SEQUENCE LISTING

<110> Regeneron Pharmaceuticals, Inc.

<120> Human Antibodies to PD-1

<130> A0028WO01

<140> To be assigned
<141> Filed herewith

<150> 61/930,576
<151> 2014-01-23

<150> 62/014,181
<151> 2014-06-19

<160> 337

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ccagggaagg ggctggagtg ggtctcaggt attagtgata ccggtggtaa cacatactac 180
acagactccg tgaagggccg gttcaccgtc tccagagaca attccaagaa cacactgtct 240
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagatcag 300
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            20   25   30
Thr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Gly Ile Ser Asp Thr Gly Gly Asn Thr Tyr Tyr Thr Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Ser
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 Lys Asp Gln Gly Gly Ser Tyr Pro Tyr Tyr Phe His Tyr Trp Gly
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Gln Gly Ser Leu Val Thr Val Ser Ser
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<210> 6
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gggacagccc ctaagttcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagtg gctgtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccctccgat caccttcggc 300
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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
            20   25   30
Leu Ile Trp Tyr Gln Gln Lys Pro Gly Thr Ala Pro Lys Phe Leu Ile
        35   40   45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Cys Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Pro
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ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtttcac atactacaca 180
gactccgtga agggccgatt caccatctcc agacacaatt ccaagaacac gctgtatctt 240
caaatgaaca gcctgagagc tgaggacacg gccgtgtatt actgtgcgag gtattactat 300
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20 25 30
Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Val Ile Tyr Ser Gly Gly Phe Thr Tyr Tyr Thr Asp Ser Val Lys
50 55 60
Gly Arg Phe Thr Ile Ser Arg His Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95
Arg Tyr Tyr Tyr Asp Thr Ser Asp Tyr Trp Thr Phe Phe Asp Tyr Trp
100 105 110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

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<400> 20
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<400> 22
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<210> 23
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<400> 23
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<400> 24
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ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccagcc 180
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gggaccaagg tggagatcaa t   321

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Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
            20   25   30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35   40   45
Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65   70   75   80
Gly Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asn Asn Trp Pro Leu
                85   90   95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Asn
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<400> 28
Gln Ser Val Ser Ser Asn
1 5

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<400> 30
Gly Ala Ser
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<400> 32
Gln Gln Tyr Asn Asn Trp Pro Leu Thr
 1   5

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ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtttcac atactacaca 180
gactccgtga agggccgatt caccatctcc agacacaatt ccaagaacac gctgtatctt 240
caaatgaaca gcctgagagc tgaggacacg gccgtgtatt actgtgcgag gtattactat 300
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Val Ser Asn Asn
            20   25   30
Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Val Ile Tyr Ser Gly Gly Phe Thr Tyr Tyr Thr Asp Ser Val Lys
    50   55   60
Gly Arg Phe Thr Ile Ser Arg His Asn Ser Lys Asn Thr Leu Tyr Leu
65   70   75   80
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85   90   95
Arg Tyr Tyr Tyr Asp Thr Ser Asp Tyr Trp Thr Phe Phe Asp Tyr Trp
            100   105   110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

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<400> 36
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<400> 38
Ile Tyr Ser Gly Gly Phe Thr
1 5

<210> 39
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<400> 39
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<400> 40
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ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccagcc 180
aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagtag cctgcagtct 240
ggagattttg cagtttatta ctgtcagcag tataataact ggccgctcac tttcggcgga 300
gggaccaagg tggagatcaa t   321

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

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<400> 44
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<400> 46
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<210> 47
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<210> 49
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ccaggcaagg ggctggagtg ggtggcagtt atatggtatg atggaagtaa tatatactat 180
tcagactccg tgaagggccg attcaccatc tccagagcca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgag agccgaggac acggctgttt attactgtgc gagaccggga 300
cactggaact acttctttga tactggggc cagggaaccc tggtcaccgt ctcctca 357

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20   25   30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ala Val Ile Trp Tyr Asp Gly Ser Asn Ile Tyr Tyr Ser Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Ala Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Pro Gly His Trp Asn Tyr Phe Phe Glu Tyr Trp Gly Gln Gly
            100   105   110
Thr Leu Val Thr Val Ser Ser
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Gly Phe Thr Phe Ser Ser Tyr Gly
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<400> 56
Ala Arg Pro Gly His Trp Asn Tyr Phe Phe Glu Tyr
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<210> 57

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gggaaagccc ctaagctcct gatctatact gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
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caagggacac aactggagat taaa 324

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

<210> 59
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<220>
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<400> 59
cagagcatta acaactat 18

<210> 60
<211> 6
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<220>
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<400> 60
Gln Ser Ile Asn Asn Tyr
 1   5

<210> 61
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<400> 61
actgcatcc   9

<210> 62
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<400> 62
Thr Ala Ser
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<210> 63
<211> 30
<212> DNA
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<400> 63
caacagagtt acagtacccc tccgctcacc   30

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<400> 64
Gln Gln Ser Tyr Ser Thr Pro Pro Leu Thr
 1   5   10

<210> 65
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<223> Synthetic

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tcctgtggag cctctggatt caccttcagg aactacgaca tgcactgggt ccgccaaatt 120
acaggaaaag gtctggagtg ggtctcagct attggtagtg ctggtgacac atactatcca 180
gactccgtga agggccgatt caccatctcc agagaaaatg ccaagaactc cttgtatctt 240
caaatgaaca gcctgagagt cggggacacg gctgtgtatt actgtacaag agatatccat 300
tgtagtagta ccaggtgcta cggtatggac gtctggggcc aagggaccac ggtcaccgtc 360
tcctca 366

<210> 66
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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
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Ser Leu Arg Leu Ser Cys Gly Ala Ser Gly Phe Thr Phe Arg Asn Tyr
            20   25   30
Asp Met His Trp Val Arg Gln Ile Thr Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Ala Ile Gly Ser Ala Gly Asp Thr Tyr Tyr Pro Asp Ser Val Lys
    50   55   60
Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn Ser Leu Tyr Leu
65   70   75   80
Gln Met Asn Ser Leu Arg Val Gly Asp Thr Ala Val Tyr Tyr Cys Thr
                85   90   95
Arg Asp Ile His Cys Ser Ser Thr Arg Cys Tyr Gly Met Asp Val Trp
            100   105   110
Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120

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<210> 68
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Gly Phe Thr Phe Arg Asn Tyr Asp

1 5

<210> 69
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<220>
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<400> 69
attggtagtg ctggtgacac a 21

<210> 70
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<220>
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<400> 70
Ile Gly Ser Ala Gly Asp Thr
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<210> 71
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<400> 71
acaagagata tccattgtag tagtaccagg tgctacggta tggacgtc 48

<210> 72
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<400> 72
Thr Arg Asp Ile His Cys Ser Ser Thr Arg Cys Tyr Gly Met Asp Val
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atcacttgcc gggcaagtca gagcattagc aactatttaa attggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccctccgat caccttcggc 300
caagggacac gactggagat taaa 324

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

<220>
<223> Synthetic

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

<210> 75
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 75
cagagcatta gcaactat 18

<210> 76
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 76
Gln Ser Ile Ser Asn Tyr
 1   5

<210> 77
<211> 9

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 77
gctgcatcc 9

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

<220>
<223> Synthetic

<400> 78
Ala Ala Ser
1

<210> 79
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 79
caacagagtt acagtacccc tccgatcacc 30

<210> 80
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 80
Gln Gln Ser Tyr Ser Thr Pro Pro Ile Thr
1 5 10

<210> 81
<211> 390
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 81
gaggtgcagc tggtggagtc tgggggaggc ttggtaaagc ctgggggggtc ccttcgactc 60
tcctgtgcag cctctggatt caaattcagt aatgaatgga tgagctgggt ccgccaggct 120
ccagggaagg ggctggagtg ggttggccgt attaaaagca aaactgatgg tgggacaaca 180
gactacgctg cacccgtgaa aggcagattc accatctcaa gagatgattc aaaaaatacg 240

ctgtatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtatta ctgtaccaca 300
gatcaagatt tttggagtgg ttattatacc ggggctgact actacggtat ggacgtctgg 360
ggccaaggga ccatggtcac cgtctcctca 390

