SEQUENCE LISTING

<110> Regeneron Pharmaceuticals, Inc.

<120> Human Antibodies to Human TNF-Like Ligand 1A (TL1A)

<130> 6400A-WO

<140> To be assigned
<141> 2011-11-08

<150> 61/411,276
<151> 2010-11-08

<150> 61/478,309
<151> 2011-04-22

<160> 259

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ccagggaagg ggctggaatg ggtggccaac ataaaggaag atggaagtga gaaaaactat 180
gtggactctg tgaagggccg attcaccctc tccagcgaca acgccaagaa ctcactgtat 240
ctgcaaatga acagcctgag agccgaggac acggctgttt attactgtgc gagagaggac 300
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            20   25   30
Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ala Asn Ile Lys Glu Asp Gly Ser Glu Lys Asn Tyr Val Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Leu Ser Ser Asp Asn Ala Lys Asn Ser Leu Tyr
65   70   75   80

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Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
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Ala Arg Glu Asp Tyr Asp Ser Tyr Tyr Lys Tyr Gly Met Asp Val Trp
            100                 105                 110
Gly Gln Gly Thr Ala Val Ile Val Ser Ser
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tggtatcagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180
gaatccgggg tccctgaccg attcagtggc agcgggtctg gaacagattt cactctcacc 240
atcagcagcc tgcaggctga agatgtgtca gtttattact gtcaacaata ttatagtact 300
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20 25 30
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80
Ile Ser Ser Leu Gln Ala Glu Asp Val Ser Val Tyr Tyr Cys Gln Gln

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                85                  90                  95
Tyr Tyr Ser Thr Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile
            100                 105                 110
Lys
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<210> 14
<211> 3
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<400> 14
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ccagggaagg ggctggagtg ggtctcaagt attagtggta ctggtcgtac cacataccat 180
gcagactccg tgcagggccg gttcaccgtc tccagagaca attccaagaa cattctatat 240
ttacagatga acagtctgcg agccgacgac acggccgtat atttctgtac gaaagagcgg 300
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<220>
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Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30
Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Ser Ile Ser Gly Thr Gly Arg Thr Thr Tyr His Ala Asp Ser Val
50 55 60
Gln Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Ile Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Phe Cys

```
                85                  90                  95
Thr Lys Glu Arg Gly Asp Tyr Tyr Tyr Gly Val Phe Asp Tyr Trp Gly
            100                 105                 110
Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
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<400> 19
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<210> 21
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<400> 21
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<210> 22
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<400> 22
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<210> 23
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<400> 23
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gagaaagccc ctaagctcct gatctatgcg gcgtctaatt tacaaagtgg agtcccatca 180
aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctacagcct 240
gatgattttg caacttatta ctgccagcag tatcatcgtt cttggacgtt cggccaaggg 300
accaaggtgg aaatcaca 318

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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Ser Ser Trp
20 25 30
Leu Ala Trp Tyr Gln Gln Thr Pro Glu Lys Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Ala Ala Ser Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr His Arg Ser Trp Thr
85 90 95

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

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<400> 27
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<210> 28
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<400> 28
Gln Thr Ile Ser Ser Trp
1 5

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

<220>
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<400> 29
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<210> 30
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<400> 30
Ala Ala Ser
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<210> 31
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<400> 31
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<400> 32
Gln Gln Tyr His Arg Ser Trp Thr
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ccagggaagg ggctggagtg gattggggat atcaatcatc gtggaaggac caactacaac 180
ccgtccctca agagtcgagt caccatatca cttgacacgt ccgggaaccc gttctccctg 240
aagctgacct ctgtgaccgc cgcggacacg gctgtttatt actgtgcgag agattttccc 300
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20 25 30
His Trp Ala Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45
Gly Asp Ile Asn His Arg Gly Arg Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60
Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Gly Asn Pro Phe Ser Leu
65 70 75 80
Lys Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95
Arg Asp Phe Pro Asn Trp Val Phe Asp Ser Trp Gly Gln Gly Ile Leu
100 105 110
Val Thr Val Ser Ser

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<400> 36
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<400> 38
Ile Asn His Arg Gly Arg Thr
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<400> 39
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<400> 40
Ala Arg Asp Phe Pro Asn Trp Val Phe Asp Ser
1 5 10

<210> 41
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<212> DNA
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<220>
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<400> 41
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cctggccagg ctcccaggct cctcatctat ggtgcatcca gaagggccac tggcatccca 180
gacaggttcc gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgta ttactgtcaa caatatggta gttcaccgct caccttcggc 300
ggagggacca aggtggagaa caaa 324

<210> 42
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<212> PRT
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<220>
<223> Synthetic

<400> 42
Glu Ile Val Leu Ser Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
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Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30
Phe Leu Ala Trp Tyr Gln Gln Tyr Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
Ile Tyr Gly Ala Ser Arg Arg Ala Thr Gly Ile Pro Asp Arg Phe Arg
50 55 60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95
Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Asn Lys
100 105

<210> 43
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<212> DNA
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<400> 43
cagagtgtta gcagcagctt c 21

<210> 44
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<400> 44
Gln Ser Val Ser Ser Ser Phe
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<210> 45
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<400> 45
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<210> 46
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<400> 46
Gly Ala Ser
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<210> 47
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<400> 47
caacaatatg gtagttcacc gctcacc 27

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<211> 9
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<400> 48
Gln Gln Tyr Gly Ser Ser Pro Leu Thr
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cccgggaagg ggctggagtg gattggggaa atcaatcatc gtggaaacac caactacaat 180
ccgtccctca agagtcgagt caccatgtca gtagacacgt ccaagaacca gttctccctg 240
aacatgatct ctgtgaccgc cgcggacacg gctatgtatt tctgtgcgag tccttttttac 300
gatttttgga gtggttccga ctactggggc cagggaaccc tggtcaccgt ctcctca   357

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Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Thr Gly Phe
            20   25   30
Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
        35   40   45
Gly Glu Ile Asn His Arg Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys
    50   55   60
Ser Arg Val Thr Met Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65   70   75   80
Asn Met Ile Ser Val Thr Ala Ala Asp Thr Ala Met Tyr Phe Cys Ala
                85   90   95
Ser Pro Phe Tyr Asp Phe Trp Ser Gly Ser Asp Tyr Trp Gly Gln Gly
            100   105   110
Thr Leu Val Thr Val Ser Ser
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<400> 51
ggtgggtcct tcactggttt ctac 24

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<400> 52
Gly Gly Ser Phe Thr Gly Phe Tyr
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<210> 53
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<400> 53
atcaatcatc gtggaaacac c 21

<210> 54
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<400> 54
Ile Asn His Arg Gly Asn Thr
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<210> 55
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<400> 55
gcgagtcctt tttacgattt ttggagtggt tccgactac 39

<210> 56
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<400> 56
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<400> 57
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cttcagcaga ggccaggcca gcctccaaga ctcctatttt ataagatttc taaccggttc 180
tctggagtcc cagacagatt cagtggcagt ggggcaggga cagatttcac actgaaaatc 240
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            20   25   30
Asp Gly Asn Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
        35   40   45
Pro Arg Leu Leu Phe Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
    50   55   60
Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
65   70   75   80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
                85   90   95
Thr Gln Phe Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 59
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<220>
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<400> 59
caaagcctcg tacacagtga tggaaacacc tac 33

<210> 60
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<220>
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<400> 60
Gln Ser Leu Val His Ser Asp Gly Asn Thr Tyr
1 5 10

<210> 61
<211> 9
<212> DNA
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<220>
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<400> 61
aagatttct 9

<210> 62
<211> 3
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<400> 62
Lys Ile Ser
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<210> 63
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<220>
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<400> 63
atgcaagcta cacaatttcc tctcact 27

<210> 64
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<220>
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<400> 64
Met Gln Ala Thr Gln Phe Pro Leu Thr
 1   5

<210> 65
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<220>
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<400> 65
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cccgggaagg ggctggagtg gattggggaa atcagtcata gtggaagaac caactacaac 180
ccgtccctca agagtcgagt caccatatca gttgacacgt ccatgagcca gttctccctg 240
aagatgacct ctgtgaccgc cgcggactcg gctgtatatt actgtgcgag agattatccc 300
aactgggttt ttgactactg gggccaggga accctggtca ccgtctcctc a   351

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<220>
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<400> 66
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Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Phe Ser Asp Tyr
            20   25   30
Phe Trp Thr Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
        35   40   45
Gly Glu Ile Ser His Ser Gly Arg Thr Asn Tyr Asn Pro Ser Leu Lys
    50   55   60
Ser Arg Val Thr Ile Ser Val Asp Thr Ser Met Ser Gln Phe Ser Leu
65   70   75   80
Lys Met Thr Ser Val Thr Ala Ala Asp Ser Ala Val Tyr Tyr Cys Ala
                85   90   95
Arg Asp Tyr Pro Asn Trp Val Phe Asp Tyr Trp Gly Gln Gly Thr Leu
            100   105   110
Val Thr Val Ser Ser
        115

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<400> 67
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<210> 68
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<220>
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<400> 68
Gly Gly Ser Phe Ser Asp Tyr Phe
1 5

<210> 69
<211> 21
<212> DNA
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<220>
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<400> 69
atcagtcata gtggaagaac c 21

<210> 70
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<220>
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<400> 70
Ile Ser His Ser Gly Arg Thr
1 5

<210> 71
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<220>
<223> Synthetic

<400> 71
gcgagagatt atcccaactg ggtttttgac tac 33

<210> 72
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<212> PRT
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<220>
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<400> 72
Ala Arg Asp Tyr Pro Asn Trp Val Phe Asp Tyr
 1   5   10

<210> 73
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ctctcctgca gggccagtca gagtgttttc aacagctact tagcgtggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggtgcatcca ggagggccac tggcatccct 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctggagatt ttgcagtata tttctgtcag cagtatggta actcaccgct cactttcggc 300
ggagggacca aggtggagat caaa   324

<210> 74
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 74
Glu Ile Glu Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 1   5   10   15
Glu Gly Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Phe Asn Ser
            20   25   30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35   40   45
Ile Tyr Gly Ala Ser Arg Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50   55   60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65   70   75   80
Pro Gly Asp Phe Ala Val Tyr Phe Cys Gln Gln Tyr Gly Asn Ser Pro
                85   90   95
Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 75
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 75
cagagtgttt tcaacagcta c 21

<210> 76
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 76
Gln Ser Val Phe Asn Ser Tyr
1 5

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

<220>
<223> Synthetic

<400> 77
ggtgcatcc 9

<210> 78
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 78
Gly Ala Ser
1

<210> 79
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 79
cagcagtatg gtaactcacc gctcact 27

<210> 80
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 80
Gln Gln Tyr Gly Asn Ser Pro Leu Thr
 1   5

<210> 81
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 81
cggttgcagc tggtggagtc tgggggaggc ttggtcaagc ctggagggtc cctgaaactc 60
tcctgtgcag cctctggatt caccatcagt gactactaca tgagctggat ccgccaggct 120
ccagggaagg ggctggagtg ggtttcgtac attggtggta gtggtagtac catatattac 180
gcagactctg tgaagggccg attcaccatc tccagggaca acgccaagaa ctcactgtat 240
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gagagaggac 300
gctgactcct actactacta cggtatggac gtctggggcc aagggaccac ggtcaccgtc 360
tcctca   366

<210> 82
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 82
Arg Leu Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
 1   5   10   15
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Ile Ser Asp Tyr
            20   25   30
Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Tyr Ile Gly Gly Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Glu Asp Ala Asp Ser Tyr Tyr Tyr Tyr Gly Met Asp Val Trp
            100   105   110
Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 83
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 83
ggattcacca tcagtgacta ctac 24

<210> 84
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 84
Gly Phe Thr Ile Ser Asp Tyr Tyr
1 5

<210> 85
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 85
attggtggta gtggtagtac cata 24

<210> 86
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 86
Ile Gly Gly Ser Gly Ser Thr Ile
1 5

<210> 87
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 87
gcgagagagg acgctgactc ctactactac tacggtatgg acgtc 45

<210> 88
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 88
Ala Arg Glu Asp Ala Asp Ser Tyr Tyr Tyr Tyr Gly Met Asp Val
 1   5   10   15

<210> 89
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 89
gatattgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60
atcaactgca agtccagcca gagtgtttta tacagctcca acaataagaa ccacttatct 120
tggtatcagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180
gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240
atcagcagcc tgcaggctga agatgtggca gtttattact gtcaacaata ttatagtact 300
cctcggacgt tcggccaagg gaccaaggtg gaaatcaaa   339

<210> 90
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 90
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1   5   10   15
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
            20   25   30
Ser Asn Asn Lys Asn His Leu Ser Trp Tyr Gln Gln Lys Pro Gly Gln
        35   40   45
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50   55   60
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
                85   90   95
Tyr Tyr Ser Thr Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
            100   105   110
Lys

<210> 91
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 91

cagagtgttt tatacagctc caacaataag aaccac 36

<210> 92
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 92
Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn His
1 5 10

<210> 93
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 93
tgggcatct 9

<210> 94
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 94
Trp Ala Ser
1

<210> 95
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 95
caacaatatt atagtactcc tcggacg 27

<210> 96
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 96
Gln Gln Tyr Tyr Ser Thr Pro Arg Thr
 1   5

<210> 97
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 97
gaagtgcaac tggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60
tcctgtgtag cctctggatt cacctttcaa gattatgcca tgcactgggt ccggcaagct 120
ccaggaaagg gcctggagtg ggtctcaggt attaattgga ttagtgatga catgggctat 180
gcggactctg tgatgggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
ctgcaaatgg acagtctgag agctgaggac acggccttgt attactgtgc aaaagataag 300
ggattacgat ttttggacta tgttatggac gtctggggcc aagggaccac ggtcaccgtc 360
tcctca   366

<210> 98
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 98
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1   5   10   15
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Gln Asp Tyr
            20   25   30
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Gly Ile Asn Trp Ile Ser Asp Asp Met Gly Tyr Ala Asp Ser Val
    50   55   60
Met Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65   70   75   80
Leu Gln Met Asp Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
                85   90   95
Ala Lys Asp Lys Gly Leu Arg Phe Leu Asp Tyr Val Met Asp Val Trp
            100   105   110
Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 99
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 99

ggattcacct ttcaagatta tgcc 24

<210> 100
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 100
Gly Phe Thr Phe Gln Asp Tyr Ala
1 5

<210> 101
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 101
attaattgga ttagtgatga catg 24

<210> 102
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 102
Ile Asn Trp Ile Ser Asp Asp Met
1 5

<210> 103
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 103
gcaaaagata agggattacg atttttggac tatgttatgg acgtc 45

<210> 104
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 104
Ala Lys Asp Lys Gly Leu Arg Phe Leu Asp Tyr Val Met Asp Val
 1   5   10   15

<210> 105
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 105
gacatccagt tgacccagtc tcctctctcc ctgcccgtca cccctggaga gccggcctcc 60
atctcctgca ggtctactca gagcctcctg cataggaatg gccacaacta tttgcattgg 120
tacctacata agccagggca gtctccacaa ctcctgattc atctgggttc taatcgggcc 180
tccggggtcc ctgacaggtt cagtggcagt ggatcaggca cagattttac actgaaaatc 240
agcagagtgg aggctgagga tgttggggtc tattactgca tgcaagctct acagactccg 300
tacacttttg gccaggggac caaggtggag atcaaacga   339

<210> 106
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 106
Asp Ile Gln Leu Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
 1   5   10   15
Glu Pro Ala Ser Ile Ser Cys Arg Ser Thr Gln Ser Leu Leu His Arg
            20   25   30
Asn Gly His Asn Tyr Leu His Trp Tyr Leu His Lys Pro Gly Gln Ser
        35   40   45
Pro Gln Leu Leu Ile His Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
    50   55   60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65   70   75   80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
                85   90   95
Leu Gln Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100   105   110
Arg

<210> 107
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 107
cagagcctcc tgcataggaa tggccacaac tat   33

<210> 108
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 108
Gln Ser Leu Leu His Arg Asn Gly His Asn Tyr
 1   5   10

<210> 109
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 109
ctgggttct   9

<210> 110
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 110
Leu Gly Ser
 1

<210> 111
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 111
atgcaagctc tacagactcc gtacact   27

<210> 112
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 112

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Met Gln Ala Leu Gln Thr Pro Tyr Thr
 1               5


<210> 113
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 113
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60
tcctgtgtag cctctggatt cacctttcaa gattatgcca tgcactgggt ccggcaagct 120
ccaggaaagg gcctggagtg ggtctcaggt attaattgga ttagtgatga catgggctat 180
gcggactctg tgatgggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
ctgcaaatgg acagtctgag agctgaggac acggccttgt attactgtgc aaaagataag 300
ggattacgat ttttggacta tgttatggac gtctggggcc aagggaccac ggtcaccgtc 360
tcc                                                               363

<210> 114
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 114
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Gln Asp Tyr
            20                  25                  30
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Gly Ile Asn Trp Ile Ser Asp Asp Met Gly Tyr Ala Asp Ser Val
    50                  55                  60
Met Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80
Leu Gln Met Asp Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95
Ala Lys Asp Lys Gly Leu Arg Phe Leu Asp Tyr Val Met Asp Val Trp
            100                 105                 110
Gly Gln Gly Thr Thr Val Thr Val Ser
        115                 120


<210> 115
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 115
gacatcgtga tgacccagtc tcctctctcc ctgcccgtca cccctggaga gccggcctcc 60
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atctcctgca ggtctactca gagcctcctg cataggaatg gccacaacta tttgcattgg 120
tacctacata agccagggca gtctccacaa ctcctgattc atctgggttc taatcgggcc 180
tccggggtcc ctgacaggtt cagtggcagt ggatcaggca cagattttac actgaaaatc 240
agcagagtgg aggctgagga tgttggggtc tattactgca tgcaagctct acagactccg 300
tacacttttg gccaggggac caagctggag atcaaa 336

<210> 116
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 116
Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15
Glu Pro Ala Ser Ile Ser Cys Arg Ser Thr Gln Ser Leu Leu His Arg
20 25 30
Asn Gly His Asn Tyr Leu His Trp Tyr Leu His Lys Pro Gly Gln Ser
35 40 45
Pro Gln Leu Leu Ile His Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
50 55 60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
85 90 95
Leu Gln Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 117
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 117
caggtgcagc tggtggagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60
tcctgcaagg cttctggata caccttcacc ggctactata tgcactgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatgggatgg atcaaaccta aaagtggtgg cacaaactat 180
gtacagaagt ttcagggcag ggtcaccatg accagggaca cgtccatcaa cacagcctac 240
atggaactaa acaatctgaa atctgacgac acggccgttt attactgtgc gactggaggg 300
agtcaagatg cttctgattt ctggggccaa gggacaatgg tcaccgtctc ttca 354

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

<220>
<223> Synthetic

<400> 118
Gln Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

