctta ttgaaaatga tggagtgcat 1440

agacaatggt atatgcatct aagtaaatat aatgttaaag taggagatta tgtcaaagct 1500

ggtcaaataa tcggttggtc tggaagcact ggttattcta cagcaccaca tttacacttc 1560

caaagaatgg ttaattcatt ttcaaattca actgcccaag atccaatgcc tttcttaaag 1620

agcgcaggat atggaaaagc aggtggtaca gtaactccaa cgccgaatac aggttggaaa 1680

acaaacaaat atggcacact atataaatca gagtcagcta gcttcacacc taatacagat 1740

ataataacaa gaacgactgg tccatttaga agcatgccgc agtcaggagt cttaaaagca 1800

ggtcaaacaa ttcattatga tgaagtgatg aaacaagacg gtcatgtttg ggtaggttat 1860

acaggtaaca gtggccaacg tatttacttg cctgtaagaa catggaataa atctactaat 1920

actttaggtg ttctttgggg aactataaag taa 1953

<210> 92
<211> 650
<212> PRT
<213> artificial

<220>
<223> artificial construct

<400> 92

Met Arg Gly Ser His His His His His His Gly Ser Met Lys Thr Leu
1 5 10 15

Lys Gln Ala Glu Ser Tyr Ile Lys Ser Lys Val Asn Thr Gly Thr Asp
20 25 30

Phe Asp Gly Leu Tyr Gly Tyr Gln Cys Met Asp Leu Ala Val Asp Tyr
35 40 45

Ile Tyr His Val Thr Asp Gly Lys Ile Arg Met Trp Gly Asn Ala Lys
50 55 60

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

Tyr Pro Ala Phe Arg Pro Lys Tyr Gly Asp Val Val Val Trp Thr Thr
85 90 95

Gly Asn Phe Ala Thr Tyr Gly His Ile Ala Ile Val Thr Asn Pro Asp
100 105 110

Pro Tyr Gly Asp Leu Gln Tyr Val Thr Val Leu Glu Gln Asn Trp Asn
115 120 125

Gly Asn Gly Ile Tyr Lys Thr Glu Leu Ala Thr Ile Arg Thr His Asp
130 135 140

Tyr Thr Gly Ile Thr His Phe Ile Lys Asp Ala Lys Lys Asp Glu Lys
145 150 155 160

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Ser Gln Val Cys Ser Gly Leu Ala Met Glu Lys Tyr Asp Ile Thr Asn
                165                 170                 175

Leu Asn Ala Lys Gln Asp Lys Ser Lys Asn Gly Ser Val Lys Glu Leu
            180                 185                 190

Lys His Ile Tyr Ser Asn His Ile Lys Gly Asn Lys Ile Thr Ala Pro
        195                 200                 205

Lys Pro Ser Ile Gln Gly Val Val Ile His Asn Asp Tyr Gly Ser Met
    210                 215                 220

Thr Pro Ser Gln Tyr Leu Pro Trp Leu Tyr Ala Arg Glu Asn Asn Gly
225                 230                 235                 240

Thr His Val Asn Gly Trp Ala Ser Val Tyr Ala Asn Arg Asn Glu Val
                245                 250                 255

Leu Trp Tyr His Pro Thr Asp Tyr Val Glu Trp His Cys Gly Asn Gln
            260                 265                 270

Trp Ala Asn Ala Asn Leu Ile Gly Phe Glu Val Cys Glu Ser Tyr Pro
        275                 280                 285

Gly Arg Ile Ser Asp Lys Leu Phe Leu Glu Asn Glu Glu Ala Thr Leu
    290                 295                 300

Lys Val Ala Ala Asp Val Met Lys Ser Tyr Gly Leu Pro Val Asn Arg
305                 310                 315                 320

Asn Thr Val Arg Leu His Asn Glu Phe Phe Gly Thr Ser Cys Pro His
                325                 330                 335

Arg Ser Trp Asp Leu His Val Gly Lys Gly Glu Pro Tyr Thr Thr Thr
            340                 345                 350

Asn Ile Asn Lys Met Lys Asp Tyr Phe Ile Lys Arg Ile Lys His Tyr
        355                 360                 365

Tyr Asp Gly Gly Lys Leu Glu Val Ser Lys Ala Ala Thr Ile Lys Gln
    370                 375                 380

