SEQUENCE LISTING

<110> Calmune Corporation
Williamson, Robert Anthony
Wadia, Jehangir
Pascual, Gabriel
Keogh, Elissa

<120> ANTI-HUMAN RESPIRATORY SYNCYTIAL VIRUS ANTIBODIES (RSV) AND METHODS OF USE

<130> 33335.01161.WO11/1161PC

<150> 61/399,310
<151> 2010-07-09

<150> 61/456,454
<151> 2010-11-05

<160> 487

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 228
<212> PRT
<213> Homo sapiens

<220>
<223> 58c5 Fab Heavy Chain

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

<210> 2
<211> 12

<212> PRT
<213> Homo sapiens

<220>
<223> 58c5 VH CDR1

<400> 2
Gly Ala Ser Ile Asn Ser Asp Asn Tyr Tyr Trp Thr
 1   5   10

<210> 3
<211> 16
<212> PRT
<213> Homo sapiens

<220>
<223> 58c5 VH CDR2

<400> 3
His Ile Ser Tyr Thr Gly Asn Thr Tyr Tyr Thr Pro Ser Leu Lys Ser
 1   5   10   15

<210> 4
<211> 15
<212> PRT
<213> Homo sapiens

<220>
<223> 58c5 VH CDR3

<400> 4
Cys Gly Ala Tyr Val Leu Ile Ser Asn Cys Gly Trp Phe Asp Ser
 1   5   10   15

<210> 5
<211> 214
<212> PRT
<213> Homo sapiens

<220>
<223> 58c5 Light Chain

<400> 5
Glu Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Thr Tyr
            20   25   30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35   40   45
Tyr Gly Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Thr Gly
    50   55   60
Ser Gly Tyr Gly Thr Asp Phe Ser Val Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Gln Tyr Leu Pro Tyr
                85   90   95
Thr Phe Ala Pro 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> 6
<211> 11
<212> PRT
<213> Homo sapiens

<220>
<223> 58c5 VL CDR1

<400> 6
Gln Ala Ser Gln Asp Ile Ser Thr Tyr Leu Asn
 1               5                  10


<210> 7
<211> 7
<212> PRT
<213> Homo sapiens

<220>
<223> 58c5 VL CDR2

<400> 7
Gly Ala Ser Asn Leu Glu Thr
 1               5


<210> 8
<211> 9
<212> PRT
<213> Homo sapiens

<220>
<223> 58c5 VL CDR3

<400> 8
Gln Gln Tyr Gln Tyr Leu Pro Tyr Thr
 1               5


<210> 9
<211> 228
<212> PRT
<213> Homo sapiens

<220>
<223> sc5 Fab Heavy Chain

<400> 9
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gly
 1               5                  10                  15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Ile Ser Gly Ser
            20                  25                  30
Asn Trp Trp Asn Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
        35                  40                  45
Ile Gly Glu Ile Tyr Tyr Arg Gly Thr Thr Asn Tyr Lys Ser Ser Leu
    50                  55                  60
Lys Gly Arg Val Thr Met Ser Val Asp Thr Ser Lys Asn Gln Phe Ser
65                  70                  75                  80
Leu Lys Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
```

```
Ala Arg Gly Gly Arg Ser Thr Phe Gly Pro Asp Tyr Tyr Tyr Tyr Met
            100                 105                 110
Asp Val Trp Gly Arg Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr
        115                 120                 125
Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
    130                 135                 140
Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
145                 150                 155                 160
Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
                165                 170                 175
Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
            180                 185                 190
Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
        195                 200                 205
Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
    210                 215                 220
Pro Lys Ser Cys
225
```

<210> 10
<211> 11
<212> PRT
<213> Homo sapiens

<220>
<223> sc5 VH CDR1

<400> 10
```
Gly Asp Ser Ile Ser Gly Ser Asn Trp Trp Asn
 1               5                  10
```

<210> 11
<211> 16
<212> PRT
<213> Homo sapiens

<220>
<223> sc5 VH CDR2

<400> 11
```
Glu Ile Tyr Tyr Arg Gly Thr Thr Asn Tyr Lys Ser Ser Leu Lys Gly
 1               5                  10                  15
```

<210> 12
<211> 16
<212> PRT
<213> Homo sapiens

<220>
<223> sc5 VH CDR3

<400> 12
```
Gly Gly Arg Ser Thr Phe Gly Pro Asp Tyr Tyr Tyr Tyr Met Asp Val
 1               5                  10                  15
```

<210> 13
<211> 214
<212> PRT
<213> Homo sapiens

<220>
<223> sc5 Light Chain

<400> 13

```
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 Asn Ile Lys Asn Tyr
            20                  25                  30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile
        35                  40                  45
Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
Glu Asp Phe Ala Thr Tyr Ser Cys Gln Gln Ser Tyr Asn Asn Gln 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> 14
<211> 11
<212> PRT
<213> Homo sapiens

<220>
<223> sc5 VL CDR1

<400> 14
```
Arg Ala Ser Gln Asn Ile Lys Asn Tyr Leu Asn
 1               5                  10
```

<210> 15
<211> 7
<212> PRT
<213> Homo sapiens

<220>
<223> sc5 VL CDR2

<400> 15
```
Ala Ala Ser Thr Leu Gln Ser
 1               5
```

<210> 16
<211> 9
<212> PRT
<213> Homo sapiens

<220>
<223> sc5 VL CDR3

<400> 16
```
Gln Gln Ser Tyr Asn Asn Gln Leu Thr
 1               5
```

<210> 17
<211> 702
<212> DNA
<213> Homo sapiens

<220>
<223> 58c5 Heavy Chain

<400> 17
caggtccagc ttgtgcagtc gggcccagga ctggtgaagc cttcacagac cctggccctc 60
acctgcaatg tctctggtgc ctccatcaat agtgataatt actactggac gtggatccgt 120
cagcgcccag gggggggcct ggagtggatt ggccacatct cttacactgg gaacacctac 180
tacaccccgt cactcaagag ccgactttcc atgtcactag agacatctca gagccaattc 240
tccctgaggc tgacctctgt gactgccgcg gactcggccg tctatttctg tgcggcctgc 300
ggggcatatg ttttaatatc aaactgtggc tggttcgact cctggggcca gggaacccag 360
gtcaccgtct cctcagcctc caccaagggc ccatcggtct tcccccctggc accctcctcc 420
aagagcacct ctgggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa 480
ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct 540
gtcctacagt cctcaggact ctactccctc agcagcgtgg tgaccgtgcc ctccagcagc 600
ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac 660
aagaaagttg agcccaaatc ttgtggtcgg ccaggccggc cg 702

<210> 18
<211> 645
<212> DNA
<213> Homo sapiens

<220>
<223> 58c5 Light Chain

<400> 18
gaaatagtga tgacgcagtc tccatcctcc ctgtctgcat ctataggaga cagagtcacc 60
atcacttgcc aggcgagtca ggacattagc acctatttaa attggtatca gcagaaacca 120
gggcaagccc ctaggctcct gatctacgga gcgtccaatt tggagacagg ggtcccatca 180
aggttcactg gaagtggata tgggacagac ttctctgtca ccatcagcag cctgcagcct 240
gaagatattg caacatatta ctgtcaacag taccaatatc tcccgtacac ttttgccccg 300
gggaccaagg tcgagatcaa acgaactgtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gctaa 645

<210> 19
<211> 687
<212> DNA
<213> Homo sapiens

<220>
<223> sc5 Heavy Chain

<400> 19
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggggac cctgtccctc 60
acttgcactg tctctggtga ctccatcagc ggctctaact ggtggaattg ggtccgccag 120
cccccaggga aggggctgga gtggattggg gaaatctatt atcgtgggac taccaattat 180
aagtcgtccc tcaagggtcg agtcaccatg tcagttgaca cgtccaagaa ccagttctcc 240
ctgaagctga cctctgtgac cgccgcggac acggccgtat attattgtgc gagaggggag 300
aggtccacct ttggtccgga ctactactac tacatggacg tctggggcag agggaccacg 360
gtcaccgtct cctcagcgtc gaccaaaggt ccgtctgttt tcccgctggc tccgtcttct 420
aaatctacct ctggtggtac cgctgctctg ggttgcctgg ttaaagacta cttccccggaa 480
ccggttaccg tttcttggaa ctctggtgct ctgacctctg gtgttcacac cttcccggct 540
gttctgcagt cttctggtct gtactctctg tcttctgttg ttaccgttcc gtcttcttct 600
ctgggtaccc agacctacat ctgcaacgtt aaccacaaac cgtctaacac caaagttgac 660
aagaaagttg aaccgaaatc ttgcctg 687

<210> 20
<211> 642

<212> DNA
<213> Homo sapiens

<220>
<223> sc5 Light Chain

<400> 20
gacatccaga tgacccagtc tccatcctcc ctgtctgcct ctgtaggtga cagagtcacc 60
atcacttgcc gggcaagtca gaacattaag aactatttaa attggtatca acaaaaacca 120
gggaaagtcc cgaagctcct gatctatgct gcatccactt tgcagagtgg ggtcccatcg 180
aggttcagtg gcagtggatc tgggacagac ttcactctca ccatcagcag tctgcaacct 240
gaagattttg caacttactc ctgtcaacag agttacaata accagctcac tttcggcggt 300
gggaccaagg tggagatcaa acgaactgtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gc 642

<210> 21
<211> 1665
<212> DNA
<213> Artificial Sequence

<220>
<223> RSV A2 F protein

<400> 21
gctagcggta ccatgggcga gctcctcatc ctgaaggcca acgccatcac caccatcctg 60
accgctgtga ccttctgctt cgccagcggc cagaacatca ccgaggaatt ctaccagagc 120
acctgcagcg ccgtgagcaa gggctacctg agcgccctgc ggaccggctg gtacaccagc 180
gtgatcacca tcgagctgtc caacatcaaa gaaaacaagt gcaacggcac cgacgccaaa 240
gtgaagctga tcaagcagga actggacaag tacaagaacg ccgtgaccga gctgcagctg 300
ctgatgcaga gcacccccc caccaacaac cgggccagaa gagaactgcc ccggttcatg 360
aactacaccc tgaacaacgc caagaaaacc aacgtgaccc tgagcaagaa gcggaagcgg 420
cggttcctgg gcttcctgct gggcgtgggc agcgccattg ccagcggcgt ggccgtgtcc 480
aaagtgctgc acctggaagg cgaagtgaac aagatcaagt ccgccctgct gtccaccaac 540
aaggccgtgg tgtccctgag caacggcgtg agcgtgctga ccagcaaggt gctggatctg 600
aagaactaca tcgacaagca gctgctgccc atcgtgaaca agcagagctg cagcatcagc 660
aacatcgaga cagtgatcga gttccagcag aagaacaacc ggctgctgga aatcacccgg 720
gagttcagcg tgaacgctgg cgtgaccacc cccgtgtcca cctacatgct gaccaactcc 780
gagctgctct ccctgatcaa tgacatgccc atcaccaacg accagaaaaa gctgatgagc 840
aacaacgtgc agatcgtgcg gcagcagagc tactccatca tgagcatcat caaagaagag 900
gtgctggcct acgtggtgca gctgcccctg tacggcgtga tcgacacccc ctgctggaag 960
ctgcacacca gccccctgtg caccaccaac accaaagagg gcagcaacat ctgcctgacc 1020
cggaccgacc ggggctggta ctgcgacaac gccggcagcg tgtcattctt cccacaagcc 1080
gagacatgca aggtgcagag caaccgggtg ttctgcgaca ccatgaacag cctgaccctg 1140
cccagcgaga tcaacctgtg caacgtggac atcttcaacc ccaagtacga ctgcaagatc 1200
atgacctcca agaccgacgt gtccagctcc gtgatcacct ccctgggcgc catcgtgtcc 1260
tgctacggca agaccaagtg caccgccagc aacaagaacc ggggcatcat caagaccttc 1320
agcaacggct gcgactacgt gtccaacaag ggcatggaca ccgtgtccgt gggcaacaca 1380
ctgtactacg tgaataagca ggaaggcaag agcctgtacg tgaagggcga gcccatcatc 1440
aacttctacg acccccctggt gttccccagc gacgagttcg acgccagcat cagccaggtg 1500
aacgagaaga tcaaccagag cctggccttc atcagaaaga gcgacgagct gctgcacaat 1560
gtgaatgccg gcaagtccac caccaaccaa gcttacgtag aacaaaaact catctcagaa 1620
gaggatctga atagcgccgt cgaccatcat catcatcatc attga 1665