<210> 82
<211> 130
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 82
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Lys Phe Ser Asn Glu
20 25 30
Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Gly Arg Ile Lys Ser Lys Thr Asp Gly Gly Thr Thr Asp Tyr Ala Ala
50 55 60
Pro Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80
Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
85 90 95
Tyr Cys Thr Thr Asp Gln Asp Phe Trp Ser Gly Tyr Tyr Thr Gly Ala
100 105 110
Asp Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Met Val Thr Val
115 120 125
Ser Ser
130

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

<220>
<223> Synthetic

<400> 83
ggattcaaat tcagtaatga atgg 24

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

<220>
<223> Synthetic

<400> 84
Gly Phe Lys Phe Ser Asn Glu Trp
1 5

<210> 85
<211> 30

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 85
attaaaagca aaactgatgg tgggacaaca 30

<210> 86
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 86
Ile Lys Ser Lys Thr Asp Gly Gly Thr Thr
1 5 10

<210> 87
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 87
accacagatc aagatttttg gagtggttat tataccgggg ctgactacta cggtatggac 60
gtc 63

<210> 88
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 88
Thr Thr Asp Gln Asp Phe Trp Ser Gly Tyr Tyr Thr Gly Ala Asp Tyr
1 5 10 15
Tyr Gly Met Asp Val
20

<210> 89
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 89
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccctccgat caccttcggc 300
caagggacac gactggagat taaa 324

<210> 90
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

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

<210> 91
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 91
cagagcatta gcagctat 18

<210> 92
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 92
Gln Ser Ile Ser Ser Tyr
1 5

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

<220>
<223> Synthetic

<400> 93
gctgcatcc 9

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

<220>
<223> Synthetic

<400> 94
Ala Ala Ser
 1

<210> 95
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 95
caacagagtt acagtacccc tccgatcacc 30

<210> 96
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 96
Gln Gln Ser Tyr Ser Thr Pro Pro Ile Thr
 1   5   10

<210> 97
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 97
cagatgcagc tccaacagtg gggcgcagga ctattgaagc cttcggagac cctgtccctc 60
acctgcgttg tctatggtgg gtccctcaat ggatactatt ggagctggat ccgccagtcc 120
cccgggaagg ggctggagtg gattggggaa atcgatcata gtggaagcac caactacaac 180
ccgtccctca agaatcgagt caccatgtca gtagacacgt ctaagattca gttctccctg 240
aaactgacct ctgtgaccgt cgcggacacg gctgtgtatt actgtgcgag agaaggatta 300
ttacccttta actattgggg ccagggaacc ctggtcaccg tctcctca 348

<210> 98
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

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

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

<220>
<223> Synthetic

<400> 99
ggtgggtccc tcaatggata ctat   24

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

<220>
<223> Synthetic

<400> 100
Gly Gly Ser Leu Asn Gly Tyr Tyr
 1   5

<210> 101
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 101
atcgatcata gtggaagcac c 21

<210> 102
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 102
Ile Asp His Ser Gly Ser Thr
1 5

<210> 103
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 103
gcgagagaag gattattacc ctttgactat 30

<210> 104
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 104
Ala Arg Glu Gly Leu Leu Pro Phe Asp Tyr
1 5 10

<210> 105
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 105
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagtcacc 60
ctctcctgca gggccagtca gagtgtttac agcaactact tagcctggta ccagcagaat 120
cctggccagg ctcccaggct cctcatctat gctgcatcca acagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcggtgta ttactgtcat cagtatgcta cctcaccttg gacgttcggc 300
caagggacca aggtggaaat caaa 324

<210> 106
<211> 108

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

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

<210> 107
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 107
cagagtgttt acagcaacta c   21

<210> 108
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 108
Gln Ser Val Tyr Ser Asn Tyr
 1   5

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

<220>
<223> Synthetic

<400> 109
gctgcatcc   9

<210> 110

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

<220>
<223> Synthetic

<400> 110
Ala Ala Ser
 1

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

<220>
<223> Synthetic

<400> 111
catcagtatg ctacctcacc ttggacg 27

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

<220>
<223> Synthetic

<400> 112
His Gln Tyr Ala Thr Ser Pro Trp Thr
 1   5

<210> 113
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 113
cagctgcagc tgcaggagtc gggcccagat ctggtgaagc cttcggatac cctgtccctc 60
acctgcactg tctctgatga ctccatcagc agtactactt actactgggc ctggatccgc 120
cagcccccag ggaaggggct ggaatggatt ggcagtatgt cttataatgg gaacaactac 180
tacaacccgt ccctcaagag tcgagtcgcc atatccgcag gcacgtccca gaaacagttc 240
tccctgaaac tgacctctgt gactgccgca gacacggctg tttatcactg tgcgagacat 300
cttggatata acggcaactg gtaccccttt gacttctggg gccagggaat tctggtcacc 360
gtctcctct 369

<210> 114
<211> 123
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

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

<210> 115
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 115
gatgactcca tcagcagtac tacttactac   30

<210> 116
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 116
Asp Asp Ser Ile Ser Ser Thr Thr Tyr Tyr
 1   5   10

<210> 117
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 117
atgtcttata atgggaacaa c   21

<210> 118
<211> 7
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 118
Met Ser Tyr Asn Gly Asn Asn
 1   5

<210> 119
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 119
gcgagacatc ttggatataa cggcaactgg tacccctttg acttc   45

<210> 120
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 120
Ala Arg His Leu Gly Tyr Asn Gly Asn Trp Tyr Pro Phe Asp Phe
 1   5   10   15

<210> 121
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 121
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccaggaga aagagccacc 60
ctctcctgca gggccagtca gagtgttagt agtagttatt tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcaggaccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccttg gacgttcggc 300
caagggacca aggtggaaat caaa   324

<210> 122
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 122

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Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 1               5                  10                  15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
            20                  25                  30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45
Ile Tyr Gly Ala Ser Ser Arg Thr Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85                  90                  95
Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105
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<210> 123
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 123
cagagtgtta gtagtagtta t 21

<210> 124
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 124
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Gln Ser Val Ser Ser Ser Tyr
 1               5
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<210> 125
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 125
ggtgcatcc 9

<210> 126
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 126
Gly Ala Ser
 1

<210> 127
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 127
cagcagtatg gtagctcacc ttggacg 27

<210> 128
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 128
Gln Gln Tyr Gly Ser Ser Pro Trp Thr
 1   5

<210> 129
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 129
gaagtgcagg tggtagagtc tgggggcggc ttggtcgagc ctggcaggtc cctgagactc 60
tcctgtaaag cctctggatt cacctttgat gattatgcca tgcactgggt ccgacaaact 120
ccagggaagg ccctggagtg ggtctcgggt attaattgga gtggtaataa cataggctat 180
gcggactctg tgaagggccg attcaccatc tccaaggacg acgccaagaa ctccctgtat 240
ctgcaaatga acagtctgag acctgaggac acggccttat attactgtac aaaagatata 300
agtataactg gaaccctcga tgcttttgat gtctggggcc aagggacaat ggtcaccgtc 360
tcttca 366

<210> 130
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 130
Glu Val Gln Val Val Glu Ser Gly Gly Gly Leu Val Glu Pro Gly Arg
 1   5   10   15
Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Phe Thr Phe Asp Asp Tyr
            20   25   30

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


<210> 131
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 131
ggattcacct ttgatgatta tgcc                                          24

<210> 132
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 132
Gly Phe Thr Phe Asp Asp Tyr Ala
 1               5


<210> 133
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 133
attaattgga gtggtaataa cata                                          24

<210> 134
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 134
Ile Asn Trp Ser Gly Asn Asn Ile
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 1               5


<210> 135
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 135
acaaaagata taagtataac tggaaccctc gatgcttttg atgtc                  45

<210> 136
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 136
Thr Lys Asp Ile Ser Ile Thr Gly Thr Leu Asp Ala Phe Asp Val
 1               5                  10                  15