Ser Asp Val Lys Gln Glu Val Lys Lys Gln Glu Ala Lys Gln Ile Val
385                 390                 395                 400

Lys Ala Thr Asp Ala Ala Thr His Glu His Ser Ala Gln Trp Leu Asn
                405                 410                 415

Asn Tyr Lys Lys Gly Tyr Gly Tyr Gly Pro Tyr Pro Leu Gly Ile Asn
            420                 425                 430
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Gly Gly Met His Tyr Gly Val Asp Phe Phe Met Asn Ile Gly Thr Pro
435 440 445

Val Lys Ala Ile Ser Ser Gly Lys Ile Val Glu Ala Gly Trp Ser Asn
450 455 460

Tyr Gly Gly Gly Asn Gln Ile Gly Leu Ile Glu Asn Asp Gly Val His
465 470 475 480

Arg Gln Trp Tyr Met His Leu Ser Lys Tyr Asn Val Lys Val Gly Asp
485 490 495

Tyr Val Lys Ala Gly Gln Ile Ile Gly Trp Ser Gly Ser Thr Gly Tyr
500 505 510

Ser Thr Ala Pro His Leu His Phe Gln Arg Met Val Asn Ser Phe Ser
515 520 525

Asn Ser Thr Ala Gln Asp Pro Met Pro Phe Leu Lys Ser Ala Gly Tyr
530 535 540

Gly Lys Ala Gly Gly Thr Val Thr Pro Thr Pro Asn Thr Gly Trp Lys
545 550 555 560

Thr Asn Lys Tyr Gly Thr Leu Tyr Lys Ser Glu Ser Ala Ser Phe Thr
565 570 575

Pro Asn Thr Asp Ile Ile Thr Arg Thr Thr Gly Pro Phe Arg Ser Met
580 585 590

Pro Gln Ser Gly Val Leu Lys Ala Gly Gln Thr Ile His Tyr Asp Glu
595 600 605

Val Met Lys Gln Asp Gly His Val Trp Val Gly Tyr Thr Gly Asn Ser
610 615 620

Gly Gln Arg Ile Tyr Leu Pro Val Arg Thr Trp Asn Lys Ser Thr Asn
625 630 635 640

Thr Leu Gly Val Leu Trp Gly Thr Ile Lys
645 650

<210> 93
<211> 1521
<212> DNA
<213> artificial

<220>
<223> artificial construct

<400> 93
atgagaggat cgcatcacca tcaccatcac ggatccgctg caacacatga acattcagca 60

caatggttga ataattacaa aaaaggatat ggttacggtc cttatccatt aggtataaat 120

ggcggtatgc actacggagt tgatttttt atgaatattg gaacaccagt aaaagctatt 180

tcaagcggaa aaatagttga agctggttgg agtaattacg gaggaggtaa tcaaataggt 240

cttattgaaa atgatggagt gcatagacaa tggtatatgc atctaagtaa atataatgtt 300

aaagtaggag attatgtcaa agctggtcaa ataatcggtt ggtctggaag cactggttat 360

tctacagcac cacatttaca cttccaaaga atggttaatt cattttcaaa ttcaactgcc 420

caagatccaa tgcctttctt aaagagcgca ggatatggaa aagcaggtgg tacagtaact 480

ccaacgccga atacaggttg gaaaacaaac aaatatggca cactatataa atcagagtca 540

gctagcttca cacctaatac agatataata acaagaacga ctggtccatt tagaagcatg 600

ccgcagtcag gagtcttaaa agcaggtcaa acaattcatt atgatgaagt gatgaaacaa 660

gacggtcatg tttgggtagg ttatacaggt aacagtggcc aacgtattta cttgcctgta 720

agaacatgga ataaatctac taatacttta ggtgttcttt ggggaactat aaaggagctc 780

gctgcaacac atgaacattc agcacaatgg ttgaataatt acaaaaaagg atatggttac 840

ggtccttatc cattaggtat aaatggcggt atgcactacg gagttgattt ttttatgaat 900

attggaacac cagtaaaagc tatttcaagc ggaaaaatag ttgaagctgg ttggagtaat 960

tacggaggag gtaatcaaat aggtcttatt gaaaatgatg gagtgcatag acaatggtat 1020

atgcatctaa gtaaatataa tgttaaagta ggagattatg tcaaagctgg tcaaataatc 1080

ggttggtctg gaagcactgg ttattctaca gcaccacatt tacacttcca aagaatggtt 1140

aattcatttt caaattcaac tgcccaagat ccaatgcctt tcttaaagag cgcaggatat 1200