<210> 22
<211> 6
<212> DNA
<213> Artificial Sequence

<220>
<223> NheI Restriction Site

<400> 22
gctagc 6

<210> 23
<211> 6
<212> DNA
<213> Artificial Sequence

<220>
<223> HindIII Restriction Site

<400> 23
aagctt 6

<210> 24
<211> 5521
<212> DNA
<213> Artificial Sequence

<220>
<223> pcDNA 3.1/myc-His(-) C vector

<400> 24
gacggatcgg gagatctccc gatcccctat ggtgcactct cagtacaatc tgctctgatg 60
ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg 120
cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc 180
ttagggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt 240
gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata 300
tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc 360
cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc 420
attgacgtca atgggtggag tatttacggt aaactgccca cttggcagta catcaagtgt 480
atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt 540
atgcccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca 600
tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg 660
actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc 720
aaaatcaacg ggactttcca aaatgtcgta acaactccgc cccattgacg caaatgggcg 780
gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaaccca 840
ctgcttactg gcttatcgaa attaatacga ctcactatag ggagacccaa gctggctagc 900
gtttaaacgg gccctctaga ctcgagcggc cgccactgtg ctggatatct gcagaattcc 960
accacactgg actagtggat ccgagctcgg taccaagctt acgtagaaca aaaactcatc 1020
tcagaagagg atctgaatag cgccgtcgac catcatcatc atcatcattg agtttaaacg 1080
gtctccagct taagtttaaa ccgctgatca gcctcgactg tgccttctag ttgccagcca 1140
tctgttgttt gcccctcccc cgtgccttcc ttgaccctgg aaggtgccac tcccactgtc 1200
ctttcctaat aaaatgagga aattgcatcg cattgtctga gtaggtgtca ttctattctg 1260
gggggtgggg tggggcagga cagcaagggg gaggattggg aagacaatag caggcatgct 1320
ggggatgcgg tgggctctat ggcttctgag gcggaaagaa ccagctgggg ctctaggggg 1380
tatccccacg cgccctgtag cggcgcatta agcgcggcgg gtgtggtggt tacgcgcagc 1440
gtgaccgcta cacttgccag cgccctagcg cccgctcctt tcgctttctt cccttccttt 1500
ctcgccacgt tcgccggctt tccccgtcaa gctctaaatc gggggctccc tttagggttc 1560
cgatttagtg ctttacggca cctcgacccc aaaaaacttg attagggtga tggttcacgt 1620
agtgggccat cgccctgata gacggttttt cgcccctttga cgttggagtc cacgttcttt 1680
aatagtggac tcttgttcca aactggaaca acactcaacc ctatctcggt ctattctttt 1740
gatttataag ggattttgcc gatttcggcc tattggttaa aaaatgagct gatttaacaa 1800
aaatttaacg cgaattaatt ctgtggaatg tgtgtcagtt agggtgtgga aagtccccag 1860
gctccccagc aggcagaagt atgcaaagca tgcatctcaa ttagtcagca accaggtgtg 1920
gaaagtcccc aggctcccca gcaggcagaa gtatgcaaag catgcatctc aattagtcag 1980
caaccatagt cccgccccta actccgccca tcccgcccct aactccgccc agttccgccc 2040
attctccgcc ccatggctga ctaatttttt ttatttatgc agaggccgag gccgcctctg 2100
cctctgagct attccagaag tagtgaggag gcttttttgg aggcctaggc ttttgcaaaa 2160
agctcccggg agcttgtata tccattttcg gatctgatca agagacagga tgaggatcgt 2220
ttcgcatgat tgaacaagat ggattgcacg caggttctcc ggccgcttgg gtggagaggc 2280
tattcggcta tgactgggca caacagacaa tcggctgctc tgatgccgcc gtgttccggc 2340
tgtcagcgca ggggcgcccg gttcttttttg tcaagaccga cctgtccggt gccctgaatg 2400
aactgcagga cgaggcagcg cggctatcgt ggctggccac gacgggcgtt ccttgcgcag 2460
ctgtgctcga cgttgtcact gaagcgggaa gggactggct gctattgggc gaagtgccgg 2520
ggcaggatct cctgtcatct caccttgctc ctgccgagaa agtatccatc atggctgatg 2580
caatgcggcg gctgcatacg cttgatccgg ctacctgccc attcgaccac caagcgaaac 2640
atcgcatcga gcgagcacgt actcggatgg aagccggtct tgtcgatcag gatgatctgg 2700
acgaagagca tcaggggctc gcgccagccg aactgttcgc caggctcaag gcgcgcatgc 2760
ccgacggcga ggatctcgtc gtgacccatg gcgatgcctg cttgccgaat atcatggtgg 2820
aaaatggccg cttttctgga ttcatcgact gtggccggct gggtgtggcg gaccgctatc 2880

```
aggacatagc gttggctacc cgtgatattg ctgaagagct tggcggcgaa tgggctgacc 2940
gcttcctcgt gctttacggt atcgccgctc ccgattcgca gcgcatcgcc ttctatcgcc 3000
ttcttgacga gttcttctga gcgggactct ggggttcgaa atgaccgacc aagcgacgcc 3060
caacctgcca tcacgagatt tcgattccac cgccgccttc tatgaaaggt tgggcttcgg 3120
aatcgttttc cgggacgccg gctggatgat cctccagcgc ggggatctca tgctggagtt 3180
cttcgcccac cccaacttgt ttattgcagc ttataatggt tacaaataaa gcaatagcat 3240
cacaaatttc acaaataaag cattttttc actgcattct agttgtggtt tgtccaaact 3300
catcaatgta tcttatcatg tctgtatacc gtcgacctct agctagagct tggcgtaatc 3360
atggtcatag ctgtttcctg tgtgaaattg ttatccgctc acaattccac acaacatacg 3420
agccggaagc ataaagtgta aagcctgggg tgcctaatga gtgagctaac tcacattaat 3480
tgcgttgcgc tcactgcccg ctttccagtc gggaaacctg tcgtgccagc tgcattaatg 3540
aatcggccaa cgcgcgggga gaggcggttt gcgtattggg cgctcttccg cttcctcgct 3600
cactgactcg ctgcgctcgg tcgttcggct gcggcgagcg gtatcagctc actcaaaggc 3660
ggtaatacgg ttatccacag aatcagggga taacgcagga aagaacatgt gagcaaaagg 3720
ccagcaaaag gccaggaacc gtaaaaaggc cgcgttgctg gcgtttttcc ataggctccg 3780
ccccccctgac gagcatcaca aaaatcgacg ctcaagtcag aggtggcgaa acccgacagg 3840
actataaaga taccaggcgt ttcccccctgg aagctccctc gtgcgctctc ctgttccgac 3900
cctgccgctt accggatacc tgtccgcctt tctcccttcg ggaagcgtgg cgctttctca 3960
tagctcacgc tgtaggtatc tcagttcggt gtaggtcgtt cgctccaagc tgggctgtgt 4020
gcacgaaccc cccgttcagc ccgaccgctg cgccttatcc ggtaactatc gtcttgagtc 4080
caacccggta agacacgact tatcgccact ggcagcagcc actggtaaca ggattagcag 4140
agcgaggtat gtaggcggtg ctacagagtt cttgaagtgg tggcctaact acggctacac 4200
tagaagaaca gtatttggta tctgcgctct gctgaagcca gttaccttcg gaaaaagagt 4260
tggtagctct tgatccggca aacaaaccac cgctggtagc ggtggttttt ttgtttgcaa 4320
gcagcagatt acgcgcagaa aaaaaggatc tcaagaagat cctttgatct tttctacggg 4380
gtctgacgct cagtggaacg aaaactcacg ttaagggatt ttggtcatga gattatcaaa 4440
aaggatcttc acctagatcc ttttaaatta aaaatgaagt tttaaatcaa tctaaagtat 4500
atatgagtaa acttggtctg acagttacca atgcttaatc agtgaggcac ctatctcagc 4560
gatctgtcta tttcgttcat ccatagttgc ctgactcccc gtcgtgtaga taactacgat 4620
acgggagggc ttaccatctg gccccagtgc tgcaatgata ccgcgagacc cacgctcacc 4680
ggctccagat ttatcagcaa taaaccagcc agccggaagg gccgagcgca gaagtggtcc 4740
tgcaacttta tccgcctcca tccagtctat taattgttgc cgggaagcta gagtaagtag 4800
ttcgccagtt aatagtttgc gcaacgttgt tgccattgct acaggcatcg tggtgtcacg 4860
ctcgtcgttt ggtatggctt cattcagctc cggttcccaa cgatcaaggc gagttacatg 4920
atcccccatg ttgtgcaaaa aagcggttag ctccttcggt cctccgatcg ttgtcagaag 4980
taagttggcc gcagtgttat cactcatggt tatggcagca ctgcataatt ctcttactgt 5040
catgccatcc gtaagatgct tttctgtgac tggtgagtac tcaaccaagt cattctgaga 5100
atagtgtatg cggcgaccga gttgctcttg cccggcgtca atacgggata ataccgcgcc 5160
acatagcaga actttaaaag tgctcatcat tggaaaacgt tcttcggggc gaaaactctc 5220
aaggatctta ccgctgttga gatccagttc gatgtaaccc actcgtgcac ccaactgatc 5280
ttcagcatct tttactttca ccagcgtttc tgggtgagca aaaacaggaa ggcaaaatgc 5340
cgcaaaaaag ggaataaggg cgacacggaa atgttgaata ctcatactct tccttttca 5400
atattattga agcatttatc agggttattg tctcatgagc ggatacatat ttgaatgtat 5460
ttagaaaaat aaacaaatag gggttccgcg cacatttccc cgaaaagtgc cacctgacgt 5520
c                                                                  5521
```

<210> 25
<211> 550
<212> PRT
<213> Artificial Sequence

<220>
<223> RSV A2 F protein

<400> 25

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

```
                85                  90                  95
Leu Met Gln Ser Thr Pro Pro Thr Asn Asn Arg Ala Arg Arg Glu Leu
            100                 105                 110
Pro Arg Phe Met Asn Tyr Thr Leu Asn Asn Ala Lys Lys Thr Asn Val
        115                 120                 125
Thr Leu Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly
    130                 135                 140
Val Gly Ser Ala Ile Ala Ser Gly Val Ala Val Ser Lys Val Leu His
145                 150                 155                 160
Leu Glu Gly Glu Val Asn Lys Ile Lys Ser Ala Leu Leu Ser Thr Asn
                165                 170                 175
Lys Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Ser Lys
            180                 185                 190
Val Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Val
        195                 200                 205
Asn Lys Gln Ser Cys Ser Ile Ser Asn Ile Glu Thr Val Ile Glu Phe
    210                 215                 220
Gln Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val
225                 230                 235                 240
Asn Ala Gly Val Thr Thr Pro Val Ser Thr Tyr Met Leu Thr Asn Ser
                245                 250                 255
Glu Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys
            260                 265                 270
Lys Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser
        275                 280                 285
Ile Met Ser Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu
    290                 295                 300
Pro Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser
305                 310                 315                 320
Pro Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr
                325                 330                 335
Arg Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe
            340                 345                 350
Phe Pro Gln Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys
        355                 360                 365
Asp Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Ile Asn Leu Cys Asn
    370                 375                 380
Val Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys
385                 390                 395                 400
Thr Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser
                405                 410                 415
Cys Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile
            420                 425                 430
Ile Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Met
        435                 440                 445
Asp Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu
    450                 455                 460
Gly Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp
465                 470                 475                 480
Pro Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val
                485                 490                 495
Asn Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Lys Ser Asp Glu
            500                 505                 510
Leu Leu His Asn Val Asn Ala Gly Lys Ser Thr Thr Asn Gln Ala Tyr
        515                 520                 525
Val Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp
    530                 535                 540
His His His His His His
545                 550
```

<210> 26
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> VH1a Forward Primer

<400> 26
ggatcctctt cttggtggca gcag 24

<210> 27
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> VH1b Forward Primer

<400> 27
gcatcctttt cttggtggca gcac 24

<210> 28
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> VH1c Forward Primer

<400> 28
gggtcttctg cttgctggct gtag 24

<210> 29
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> VH1d Forward Primer

<400> 29
ggatcctctt cttggtggga gcag 24

<210> 30
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> VH2a Forward Primer

<400> 30
ctgaccatcc cttcatggct cttg 24

<210> 31
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> VH2b Forward Primer

<400> 31
ctgaccaccc cttcctgggt cttg 24

<210> 32
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> VH3a Forward Primer

<400> 32

gctattttar aaggtgtcca gtgt 24

<210> 33
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> VH3b Forward Primer

<400> 33
gctcttttaa gaggtgtcca gtgt 24

<210> 34
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> VH3c Forward Primer

<400> 34
gctatttaaa aaggtgtcca atgt 24

<210> 35
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> VH4a Forward Primer

<400> 35
ctggtggcag ctcccagatg ggtc 24

<210> 36
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> VH5a Forward Primer

<400> 36
ctcctggctg ttctccaagg agtc 24

<210> 37
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> VH-g 1-REV Reverse Primer

<400> 37
acaagatttg ggctcaactt tcttgtcc 28

<210> 38
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> VH-g 2-REV Reverse Primer

<400> 38
tttgcgctca actgtcttgt ccaccttg 28

<210> 39
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> VH-g 3-REV Reverse Primer

<400> 39
tttgagctca actctcttgt ccaccttg 28

<210> 40
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> VH-g 4-REV Reverse Primer

<400> 40
atatttggac tcaactctct tgtccacc 28

<210> 41
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> SfiI Restriction Site

<220>
<221> misc_feature
<222> (5)...(9)
<223> N = a or g or c or t

<400> 41
ggccnnnnng gcc 13

<210> 42
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> pCal30 VH1a Forward Primer

<400> 42
ggctttgcta ccgtagcgca ggcggccgca caggtkcagc tggtgcag 48

<210> 43
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> pCal30 VH1b Forward Primer

<400> 43
ggctttgcta ccgtagcgca ggcggccgca caggtccagc ttgtgcag 48

<210> 44
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> pCal30 VH1c Forward Primer

