SEQUENCE LISTING

<110> SICHUAN BAILI PHARMACEUTICAL CO. LTD.

<120> GUIDANCE AND NAVIGATION CONTROL PROTEINS AND METHOD OF MAKING AND USING THEREOF

<130> SIBA103PCT

<150> US62648880
<151> 2018-03-27

<150> US62648888
<151> 2018-03-27

<160> 110

<170> PatentIn version 3.5

<210> 1
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ccagggaagg ggctggagtg gatcggagtc attactggtc gtgatatcac atactacgcg 180

agctgggcga aaggcagatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgcg cgacggtgga 300

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

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

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

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

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

Arg Asp Gly Gly Ser Ser Ala Ile Thr Ser Asn Asn Ile Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
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gggaaagccc ctaagctcct gatctatgaa gcatccaaac tggcatctgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagag ttcactctca ccatcagcag cctgcagcct 240

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

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

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

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

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gly Tyr Phe Tyr Phe Ile Ser
85 90 95

Arg Thr Tyr Val Asn Ser Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

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ccagggaagg ggctggagtg gatcggagtc attactggtc gtgatatcac atactacgcg 180

agctgggcga aaggcagatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgcg cgacggtgga 300

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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ile Asp Leu Ser Ser Asn
20 25 30

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

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

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

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

Arg Asp Gly Gly Ser Ser Ala Ile Asn Ser Lys Asn Ile Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
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gggaaagccc ctaagctcct gatctatgaa gcatccaaac tggcatctgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagag ttcactctca ccatcagcag cctgcagcct 240

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

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

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

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

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gly Tyr Phe Tyr Phe Ile Ser
85 90 95

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

<210> 9
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tgggcgaaag gccgattcac catctccaaa gacaatacca agaacacggt gtatctgcaa 240

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ggttcccact tgtggggcca gggaaccctg gtcaccgtct ctagt 345

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

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<223> Synthesized

<400> 10

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

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

Ile Ile Thr Tyr Ser Gly Ser Arg Tyr Tyr Ala Asn Trp Ala Lys Gly
50 55 60

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

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

Asp Tyr Met Ser Gly Ser His Leu Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 11
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gggaaagccc ctaagctcct gatccattct gcatcctctc tggcatctgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240

gaagattttg caacttacta ttgtcaacag ggttatggta aaaataatgt tgataatgct 300

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<210> 12
<211> 110
<212> PRT
<213> Artificial Sequence

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<400> 12

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

Asp Arg Val Thr Ile Lys Cys Gln Ala Ser Glu Asp Ile Tyr Ser Phe
20 25 30

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Tyr Gly Lys Asn Asn
85 90 95

Val Asp Asn Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 13
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tacgcgagct ccgcgaaagg ccggttcacc atctccagag acaattccaa gaacacgctg 240

tatctgcaaa tgaacagcct gagagccgag gacacggccg tatattactg tgcgagagat 300

agtagtagtt attatatgtt taacttgtgg ggccagggaa ccctggtcac cgtctcgagc 360

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

<220>
<223> Synthesized

<400> 14

Gln Ser Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser

1 5 10 15

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

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

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

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

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

Cys Ala Arg Asp Ser Ser Ser Tyr Tyr Met Phe Asn Leu Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 15
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aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240

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ggtgctttcg gcggagggac caaggtggag atcaaa 336

<210> 16
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
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<400> 16

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

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

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

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

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

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

<210> 17
<211> 345
<212> DNA
<213> Artificial Sequence

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tccgcgagag gcagattcac catctccaga ccctcgtcca agaacacggt ggatcttcaa 240

atgaacagcc tgagagccga ggacacggct gtgtattact gtgcgagaga ctctggttat 300

agtgatccta tgtggggcca gggaaccctg gtcaccgtct cgagc 345

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<212> PRT
<213> Artificial Sequence

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<223> Synthesized

<400> 18

Arg Ser Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
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Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Ile Ser Ser Tyr His
20 25 30

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

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

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

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

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

Val Ser Ser
115

<210> 19
<211> 333
<212> DNA
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gggaaagccc ctaagctcct gatctatgct gcagccaatc tggcatctgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcga cctggagcct 240

ggcgatgctg caacttacta ttgtcagtct acctatcttg gtactgatta tgttggcggt 300

gctttcggcg gagggaccaa ggtggagatc aaa 333

<210> 20
<211> 111
<212> PRT
<213> Artificial Sequence

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<223> Synthesized

<400> 20

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

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

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

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

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

Gly Asp Ala Ala Thr Tyr Tyr Cys Gln Ser Thr Tyr Leu Gly Thr Asp
85 90 95

Tyr Val Gly Gly Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys

100 105 110

<210> 21
<211> 345
<212> DNA
<213> Artificial Sequence

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gctccaggga aggggctgga gtggatcgca tgcatatata ctggtagccg cgatactcct 180

cactacgcga gctccgcgaa aggccggttc accatctcca gagacaattc caagaacacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg ccgtatatta ctgtgcgaga 300

gaaggtagcc tgtggggcca gggaaccctg gtcaccgtct cgagc 345

<210> 22
<211> 115
<212> PRT
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<400> 22

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ile Asp Phe Ser Arg Arg
20 25 30

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

Ile Ala Cys Ile Tyr Thr Gly Ser Arg Asp Thr Pro His Tyr Ala Ser
50 55 60

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

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

Tyr Cys Ala Arg Glu Gly Ser Leu Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 23
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
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atcacttgcc agtccagtca gagtgtttat agtaactggt tctcctggta tcagcagaaa 120

ccagggaaag cccctaagct cctgatctat tctgcatcca ctctggcatc tggggtccca 180

tcaaggttca gcggcagtgg atctgggaca gaattcactc tcaccatcag cagcctgcag 240

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gctttcggcg gagggaccaa ggtggagatc aaa 333

<210> 24
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 24

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

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

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

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

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

Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Ala Gly Gly Tyr Asn Thr Val
85 90 95

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

<210> 25
<211> 357
<212> DNA
<213> Artificial Sequence

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tggacaaaag gcagattcac catctccaaa gacaatacca agaacacggt ggatcttcaa 240

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ggtgataaga ctggtttagg catctggggc cagggaactc tggttaccgt ctcttca 357

<210> 26
<211> 119
<212> PRT
<213> Artificial Sequence

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<400> 26

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

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

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

Thr Ile Tyr Thr Ser Gly Ser Thr Trp Tyr Ala Ser Trp Thr Lys Gly
50 55 60

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

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

Ser Tyr Tyr Gly Gly Asp Lys Thr Gly Leu Gly Ile Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 27
<211> 339
<212> DNA
<213> Artificial Sequence

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aggttcagcg gcagtggatc tgggacagag ttcactctca ccatcagcag cctgcagcct 240

gatgattttg caacttatta ctgccaatct gcttatggtg ttagtggtac tagtagttat 300

ttatatactt tcggcggagg gaccaaggtg gagatcaaa 339

<210> 28
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 28

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

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

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

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

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

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

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

Lys

<210> 29
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized

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ccagggaagg ggctggagtg gatcggacat atttatgtta ataatgatga cacagactac 180

gcgagctccg cgaaaggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccacct atttctgtgc gagattggat 300

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tcttca 366

<210> 30
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 30

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

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

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

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

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

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

Ala Arg Leu Asp Val Gly Gly Gly Gly Ala Tyr Ile Gly Asp Ile Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 31
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<212> DNA
<213> Artificial Sequence

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atcacttgcc agtccagtca gagtgtttat aacaacaacg acttagcctg gtatcagcag 120

aaaccaggga aagttcctaa gctcctgatc tattatgctt ccactctggc atctggggtc 180

ccatctcggt tcagtggcag tggatctggg acagatttca ctctcaccat cagcagcctg 240

cagcctgaag atgttgcaac ttattactgt gcaggcggtt atgatacgga tggtcttgat 300

acgtttgctt tcggcggagg gaccaaggtg gagatcaaa 339

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<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 32

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

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

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

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

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

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

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

Lys

<210> 33
<211> 345
<212> DNA
<213> Artificial Sequence

<220>
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tcctgtactg cctctggatt ctccctcagt agctatgcaa tgagctgggt ccgccaggct 120

ccagggaggg ggctggagtg gatcggaatc atttatgcta gtggtagcac atactacgcg 180

agctcggcga aaggcagatt caccatctcc aaagacaata ccaagaacac ggtggatctt 240

caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag aatttatgac 300

ggcatggacc tctggggcca gggaactctg gttaccgtct cttca 345

<210> 34
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 34

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

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

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

Gly Ile Ile Tyr Ala Ser Gly Ser Thr Tyr Tyr Ala Ser Ser Ala Lys
50 55 60

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

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

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

Val Ser Ser
115

<210> 35
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 35
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcaattgcc aggccagtca gaacatttac agctacttat cctggtatca gcagaaacca 120

gggaaagttc ctaagcgcct gatctatctg gcatctactc tggcatctgg ggtcccatct 180

cggttcagtg gcagtggatc tgggacagat tacactctca ccatcagcag cctgcagcct 240

gaagatgttg caacttatta ctgtcaaagc aattataacg gtaattatgg tttcggcgga 300

gggaccaagg tggagatcaa a 321

<210> 36
<211> 107
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthesized

<400> 36

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

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

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

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

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

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

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

<210> 37
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 37
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt ctccctcaat aactactgga tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg gatcggaacc attagtagtg gtgcgtatac atggttcgcc 180

acctgggcga caggcagatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag atattcttct 300

actactgatt ggacctactt taacatctgg ggccagggaa ctctggttac cgtctcttca 360

<210> 38
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 38

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

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

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

Gly Thr Ile Ser Ser Gly Ala Tyr Thr Trp Phe Ala Thr Trp Ala Thr
50 55 60

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

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

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 39
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 39
gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc aggccagtca gagcattaat aactacttag cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatagg gcatccactc tggaatctgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240

gatgattttg caacttatta ctgccaaagc tataatggtg ttggtaggac tgctttcggc 300

ggagggacca aggtggagat caaa 324

<210> 40
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 40

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

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

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

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

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

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

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

<210> 41
<211> 354
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthesized

<400> 41
gaggtgaagc tggatgagac tggaggaggc ttggtgcaac ctgggaggcc catgaaactc 60

tcctgtgttg cctctggatt cacttttagt gactactgga tgaactgggt ccgccagtct 120

ccagagaaag gactggagtg ggtagcacaa attagaaaca aaccttataa ttatgaaaca 180

tattattcag attctgtgaa aggcagattc accatctcaa gagatgattc caaaagtagt 240

gtctacctgc aaatgaacaa cttaagagtt gaagacatgg gtatctatta ctgtacgggt 300

tcttactatg gtatggacta ctggggtcaa ggaacctcag tcaccgtctc ctca 354

<210> 42
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 42

Glu Val Lys Leu Asp Glu Thr Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

Pro Met Lys Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

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

Ala Gln Ile Arg Asn Lys Pro Tyr Asn Tyr Glu Thr Tyr Tyr Ser Asp
50 55 60

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

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

Tyr Cys Thr Gly Ser Tyr Tyr Gly Met Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Ser Val Thr Val Ser Ser
115

<210> 43
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 43
gatgtcgtga tgacccaaac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc 60

atctcttgca gatctagtca gagccttgta cacagtaatg gaaacaccta tttacgttgg 120

tacctgcaga agccaggcca gtctccaaag gtcctgatct acaaagtttc caaccgattt 180

tctggggtcc cagacaggtt cagtggcagt ggatcaggga cagatttcac actcaagatc 240

agcagagtgg aggctgagga tctgggagtt tatttctgct ctcaaagtac acatgttccg 300

tggacgttcg gtggaggcac caagctggaa atcaaa 336

<210> 44
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 44

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

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

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

Pro Lys Val Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro

50 55 60

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

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

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

<210> 45
<211> 987
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 45
gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 60

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 120

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 180

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 240

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagag agttgagccc 300

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaagc cgcgggggca 360

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct 420

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 480

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 540

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 600

gagtacaagt gcgcggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 660

aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggatgag 720

ctgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc 780

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 840

ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg 900

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 960

cagaagagcc tctccctgtc tccgggt 987

<210> 46
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 46

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

145 150 155 160

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

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Ala Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225 230 235 240