ggaaaagcag gtggtacagt aactccaacg ccgaatacag gttggaaaac aaacaaatat 1260

ggcacactat ataaatcaga gtcagctagc ttcacaccta atacagatat aataacaaga 1320

acgactggtc catttagaag catgccgcag tcaggagtct taaaagcagg tcaaacaatt 1380

cattatgatg aagtgatgaa acaagacggt catgtttggg taggttatac aggtaacagt 1440

ggccaacgta tttacttgcc tgtaagaaca tggaataaat ctactaatac tttaggtgtt 1500

ctttggggaa ctataaagtg a 1521

<210> 94
<211> 506
<212> PRT
<213> artificial

<220>
<223> artificial construct

<400> 94

Met Arg Gly Ser His His His His His His Gly Ser Ala Ala Thr His
1 5 10 15

Glu His Ser Ala Gln Trp Leu Asn Asn Tyr Lys Lys Gly Tyr Gly Tyr
20 25 30

```
Gly Pro Tyr Pro Leu Gly Ile Asn Gly Gly Met His Tyr Gly Val Asp
        35                  40                  45

Phe Phe Met Asn Ile Gly Thr Pro Val Lys Ala Ile Ser Ser Gly Lys
    50                  55                  60

Ile Val Glu Ala Gly Trp Ser Asn Tyr Gly Gly Gly Asn Gln Ile Gly
65                  70                  75                  80

Leu Ile Glu Asn Asp Gly Val His Arg Gln Trp Tyr Met His Leu Ser
                85                  90                  95

Lys Tyr Asn Val Lys Val Gly Asp Tyr Val Lys Ala Gly Gln Ile Ile
            100                 105                 110

Gly Trp Ser Gly Ser Thr Gly Tyr Ser Thr Ala Pro His Leu His Phe
        115                 120                 125

Gln Arg Met Val Asn Ser Phe Ser Asn Ser Thr Ala Gln Asp Pro Met
    130                 135                 140

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

Pro Thr Pro Asn Thr Gly Trp Lys Thr Asn Lys Tyr Gly Thr Leu Tyr
                165                 170                 175

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

Thr Thr Gly Pro Phe Arg Ser Met Pro Gln Ser Gly Val Leu Lys Ala
        195                 200                 205

Gly Gln Thr Ile His Tyr Asp Glu Val Met Lys Gln Asp Gly His Val
    210                 215                 220

Trp Val Gly Tyr Thr Gly Asn Ser Gly Gln Arg Ile Tyr Leu Pro Val
225                 230                 235                 240

Arg Thr Trp Asn Lys Ser Thr Asn Thr Leu Gly Val Leu Trp Gly Thr
                245                 250                 255

Ile Lys Glu Leu Ala Ala Thr His Glu His Ser Ala Gln Trp Leu Asn
            260                 265                 270

Asn Tyr Lys Lys Gly Tyr Gly Tyr Gly Pro Tyr Pro Leu Gly Ile Asn
        275                 280                 285

Gly Gly Met His Tyr Gly Val Asp Phe Phe Met Asn Ile Gly Thr Pro
    290                 295                 300
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```
Val Lys Ala Ile Ser Ser Gly Lys Ile Val Glu Ala Gly Trp Ser Asn
305                 310                 315                 320

Tyr Gly Gly Gly Asn Gln Ile Gly Leu Ile Glu Asn Asp Gly Val His
                325                 330                 335

Arg Gln Trp Tyr Met His Leu Ser Lys Tyr Asn Val Lys Val Gly Asp
            340                 345                 350

Tyr Val Lys Ala Gly Gln Ile Ile Gly Trp Ser Gly Ser Thr Gly Tyr