<400> 44
ggctttgcta ccgtagcgca ggcggccgca saggtccagc tggtacag 48

<210> 45
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> pCal30 VH1d Forward Primer

<400> 45
ggctttgcta ccgtagcgca ggcggccgca caratgcagc tggtgcag 48

<210> 46
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> pCal30 VH2a Forward Primer

<400> 46
ggctttgcta ccgtagcgca ggcggccgca cagatcacct tgaaggag 48

<210> 47
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> pCal30 VH3a Forward Primer

<400> 47
ggctttgcta ccgtagcgca ggcggccgca gargtgcagc tggtggag 48

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

<220>
<223> pCal30 VH4a Forward Primer

<400> 48
ggctttgcta ccgtagcgca ggcggccgca cagstgcagc tgcaggag 48

<210> 49
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> pCal30 VH4b Forward Primer

<400> 49
ggctttgcta ccgtagcgca ggcggccgca caggtgcagc tacagcag 48

<210> 50
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> pCal30 VH5a Forward Primer

<400> 50
ggctttgcta ccgtagcgca ggcggccgca gargtgcagc tggtgcag 48

<210> 51
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> pCal30 VH6 Forward Primer

<400> 51
ggctttgcta ccgtagcgca ggcggccgca caggtacagc tgcagcag 48

<210> 52
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> pCal30 VH7 Forward Primer

<400> 52
ggctttgcta ccgtagcgca ggcggccgca caggtscagc tggtgcaa 48

<210> 53
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> VHII-g1-Rev Reverse Primer

<400> 53
tgcggccggc ctggccgacc acaagatttg ggctcaactt tc 42

<210> 54
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> VHII-g2-Rev Reverse Primer

<400> 54
tgcggccggc ctggccgacc tttgcgctca actgtcttgt cc 42

<210> 55
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> VHII-g3-Rev Reverse Primer

<400> 55
tgcggccggc ctggccgacc tttgagctca actctcttgt cc 42

<210> 56
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> VHII-g4-Rev Reverse Primer

<400> 56
tgcggccggc ctggccgacc atatttggac tcaactctct tg 42

<210> 57

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

<220>
<223> VK 1a Forward Primer

<400> 57
aaggcccagc cggccatggc cgccggtgac atccagatga cccag 45

<210> 58
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> VK 1b Forward Primer

<400> 58
aaggcccagc cggccatggc cgccggtgac atccagttga cccag 45

<210> 59
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> VK 1c Forward Primer

<400> 59
aaggcccagc cggccatggc cgccggtgcc atccggttga cccag 45

<210> 60
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> VK 2a Forward Primer

<400> 60
aaggcccagc cggccatggc cgccggtgat attgtgatga cycag 45

<210> 61
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> VK 3a Forward Primer

<400> 61
aaggcccagc cggccatggc cgccggtgaa attgtgttga cgcag 45

<210> 62
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> VK 3b Forward Primer

<400> 62
aaggcccagc cggccatggc cgccggtgaa attgtgttga cacag 45

<210> 63
<211> 45
<212> DNA

<213> Artificial Sequence

<220>
<223> VK 4a Forward Primer

<400> 63
aaggcccagc cggccatggc cgccggtgaa atagtgatga cgcag 45

<210> 64
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> VK 4a Forward Primer

<400> 64
aaggcccagc cggccatggc cgccggtgac atcgtgatga cccag 45

<210> 65
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> VK 5a Forward Primer

<400> 65
aaggcccagc cggccatggc cgccggtgaa acgacactca cgcag 45

<210> 66
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> VK 6a Forward Primer

<400> 66
aaggcccagc cggccatggc cgccggtgaa attgtgctga ctcag 45

<210> 67
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> VK 6b Forward Primer

<400> 67
aaggcccagc cggccatggc cgccggtgat gttgtgatga cacag 45

<210> 68
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> pCALCK(G)L Reverse Primer

<400> 68
ctccttatta attaattagc actctcccct gttgaagctc tttg 44

<210> 69
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> VL1-F Forward Primer

<400> 69
aaggcccagc cggccatggc cgccggtgtt cagtctgtgc tgackcagcc 50

<210> 70
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> VL2-F Forward Primer

<400> 70
aaggcccagc cggccatggc cgccggtgtt cagtctgccc tgactcagcc 50

<210> 71
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> VL3A-F Forward Primer

<400> 71
aaggcccagc cggccatggc cgccggtgtt tcctatgagc tgacwcagcy 50

<210> 72
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> VL3B-F Forward Primer

<400> 72
aaggcccagc cggccatggc cgccggtgtt tcttctgagc tgactcagga c 51

<210> 73
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> VL3C-F Forward Primer

<400> 73
aaggcccagc cggccatggc cgccggtgtt tcctatgwgc tgactcagcc 50

<210> 74
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> VL4A-F Forward Primer

<400> 74
aaggcccagc cggccatggc cgccggtgtt ctgcctgtgc tgactcagcc c 51

<210> 75
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> VL4B-F Forward Primer

<400> 75
aaggcccagc cggccatggc cgccggtgtt cagcytgtgc tgactcaatc r 51

<210> 76
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> VL5/9-F Forward Primer

<400> 76
aaggcccagc cggccatggc cgccggtgtt cagsctgtgc tgactcagcc r 51

<210> 77
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> VL6-F Forward Primer

<400> 77
aaggcccagc cggccatggc cgccggtgtt aattttatgc tgactcagcc c 51

<210> 78
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> VL7/8-F Forward Primer

<400> 78
aaggcccagc cggccatggc cgccggtgtt cagrctgtgg tgactcagga g 51

<210> 79
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> VL10-F Forward Primer

<400> 79
aaggcccagc cggccatggc cgccggtgtt caggcagggc tgactcagcc a 51

<210> 80
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> pCALCL(T)-R Reverse Primer

<400> 80
ctccttatta attaattatg agcattctgy akgggcmayt gtc 43

<210> 81
<211> 4765
<212> DNA
<213> Artificial Sequence

<220>
<223> 2g12/pCal Vector

<400> 81

gtggcacttt tcggggaaat gtgcgcggaa cccctatttg tttatttttc taaatacatt 60
caaatatgta tccgctcatg agacaataac cctgataaat gcttcaataa tattgaaaaa 120
ggaagagtat gagtattcaa catttccgtg tcgcccttat tccctttttt gcggcatttt 180
gccttcctgt ttttgctcac ccagaaacgc tggtgaaagt aaaagatgct gaagatcagt 240
tgggtgcacg agtgggttac atcgaactgg atctcaacag cggtaagatc cttgagagtt 300
ttcgccccga agaacgtttt ccaatgatga gcacttttaa agttctgcta tgtggcgcgg 360
tattatcccg tattgacgcc gggcaagagc aactcggtcg ccgcatacac tattctcaga 420
atgacttggt tgagtactca ccagtcacag aaaagcatct tacggatggc atgacagtaa 480
gagaattatg cagtgctgcc ataaccatga gtgataacac tgcggccaac ttacttctga 540
caacgatcgg aggaccgaag gagctaaccg ctttttgca caacatgggg gatcatgtaa 600
ctcgccttga tcgttgggaa ccggagctga atgaagccat accaaacgac gagcgtgaca 660
ccacgatgcc tgtagcaatg gcaacaacgt tgcgcaaact attaactggc gaactactta 720
ctctagcttc ccggcaacaa ttaatagact ggatggaggc ggataaagtt gcaggaccac 780
ttctgcgctc ggcccttccg gctggctggt ttattgctga taaatctgga gccggtgagc 840
gtgggtctcg cggtatcatt gcagcactgg ggccagatgg taagccctcc cgtatcgtag 900
ttatctacac gacggggagt caggcaacta tggatgaacg aaatagacag atcgctgaga 960
taggtgcctc actgattaag cattggtaac tgtcagacca agtttactca tatatacttt 1020
agattgattt aaaacttcat ttttaattta aaaggatcta ggtgaagatc ctttttgata 1080
atctcatgac caaaatccct taacgtgagt tttcgttcca ctgagcgtca gaccccgtag 1140
aaaagatcaa aggatcttct tgagatcctt tttttctgcg cgtaatctgc tgcttgcaaa 1200
caaaaaaacc accgctacca gcggtggttt gtttgccgga tcaagagcta ccaactcttt 1260
ttccgaaggt aactggcttc agcagagcgc agataccaaa tactgtcctt ctagtgtagc 1320
cgtagttagg ccaccacttc aagaactctg tagcaccgcc tacatacctc gctctgctaa 1380
tcctgttacc agtggctgct gccagtggcg ataagtcgtg tcttaccggg ttggactcaa 1440
gacgatagtt accggataag gcgcagcggt cgggctgaac gggggttcg tgcacacagc 1500
ccagcttgga gcgaacgacc tacaccgaac tgagatacct acagcgtgag ctatgagaaa 1560
gcgccacgct tcccgaaggg agaaaggcgg acaggtatcc ggtaagcggc agggtcggaa 1620
caggagagcg cacgagggag cttccagggg gaaacgcctg gtatctttat agtcctgtcg 1680
ggtttcgcca cctctgactt gagcgtcgat ttttgtgatg ctcgtcaggg gggcggagcc 1740
tatggaaaaa cgccagcaac gcggcctttt tacggttcct ggccttttgc tggccttttg 1800
ctcacatgtt ctttcctgcg ttatcccctg attctgtgga taaccgtatt accgcctttg 1860
agtgagctga taccgctcgc cgcagccgaa cgaccgagcg cagcgagtca gtgagcgagg 1920
aagcggaaga gcgcccaata cgcaaaccgc ctctccccgc gcgttggccg attcattaat 1980
gcagctggca cgacaggttt cccgactgga aagcgggcag tgagcgcaac gcaattaatg 2040
tgagttagct cactcattag gcaccccagg ctttacactt tatgcttccg gctcgtatgt 2100
tgtgtggaat tgtgagcgga taacaattga attaaggagg atataattat gaaatacctg 2160
ctgccgaccg cagccgctgg tctgctgctg ctcgcggccc agccggccat ggccgccggt 2220
gttgttatga cccagtctcc gtctaccctg tctgcttctg ttggtgacac catcaccatc 2280
acctgccgtg cttctcagtc tatcgaaacc tggctggctt ggtaccagca gaaaccgggt 2340
aaagctccga aactgctgat ctacaaggct tctaccctga aaaccggtgt tccgtctcgt 2400
ttctctggtt ctggttctgg taccgagttc accctgacca tctctggtct gcagttcgac 2460
gacttcgcta cctaccactg ccagcactac gctggttact ctgctacctt cggtcagggt 2520
acccgtgttg aaatcaaacg taccgttgct gctccgtctg ttttcatctt cccgccgtct 2580
gacgaacagc tgaaatctgg taccgcttct gttgtttgcc tgctgaacaa cttctacccg 2640
cgtgaagcta aagttcagtg gaaagttgac aacgctctgc agtctggtaa ctctcaggaa 2700
tctgttaccg aacaggactc taaagactct acctactctc tgtcttctac cctgaccctg 2760
tctaaagctg actacgaaaa gcacaaagtt tacgcttgcg aagttaccca ccagggtctg 2820
tcttctccgg ttaccaaatc tttcaaccgt ggtgaatgct aattaattaa taaggaggat 2880
ataattatga aaaagacagc tatcgcgatt gcagtggcac tggctggttt cgctaccgta 2940
gcccaggcgg ccgcagaagt tcagctggtt gaatctggtg gtggtctggt taaagctggt 3000
ggttctctga tcctgtcttg cggtgtttct aacttccgta tctctgctca caccatgaac 3060
tgggttcgtc gtgttccggg tggtggtctg gaatgggttg cttctatctc tacctcttct 3120
acctaccgtg actacgctga cgctgttaaa ggtcgtttca ccgtttctcg tgacgacctg 3180
gaagacttcg tttacctgca gatgcataaa atgcgtgttg aagacaccgc tatctactac 3240
tgcgctcgta aaggttctga ccgtctgtct gacaacgacc cgttcgacgc ttggggtccg 3300
ggtaccgttg ttaccgtttc tccggcgtcg accaaaggtc cgtctgtttt cccgctggct 3360
ccgtcttcta aatctacctc tggtggtacc gctgctctgg gttgcctggt taaagactac 3420
ttcccggaac cggttaccgt ttcttggaac tctggtgctc tgacctctgg tgttcacacc 3480
ttcccggctg ttctgcagtc ttctggtctg tactctctgt cttctgttgt taccgttccg 3540
tcttcttctc tgggtaccca gacctacatc tgcaacgtta accacaaacc gtctaacacc 3600
aaagttgaca agaaagttga accgaaatct tgcctgcgat cgcggccagg ccggccgcac 3660
catcaccatc accatggcgc atacccgtac gacgttccgg actacgcttc tactagttag 3720
aagggtggtg gctctgaggg tggcggttct gagggtggcg gctctgaggg aggcggttcc 3780
ggtggtggct ctggttccgg tgattttgat tatgaaaaga tggcaaacgc taataagggg 3840
gctatgaccg aaaatgccga tgaaaacgcg ctacagtctg acgctaaagg caaacttgat 3900
tctgtcgcta ctgattacgg tgctgctatc gatggtttca ttggtgacgt ttccggcctt 3960
gctaatggta atggtgctac tggtgatttt gctggctcta attcccaaat ggctcaagtc 4020
ggtgacggtg ataattcacc tttaatgaat aatttccgtc aatatttacc ttccctccct 4080

caatcggttg aatgtcgccc ttttgtcttt ggcgctggta aaccatatga attttctatt 4140
gattgtgaca aaataaactt attccgtggt gtctttgcgt ttcttttata tgttgccacc 4200
tttatgtatg tattttctac gtttgctaac atactgcgta ataaggagtc ttaagctagc 4260
taacgatcgc ccttcccaac agttgcgcag cctgaatggc gaatgggacg cgccctgtag 4320
cggcgcatta agcgcggcgg gtgtggtggt tacgcgcagc gtgaccgcta cacttgccag 4380
cgccctagcg cccgctcctt tcgctttctt cccttccttt ctcgccacgt tcgccggctt 4440
tccccgtcaa gctctaaatc gggggctccc tttagggttc cgatttagtg ctttacggca 4500
cctcgacccc aaaaaacttg attagggtga tggttcacgt agtgggccat cgccctgata 4560
gacggttttt cgccctttga cgttggagtc cacgttcttt aatagtggac tcttgttcca 4620
aactggaaca acactcaacc ctatctcggt ctattctttt gatttataag ggattttgcc 4680
gatttcggcc tattggttaa aaaatgagct gatttaacaa aaatttaacg cgaattttaa 4740
caaaatatta acgcttacaa tttag 4765