```
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
            20                  25                  30
Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45
Gly Trp Ile Lys Pro Lys Ser Gly Gly Thr Asn Tyr Val Gln Lys Phe
    50                  55                  60
Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Asn Thr Ala Tyr
65                  70                  75                  80
Met Glu Leu Asn Asn Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Thr Gly Gly Ser Gln Asp Ala Ser Asp Phe Trp Gly Gln Gly Thr
            100                 105                 110
Met Val Thr Val Ser Ser
        115
```

<210> 119
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 119
ggatacacct tcaccggcta ctat 24

<210> 120
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 120
```
Gly Tyr Thr Phe Thr Gly Tyr Tyr
 1               5
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<210> 121
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 121
atcaaaccta aaagtggtgg caca 24

<210> 122
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 122
Ile Lys Pro Lys Ser Gly Gly Thr
 1   5

<210> 123
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 123
gcgactggag ggagtcaaga tgcttctgat ttc   33

<210> 124
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 124
Ala Thr Gly Gly Ser Gln Asp Ala Ser Asp Phe
 1   5   10

<210> 125
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 125
gacatccagt tgacccagtc tccatcttcc gtgtctgcat ctgtaggagg cagagtcacc 60
atcacttgtc gggcgagtca ggatattagc atctggttag cctggtatca acagaaacca 120
gggaaagccc ctaacctcct gatctatgct gcatccagtt tacaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
gaagattttg caacttacta ttgtcaacag gctgacagtt tcccgctcac tttcggcggt 300
gggaccaagc tggagatcaa acga   324