        355                 360                 365

Ser Thr Ala Pro His Leu His Phe Gln Arg Met Val Asn Ser Phe Ser
    370                 375                 380

Asn Ser Thr Ala Gln Asp Pro Met Pro Phe Leu Lys Ser Ala Gly Tyr
385                 390                 395                 400

Gly Lys Ala Gly Gly Thr Val Thr Pro Thr Pro Asn Thr Gly Trp Lys
                405                 410                 415

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

Pro Asn Thr Asp Ile Ile Thr Arg Thr Thr Gly Pro Phe Arg Ser Met
        435                 440                 445

Pro Gln Ser Gly Val Leu Lys Ala Gly Gln Thr Ile His Tyr Asp Glu
    450                 455                 460

Val Met Lys Gln Asp Gly His Val Trp Val Gly Tyr Thr Gly Asn Ser
465                 470                 475                 480

Gly Gln Arg Ile Tyr Leu Pro Val Arg Thr Trp Asn Lys Ser Thr Asn
                485                 490                 495

Thr Leu Gly Val Leu Trp Gly Thr Ile Lys
            500                 505


<210>  95
<211>  1143
<212>  DNA
<213>  artificial

<220>
<223>  artificial construct

<400>  95
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actggagttg tcccaattct tgttgaatta gatggtgatg ttaatgggca caaattttct    120

gtcagtggag agggtgaagg tgatgcaaca tacggaaaac ttacccttaa atttatttgc    180

actactggaa aactacctgt tccatggcca acacttgtca ctactttcgc gtatggtctt    240
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caatgctttg cgagataccc agatcatatg aaacggcatg acttttttcaa gagtgccatg 300

cccgaaggtt atgtacagga aagaactata tttttcaaag atgacgggaa ctacaagaca 360

cgtgctgaag tcaagtttga aggtgatacc cttgttaata gaatcgagtt aaaaggtatt 420

gattttaaag aagatggaaa cattcttgga cacaaattgg aatacaacta taactcacac 480

aatgtataca tcatggcaga caaacaaaag aatggaatca aagttaactt caaaattaga 540

cacaacattg aagatggaag cgttcaacta gcagaccatt atcaacaaaa tactccaatt 600

ggcgatggcc ctgtcctttt accagacaac cattacctgt ccacacaatc tgccctttcg 660

aaagatccca acgaaaagag agaccacatg gtccttcttg agtttgtaac agctgctggg 720

attacacatg gcatggatga actatacaaa gagctcggtg gaaagctaga agtaagcaaa 780

gcagcaacta tcaaacaatc tgacgttaag caagaagtta aaaagcaaga agcaaaacaa 840

attgtgaaag caacagattg gaaacagaat aaagatggca tttggtataa agctgaacat 900

gcttcgttca cagtgacagc accagaggga attatcacaa gatacaaagg tccttggact 960

ggtcacccac aagctggtgt attacaaaaa ggtcaaacga ttaaatatga tgaggttcaa 1020

aaatttgacg gtcatgtttg ggtatcgtgg gaaacgtttg agggcgaaac tgtatacatg 1080

ccggtacgca catgggacgc taaaactggt aaagttggta agttgtgggg cgaaattaaa 1140

taa 1143

<210> 96
<211> 380
<212> PRT
<213> artificial

<220>
<223> artificial construct

<400> 96

Met Arg Gly Ser His His His His His His Gly Ser Met Ser Lys Gly
1 5 10 15

Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly
20 25 30

Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp
35 40 45

Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys
50 55 60

Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ala Tyr Gly Leu
65 70 75 80

Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe
85 90 95