<210> 137
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 137
gacatccaga tgacccagtc tccaatttcc gtgtctgcat ctgtaggaga cagagtcacc 60
atcacttgtc gggcgagtca gggtattagc aactggttag cctggtatca gcagaaacca 120
gggatagccc ctaaactcct gatctattct gcatccagtt tacaaagtgg ggtcccatca 180
aggttcagag gcagtggatc tgggacagac ttcactctca ccatcggcag cctgcagcct 240
gaagattttg caacttacta ttgtcaacag gctcacagtt tcccgctcac tttcggcgga 300
gggaccaagg tggagatcaa a                                             321

<210> 138
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 138
Asp Ile Gln Met Thr Gln Ser Pro Ile Ser Val Ser Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Trp
            20                  25                  30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Ile Ala Pro Lys Leu Leu Ile
        35                  40                  45
Tyr Ser Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Arg Gly
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```
    50                  55                  60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Gly Ser Leu Gln Pro
65                  70                  75                  80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala His Ser Phe Pro Leu
                85                  90                  95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105
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<210> 139
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 139
cagggtatta gcaactgg 18

<210> 140
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 140
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Gln Gly Ile Ser Asn Trp
 1               5
```

<210> 141
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 141
tctgcatcc 9

<210> 142
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 142
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Ser Ala Ser
 1
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<210> 143
<211> 27

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 143
caacaggctc acagtttccc gctcact 27

<210> 144
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 144
Gln Gln Ala His Ser Phe Pro Leu Thr
1 5

<210> 145
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 145
caggtgcaat tagtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60
tcctgtgcag cgtctggatt caccttcagt agctatggca tgcactgggt ccgccaggct 120
ccaggcaagg ggctggagtg ggtggcaatt atatggtctg atggagatag tgaatataat 180
ctagactccg taaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatga acagtctgag agtcgaagac tcggctgtat attactgtgc gagagatcga 300
gaccttgagg atatctgggg ccaagggaca atggtcaccg tctcttca 348

<210> 146
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 146
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ala Ile Ile Trp Ser Asp Gly Asp Ser Glu Tyr Asn Leu 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 Val Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg Asp Leu Glu Asp Ile Trp Gly Gln Gly Thr Met Val
100 105 110
Thr Val Ser Ser
115

<210> 147
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 147
ggattcacct tcagtagcta tggc 24

<210> 148
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 148
Gly Phe Thr Phe Ser Ser Tyr Gly
1 5

<210> 149
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 149
atatggtctg atggagatag tgaa 24

<210> 150
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 150
Ile Trp Ser Asp Gly Asp Ser Glu
1 5

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

<220>
<223> Synthetic

<400> 151
gcgagagatc gagaccttga ggatatc 27

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

<220>
<223> Synthetic

<400> 152
Ala Arg Asp Arg Asp Leu Glu Asp Ile
1 5

<210> 153
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 153
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtcggaga cagagtcacc 60
atcacttgcc gggcaagtca gggcattaga aatgatttag gctggtatca gcagaaacca 120
gggaaagccc ctaagcgcct gatctatgct gcatccaatt tgcaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagag ttcactctca caatcagcag cctgcagcct 240
gaagattttg caacttatta ctgtctacag cataatagtt atccgctcac tttcggcgga 300
gggaccaagg tggagatcaa a 321

<210> 154
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 154
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile 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 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
Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu
85 90 95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 155
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 155
cagggcatta gaaatgat 18

<210> 156
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 156
Gln Gly Ile Arg Asn Asp
1 5

<210> 157
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 157
gctgcatcc 9

<210> 158
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 158
Ala Ala Ser
1

<210> 159
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 159
ctacagcata atagttatcc gctcact 27

<210> 160
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 160
Leu Gln His Asn Ser Tyr Pro Leu Thr
 1   5

<210> 161
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 161
gaggtgcagt tgttggagtc tgggggagtt ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttagt aattttggca tgacgtgggt ccgccaggct 120
ccagggaagg gactggagtg ggtctcaggt attagtggtg gcggtcgtga cacatacttc 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa tacgttgtat 240
ctacagatga acagcctgaa aggcgaggac acggccgtat attactgtgt gaagtgggga 300
aatatttact ttgactactg gggccaggga accctggtca ccgtctcatc a   351

<210> 162
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 162
Glu Val Gln Leu Leu Glu Ser Gly Gly Val 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 Phe
            20   25   30
Gly Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Gly Ile Ser Gly Gly Gly Arg Asp Thr Tyr Phe 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 Lys Gly Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Val Lys Trp Gly Asn Ile Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
            100   105   110
Val Thr Val Ser Ser
        115

<210> 163
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 163
ggattcacct ttagtaattt tggc 24

<210> 164
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 164
Gly Phe Thr Phe Ser Asn Phe Gly
1 5

<210> 165
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 165
attagtggtg gcggtcgtga caca 24

<210> 166
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 166
Ile Ser Gly Gly Gly Arg Asp Thr
1 5

<210> 167
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 167
gtgaagtggg gaaatattta ctttgactac 30

<210> 168
<211> 10

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 168
Val Lys Trp Gly Asn Ile Tyr Phe Asp Tyr
 1   5   10

<210> 169
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 169
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtcggaga cagcatcacc 60
atcacttgcc gggcgagtct gtccattaac acctttttaa attggtatca gcagaaacca 120
gggaaagccc ctaacctcct gatctatgct gcgtccagtt tacatggtgg ggtcccatca 180
aggttcagtg gcagcggctc tgggacagat ttcactctca ccatcagaac tcttcaacct 240
gaagattttg caacttacta ctgtcaacag agttccaata ccccattcac tttcggccct 300
gggaccgtag tggatttcag a   321

<210> 170
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 170
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Ser Ile Thr Ile Thr Cys Arg Ala Ser Leu Ser Ile Asn Thr Phe
            20   25   30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile
        35   40   45
Tyr Ala Ala Ser Ser Leu His Gly Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Arg Thr Leu Gln Pro
65   70   75   80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Ser Asn Thr Pro Phe
                85   90   95
Thr Phe Gly Pro Gly Thr Val Val Asp Phe Arg
            100   105

<210> 171
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 171
ctgtccatta acaccttt 18

<210> 172
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 172
Leu Ser Ile Asn Thr Phe
1 5

<210> 173
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 173
gctgcgtcc 9

<210> 174
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 174
Ala Ala Ser
1

<210> 175
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 175
caacagagtt ccaatacccc attcact 27

<210> 176
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 176
Gln Gln Ser Ser Asn Thr Pro Phe Thr
 1   5

<210> 177
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 177
gaggtgcagc tggtggagtc tgggggagga gtggtacggc cgggggggtc cctgagactc 60
tcctgtgcag cctctggatt cacttttgat gactatggca tgagttgggt ccgccaagtt 120
ccagggaagg ggctggagtg ggtctcaggt attagttgga atgatggtaa gacagtttat 180
gcagagtctg tgaagggccg attcatcatc tccagagaca acgccaagaa ctccctgtat 240
ctggaaatga atagtctgag agccgaggac acggccttat attactgtgc gagagattgg 300
cagtacttga tagagcggta ctttgactac tggggccagg gaaccctggt caccgtctcc 360
tca   363

<210> 178
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

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

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

<220>
<223> Synthetic

<400> 179

ggattcactt ttgatgacta tggc 24

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

<220>
<223> Synthetic

<400> 180
Gly Phe Thr Phe Asp Asp Tyr Gly
1 5

<210> 181
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 181
attagttgga atgatggtaa gaca 24

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

<220>
<223> Synthetic

<400> 182
Ile Ser Trp Asn Asp Gly Lys Thr
1 5

<210> 183
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 183
gcgagagatt ggcagtactt gatagagcgg tactttgact ac 42

<210> 184
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 184

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Ala Arg Asp Trp Gln Tyr Leu Ile Glu Arg Tyr Phe Asp Tyr
 1               5                  10
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<210> 185
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 185
gaaatagttt tgacacagag tcccggcaca ctgtcactct ctcccgggga aagagccacc 60
ttgtcatgta gagcaagtca gtcagtctct agctcttatc tcgcctggta ccagcagaag 120
ccgggacagg cccctagact gctgatctac ggggcaagtt ccagggccac cggaatcccc 180
gaccggttca gtggaagcgg aagcggaacc gattttactt tgacgatttc tagactggag 240
ccagaggatt tcgccgttta ctattgtcaa cagtacggaa gcagcccgtg gacgtttggc 300
cagggcacga aggtagaaat caag 324

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

<220>
<223> Synthetic

<400> 186
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Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 1               5                  10                  15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
            20                  25                  30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85                  90                  95
Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105
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<210> 187
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 187
cagtcagtct ctagctctta t 21

<210> 188
<211> 7
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 188
Gln Ser Val Ser Ser Ser Tyr
 1   5

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

<220>
<223> Synthetic

<400> 189
ggggcaagt   9

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