<210> 82
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> FabLinkerCK-Fwd

<400> 82
gagcttcaac aggggagagt gctaattaat taataaggag 40

<210> 83
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> FabLinker-Rev

<400> 83
tgcggccgcc tgcgctacgg tagcaaagcc agccagtgcc ac 42

<210> 84
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Sfi Forward Primer

<400> 84
tcgcggccca gccggccatg gc 22

<210> 85
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Sfi Reverse Primer

<400> 85
tgcggccggc ctggccga 18

<210> 86
<211> 4779
<212> DNA
<213> Artificial Sequence

<220>
<223> 4E10 pCAL vector

<400> 86
gtggcacttt tcggggaaat gtgcgcggaa cccctatttg tttatttttc taaatacatt 60
caaatatgta tccgctcatg agacaataac cctgataaat gcttcaataa tattgaaaaa 120

ggaagagtat gagtattcaa catttccgtg tcgcccttat tccctttttt gcggcatttt 180
gccttcctgt ttttgctcac ccagaaacgc tggtgaaagt aaaagatgct gaagatcagt 240
tgggtgcacg agtgggttac atcgaactgg atctcaacag cggtaagatc cttgagagtt 300
ttcgccccga agaacgtttt ccaatgatga gcacttttaa agttctgcta tgtggcgcgg 360
tattatcccg tattgacgcc gggcaagagc aactcggtcg ccgcatacac tattctcaga 420
atgacttggt tgagtactca ccagtcacag aaaagcatct tacggatggc atgacagtaa 480
gagaattatg cagtgctgcc ataaccatga gtgataacac tgcggccaac ttacttctga 540
caacgatcgg aggaccgaag gagctaaccg ctttttgca caacatgggg gatcatgtaa 600
ctcgccttga tcgttgggaa ccggagctga atgaagccat accaaacgac gagcgtgaca 660
ccacgatgcc tgtagcaatg gcaacaacgt tgcgcaaact attaactggc gaactactta 720
ctctagcttc ccggcaacaa ttaatagact ggatggaggc ggataaagtt gcaggaccac 780
ttctgcgctc ggcccttccg gctggctggt ttattgctga taaatctgga gccggtgagc 840
gtgggtctcg cggtatcatt gcagcactgg ggccagatgg taagccctcc cgtatcgtag 900
ttatctacac gacggggagt caggcaacta tggatgaacg aaatagacag atcgctgaga 960
taggtgcctc actgattaag cattggtaac tgtcagacca agtttactca tatatacttt 1020
agattgattt aaaacttcat ttttaattta aaaggatcta ggtgaagatc ctttttgata 1080
atctcatgac caaaatccct taacgtgagt tttcgttcca ctgagcgtca gaccccgtag 1140
aaaagatcaa aggatcttct tgagatcctt tttttctgcg cgtaatctgc tgcttgcaaa 1200
caaaaaaacc accgctacca gcggtggttt gtttgccgga tcaagagcta ccaactcttt 1260
ttccgaaggt aactggcttc agcagagcgc agataccaaa tactgtcctt ctagtgtagc 1320
cgtagttagg ccaccacttc aagaactctg tagcaccgcc tacatacctc gctctgctaa 1380
tcctgttacc agtggctgct gccagtggcg ataagtcgtg tcttaccggg ttggactcaa 1440
gacgatagtt accggataag gcgcagcggt cgggctgaac ggggggttcg tgcacacagc 1500
ccagcttgga gcgaacgacc tacaccgaac tgagatacct acagcgtgag ctatgagaaa 1560
gcgccacgct tcccgaaggg agaaaggcgg acaggtatcc ggtaagcggc agggtcggaa 1620
caggagagcg cacgagggag cttccagggg gaaacgcctg gtatctttat agtcctgtcg 1680
ggtttcgcca cctctgactt gagcgtcgat ttttgtgatg ctcgtcaggg gggcggagcc 1740
tatggaaaaa cgccagcaac gcggcctttt tacggttcct ggccttttgc tggccttttg 1800
ctcacatgtt ctttcctgcg ttatcccctg attctgtgga taaccgtatt accgcctttg 1860
agtgagctga taccgctcgc cgcagccgaa cgaccgagcg cagcgagtca gtgagcgagg 1920
aagcggaaga gcgcccaata cgcaaaccgc ctctccccgc gcgttggccg attcattaat 1980
gcagctggca cgacaggttt cccgactgga aagcgggcag tgagcgcaac gcaattaatg 2040
tgagttagct cactcattag gcaccccagg ctttacactt tatgcttccg gctcgtatgt 2100
tgtgtggaat tgtgagcgga taacaattga attaaggagg atataattat gaaatacctg 2160
ctgccgaccg cagccgctgg tctgctgctg ctcgcggccc agccggccat ggccgccggt 2220
gaaattgtct tgacgcaaag cccggggacc cagtcgctgt ccccgggaga gcgcgcgacc 2280
ctgtcatgtc gtgcgagtca aagtgtcggt aacaataaac tggcttggta ccagcaacgt 2340
cctgggcagg caccgcgctt actcatttac ggagcctctt cacgtcccag cggggtagcg 2400
gatcgtttct ccggttctgg cagcggcact gatttcacct taacaatctc gcgtctggaa 2460
ccggaagatt ttgccgtcta ttactgtcag caatacggcc agtccttgtc tacatttggc 2520
cagggaacga aagtggaggt aaaacgtacc gttgctgccc ccagtgtttt catctttcca 2580
ccgtcagacg agcagctgaa gtctggtacc gcaagtgtgg tttgcctcct gaataacttt 2640
tatcctcgcg aagcgaaagt tcagtggaag gtggataatg ccctgcagtc gggtaatagc 2700
caggaaagcg tgaccgaaca agattcaaaa gactccacat attctctgag ttcgactctt 2760
acgttaagca aagctgacta tgaaaagcac aaagtttatg catgcgaggt gacgcatcag 2820
ggtctttcca gcccagtaac taaatcattc aaccgcggcg aatgttaatt aataaggagg 2880
atataattat gaaaaagaca gctatcgcga ttgcagtggc actggctggt ttcgctaccg 2940
tagcccaggc ggccgcacag gtgcaactgg tgcagagtgg ggccgaagtt aaacgcccag 3000
gttcgtccgt aaccgtctca tgcaaggcca gcggtggctc tttctctacg tacgcgctgt 3060
cctgggttcg tcaggccccg ggtcgtggac ttgaatggat gggcggcgta ataccgctgc 3120
tcaccatcac taattacgca ccgcgtttcc agggccgcat tacaatcacc gcggaccgtt 3180
cgacctcaac ggcatatctc gagttaaact cactgcgtcc tgaagatacc gcagtgtatt 3240
actgcgctcg tgaaggtacc actggctggg gctggttggg taaaccgatt ggtgcgttcg 3300
cacattgggg gcaaggcaca cttgttactg tcagctctgc ctctacgaaa ggaccgagcg 3360
tctttccctt ggctccaagt agcaaatcaa cgagcggagg gacagccgcg ttaggatgtc 3420
tggtgaagga ctattttccg gaaccagtta ccgtcagttg gaactcgggc gcgttaactt 3480
ccggtgttca cacatttccc gctgttctgc aaagtagcgg tctgtattcc ctgtcctcag 3540
tagtgacagt tccttcgagt tctctgggca ctcagaccta tatttgcaat gtgaaccata 3600
aacctagcaa tacgaaagtg gataagaaag tagagccgaa atcttgtctg cgatcgcggc 3660
caggccggcc gcaccatcac catcaccatg gcgcataccc gtacgacgtt ccggactacg 3720
cttctactag ttagaagggt ggtggctctg agggtggcgg ttctgagggt ggcggctctg 3780
agggaggcgg ttccggtggt ggctctggtt ccggtgattt tgattatgaa aagatggcaa 3840
acgctaataa gggggctatg accgaaaatg ccgatgaaaa cgcgctacag tctgacgcta 3900
aaggcaaact tgattctgtc gctactgatt acggtgctgc tatcgatggt ttcattggtg 3960
acgtttccgg ccttgctaat ggtaatggtg ctactggtga ttttgctggc tctaattccc 4020
aaatggctca agtcggtgac ggtgataatt caccttaat gaataatttc cgtcaatatt 4080
taccttccct ccctcaatcg gttgaatgtc gccctttgt ctttggcgct ggtaaaccat 4140
atgaattttc tattgattgt gacaaaataa acttattccg tggtgtcttt gcgtttcttt 4200

tatatgttgc cacctttatg tatgtatttt ctacgtttgc taacatactg cgtaataagg 4260
agtcttaagc tagctaacga tcgcccttcc caacagttgc gcagcctgaa tggcgaatgg 4320
gacgcgccct gtagcggcgc attaagcgcg gcgggtgtgg tggttacgcg cagcgtgacc 4380
gctacacttg ccagcgccct agcgcccgct cctttcgctt tcttcccttc ctttctcgcc 4440
acgttcgccg gctttccccg tcaagctcta aatcgggggc tcccttttagg gttccgattt 4500
agtgctttac ggcacctcga ccccaaaaaa cttgattagg gtgatggttc acgtagtggg 4560
ccatcgccct gatagacggt ttttcgccct ttgacgttgg agtccacgtt ctttaatagt 4620
ggactcttgt tccaaactgg aacaacactc aaccctatct cggtctattc ttttgattta 4680
taagggattt tgccgatttc ggcctattgg ttaaaaaatg agctgattta acaaaaattt 4740
aacgcgaatt ttaacaaaat attaacgctt acaatttag 4779

<210> 87
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' LVKappa1/2 Forward Primer

<400> 87
atgaggstcc cygctcagct gctgg 25

<210> 88
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' LVKappa3 Forward Primer

<400> 88
ctcttcctcc tgctactctg gctcccag 28

<210> 89
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' LVKappa4 Forward Primer

<400> 89
atttctctgt tgctctggat ctctg 25

<210> 90
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> VK-rev Reverse Primer

<400> 90
gcactctccc ctgttgaagc tctttg 26

<210> 91
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' L-VH1 Forward Primer

<400> 91
acaggtgccc actcccaggt gcag 24

<210> 92
<211> 23

<212> DNA
<213> Artificial Sequence

<220>
<223> 5' L-VH3 Forward Primer

<400> 92
aaggtgtcca gtgtgargtg cag 23

<210> 93
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' L-VH4/6 Forward Primer

<400> 93
cccagatggg tcctgtccca ggtgcag 27

<210> 94
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' L-VH5 Forward Primer

<400> 94
caaggagtct gttccgaggt gcag 24

<210> 95
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' CgammaCH1 Reverse Primer

<400> 95
ggaaggtgtg cacgccgctg gtc 23

<210> 96
<211> 6
<212> DNA
<213> Artificial Sequence

<220>
<223> SalI restriction site

<400> 96
gtcgac 6

<210> 97
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' SalIJH 1/2/4/5 Forward Primer

<400> 97
tgcgaagtcg acgctgagga gacggtgacc ag 32

<210> 98
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' SalIJH3 Forward Primer

<400> 98
tgcgaagtcg acgctgaaga gacggtgacc attg 34

<210> 99
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' SalIJH6 Forward Primer

<400> 99
tgcgaagtcg acgctgagga gacggtgacc gtg 33

<210> 100
<211> 118
<212> DNA
<213> Artificial Sequence

<220>
<223> Fab Linker

<400> 100
gagcttcaac aggggagagt gctaattaat taataaggag gatataatta tgaaaaagac 60
agctatcgcg attgcagtgg cactggctgg ctttgctacc gtagcgcagg cggccgca 118

<210> 101
<211> 391
<212> DNA
<213> Artificial Sequence

<220>
<223> CH1 fragment

<400> 101
gtcgaccaaa ggtccgtctg ttttcccgct ggctccgtct tctaaatcta cctctggtgg 60
taccgctgct ctgggttgcc tggttaaaga ctacttcccg gaaccggtta ccgtttcttg 120
gaactctggt gctctgacct ctggtgttca caccttcccg gctgttctgc agtcttctgg 180
tctgtactct ctgtcttctg ttgttaccgt tccgtcttct tctctgggta cccagaccta 240
catctgcaac gttaaccaca aaccgtctaa caccaaagtt gacaagaaag ttgaaccgaa 300
atcttgcctg cgatcgcggc caggccggcc gcaccatcac catcaccatg gcgcataccc 360
gtacgacgtt ccggactacg cttctactag t 391