<210> 126
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 126
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
 1   5   10   15
Gly Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Ile Trp

```
            20                  25                  30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile
        35                  40                  45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asp Ser Phe Pro Leu
                85                  90                  95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
            100                 105
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<210> 127
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 127
caggatatta gcatctgg 18

<210> 128
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 128
Gln Asp Ile Ser Ile Trp
 1   5

<210> 129
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 129
gctgcatcc 9

<210> 130
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 130
Ala Ala Ser

1

<210> 131
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 131
caacaggctg acagtttccc gctcact 27

<210> 132
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 132
Gln Gln Ala Asp Ser Phe Pro Leu Thr
1 5

<210> 133
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 133
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60
tcctgcaagg cttctggata caccttcacc ggctactata tgcactgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatgggatgg atcaaaccta aaagtggtgg cacaaactat 180
gtacagaagt ttcagggcag ggtcaccatg accagggaca cgtccatcaa cacagcctac 240
atggaactaa acaatctgaa atctgacgac acggccgttt attactgtgc gactggaggg 300
agtcaagatg cttctgattt ctggggccaa gggacaatgg tcaccgtctc ttca 354

<210> 134
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 134
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30
Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

```
Gly Trp Ile Lys Pro Lys Ser Gly Gly Thr Asn Tyr Val Gln Lys Phe
    50                  55                  60
Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Asn Thr Ala Tyr
65                  70                  75                  80
Met Glu Leu Asn Asn Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Thr Gly Gly Ser Gln Asp Ala Ser Asp Phe Trp Gly Gln Gly Thr
            100                 105                 110
Met Val Thr Val Ser Ser
        115
```

<210> 135
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 135
gacatccaga tgacccagtc tccatcttcc gtgtctgcat ctgtaggagg cagagtcacc 60
atcacttgtc gggcgagtca ggatattagc atctggttag cctggtatca acagaaacca 120
gggaaagccc ctaacctcct gatctatgct gcatccagtt tacaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
gaagattttg caacttacta ttgtcaacag gctgacagtt tcccgctcac tttcggcggt 300
gggaccaagg tggagatcaa a 321

<210> 136
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 136
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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
 1               5                  10                  15
Gly Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Ile Trp
            20                  25                  30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile
        35                  40                  45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asp Ser Phe Pro Leu
                85                  90                  95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105
```

<210> 137
<211> 378
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 137
caggtgcagc tggtggagtc tgggggagcc ttggtaaagc ctgggggtc ccttagactc 60
tcctgtgcag tctctggatt cactttcatt aatgactgga tgaactgggt ccgccaggct 120
ccagggaagg ggctggaatg ggttggccgt attaaaagca caactgatgg tgggacaaca 180
gacgacgctg cacccgtgaa aggcagattc accatctcaa gagatgactc aaaaaacacg 240
ctatatctgc aaatgaatag cctgaaaacc gaggacacag ccgtgtatta ctgtaccaga 300
gataggaacc gacagagaaa ttacttctat gacggtatgg acgtctgggg ccaagggacc 360
acggtcaccg tctcctca 378

<210> 138
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 138
Gln Val Gln Leu Val Glu Ser Gly Gly Ala Leu Val Lys Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Thr Phe Ile Asn Asp
20 25 30
Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Gly Arg Ile Lys Ser Thr Thr Asp Gly Gly Thr Thr Asp Asp Ala Ala
50 55 60
Pro Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80
Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
85 90 95
Tyr Cys Thr Arg Asp Arg Asn Arg Gln Arg Asn Tyr Phe Tyr Asp Gly
100 105 110
Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 139
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 139
ggattcactt tcattaatga ctgg 24

<210> 140
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 140
Gly Phe Thr Phe Ile Asn Asp Trp
 1   5

<210> 141
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 141
attaaaagca caactgatgg tgggacaaca   30

<210> 142
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 142
Ile Lys Ser Thr Thr Asp Gly Gly Thr Thr
 1   5   10

<210> 143
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 143
accagagata ggaaccgaca gagaaattac ttctatgacg gtatggacgt c   51

<210> 144
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 144
Thr Arg Asp Arg Asn Arg Gln Arg Asn Tyr Phe Tyr Asp Gly Met Asp
 1   5   10   15
Val

<210> 145
<211> 339
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 145
gacatccagt tgacccagtc tccagtctcc ctgcccgtca cccctggaga gccggcctcc 60
atctcctgca ggtctagtca gaggctcctg cataataatg gaaacaacta tttggattgg 120
tacctgcaga agccagggca gtctccacaa ctcctgatct atttgggctc taatcgggcc 180
tccggggtcc ctgacaggtt cagtggcagt ggatcaggca cagatttcac actgaaagtc 240
agtagagtgg aggctgagga tgttggggtt tattactgca tgcaagctct acaaactccg 300
tacacttttg gccaggggac caagctggag atcaaacga 339

<210> 146
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 146
Asp Ile Gln Leu Thr Gln Ser Pro Val Ser Leu Pro Val Thr Pro Gly
 1   5   10   15
Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Arg Leu Leu His Asn
            20   25   30
Asn Gly Asn Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
        35   40   45
Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
    50   55   60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Val
65   70   75   80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
                85   90   95
Leu Gln Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100   105   110
Arg

<210> 147
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 147
cagaggctcc tgcataataa tggaaacaac tat 33

<210> 148
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 148
Gln Arg Leu Leu His Asn Asn Gly Asn Asn Tyr
 1   5   10

<210> 149
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 149
ttgggctct   9

<210> 150
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 150
Leu Gly Ser
 1

<210> 151
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 151
atgcaagctc tacaaactcc gtacact   27

<210> 152
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 152
Met Gln Ala Leu Gln Thr Pro Tyr Thr
 1   5

<210> 153
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 153
gaggtgcagc tggtggagtc tgggggagcc ttggtaaagc ctgggggtc ccttagactc 60
tcctgtgcag tctctggatt cactttcatt aatgactgga tgaactgggt ccgccaggct 120
ccagggaagg ggctggaatg ggttggccgt attaaaagca caactgatgg tgggacaaca 180
gacgacgctg cacccgtgaa aggcagattc accatctcaa gagatgactc aaaaaacacg 240
ctatatctgc aaatgaatag cctgaaaacc gaggacacag ccgtgtatta ctgtaccaga 300
gataggaacc gacagagaaa ttacttctat gacggtatgg acgtctgggg ccaagggacc 360
acggtcaccg tctcc 375

<210> 154
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 154
Glu Val Gln Leu Val Glu Ser Gly Gly Ala Leu Val Lys Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Thr Phe Ile Asn Asp
20 25 30
Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Gly Arg Ile Lys Ser Thr Thr Asp Gly Gly Thr Thr Asp Asp Ala Ala
50 55 60
Pro Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80
Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
85 90 95
Tyr Cys Thr Arg Asp Arg Asn Arg Gln Arg Asn Tyr Phe Tyr Asp Gly
100 105 110
Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
115 120 125

<210> 155
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 155
gacatcgtga tgacccagtc tccagtctcc ctgcccgtca cccctggaga gccggcctcc 60
atctcctgca ggtctagtca gaggctcctg cataataatg gaaacaacta tttggattgg 120
tacctgcaga agccagggca gtctccacaa ctcctgatct atttgggctc taatcgggcc 180
tccggggtcc ctgacaggtt cagtggcagt ggatcaggca cagatttcac actgaaagtc 240
agtagagtgg aggctgagga tgttggggtt tattactgca tgcaagctct acaaactccg 300
tacacttttg gccaggggac caagctggag atcaaa 336

<210> 156
<211> 112

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 156
Asp Ile Val Met Thr Gln Ser Pro Val Ser Leu Pro Val Thr Pro Gly
 1   5   10   15
Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Arg Leu Leu His Asn
            20   25   30
Asn Gly Asn Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
        35   40   45
Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
    50   55   60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Val
65   70   75   80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
                85   90   95
Leu Gln Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100   105   110

<210> 157
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 157
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttagc agttatgcca tgacctgggt ccgccaggct 120
ccagggaagg ggcttgagtg ggtctcaggt gtaagtggaa gaggtggtag tacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
cttcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gtattgggat 300
atcagctcgt ttgactactg gggccaggga accctggtca ctgtctcctc a   351

<210> 158
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 158
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20   25   30
Ala Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Gly Val Ser Gly Arg Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Tyr Trp Asp Ile Ser Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110
Val Thr Val Ser Ser
115

<210> 159
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 159
ggattcacct ttagcagtta tgcc 24

<210> 160
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 160
Gly Phe Thr Phe Ser Ser Tyr Ala
1 5

<210> 161
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 161
gtaagtggaa gaggtggtag taca 24

<210> 162
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 162
Val Ser Gly Arg Gly Gly Ser Thr
1 5

<210> 163
<211> 30

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 163
gcgtattggg atatcagctc gtttgactac 30

<210> 164
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 164
Ala Tyr Trp Asp Ile Ser Ser Phe Asp Tyr
1 5 10

<210> 165
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 165
gacatccagt tgacccagtc tccatccttc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgct gggccagtca gggcattagc acttatttag cctggtatca gcaaaaacca 120
gggaaaaccc ctaaactcct gatctatgct gcatccactt tgcaaagtgg agtcccatca 180
aggttcagcg gcagtggatc tgggacagat ttcactctca caatcagcag cctgcagcct 240
gaagattttg caacttatta ctgtcaacag tttaatagtt acccgctcac tttcggcgga 300
gggaccaagc tggagatcaa acga 324

<210> 166
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 166
Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Trp Ala Ser Gln Gly Ile Ser Thr Tyr
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Thr Pro Lys Leu Leu Ile
35 40 45
Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr 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 Leu

85 90 95

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

<210> 167
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 167
cagggcatta gcacttat 18

<210> 168
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 168
Gln Gly Ile Ser Thr Tyr
1 5

<210> 169
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 169
gctgcatcc 9

<210> 170
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 170
Ala Ala Ser
1

<210> 171
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 171
caacagttta atagttaccc gctcact 27

<210> 172
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 172
Gln Gln Phe Asn Ser Tyr Pro Leu Thr
1 5

<210> 173
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 173
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttagc agttatgcca tgacctgggt ccgccaggct 120
ccagggaagg ggcttgagtg ggtctcaggt gtaagtggaa gaggtggtag tacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
cttcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gtattgggat 300
atcagctcgt ttgactactg gggccaggga accctggtca ctgtctcctc a 351