<220>
<223> Synthetic

<400> 190
Gly Ala Ser
 1

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

<220>
<223> Synthetic

<400> 191
caacagtacg gaagcagccc gtggacg   27

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

<220>
<223> Synthetic

<400> 192
Gln Gln Tyr Gly Ser Ser Pro Trp Thr
 1   5

<210> 193

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

<220>
<223> Synthetic

<400> 193
gaggtgcagc tggtggagtc tgggggaggt gtggtacggc ctgggggtc cctgagactc 60
tcctgtacag cctctggatt cacctttgat gattatggca tgagctgggt ccgccaagct 120
ccagggaagg ggctggagtg gatctctggt attggttgga ctggtggtcg gtcaagttat 180
gcagactctg tgaggggccg attcaccatc tccagagaca acgccaagaa ttccctgtat 240
ctgcaaatga acagtctggg agccgaggac acggccttgt attattgtgc aagagatcgg 300
cagtggctgg tgcagtggta ctttgactac tggggccagg gaaccctggt caccgtctcc 360
tca 363

<210> 194
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

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

<210> 195
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 195
ggattcacct ttgatgatta tggc 24

<210> 196
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 196
Gly Phe Thr Phe Asp Asp Tyr Gly
 1   5

<210> 197
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 197
attggttgga ctggtggtcg gtca   24

<210> 198
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 198
Ile Gly Trp Thr Gly Gly Arg Ser
 1   5

<210> 199
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 199
gcaagagatc ggcagtggct ggtgcagtgg tactttgact ac   42

<210> 200
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 200
Ala Arg Asp Arg Gln Trp Leu Val Gln Trp Tyr Phe Asp Tyr
 1   5   10

<210> 201
<211> 324
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 201
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccgtca 180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccctccgat caccttcggc 300
caagggacac gactggagat taaa 324

<210> 202
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 202
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Pro
85 90 95
Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 203
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 203
cagagcatta gcagctat 18

<210> 204
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 204
Gln Ser Ile Ser Ser Tyr

1 5

<210> 205
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 205
gctgcatcc 9

<210> 206
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 206
Ala Ala Ser
1

<210> 207
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 207
caacagagtt acagtacccc tccgatcacc 30

<210> 208
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 208
Gln Gln Ser Tyr Ser Thr Pro Pro Ile Thr
1 5 10

<210> 209
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 209
gaggtgcagc tggtggagtc tgggggaaga gtggtacggc cgggggggtc cctgagactc 60
tcctgtgcag cctctggatt cacttttgat gactatggca tgagttgggt ccgccaactt 120
ccagggaagg gcctggagtg ggtcgcaggt attagttgga atgatggtaa gacagtttat 180
gcagagtctg tgaagggccg attcatcatc tccagagaca acgccaagaa ctccctgcat 240
ctggagatga acagtctgag agccgaggac acggccttat attactgtgc gcgagattgg 300
caatacttaa tagatcgtta ctttgacttc tggggtcagg gaaccctggt caccgtctcc 360
tca 363

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

<220>
<223> Synthetic

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

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

<220>
<223> Synthetic

<400> 211
ggattcactt ttgatgacta tggc 24

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

<220>
<223> Synthetic

<400> 212
Gly Phe Thr Phe Asp Asp Tyr Gly
 1   5

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

<220>
<223> Synthetic

<400> 213
attagttgga atgatggtaa gaca 24

<210> 214
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 214
Ile Ser Trp Asn Asp Gly Lys Thr
1 5

<210> 215
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 215
gcgcgagatt ggcaatactt aatagatcgt tactttgact tc 42

<210> 216
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 216
Ala Arg Asp Trp Gln Tyr Leu Ile Asp Arg Tyr Phe Asp Phe
1 5 10

<210> 217
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 217
gaagtgcagc tggtggagtc tgggggaggc ttggtgcagc ctggcgggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgat gattatgcca tgcactgggt ccggcaagct 120
ccagggaagg gcctggagtg ggtctcaggt attggttgga gtagtggtag cataggctat 180
gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccttgtat 240
ctgcaaatgg acagtctgag acctgaggac tcagccttat attactgtgc aaaagcctat 300
acatttatga ttaccctcta ctttgactac tggggccagg gaaccctggt caccgtctcc 360
tca 363

<210> 218
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

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

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

<220>
<223> Synthetic

<400> 219
ggattcacct ttgatgatta tgcc 24

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

<220>
<223> Synthetic

<400> 220
Gly Phe Thr Phe Asp Asp Tyr Ala
 1   5

<210> 221

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

<220>
<223> Synthetic

<400> 221
attggttgga gtagtggtag cata 24

<210> 222
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

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

<210> 223
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 223
gcaaaagcct atacatttat gattaccctc tactttgact ac 42

<210> 224
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 224
Ala Lys Ala Tyr Thr Phe Met Ile Thr Leu Tyr Phe Asp Tyr
1 5 10

<210> 225
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 225
gaagtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttgat gattatgaca tgcactgggt ccggcaagct 120
ccagggaagg gcctggagtg ggtgtcaggg agtggttgga ataggggtag tttaggctat 180

gcggattctg tgaagggccg attcaccatc tccagagaca acgccaagaa gtccctgtat 240
ctgcaaatga acagtgtgag agttgaggac acggccttgt attactgtgc aaaaggcttt 300
gtagtggtat cagctgctta ctttgactac tggggccagg gaaccctggt caccgtctcc 360
tca 363

<210> 226
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 226
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
            20   25   30
Asp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Gly Ser Gly Trp Asn Arg Gly Ser Leu Gly Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Ser Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Val Arg Val Glu Asp Thr Ala Leu Tyr Tyr Cys
                85   90   95
Ala Lys Gly Phe Val Val Val Ser Ala Ala Tyr Phe Asp Tyr Trp Gly
            100   105   110
Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 227
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 227
ggattcacct ttgatgatta tgac 24

<210> 228
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 228
Gly Phe Thr Phe Asp Asp Tyr Asp
 1   5

<210> 229
<211> 24
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 229
agtggttgga ataggggtag ttta 24

<210> 230
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 230
Ser Gly Trp Asn Arg Gly Ser Leu
1 5

<210> 231
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 231
gcaaaaggct ttgtagtggt atcagctgct tactttgact ac 42

<210> 232
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 232
Ala Lys Gly Phe Val Val Val Ser Ala Ala Tyr Phe Asp Tyr
1 5 10

<210> 233
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 233
caggtgcagc tggtgcagtc tggggctgag gtgaagaggc ctgggtcctc ggtgaaggtc 60
tcctgcaagg tatctggagt caccttcagg aattttgcta tcatctgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatgggagga atcatccctt tctttagtgc agcaaattac 180
gcacagagct tccagggcag agtcacgatt accccggacg aatccacgag cacagccttc 240
atggagctgg ccagtctgag atctgaggac acggccgttt attattgtgc gagagagggg 300

gaacgtggac acacctatgg gtttgactac tggggccagg gaaccctggt caccgtctcc 360
tca 363

<210> 234
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 234
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Arg Pro Gly Ser
1 5 10 15
Ser Val Lys Val Ser Cys Lys Val Ser Gly Val Thr Phe Arg Asn Phe
20 25 30
Ala Ile Ile Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Gly Ile Ile Pro Phe Phe Ser Ala Ala Asn Tyr Ala Gln Ser Phe
50 55 60
Gln Gly Arg Val Thr Ile Thr Pro Asp Glu Ser Thr Ser Thr Ala Phe
65 70 75 80
Met Glu Leu Ala Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Glu Gly Glu Arg Gly His Thr Tyr Gly Phe Asp Tyr Trp Gly
100 105 110
Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 235
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 235
ggagtcacct tcaggaattt tgct 24

<210> 236
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 236
Gly Val Thr Phe Arg Asn Phe Ala
1 5

<210> 237
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 237
atcatccctt tctttagtgc agca 24

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

<220>
<223> Synthetic

<400> 238
Ile Ile Pro Phe Phe Ser Ala Ala
1 5

<210> 239
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 239
gcgagagagg gggaacgtgg acacacctat gggtttgact ac 42

<210> 240
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 240
Ala Arg Glu Gly Glu Arg Gly His Thr Tyr Gly Phe Asp Tyr
1 5 10

<210> 241
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 241
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tcctgtgcag cctctggatt cacctttgat gattatgcca tgcactgggt ccgacaacct 120
ccagggaagg gcctggaatg ggtctcaggt attaactgga atagaggtag gacaggctat 180
gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
ctgcaaatga acgatctgag agttgaggat acggccttgt attactgtgc aaaagccgaa 300
cagtggctgg acgagggata ctttgactac tggggccagg gaaccctggt caccgtctcc 360
tca 363

<210> 242
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 242
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Ser Gly Arg
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
            20   25   30
Ala Met His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Gly Ile Asn Trp Asn Arg Gly Arg Thr Gly Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65   70   75   80
Leu Gln Met Asn Asp Leu Arg Val Glu Asp Thr Ala Leu Tyr Tyr Cys
                85   90   95
Ala Lys Ala Glu Gln Trp Leu Asp Glu Gly Tyr Phe Asp Tyr Trp Gly
            100   105   110
Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 243
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 243
ggattcacct ttgatgatta tgcc   24

<210> 244
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 244
Gly Phe Thr Phe Asp Asp Tyr Ala
 1   5

<210> 245
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 245
attaactgga atagaggtag gaca 24

<210> 246
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 246
Ile Asn Trp Asn Arg Gly Arg Thr
1 5

<210> 247
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 247
gcaaaagccg aacagtggct ggacgaggga tactttgact ac 42

<210> 248
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 248
Ala Lys Ala Glu Gln Trp Leu Asp Glu Gly Tyr Phe Asp Tyr
1 5 10

<210> 249
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 249
gaggtgcagc tggtggagtc tgggggaggc ttggtgcagc ggggggggtc cctgagactc 60
tcctgtgcag cctctggatt cagctttagc agctatgcca tgaactgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtctcaact attagtgata gtggtggtag tacatactac 180
gcagactccg tgaagggccg gttcaccatt tccagagaca attccaagaa cacgctgtct 240
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagatcag 300
ggtgggagtt acccctacta ctttcactac tggggccagg gaaccctggt caccgtctcc 360
tca 363

<210> 250