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

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

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly
325

<210> 47
<211> 321
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthesized

<400> 47
cgtacggtgg ctgcaccatc tgtcttcatc ttcccgccat ctgatgagca gttgaaatct 60

ggaactgcct ctgttgtgtg cctgctgaat aacttctatc ccagagaggc caaagtacag 120

tggaaggtgg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac 180

agcaaggaca gcacctacag cctcagcagc accctgacgc tgagcaaagc agactacgag 240

aaacacaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaag 300

agcttcaaca ggggagagtg t 321

<210> 48
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 48

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1 5 10 15

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

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

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
50 55 60

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65 70 75 80

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
85 90 95

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 49
<211> 3681
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 49
gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc agtccagtca gagtgtttat agtaactggt tctcctggta tcagcagaaa 120

ccagggaaag cccctaagct cctgatctat tctgcatcca ctctggcatc tggggtccca 180

tcaaggttca gcggcagtgg atctgggaca gaattcactc tcaccatcag cagcctgcag 240

cctgatgatt ttgcaactta ttactgcgca ggcggttaca atactgttat tgatactttt 300

gctttcggcg gagggaccaa ggtggagatc aaaggcggtg gcggtagtgg gggaggcggt 360

tctggcggcg gagggtccgg cggtggagga tcagaggtgc agctgttgga gtctggggga 420

ggcttggtac agcctggggg gtccctgaga ctctcctgtg cagcctctgg aatcgacttc 480

agtaggagat actacatgtg ctgggtccgc caggctccag ggaaggggct ggagtggatc 540

gcatgcatat atactggtag ccgcgatact cctcactacg cgagctccgc gaaaggccgg 600

ttcaccatct ccagagacaa ttccaagaac acgctgtatc tgcaaatgaa cagcctgaga 660

gccgaggaca cggccgtata ttactgtgcg agagaaggta gcctgtgggg ccagggaacc 720

ctggtcaccg tctcgagcgg cggtggaggg tccggcggtg gtggatccca gtcggtggag 780

gagtctgggg gaggcttggt ccagcctggg gggtccctga gactctcctg tacagcctct 840

ggaatcgacc ttaataccta cgacatgatc tgggtccgcc aggctccagg caaggggcta 900

gagtgggttg gaatcattac ttatagtggt agtagatact acgcgaactg ggcgaaaggc 960

cgattcacca tctccaaaga caataccaag aacacggtgt atctgcaaat gaacagcctg 1020

agagctgagg acacggctgt gtattactgt gccagagatt atatgagtgg ttcccacttg 1080

tggggccagg gaaccctggt caccgtctct agtgctagca ccaagggccc atcggtcttc 1140

cccctggcac cctcctccaa gagcacctct gggggcacag cggccctggg ctgcctggtc 1200

aaggactact tccccgaacc ggtgacggtg tcgtggaact caggcgccct gaccagcggc 1260

gtgcacacct tcccggctgt cctacagtcc tcaggactct actccctcag cagcgtggtg 1320

accgtgccct ccagcagctt gggcacccag acctacatct gcaacgtgaa tcacaagccc 1380

agcaacacca aggtggacaa gagagttgag cccaaatctt gtgacaaaac tcacacatgc 1440

ccaccgtgcc cagcacctga agccgcgggg gcaccgtcag tcttcctctt cccccaaaa 1500

cccaaggaca ccctcatgat ctcccggacc cctgaggtca catgcgtggt ggtggacgtg 1560

agccacgaag accctgaggt caagttcaac tggtacgtgg acggcgtgga ggtgcataat 1620

gccaagacaa agccgcggga ggagcagtac aacagcacgt accgtgtggt cagcgtcctc 1680

accgtcctgc accaggactg gctgaatggc aaggagtaca agtgcgcggt ctccaacaaa 1740

gccctcccag cccccatcga gaaaaccatc tccaaagcca aagggcagcc ccgagaacca 1800

caggtgtata ccctgccccc atcccgggat gagctgacca agaaccaggt cagcctgacc 1860

tgcctggtca aaggcttcta tcccagcgac atcgccgtgg agtgggagag caatgggcag 1920

ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc 1980

tatagcaagc tcaccgtgga caagagcagg tggcagcagg ggaacgtctt ctcatgctcc 2040

gtgatgcatg aggctctgca caaccactac acgcagaaga gcctctccct gtctccgggt 2100

ggcggtggag ggtccggcgg tggtggatcc gaggtgcagc tgttggagtc tgggggaggc 2160

ttggtacagc ctgggggtc cctgagactc tcctgtgcag cctctggatt caccatcagt 2220

cgctaccaca tgacttgggt ccgccaggct ccagggaagg ggctggagtg gatcggacat 2280

atttatgtta ataatgatga cacagactac gcgagctccg cgaaaggccg gttcaccatc 2340

tccagagaca attccaagaa cacgctgtat ctgcaaatga acagcctgag agccgaggac 2400

acggccacct atttctgtgc gagattggat gttggtggtg gtggtgctta tattggggac 2460

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gtttataaca acaacgactt agcctggtat cagcagaaac cagggaaagt tcctaagctc 2700

ctgatctatt atgcttccac tctggcatct ggggtcccat ctcggttcag tggcagtgga 2760

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aaggtggaga tcaaaggcgg tggagggtcc ggcggtggtg gatccgaggt gcagctggtg 2940

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ggattcacca tcagtaccaa tgcaatgagc tgggtccgcc aggctccagg gaaggggctg 3060

gagtggatcg gagtcattac tggtcgtgat atcacatact acgcgagctg ggcgaaaggc 3120

agattcacca tctccagaga caattccaag aacacgctgt atcttcaaat gaacagcctg 3180

agagccgagg acacggctgt gtattactgt gcgcgcgacg gtggatcatc tgctattact 3240

agtaacaaca tttggggcca aggaactctg gtcaccgttt cttcaggcgg tggcggtagt 3300

gggggaggcg gttctggcgg cggagggtcc ggcggtggag gatcagacgt cgtgatgacc 3360

cagtctcctt ccaccctgtc tgcatctgta ggagacagag tcaccatcaa ttgccaagcc 3420

agtgagagca ttagcagttg gttagcctgg tatcagcaga aaccagggaa agcccctaag 3480

ctcctgatct atgaagcatc caaactggca tctggggtcc catcaaggtt cagcggcagt 3540

ggatctggga cagagttcac tctcaccatc agcagcctgc agcctgatga ttttgcaact 3600

tattactgcc aaggctattt ttattttatt agtcgtactt atgtaaattc tttcggcgga 3660

gggaccaagg tggagatcaa a 3681

<210> 50
<211> 1227
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 50

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

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

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

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

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

Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Ala Gly Gly Tyr Asn Thr Val
85 90 95

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

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

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

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ile Asp Phe
145 150 155 160

Ser Arg Arg Tyr Tyr Met Cys Trp Val Arg Gln Ala Pro Gly Lys Gly
165 170 175

Leu Glu Trp Ile Ala Cys Ile Tyr Thr Gly Ser Arg Asp Thr Pro His
180 185 190

Tyr Ala Ser Ser Ala Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
195 200 205

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

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

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
245 250 255

Gln Ser Val Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
260 265 270

Leu Arg Leu Ser Cys Thr Ala Ser Gly Ile Asp Leu Asn Thr Tyr Asp
275 280 285

Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly
290 295 300

Ile Ile Thr Tyr Ser Gly Ser Arg Tyr Tyr Ala Asn Trp Ala Lys Gly
305 310 315 320

Arg Phe Thr Ile Ser Lys Asp Asn Thr Lys Asn Thr Val Tyr Leu Gln
325 330 335

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
340 345 350

Asp Tyr Met Ser Gly Ser His Leu Trp Gly Gln Gly Thr Leu Val Thr
355 360 365

Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
370 375 380

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
385 390 395 400

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

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
420 425 430

Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
435 440 445

Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
450 455 460

Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
465 470 475 480

Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu
485 490 495

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
500 505 510

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
515 520 525

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
530 535 540

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
545 550 555 560

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Ala
565 570 575

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

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
595 600 605

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
610 615 620

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
625 630 635 640

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
645 650 655

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
660 665 670

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
675 680 685

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly

690 695 700

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly
705 710 715 720

Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
725 730 735

Phe Thr Ile Ser Arg Tyr His Met Thr Trp Val Arg Gln Ala Pro Gly
740 745 750

Lys Gly Leu Glu Trp Ile Gly His Ile Tyr Val Asn Asn Asp Asp Thr
755 760 765

Asp Tyr Ala Ser Ser Ala Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
770 775 780

Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
785 790 795 800

Thr Ala Thr Tyr Phe Cys Ala Arg Leu Asp Val Gly Gly Gly Gly Ala
805 810 815

Tyr Ile Gly Asp Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
820 825 830

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
835 840 845

Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
850 855 860

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ser Ser Gln Ser
865 870 875 880

Val Tyr Asn Asn Asn Asp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
885 890 895

Val Pro Lys Leu Leu Ile Tyr Tyr Ala Ser Thr Leu Ala Ser Gly Val
900 905 910

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
915 920 925

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Ala Gly
930 935 940

Gly Tyr Asp Thr Asp Gly Leu Asp Thr Phe Ala Phe Gly Gly Gly Thr
945 950 955 960

Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
965 970 975

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
980 985 990

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Ile Ser Thr Asn Ala
995 1000 1005

Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
1010 1015 1020

Gly Val Ile Thr Gly Arg Asp Ile Thr Tyr Tyr Ala Ser Trp Ala
1025 1030 1035

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
1040 1045 1050

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
1055 1060 1065

Tyr Cys Ala Arg Asp Gly Gly Ser Ser Ala Ile Thr Ser Asn Asn
1070 1075 1080

Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
1085 1090 1095

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
1100 1105 1110

Gly Ser Asp Val Val Met Thr Gln Ser Pro Ser Thr Leu Ser Ala
1115 1120 1125

Ser Val Gly Asp Arg Val Thr Ile Asn Cys Gln Ala Ser Glu Ser
1130 1135 1140

Ile Ser Ser Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala
1145 1150 1155

Pro Lys Leu Leu Ile Tyr Glu Ala Ser Lys Leu Ala Ser Gly Val
1160 1165 1170

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu
1175 1180 1185

Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
1190 1195 1200

Gln Gly Tyr Phe Tyr Phe Ile Ser Arg Thr Tyr Val Asn Ser Phe
1205 1210 1215

Gly Gly Gly Thr Lys Val Glu Ile Lys
1220 1225

<210> 51
<211> 651
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 51
gcctatgata tgacccagtc tccatcttcc gtgtctgcat ctgtaggaga cagagtcacc 60

atcaagtgtc aggccagtga ggacatttat agcttcttgg cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatccattct gcatcctctc tggcatctgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240

gaagattttg caacttacta ttgtcaacag ggttatggta aaaataatgt tgataatgct 300

ttcggcggag ggaccaaggt ggagatcaaa cgtacggtgg ctgcaccatc tgtcttcatc 360

ttcccgccat ctgatgagca gttgaaatct ggaactgcct ctgttgtgtg cctgctgaat 420

aacttctatc ccagagaggc caaagtacag tggaaggtgg ataacgccct ccaatcgggt 480

aactcccagg agagtgtcac agagcaggac agcaaggaca gcacctacag cctcagcagc 540

accctgacgc tgagcaaagc agactacgag aaacacaaag tctacgcctg cgaagtcacc 600

catcagggcc tgagctcgcc cgtcacaaag agcttcaaca ggggagagtg t 651

<210> 52
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 52

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

Asp Arg Val Thr Ile Lys Cys Gln Ala Ser Glu Asp Ile Tyr Ser Phe
20 25 30

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Tyr Gly Lys Asn Asn
85 90 95

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

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

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

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

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

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

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

Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 53
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> Syntheized

<400> 53
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt caccatcagt accaatgcaa tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg gatcggagtc attactggtc gtgatatcac atactacgcg 180

agctgggcga aaggcagatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag agacggtggt 300

tcttctgcta ttactagtaa caacatttgg ggccagggaa ccctggtcac cgtgtcgaca 360

<210> 54
<211> 120
<212> PRT
<213> Artificial Sequence

<220>

<223> Syntheized

<400> 54

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

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

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

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

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

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

Arg Asp Gly Gly Ser Ser Ala Ile Thr Ser Asn Asn Ile Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Thr
115 120

<210> 55
<211> 345
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 55
cggtcgctgg tggagtctgg gggaggcttg gtccagcctg gggggtccct gagactctcc 60

tgtacagcct ctggattcac catcagtagc taccacatgc agtgggtccg ccaggctcca 120

gggaaggggc tggagtacat cggaaccatt agtagtggtg gtaatgtata ctacgcaagc 180

tccgctagag gcagattcac catctccaga ccctcgtcca agaacacggt ggatcttcaa 240

atgaacagcc tgagagccga ggacacggct gtgtattact gtgcgagaga ctctggttat 300

agtgatccta tgtggggcca gggaaccctg gtcaccgtgt cgaca 345

<210> 56
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 56

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

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

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

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

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

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

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

Val Ser Thr
115

<210> 57
<211> 345
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthesized

<400> 57
cagtcggtgg aggagtctgg gggaggcttg gtccagcctg gggggtccct gagactctcc 60

tgtaccgcct ctggaatcga ccttaatacc tacgacatga tctgggtccg ccaggctcca 120

ggcaaggggc tagagtgggt tggaatcatt acttatagtg gtagtagata ctacgcgaac 180

tgggcgaaag gccgattcac catctccaaa gacaatacca agaacacggt gtatctgcaa 240

atgaacagcc tgagagctga ggacacggct gtgtattact gtgcgagaga ttatatgagt 300

ggttcccact tgtggggcca gggaaccctg gtcaccgtgt cgaca 345

<210> 58
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 58

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

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

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

Ile Ile Thr Tyr Ser Gly Ser Arg Tyr Tyr Ala Asn Trp Ala Lys Gly
50 55 60

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

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

Asp Tyr Met Ser Gly Ser His Leu Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Thr
115