<210> 174
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 174
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30
Ala Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Gly Val Ser Gly Arg Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Tyr Trp Asp Ile Ser Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 175
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 175
gacatccagt tgacccagtc tccatccttc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgct gggccagtca gggcattagc acttatttag cctggtatca gcaaaaacca 120
gggaaaaccc ctaaactcct gatctatgct gcatccactt tgcaaagtgg agtcccatca 180
aggttcagcg gcagtggatc tgggacagat ttcactctca caatcagcag cctgcagcct 240
gaagattttg caacttatta ctgtcaacag tttaatagtt acccgctcac tttcggcgga 300
gggaccaagg tggagatcaa a 321

<210> 176
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 176
Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Trp Ala Ser Gln Gly Ile Ser Thr Tyr
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Thr Pro Lys Leu Leu Ile
35 40 45
Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr 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 Leu
85 90 95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 177
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 177
gaggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggagatc cctgagactc 60
tcctgtgtgg cctctggatt caccttcagt aactatggca tgcactgggt ccgccaggct 120
ccaggcaagg ggctggaatg ggtggcagtt atatcatatg atggaaataa tgatttgtat 180
tcagactccg tgaagggccg attcaccatc tccagagaca atgccaagaa cgcgctgtct 240

ctgcaaatga ccagcctgag agctgaggac acggctgtct attactgtgc gagagatagt 300
acgatgactc cctactacta ccacggtata gacgtctggg gccaagggac cacggtcacc 360
gtctcctca 369

<210> 178
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 178
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1   5   10   15
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Asn Tyr
            20   25   30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ala Val Ile Ser Tyr Asp Gly Asn Asn Asp Leu Tyr Ser Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ala Leu Ser
65   70   75   80
Leu Gln Met Thr Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Asp Ser Thr Met Thr Pro Tyr Tyr Tyr His Gly Ile Asp Val
            100   105   110
Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 179
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 179
ggattcacct tcagtaacta tggc 24

<210> 180
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 180
Gly Phe Thr Phe Ser Asn Tyr Gly
 1   5

<210> 181
<211> 24
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 181
atatcatatg atggaaataa tgat 24

<210> 182
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 182
Ile Ser Tyr Asp Gly Asn Asn Asp
1 5

<210> 183
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 183
gcgagagata gtacgatgac tccctactac taccacggta tagacgtc 48

<210> 184
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 184
Ala Arg Asp Ser Thr Met Thr Pro Tyr Tyr Tyr His Gly Ile Asp Val
1 5 10 15

<210> 185
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 185
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca ggacattaga aatgatttag gctggtatca gcagaaacca 120
gggaaagccc ctaagcgcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagac ttcactctca caatcagcag cctgcagcct 240

gaagattttg caacttatta ctgtctacag cataatagtt accctccgac gttcggccaa 300
gggaccaagg tggagatcaa acga 324

<210> 186
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 186
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Arg Asn Asp
20 25 30
Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
35 40 45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Pro
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 187
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 187
caggacatta gaaatgat 18

<210> 188
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 188
Gln Asp Ile Arg Asn Asp
1 5

<210> 189
<211> 9
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 189
gctgcatcc 9

<210> 190
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 190
Ala Ala Ser
1

<210> 191
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 191
ctacagcata atagttaccc tccgacg 27

<210> 192
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 192
Leu Gln His Asn Ser Tyr Pro Pro Thr
1 5

<210> 193
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 193
caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggagatc cctgagactc 60
tcctgtgtgg cctctggatt caccttcagt aactatggca tgcactgggt ccgccaggct 120
ccaggcaagg ggctggaatg ggtggcagtt atatcatatg atggaaataa tgatttgtat 180
tcagactccg tgaagggccg attcaccatc tccagagaca atgccaagaa cgcgctgtct 240
ctgcaaatga ccagcctgag agctgaggac acggctgtct attactgtgc gagagatagt 300
acgatgactc cctactacta ccacggtata gacgtctggg gccaagggac cacggtcacc 360
gtctcc 366

<210> 194
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 194
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1   5   10   15
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Asn Tyr
            20   25   30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ala Val Ile Ser Tyr Asp Gly Asn Asn Asp Leu Tyr Ser Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ala Leu Ser
65   70   75   80
Leu Gln Met Thr Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Asp Ser Thr Met Thr Pro Tyr Tyr Tyr His Gly Ile Asp Val
            100   105   110
Trp Gly Gln Gly Thr Thr Val Thr Val Ser
        115   120

<210> 195
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 195
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca ggacattaga aatgatttag gctggtatca gcagaaacca 120
gggaaagccc ctaagcgcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagac ttcactctca caatcagcag cctgcagcct 240
gaagattttg caacttatta ctgtctacag cataatagtt accctccgac gttcggccaa 300
gggaccaagg tggagatcaa a   321