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

<220>
<223> Synthetic

<400> 250
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Arg Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr
            20   25   30
Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Thr Ile Ser Asp Ser 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 Ser
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 Asp Gln Gly Gly Ser Tyr Pro Tyr Tyr Phe His Tyr Trp Gly
            100   105   110
Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 251
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 251
ggattcagct ttagcagcta tgcc   24

<210> 252
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 252
Gly Phe Ser Phe Ser Ser Tyr Ala
 1   5

<210> 253
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 253

attagtgata gtggtggtag taca 24

<210> 254
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 254
Ile Ser Asp Ser Gly Gly Ser Thr
1 5

<210> 255
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 255
gcgaaagatc agggtgggag ttacccctac tactttcact ac 42

<210> 256
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 256
Ala Lys Asp Gln Gly Gly Ser Tyr Pro Tyr Tyr Phe His Tyr
1 5 10

<210> 257
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 257
gaagtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttgag gattatgcca tgcactgggt ccggcaagct 120
ccagggaagg gcctggagtg ggtctcaggt attggttgga gtaatgtaaa gataggctat 180
gcggactctg tgaagggccg attcaccatc tccagagaca atgtcaggaa ctccctatat 240
ctgcaaatga acagtctgag aactgaggac acggccttct attactgtgt aaaagcctat 300
acatctatgc ttaccctcta ctttgactat tggggccagg gaaccctggt caccgtctcc 360
tca 363

<210> 258
<211> 121
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 258
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu 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 Gly Trp Ser Asn Val Lys Ile Gly Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Val Arg Asn Ser Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Phe Tyr Tyr Cys
                85   90   95
Val Lys Ala Tyr Thr Ser Met Leu Thr Leu Tyr Phe Asp Tyr Trp Gly
            100   105   110
Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 259
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 259
ggattcacct ttgaggatta tgcc   24

<210> 260
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 260
Gly Phe Thr Phe Glu Asp Tyr Ala
 1   5

<210> 261
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 261
attggttgga gtaatgtaaa gata   24

<210> 262
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 262
Ile Gly Trp Ser Asn Val Lys Ile
 1   5

<210> 263
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 263
gtaaaagcct atacatctat gcttaccctc tactttgact at   42

<210> 264
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 264
Val Lys Ala Tyr Thr Ser Met Leu Thr Leu Tyr Phe Asp Tyr
 1   5   10

<210> 265
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 265
caggtgcagc tggtgcagtc tggggctgag gtgaagaggc ctggggcctc agtgaaggtt 60
tcctgcaagg catctggata caccttcacc agcttctata tgtactgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatgggaata atcaacccta gtgatggtag cacaagcaac 180
gcacagaagt tccagggcag agtcaccatg accagggaca cgtccacgag tacagtctac 240
atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagacgggtg 300
gctggggata tttttgatat ctggggccaa gggacaatgg tcaccgtctc ttca   354

<210> 266
<211> 118
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 266
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Arg Pro Gly Ala
 1   5   10   15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Phe
            20   25   30
Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45
Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Asn Ala Gln Lys Phe
    50   55   60
Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65   70   75   80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Arg Val Ala Gly Asp Ile Phe Asp Ile Trp Gly Gln Gly Thr
            100   105   110
Met Val Thr Val Ser Ser
        115

<210> 267
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 267
ggatacacct tcaccagctt ctat   24

<210> 268
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 268
Gly Tyr Thr Phe Thr Ser Phe Tyr
 1   5

<210> 269
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 269
atcaacccta gtgatggtag caca   24

<210> 270
<211> 8
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 270
Ile Asn Pro Ser Asp Gly Ser Thr
 1   5

<210> 271
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 271
gcgagacggg tggctgggga tatttttgat atc   33

<210> 272
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 272
Ala Arg Arg Val Ala Gly Asp Ile Phe Asp Ile
 1   5   10

<210> 273
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 273
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60
acctgcactg tctctggtgg ctccatcagt agttaccact ggaactggat ccggcagagt 120
ccagggaagg gactggaatg gattggatat atctattata ttgggagcac cgactataat 180
ccctccctcg agagtcgagt caccatatca gtagacacgt ccaagaacca gttctccctg 240
aagctgagtt ctgtgaccgc tgcggacacg gccgtgtatt actgtgcgag agtccccgtg 300
ggagctacag gggcttctga tgtctggggc caagggacaa tggtcaccgt ctcttca   357

<210> 274
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 274

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Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1               5                  10                  15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
            20                  25                  30
His Trp Asn Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile
        35                  40                  45
Gly Tyr Ile Tyr Tyr Ile Gly Ser Thr Asp Tyr Asn Pro Ser Leu Glu
    50                  55                  60
Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65                  70                  75                  80
Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95
Arg Val Pro Val Gly Ala Thr Gly Ala Ser Asp Val Trp Gly Gln Gly
            100                 105                 110
Thr Met Val Thr Val Ser Ser
        115
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<210> 275
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 275
ggtggctcca tcagtagtta ccac 24

<210> 276
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 276
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Gly Gly Ser Ile Ser Ser Tyr His
 1               5
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<210> 277
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 277
atctattata ttgggagcac c 21

<210> 278
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 278
Ile Tyr Tyr Ile Gly Ser Thr
 1   5

<210> 279
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 279
gcgagagtcc ccgtgggagc tacaggggct tctgatgtc   39

<210> 280
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 280
Ala Arg Val Pro Val Gly Ala Thr Gly Ala Ser Asp Val
 1   5   10

<210> 281
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 281
gaggtgcagc tggtggagtc tgggggaagt gtggttcgac ctgggggtc cctgagactc 60
tcctgtgtag tctctggatt cacctttgag gattatggtt tgagctgggt ccgccaaatt 120
ccagggaaag gactggagtg ggtctctggt attagttgga ctggtggtaa cacaggttat 180
gcagactctg tgaagggccg cttcaccatc tccagagaca acgccaagaa ctccctgtat 240
ctgcaaatga acagtctgag agccgaagac acggccctgt atcactgtac gagagatcga 300
cagtggctga tgcagtggta ttttgactat tggggccagg gaaccctggt caccgtctcc 360
tca   363

<210> 282
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 282
Glu Val Gln Leu Val Glu Ser Gly Gly Ser Val Val Arg Pro Gly Gly
 1   5   10   15

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Ser Leu Arg Leu Ser Cys Val Val Ser Gly Phe Thr Phe Glu Asp Tyr
            20                  25                  30
Gly Leu Ser Trp Val Arg Gln Ile Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Gly Ile Ser Trp Thr Gly Gly Asn Thr Gly Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr His Cys
                85                  90                  95
Thr Arg Asp Arg Gln Trp Leu Met Gln Trp Tyr Phe Asp Tyr Trp Gly
            100                 105                 110
Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
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<210> 283
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 283
ggattcacct ttgaggatta tggt 24

<210> 284
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 284
```
Gly Phe Thr Phe Glu Asp Tyr Gly
 1               5
```

<210> 285
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 285
attagttgga ctggtggtaa caca 24

<210> 286
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 286
Ile Ser Trp Thr Gly Gly Asn Thr
 1   5

<210> 287
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 287
acgagagatc gacagtggct gatgcagtgg tattttgact at   42

<210> 288
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 288
Thr Arg Asp Arg Gln Trp Leu Met Gln Trp Tyr Phe Asp Tyr
 1   5   10

<210> 289
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 289
caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60
tcctgttcag cctctggatt caccttcagt gcctatgcca tgcactgggt ccgccaggct 120
ccaggcaagg ggctggaatg ggtggcagct atctcatatg gtggaagtga taaatactat 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctatat 240
ctgcaaatga acagcctgag aactgacgac acggctgtgt attactgtgc gaaatccgct 300
cactggaact tcttctttga ctactggggc cagggaaccc tggtcactgt ctcctca   357

<210> 290
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 290
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 Ser Ala Ser Gly Phe Thr Phe Ser Ala Tyr
            20   25   30
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

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

<210> 291
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 291
ggattcacct tcagtgccta tgcc 24

<210> 292
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 292
Gly Phe Thr Phe Ser Ala Tyr Ala
 1   5

<210> 293
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 293
atctcatatg gtggaagtga taaa 24

<210> 294
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 294
Ile Ser Tyr Gly Gly Ser Asp Lys
 1   5

<210> 295
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 295
gcgaaatccg ctcactggaa cttcttcttt gactac 36

<210> 296
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 296
Ala Lys Ser Ala His Trp Asn Phe Phe Phe Asp Tyr
 1 5 10

<210> 297
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 297
gaagtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60
tcctgtgtag cctctggatt cgcccttcat gattatgcca tgcactgggt ccggcaagtt 120
ccagggaagg gcctggagtg ggtctcaagt attagttgga atagtggtgt cataggctat 180
gcggactctc tgaagggccg cttcaccatc tccagagaca acgccaagaa ctccctgtat 240
ctgcaaatga acagtctgag agcagaggac acggccttat actactgtgc aaaaggtagt 300
gggagctact acgtcagttg gttcgacccc tggggccagg gaaccctggt caccgtctcc 360
tca 363

<210> 298
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 298
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1 5 10 15
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Ala Leu His Asp Tyr
            20 25 30
Ala Met His Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val
        35 40 45
Ser Ser Ile Ser Trp Asn Ser Gly Val Ile Gly Tyr Ala Asp Ser Leu