<210> 59
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 59
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt ctccttcagt agcgggtacg acatgtgctg ggtccgccag 120

gctccaggga aggggctgga gtggatcgca tgcattgctg ctggtagtgc tggtatcact 180

tacgacgcga actgggcgaa aggccggttc accatctcca gagacaattc caagaacacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg ccgtatatta ctgtgcgaga 300

tcggcgtttt cgttcgacta cgccatggac ctctggggcc agggaaccct ggtcaccgtc 360

tcgagc 366

<210> 60
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 60

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

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

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

Ile Ala Cys Ile Ala Ala Gly Ser Ala Gly Ile Thr Tyr Asp Ala Asn
50 55 60

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

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

Tyr Cys Ala Arg Ser Ala Phe Ser Phe Asp Tyr Ala Met Asp Leu Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 61
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 61
gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc aggccagtca gagcattagt tcccacttaa actggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctataag gcatccactc tggcatctgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa tttactctca ccatcagcag cctgcagcct 240

gatgattttg caacttatta ctgccaacag ggttatagtt ggggtaatgt tgataatgtt 300

ttcggcggag ggaccaaggt ggagatcaaa 330

<210> 62
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 62

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

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

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

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

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

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

Val Asp Asn Val Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 63
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 63
gaggtgcagc tggtgcagtc tggagcagag gtgaagaaac caggagagtc tctgaagatc 60

tcctgtaagg gttctggata cagctttagc agttcatgga tcggctgggt gcgccaggca 120

cctgggaaag gcctggaatg gatggggatc atctatcctg atgactctga taccagatac 180

agtccatcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag gactgcctac 240

ctgcagtgga gtagcctgaa ggcctcggac accgctatgt attactgtgc gagacatgtt 300

actatgattt ggggagttat tattgacttc tggggccagg gaaccctggt caccgtctcc 360

tca 363

<210> 64
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 64

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Ser Ser Ser
20 25 30

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

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

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

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

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

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 65
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 65
gccatccagt tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gggcattagc agtgctttag cctggtatca gcagaaacca 120

gggaaagctc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240

gaagattttg caacttatta ctgtcaacag tttaatagtt acccattcac tttcggccct 300

gggaccaaag tggatatcaa a 321

<210> 66
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 66

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

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

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

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

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

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

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

<210> 67
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 67
gatgtgcagc ttcaggagtc gggacctagc ctggtgaaac cttctcagtc tctgtccctc 60

acctgcactg tcactggcta ctcaatcacc agtgattttg cctggaactg gattcggcag 120

tttccaggaa acaagctgga gtggatgggc tacataagtt atagtggtaa cactaggtac 180

aacccatctc tcaaaagtcg aatctctatc actcgcgaca catccaagaa ccaattcttc 240

ctgcagttga actctgtgac tattgaggac acagccacat attactgtgt aacggcggga 300

cgcgggtttc cttattgggg ccaagggact ctggtcactg tctctgca 348

<210> 68
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 68

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

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

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

Met Gly Tyr Ile Ser Tyr Ser Gly Asn Thr Arg Tyr Asn Pro Ser Leu
50 55 60

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

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

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

Thr Val Ser Ala

115

<210> 69
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 69
gacatcctga tgacccaatc tccatcctcc atgtctgtat ctctgggaga cacagtcagc 60

atcacttgcc attcaagtca ggacattaac agtaatatag ggtggttgca gcagagacca 120

gggaaatcat ttaagggcct gatctatcat ggaaccaact tggacgatga agttccatca 180

aggttcagtg gcagtggatc tggagccgat tattctctca ccatcagcag cctggaatct 240

gaagattttg cagactatta ctgtgtacag tatgctcagt ttccgtggac gttcggtgga 300

ggcaccaagc tggaaatcaa a 321

<210> 70
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 70

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

Asp Thr Val Ser Ile Thr Cys His Ser Ser Gln Asp Ile Asn Ser Asn
20 25 30

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

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

Ser Gly Ser Gly Ala Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser
65 70 75 80

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

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

<210> 71
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 71
ggcggtggag ggtccggcgg tggtggctcc gga 33

<210> 72
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 72

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10

<210> 73
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 73
ggcggtggag ggtccggcgg tggtggatca 30

<210> 74
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 74

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 75
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 75
ggcggtggag ggtccggcgg tggtggatcc 30

<210> 76
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 76

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 77
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 77
ggcggtggcg gtagtggggg aggcggttct ggcggcggag ggtccggcgg tggaggatca 60

<210> 78
<211> 20
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthesized

<400> 78

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser
20

<210> 79
<211> 3693
<212> DNA
<213> Artificial Sequence

<220>
<223> synthesized

<400> 79
gacgtcgtga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga cagagtcacc 60

atcaattgcc aagccagtga gagcattagc agttggttag cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgaa gcatccaaac tggcatctgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagag ttcactctca ccatcagcag cctgcagcct 240

gatgattttg caacttatta ctgccaaggc tatttttatt ttattagtcg tacttatgta 300

aattctttcg gcggagggac caaggtggag atcaaaggcg gtggcggtag tgggggaggc 360

ggttctggcg gcggagggtc cggcggtgga ggatcagagg tgcagctggt ggagtctggg 420

ggaggcttgg tccagcctgg ggggtccctg agactctcct gtgcagcctc tggattcacc 480

atcagtacca atgcaatgag ctgggtccgc caggctccag ggaaggggct ggagtggatc 540

ggagtcatta ctggtcgtga tatcacatac tacgcgagct gggcgaaagg cagattcacc 600

atctccagag acaattccaa gaacacgctg tatcttcaaa tgaacagcct gagagccgag 660

gacacggctg tgtattactg tgcgcgcgac ggtggatcat ctgctattac tagtaacaac 720

atttggggcc aaggaactct ggtcaccgtt tcttcaggcg gtggagggtc cggcggtggt 780

ggatccgatg tgcagcttca ggagtcggga cctagcctgg tgaaaccttc tcagtctctg 840

tccctcacct gcactgtcac tggctactca atcaccagtg attttgcctg gaactggatt 900

cggcagtttc caggaaacaa gctggagtgg atgggctaca taagttatag tggtaacact 960

aggtacaacc catctctcaa aagtcgaatc tctatcactc gcgacacatc caagaaccaa 1020

ttcttcctgc agttgaactc tgtgactatt gaggacacag ccacatatta ctgtgtaacg 1080

gcgggacgcg ggtttcctta ttggggccaa gggactctgg tcactgtctc tgcagctagc 1140

accaagggcc catcggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca 1200

gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 1260

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 1320

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 1380

tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agagagttga gcccaaatct 1440

tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagccgcggg ggcaccgtca 1500

gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 1560

acatgcgtgg tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 1620

gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 1680

taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 1740

aagtgcgcgg tctccaacaa agccctccca gcccccatcg agaaaaccat ctccaaagcc 1800

aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc 1860

aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1920

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1980

tccgacggct ccttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag 2040

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 2100

agcctctccc tgtctccggg tggcggtgga gggtccggcg gtggtggatc cgaggtgcag 2160

ctgttggagt ctgggggagg cttggtacag cctgggggt ccctgagact ctcctgtgca 2220

gcctctggat tctccttcag tagcgggtac gacatgtgct gggtccgcca ggctccaggg 2280

aaggggctgg agtggatcgc atgcattgct gctggtagtg ctggtatcac ttacgacgcg 2340

aactgggcga aaggccggtt caccatctcc agagacaatt ccaagaacac gctgtatctg 2400

caaatgaaca gcctgagagc cgaggacacg gccgtatatt actgtgcgag atcggcgttt 2460

tcgttcgact acgccatgga cctctggggc cagggaaccc tggtcaccgt ctcgagcggc 2520

ggtggcggta gtgggggagg cggttctggc ggcggagggt ccggcggtgg aggatcagac 2580

atccagatga cccagtctcc ttccaccctg tctgcatctg taggagacag agtcaccatc 2640

acttgccagg ccagtcagag cattagttcc cacttaaact ggtatcagca gaaaccaggg 2700

aaagccccta agctcctgat ctataaggca tccactctgg catctggggt cccatcaagg 2760

ttcagcggca gtggatctgg gacagaattt actctcacca tcagcagcct gcagcctgat 2820

gattttgcaa cttattactg ccaacagggt tatagttggg gtaatgttga taatgttttc 2880

ggcggaggga ccaaggtgga gatcaaaggc ggtggagggt ccggcggtgg tggatcccag 2940

tcgctggtgg agtctggggg aggcttggta cagcctgggg ggtccctgag actctcctgt 3000

gcagcctctg gattctcctt cagtagcaac tactggatat gctgggtccg ccaggctcca 3060

gggaaggggc tggagtggat cgcatgtatt tatgttggta gtagtggtga cacttactac 3120

gcgagctccg cgaaaggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 3180

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gagagatagt 3240

agtagttatt atatgtttaa cttgtggggc cagggaaccc tggtcaccgt ctcttcaggc 3300

ggtggcggta gtgggggagg cggttctggc ggcggagggt ccggcggtgg aggatcagcc 3360

cttgtgatga cccagtctcc ttccaccctg tctgcatctg taggagacag agtcaccatc 3420

aattgccagg ccagtgagga cattgatacc tatttagcct ggtatcagca gaaaccaggg 3480

aaagccccta agctcctgat cttttacgca tccgatctgg catctggggt cccatcaagg 3540

ttcagcggca gtggatctgg gacagaattt actctcacca tcagcagcct gcagcctgat 3600

gattttgcaa cttattactg ccaaggcggt tactatacta gtagtgctga tacgaggggt 3660

gctttcggcg gagggaccaa ggtggagatc aaa 3693

<210> 80
<211> 1231
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 80

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

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

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

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

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

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gly Tyr Phe Tyr Phe Ile Ser
85 90 95

Arg Thr Tyr Val Asn Ser Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

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

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

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Ile Ser Thr Asn Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
165 170 175

Leu Glu Trp Ile Gly Val Ile Thr Gly Arg Asp Ile Thr Tyr Tyr Ala
180 185 190

Ser Trp Ala Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
195 200 205

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

Tyr Tyr Cys Ala Arg Asp Gly Gly Ser Ser Ala Ile Thr Ser Asn Asn
225 230 235 240

Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
245 250 255

Ser Gly Gly Gly Gly Ser Asp Val Gln Leu Gln Glu Ser Gly Pro Ser
260 265 270

Leu Val Lys Pro Ser Gln Ser Leu Ser Leu Thr Cys Thr Val Thr Gly
275 280 285

Tyr Ser Ile Thr Ser Asp Phe Ala Trp Asn Trp Ile Arg Gln Phe Pro
290 295 300

Gly Asn Lys Leu Glu Trp Met Gly Tyr Ile Ser Tyr Ser Gly Asn Thr
305 310 315 320

Arg Tyr Asn Pro Ser Leu Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr
325 330 335

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

Thr Ala Thr Tyr Tyr Cys Val Thr Ala Gly Arg Gly Phe Pro Tyr Trp
355 360 365

Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro
370 375 380

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

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
405 410 415

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
420 425 430

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr

435 440 445

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

His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser
465 470 475 480

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala
485 490 495

Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
500 505 510

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
515 520 525

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
530 535 540

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
545 550 555 560

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
565 570 575

Gly Lys Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro
580 585 590

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
595 600 605

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
610 615 620

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
625 630 635 640

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
645 650 655

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
660 665 670

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
675 680 685

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
690 695 700

Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln
705 710 715 720

Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
725 730 735

Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Gly Tyr Asp Met
740 745 750

Cys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Ala Cys
755 760 765

Ile Ala Ala Gly Ser Ala Gly Ile Thr Tyr Asp Ala Asn Trp Ala Lys
770 775 780

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
785 790 795 800

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
805 810 815

Arg Ser Ala Phe Ser Phe Asp Tyr Ala Met Asp Leu Trp Gly Gln Gly
820 825 830

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
835 840 845

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr
850 855 860

Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
865 870 875 880

Thr Cys Gln Ala Ser Gln Ser Ile Ser Ser His Leu Asn Trp Tyr Gln
885 890 895

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Ala Ser Thr
900 905 910

Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
915 920 925

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr
930 935 940

Tyr Tyr Cys Gln Gln Gly Tyr Ser Trp Gly Asn Val Asp Asn Val Phe
945 950 955 960

Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly
965 970 975

Gly Gly Ser Gln Ser Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
980 985 990

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser
995 1000 1005

Ser Asn Tyr Trp Ile Cys Trp Val Arg Gln Ala Pro Gly Lys Gly
1010 1015 1020

Leu Glu Trp Ile Ala Cys Ile Tyr Val Gly Ser Ser Gly Asp Thr
1025 1030 1035

Tyr Tyr Ala Ser Ser Ala Lys Gly Arg Phe Thr Ile Ser Arg Asp
1040 1045 1050

Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala
1055 1060 1065

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Ser Ser Ser Tyr
1070 1075 1080

Tyr Met Phe Asn Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser
1085 1090 1095

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
1100 1105 1110

Ser Gly Gly Gly Gly Ser Ala Leu Val Met Thr Gln Ser Pro Ser
1115 1120 1125

Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Asn Cys Gln
1130 1135 1140

Ala Ser Glu Asp Ile Asp Thr Tyr Leu Ala Trp Tyr Gln Gln Lys
1145 1150 1155

Pro Gly Lys Ala Pro Lys Leu Leu Ile Phe Tyr Ala Ser Asp Leu
1160 1165 1170

Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
1175 1180 1185

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala
1190 1195 1200

Thr Tyr Tyr Cys Gln Gly Gly Tyr Tyr Thr Ser Ser Ala Asp Thr
1205 1210 1215

Arg Gly Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
1220 1225 1230

<210> 81
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 81

gacatcctga tgacccaatc tccatcctcc atgtctgtat ctctgggaga cacagtcagc 60

atcacttgcc attcaagtca ggacattaac agtaatatag ggtggttgca gcagagacca 120

gggaaatcat ttaagggcct gatctatcat ggaaccaact tggacgatga agttccatca 180

aggttcagtg gcagtggatc tggagccgat tattctctca ccatcagcag cctggaatct 240

gaagattttg cagactatta ctgtgtacag tatgctcagt ttccgtggac gttcggtgga 300

ggcaccaagc tggaaatcaa acgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 82
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 82