```
Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe
            100                 105                 110

Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly
        115                 120                 125

Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
    130                 135                 140

Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His
145                 150                 155                 160

Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn
                165                 170                 175

Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp
            180                 185                 190

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

Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn
    210                 215                 220

Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly
225                 230                 235                 240

Ile Thr His Gly Met Asp Glu Leu Tyr Lys Glu Leu Gly Gly Lys Leu
                245                 250                 255

Glu Val Ser Lys Ala Ala Thr Ile Lys Gln Ser Asp Val Lys Gln Glu
            260                 265                 270

Val Lys Lys Gln Glu Ala Lys Gln Ile Val Lys Ala Thr Asp Trp Lys
        275                 280                 285

Gln Asn Lys Asp Gly Ile Trp Tyr Lys Ala Glu His Ala Ser Phe Thr
    290                 295                 300

Val Thr Ala Pro Glu Gly Ile Ile Thr Arg Tyr Lys Gly Pro Trp Thr
305                 310                 315                 320

Gly His Pro Gln Ala Gly Val Leu Gln Lys Gly Gln Thr Ile Lys Tyr
                325                 330                 335

Asp Glu Val Gln Lys Phe Asp Gly His Val Trp Val Ser Trp Glu Thr
            340                 345                 350

Phe Glu Gly Glu Thr Val Tyr Met Pro Val Arg Thr Trp Asp Ala Lys
        355                 360                 365
```

Thr Gly Lys Val Gly Lys Leu Trp Gly Glu Ile Lys
370 375 380

<210> 97
<211> 516
<212> DNA
<213> Staphylococcus bacteriophage phi 11

<400> 97
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caattcaatg tggacttatg gtatggattt caatgctttg attatgccaa tgctggttgg 120

aaagttttgt ttggattact tctaaaaggt ttaggtgcaa aagatattcc gttcgctaac 180

aacttcgacg gattagctac tgtataccaa aatacaccgg acttcttagc acaacctggc 240

gacatggtgg tattcggtag caactacggt gctggatatg gtcacgttgc atgggtaatt 300

gaagcaactt tagattacat cattgtatat gagcagaatt ggctaggcgg tggctggact 360

gacggaatcg aacaacccgg ctggggttgg gaaaaagtta caagacgaca acatgcttat 420

gatttcccta tgtggtttat ccgtccgaat tttaaaagtg agacagcgcc acgatcagtt 480

caatctccta cacaagcacc taaaaaagaa acagct 516

<210> 98
<211> 158
<212> PRT
<213> Staphylococcus bacteriophage phi 11

<400> 98

Met Ser Ile Ile Met Glu Val Ala Thr Met Gln Ala Lys Leu Thr Lys
1 5 10 15

Asn Glu Phe Ile Glu Trp Leu Lys Thr Ser Glu Gly Lys Gln Phe Asn
20 25 30

Val Asp Leu Trp Tyr Gly Phe Gln Cys Phe Asp Tyr Ala Asn Ala Gly
35 40 45

Trp Lys Val Leu Phe Gly Leu Leu Leu Lys Gly Leu Gly Ala Lys Asp
50 55 60

Ile Pro Phe Ala Asn Asn Phe Asp Gly Leu Ala Thr Val Tyr Gln Asn
65 70 75 80

Thr Pro Asp Phe Leu Ala Gln Pro Gly Asp Met Val Val Phe Gly Ser
85 90 95

Asn Tyr Gly Ala Gly Tyr Gly His Val Ala Trp Val Ile Glu Ala Thr
100 105 110

Leu Asp Tyr Ile Ile Val Tyr Glu Gln Asn Trp Leu Gly Gly Gly Trp
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Thr Asp Gly Ile Glu Gln Pro Gly Trp Gly Trp Glu Lys Val Thr Arg
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Arg Gln His Ala Tyr Asp Phe Pro Met Trp Phe Ile Arg Pro
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<400> 99
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ggggcgactg ctgaagcata tcgtaacgga ttagtaaatg cacctttatc aagattagaa 180

gcgggcattg cgcatagtta cgtatcaggc aacacagttt ggcaagcctt agatgaatca 240

caagtaggtt ggcataccgc taatcaaata ggtaataaat attattacgg tattgaagta 300

tgtcaatcaa tgggcgcaga taacgcgaca ttcttaaaaa atgaacaggc aactttccaa 360

gaatgcgcta gattgttgaa aaaatgggga ttaccagcaa acagaaatac aatcagattg 420

cacaatgaat ttacttcaac atcatgccct catagaagtt cggttttaca cactggtttt 480

gacccagtaa ctcgcggtct attgccagaa gacaagcggt tgcaacttaa agactacttt 540

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

Gln Ala Leu Asp Glu Ser Gln Val Gly Trp His Thr Ala Asn Gln Ile
50 55 60

Gly Asn Lys Tyr Tyr Tyr Gly Ile Glu Val Cys Gln Ser Met Gly Ala
65 70 75 80

Asp Asn Ala Thr Phe Leu Lys Asn Glu Gln Ala Thr Phe Gln Glu Cys
85 90 95

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Ala Arg Leu Leu Lys Lys Trp Gly Leu Pro Ala Asn Arg Asn Thr Ile
            100                 105                 110

Arg Leu His Asn Glu Phe Thr Ser Thr Ser Cys Pro His Arg Ser Ser
        115                 120                 125

Val Leu His Thr Gly Phe Asp Pro Val Thr Arg Gly Leu Leu Pro Glu
    130                 135                 140

Asp Lys Arg Leu Gln Leu Lys Asp Tyr Phe Ile Lys Gln Ile Arg Ala
145                 150                 155                 160

Tyr Met Asp
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