```
    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 Leu Tyr Tyr Cys
                85                  90                  95
Ala Lys Gly Ser Gly Ser Tyr Tyr Val Ser Trp Phe Asp Pro Trp Gly
            100                 105                 110
Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
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<210> 299
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 299
ggattcgccc ttcatgatta tgcc 24

<210> 300
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 300
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Gly Phe Ala Leu His Asp Tyr Ala
 1               5
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<210> 301
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 301
attagttgga atagtggtgt cata 24

<210> 302
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 302
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Ile Ser Trp Asn Ser Gly Val Ile
 1               5
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<210> 303
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 303
gcaaaaggta gtgggagcta ctacgtcagt tggttcgacc cc 42

<210> 304
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 304
Ala Lys Gly Ser Gly Ser Tyr Tyr Val Ser Trp Phe Asp Pro
 1   5   10

<210> 305
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 305
cagctgcagc tgcaggagtc gggcccagga ctggttcagc cttcggagac cctgtccctc 60
acctgcactg tctctggtga ctccatcagt agtactgctt accactggga ctggatccgc 120
cagccccccg ggaagggact ggagtggatt gggaccatca cttataatgg gaacacctac 180
ttcaacccgt ccctcaagag tcgagtcacc atatccgttg acacgtccaa gaaccagttc 240
tccctgaagc tactctctat gaccgccgca gaaacggctg ttttttactg tgcgcgacat 300
ctaggatata acagtgactt ctttcccttt gacttctggg gccagggaac cctggtcact 360
gtctcctca 369

<210> 306
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 306
Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Gln Pro Ser Glu
 1   5   10   15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Ile Ser Ser Thr
            20   25   30
Ala Tyr His Trp Asp Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35   40   45
Trp Ile Gly Thr Ile Thr Tyr Asn Gly Asn Thr Tyr Phe Asn Pro Ser
    50   55   60
Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80
Ser Leu Lys Leu Leu Ser Met Thr Ala Ala Glu Thr Ala Val Phe Tyr
85 90 95
Cys Ala Arg His Leu Gly Tyr Asn Ser Asp Phe Phe Pro Phe Asp Phe
100 105 110
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 307
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 307
ggtgactcca tcagtagtac tgcttaccac 30

<210> 308
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 308
Gly Asp Ser Ile Ser Ser Thr Ala Tyr His
1 5 10

<210> 309
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 309
atcacttata atgggaacac c 21

<210> 310
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 310
Ile Thr Tyr Asn Gly Asn Thr
1 5

<210> 311
<211> 45

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 311
gcgcgacatc taggatataa cagtgacttc tttccctttg acttc 45

<210> 312
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 312
Ala Arg His Leu Gly Tyr Asn Ser Asp Phe Phe Pro Phe Asp Phe
 1   5   10   15

<210> 313
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 313
gaggtgcagc tggtggagtc tgggggaggc ctggtacggc cgggggggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttagc acctatgcca tggcctgggt ccgccagact 120
ccagggaagg ggctggaggg ggtctcagct attgggggta gtggtgatag tacctattat 180
gtcgactccg tgaagggccg gttcaccatc tccagggaca actccaagag cacgcttttt 240
ctgcaaatga atagcctgag agccgaggac acggccgttt attactgtgt gaaagtccgg 300
aattacgacg gttcttttga tatctggggc caagggacaa tggtcaccgt ctcttca 357