<210> 196
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 196
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Arg Asn Asp
            20   25   30
Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile

```
        35                  40                  45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Pro
                85                  90                  95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105
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<210> 197
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 197
gaggtgcagc tggtggagtc tgggggaggc ttggtgcagc ctgggggtc cctgagactc 60
tcctgttcag cctctggatt cacctttagt aaatatgtca tgacctgggt ccgccaggct 120
ccagggaagg gactggagtg ggtctcagct attggtccta ctggtcgtac cacggaatac 180
gcagactccg tgcagggccg cttcaccatc tccagagaca attccatgaa cacggttttt 240
cttcacttga acagtctgac agccgaggac acggccgaat attattgtgc gaagatgttt 300
gactggaatt acgacgtgta ctttgactcc tggggccagg gaaccctggt cactgtctcc 360
tca 363

<210> 198
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 198
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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Thr Phe Ser Lys Tyr
            20                  25                  30
Val Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Ala Ile Gly Pro Thr Gly Arg Thr Thr Glu Tyr Ala Asp Ser Val
    50                  55                  60
Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Met Asn Thr Val Phe
65                  70                  75                  80
Leu His Leu Asn Ser Leu Thr Ala Glu Asp Thr Ala Glu Tyr Tyr Cys
                85                  90                  95
Ala Lys Met Phe Asp Trp Asn Tyr Asp Val Tyr Phe Asp Ser Trp Gly
            100                 105                 110
Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
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<210> 199
<211> 24
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 199
ggattcacct ttagtaaata tgtc 24

<210> 200
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 200
Gly Phe Thr Phe Ser Lys Tyr Val
1 5

<210> 201
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 201
attggtccta ctggtcgtac cacg 24

<210> 202
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 202
Ile Gly Pro Thr Gly Arg Thr Thr
1 5

<210> 203
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 203
gcgaagatgt ttgactggaa ttacgacgtg tactttgact cc 42

<210> 204
<211> 14

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 204
Ala Lys Met Phe Asp Trp Asn Tyr Asp Val Tyr Phe Asp Ser
 1   5   10

<210> 205
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 205
gacatccaga tgacccagtc tccctccatc ttgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc ggaccagtca gagtattagt aattggttgg cctggtatca gcagaaacca 120
gggaaagccc ctaacctcct gatctataag gcgtctagtt tagaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240
gatgattttg caacttatta ctgtcaacag tattatagat attggacgtt cggccaaggg 300
accaaggtgg agatcaaacg a   321

<210> 206
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 206
Asp Ile Gln Met Thr Gln Ser Pro Ser Ile Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Gln Ser Ile Ser Asn Trp
            20   25   30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile
        35   40   45
Tyr Lys Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Arg Tyr Trp Thr
                85   90   95
Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100   105

<210> 207
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 207
cagagtatta gtaattgg 18

<210> 208
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 208
Gln Ser Ile Ser Asn Trp
1 5

<210> 209
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 209
aaggcgtct 9

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

<220>
<223> Synthetic

<400> 210
Lys Ala Ser
1

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

<220>
<223> Synthetic

<400> 211
caacagtatt atagatattg gacg 24

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

<220>
<223> Synthetic

<400> 212
Gln Gln Tyr Tyr Arg Tyr Trp Thr
 1   5

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

<220>
<223> Synthetic

<400> 213
gaggtgcagc tggtggagtc tgggggaggc ttggtgcagc ctgggggtc cctgagactc 60
tcctgttcag cctctggatt cacctttagt aaatatgtca tgacctgggt ccgccaggct 120
ccagggaagg gactggagtg ggtctcagct attggtccta ctggtcgtac cacggaatac 180
gcagactccg tgcagggccg cttcaccatc tccagagaca attccatgaa cacggttttt 240
cttcacttga acagtctgac agccgaggac acggccgaat attattgtgc gaagatgttt 300
gactggaatt acgacgtgta ctttgactcc tggggccagg gaaccctggt caccgtctcc 360
tca   363

<210> 214
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 214
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 Ser Ala Ser Gly Phe Thr Phe Ser Lys Tyr
            20   25   30
Val Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Ala Ile Gly Pro Thr Gly Arg Thr Thr Glu Tyr Ala Asp Ser Val
    50   55   60
Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Met Asn Thr Val Phe
65   70   75   80
Leu His Leu Asn Ser Leu Thr Ala Glu Asp Thr Ala Glu Tyr Tyr Cys
                85   90   95
Ala Lys Met Phe Asp Trp Asn Tyr Asp Val Tyr Phe Asp Ser Trp Gly
            100   105   110
Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 215
<211> 318
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 215
gacatccaga tgacccagtc tccctccatc ttgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc ggaccagtca gagtattagt aattggttgg cctggtatca gcagaaacca 120
gggaaagccc ctaacctcct gatctataag gcgtctagtt tagaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240
gatgattttg caacttatta ctgtcaacag tattatagat attggacgtt cggccaaggg 300
accaaggtgg agatcaaa 318

<210> 216
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 216
Asp Ile Gln Met Thr Gln Ser Pro Ser Ile Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Gln Ser Ile Ser Asn Trp
            20   25   30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile
        35   40   45
Tyr Lys Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Arg Tyr Trp Thr
                85   90   95
Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 217
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 217
caggttcagc tggtgcagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttagt aattatgtca tgaactgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtctcagtt ataagtggta gtggcggtag cacacactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaaaga cgcgctgtat 240
ctacaaatga acagcctgag agccgaggac acggccgttt attactgtgc gaaaggcccg 300
ctggaggctt actactacta caacggtatg gacgtctggg gccaagggac cacggtcacc 360
gtctcctca 369

<210> 218
<211> 123
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 218
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
            20   25   30
Val Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Val Ile Ser Gly Ser Gly Gly Ser Thr His Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asp Ala Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Lys Gly Pro Leu Glu Ala Tyr Tyr Tyr Tyr Asn Gly Met Asp Val
            100   105   110
Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 219
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 219
ggattcacct ttagtaatta tgtc   24

<210> 220
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 220
Gly Phe Thr Phe Ser Asn Tyr Val
 1   5

<210> 221
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 221
ataagtggta gtggcggtag caca   24

<210> 222
<211> 8

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 222
Ile Ser Gly Ser Gly Gly Ser Thr
 1   5

<210> 223
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 223
gcgaaaggcc cgctggaggc ttactactac tacaacggta tggacgtc   48

<210> 224
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 224
Ala Lys Gly Pro Leu Glu Ala Tyr Tyr Tyr Tyr Asn Gly Met Asp Val
 1   5   10   15

<210> 225
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 225
gccatccaga tgacccagtc tccatccttc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgct gggccagtca ggccattagc agttatttag cctggtatca gcacaaacca 120
gggagagccc ctaagctcct gatctattct acatccactt tgcaaagtgg agtcccatca 180
aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240
gaagattttg caacttatta ctgtcaacag cttaatagtt accccacctt cggccaaggg 300
accaagctgg agatcaaacg a   321

<210> 226
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 226
Ala Ile Gln Met Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Trp Ala Ser Gln Ala Ile Ser Ser Tyr
            20   25   30
Leu Ala Trp Tyr Gln His Lys Pro Gly Arg Ala Pro Lys Leu Leu Ile
        35   40   45
Tyr Ser Thr Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Asn Ser Tyr Pro Thr
                85   90   95
Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
            100   105

<210> 227
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 227
caggccatta gcagttat 18

<210> 228
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 228
Gln Ala Ile Ser Ser Tyr
 1   5

<210> 229
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 229
tctacatcc 9

<210> 230
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 230
Ser Thr Ser
 1

<210> 231
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 231
caacagctta atagttaccc cacc 24

<210> 232
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 232
Gln Gln Leu Asn Ser Tyr Pro Thr
 1   5

<210> 233
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 233
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttagt aattatgtca tgaactgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtctcagtt ataagtggta gtggcggtag cacacactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaaaga cgcgctgtat 240
ctacaaatga acagcctgag agccgaggac acggccgttt attactgtgc gaaaggcccg 300
ctggaggctt actactacta caacggtatg gacgtctggg gccaagggac cacggtcacc 360
gtctcctca 369

<210> 234
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 234

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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
            20                  25                  30
Val Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Val Ile Ser Gly Ser Gly Gly Ser Thr His Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asp Ala Leu Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Lys Gly Pro Leu Glu Ala Tyr Tyr Tyr Tyr Asn Gly Met Asp Val
            100                 105                 110
Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120
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<210> 235
<211> 318
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 235
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gacatccagt tgacccagtc tccatccttc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgct gggccagtca ggccattagc agttatttag cctggtatca gcacaaacca 120
gggagagccc ctaagctcct gatctattct acatccactt tgcaaagtgg agtcccatca 180
aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240
gaagattttg caacttatta ctgtcaacag cttaatagtt accccacctt cggccaaggg 300
accaagctgg agatcaaa                                              318
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<210> 236
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 236
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Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Thr Ile Thr Cys Trp Ala Ser Gln Ala Ile Ser Ser Tyr
            20                  25                  30
Leu Ala Trp Tyr Gln His Lys Pro Gly Arg Ala Pro Lys Leu Leu Ile
        35                  40                  45
Tyr Ser Thr Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Asn Ser Tyr Pro Thr
                85                  90                  95
Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105
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<210> 237
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> VARIANT
<222> (1)...(1)
<223> Xaa = Gly

<220>
<221> VARIANT
<222> (2)...(2)
<223> Xaa = Phe

<220>
<221> VARIANT
<222> (3)...(3)
<223> Xaa = Thr

<220>
<221> VARIANT
<222> (4)...(4)
<223> Xaa = Phe

<220>
<221> VARIANT
<222> (5)...(5)
<223> Xaa = Ser

<220>
<221> VARIANT
<222> (6)...(6)
<223> Xaa = Thr, Ser, or Asn

<220>
<221> VARIANT
<222> (7)...(7)
<223> Xaa = Tyr

<220>
<221> VARIANT
<222> (8)...(8)
<223> Xaa = Gly, Trp, Val, or Ala

<400> 237
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1   5

<210> 238
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> VARIANT
<222> (1)...(1)
<223> Xaa = Ile or Val

<220>
<221> VARIANT
<222> (2)...(2)
<223> Xaa = Ser or Lys

<220>
<221> VARIANT
<222> (3)...(3)
<223> Xaa = Gly or Glu

<220>
<221> VARIANT
<222> (4)...(4)
<223> Xaa = Thr, Asp, Ser, or Arg

<220>
<221> VARIANT
<222> (5)...(5)
<223> Xaa = Gly

<220>
<221> VARIANT
<222> (6)...(6)
<223> Xaa = Arg, Ser, or Gly

<220>
<221> VARIANT
<222> (7)...(7)
<223> Xaa = Thr, Glu, or Ser

<220>
<221> VARIANT
<222> (8)...(8)
<223> Xaa = Thr or Lys

<400> 238
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1   5

<210> 239

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

<220>
<223> Synthetic

<220>
<221> VARIANT
<222> (1)...(1)
<223> Xaa = Thr or Ala

<220>
<221> VARIANT
<222> (2)...(2)
<223> Xaa = Lys, Arg or absent

<220>
<221> VARIANT
<222> (3)...(3)
<223> Xaa = Glu, Gly or absent

<220>
<221> VARIANT
<222> (4)...(4)
<223> Xaa = Asp, Pro or absent

<220>
<221> VARIANT
<222> (5)...(5)
<223> Xaa = Leu or absent

<220>
<221> VARIANT
<222> (6)...(6)
<223> Xaa = Arg, Tyr, Glu or absent

<220>
<221> VARIANT
<222> (7)...(7)
<223> Xaa = Gly, Asp, Ala or absent

<220>
<221> VARIANT
<222> (8)...(8)
<223> Xaa = Asp, Ser or Tyr

<220>
<221> VARIANT
<222> (9)...(9)
<223> Xaa = Tyr or Trp

<220>
<221> VARIANT
<222> (10)...(10)
<223> Xaa = Tyr or Asp

<220>
<221> VARIANT
<222> (11)...(11)
<223> Xaa =Tyr, Lys or Ile

<220>
<221> VARIANT
<222> (12)...(12)
<223> Xaa = Gly, Tyr, Asn, or Ser

<220>
<221> VARIANT
<222> (13)...(13)
<223> Xaa =Val, Gly or Ser

<220>
<221> VARIANT
<222> (14)...(14)
<223> Xaa = Phe or Met

<220>
<221> VARIANT
<222> (15)...(15)
<223> Xaa = Asp

<220>
<221> VARIANT
<222> (16)...(16)
<223> Xaa = Tyr or Val

<400> 239
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1   5   10   15

<210> 240
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> VARIANT
<222> (1)...(1)
<223> Xaa = Gln

<220>
<221> VARIANT
<222> (2)...(2)
<223> Xaa = Thr, Ser, Ala or Gly

<220>
<221> VARIANT
<222> (3)...(3)
<223> Xaa = Ile

<220>
<221> VARIANT
<222> (4)...(4)
<223> Xaa = Ser or Leu

<220>
<221> VARIANT
<222> (5)...(5)
<223> Xaa = Tyr or absent

<220>
<221> VARIANT
<222> (6)...(6)
<223> Xaa = Ser or absent

<220>
<221> VARIANT
<222> (7)...(7)
<223> Xaa = Ser or absent

<220>
<221> VARIANT
<222> (8)...(8)
<223> Xaa = Asn or absent

<220>
<221> VARIANT
<222> (9)...(9)
<223> Xaa = Asn or absent

<220>
<221> VARIANT
<222> (10)...(10)
<223> Xaa = Lys or absent

<220>
<221> VARIANT
<222> (11)...(11)
<223> Xaa = Ser, Asn or Thr

<220>
<221> VARIANT
<222> (12)...(12)
<223> Xaa = Trp or Tyr

<400> 240
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1   5   10

<210> 241
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> VARIANT
<222> (1)...(1)
<223> Xaa = Ala, Trp or Ser

<220>
<221> VARIANT
<222> (2)...(2)
<223> Xaa = Ala or Thr

<220>
<221> VARIANT
<222> (3)...(3)
<223> Xaa = Ser

<400> 241
Xaa Xaa Xaa
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<210> 242
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> VARIANT
<222> (1)...(1)
<223> Xaa =Gln

<220>
<221> VARIANT
<222> (2)...(2)
<223> Xaa = Gln

<220>

<221> VARIANT
<222> (3)...(3)
<223> Xaa = Tyr, Leu or Phe

<220>
<221> VARIANT
<222> (4)...(4)
<223> Xaa = His, Tyr or Asn

<220>
<221> VARIANT
<222> (5)...(5)
<223> Xaa = Arg or Ser

<220>
<221> VARIANT
<222> (6)...(6)
<223> Xaa = Ser, Thr or Tyr

<220>
<221> VARIANT
<222> (7)...(7)
<223> Xaa =Trp or Pro

<220>
<221> VARIANT
<222> (8)...(8)
<223> Xaa = Phe, Leu or absent

<220>
<221> VARIANT
<222> (9)...(9)
<223> Xaa = Thr

<400> 242
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 243
<211> 756
<212> DNA
<213> Homo sapiens

<400> 243
atggccgagg atctgggact gagctttggg gaaacagcca gtgtggaaat gctgccagag 60
cacggcagct gcaggcccaa ggccaggagc agcagcgcac gctgggctct cacctgctgc 120
ctggtgttgc tccccttcct tgcaggactc accacatacc tgcttgtcag ccagctccgg 180
gcccagggag aggcctgtgt gcagttccag gctctaaaag gacaggagtt tgcaccttca 240
catcagcaag tttatgcacc tcttagagca gacggagata agccaagggc acacctgaca 300
gttgtgagac aaactcccac acagcacttt aaaaatcagt tcccagctct gcactgggaa 360
catgaactag gcctggcctt caccaagaac cgaatgaact ataccaacaa attcctgctg 420
atcccagagt cgggagacta cttcatttac tcccaggtca cattccgtgg gatgacctct 480

gagtgcagtg aaatcagaca agcaggccga ccaaacaagc cagactccat cactgtggtc 540
atcaccaagg taacagacag ctaccctgag ccaacccagc tcctcatggg gaccaagtct 600
gtatgcgaag taggtagcaa ctggttccag cccatctacc tcggagccat gttctccttg 660
caagaagggg acaagctaat ggtgaacgtc agtgacatct ctttggtgga ttacacaaaa 720
gaagataaaa ccttctttgg agccttctta ctatag 756

<210> 244
<211> 251
<212> PRT
<213> Homo sapiens

<400> 244
Met Ala Glu Asp Leu Gly Leu Ser Phe Gly Glu Thr Ala Ser Val Glu
 1   5   10   15
Met Leu Pro Glu His Gly Ser Cys Arg Pro Lys Ala Arg Ser Ser Ser
            20   25   30
Ala Arg Trp Ala Leu Thr Cys Cys Leu Val Leu Leu Pro Phe Leu Ala
        35   40   45
Gly Leu Thr Thr Tyr Leu Leu Val Ser Gln Leu Arg Ala Gln Gly Glu
    50   55   60
Ala Cys Val Gln Phe Gln Ala Leu Lys Gly Gln Glu Phe Ala Pro Ser
65   70   75   80
His Gln Gln Val Tyr Ala Pro Leu Arg Ala Asp Gly Asp Lys Pro Arg
                85   90   95
Ala His Leu Thr Val Val Arg Gln Thr Pro Thr Gln His Phe Lys Asn
            100   105   110
Gln Phe Pro Ala Leu His Trp Glu His Glu Leu Gly Leu Ala Phe Thr
        115   120   125
Lys Asn Arg Met Asn Tyr Thr Asn Lys Phe Leu Leu Ile Pro Glu Ser
    130   135   140
Gly Asp Tyr Phe Ile Tyr Ser Gln Val Thr Phe Arg Gly Met Thr Ser
145   150   155   160
Glu Cys Ser Glu Ile Arg Gln Ala Gly Arg Pro Asn Lys Pro Asp Ser
                165   170   175
Ile Thr Val Val Ile Thr Lys Val Thr Asp Ser Tyr Pro Glu Pro Thr
            180   185   190
Gln Leu Leu Met Gly Thr Lys Ser Val Cys Glu Val Gly Ser Asn Trp
        195   200   205
Phe Gln Pro Ile Tyr Leu Gly Ala Met Phe Ser Leu Gln Glu Gly Asp
    210   215   220
Lys Leu Met Val Asn Val Ser Asp Ile Ser Leu Val Asp Tyr Thr Lys
225   230   235   240
Glu Asp Lys Thr Phe Phe Gly Ala Phe Leu Leu
                245   250

<210> 245
<211> 756
<212> DNA
<213> Homo sapiens

<400> 245
atggccgagg atctgggact gagctttggg gaaacagcca gtgtggaaat gctgccagag 60
cacggcagct gcaggcccaa ggccaggagc agcagcgcac gctgggctct cacctgctgc 120
ctggtgttgc tccccttcct tgcaggactc accacatacc tgcttgtcag ccagctccgg 180
gcccagggag aggcctgtgt gcagttccag gctctaaaag gacaggagtt tgcaccttca 240
catcagcaag tttatgcacc tcttagagca gacggagata agccaagggc acacctgaca 300
gttgtgagac aaactcccac acagcacttt aaaaatcagt tcccagctct gcactgggaa 360

catgaactag gcctggcctt caccaagaac cgaatgaact ataccaacaa attcctgctg 420
atcccagagt cgggagacta cttcatttac tcccaggtca cattccgtgg gatgacctct 480
gagtgcagtg aaatcagacg agcaggccga ccaaacaagc cagactccat cactgtggtc 540
atcaccaagg taacagacag ctaccctgag ccaacccagc tcctcatggg gaccaagtct 600
gtatgcgaag taggtagcaa ctggttccag cccatctacc tcggagccat gttctccttg 660
caagaagggg acaagctaat ggtgaacgtc agtgacatct ctttggtgga ttacacaaaa 720
gaagataaaa ccttctttgg agccttctta ctatag 756

<210> 246
<211> 251
<212> PRT
<213> Homo sapiens

<400> 246
Met Ala Glu Asp Leu Gly Leu Ser Phe Gly Glu Thr Ala Ser Val Glu
1 5 10 15
Met Leu Pro Glu His Gly Ser Cys Arg Pro Lys Ala Arg Ser Ser Ser
20 25 30
Ala Arg Trp Ala Leu Thr Cys Cys Leu Val Leu Leu Pro Phe Leu Ala
35 40 45
Gly Leu Thr Thr Tyr Leu Leu Val Ser Gln Leu Arg Ala Gln Gly Glu
50 55 60
Ala Cys Val Gln Phe Gln Ala Leu Lys Gly Gln Glu Phe Ala Pro Ser
65 70 75 80
His Gln Gln Val Tyr Ala Pro Leu Arg Ala Asp Gly Asp Lys Pro Arg
85 90 95
Ala His Leu Thr Val Val Arg Gln Thr Pro Thr Gln His Phe Lys Asn
100 105 110
Gln Phe Pro Ala Leu His Trp Glu His Glu Leu Gly Leu Ala Phe Thr
115 120 125
Lys Asn Arg Met Asn Tyr Thr Asn Lys Phe Leu Leu Ile Pro Glu Ser
130 135 140
Gly Asp Tyr Phe Ile Tyr Ser Gln Val Thr Phe Arg Gly Met Thr Ser
145 150 155 160
Glu Cys Ser Glu Ile Arg Arg Ala Gly Arg Pro Asn Lys Pro Asp Ser
165 170 175
Ile Thr Val Val Ile Thr Lys Val Thr Asp Ser Tyr Pro Glu Pro Thr
180 185 190
Gln Leu Leu Met Gly Thr Lys Ser Val Cys Glu Val Gly Ser Asn Trp
195 200 205
Phe Gln Pro Ile Tyr Leu Gly Ala Met Phe Ser Leu Gln Glu Gly Asp
210 215 220
Lys Leu Met Val Asn Val Ser Asp Ile Ser Leu Val Asp Tyr Thr Lys
225 230 235 240
Glu Asp Lys Thr Phe Phe Gly Ala Phe Leu Leu
245 250

<210> 247
<211> 756
<212> DNA
<213> Macaca fascicularis

<400> 247
atggccgagg atctgggact gagctttggg gagacagcca gtgtggaaat gctgccagag 60
cacggcagct gcaggcccaa ggccaggagc agcagcgcat gctgggctct cacctgctgc 120
ctggtgttgc tccccttcct tgcagggctc accacctacc tgcttgtcag ccagctccgg 180
gcccaaggag aggcctgtgt gcagctccag gatctaaaag gacaggagtt tgcaccttca 240

catcagcaag tttatgcacc tcttagagca gatggagata agccaagggc acacctgaca 300
gttgtgagac aaactcccac acagcactta aaaaatcagt tcccagctct gcactgggaa 360
catgaactag gcctggcctt caccaagaac cgaatgaact acaccaacaa attcctgctg 420
atcccagagt cgggagacta cttcgtttac tcccaggtca cattccgtgg gatgacctct 480
gagtgcagtg aaatcagaca agcaggccga ccaaacaagc cagactccat cactgtggtc 540
atcaccaagg taacagacag ctaccctgag ccaacccagc tcctcatggg gaccaagtct 600
gtgtgtgaag taggcagtaa ctggttccag cccatctacc tcggagccat gttctccttg 660
caagaagggg acaagctcat ggtgaacgtc agtgacatct ctttggtgga ttacacaaaa 720
gaagataaaa ccttctttgg agccttctta ctatag 756

<210> 248
<211> 251
<212> PRT
<213> Macaca fascicularis

<400> 248
Met Ala Glu Asp Leu Gly Leu Ser Phe Gly Glu Thr Ala Ser Val Glu
 1   5   10   15
Met Leu Pro Glu His Gly Ser Cys Arg Pro Lys Ala Arg Ser Ser Ser
            20   25   30
Ala Cys Trp Ala Leu Thr Cys Cys Leu Val Leu Leu Pro Phe Leu Ala
        35   40   45
Gly Leu Thr Thr Tyr Leu Leu Val Ser Gln Leu Arg Ala Gln Gly Glu
    50   55   60
Ala Cys Val Gln Leu Gln Asp Leu Lys Gly Gln Glu Phe Ala Pro Ser
65   70   75   80
His Gln Gln Val Tyr Ala Pro Leu Arg Ala Asp Gly Asp Lys Pro Arg
                85   90   95
Ala His Leu Thr Val Val Arg Gln Thr Pro Thr Gln His Leu Lys Asn
            100   105   110
Gln Phe Pro Ala Leu His Trp Glu His Glu Leu Gly Leu Ala Phe Thr
        115   120   125
Lys Asn Arg Met Asn Tyr Thr Asn Lys Phe Leu Leu Ile Pro Glu Ser
    130   135   140
Gly Asp Tyr Phe Val Tyr Ser Gln Val Thr Phe Arg Gly Met Thr Ser
145   150   155   160
Glu Cys Ser Glu Ile Arg Gln Ala Gly Arg Pro Asn Lys Pro Asp Ser
                165   170   175
Ile Thr Val Val Ile Thr Lys Val Thr Asp Ser Tyr Pro Glu Pro Thr
            180   185   190
Gln Leu Leu Met Gly Thr Lys Ser Val Cys Glu Val Gly Ser Asn Trp
        195   200   205
Phe Gln Pro Ile Tyr Leu Gly Ala Met Phe Ser Leu Gln Glu Gly Asp
    210   215   220
Lys Leu Met Val Asn Val Ser Asp Ile Ser Leu Val Asp Tyr Thr Lys
225   230   235   240
Glu Asp Lys Thr Phe Phe Gly Ala Phe Leu Leu
                245   250

<210> 249
<211> 759
<212> DNA
<213> Mus musculus

<400> 249
atggcagagg agctggggtt gggcttcgga gaaggagtcc cagtggaagt gctgccggaa 60
ggctgtagac acaggccaga ggccagggcc gggctagctg ccaggagcaa agcctgcctg 120