<210> 102
<211> 5432
<212> DNA
<213> pCALM

<400> 102
atgcattagt tattaatagt aatcaattac ggggtcatta gttcatagcc catatatgga 60
gttccgcgtt acataactta cggtaaatgg cccgcctggc tgaccgccca acgacccccg 120
cccattgacg tcaataatga cgtatgttcc catagtaacg ccaataggga ctttccattg 180
acgtcaatgg gtggagtatt tacggtaaac tgcccacttg gcagtacatc aagtgtatca 240
tatgccaagt acgccccccta ttgacgtcaa tgacggtaaa tggcccgcct ggcattatgc 300
ccagtacatg accttatggg actttcctac ttggcagtac atctacgtat tagtcatcgc 360
tattaccatg gtgatgcggt tttggcagta catcaatggg cgtggatagc ggtttgactc 420
acggggattt ccaagtctcc accccattga cgtcaatggg agtttgtttt ggcaccaaaa 480
tcaacgggac tttccaaaat gtcgtaacaa ctccgcccca ttgacgcaaa tgggcggtag 540
gcgtgtacgg tgggaggtct atataagcag agctggttta gtgaaccgtc agatccgcta 600
gcgattacgc caagctcgaa attaaccctc actaaaggga acaaaagctg gagctccacc 660
gcggtggcgg ccgcccacca tggactggac ctggcggatc ctgttcctgg tggccgcggc 720
caccggggcc cacagcaaag ggaaagggaa aggggctagc accaagggcc ccagcgtgtt 780
ccccctggcc cccagcagca agagcaccag cggcggcacc gccgccctgg gctgcctggt 840
gaaggactac ttccccgagc ccgtgaccgt gagctggaac agcggcgccc tgaccagcgg 900

cgtgcacacc ttccccgccg tgctgcagag cagcggcctg tacagcctga gcagcgtggt 960
gaccgtgccc agcagcagcc tgggcaccca gacctacatc tgcaacgtga accacaagcc 1020
cagcaacacc aaggtggaca agaaggtgga gcccaagagc tgcgacaaaa ctcacacatg 1080
cccaccgtgc ccagcacctg aactcctggg gggaccgtca gtcttcctct tccccccaaa 1140
acccaaggac accctcatga tctcccggac ccctgaggtc acatgcgtgg tggtggacgt 1200
gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa 1260
tgccaagaca aagccgcggg aggagcagta caacagcacg taccgggtgg tcagcgtcct 1320
caccgtcctg caccaggact ggctgaatgg caaggagtac aagtgcaagg tctccaacaa 1380
agccctccca gcccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc 1440
acaggtgtac accctgcccc catcccggga tgagctgacc aagaaccagg tcagcctgac 1500
ctgcctggtc aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca 1560
gccggagaac aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttcct 1620
ctacagcaag ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc 1680
cgtgatgcat gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg 1740
taaacgggcc aagcgggcac ccgtgaagca gaccctgaac ttcgacctgc tgaagctggc 1800
cggcgacgtg gagagcaacc ccggccccat gaggctccct gctcagctcc tggggctgct 1860
aatgctctgg gtccctggct cgagtgagaa agggaaaggg aaataaggta ccaggtaagt 1920
gtacccaatt cgccctatag tgagtcgtat tacaattcac tcgatcgccc ttcccaacag 1980
ttgcgcagcc tgaatggcga atggagatcc aatttttaag tgtataatgt gttaaactac 2040
tgattctaat tgtttgtgta ttttagattc acagtcccaa ggctcatttc aggcccctca 2100
gtcctcacag tctgttcatg atcataatca gccataccac atttgtagag gttttacttg 2160
ctttaaaaaa cctcccacac ctccccctga acctgaaaca taaaatgaat gcaattgttg 2220
ttgttaactt gtttattgca gcttataatg gttacaaata aagcaatagc atcacaaatt 2280
tcacaaataa agcatttttt tcactgcatt ctagttgtgg tttgtccaaa ctcatcaatg 2340
tatcttaacg cgtaaattgt aagcgttaat attttgttaa aattcgcgtt aaatttttgt 2400
taaatcagct catttttaa ccaataggcc gaaatcggca aaatccctta taaatcaaaa 2460
gaatagaccg agatagggtt gagtgttgtt ccagtttgga acaagagtcc actattaaag 2520
aacgtggact ccaacgtcaa agggcgaaaa accgtctatc agggcgatgg cccactacgt 2580
gaaccatcac cctaatcaag ttttttgggg tcgaggtgcc gtaaagcact aaatcggaac 2640
cctaaaggga gcccccgatt tagagcttga cggggaaagc cggcgaacgt ggcgagaaag 2700
gaagggaaga aagcgaaagg agcgggcgct agggcgctgg caagtgtagc ggtcacgctg 2760
cgcgtaacca ccacacccgc cgcgcttaat gcgccgctac agggcgcgtc aggtggcact 2820
tttcggggaa atgtgcgcgg aacccctatt tgtttatttt tctaaataca ttcaaatatg 2880
tatccgctca tgagacaata accctgataa atgcttcaat aatattgaaa aaggaagaat 2940
cctgaggcgg aaagaaccag ctgtggaatg tgtgtcagtt agggtgtgga aagtccccag 3000
gctccccagc aggcagaagt atgcaaagca tgcatctcaa ttagtcagca accaggtgtg 3060
gaaagtcccc aggctcccca gcaggcagaa gtatgcaaag catgcatctc aattagtcag 3120
caaccatagt cccgccccta actccgccca tcccgccccc aactccgccc agttccgccc 3180
attctccgcc ccatggctga ctaatttttt ttatttatgc agaggccgag gccgcctcgg 3240
cctctgagct attccagaag tagtgaggag gctttttttgg aggcctaggc ttttgcaaag 3300
atcgatcaag agacaggatg aggatcgttt cgcatgattg aacaagatgg attgcacgca 3360
ggttctccgg ccgcttgggt ggagaggcta ttcggctatg actgggcaca acagacaatc 3420
ggctgctctg atgccgccgt gttccggctg tcagcgcagg ggcgcccggt tctttttgtc 3480
aagaccgacc tgtccggtgc cctgaatgaa ctgcaagacg aggcagcgcg gctatcgtgg 3540
ctggccacga cgggcgttcc ttgcgcagct gtgctcgacg ttgtcactga agcgggaagg 3600
gactggctgc tattgggcga agtgccgggg caggatctcc tgtcatctca ccttgctcct 3660
gccgagaaag tatccatcat ggctgatgca atgcggcggc tgcatacgct tgatccggct 3720
acctgcccat tcgaccacca agcgaaacat cgcatcgagc gagcacgtac tcggatggaa 3780
gccggtcttg tcgatcagga tgatctggac gaagaacatc aggggctcgc gccagccgaa 3840
ctgttcgcca ggctcaaggc gagcatgccc gacggcgagg atctcgtcgt gacccatggc 3900
gatgcctgct tgccgaatat catggtggaa aatggccgct tttctggatt catcgactgt 3960
ggccggctgg gtgtggcgga ccgctatcag gacatagcgt tggctacccg tgatattgct 4020
gaagaacttg gcggcgaatg ggctgaccgc ttcctcgtgc tttacggtat cgccgctccc 4080
gattcgcagc gcatcgcctt ctatcgcctt cttgacgagt tcttctgagc gggactctgg 4140
ggttcgaaat gaccgaccaa gcgacgccca acctgccatc acgagatttc gattccaccg 4200
ccgccttcta tgaaaggttg ggcttcggaa tcgttttccg ggacgccggc tggatgatcc 4260
tccagcgcgg ggatctcatg ctggagttct tcgcccaccc taggggggagg ctaactgaaa 4320
cacggaagga gacaataccg gaaggaaccc gcgctatgac ggcaataaaa agacagaata 4380
aaacgcacgg tgttgggtcg tttgttcata aacgcggggt tcggtcccag ggctggcact 4440
ctgtcgatac cccaccgaga ccccattggg gccaatacgc ccgcgtttct tccttttccc 4500
caccccaccc cccaagttcg ggtgaaggcc cagggctcgc agccaacgtc ggggcggcag 4560
gccctgccat agcctcaggt tactcatata tactttagat tgatttaaaa cttcattttt 4620
aatttaaaag gatctaggtg aagatccttt ttgataatct catgaccaaa atcccttaac 4680
gtgagttttc gttccactga gcgtcagacc ccgtagaaaa gatcaaagga tcttcttgag 4740
atccttttt tctgcgcgta atctgctgct tgcaaacaaa aaaaccaccg ctaccagcgg 4800
tggtttgttt gccggatcaa gagctaccaa ctcttttttcc gaaggtaact ggcttcagca 4860
gagcgcagat accaaatact gtccttctag tgtagccgta gttaggccac cacttcaaga 4920
actctgtagc accgcctaca tacctcgctc tgctaatcct gttaccagtg gctgctgcca 4980

gtggcgataa gtcgtgtctt accgggttgg actcaagacg atagttaccg gataaggcgc 5040
agcggtcggg ctgaacgggg ggttcgtgca cacagcccag cttggagcga acgacctaca 5100
ccgaactgag atacctacag cgtgagctat gagaaagcgc cacgcttccc gaagggagaa 5160
aggcggacag gtatccggta agcggcaggg tcggaacagg agagcgcacg agggagcttc 5220
caggggaaa cgcctggtat ctttatagtc ctgtcgggtt tcgccacctc tgacttgagc 5280
gtcgattttt gtgatgctcg tcaggggggc ggagcctatg gaaaaacgcc agcaacgcgg 5340
ccttttacg gttcctggcc ttttgctggc cttttgctca catgttcttt cctgcgttat 5400
cccctgattc tgtggataac cgtattaccg cc 5432

<210> 103
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Synagis VH chain

<400> 103
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1   5   10   15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
            20   25   30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35   40   45
Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser
    50   55   60
Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65   70   75   80
Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
                85   90   95
Cys Ala Arg Ser Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly Gln
            100   105   110
Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115   120   125
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130   135   140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145   150   155   160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165   170   175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180   185   190
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195   200   205
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
    210   215   220
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225   230   235   240
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245   250   255
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260   265   270
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275   280   285
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290   295   300
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305   310   315   320
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325   330   335
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340   345   350
Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
        355   360   365
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370   375   380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
405 410 415
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445
Gly Lys
450

<210> 104
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synagis VH domain

<400> 104
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1 5 10 15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45
Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser
50 55 60
Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65 70 75 80
Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
85 90 95
Cys Ala Arg Ser Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly Ala
100 105 110
Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 105
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synagis VH CDR1

<400> 105
Thr Ser Gly Met Ser Val Gly
1 5

<210> 106
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synagis VH CDR2

<400> 106
Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

<210> 107
<211> 10
<212> PRT

<213> Artificial Sequence

<220>
<223> Synagis VH CDR3

<400> 107
Ser Met Ile Thr Asn Trp Tyr Phe Asp Val
 1   5   10

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

<220>
<223> Synagis VL chain

<400> 108
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Lys Cys Gln Leu Ser Val Gly Tyr Met
            20   25   30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
        35   40   45
Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50   55   60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65   70   75   80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
                85   90   95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
            100   105   110
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
        115   120   125
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
    130   135   140
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145   150   155   160
Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
                165   170   175
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
            180   185   190
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
        195   200   205
Asn Arg Gly Glu Cys
    210

<210> 109
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Synagis VL domain

<400> 109
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Lys Cys Gln Leu Ser Val Gly Tyr Met
            20   25   30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
        35   40   45
Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50   55   60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65   70   75   80

Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
85 90 95
Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 110
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synagis VL CDR1

<400> 110
Lys Cys Gln Leu Ser Val Gly Tyr Met His
1 5 10

<210> 111
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synagis VL CDR2

<400> 111
Asp Thr Ser Lys Leu Ala Ser
1 5

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

<220>
<223> Synagis VL CDR3

<400> 112
Phe Gln Gly Ser Gly Tyr Pro Phe Thr
1 5

<210> 113
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> AFFF VH CHAIN

<400> 113
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1 5 10 15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
20 25 30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45
Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser
50 55 60
Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65 70 75 80
Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
85 90 95
Cys Ala Arg Ser Met Ile Thr Asn Phe Tyr Phe Asp Val Trp Gly Gln
100 105 110

```
Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
    210                 215                 220
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350
Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
        355                 360                 365
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445
Gly Lys
    450


<210> 114
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> AFFF VH DOMAIN

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

```
            100                 105                 110
Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210> 115
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> AFFF VH CDR1

<400> 115
Thr Ala Gly Met Ser Val Gly
 1               5


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

<220>
<223> AFFF VH CDR3

<400> 116
Ser Met Ile Thr Asn Phe Tyr Phe Asp Val
 1               5                  10