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

Asp Thr Val Ser Ile Thr Cys His Ser Ser Gln Asp Ile Asn Ser Asn
20 25 30

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

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

Ser Gly Ser Gly Ala Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser
65 70 75 80

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

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

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys
210

<210> 83
<211> 3678
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 83
gacatcctga tgacccaatc tccatcctcc atgtctgtat ctctgggaga cacagtcagc 60

atcacttgcc attcaagtca ggacattaac agtaatatag ggtggttgca gcagagacca 120

gggaaatcat ttaagggcct gatctatcat ggaaccaact tggacgatga agttccatca 180

aggttcagtg gcagtggatc tggagccgat tattctctca ccatcagcag cctggaatct 240

gaagattttg cagactatta ctgtgtacag tatgctcagt ttccgtggac gttcggtgga 300

ggcaccaagc tggaaatcaa aggcggtggc ggtagtgggg gaggcggttc tggcggcgga 360

gggtccggcg gtggaggatc agatgtgcag cttcaggagt cgggacctag cctggtgaaa 420

ccttctcagt ctctgtccct cacctgcact gtcactggct actcaatcac cagtgatttt 480

gcctggaact ggattcggca gtttccagga aacaagctgg agtggatggg ctacataagt 540

tatagtggta acactaggta caacccatct ctcaaaagtc gaatctctat cactcgcgac 600

acatccaaga accaattctt cctgcagttg aactctgtga ctattgagga cacagccaca 660

tattactgtg taacggcggg acgcgggttt ccttattggg gccaagggac tctggtcact 720

gtctctgcag gcggtggagg gtccggcggt ggtggatccg aggtgcagct ggtggagtct 780

gggggaggct tggtccagcc tgggggtcc ctgagactct cctgtgcagc ctctggattc 840

accatcagta ccaatgcaat gagctgggtc cgccaggctc cagggaaggg gctggagtgg 900

atcggagtca ttactggtcg tgatatcaca tactacgcga gctgggcgaa aggcagattc 960

accatctcca gagacaattc caagaacacg ctgtatcttc aaatgaacag cctgagagcc 1020

gaggacacgg ctgtgtatta ctgtgcgcgc gacggtggat catctgctat tactagtaac 1080

aacatttggg gccaaggaac tctggtcacc gtttcttcag ctagcaccaa gggcccatcg 1140

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gtggtgaccg tgccctccag cagcttgggc acccagacct acatctgcaa cgtgaatcac 1380

aagcccagca acaccaaggt ggacaagaga gttgagccca aatcttgtga caaaactcac 1440

acatgcccac cgtgcccagc acctgaagcc gcgggggcac cgtcagtctt cctcttcccc 1500

ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtggtggtg 1560

gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg 1620

cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 1680

gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg cgcggtctcc 1740

aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 1800

gaaccacagg tgtacaccct gcccccatcc cgggatgagc tgaccaagaa ccaggtcagc 1860

ctgacctgcc tggtcaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 1920

gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1980

ttcctctata gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 2040

tgctccgtga tgcatgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 2100

ccgggtggcg gtggagggtc cggcggtggt ggatccgagg tgcagctgtt ggagtctggg 2160

ggaggcttgg tacagcctgg ggggtccctg agactctcct gtgcagcctc tggattctcc 2220

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atcgcatgca ttgctgctgg tagtgctggt atcacttacg acgcgaactg ggcgaaaggc 2340

cggttcacca tctccagaga caattccaag aacacgctgt atctgcaaat gaacagcctg 2400

agagccgagg acacggccgt atattactgt gcgagatcgg cgttttcgtt cgactacgcc 2460

atggacctct ggggccaggg aaccctggtc accgtctcga gcggcggtgg cggtagtggg 2520

ggaggcggtt ctggcggcgg agggtccggc ggtggaggat cagacatcca gatgacccag 2580

tctccttcca ccctgtctgc atctgtagga gacagagtca ccatcacttg ccaggccagt 2640

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ctgatctata aggcatccac tctggcatct ggggtcccat caaggttcag cggcagtgga 2760

tctgggacag aatttactct caccatcagc agcctgcagc ctgatgattt tgcaacttat 2820

tactgccaac agggttatag ttggggtaat gttgataatg ttttcggcgg agggaccaag 2880

gtggagatca aaggcggtgg agggtccggc ggtggtggat cccagtcgct ggtggagtct 2940

gggggaggct tggtacagcc tgggggggtcc ctgagactct cctgtgcagc ctctggattc 3000

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tggatcgcat gtatttatgt tggtagtagt ggtgacactt actacgcgag ctccgcgaaa 3120

ggccggttca ccatctccag agacaattcc aagaacacgc tgtatctgca aatgaacagc 3180

ctgagagccg aggacacggc cgtatattac tgtgcgagag atagtagtag ttattatatg 3240

tttaacttgt ggggccaggg aaccctggtc accgtctctt caggcggtgg cggtagtggg 3300

ggaggcggtt ctggcggcgg agggtccggc ggtggaggat cagcccttgt gatgacccag 3360

tctccttcca ccctgtctgc atctgtagga gacagagtca ccatcaattg ccaggccagt 3420

gaggacattg atacctattt agcctggtat cagcagaaac cagggaaagc ccctaagctc 3480

ctgatctttt acgcatccga tctggcatct ggggtcccat caaggttcag cggcagtgga 3540

tctgggacag aatttactct caccatcagc agcctgcagc ctgatgattt tgcaacttat 3600

tactgccaag gcggttacta tactagtagt gctgatacga ggggtgcttt cggcggaggg 3660

accaaggtgg agatcaaa 3678

<210> 84
<211> 1226
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 84

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

Asp Thr Val Ser Ile Thr Cys His Ser Ser Gln Asp Ile Asn Ser Asn
20 25 30

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

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

Ser Gly Ser Gly Ala Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser
65 70 75 80

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

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser
100 105 110

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

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

Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Asp Phe
145 150 155 160

Ala Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp Met
165 170 175

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

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

Gln Leu Asn Ser Val Thr Ile Glu Asp Thr Ala Thr Tyr Tyr Cys Val
210 215 220

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

Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln
245 250 255

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
260 265 270

Leu Ser Cys Ala Ala Ser Gly Phe Thr Ile Ser Thr Asn Ala Met Ser
275 280 285

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Gly Val Ile
290 295 300

Thr Gly Arg Asp Ile Thr Tyr Tyr Ala Ser Trp Ala Lys Gly Arg Phe
305 310 315 320

Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn
325 330 335

Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Gly

340 345 350

Gly Ser Ser Ala Ile Thr Ser Asn Asn Ile Trp Gly Gln Gly Thr Leu
355 360 365

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
370 375 380

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
385 390 395 400

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
405 410 415

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
420 425 430

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
435 440 445

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
450 455 460

Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His
465 470 475 480

Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val
485 490 495

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
500 505 510

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
515 520 525

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
530 535 540

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
545 550 555 560

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
565 570 575

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

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
595 600 605

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
610 615 620

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
625 630 635 640

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
645 650 655

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
660 665 670

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
675 680 685

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly
690 695 700

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly
705 710 715 720

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
725 730 735

Ser Gly Phe Ser Phe Ser Ser Gly Tyr Asp Met Cys Trp Val Arg Gln
740 745 750

Ala Pro Gly Lys Gly Leu Glu Trp Ile Ala Cys Ile Ala Ala Gly Ser
755 760 765

Ala Gly Ile Thr Tyr Asp Ala Asn Trp Ala Lys Gly Arg Phe Thr Ile
770 775 780

Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu
785 790 795 800

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Ala Phe Ser
805 810 815

Phe Asp Tyr Ala Met Asp Leu Trp Gly Gln Gly Thr Leu Val Thr Val
820 825 830

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
835 840 845

Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr
850 855 860

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ala Ser
865 870 875 880

Gln Ser Ile Ser Ser His Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
885 890 895

Ala Pro Lys Leu Leu Ile Tyr Lys Ala Ser Thr Leu Ala Ser Gly Val
900 905 910

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
915 920 925

Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
930 935 940

Gly Tyr Ser Trp Gly Asn Val Asp Asn Val Phe Gly Gly Gly Thr Lys
945 950 955 960

Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser
965 970 975

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
980 985 990

Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Asn Tyr Trp Ile
995 1000 1005

Cys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Ala
1010 1015 1020

Cys Ile Tyr Val Gly Ser Ser Gly Asp Thr Tyr Tyr Ala Ser Ser
1025 1030 1035

Ala Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
1040 1045 1050

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
1055 1060 1065

Tyr Tyr Cys Ala Arg Asp Ser Ser Ser Tyr Tyr Met Phe Asn Leu
1070 1075 1080

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
1085 1090 1095

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
1100 1105 1110

Ser Ala Leu Val Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser
1115 1120 1125

Val Gly Asp Arg Val Thr Ile Asn Cys Gln Ala Ser Glu Asp Ile
1130 1135 1140

Asp Thr Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
1145 1150 1155

Lys Leu Leu Ile Phe Tyr Ala Ser Asp Leu Ala Ser Gly Val Pro
1160 1165 1170

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr

1175 1180 1185

Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln
1190 1195 1200

Gly Gly Tyr Tyr Thr Ser Ser Ala Asp Thr Arg Gly Ala Phe Gly
1205 1210 1215

Gly Gly Thr Lys Val Glu Ile Lys
1220 1225

<210> 85
<211> 657
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 85
gacgtcgtga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga cagagtcacc 60

atcaattgcc aagccagtga gagcattagc agttggttag cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgaa gcatccaaac tggcatctgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240

gatgattttg caacttatta ctgccaaggc tatttttatt ttattagtcg tacttatgta 300

aattctttcg gcggagggac caaggtggag atcaaacgta cggtggctgc accatctgtc 360

ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg 420

ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa 480

tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc 540

agcagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 600

gtcacccatc agggcctgag ctcgcccgtc acaaagagct tcaacagggg agagtgt 657

<210> 86
<211> 219
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthesized

<400> 86

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

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

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

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

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

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gly Tyr Phe Tyr Phe Ile Ser
85 90 95

Arg Thr Tyr Val Asn Ser Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

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

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

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

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

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

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

195 200 205

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

<210> 87
<211> 3681
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 87
gacgttgtga tgacccagtc tccatcttcc gtgtctgcat ctgtaggaga cagagtcacc 60

atcacctgtc aggccagtca gaacattagg acttacttat cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgct gcagccaatc tggcatctgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcga cctggagcct 240

ggcgatgctg caacttacta ttgtcagtct acctatcttg gtactgatta tgttggcggt 300

gctttcggcg gagggaccaa ggtggagatc aaaggcggtg gcggtagtgg gggaggcggt 360

tctggcggcg gagggtccgg cggtggagga tcacggtcgc tggtggagtc tgggggaggc 420

ttggtccagc ctgggggtc cctgagactc tcctgtacag cctctggatt caccatcagt 480

agctaccaca tgcagtgggt ccgccaggct ccagggaagg ggctggagta catcggaacc 540

attagtagtg gtggtaatgt atactacgcg agctccgcga gaggcagatt caccatctcc 600

agaccctcgt ccaagaacac ggtggatctt caaatgaaca gcctgagagc cgaggacacg 660

gctgtgtatt actgtgcgag agactctggt tatagtgatc ctatgtgggg ccagggaacc 720

ctggtcaccg tctcgagcgg cggtggaggg tccggcggtg gtggatccca gtcggtggag 780

gagtctgggg gaggcttggt ccagcctggg gggtccctga gactctcctg tacagcctct 840

ggaatcgacc ttaataccta cgacatgatc tgggtccgcc aggctccagg caaggggcta 900

gagtgggttg gaatcattac ttatagtggt agtagatact acgcgaactg ggcgaaaggc 960

cgattcacca tctccaaaga caataccaag aacacggtgt atctgcaaat gaacagcctg 1020

agagctgagg acacggctgt gtattactgt gccagagatt atatgagtgg ttcccacttg 1080

tggggccagg gaaccctggt caccgtctct agtgctagca ccaagggccc atcggtcttc 1140

cccctggcac cctcctccaa gagcacctct gggggcacag cggccctggg ctgcctggtc 1200

aaggactact tccccgaacc ggtgacggtg tcgtggaact caggcgccct gaccagcggc 1260

gtgcacacct tcccggctgt cctacagtcc tcaggactct actccctcag cagcgtggtg 1320

accgtgccct ccagcagctt gggcacccag acctacatct gcaacgtgaa tcacaagccc 1380

agcaacacca aggtggacaa gagagttgag cccaaatctt gtgacaaaac tcacacatgc 1440

ccaccgtgcc cagcacctga agccgcgggg gcaccgtcag tcttcctctt cccccaaaa 1500

cccaaggaca ccctcatgat ctcccggacc cctgaggtca catgcgtggt ggtggacgtg 1560

agccacgaag accctgaggt caagttcaac tggtacgtgg acggcgtgga ggtgcataat 1620

gccaagacaa agccgcggga ggagcagtac aacagcacgt accgtgtggt cagcgtcctc 1680

accgtcctgc accaggactg gctgaatggc aaggagtaca agtgcgcggt ctccaacaaa 1740

gccctcccag cccccatcga gaaaaccatc tccaaagcca aagggcagcc ccgagaacca 1800

caggtgtata ccctgccccc atcccgggat gagctgacca agaaccaggt cagcctgacc 1860

tgcctggtca aaggcttcta tcccagcgac atcgccgtgg agtgggagag caatgggcag 1920

ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc 1980

tatagcaagc tcaccgtgga caagagcagg tggcagcagg ggaacgtctt ctcatgctcc 2040

gtgatgcatg aggctctgca caaccactac acgcagaaga gcctctccct gtctccgggt 2100

ggcggtggag ggtccggcgg tggtggatcc gaggtgcagc tgttggagtc tgggggaggc 2160

ttggtacagc ctgggggtc cctgagactc tcctgtgcag cctctggatt caccatcagt 2220

cgctaccaca tgacttgggt ccgccaggct ccagggaagg ggctggagtg gatcggacat 2280

atttatgtta ataatgatga cacagactac gcgagctccg cgaaaggccg gttcaccatc 2340

tccagagaca attccaagaa cacgctgtat ctgcaaatga acagcctgag agccgaggac 2400

acggccacct atttctgtgc gagattggat gttggtggtg gtggtgctta tattggggac 2460

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gtttataaca acaacgactt agcctggtat cagcagaaac cagggaaagt tcctaagctc 2700