<210> 314
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 314
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Arg Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
            20   25   30
Ala Met Ala Trp Val Arg Gln Thr Pro Gly Lys Gly Leu Glu Gly Val
        35   40   45
Ser Ala Ile Gly Gly Ser Gly Asp Ser Thr Tyr Tyr Val Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Ser Thr Leu Phe
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Val Lys Val Arg Asn Tyr Asp Gly Ser Phe Asp Ile Trp Gly Gln Gly
100 105 110
Thr Met Val Thr Val Ser Ser
115

<210> 315
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 315
ggattcacct ttagcaccta tgcc 24

<210> 316
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 316
Gly Phe Thr Phe Ser Thr Tyr Ala
1 5

<210> 317
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 317
attgggggta gtggtgatag tacc 24

<210> 318
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 318
Ile Gly Gly Ser Gly Asp Ser Thr
1 5

<210> 319
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 319
gtgaaagtcc ggaattacga cggttctttt gatatc 36

<210> 320
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 320
Val Lys Val Arg Asn Tyr Asp Gly Ser Phe Asp Ile
 1   5   10

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

<220>
<223> hPD-1-MMH

<220>
<223> 1-146: aa 25-170 of NP_005009.2 with C93S

<220>
<223> 147-174: myc-myc-hexahistidine

<400> 321
Leu Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala
 1   5   10   15
Leu Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe
            20   25   30
Ser Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro
        35   40   45
Ser Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln
    50   55   60
Pro Gly Gln Asp Ser Arg Phe Arg Val Thr Gln Leu Pro Asn Gly Arg
65   70   75   80
Asp Phe His Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr
                85   90   95
Tyr Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu
            100   105   110
Ser Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg Ala Glu Val Pro
        115   120   125
Thr Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly Gln Phe Gln Thr
    130   135   140
Leu Val Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Gly Gly Glu Gln
145   150   155   160
Lys Leu Ile Ser Glu Glu Asp Leu His His His His His His
                165   170

<210> 322

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

<220>
<223> MfPD-1-MMH

<220>
<223> 1-146: M.fascicularis PD-1 with C93S

<220>
<223> 147-174: myc-myc-hexahistidine

<400> 322
Leu Glu Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala
 1   5   10   15
Leu Leu Leu Val Thr Glu Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe
            20   25   30
Ser Asn Ala Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro
        35   40   45
Ser Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln
    50   55   60
Pro Gly Arg Asp Ser Arg Phe Arg Val Thr Gln Leu Pro Asn Gly Arg
65   70   75   80
Asp Phe His Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr
                85   90   95
Tyr Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu
            100   105   110
Ser Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg Ala Glu Val Pro
        115   120   125
Thr Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly Gln Phe Gln Ala
    130   135   140
Leu Val Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Gly Gly Glu Gln
145   150   155   160
Lys Leu Ile Ser Glu Glu Asp Leu His His His His His His
                165   170

<210> 323
<211> 379
<212> PRT
<213> Artificial Sequence

<220>
<223> hPD-1-mFc

<220>
<223> 1-146: aa 25-170 of NP-005009.2 with C93S

<220>
<223> 147-379: mFc: aa 98-330 of P01863

<400> 323
Leu Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala
 1   5   10   15
Leu Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe
            20   25   30
Ser Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro
        35   40   45

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Ser Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln
    50                  55                  60
Pro Gly Gln Asp Ser Arg Phe Arg Val Thr Gln Leu Pro Asn Gly Arg
65                  70                  75                  80
Asp Phe His Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr
                85                  90                  95
Tyr Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu
            100                 105                 110
Ser Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg Ala Glu Val Pro
        115                 120                 125
Thr Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly Gln Phe Gln Thr
    130                 135                 140
Leu Val Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys
145                 150                 155                 160
Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro
                165                 170                 175
Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr
            180                 185                 190
Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser
        195                 200                 205
Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His
    210                 215                 220
Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile
225                 230                 235                 240
Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn
                245                 250                 255
Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys
            260                 265                 270
Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu
        275                 280                 285
Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe
    290                 295                 300
Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu
305                 310                 315                 320
Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr
                325                 330                 335
Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg
            340                 345                 350
Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His
        355                 360                 365
Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
    370                 375


<210> 324
<211> 373
<212> PRT
<213> Artificial Sequence

<220>
<223> hPD-1-hFc

<220>
<223> 1-146: aa 25-170 of NP_005009.2 with C93S

<220>
<223> 147-373: hFc: aa 104-330 of P01857

<400> 324
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Leu Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala
 1               5                  10                  15
Leu Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe
            20                  25                  30
Ser Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro
        35                  40                  45
Ser Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln
    50                  55                  60
Pro Gly Gln Asp Ser Arg Phe Arg Val Thr Gln Leu Pro Asn Gly Arg
65                  70                  75                  80
Asp Phe His Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr
                85                  90                  95
Tyr Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu
            100                 105                 110
Ser Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg Ala Glu Val Pro
        115                 120                 125
Thr Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly Gln Phe Gln Thr
    130                 135                 140
Leu Val Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
145                 150                 155                 160
Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                165                 170                 175
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            180                 185                 190
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        195                 200                 205
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    210                 215                 220
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
225                 230                 235                 240
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                245                 250                 255
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            260                 265                 270
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
        275                 280                 285
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    290                 295                 300
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
305                 310                 315                 320
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                325                 330                 335
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            340                 345                 350
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        355                 360                 365
Leu Ser Pro Gly Lys
    370
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<210> 325
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> hPD-L1-hFc

<220>

<223> 1-221: aa 19-239 of NP_054862.1

<220>
<223> 222-448: hFc: aa 104-330 of P01857

<400> 325
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
 1   5   10   15
Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20   25   30
Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35   40   45
Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50   55   60
Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65   70   75   80
Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85   90   95
Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100   105   110
Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115   120   125
Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130   135   140
Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145   150   155   160
Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165   170   175
Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180   185   190
Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195   200   205
Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr Asp Lys Thr
    210   215   220
His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
225   230   235   240
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245   250   255
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            260   265   270
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275   280   285
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
    290   295   300
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305   310   315   320
Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
                325   330   335
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
            340   345   350
Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
        355   360   365
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
    370   375   380
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385   390   395   400
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
                405   410   415
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala

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            420                 425                 430
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445


<210> 326
<211> 454
<212> PRT
<213> Artificial Sequence

<220>
<223> hPD-L1-mFc

<220>
<223> 1-221: aa 19-239 of NP_054862.1

<220>
<223> 222-454: mFc: aa 98-330 of P01863

<400> 326
Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
 1               5                  10                  15
Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
            20                  25                  30
Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45
Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
    50                  55                  60
Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65                  70                  75                  80
Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
                85                  90                  95
Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
            100                 105                 110
Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125
Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140
Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160
Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175
Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190
Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205
Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr Glu Pro Arg
    210                 215                 220
Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn
225                 230                 235                 240
Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp
                245                 250                 255
Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val Val Asp
            260                 265                 270
Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn
        275                 280                 285
Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn
    290                 295                 300
Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp
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305                 310                 315                 320
Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro
                325                 330                 335
Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala
            340                 345                 350
Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys
        355                 360                 365
Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile
    370                 375                 380
Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn
385                 390                 395                 400
Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys
                405                 410                 415
Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys
            420                 425                 430
Ser Val Val His Glu Gly Leu His Asn His His Thr Thr Lys Ser Phe
        435                 440                 445
Ser Arg Thr Pro Gly Lys
    450
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<210> 327
<211> 288
<212> PRT
<213> Artificial Sequence

<220>
<223> hPD-1 NP_005009.2

<400> 327

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

225 230 235 240
Cys Val Pro Glu Gln Thr Glu Tyr Ala Thr Ile Val Phe Pro Ser Gly
245 250 255
Met Gly Thr Ser Ser Pro Ala Arg Arg Gly Ser Ala Asp Gly Pro Arg
260 265 270
Ser Ala Gln Pro Leu Arg Pro Glu Asp Gly His Cys Ser Trp Pro Leu
275 280 285