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

<220>
<223> AFFF VL CHAIN

<400> 117
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Gly Tyr Met
            20                  25                  30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
        35                  40                  45
Asp Thr Phe Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50                  55                  60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65                  70                  75                  80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Phe Ser Gly Tyr Pro Phe Thr
                85                  90                  95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
            100                 105                 110
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
        115                 120                 125
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
    130                 135                 140
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145                 150                 155                 160
Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
                165                 170                 175
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
            180                 185                 190
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
        195                 200                 205
Asn Arg Gly Glu Cys
    210
```

<210> 118
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> AFFF VL DOMAIN

<400> 118
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Gly Tyr Met
            20   25   30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
        35   40   45
Asp Thr Phe Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50   55   60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65   70   75   80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Phe Ser Gly Tyr Pro Phe Thr
                85   90   95
Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100   105

<210> 119
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> AFFF VL CDR1

<400> 119
Ser Ala Ser Ser Ser Val Gly Tyr Met His
 1   5   10

<210> 120
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> AFFF VL CDR2

<400> 120
Asp Thr Phe Lys Leu Ala Ser
 1   5

<210> 121
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> AFFF VL CDR3

<400> 121
Phe Gln Phe Ser Gly Tyr Pro Phe Thr
 1   5

<210> 122
<211> 450

<212> PRT
<213> Artificial Sequence

<220>
<223> P1212 VH CHAIN

<400> 122
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1   5   10   15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Pro
            20   25   30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35   40   45
Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys His Tyr Asn Pro Ser
    50   55   60
Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65   70   75   80
Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
                85   90   95
Cys Ala Arg Asp Met Ile Phe Asn Phe Tyr Phe Asp Val Trp Gly Gln
            100   105   110
Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115   120   125
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130   135   140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145   150   155   160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165   170   175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180   185   190
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195   200   205
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
    210   215   220
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225   230   235   240
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245   250   255
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260   265   270
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275   280   285
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290   295   300
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305   310   315   320
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325   330   335
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340   345   350
Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
        355   360   365
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370   375   380
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385   390   395   400
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405   410   415
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420   425   430
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435   440   445
Gly Lys
    450

<210> 123

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

<220>
<223> P1212 VH DOMAIN

<400> 123
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1   5   10   15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Pro
            20   25   30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35   40   45
Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys His Tyr Asn Pro Ser
    50   55   60
Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65   70   75   80
Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
                85   90   95
Cys Ala Arg Asp Met Ile Phe Asn Phe Tyr Phe Asp Val Trp Gly Ala
            100   105   110
Gly Thr Thr Val Thr Val Ser Ser
        115   120

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

<220>
<223> P1212 VH CDR1

<400> 124
Thr Pro Gly Met Ser Val Gly
 1   5

<210> 125
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> P1212 VH CDR2

<400> 125
Asp Ile Trp Trp Asp Asp Lys Lys His Tyr Asn Pro Ser Leu Lys Asp
 1   5   10   15

<210> 126
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> P1212 VH CDR3

<400> 126
Asp Met Ile Phe Asn Phe Tyr Phe Asp Val
 1   5   10

<210> 127
<211> 213
<212> PRT

<213> Artificial Sequence

<220>
<223> P1212 VL CHAIN

<400> 127
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Ser Leu Ser Ser Arg Val Gly Tyr Met
            20   25   30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
        35   40   45
Asp Thr Phe Tyr Leu Ser Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50   55   60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65   70   75   80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
                85   90   95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
            100   105   110
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
        115   120   125
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
    130   135   140
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145   150   155   160
Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
                165   170   175
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
            180   185   190
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
        195   200   205
Asn Arg Gly Glu Cys
    210

<210> 128
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> P1212 VL DOMAIN

<400> 128
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Ser Leu Ser Ser Arg Val Gly Tyr Met
            20   25   30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
        35   40   45
Asp Thr Phe Tyr Leu Ser Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50   55   60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65   70   75   80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
                85   90   95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 129
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> P1212 VL CDR1

<400> 129
Ser Leu Ser Ser Arg Val Gly Tyr Met His
 1   5   10

<210> 130
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> P1212 VL CDR2

<400> 130
Asp Thr Phe Tyr Leu Ser Ser
 1   5

<210> 131
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> P12f4 VH CHAIN

<400> 131
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1   5   10   15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Pro
            20   25   30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35   40   45
Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys His Tyr Asn Pro Ser
    50   55   60
Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65   70   75   80
Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
                85   90   95
Cys Ala Arg Asp Met Ile Phe Asn Phe Tyr Phe Asp Val Trp Gly Gln
            100   105   110
Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115   120   125
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130   135   140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145   150   155   160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165   170   175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180   185   190
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195   200   205
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
    210   215   220
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225   230   235   240
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245   250   255
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260   265   270
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275   280   285
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290   295   300
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305   310   315   320

```
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350
Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
        355                 360                 365
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445
Gly Lys
    450


<210> 132
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> P12f4 VH DOMAIN

<400> 132
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1               5                  10                  15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Pro
            20                  25                  30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35                  40                  45
Trp Leu Ala Asp Ile Trp Trp Asp Gly Lys Lys His Tyr Asn Pro Ser
    50                  55                  60
Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65                  70                  75                  80
Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
                85                  90                  95
Cys Ala Arg Asp Met Ile Phe Asn Phe Tyr Phe Asp Val Trp Gly Gln
            100                 105                 110
Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210> 133
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> P12f4 VH CDR2

<400> 133
Asp Ile Trp Trp Asp Gly Lys Lys His Tyr Asn Pro Ser Leu Lys Asp
 1               5                  10                  15


<210> 134
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> P12f4 VL CHAIN
```

<400> 134
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Ser Leu Ser Ser Arg Val Gly Tyr Met
            20   25   30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
        35   40   45
Asp Thr Arg Gly Leu Pro Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50   55   60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65   70   75   80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
                85   90   95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
            100   105   110
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
        115   120   125
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
    130   135   140
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145   150   155   160
Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
                165   170   175
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
            180   185   190
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
        195   200   205

<210> 135
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> P12f4 VL DOMAIN

<400> 135
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Ser Leu Ser Ser Arg Val Gly Tyr Met
            20   25   30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
        35   40   45
Asp Thr Arg Gly Leu Pro Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50   55   60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65   70   75   80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
                85   90   95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 136
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> P12f4 VL CDR2

<400> 136
Asp Thr Arg Gly Leu Pro Ser
 1   5

<210> 137

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

<220>
<223> P11d4 VH CHAIN

<400> 137
```
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1               5                  10                  15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Pro
            20                  25                  30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35                  40                  45
Trp Leu Ala Asp Ile Trp Trp Asp Gly Lys Lys His Tyr Asn Pro Ser
    50                  55                  60
Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65                  70                  75                  80
Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
                85                  90                  95
Cys Ala Arg Asp Met Ile Phe Asn Trp Tyr Phe Asp Val Trp Gly Gln
            100                 105                 110
Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
    210                 215                 220
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350
Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
        355                 360                 365
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445
Gly Lys
    450
```

<210> 138
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> P11d4 VH DOMAIN

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

<210> 139
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> P11d4 VH CDR3

<400> 139
Asp Met Ile Phe Asn Trp Tyr Phe Asp Val
 1   5   10

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

<220>
<223> P11d4 VL CHAIN

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

```
145                 150                 155                 160
Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
                165                 170                 175
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
            180                 185                 190
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
        195                 200                 205
Asn Arg Gly Glu Cys
    210
```

<210> 141
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> P11d4 VL DOMAIN

<400> 141
```
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Thr Ile Thr Cys Ser Pro Ser Ser Arg Val Gly Tyr Met
            20                  25                  30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
        35                  40                  45
Asp Thr Met Arg Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50                  55                  60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65                  70                  75                  80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
                85                  90                  95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105
```

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

<220>
<223> P11d4 VL CDR1

<400> 142
```
Ser Pro Ser Ser Arg Val Gly Tyr Met His
 1               5                  10
```

<210> 143
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> P11d4 VL CDR2

<400> 143
```
Asp Thr Met Arg Leu Ala Ser
 1               5
```

<210> 144
<211> 450
<212> PRT
<213> Artificial Sequence

<220>

<223> A1e9 VH CHAIN

<400> 144
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1   5   10   15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
            20   25   30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35   40   45
Trp Leu Ala Asp Ile Trp Trp Asp Gly Lys Lys His Tyr Asn Pro Ser
    50   55   60
Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65   70   75   80
Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
                85   90   95
Cys Ala Arg Asp Met Ile Phe Asn Trp Tyr Phe Asp Val Trp Gly Gln
            100   105   110
Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115   120   125
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130   135   140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145   150   155   160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165   170   175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180   185   190
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195   200   205
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
    210   215   220
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225   230   235   240
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245   250   255
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260   265   270
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275   280   285
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290   295   300
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305   310   315   320
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325   330   335
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340   345   350
Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
        355   360   365
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370   375   380
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385   390   395   400
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405   410   415
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420   425   430
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435   440   445
Gly Lys
    450

<210> 145
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> A1e9 VH DOMAIN

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

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

<220>
<223> A1e9 VL CHAIN

<400> 146
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Ser Leu Ser Ser Arg Val Gly Tyr Met
            20   25   30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
        35   40   45
Asp Thr Phe Lys Leu Ser Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50   55   60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65   70   75   80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
                85   90   95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
            100   105   110
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
        115   120   125
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
    130   135   140
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145   150   155   160
Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
                165   170   175
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
            180   185   190
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
        195   200   205
Asn Arg Gly Glu Cys
    210

<210> 147
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> A1e9 VL DOMAIN

<400> 147
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Ser Leu Ser Ser Arg Val Gly Tyr Met
            20   25   30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
        35   40   45
Asp Thr Phe Lys Leu Ser Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50   55   60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65   70   75   80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
                85   90   95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 148
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> A1e9 VL CDR2

<400> 148
Asp Thr Phe Lys Leu Ser Ser
 1   5

<210> 149
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> A12a6 VH CHAIN

<400> 149
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1   5   10   15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
            20   25   30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35   40   45
Trp Leu Ala Asp Ile Trp Trp Asp Gly Lys Lys Asp Tyr Asn Pro Ser
    50   55   60
Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65   70   75   80
Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
                85   90   95
Cys Ala Arg Asp Met Ile Phe Asn Phe Tyr Phe Asp Val Trp Gly Gln
            100   105   110
Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115   120   125
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130   135   140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145   150   155   160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165   170   175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180   185   190
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195   200   205
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
    210   215   220

```
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350
Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
        355                 360                 365
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445
Gly Lys
    450
```

<210> 150
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> A12a6 VH DOMAIN

<400> 150

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

<210> 151
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> A12a6 VH CDR2

<400> 151

```
Asp Ile Trp Trp Asp Gly Lys Lys Asp Tyr Asn Pro Ser Leu Lys Asp
 1               5                  10                  15


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

<220>
<223> A12a6 VL CHAIN

<400> 152
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Arg Val Gly Tyr Met
            20                  25                  30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
        35                  40                  45
Asp Thr Phe Lys Leu Ser Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50                  55                  60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65                  70                  75                  80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
                85                  90                  95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
            100                 105                 110
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
        115                 120                 125
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
    130                 135                 140
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145                 150                 155                 160
Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
                165                 170                 175
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
            180                 185                 190
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
        195                 200                 205
Asn Arg Gly Glu Cys
    210


<210> 153
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> A12a6 VL DOMAIN

<400> 153
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Arg Val Gly Tyr Met
            20                  25                  30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
        35                  40                  45
Asp Thr Phe Lys Leu Ser Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50                  55                  60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65                  70                  75                  80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
                85                  90                  95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105
```

<210> 154
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> A12a6 VL CDR1

<400> 154
Ser Ala Ser Ser Arg Val Gly Tyr Met His
 1   5   10

<210> 155
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> A13c4 VH CHAIN

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

```
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445
Gly Lys
    450


<210> 156
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> A13c4 VH DOMAIN

<400> 156
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1               5                  10                  15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
            20                  25                  30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35                  40                  45
Trp Leu Ala Asp Ile Trp Trp Asp Gly Lys Lys Ser Tyr Asn Pro Ser
    50                  55                  60
Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65                  70                  75                  80
Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
                85                  90                  95
Cys Ala Arg Asp Met Ile Phe Asn Phe Tyr Phe Asp Val Trp Gly Gln
            100                 105                 110
Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210> 157
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> A13c4 VH CDR2

<400> 157
Asp Ile Trp Trp Asp Gly Lys Lys Ser Tyr Asn Pro Ser Leu Lys Asp
 1               5                  10                  15


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

<220>
<223> A13c4 VL CHAIN

<400> 158
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Thr Ile Thr Cys Ser Leu Ser Ser Arg Val Gly Tyr Met
            20                  25                  30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
```

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


<210> 159
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> A13c4 VL DOMAIN

<400> 159
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Thr Ile Thr Cys Ser Leu Ser Ser Arg Val Gly Tyr Met
            20                  25                  30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
        35                  40                  45
Asp Thr Met Tyr Gln Ser Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50                  55                  60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65                  70                  75                  80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
                85                  90                  95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105


<210> 160
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> A13c4 VL CDR2

<400> 160
Asp Thr Met Tyr Gln Ser Ser
 1               5


<210> 161
<211> 450
<212> PRT
<213> Artificial Sequence
```