ctgatctatt atgcttccac tctggcatct ggggtcccat ctcggttcag tggcagtgga 2760

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gagtggatcg gagtcattac tggtcgtgat atcacatact acgcgagctg ggcgaaaggc 3120

agattcacca tctccagaga caattccaag aacacgctgt atcttcaaat gaacagcctg 3180

agagccgagg acacggctgt gtattactgt gcgcgcgacg gtggatcatc tgctattact 3240

agtaacaaca tttggggcca aggaactctg gtcaccgttt cttcaggcgg tggcggtagt 3300

gggggaggcg gttctggcgg cggagggtcc ggcggtggag gatcagacgt cgtgatgacc 3360

cagtctcctt ccaccctgtc tgcatctgta ggagacagag tcaccatcaa ttgccaagcc 3420

agtgagagca ttagcagttg gttagcctgg tatcagcaga aaccagggaa agcccctaag 3480

ctcctgatct atgaagcatc caaactggca tctggggtcc catcaaggtt cagcggcagt 3540

ggatctggga cagagttcac tctcaccatc agcagcctgc agcctgatga ttttgcaact 3600

tattactgcc aaggctattt ttattttatt agtcgtactt atgtaaattc tttcggcgga 3660

gggaccaagg tggagatcaa a 3681

<210> 88
<211> 1227
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 88

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

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

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

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

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

Gly Asp Ala Ala Thr Tyr Tyr Cys Gln Ser Thr Tyr Leu Gly Thr Asp
85 90 95

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

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

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

Gly Gly Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Ile Ser
145 150 155 160

Ser Tyr His Met Gln Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
165 170 175

Tyr Ile Gly Thr Ile Ser Ser Gly Gly Asn Val Tyr Tyr Ala Ser Ser
180 185 190

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

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

Cys Ala Arg Asp Ser Gly Tyr Ser Asp Pro Met Trp Gly Gln Gly Thr
225 230 235 240

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

245 250 255

Gln Ser Val Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
260 265 270

Leu Arg Leu Ser Cys Thr Ala Ser Gly Ile Asp Leu Asn Thr Tyr Asp
275 280 285

Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly
290 295 300

Ile Ile Thr Tyr Ser Gly Ser Arg Tyr Tyr Ala Asn Trp Ala Lys Gly
305 310 315 320

Arg Phe Thr Ile Ser Lys Asp Asn Thr Lys Asn Thr Val Tyr Leu Gln
325 330 335

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
340 345 350

Asp Tyr Met Ser Gly Ser His Leu Trp Gly Gln Gly Thr Leu Val Thr
355 360 365

Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
370 375 380

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
385 390 395 400

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

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
420 425 430

Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
435 440 445

Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
450 455 460

Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
465 470 475 480

Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu
485 490 495

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
500 505 510

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
515 520 525

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
530 535 540

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
545 550 555 560

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Ala
565 570 575

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

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
595 600 605

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
610 615 620

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
625 630 635 640

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
645 650 655

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
660 665 670

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
675 680 685

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly
690 695 700

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly
705 710 715 720

Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
725 730 735

Phe Thr Ile Ser Arg Tyr His Met Thr Trp Val Arg Gln Ala Pro Gly
740 745 750

Lys Gly Leu Glu Trp Ile Gly His Ile Tyr Val Asn Asn Asp Asp Thr
755 760 765

Asp Tyr Ala Ser Ser Ala Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
770 775 780

Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
785 790 795 800

Thr Ala Thr Tyr Phe Cys Ala Arg Leu Asp Val Gly Gly Gly Gly Ala
805 810 815

Tyr Ile Gly Asp Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
820 825 830

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
835 840 845

Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
850 855 860

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ser Ser Gln Ser
865 870 875 880

Val Tyr Asn Asn Asn Asp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
885 890 895

Val Pro Lys Leu Leu Ile Tyr Tyr Ala Ser Thr Leu Ala Ser Gly Val
900 905 910

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
915 920 925

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Ala Gly
930 935 940

Gly Tyr Asp Thr Asp Gly Leu Asp Thr Phe Ala Phe Gly Gly Gly Thr
945 950 955 960

Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
965 970 975

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
980 985 990

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Ile Ser Thr Asn Ala
995 1000 1005

Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
1010 1015 1020

Gly Val Ile Thr Gly Arg Asp Ile Thr Tyr Tyr Ala Ser Trp Ala
1025 1030 1035

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
1040 1045 1050

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
1055 1060 1065

Tyr Cys Ala Arg Asp Gly Gly Ser Ser Ala Ile Thr Ser Asn Asn
1070 1075 1080

Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly

1085 1090 1095

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
1100 1105 1110

Gly Ser Asp Val Val Met Thr Gln Ser Pro Ser Thr Leu Ser Ala
1115 1120 1125

Ser Val Gly Asp Arg Val Thr Ile Asn Cys Gln Ala Ser Glu Ser
1130 1135 1140

Ile Ser Ser Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala
1145 1150 1155

Pro Lys Leu Leu Ile Tyr Glu Ala Ser Lys Leu Ala Ser Gly Val
1160 1165 1170

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu
1175 1180 1185

Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
1190 1195 1200

Gln Gly Tyr Phe Tyr Phe Ile Ser Arg Thr Tyr Val Asn Ser Phe
1205 1210 1215

Gly Gly Gly Thr Lys Val Glu Ile Lys
1220 1225

<210> 89
<211> 651
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 89
gcctatgata tgacccagtc tccatcttcc gtgtctgcat ctgtaggaga cagagtcacc 60

atcaagtgtc aggccagtga ggacatttat agcttcttgg cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatccattct gcatcctctc tggcatctgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240

gaagattttg caacttacta ttgtcaacag ggttatggta aaaataatgt tgataatgct 300

ttcggcggag ggaccaaggt ggagatcaaa cgtacggtgg ctgcaccatc tgtcttcatc 360

ttcccgccat ctgatgagca gttgaaatct ggaactgcct ctgttgtgtg cctgctgaat 420

aacttctatc ccagagaggc caaagtacag tggaaggtgg ataacgccct ccaatcgggt 480

aactcccagg agagtgtcac agagcaggac agcaaggaca gcacctacag cctcagcagc 540

accctgacgc tgagcaaagc agactacgag aaacacaaag tctacgcctg cgaagtcacc 600

catcagggcc tgagctcgcc cgtcacaaag agcttcaaca ggggagagtg t 651

<210> 90
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 90

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

Asp Arg Val Thr Ile Lys Cys Gln Ala Ser Glu Asp Ile Tyr Ser Phe
20 25 30

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Tyr Gly Lys Asn Asn
85 90 95

Val Asp Asn Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr

100 105 110

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

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

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

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

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

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

Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 91
<211> 3687
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 91
gacgtcgtga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga cagagtcacc 60

atcaattgcc aagccagtga gagcattagc agttggttag cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgaa gcatccaaac tggcatctgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa tttactctca ccatcagcag cctgcagcct 240

gatgattttg caacttatta ctgccaaggc tatttttatt ttattagtcg tacttatgta 300

aattctttcg gcggagggac caaggtggag atcaaaggcg gtggcggtag tgggggaggc 360

ggttctggcg gcggagggtc cggcggtgga ggatcagagg tgcagctggt ggagtctggg 420

ggaggcttgg tccagcctgg ggggtccctg agactctcct gtgcagcctc tggattcacc 480

atcagtacca atgcaatgag ctgggtccgc caggctccag ggaaggggct ggagtggatc 540

ggagtcatta ctggtcgtga tatcacatac tacgcgagct gggcgaaagg cagattcacc 600

atctccagag acaattccaa gaacacgctg tatcttcaaa tgaacagcct gagagccgag 660

gacacggctg tgtattactg tgcgagagac ggtggttctt ctgctattac tagtaacaac 720

atttggggcc agggaaccct ggtcaccgtg tcgacaggcg gtggagggtc cggcggtggt 780

ggatcccagt cggtggagga gtctggggga ggcttggtcc agcctggggg gtccctgaga 840

ctctcctgta ccgcctctgg aatcgacctt aatacctacg acatgatctg ggtccgccag 900

gctccaggca aggggctaga gtgggttgga atcattactt atagtggtag tagatactac 960

gcgaactggg cgaaaggccg attcaccatc tccaaagaca ataccaagaa cacggtgtat 1020

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gagagattat 1080

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aacgtgaatc acaagcccag caacaccaag gtggacaaga gagttgagcc caaatcttgt 1440

gacaaaactc acacatgccc accgtgccca gcacctgaag ccgcgggggc accgtcagtc 1500

ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 1560

tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 1620

ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac 1680

cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 1740

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gggcagcccc gagaaccaca ggtgtatacc ctgcccccat cccgggatga gctgaccaag 1860

aaccaggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag 1920

tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 1980

gacggctcct tcttcctcta tagcaagctc accgtggaca agagcaggtg gcagcagggg 2040

aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 2100

ctctccctgt ctccgggtgg cggtggaggg tccggcggtg gtgggtccgg agaggtgcag 2160

ctgttggagt ctgggggagg cttggtacag cctggggggt ccctgagact ctcctgtgca 2220

gcctctggat tcaccatcag tcgctaccac atgacttggg tccgccaggc tccagggaag 2280

gggctggagt ggatcggaca tatttatgtt aataatgatg acacagacta cgcgagctcc 2340

gcgaaaggcc ggttcaccat ctccagagac aattccaaga acacgctgta tctgcaaatg 2400

aacagcctga gagccgagga cacggccacc tatttctgtg cgagattgga tgttggtggt 2460

ggtggtgctt atattgggga catctggggc cagggaactc tggttaccgt ctcttcaggc 2520

ggtggcggta gtgggggagg cggttctggc ggcggagggt ccggcggtgg aggatcagac 2580

atccagatga cccagtctcc atcctccctg tctgcatctg taggagacag agtcaccatc 2640

acttgccagt ccagtcagag tgtttataac aacaacgact tagcctggta tcagcagaaa 2700

ccagggaaag ttcctaagct cctgatctat tatgcttcca ctctggcatc tggggtccca 2760

tctcggttca gtggcagtgg atctgggaca gatttcactc tcaccatcag cagcctgcag 2820

cctgaagatg ttgcaactta ttactgtgca ggcggttatg atacggatgg tcttgatacg 2880

tttgctttcg gcggagggac caaggtggag atcaaaggcg gtggagggtc cggcggtggt 2940

gggtccggac ggtcgctggt ggagtctggg ggaggcttgg tccagcctgg ggggtccctg 3000

agactctcct gtactgcctc tggattcacc atcagtagct accacatgca gtgggtccgc 3060

caggctccag ggaaggggct ggagtacatc ggaaccatta gtagtggtgg taatgtatac 3120

tacgcaagct ccgctagagg cagattcacc atctccagac cctcgtccaa gaacacggtg 3180

gatcttcaaa tgaacagcct gagagccgag gacacggctg tgtattactg tgcgagagac 3240

tctggttata gtgatcctat gtggggccag ggaaccctgg tcaccgtctc ttcaggcggt 3300

ggcggtagtg ggggaggcgg ttctggcggc ggagggtccg gcggtggagg atcagacgtt 3360

gtgatgaccc agtctccatc ttccgtgtct gcatctgtag gagacagagt caccatcacc 3420

tgtcaggcca gtcagaacat taggacttac ttatcctggt atcagcagaa accagggaaa 3480

gcccctaagc tcctgatcta tgctgcagcc aatctggcat ctggggtccc atcaaggttc 3540

agcggcagtg gatctgggac agatttcact ctcaccatca gcgacctgga gcctggcgat 3600

gctgcaactt actattgtca gtctacctat cttggtactg attatgttgg cggtgctttc 3660

ggcggaggga ccaaggtgga gatcaaa 3687

<210> 92
<211> 1229
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 92

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

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

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

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

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

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gly Tyr Phe Tyr Phe Ile Ser
85 90 95