```
gctctcacct gctgcctgtt gtcatttccc atcctcgcag gacttagcac cctcctaatg 180
gctggccagc tccgggtccc cggaaaagac tgtatgcttc gggccataac agaagagaga 240
tctgagcctt caccacagca agtttactca cctcccagag gcaagccgag agcacacctg 300
acaattaaga aacaaacccc agcaccacat ctgaaaaatc agctctctgc tctacactgg 360
gaacatgacc tagggatggc cttcaccaag aacgggatga agtacatcaa caaatccctg 420
gtgatcccag agtcaggaga ctatttcatc tactcccaga tcacattccg agggaccaca 480
tctgtgtgtg gtgacatcag tcgggggaga cgaccaaaca agccagactc catcaccatg 540
gttatcacca aggtagcaga cagctaccct gagcctgccc gcctactaac agggtccaag 600
tctgtgtgtg aaataagcaa caactggttc cagtccctct accttggggc cacgttctcc 660
ttggaagaag gagacagact aatggtaaac gtcagtgaca tctccttggt ggattacaca 720
aaagaagata aaactttctt tggagctttc ttgctataa                        759
```

<210> 250
<211> 252
<212> PRT
<213> Mus musculus

<400> 250

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Met Ala Glu Glu Leu Gly Leu Gly Phe Gly Glu Gly Val Pro Val Glu
 1               5                  10                  15
Val Leu Pro Glu Gly Cys Arg His Arg Pro Glu Ala Arg Ala Gly Leu
            20                  25                  30
Ala Ala Arg Ser Lys Ala Cys Leu Ala Leu Thr Cys Cys Leu Leu Ser
        35                  40                  45
Phe Pro Ile Leu Ala Gly Leu Ser Thr Leu Leu Met Ala Gly Gln Leu
    50                  55                  60
Arg Val Pro Gly Lys Asp Cys Met Leu Arg Ala Ile Thr Glu Glu Arg
65                  70                  75                  80
Ser Glu Pro Ser Pro Gln Gln Val Tyr Ser Pro Pro Arg Gly Lys Pro
                85                  90                  95
Arg Ala His Leu Thr Ile Lys Lys Gln Thr Pro Ala Pro His Leu Lys
            100                 105                 110
Asn Gln Leu Ser Ala Leu His Trp Glu His Asp Leu Gly Met Ala Phe
        115                 120                 125
Thr Lys Asn Gly Met Lys Tyr Ile Asn Lys Ser Leu Val Ile Pro Glu
    130                 135                 140
Ser Gly Asp Tyr Phe Ile Tyr Ser Gln Ile Thr Phe Arg Gly Thr Thr
145                 150                 155                 160
Ser Val Cys Gly Asp Ile Ser Arg Gly Arg Arg Pro Asn Lys Pro Asp
                165                 170                 175
Ser Ile Thr Met Val Ile Thr Lys Val Ala Asp Ser Tyr Pro Glu Pro
            180                 185                 190
Ala Arg Leu Leu Thr Gly Ser Lys Ser Val Cys Glu Ile Ser Asn Asn
        195                 200                 205
Trp Phe Gln Ser Leu Tyr Leu Gly Ala Thr Phe Ser Leu Glu Glu Gly
    210                 215                 220
Asp Arg Leu Met Val Asn Val Ser Asp Ile Ser Leu Val Asp Tyr Thr
225                 230                 235                 240
Lys Glu Asp Lys Thr Phe Phe Gly Ala Phe Leu Leu
                245                 250
```