<220>
<223> A17d4 VH CHAIN

<400> 161
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1   5   10   15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
            20   25   30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35   40   45
Trp Leu Ala Asp Ile Trp Trp Asp Gly Lys Lys Ser Tyr Asn Pro Ser
    50   55   60
Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65   70   75   80
Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
                85   90   95
Cys Ala Arg Asp Met Ile Phe Asn Phe Tyr Phe Asp Val Trp Gly Gln
            100   105   110
Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115   120   125
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130   135   140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145   150   155   160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165   170   175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180   185   190
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195   200   205
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
    210   215   220
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225   230   235   240
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245   250   255
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260   265   270
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275   280   285
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290   295   300
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305   310   315   320
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325   330   335
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340   345   350
Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
        355   360   365
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370   375   380
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385   390   395   400
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405   410   415
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420   425   430
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435   440   445
Gly Lys
    450

<210> 162
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> A17d4 VH DOMAIN

<400> 162
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1   5   10   15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
            20   25   30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35   40   45
Trp Leu Ala Asp Ile Trp Trp Asp Gly Lys Lys Ser Tyr Asn Pro Ser
    50   55   60
Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65   70   75   80
Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
                85   90   95
Cys Ala Arg Asp Met Ile Phe Asn Phe Tyr Phe Asp Val Trp Gly Gln
            100   105   110
Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 163
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> A17d4 VH CDR2

<400> 163
Asp Ile Trp Trp Asp Asp Lys Lys Ser Tyr Asn Pro Ser Leu Lys Asp
 1   5   10   15

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

<220>
<223> A17d4 VL CHAIN

<400> 164
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Leu Pro Ser Ser Arg Val Gly Tyr Met
            20   25   30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
        35   40   45
Asp Thr Met Tyr Gln Ser Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50   55   60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65   70   75   80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
                85   90   95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
            100   105   110
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
        115   120   125
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
    130   135   140
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145   150   155   160
Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
                165   170   175
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala

```
            180                 185                 190
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
        195                 200                 205
Asn Arg Gly Glu Cys
    210


<210> 165
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> A17d4 VL DOMAIN

<400> 165
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Thr Ile Thr Cys Leu Pro Ser Ser Arg Val Gly Tyr Met
            20                  25                  30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
        35                  40                  45
Asp Thr Met Tyr Gln Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50                  55                  60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65                  70                  75                  80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Phe Ser Gly Tyr Pro Phe Thr
                85                  90                  95
Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105


<210> 166
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> A17d4 VL CDR1

<400> 166
Leu Pro Ser Ser Arg Val Gly Tyr Met His
 1               5                  10


<210> 167
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> A4B4 VH CHAIN

<400> 167
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1               5                  10                  15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
            20                  25                  30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35                  40                  45
Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys His Tyr Asn Pro Ser
    50                  55                  60
Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65                  70                  75                  80
Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
                85                  90                  95
Cys Ala Arg Asp Met Ile Phe Asn Phe Tyr Phe Asp Val Trp Gly Gln
            100                 105                 110
```

```
Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
    210                 215                 220
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350
Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
        355                 360                 365
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445
Gly Lys
    450


<210> 168
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> A4B4 VH DOMAIN

<400> 168
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1               5                  10                  15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
            20                  25                  30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35                  40                  45
Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys His Tyr Asn Pro Ser
    50                  55                  60
Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65                  70                  75                  80
Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
                85                  90                  95
Cys Ala Arg Asp Met Ile Phe Asn Phe Tyr Phe Asp Val Trp Gly Gln
```

```
            100                 105                 110
Gly Thr Thr Val Thr Val Ser Ser
        115                 120


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

<220>
<223> A4B4 VL CHAIN

<400> 169
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Arg Val Gly Tyr Met
            20                  25                  30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
        35                  40                  45
Asp Thr Phe Phe Leu Asp Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50                  55                  60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65                  70                  75                  80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
                85                  90                  95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
            100                 105                 110
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
        115                 120                 125
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
    130                 135                 140
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145                 150                 155                 160
Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
                165                 170                 175
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
            180                 185                 190
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
        195                 200                 205
Asn Arg Gly Glu Cys
    210


<210> 170
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> A4B4 VL DOMAIN

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

<210> 171
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> A4B4 VL CDR2

<400> 171
Asp Thr Phe Phe Leu Asp Ser
 1   5

<210> 172
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> A8c7 VH CHAIN

<400> 172
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1   5   10   15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
            20   25   30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35   40   45
Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Ser Tyr Asn Pro Ser
    50   55   60
Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65   70   75   80
Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
                85   90   95
Cys Ala Arg Asp Met Ile Phe Asn Trp Tyr Phe Asp Val Trp Gly Gln
            100   105   110
Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115   120   125
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130   135   140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145   150   155   160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165   170   175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180   185   190
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195   200   205
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
    210   215   220
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225   230   235   240
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245   250   255
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260   265   270
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275   280   285
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290   295   300
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305   310   315   320
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325   330   335
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340   345   350
Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu

```
        355                 360                 365
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445
Gly Lys
    450


<210> 173
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> A8c7 VH DOMAIN

<400> 173
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1               5                  10                  15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
            20                  25                  30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35                  40                  45
Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Ser Tyr Asn Pro Ser
    50                  55                  60
Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65                  70                  75                  80
Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
                85                  90                  95
Cys Ala Arg Asp Met Ile Phe Asn Trp Tyr Phe Asp Val Trp Gly Gln
            100                 105                 110
Gly Thr Thr Val Thr Val Ser Ser
        115                 120


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

<220>
<223> A8c7 VL CHAIN

<400> 174
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Thr Ile Thr Cys Ser Pro Ser Ser Arg Val Gly Tyr Met
            20                  25                  30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
        35                  40                  45
Asp Thr Arg Tyr Gln Ser Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50                  55                  60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65                  70                  75                  80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
                85                  90                  95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
            100                 105                 110
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
        115                 120                 125
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
```

```
    130                 135                 140
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145                 150                 155                 160
Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
                165                 170                 175
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
            180                 185                 190
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
        195                 200                 205
Asn Arg Gly Glu Cys
    210


<210> 175
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> A8c7 VL DOMAIN

<400> 175
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1                  5                  10                  15
Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Arg Val Gly Tyr Met
            20                  25                  30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
        35                  40                  45
Asp Thr Arg Tyr Gln Ser Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50                  55                  60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65                  70                  75                  80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
                85                  90                  95
Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105


<210> 176
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> IX-493L1FR VH CHAIN

<400> 176
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1                  5                  10                  15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
            20                  25                  30
Gly Met Ser Val Gly Tyr Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu
        35                  40                  45
Glu Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro
    50                  55                  60
Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln
65                  70                  75                  80
Val Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr
                85                  90                  95
Tyr Cys Ala Arg Ser Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly
            100                 105                 110
Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
        115                 120                 125
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
    130                 135                 140
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
```

```
                165                 170                 175
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
    210                 215                 220
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225                 230                 235                 240
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
                325                 330                 335
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
        355                 360                 365
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                405                 410                 415
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445
Pro Gly Lys
    450
```

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

<220>
<223> IX-493L1FR VL CHAIN

<400> 177

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

```
Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
                165                 170                 175
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
            180                 185                 190
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
        195                 200                 205
Asn Arg Gly Glu Cys
    210
```

<210> 178
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> IX-493L1FR VL DOMAIN

<400> 178

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

<210> 179
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> M3H9 VH CHAIN

<400> 179

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

```
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
    210                 215                 220
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350
Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
        355                 360                 365
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445
Gly Lys
    450


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

<220>
<223> M3H9 VL CHAIN

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

```
            180                 185                 190
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
        195                 200                 205
Asn Arg Gly Glu Cys
    210


<210> 181
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> M3H9 VL DOMAIN

<400> 181
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Gly Tyr Met
            20                  25                  30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
        35                  40                  45
Asp Thr Tyr Lys Gln Thr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50                  55                  60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65                  70                  75                  80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
                85                  90                  95
Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105


<210> 182
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Y10H6 VH CHAIN

<400> 182
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1               5                  10                  15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
            20                  25                  30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35                  40                  45
Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser
    50                  55                  60
Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65                  70                  75                  80
Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
                85                  90                  95
Cys Ala Arg Asp Met Ile Phe Asn Trp Tyr Phe Asp Val Trp Gly Gln
            100                 105                 110
Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
```

```
    210                 215                 220
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350
Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
        355                 360                 365
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445
Gly Lys
    450


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

<220>
<223> Y10H6 VL CHAIN

<400> 183
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1                5                  10                  15
Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Gly Tyr Met
            20                  25                  30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
        35                  40                  45
Asp Thr Arg Tyr Leu Ser Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50                  55                  60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65                  70                  75                  80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
                85                  90                  95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
            100                 105                 110
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
        115                 120                 125
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
    130                 135                 140
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145                 150                 155                 160
Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
                165                 170                 175
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
            180                 185                 190
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
        195                 200                 205
```

Asn Arg Gly Glu Cys
    210

<210> 184
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Y10H6 VL DOMAIN

<400> 184
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Gly Tyr Met
            20   25   30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
        35   40   45
Asp Thr Arg Tyr Leu Ser Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50   55   60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65   70   75   80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
                85   90   95
Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100   105

<210> 185
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Y10H6 VL CDR2

<400> 185
Asp Thr Arg Tyr Leu Ser Ser
 1   5

<210> 186
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> DG VH CHAIN

<400> 186
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1   5   10   15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
            20   25   30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35   40   45
Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser
    50   55   60
Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65   70   75   80
Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
                85   90   95
Cys Ala Arg Asp Met Ile Thr Asn Phe Tyr Phe Asp Val Trp Gly Gln
            100   105   110
Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115   120   125
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala

```
    130                 135                 140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
    210                 215                 220
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350
Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
        355                 360                 365
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445
Gly Lys
    450


<210> 187
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> DG VH DOMAIN

<400> 187
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1                5                  10                  15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
            20                  25                  30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35                  40                  45
Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser
    50                  55                  60
Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65                  70                  75                  80
Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
                85                  90                  95
Cys Ala Arg Asp Met Ile Thr Asn Phe Tyr Phe Asp Val Trp Gly Ala
            100                 105                 110
Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 188
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> DG VH CDR3

<400> 188
Asp Met Ile Thr Asn Phe Tyr Phe Asp Val
 1   5   10

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

<220>
<223> DG VL CHAIN

<400> 189
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Gly Tyr Met
            20   25   30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
        35   40   45
Asp Thr Phe Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50   55   60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65   70   75   80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
                85   90   95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
            100   105   110
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
        115   120   125
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
    130   135   140
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145   150   155   160
Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
                165   170   175
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
            180   185   190
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
        195   200   205
Asn Arg Gly Glu Cys
    210

<210> 190
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> AFFF(1) VH CHAIN

<400> 190
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1   5   10   15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
            20   25   30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu

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


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

<220>
<223> AFFF(1) VL CHAIN

<400> 191
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Gly Tyr Met
            20                  25                  30
```

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

<210> 192
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> AFFF(1) VL DOMAIN

<400> 192

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

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

<220>
<223> AFFF(1) VL CDR3

<400> 193

```
Phe Gln Gly Ser Phe Tyr Pro Phe Thr
 1               5
```

<210> 194
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> 6H8 VH CHAIN

<400> 194
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1   5   10   15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
            20   25   30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35   40   45
Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser
    50   55   60
Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65   70   75   80
Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
                85   90   95
Cys Ala Arg Asp Met Ile Thr Asn Phe Tyr Phe Asp Val Trp Gly Gln
            100   105   110
Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115   120   125
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130   135   140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145   150   155   160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165   170   175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180   185   190
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195   200   205
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
    210   215   220
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225   230   235   240
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245   250   255
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260   265   270
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275   280   285
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290   295   300
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305   310   315   320
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325   330   335
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340   345   350
Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
        355   360   365
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370   375   380
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385   390   395   400
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405   410   415
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420   425   430
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435   440   445
Gly Lys
    450

<210> 195
<211> 213
<212> PRT

<213> Artificial Sequence

<220>
<223> 6H8 VL CHAIN

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

<210> 196
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> 6H8 VL DOMAIN

<400> 196
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Gly Tyr Met
            20   25   30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
        35   40   45
Asp Thr Phe Lys Leu Thr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50   55   60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65   70   75   80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
                85   90   95
Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100   105

<210> 197
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 6H8 VL CDR2

<400> 197
Asp Thr Phe Lys Leu Thr Ser
 1   5

<210> 198
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> L1-7E5 VH CHAIN

<400> 198
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1   5   10   15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
            20   25   30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35   40   45
Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser
    50   55   60
Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65   70   75   80
Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
                85   90   95
Cys Ala Arg Asp Met Ile Thr Asn Phe Tyr Phe Asp Val Trp Gly Gln
            100   105   110
Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115   120   125
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130   135   140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145   150   155   160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165   170   175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180   185   190
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195   200   205
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
    210   215   220
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225   230   235   240
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245   250   255
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260   265   270
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275   280   285
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290   295   300
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305   310   315   320
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325   330   335
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340   345   350
Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
        355   360   365
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370   375   380
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385   390   395   400
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405   410   415
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His

```
            420                 425                 430
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445
Gly Lys
    450


<210> 199
<211> 213
<212> PRT
<213> Artificial Sequence

<220>
<223> L1-7E5 VL CHAIN

<400> 199
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Arg Val Gly Tyr Met
            20                  25                  30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
        35                  40                  45
Asp Thr Phe Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50                  55                  60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65                  70                  75                  80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
                85                  90                  95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
            100                 105                 110
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
        115                 120                 125
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
    130                 135                 140
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145                 150                 155                 160
Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
                165                 170                 175
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
            180                 185                 190
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
        195                 200                 205
Asn Arg Gly Glu Cys
    210


<210> 200
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> L1-7E5 VL DOMAIN

<400> 200
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Gly Tyr Met
            20                  25                  30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
        35                  40                  45
Asp Thr Phe Arg Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50                  55                  60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65                  70                  75                  80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
                85                  90                  95
Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
```