Arg Thr Tyr Val Asn Ser Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

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

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

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr

145 150 155 160

Ile Ser Thr Asn Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
165 170 175

Leu Glu Trp Ile Gly Val Ile Thr Gly Arg Asp Ile Thr Tyr Tyr Ala
180 185 190

Ser Trp Ala Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
195 200 205

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

Tyr Tyr Cys Ala Arg Asp Gly Gly Ser Ser Ala Ile Thr Ser Asn Asn
225 230 235 240

Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Thr Gly Gly Gly Gly
245 250 255

Ser Gly Gly Gly Gly Ser Gln Ser Val Glu Glu Ser Gly Gly Gly Leu
260 265 270

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Ile
275 280 285

Asp Leu Asn Thr Tyr Asp Met Ile Trp Val Arg Gln Ala Pro Gly Lys
290 295 300

Gly Leu Glu Trp Val Gly Ile Ile Thr Tyr Ser Gly Ser Arg Tyr Tyr
305 310 315 320

Ala Asn Trp Ala Lys Gly Arg Phe Thr Ile Ser Lys Asp Asn Thr Lys
325 330 335

Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
340 345 350

Val Tyr Tyr Cys Ala Arg Asp Tyr Met Ser Gly Ser His Leu Trp Gly
355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
370 375 380

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

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
405 410 415

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
420 425 430

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
435 440 445

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
450 455 460

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
465 470 475 480

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
485 490 495

Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
500 505 510

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
515 520 525

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
530 535 540

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
545 550 555 560

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
565 570 575

Lys Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
580 585 590

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
595 600 605

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
610 615 620

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
625 630 635 640

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
645 650 655

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
660 665 670

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
675 680 685

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
690 695 700

Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Glu Val Gln
705 710 715 720

Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
725 730 735

Leu Ser Cys Ala Ala Ser Gly Phe Thr Ile Ser Arg Tyr His Met Thr
740 745 750

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Gly His Ile
755 760 765

Tyr Val Asn Asn Asp Asp Thr Asp Tyr Ala Ser Ser Ala Lys Gly Arg
770 775 780

Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met
785 790 795 800

Asn Ser Leu Arg Ala Glu Asp Thr Ala Thr Tyr Phe Cys Ala Arg Leu
805 810 815

Asp Val Gly Gly Gly Gly Ala Tyr Ile Gly Asp Ile Trp Gly Gln Gly
820 825 830

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
835 840 845

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr
850 855 860

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
865 870 875 880

Thr Cys Gln Ser Ser Gln Ser Val Tyr Asn Asn Asn Asp Leu Ala Trp
885 890 895

Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile Tyr Tyr Ala
900 905 910

Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
915 920 925

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Val
930 935 940

Ala Thr Tyr Tyr Cys Ala Gly Gly Tyr Asp Thr Asp Gly Leu Asp Thr
945 950 955 960

Phe Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly
965 970 975

Ser Gly Gly Gly Gly Ser Gly Arg Ser Leu Val Glu Ser Gly Gly Gly
980 985 990

Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly

995 1000 1005

Phe Thr Ile Ser Ser Tyr His Met Gln Trp Val Arg Gln Ala Pro
1010 1015 1020

Gly Lys Gly Leu Glu Tyr Ile Gly Thr Ile Ser Ser Gly Gly Asn
1025 1030 1035

Val Tyr Tyr Ala Ser Ser Ala Arg Gly Arg Phe Thr Ile Ser Arg
1040 1045 1050

Pro Ser Ser Lys Asn Thr Val Asp Leu Gln Met Asn Ser Leu Arg
1055 1060 1065

Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Ser Gly Tyr
1070 1075 1080

Ser Asp Pro Met Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
1085 1090 1095

Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1100 1105 1110

Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln Ser Pro Ser Ser
1115 1120 1125

Val Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ala
1130 1135 1140

Ser Gln Asn Ile Arg Thr Tyr Leu Ser Trp Tyr Gln Gln Lys Pro
1145 1150 1155

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ala Asn Leu Ala
1160 1165 1170

Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
1175 1180 1185

Phe Thr Leu Thr Ile Ser Asp Leu Glu Pro Gly Asp Ala Ala Thr
1190 1195 1200

Tyr Tyr Cys Gln Ser Thr Tyr Leu Gly Thr Asp Tyr Val Gly Gly
1205 1210 1215

Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
1220 1225

<210> 93
<211> 651
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 93
gcctatgata tgacccagtc tccatcttcc gtgtctgcat ctgtaggaga cagagtcacc 60

atcaagtgtc aggccagtga ggacatttat agcttcttgg cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatccattct gcatcctctc tggcatctgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240

gaagattttg caacttacta ttgtcaacag ggttatggta aaaataatgt tgataatgct 300

ttcggcggag ggaccaaggt ggagatcaaa cgtacggtgg ctgcaccatc tgtcttcatc 360

ttcccgccat ctgatgagca gttgaaatct ggaactgcct ctgttgtgtg cctgctgaat 420

aacttctatc ccagagaggc caaagtacag tggaaggtgg ataacgccct ccaatcgggt 480

aactcccagg agagtgtcac agagcaggac agcaaggaca gcacctacag cctcagcagc 540

accctgacgc tgagcaaagc agactacgag aaacacaaag tctacgcctg cgaagtcacc 600

catcagggcc tgagctcgcc cgtcacaaag agcttcaaca ggggagagtg t 651

<210> 94
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 94

Ala Tyr Asp Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Lys Cys Gln Ala Ser Glu Asp Ile Tyr Ser Phe
20 25 30

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Tyr Gly Lys Asn Asn
85 90 95

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

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

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

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

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

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

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

Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 95
<211> 3675
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 95
gacgtcgtga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga cagagtcacc 60

atcaattgcc aagccagtga gagcattagc agttggttag cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgaa gcatccaaac tggcatctgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa tttactctca ccatcagcag cctgcagcct 240

gatgattttg caacttatta ctgccaaggc tatttttatt ttattagtcg tacttatgta 300

aattctttcg gcggagggac caaggtggag atcaaaggcg gtggcggtag tgggggaggc 360

ggttctggcg gcggagggtc cggcggtgga ggatcagagg tgcagctggt ggagtctggg 420

ggaggcttgg tccagcctgg ggggtccctg agactctcct gtgcagcctc tggattcacc 480

atcagtacca atgcaatgag ctgggtccgc caggctccag ggaaggggct ggagtggatc 540

ggagtcatta ctggtcgtga tatcacatac tacgcgagct gggcgaaagg cagattcacc 600

atctccagag acaattccaa gaacacgctg tatcttcaaa tgaacagcct gagagccgag 660

gacacggctg tgtattactg tgcgagagac ggtggttctt ctgctattac tagtaacaac 720

atttggggcc agggaaccct ggtcaccgtg tcgacaggcg gtggagggtc cggcggtggt 780

ggatccgagg tgcagctgtt ggagtctggg ggaggcttgg tacagcctgg ggggtccctg 840

agactctcct gtgcagcctc tggattcacc atcagtcgct accacatgac ttgggtccgc 900

caggctccag ggaaggggct ggagtggatc ggacatattt atgttaataa tgatgacaca 960

gactacgcga gctccgcgaa aggccggttc accatctcca gagacaattc caagaacacg 1020

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg ccacctattt ctgtgcgaga 1080

ttggatgttg gtggtggtgg tgcttatatt ggggacatct ggggccaggg aaccctggtc 1140

accgtctcga gcgctagcac caagggccca tcggtcttcc ccctggcacc ctcctccaag 1200

agcacctctg ggggcacagc ggccctgggc tgcctggtca aggactactt ccccgaaccg 1260

gtgacggtgt cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc 1320

ctacagtcct caggactcta ctccctcagc agcgtggtga ccgtgccctc cagcagcttg 1380

ggcacccaga cctacatctg caacgtgaat cacaagccca gcaacaccaa ggtggacaag 1440

agagttgagc ccaaatcttg tgacaaaact cacacatgcc caccgtgccc agcacctgaa 1500

gccgcggggg caccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgatc 1560

tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc 1620

aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag 1680

gagcagtaca acagcacgta ccgtgtggtc agcgtcctca ccgtcctgca ccaggactgg 1740

ctgaatggca aggagtacaa gtgcgcggtc tccaacaaag ccctcccagc ccccatcgag 1800

aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtatac cctgccccca 1860

tcccgggatg agctgaccaa gaaccaggtc agcctgacct gcctggtcaa aggcttctat 1920

cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1980

acgcctcccg tgctggactc cgacggctcc ttcttcctct atagcaagct caccgtggac 2040

aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 2100

aaccactaca cgcagaagag cctctccctg tctccgggtg gcggtggagg gtccggcggt 2160

ggtggatccc agtcggtgga ggagtctggg ggaggcttgg tccagcctgg ggggtccctg 2220

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tatctgcaaa tgaacagcct gagagctgag gacacggctg tgtattactg tgcgagagat 2460

tatatgagtg gttcccactt gtggggccag ggaaccctgg tcaccgtctc ttccggtgga 2520

ggcggttcag gcggaggtgg aagtggtggt ggcggctctg gaggcggcgg atctgcctat 2580

gatatgaccc agtctccatc ttccgtgtct gcatctgtag gagacagagt caccatcaag 2640

tgtcaggcca gtgaggacat ttatagcttc ttggcctggt atcagcagaa accagggaaa 2700

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ggagggacca aggtggagat caaaggcggt ggagggtccg gcggtggtgg gtccggacgg 2940

tcgctggtgg agtctggggg aggcttggtc cagcctgggg ggtccctgag actctcctgt 3000

actgcctctg gattcaccat cagtagctac cacatgcagt gggtccgcca ggctccaggg 3060

aaggggctgg agtacatcgg aaccattagt agtggtggta atgtatacta cgcaagctcc 3120

gctagaggca gattcaccat ctccagaccc tcgtccaaga acacggtgga tcttcaaatg 3180

aacagcctga gagccgagga cacggctgtg tattactgtg cgagagactc tggttatagt 3240

gatcctatgt ggggccaggg aaccctggtc accgtctctt caggcggtgg cggtagtggg 3300

ggaggcggtt ctggcggcgg agggtccggc ggtggaggat cagacgttgt gatgacccag 3360

tctccatctt ccgtgtctgc atctgtagga gacagagtca ccatcacctg tcaggccagt 3420

cagaacatta ggacttactt atcctggtat cagcagaaac cagggaaagc ccctaagctc 3480

ctgatctatg ctgcagccaa tctggcatct ggggtcccat caaggttcag cggcagtgga 3540

tctgggacag atttcactct caccatcagc gacctggagc ctggcgatgc tgcaacttac 3600

tattgtcagt ctacctatct tggtactgat tatgttggcg gtgctttcgg cggagggacc 3660

aaggtggaga tcaaa 3675

<210> 96
<211> 1225
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 96

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

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

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

Tyr Glu Ala Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

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

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gly Tyr Phe Tyr Phe Ile Ser
85 90 95

Arg Thr Tyr Val Asn Ser Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

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

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

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Ile Ser Thr Asn Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
165 170 175

Leu Glu Trp Ile Gly Val Ile Thr Gly Arg Asp Ile Thr Tyr Tyr Ala
180 185 190

Ser Trp Ala Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
195 200 205

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

Tyr Tyr Cys Ala Arg Asp Gly Gly Ser Ser Ala Ile Thr Ser Asn Asn
225 230 235 240

Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Thr Gly Gly Gly Gly
245 250 255

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly
260 265 270

Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
275 280 285

Phe Thr Ile Ser Arg Tyr His Met Thr Trp Val Arg Gln Ala Pro Gly
290 295 300

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

Asp Tyr Ala Ser Ser Ala Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
325 330 335

Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
340 345 350

Thr Ala Thr Tyr Phe Cys Ala Arg Leu Asp Val Gly Gly Gly Gly Ala
355 360 365

Tyr Ile Gly Asp Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
370 375 380

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

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
405 410 415

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
420 425 430

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
435 440 445

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
450 455 460

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
465 470 475 480

Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
485 490 495

Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro
500 505 510

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
515 520 525

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
530 535 540

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
545 550 555 560

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
565 570 575

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Ala Val Ser Asn
580 585 590

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
595 600 605

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
610 615 620

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
625 630 635 640

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
645 650 655

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
660 665 670

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
675 680 685

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
690 695 700

Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly
705 710 715 720

Gly Gly Ser Gln Ser Val Glu Glu Ser Gly Gly Gly Leu Val Gln Pro
725 730 735

Gly Gly Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Ile Asp Leu Asn
740 745 750

Thr Tyr Asp Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
755 760 765

Trp Val Gly Ile Ile Thr Tyr Ser Gly Ser Arg Tyr Tyr Ala Asn Trp
770 775 780

Ala Lys Gly Arg Phe Thr Ile Ser Lys Asp Asn Thr Lys Asn Thr Val
785 790 795 800

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
805 810 815

Cys Ala Arg Asp Tyr Met Ser Gly Ser His Leu Trp Gly Gln Gly Thr
820 825 830

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
835 840 845

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Tyr Asp Met Thr Gln
850 855 860