<210> 251
<211> 1254
<212> DNA
<213> Homo sapiens

<400> 251

atggagcagc ggccgcgggg ctgcgcggcg gtggcggcgg cgctcctcct ggtgctgctg 60
ggggcccggg cccagggcgg cactcgtagc cccaggtgtg actgtgccgg tgacttccac 120
aagaagattg gtctgttttg ttgcagaggc tgcccagcgg ggcactacct gaaggcccct 180
tgcacggagc cctgcggcaa ctccacctgc cttgtgtgtc cccaagacac cttcttggcc 240
tgggagaacc accataattc tgaatgtgcc cgctgccagg cctgtgatga gcaggcctcc 300
caggtggcgc tggagaactg ttcagcagtg gccgacaccc gctgtggctg taagccaggc 360
tggtttgtgg agtgccaggt cagccaatgt gtcagcagtt cacccttcta ctgccaacca 420
tgcctagact gcggggccct gcaccgccac acacggctac tctgttcccg cagagatact 480
gactgtggga cctgcctgcc tggcttctat gaacatggcg atggctgcgt gtcctgcccc 540
acgagcaccc tggggagctg tccagagcgc tgtgccgctg tctgtggctg gaggcagatg 600
ttctgggtcc aggtgctcct ggctggcctt gtggtccccc tcctgcttgg ggccaccctg 660
acctacacat accgccactg ctggcctcac aagcccctgg ttactgcaga tgaagctggg 720
atggaggctc tgaccccacc accggccacc catctgtcac ccttggacag cgcccacacc 780
cttctagcac ctcctgacag cagtgagaag atctgcaccg tccagttggt gggtaacagc 840
tggacccctg gctaccccga gacccaggag gcgctctgcc cgcaggtgac atggtcctgg 900
gaccagttgc ccagcagagc tcttggcccc gctgctgcgc ccacactctc gccagagtcc 960
ccagccggct cgccagccat gatgctgcag ccgggcccgc agctctacga cgtgatggac
1020
gcggtcccag cgcggcgctg gaaggagttc gtgcgcacgc tggggctgcg cgaggcagag
1080
atcgaagccg tggaggtgga gatcggccgc ttccgagacc agcagtacga gatgctcaag
1140
cgctggcgcc agcagcagcc cgcgggcctc ggagccgttt acgcggccct ggagcgcatg
1200
gggctggacg gctgcgtgga agacttgcgc agccgcctgc agcgcggccc gtga
1254

<210> 252
<211> 417
<212> PRT
<213> Homo sapiens

<400> 252
Met Glu Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu Leu
 1   5   10   15
Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr Arg Ser Pro Arg
            20   25   30
Cys Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu Phe Cys Cys
        35   40   45
Arg Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro Cys Thr Glu Pro
    50   55   60
Cys Gly Asn Ser Thr Cys Leu Val Cys Pro Gln Asp Thr Phe Leu Ala
65   70   75   80
Trp Glu Asn His His Asn Ser Glu Cys Ala Arg Cys Gln Ala Cys Asp
                85   90   95
Glu Gln Ala Ser Gln Val Ala Leu Glu Asn Cys Ser Ala Val Ala Asp
            100   105   110
Thr Arg Cys Gly Cys Lys Pro Gly Trp Phe Val Glu Cys Gln Val Ser
        115   120   125
Gln Cys Val Ser Ser Ser Pro Phe Tyr Cys Gln Pro Cys Leu Asp Cys
    130   135   140
Gly Ala Leu His Arg His Thr Arg Leu Leu Cys Ser Arg Arg Asp Thr
145   150   155   160
Asp Cys Gly Thr Cys Leu Pro Gly Phe Tyr Glu His Gly Asp Gly Cys
                165   170   175
Val Ser Cys Pro Thr Ser Thr Leu Gly Ser Cys Pro Glu Arg Cys Ala
            180   185   190
Ala Val Cys Gly Trp Arg Gln Met Phe Trp Val Gln Val Leu Leu Ala

```
        195                 200                 205
Gly Leu Val Val Pro Leu Leu Leu Gly Ala Thr Leu Thr Tyr Thr Tyr
    210                 215                 220
Arg His Cys Trp Pro His Lys Pro Leu Val Thr Ala Asp Glu Ala Gly
225                 230                 235                 240
Met Glu Ala Leu Thr Pro Pro Pro Ala Thr His Leu Ser Pro Leu Asp
                245                 250                 255
Ser Ala His Thr Leu Leu Ala Pro Pro Asp Ser Ser Glu Lys Ile Cys
            260                 265                 270
Thr Val Gln Leu Val Gly Asn Ser Trp Thr Pro Gly Tyr Pro Glu Thr
        275                 280                 285
Gln Glu Ala Leu Cys Pro Gln Val Thr Trp Ser Trp Asp Gln Leu Pro
    290                 295                 300
Ser Arg Ala Leu Gly Pro Ala Ala Ala Pro Thr Leu Ser Pro Glu Ser
305                 310                 315                 320
Pro Ala Gly Ser Pro Ala Met Met Leu Gln Pro Gly Pro Gln Leu Tyr
                325                 330                 335
Asp Val Met Asp Ala Val Pro Ala Arg Arg Trp Lys Glu Phe Val Arg
            340                 345                 350
Thr Leu Gly Leu Arg Glu Ala Glu Ile Glu Ala Val Glu Val Glu Ile
        355                 360                 365
Gly Arg Phe Arg Asp Gln Gln Tyr Glu Met Leu Lys Arg Trp Arg Gln
    370                 375                 380
Gln Gln Pro Ala Gly Leu Gly Ala Val Tyr Ala Ala Leu Glu Arg Met
385                 390                 395                 400
Gly Leu Asp Gly Cys Val Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly
                405                 410                 415
Pro
```

<210> 253
<211> 900
<212> DNA
<213> Homo sapiens

<400> 253
atgagggcgc tggaggggcc aggcctgtcg ctgctgtgcc tggtgttggc gctgcctgcc 60
ctgctgccgg tgccggctgt acgcggagtg gcagaaacac ccacctaccc ctggcgggac 120
gcagagacag gggagcggct ggtgtgcgcc cagtgccccc caggcacctt tgtgcagcgg 180
ccgtgccgcc gagacagccc cacgacgtgt ggcccgtgtc caccgcgcca ctacacgcag 240
ttctggaact acctggagcg ctgccgctac tgcaacgtcc tctgcgggga gcgtgaggag 300
gaggcacggg cttgccacgc cacccacaac cgtgcctgcc gctgccgcac cggcttcttc 360
gcgcacgctg gtttctgctt ggagcacgca tcgtgtccac ctggtgccgg cgtgattgcc 420
ccgggcaccc ccagccagaa cacgcagtgc cagccgtgcc ccccaggcac cttctcagcc 480
agcagctcca gctcagagca gtgccagccc caccgcaact gcacggccct gggcctggcc 540
ctcaatgtgc caggctcttc ctcccatgac accctgtgca ccagctgcac tggcttcccc 600
ctcagcacca gggtaccagg agctgaggag tgtgagcgtg ccgtcatcga ctttgtggct 660
ttccaggaca tctccatcaa gaggctgcag cggctgctgc aggccctcga ggccccggag 720
ggctggggtc cgacaccaag ggcgggccgc gcggccttgc agctgaagct gcgtcggcgg 780
ctcacggagc tcctgggggc gcaggacggg gcgctgctgg tgcggctgct gcaggcgctg 840
cgcgtggcca ggatgcccgg gctggagcgg agcgtccgtg agcgcttcct ccctgtgcac 900