<210> 328
<211> 290
<212> PRT
<213> Artificial Sequence

<220>
<223> hPD-L1 NP_054862.1

<400> 328
Met Arg Ile Phe Ala Val Phe Ile Phe Met Thr Tyr Trp His Leu Leu
1 5 10 15
Asn Ala Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr
20 25 30
Gly Ser Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu
35 40 45
Asp Leu Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile
50 55 60
Ile Gln Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser
65 70 75 80
Tyr Arg Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn
85 90 95
Ala Ala Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr
100 105 110
Arg Cys Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val
115 120 125
Lys Val Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val
130 135 140
Asp Pro Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr
145 150 155 160
Pro Lys Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser
165 170 175
Gly Lys Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn
180 185 190
Val Thr Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr
195 200 205
Cys Thr Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu
210 215 220
Val Ile Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr His
225 230 235 240
Leu Val Ile Leu Gly Ala Ile Leu Leu Cys Leu Gly Val Ala Leu Thr
245 250 255
Phe Ile Phe Arg Leu Arg Lys Gly Arg Met Met Asp Val Lys Lys Cys
260 265 270
Gly Ile Gln Asp Thr Asn Ser Lys Lys Gln Ser Asp Thr His Leu Glu
275 280 285
Glu Thr
290

<210> 329

<211> 379
<212> PRT
<213> Artificial Sequence

<220>
<223> aa1-146: M.fascicularis PD-1 (with C93S change)
aa147-379: mFc tag (aa 98-330 of P01863)

<400> 329

```
Leu Glu Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala
 1               5                  10                  15
Leu Leu Leu Val Thr Glu Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe
            20                  25                  30
Ser Asn Ala Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro
        35                  40                  45
Ser Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln
    50                  55                  60
Pro Gly Arg Asp Ser Arg Phe Arg Val Thr Gln Leu Pro Asn Gly Arg
65                  70                  75                  80
Asp Phe His Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr
                85                  90                  95
Tyr Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu
            100                 105                 110
Ser Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg Ala Glu Val Pro
        115                 120                 125
Thr Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly Gln Phe Gln Ala
    130                 135                 140
Leu Val Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys
145                 150                 155                 160
Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro
                165                 170                 175
Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr
            180                 185                 190
Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser
        195                 200                 205
Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His
    210                 215                 220
Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile
225                 230                 235                 240
Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn
                245                 250                 255
Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys
            260                 265                 270
Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu
        275                 280                 285
Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe
    290                 295                 300
Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu
305                 310                 315                 320
Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr
                325                 330                 335
Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg
            340                 345                 350
Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His
        355                 360                 365
Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
    370                 375
```

<210> 330
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> H4H7798N
aa1-117: HCVR
aa118-444: HC constant

<400> 330
Glu Val Gln Leu Leu Glu Ser Gly Gly Val 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 Phe
20 25 30
Gly Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Gly Ile Ser Gly Gly Gly Arg Asp Thr Tyr Phe 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 Lys Gly Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Val Lys Trp Gly Asn Ile Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110
Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
115 120 125
Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
130 135 140
Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145 150 155 160
Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
165 170 175
Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
180 185 190
Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
195 200 205
Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro
210 215 220
Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe
225 230 235 240
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
245 250 255
Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
260 265 270
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
275 280 285
Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
290 295 300
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305 310 315 320
Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
325 330 335
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln
340 345 350
Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
355 360 365
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
370 375 380

```
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
385                 390                 395                 400
Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu
                405                 410                 415
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
            420                 425                 430
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440
```

<210> 331
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> H4H7798N
aa1-107: LCVR
aa108-214: LC constant

<400> 331
```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1               5                  10                  15
Asp Ser Ile Thr Ile Thr Cys Arg Ala Ser Leu Ser Ile Asn Thr Phe
            20                  25                  30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile
        35                  40                  45
Tyr Ala Ala Ser Ser Leu His Gly Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Arg Thr Leu Gln Pro
65                  70                  75                  80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Ser Asn Thr Pro Phe
                85                  90                  95
Thr Phe Gly Pro Gly Thr Val Val Asp Phe Arg Arg Thr Val Ala Ala
            100                 105                 110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205
Phe Asn Arg Gly Glu Cys
    210
```

<210> 332
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> H4H7795N2
aa1-122: HCVR

aa123-449: HC constant

<400> 332

```
Glu Val Gln Val Val Glu Ser Gly Gly Gly Leu Val Glu Pro Gly Arg
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Phe Thr Phe Asp Asp Tyr
            20                  25                  30
Ala Met His Trp Val Arg Gln Thr Pro Gly Lys Ala Leu Glu Trp Val
        35                  40                  45
Ser Gly Ile Ser Trp Ser Gly Asn Asn Ile Gly Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Lys Asp Asp Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95
Thr Lys Asp Ile Ser Ile Thr Gly Thr Leu Asp Ala Phe Asp Val Trp
            100                 105                 110
Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
        115                 120                 125
Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr
    130                 135                 140
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145                 150                 155                 160
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
                165                 170                 175
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
            180                 185                 190
Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp
        195                 200                 205
His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr
    210                 215                 220
Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro
225                 230                 235                 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp
            260                 265                 270
Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val
    290                 295                 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys
                325                 330                 335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350
Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys
                405                 410                 415
Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
        435                 440                 445
```

Lys

<210> 333
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> H4H7795N2
aa1-107: LCVR
aa108-214: LC constant

<400> 333
Asp Ile Gln Met Thr Gln Ser Pro Ile Ser Val Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Trp
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Ile Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Ser Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Arg Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Gly Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala His Ser Phe Pro Leu
85 90 95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205
Phe Asn Arg Gly Glu Cys
210

<210> 334
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> H4H9008P
aa1-119: HCVR
aa120-446: HC constant

<400> 334
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Arg Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

```
            20                  25                  30
Ala Met Ala Trp Val Arg Gln Thr Pro Gly Lys Gly Leu Glu Gly Val
        35                  40                  45
Ser Ala Ile Gly Gly Ser Gly Asp Ser Thr Tyr Tyr Val Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Ser Thr Leu Phe
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Val Lys Val Arg Asn Tyr Asp Gly Ser Phe Asp Ile Trp Gly Gln Gly
            100                 105                 110
Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125
Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
    130                 135                 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190
Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
        195                 200                 205
Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
    210                 215                 220
Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
225                 230                 235                 240
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                245                 250                 255
Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
            260                 265                 270
Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285
Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
    290                 295                 300
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305                 310                 315                 320
Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
                325                 330                 335
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            340                 345                 350
Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
        355                 360                 365
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    370                 375                 380
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385                 390                 395                 400
Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
                405                 410                 415
Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            420                 425                 430
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440                 445
```

<210> 335
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> H4H9008P
aa1-108: LCVR
aa109-215: LC constant

<400> 335
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95
Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
100 105 110
Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125
Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140
Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160
Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175
Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190
Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
195 200 205
Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 336
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> H4H9048P2
aa1-121: HCVR
aa122-448: HC constant

<400> 336
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Arg Pro Gly Ser
1 5 10 15
Ser Val Lys Val Ser Cys Lys Val Ser Gly Val Thr Phe Arg Asn Phe
20 25 30
Ala Ile Ile Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Gly Ile Ile Pro Phe Phe Ser Ala Ala Asn Tyr Ala Gln Ser Phe
50 55 60
Gln Gly Arg Val Thr Ile Thr Pro Asp Glu Ser Thr Ser Thr Ala Phe
65 70 75 80
Met Glu Leu Ala Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys

```
                85                  90                  95
Ala Arg Glu Gly Glu Arg Gly His Thr Tyr Gly Phe Asp Tyr Trp Gly
            100                 105                 110
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
        115                 120                 125
Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
    130                 135                 140
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190
Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His
        195                 200                 205
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly
    210                 215                 220
Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser
225                 230                 235                 240
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245                 250                 255
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro
            260                 265                 270
Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275                 280                 285
Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val
    290                 295                 300
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305                 310                 315                 320
Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr
                325                 330                 335
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
            340                 345                 350
Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
        355                 360                 365
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
    370                 375                 380
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385                 390                 395                 400
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser
                405                 410                 415
Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            420                 425                 430
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440                 445
```

<210> 337
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> H4H9048P2
aa1-108: LCVR
aa109-215: LC constant

<400> 337
```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
```

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