Ser Pro Ser Ser Val Ser Ala Ser Val Gly Asp Arg Val Thr Ile Lys
865 870 875 880

Cys Gln Ala Ser Glu Asp Ile Tyr Ser Phe Leu Ala Trp Tyr Gln Gln
885 890 895

Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile His Ser Ala Ser Ser Leu

900 905 910

Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
915 920 925

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
930 935 940

Tyr Cys Gln Gln Gly Tyr Gly Lys Asn Asn Val Asp Asn Ala Phe Gly
945 950 955 960

Gly Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly
965 970 975

Gly Ser Gly Arg Ser Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
980 985 990

Gly Gly Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Ile Ser
995 1000 1005

Ser Tyr His Met Gln Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
1010 1015 1020

Glu Tyr Ile Gly Thr Ile Ser Ser Gly Gly Asn Val Tyr Tyr Ala
1025 1030 1035

Ser Ser Ala Arg Gly Arg Phe Thr Ile Ser Arg Pro Ser Ser Lys
1040 1045 1050

Asn Thr Val Asp Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
1055 1060 1065

Ala Val Tyr Tyr Cys Ala Arg Asp Ser Gly Tyr Ser Asp Pro Met
1070 1075 1080

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
1085 1090 1095

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
1100 1105 1110

Ser Asp Val Val Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser
1115 1120 1125

Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asn Ile
1130 1135 1140

Arg Thr Tyr Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
1145 1150 1155

Lys Leu Leu Ile Tyr Ala Ala Ala Asn Leu Ala Ser Gly Val Pro
1160 1165 1170

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
1175 1180 1185

Ile Ser Asp Leu Glu Pro Gly Asp Ala Ala Thr Tyr Tyr Cys Gln
1190 1195 1200

Ser Thr Tyr Leu Gly Thr Asp Tyr Val Gly Gly Ala Phe Gly Gly
1205 1210 1215

Gly Thr Lys Val Glu Ile Lys
1220 1225

<210> 97
<211> 660
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 97
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

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aaaccaggga aagttcctaa gctcctgatc tattatgcat ccactctggc atctggggtc 180

ccatctcggt tcagtggcag tggatctggg acagatttca ctctcaccat cagcagcctg 240

cagcctgaag atgttgcaac ttattactgt gcaggcggtt atgatacgga tggtcttgat 300

acgtttgctt tcggcggagg gaccaaggtg gagatcaaac gtacggtggc tgcaccatct 360

gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc 420

ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgccctc 480

caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 540

ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600

gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

<210> 98
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 98

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 99
<211> 3696
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 99
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atcaattgcc aagccagtga gagcattagc agttggttag cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgaa gcatccaaac tggcatctgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa tttactctca ccatcagcag cctgcagcct 240

gatgattttg caacttatta ctgccaaggc tatttttatt ttattagtcg tacttatgta 300

aattctttcg gcggagggac caaggtggag atcaaaggcg gtggcggtag tgggggaggc 360

ggttctggcg gcggagggtc cggcggtgga ggatcagagg tgcagctggt ggagtctggg 420

ggaggcttgg tccagcctgg ggggtccctg agactctcct gtgcagcctc tggattcacc 480

atcagtacca atgcaatgag ctgggtccgc caggctccag ggaaggggct ggagtggatc 540

ggagtcatta ctggtcgtga tatcacatac tacgcgagct gggcgaaagg cagattcacc 600

atctccagag acaattccaa gaacacgctg tatcttcaaa tgaacagcct gagagccgag 660

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atttggggcc agggaaccct ggtcaccgtg tcgacaggcg gtggagggtc cggcggtggt 780

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agactctcct gtgcagcctc tggattcacc atcagtcgct accacatgac ttgggtccgc 900

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gactacgcga gctccgcgaa aggccggttc accatctcca gagacaattc caagaacacg 1020

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg ccacctattt ctgtgcgaga 1080

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gccgcggggg caccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgatc 1560

tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc 1620

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gagcagtaca acagcacgta ccgtgtggtc agcgtcctca ccgtcctgca ccaggactgg 1740

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cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1980

acgcctcccg tgctggactc cgacggctcc ttcttcctct atagcaagct caccgtggac 2040

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aagaacacgc tgtatctgca aatgaacagc ctgagagccg aggacacggc cgtatattac 2460

tgtgcgagat cggcgttttc gttcgactac gccatggacc tctggggcca gggaaccctg 2520

gtcaccgtct cgagcggtgg aggcggatct ggcggaggtg gttccggcgg tggcggctcc 2580

ggtggaggcg gctctgacat ccagatgacc cagtctcctt ccaccctgtc tgcatctgta 2640

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tatcagcaga aaccagggaa agcccctaag ctcctgatct ataaggcatc cactctggca 2760

tctggggtcc catcaaggtt cagcggcagt ggatctggga cagaatttac tctcaccatc 2820

agcagcctgc agcctgatga ttttgcaact tattactgcc aacagggtta tagttggggt 2880

aatgttgata atgttttcgg cggagggacc aaggtggaga tcaaaggcgg tggagggtcc 2940

ggcggtggtg gctccggacg gtcgctggtg gagtctgggg gaggcttggt ccagcctggg 3000

gggtccctga gactctcctg tactgcctct ggattcacca tcagtagcta ccacatgcag 3060

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tcagacgttg tgatgaccca gtctccatct tccgtgtctg catctgtagg agacagagtc 3420

accatcacct gtcaggccag tcagaacatt aggacttact tatcctggta tcagcagaaa 3480

ccagggaaag cccctaagct cctgatctat gctgcagcca atctggcatc tggggtccca 3540

tcaaggttca gcggcagtgg atctgggaca gatttcactc tcaccatcag cgacctggag 3600

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<210> 100
<211> 1232
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 100

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

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

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

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

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gly Tyr Phe Tyr Phe Ile Ser
85 90 95

Arg Thr Tyr Val Asn Ser Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

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

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

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Ile Ser Thr Asn Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
165 170 175

Leu Glu Trp Ile Gly Val Ile Thr Gly Arg Asp Ile Thr Tyr Tyr Ala
180 185 190

Ser Trp Ala Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
195 200 205

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

Tyr Tyr Cys Ala Arg Asp Gly Gly Ser Ser Ala Ile Thr Ser Asn Asn
225 230 235 240

Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Thr Gly Gly Gly Gly
245 250 255

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly
260 265 270

Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
275 280 285

Phe Thr Ile Ser Arg Tyr His Met Thr Trp Val Arg Gln Ala Pro Gly
290 295 300

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

Asp Tyr Ala Ser Ser Ala Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
325 330 335

Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
340 345 350

Thr Ala Thr Tyr Phe Cys Ala Arg Leu Asp Val Gly Gly Gly Gly Ala
355 360 365

Tyr Ile Gly Asp Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
370 375 380

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

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
405 410 415

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
420 425 430

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
435 440 445

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
450 455 460

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
465 470 475 480

Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
485 490 495

Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro
500 505 510

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
515 520 525

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
530 535 540

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
545 550 555 560

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
565 570 575

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Ala Val Ser Asn
580 585 590

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
595 600 605

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
610 615 620

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
625 630 635 640

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
645 650 655

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
660 665 670

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
675 680 685

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
690 695 700

Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly
705 710 715 720

Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
725 730 735

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe
740 745 750

Ser Ser Gly Tyr Asp Met Cys Trp Val Arg Gln Ala Pro Gly Lys Gly
755 760 765

Leu Glu Trp Ile Ala Cys Ile Ala Ala Gly Ser Ala Gly Ile Thr Tyr
770 775 780

Asp Ala Asn Trp Ala Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
785 790 795 800

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr

805 810 815

Ala Val Tyr Tyr Cys Ala Arg Ser Ala Phe Ser Phe Asp Tyr Ala Met
820 825 830

Asp Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
835 840 845

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
850 855 860

Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val
865 870 875 880

Gly Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Ser Ile Ser Ser
885 890 895

His Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
900 905 910

Ile Tyr Lys Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Ser
915 920 925

Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln
930 935 940

Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Tyr Ser Trp Gly
945 950 955 960

Asn Val Asp Asn Val Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly
965 970 975

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Arg Ser Leu Val Glu Ser
980 985 990

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Thr
995 1000 1005

Ala Ser Gly Phe Thr Ile Ser Ser Tyr His Met Gln Trp Val Arg
1010 1015 1020

Gln Ala Pro Gly Lys Gly Leu Glu Tyr Ile Gly Thr Ile Ser Ser
1025 1030 1035

Gly Gly Asn Val Tyr Tyr Ala Ser Ser Ala Arg Gly Arg Phe Thr
1040 1045 1050

Ile Ser Arg Pro Ser Ser Lys Asn Thr Val Asp Leu Gln Met Asn
1055 1060 1065

Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp
1070 1075 1080

Ser Gly Tyr Ser Asp Pro Met Trp Gly Gln Gly Thr Leu Val Thr
1085 1090 1095

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
1100 1105 1110

Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln Ser
1115 1120 1125

Pro Ser Ser Val Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
1130 1135 1140

Cys Gln Ala Ser Gln Asn Ile Arg Thr Tyr Leu Ser Trp Tyr Gln
1145 1150 1155

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ala
1160 1165 1170

Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
1175 1180 1185

Gly Thr Asp Phe Thr Leu Thr Ile Ser Asp Leu Glu Pro Gly Asp
1190 1195 1200

Ala Ala Thr Tyr Tyr Cys Gln Ser Thr Tyr Leu Gly Thr Asp Tyr
1205 1210 1215

Val Gly Gly Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
1220 1225 1230

<210> 101
<211> 660
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 101
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atcacttgcc agtccagtca gagtgtttat aacaacaacg acttagcctg gtatcagcag 120

aaaccaggga aagttcctaa gctcctgatc tattatgcat ccactctggc atctggggtc 180

ccatctcggt tcagtggcag tggatctggg acagatttca ctctcaccat cagcagcctg 240

cagcctgaag atgttgcaac ttattactgt gcaggcggtt atgatacgga tggtcttgat 300

acgtttgctt tcggcggagg gaccaaggtg gagatcaaac gtacggtggc tgcaccatct 360

gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc 420

ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgccctc 480

caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 540

ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600

gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

<210> 102
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 102

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 103
<211> 3690
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthesized

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atcaattgcc aagccagtga gagcattagc agttggttag cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgaa gcatccaaac tggcatctgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagag ttcactctca ccatcagcag cctgcagcct 240

gatgattttg caacttatta ctgccaaggc tatttttatt ttattagtcg tacttatgta 300

aattctttcg gcggagggac caaggtggag atcaaaggcg gtggcggtag tgggggaggc 360

ggttctggcg gcggagggtc cggcggtgga ggatcagagg tgcagctggt ggagtctggg 420

ggaggcttgg tccagcctgg ggggtccctg agactctcct gtgcagcctc tggattcacc 480

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gacacggctg tgtattactg tgcgcgcgac ggtggatcat ctgctattac tagtaacaac 720

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ggatccgagg tgcagctggt gcagtctgga gcagaggtga agaaaccagg agagtctctg 840

aagatctcct gtaagggttc tggatacagc tttagcagtt catggatcgg ctgggtgcgc 900

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cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 1620

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accatctcca aagccaaagg gcagccccga gaaccacagg tgtataccct gcccccatcc 1860

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agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1980

cctcccgtgc tggactccga cggctccttc ttcctctata gcaagctcac cgtggacaag 2040

agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 2100

cactacacgc agaagagcct ctccctgtct ccgggtggcg gtggagggtc cggcggtggt 2160

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aacacgctgt atctgcaaat gaacagcctg agagccgagg acacggccgt atattactgt 2460

gcgagatcgg cgttttcgtt cgactacgcc atggacctct ggggccaggg aaccctggtc 2520

accgtctcga gcggtggagg cggatctggc ggaggtggtt ccggcggtgg cggctccggt 2580

ggaggcggct ctgacatcca gatgacccag tctccttcca ccctgtctgc atctgtagga 2640

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cagcagaaac cagggaaagc ccctaagctc ctgatctata aggcatccac tctggcatct 2760

ggggtcccat caaggttcag cggcagtgga tctgggacag aatttactct caccatcagc 2820

agcctgcagc ctgatgattt tgcaacttat tactgccaac agggttatag ttggggtaat 2880

gttgataatg ttttcggcgg agggaccaag gtggagatca aaggcggtgg agggtccggc 2940

ggtggtggat cccggtcgct ggtggagtct gggggaggct tggtccagcc tgggggtcc 3000

ctgagactct cctgtacagc ctctggattc accatcagta gctaccacat gcagtgggtc 3060

cgccaggctc cagggaaggg gctggagtac atcggaacca ttagtagtgg tggtaatgta 3120

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gtggatcttc aaatgaacag cctgagagcc gaggacacgg ctgtgtatta ctgtgcgaga 3240

gactctggtt atagtgatcc tatgtggggc cagggaaccc tggtcaccgt ctcgagcggc 3300

ggtggcggta gtgggggagg cggttctggc ggcggagggt ccggcggtgg aggatcagac 3360

gttgtgatga cccagtctcc atcttccgtg tctgcatctg taggagacag agtcaccatc 3420

acctgtcagg ccagtcagaa cattaggact tacttatcct ggtatcagca gaaaccaggg 3480

aaagccccta agctcctgat ctatgctgca gccaatctgg catctggggt cccatcaagg 3540

ttcagcggca gtggatctgg gacagatttc actctcacca tcagcgacct ggagcctggc 3600

gatgctgcaa cttactattg tcagtctacc tatcttggta ctgattatgt tggcggtgct 3660

ttcggcggag ggaccaaggt ggagatcaaa 3690

<210> 104
<211> 1230
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 104

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

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

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

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

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

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gly Tyr Phe Tyr Phe Ile Ser
85 90 95