<210> 254
<211> 300
<212> PRT
<213> Homo sapiens

<400> 254
Met Arg Ala Leu Glu Gly Pro Gly Leu Ser Leu Leu Cys Leu Val Leu
 1   5   10   15
Ala Leu Pro Ala Leu Leu Pro Val Pro Ala Val Arg Gly Val Ala Glu
            20   25   30
Thr Pro Thr Tyr Pro Trp Arg Asp Ala Glu Thr Gly Glu Arg Leu Val
        35   40   45
Cys Ala Gln Cys Pro Pro Gly Thr Phe Val Gln Arg Pro Cys Arg Arg
    50   55   60
Asp Ser Pro Thr Thr Cys Gly Pro Cys Pro Pro Arg His Tyr Thr Gln
65   70   75   80
Phe Trp Asn Tyr Leu Glu Arg Cys Arg Tyr Cys Asn Val Leu Cys Gly
                85   90   95
Glu Arg Glu Glu Glu Ala Arg Ala Cys His Ala Thr His Asn Arg Ala
            100   105   110
Cys Arg Cys Arg Thr Gly Phe Phe Ala His Ala Gly Phe Cys Leu Glu
        115   120   125
His Ala Ser Cys Pro Pro Gly Ala Gly Val Ile Ala Pro Gly Thr Pro
    130   135   140
Ser Gln Asn Thr Gln Cys Gln Pro Cys Pro Pro Gly Thr Phe Ser Ala
145   150   155   160
Ser Ser Ser Ser Ser Glu Gln Cys Gln Pro His Arg Asn Cys Thr Ala
                165   170   175
Leu Gly Leu Ala Leu Asn Val Pro Gly Ser Ser Ser His Asp Thr Leu
            180   185   190
Cys Thr Ser Cys Thr Gly Phe Pro Leu Ser Thr Arg Val Pro Gly Ala
        195   200   205
Glu Glu Cys Glu Arg Ala Val Ile Asp Phe Val Ala Phe Gln Asp Ile
    210   215   220
Ser Ile Lys Arg Leu Gln Arg Leu Leu Gln Ala Leu Glu Ala Pro Glu
225   230   235   240
Gly Trp Gly Pro Thr Pro Arg Ala Gly Arg Ala Ala Leu Gln Leu Lys
                245   250   255
Leu Arg Arg Arg Leu Thr Glu Leu Leu Gly Ala Gln Asp Gly Ala Leu
            260   265   270
Leu Val Arg Leu Leu Gln Ala Leu Arg Val Ala Arg Met Pro Gly Leu
        275   280   285
Glu Arg Ser Val Arg Glu Arg Phe Leu Pro Val His
    290   295   300

<210> 255
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 255
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
Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
            100                 105                 110
Pro Ala Pro Glu Leu Leu Gly Gly 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 Lys 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 Lys
                325                 330
```

<210> 256
<211> 327
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 256

```
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
 1               5                  10                  15
Ser Thr Ser Glu Ser 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 Lys Thr
65                  70                  75                  80
Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95
```

```
Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro
            100                 105                 110
Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
        115                 120                 125
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
    130                 135                 140
Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145                 150                 155                 160
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
                165                 170                 175
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
            180                 185                 190
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
        195                 200                 205
Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
    210                 215                 220
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
225                 230                 235                 240
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
                245                 250                 255
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
            260                 265                 270
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
        275                 280                 285
Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
    290                 295                 300
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
305                 310                 315                 320
Leu Ser Leu Ser Leu Gly Lys
                325
```

<210> 257
<211> 327
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 257

```
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
 1               5                  10                  15
Ser Thr Ser Glu Ser 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 Lys Thr
65                  70                  75                  80
Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95
Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
            100                 105                 110
Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
        115                 120                 125
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
```

```
    130                 135                 140
Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145                 150                 155                 160
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
                165                 170                 175
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
            180                 185                 190
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
        195                 200                 205
Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
    210                 215                 220
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
225                 230                 235                 240
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
                245                 250                 255
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
            260                 265                 270
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
        275                 280                 285
Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
    290                 295                 300
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
305                 310                 315                 320
Leu Ser Leu Ser Leu Gly Lys
                325
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<210> 258
<211> 252
<212> PRT
<213> Rattus norvegicus

<400> 258

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Met Ala Glu Glu Leu Gly Leu Gly Phe Gly Glu Ala Val Pro Val Glu
 1               5                  10                  15
Met Leu Pro Glu Gly Cys Arg His Arg Arg Glu Ala Arg Thr Gly Leu
            20                  25                  30
Ala Ala Arg Ser Lys Ala Cys Leu Ala Leu Thr Cys Cys Leu Leu Ser
        35                  40                  45
Phe Pro Ile Leu Ala Gly Leu Ser Thr Leu Leu Met Thr Gly Gln Leu
    50                  55                  60
Arg Ile Pro Gly Lys Asp Cys Met Phe Pro Thr Val Thr Glu Glu Arg
65                  70                  75                  80
Ser Ala Pro Ser Ala Gln Pro Val Tyr Thr Pro Ser Arg Asp Lys Pro
                85                  90                  95
Lys Ala His Leu Thr Ile Met Arg Gln Thr Pro Val Pro His Leu Lys
            100                 105                 110
Asn Glu Leu Ala Ala Leu His Trp Glu Asn Asn Leu Gly Met Ala Phe
        115                 120                 125
Thr Lys Asn Arg Met Asn Tyr Thr Asn Lys Phe Leu Val Ile Pro Glu
    130                 135                 140
Ser Gly Asp Tyr Phe Ile Tyr Ser Gln Ile Thr Phe Arg Gly Thr Thr
145                 150                 155                 160
Ser Glu Cys Gly Asp Ile Ser Arg Val Arg Arg Pro Lys Lys Pro Asp
                165                 170                 175
Ser Ile Thr Val Val Ile Thr Lys Val Ala Asp Ser Tyr Pro Glu Pro
            180                 185                 190
Ala His Leu Leu Thr Gly Thr Lys Ser Val Cys Glu Ile Ser Ser Asn
```

```
        195                 200                 205
Trp Phe Gln Pro Ile Tyr Leu Gly Ala Met Phe Ser Leu Glu Glu Gly
    210                 215                 220
Asp Arg Leu Met Val Asn Val Ser Asp Ile Ser Leu Val Asp Tyr Thr
225                 230                 235                 240
Lys Glu Asp Lys Thr Phe Phe Gly Ala Phe Leu Ile
                245                 250
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<210> 259
<211> 411
<212> PRT
<213> Mus musculus

<400> 259

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Met Glu Ala Arg Leu Leu Arg Gly Cys Val Val Glu Pro Leu Phe Leu
 1               5                  10                  15
Pro Leu Leu Leu Leu Leu Leu Leu Leu Leu Gly Gly Gln Gly Gln Gly
            20                  25                  30
Gly Met Ser Gly Arg Cys Asp Cys Ala Ser Glu Ser Gln Lys Arg Tyr
        35                  40                  45
Gly Pro Phe Cys Cys Arg Gly Cys Pro Lys Gly His Tyr Met Lys Ala
    50                  55                  60
Pro Cys Ala Glu Pro Cys Gly Asn Ser Thr Cys Leu Pro Cys Pro Ser
65                  70                  75                  80
Asp Thr Phe Leu Thr Arg Asp Asn His Phe Lys Thr Asp Cys Thr Arg
                85                  90                  95
Cys Gln Val Cys Asp Glu Glu Ala Leu Gln Val Thr Leu Glu Asn Cys
            100                 105                 110
Ser Ala Lys Ser Asp Thr His Cys Gly Cys Gln Ser Gly Trp Cys Val
        115                 120                 125
Asp Cys Ser Thr Glu Pro Cys Gly Lys Ser Ser Pro Phe Ser Cys Val
    130                 135                 140
Pro Cys Gly Ala Thr Thr Pro Val His Glu Ala Pro Thr Pro Arg Pro
145                 150                 155                 160
Cys Leu Pro Gly Phe Tyr Ile Arg Gly Asn Asp Cys Thr Ser Cys Pro
                165                 170                 175
Thr Gly Phe Ser Ser Val Cys Pro Lys Ala Cys Thr Ala Val Cys Gly
            180                 185                 190
Trp Lys Gln Met Phe Trp Val Gln Val Leu Leu Gly Val Ala Phe Leu
        195                 200                 205
Phe Gly Ala Ile Leu Ile Cys Ala Tyr Cys Arg Trp Gln Pro Cys Lys
    210                 215                 220
Ala Val Val Thr Ala Asp Thr Ala Gly Thr Glu Thr Leu Ala Ser Pro
225                 230                 235                 240
Gln Thr Ala His Leu Ser Ala Ser Asp Ser Ala His Thr Leu Leu Ala
                245                 250                 255
Pro Pro Ser Ser Thr Gly Lys Ile Cys Thr Thr Val Gln Leu Val Gly
            260                 265                 270
Asn Asn Trp Thr Pro Gly Leu Ser Gln Thr Gln Glu Val Val Cys Gly
        275                 280                 285
Gln Ala Ser Gln Pro Trp Asp Gln Leu Pro Asn Arg Thr Leu Gly Thr
    290                 295                 300
Pro Leu Ala Ser Pro Leu Ser Pro Ala Pro Pro Ala Gly Ser Pro Ala
305                 310                 315                 320
Ala Val Leu Gln Pro Gly Pro Gln Leu Tyr Asp Val Met Asp Ala Val
                325                 330                 335
Pro Ala Arg Arg Trp Lys Glu Phe Val Arg Thr Leu Gly Leu Arg Glu
```

```
            340                 345                 350
Ala Glu Ile Glu Ala Val Glu Val Glu Ile Cys Arg Phe Arg Asp Gln
        355                 360                 365
Gln Tyr Glu Met Leu Lys Arg Trp Arg Gln Gln Gln Pro Ala Gly Leu
    370                 375                 380
Gly Ala Ile Tyr Ala Ala Leu Glu Arg Met Gly Leu Glu Gly Cys Ala
385                 390                 395                 400
Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly Pro
                405                 410
```