Arg Thr Tyr Val Asn Ser Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

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

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

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Ile Ser Thr Asn Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
165 170 175

Leu Glu Trp Ile Gly Val Ile Thr Gly Arg Asp Ile Thr Tyr Tyr Ala
180 185 190

Ser Trp Ala Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
195 200 205

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

Tyr Tyr Cys Ala Arg Asp Gly Gly Ser Ser Ala Ile Thr Ser Asn Asn
225 230 235 240

Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
245 250 255

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln Ser Gly Ala Glu
260 265 270

Val Lys Lys Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly
275 280 285

Tyr Ser Phe Ser Ser Ser Trp Ile Gly Trp Val Arg Gln Ala Pro Gly
290 295 300

Lys Gly Leu Glu Trp Met Gly Ile Ile Tyr Pro Asp Asp Ser Asp Thr
305 310 315 320

Arg Tyr Ser Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys
325 330 335

Ser Ile Arg Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp
340 345 350

Thr Ala Met Tyr Tyr Cys Ala Arg His Val Thr Met Ile Trp Gly Val
355 360 365

Ile Ile Asp Phe Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala
370 375 380

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

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

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
420 425 430

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
435 440 445

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
450 455 460

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg
465 470 475 480

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
485 490 495

Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys
500 505 510

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
515 520 525

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
530 535 540

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
545 550 555 560

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
565 570 575

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Ala Val Ser Asn Lys
580 585 590

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
595 600 605

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
610 615 620

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
625 630 635 640

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
645 650 655

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
660 665 670

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
675 680 685

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
690 695 700

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly

705 710 715 720

Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro
725 730 735

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser
740 745 750

Ser Gly Tyr Asp Met Cys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
755 760 765

Glu Trp Ile Ala Cys Ile Ala Ala Gly Ser Ala Gly Ile Thr Tyr Asp
770 775 780

Ala Asn Trp Ala Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys
785 790 795 800

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
805 810 815

Val Tyr Tyr Cys Ala Arg Ser Ala Phe Ser Phe Asp Tyr Ala Met Asp
820 825 830

Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
835 840 845

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
850 855 860

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
865 870 875 880

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Ser Ile Ser Ser His
885 890 895

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
900 905 910

Tyr Lys Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
915 920 925

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
930 935 940

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Tyr Ser Trp Gly Asn
945 950 955 960

Val Asp Asn Val Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly
965 970 975

Gly Gly Ser Gly Gly Gly Gly Ser Arg Ser Leu Val Glu Ser Gly Gly
980 985 990

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Thr Ala Ser
995 1000 1005

Gly Phe Thr Ile Ser Ser Tyr His Met Gln Trp Val Arg Gln Ala
1010 1015 1020

Pro Gly Lys Gly Leu Glu Tyr Ile Gly Thr Ile Ser Ser Gly Gly
1025 1030 1035

Asn Val Tyr Tyr Ala Ser Ser Ala Arg Gly Arg Phe Thr Ile Ser
1040 1045 1050

Arg Pro Ser Ser Lys Asn Thr Val Asp Leu Gln Met Asn Ser Leu
1055 1060 1065

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Ser Gly
1070 1075 1080

Tyr Ser Asp Pro Met Trp Gly Gln Gly Thr Leu Val Thr Val Ser
1085 1090 1095

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
1100 1105 1110

Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln Ser Pro Ser
1115 1120 1125

Ser Val Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln
1130 1135 1140

Ala Ser Gln Asn Ile Arg Thr Tyr Leu Ser Trp Tyr Gln Gln Lys
1145 1150 1155

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ala Asn Leu
1160 1165 1170

Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
1175 1180 1185

Asp Phe Thr Leu Thr Ile Ser Asp Leu Glu Pro Gly Asp Ala Ala
1190 1195 1200

Thr Tyr Tyr Cys Gln Ser Thr Tyr Leu Gly Thr Asp Tyr Val Gly
1205 1210 1215

Gly Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
1220 1225 1230

<210> 105
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 105
gccatccagt tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gggcattagc agtgctttag cctggtatca gcagaaacca 120

gggaaagctc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240

gaagattttg caacttatta ctgtcaacag tttaatagtt acccattcac tttcggccct 300

gggaccaaag tggatatcaa acgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 106
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 106

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

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

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

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

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

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

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

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys
210

<210> 107
<211> 3675
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 107
gccatccagt tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gggcattagc agtgctttag cctggtatca gcagaaacca 120

gggaaagctc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240

gaagattttg caacttatta ctgtcaacag tttaatagtt acccattcac tttcggccct 300

gggaccaaag tggatatcaa aggcggtggc ggtagtgggg gaggcggttc tggcggcgga 360

gggtccggcg gtggaggatc agaggtgcag ctggtgcagt ctggagcaga ggtgaagaaa 420

ccaggagagt ctctgaagat ctcctgtaag ggttctggat acagctttag cagttcatgg 480

atcggctggg tgcgccaggc acctgggaaa ggcctggaat ggatggggat catctatcct 540

gatgactctg ataccagata cagtccatcc ttccaaggcc aggtcaccat ctcagccgac 600

aagtccatca ggactgccta cctgcagtgg agtagcctga aggcctcgga caccgctatg 660

tattactgtg cgagacatgt tactatgatt tggggagtta ttattgactt ctggggccag 720

ggaaccctgg tcaccgtctc ctcaggcggt ggagggtccg gcggtggtgg atccgaggtg 780

cagctggtgg agtctggggg aggcttggtc cagcctgggg ggtccctgag actctcctgt 840

gcagcctctg gattcaccat cagtaccaat gcaatgagct gggtccgcca ggctccaggg 900

aaggggctgg agtggatcgg agtcattact ggtcgtgata tcacatacta cgcgagctgg 960

gcgaaaggca gattcaccat ctccagagac aattccaaga acacgctgta tcttcaaatg 1020

aacagcctga gagccgagga cacggctgtg tattactgtg cgcgcgacgg tggatcatct 1080

gctattacta gtaacaacat ttggggccaa ggaactctgg tcaccgtttc ttcagctagc 1140

accaagggcc catcggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca 1200

gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 1260

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 1320

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 1380

tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agagagttga gcccaaatct 1440

tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagccgcggg ggcaccgtca 1500

gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 1560

acatgcgtgg tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 1620

gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 1680

taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 1740

aagtgcgcgg tctccaacaa agccctccca gcccccatcg agaaaaccat ctccaaagcc 1800

aaagggcagc cccgagaacc acaggtgtat accctgcccc catcccggga tgagctgacc 1860

aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1920

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1980

tccgacggct ccttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag 2040

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 2100

agcctctccc tgtctccggg tggcggtgga gggtccggcg gtggtggatc cgaggtgcag 2160

ctgttggagt ctgggggagg cttggtacag cctgggggt ccctgagact ctcctgtgca 2220

gcctctggat tctccttcag tagcgggtac gacatgtgct gggtccgcca ggctccaggg 2280

aaggggctgg agtggatcgc atgcattgct gctggtagtg ctggtatcac ttacgacgcg 2340

aactgggcga aaggccggtt caccatctcc agagacaatt ccaagaacac gctgtatctg 2400

caaatgaaca gcctgagagc cgaggacacg gccgtatatt actgtgcgag atcggcgttt 2460

tcgttcgact acgccatgga cctctggggc cagggaaccc tggtcaccgt ctcgagcggt 2520

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tcgctggtgg agtctggggg aggcttggtc cagcctgggg ggtccctgag actctcctgt 3000

acagcctctg gattcaccat cagtagctac cacatgcagt gggtccgcca ggctccaggg 3060

aaggggctgg agtacatcgg aaccattagt agtggtggta atgtatacta cgcgagctcc 3120

gcgagaggca gattcaccat ctccagaccc tcgtccaaga acacggtgga tcttcaaatg 3180

aacagcctga gagccgagga cacggctgtg tattactgtg cgagagactc tggttatagt 3240

gatcctatgt ggggccaggg aaccctggtc accgtctcga gcggcggtgg cggtagtggg 3300

ggaggcggtt ctggcggcgg agggtccggc ggtggaggat cagacgttgt gatgacccag 3360

tctccatctt ccgtgtctgc atctgtagga gacagagtca ccatcacctg tcaggccagt 3420

cagaacatta ggacttactt atcctggtat cagcagaaac cagggaaagc ccctaagctc 3480

ctgatctatg ctgcagccaa tctggcatct ggggtcccat caaggttcag cggcagtgga 3540

tctgggacag atttcactct caccatcagc gacctggagc ctggcgatgc tgcaacttac 3600

tattgtcagt ctacctatct tggtactgat tatgttggcg gtgctttcgg cggagggacc 3660

aaggtggaga tcaaa 3675

<210> 108
<211> 1225
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 108

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

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

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

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

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

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

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Gly Gly Gly Gly Ser
100 105 110

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

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

Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Ser Ser Ser Trp
145 150 155 160

Ile Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met Gly
165 170 175

Ile Ile Tyr Pro Asp Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln
180 185 190

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Arg Thr Ala Tyr Leu
195 200 205

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
210 215 220

Arg His Val Thr Met Ile Trp Gly Val Ile Ile Asp Phe Trp Gly Gln
225 230 235 240

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
245 250 255

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
260 265 270

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Ile Ser
275 280 285

Thr Asn Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
290 295 300

Trp Ile Gly Val Ile Thr Gly Arg Asp Ile Thr Tyr Tyr Ala Ser Trp
305 310 315 320

Ala Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
325 330 335

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
340 345 350

Cys Ala Arg Asp Gly Gly Ser Ser Ala Ile Thr Ser Asn Asn Ile Trp
355 360 365

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
370 375 380

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

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
405 410 415

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
420 425 430

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
435 440 445

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

His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser
465 470 475 480

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala
485 490 495

Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
500 505 510

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
515 520 525

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
530 535 540

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
545 550 555 560

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
565 570 575

Gly Lys Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro
580 585 590

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
595 600 605

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

610 615 620

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
625 630 635 640

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
645 650 655

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
660 665 670

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
675 680 685

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
690 695 700

Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln
705 710 715 720

Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
725 730 735

Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Gly Tyr Asp Met
740 745 750

Cys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Ala Cys
755 760 765

Ile Ala Ala Gly Ser Ala Gly Ile Thr Tyr Asp Ala Asn Trp Ala Lys
770 775 780

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
785 790 795 800

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
805 810 815

Arg Ser Ala Phe Ser Phe Asp Tyr Ala Met Asp Leu Trp Gly Gln Gly
820 825 830

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
835 840 845

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr
850 855 860

Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
865 870 875 880

Thr Cys Gln Ala Ser Gln Ser Ile Ser Ser His Leu Asn Trp Tyr Gln
885 890 895

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Ala Ser Thr
900 905 910

Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
915 920 925

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr
930 935 940

Tyr Tyr Cys Gln Gln Gly Tyr Ser Trp Gly Asn Val Asp Asn Val Phe
945 950 955 960

Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly
965 970 975

Gly Gly Ser Arg Ser Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
980 985 990

Gly Gly Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Ile Ser
995 1000 1005

Ser Tyr His Met Gln Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
1010 1015 1020

Glu Tyr Ile Gly Thr Ile Ser Ser Gly Gly Asn Val Tyr Tyr Ala
1025 1030 1035

Ser Ser Ala Arg Gly Arg Phe Thr Ile Ser Arg Pro Ser Ser Lys
1040 1045 1050

Asn Thr Val Asp Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
1055 1060 1065

Ala Val Tyr Tyr Cys Ala Arg Asp Ser Gly Tyr Ser Asp Pro Met
1070 1075 1080

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
1085 1090 1095

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
1100 1105 1110

Ser Asp Val Val Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser
1115 1120 1125

Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asn Ile
1130 1135 1140

Arg Thr Tyr Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
1145 1150 1155

Lys Leu Leu Ile Tyr Ala Ala Ala Asn Leu Ala Ser Gly Val Pro
1160 1165 1170

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
1175 1180 1185

Ile Ser Asp Leu Glu Pro Gly Asp Ala Ala Thr Tyr Tyr Cys Gln
1190 1195 1200

Ser Thr Tyr Leu Gly Thr Asp Tyr Val Gly Gly Ala Phe Gly Gly
1205 1210 1215

Gly Thr Lys Val Glu Ile Lys
1220 1225

<210> 109
<211> 657
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized

<400> 109
gacgtcgtga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga cagagtcacc 60

atcaattgcc aagccagtga gagcattagc agttggttag cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgaa gcatccaaac tggcatctgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240

gatgattttg caacttatta ctgccaaggc tatttttatt ttattagtcg tacttatgta 300

aattctttcg gcggagggac caaggtggag atcaaacgta cggtggctgc accatctgtc 360

ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg 420

ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa 480

tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc 540

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Tyr Glu Ala Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
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Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
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Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gly Tyr Phe Tyr Phe Ile Ser
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Arg Thr Tyr Val Asn Ser Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
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Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
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Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
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Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145 150 155 160

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

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

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

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
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