100 105

<210> 201
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> L2-15B10 VH CHAIN

<400> 201
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1 5 10 15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
20 25 30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45
Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser
50 55 60
Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65 70 75 80
Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
85 90 95
Cys Ala Arg Asp Met Ile Thr Asn Phe Tyr Phe Asp Val Trp Gly Gln
100 105 110
Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195 200 205
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
210 215 220
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225 230 235 240
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
245 250 255
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
260 265 270
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
275 280 285
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
290 295 300
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
325 330 335
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
340 345 350
Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
355 360 365
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
405 410 415
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gly Lys
    450

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

<220>
<223> L2-15B10 VL CHAIN

<400> 202
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Gly Tyr Met
            20   25   30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
        35   40   45
Asp Thr Phe Arg Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50   55   60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65   70   75   80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
                85   90   95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
            100   105   110
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
        115   120   125
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
    130   135   140
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145   150   155   160
Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
                165   170   175
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
            180   185   190
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
        195   200   205
Asn Arg Gly Glu Cys
    210

<210> 203
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> L2-15B10 VL DOMAIN

<400> 203
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Gly Tyr Met
            20   25   30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
        35   40   45
Asp Thr Phe Arg Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50   55   60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65   70   75   80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
                85   90   95
Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100   105

<210> 204
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> L2-15B10 VL CDR2

<400> 204
Asp Thr Phe Arg Leu Ala Ser
 1   5

<210> 205
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> A13a11 VH CHAIN

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

```
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445
Gly Lys
    450


<210> 206
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> A13a11 VH DOMAIN

<400> 206
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1                5                  10                  15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
            20                  25                  30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35                  40                  45
Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys His Tyr Asn Pro Ser
    50                  55                  60
Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65                  70                  75                  80
Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
                85                  90                  95
Cys Ala Arg Asp Met Ile Phe Asn Trp Tyr Phe Asp Val Trp Gly Ala
            100                 105                 110
Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210> 207
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> A13a11 VL CHAIN

<400> 207
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1                5                  10                  15
Asp Arg Val Thr Ile Thr Cys Ser Pro Ser Ser Arg Val Gly Tyr Met
            20                  25                  30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
        35                  40                  45
Asp Thr Tyr Arg His Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
Asp Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe
                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> 208
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> A13a11 VL DOMAIN

<400> 208
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Gly Tyr Met
            20                  25                  30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
        35                  40                  45
Asp Thr Tyr Arg His Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50                  55                  60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65                  70                  75                  80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
                85                  90                  95
Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105


<210> 209
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> A13a11 VL CDR2

<400> 209
Asp Thr Tyr Arg His Ser Ser
 1               5


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

<220>
<223> A1h5 VH CHAIN

<400> 210
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1               5                  10                  15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
            20                  25                  30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35                  40                  45
Trp Leu Ala Asp Ile Trp Trp Asp Gly Lys Lys His Tyr Asn Pro Ser
    50                  55                  60
Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
```

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

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

<220>
<223> A1h5 VL CHAIN

<400> 211
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Ser Leu Ser Ser Ser Val Gly Tyr Met
20 25 30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
35 40 45
Asp Thr Phe Phe His Arg Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
50 55 60

```
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65                  70                  75                  80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
                85                  90                  95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
            100                 105                 110
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
        115                 120                 125
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
    130                 135                 140
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145                 150                 155                 160
Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
                165                 170                 175
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
            180                 185                 190
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
        195                 200                 205
Asn Arg Gly Glu Cys
    210


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

<220>
<223> A1h5 VL DOMAIN

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


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

<220>
<223> A1h5 VL CDR1

<400> 213
Ser Leu Ser Ser Ser Val Gly Tyr Met His
 1               5                  10


<210> 214
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> A1h5 VL CDR2
```

<400> 214
Asp Thr Phe Phe His Arg Ser
 1   5

<210> 215
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> A4B4(1) VH CHAIN

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

```
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445
Gly Lys
    450


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

<220>
<223> A4B4(1) VL CHAIN

<400> 216
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Arg Val Gly Tyr Met
            20                  25                  30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
        35                  40                  45
Asp Thr Leu Leu Leu Asp Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50                  55                  60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65                  70                  75                  80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
                85                  90                  95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
            100                 105                 110
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
        115                 120                 125
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
    130                 135                 140
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145                 150                 155                 160
Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
                165                 170                 175
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
            180                 185                 190
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
        195                 200                 205
Asn Arg Gly Glu Cys
    210


<210> 217
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> A4B4(1) VL DOMAIN

<400> 217
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Arg Val Gly Tyr Met
            20                  25                  30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
        35                  40                  45
Asp Thr Leu Leu Leu Asp Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50                  55                  60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65                  70                  75                  80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
                85                  90                  95
Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105
```

<210> 218
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> A4B4(1) VL CDR2

<400> 218
Asp Thr Leu Leu Leu Asp Ser
 1   5

<210> 219
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> A4B4L1 VH CHAIN

<400> 219
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1   5   10   15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
            20   25   30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35   40   45
Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys His Tyr Asn Pro Ser
    50   55   60
Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65   70   75   80
Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
                85   90   95
Cys Ala Arg Asp Met Ile Phe Asn Phe Tyr Phe Asp Val Trp Gly Gln
            100   105   110
Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115   120   125
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130   135   140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145   150   155   160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165   170   175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180   185   190
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195   200   205
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
    210   215   220
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225   230   235   240
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245   250   255
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260   265   270
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275   280   285
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290   295   300
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305   310   315   320
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325   330   335
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340   345   350

```
Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
        355                 360                 365
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445
Gly Lys
    450


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

<220>
<223> A4B4L1 VL CHAIN

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


<210> 221
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> A4B4L1 VL DOMAIN

<400> 221
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Arg Val Gly Tyr Met
            20                  25                  30
```

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


<210> 222
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> A4B4-F25S VH CHAIN

<400> 222
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1               5                  10                  15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
            20                  25                  30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35                  40                  45
Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys His Tyr Asn Pro Ser
    50                  55                  60
Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65                  70                  75                  80
Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
                85                  90                  95
Cys Ala Arg Asp Met Ile Phe Asn Phe Tyr Phe Asp Val Trp Gly Gln
            100                 105                 110
Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
    210                 215                 220
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350
Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
        355                 360                 365
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
```

370 375 380
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
405 410 415
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445
Gly Lys
450

<210> 223
<211> 213
<212> PRT
<213> Artificial Sequence

<220>
<223> A4B4-F25S VL CHAIN

<400> 223
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Arg Val Gly Tyr Met
20 25 30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
35 40 45
Asp Thr Ser Phe Leu Asp Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
50 55 60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65 70 75 80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
85 90 95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
100 105 110
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
115 120 125
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160
Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205
Asn Arg Gly Glu Cys
210

<210> 224
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> A4B4-F25S VL DOMAIN

<400> 224
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Arg Val Gly Tyr Met
20 25 30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
35 40 45
Asp Thr Ser Phe Leu Asp Ser Gly Val Pro Ser Arg Phe Ser Gly Ser

```
    50                  55                  60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65                  70                  75                  80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
                85                  90                  95
Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105


<210> 225
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> A4B4-F25S VL CDR2

<400> 225
Asp Thr Ser Phe Leu Asp Ser
 1               5


<210> 226
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> H3-3F4 VH CHAIN

<400> 226
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1               5                  10                  15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
            20                  25                  30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35                  40                  45
Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser
    50                  55                  60
Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65                  70                  75                  80
Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
                85                  90                  95
Cys Ala Arg Asp Met Ile Phe Asn Trp Tyr Phe Asp Val Trp Gly Gln
            100                 105                 110
Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
    210                 215                 220
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
```

```
    290                 295                 300
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350
Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
        355                 360                 365
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445
Gly Lys
    450


<210> 227
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> H3-3F4 VH DOMAIN

<400> 227
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1               5                  10                  15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
            20                  25                  30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35                  40                  45
Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser
    50                  55                  60
Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65                  70                  75                  80
Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
                85                  90                  95
Cys Ala Arg Asp Met Ile Phe Asn Trp Tyr Phe Asp Val Trp Gly Ala
            100                 105                 110
Gly Thr Thr Val Thr Val Ser Ser
        115                 120


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

<220>
<223> H3-3F4 VL CHAIN

<400> 228
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Gly Tyr Met
            20                  25                  30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
        35                  40                  45
Asp Thr Phe Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50                  55                  60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
```

65 70 75 80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
85 90 95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
100 105 110
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
115 120 125
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160
Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205
Asn Arg Gly Glu Cys
210

<210> 229
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> H3-3F4 VL DOMAIN

<400> 229
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Gly Tyr Met
20 25 30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
35 40 45
Asp Thr Phe Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
50 55 60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65 70 75 80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
85 90 95
Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 230
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> VL CDR2

<400> 230
Asp Thr Arg Tyr Gln Ser Ser
1 5

<210> 231
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> M3H9 VL CDR2

<400> 231

Asp Thr Tyr Lys Gln Thr Ser
 1   5

<210> 232
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> IX-493L1FR VH domain

<400> 232
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1   5   10   15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
            20   25   30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35   40   45
Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser
    50   55   60
Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65   70   75   80
Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
                85   90   95
Cys Ala Arg Ser Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly Gln
            100   105   110
Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 233
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> A3e2 VH chain

<400> 233
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1   5   10   15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
            20   25   30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35   40   45
Trp Leu Ala Asp Ile Trp Trp Gly Asp Lys Gly His Tyr Asn Pro Ser
    50   55   60
Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65   70   75   80
Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
                85   90   95
Cys Ala Arg Asp Met Ile Phe Asn Trp Tyr Phe Asp Val Trp Gly Gln
            100   105   110
Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115   120   125
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130   135   140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145   150   155   160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165   170   175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180   185   190
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195   200   205
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
    210   215   220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225 230 235 240
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
245 250 255
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
260 265 270
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
275 280 285
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
290 295 300
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
325 330 335
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
340 345 350
Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
355 360 365
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
405 410 415
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445
Gly Lys
450

<210> 234
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> A3e2 VH domain

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

<210> 235
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> A3e2 VH CDR2

<400> 235

```
Asp Ile Trp Trp Gly Asp Lys Gly His Tyr Asn Pro Ser Leu Lys Asp
 1               5                  10                  15


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

<220>
<223> A3e2 VL chain

<400> 236
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Gly Tyr Met
            20                  25                  30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
        35                  40                  45
Asp Thr Phe Tyr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50                  55                  60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65                  70                  75                  80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
                85                  90                  95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
            100                 105                 110
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
        115                 120                 125
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
    130                 135                 140
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145                 150                 155                 160
Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
                165                 170                 175
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
            180                 185                 190
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
        195                 200                 205
Asn Arg Gly Glu Cys
    210


<210> 237
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> A3e2 VL domain

<400> 237
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Gly Tyr Met
            20                  25                  30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
        35                  40                  45
Asp Thr Phe Tyr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50                  55                  60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65                  70                  75                  80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
                85                  90                  95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105
```

<210> 238
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> A3e2 VL CDR2

<400> 238
Asp Thr Phe Tyr Leu His Ser
 1   5

<210> 239
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> A14a4 VH chain

<400> 239
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1   5   10   15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
            20   25   30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35   40   45
Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Ser Tyr Asn Pro Ser
    50   55   60
Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65   70   75   80
Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
                85   90   95
Cys Ala Arg Asp Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly Gln
            100   105   110
Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115   120   125
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130   135   140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145   150   155   160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165   170   175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180   185   190
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195   200   205
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
    210   215   220
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225   230   235   240
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245   250   255
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260   265   270
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275   280   285
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290   295   300
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305   310   315   320
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325   330   335
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340   345   350
Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
        355   360   365

```
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445
Gly Lys
    450


<210> 240
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> A14a4 VH domain

<400> 240
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1               5                  10                  15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
            20                  25                  30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35                  40                  45
Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Ser Tyr Asn Pro Ser
    50                  55                  60
Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65                  70                  75                  80
Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
                85                  90                  95
Cys Ala Arg Asp Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly Gln
            100                 105                 110
Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210> 241
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> A14a4 VH CDR3

<400> 241
Asp Met Ile Thr Asn Trp Tyr Phe Asp Val
 1               5                  10


<210> 242
<211> 197
<212> PRT
<213> Artificial Sequence

<220>
<223> A14a4 VL chain

<400> 242
Asp Arg Val Thr Ile Thr Cys Leu Leu Ser Ser Arg Val Gly Tyr Met
 1               5                  10                  15
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
            20                  25                  30
Asp Thr Tyr Tyr Gln Thr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
```

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


<210> 243
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> A14a4 VL domain

<400> 243
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1                  5                  10                  15
Asp Arg Val Thr Ile Thr Cys Leu Leu Ser Ser Arg Val Gly Tyr Met
            20                  25                  30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
        35                  40                  45
Asp Thr Tyr Tyr Gln Thr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50                  55                  60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65                  70                  75                  80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
                85                  90                  95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105


<210> 244
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> A14a4 VL CDR1

<400> 244
Leu Leu Ser Ser Arg Val Gly Tyr Met His
 1               5                  10


<210> 245
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> A14a4 VL CDR2
```

<400> 245
Asp Thr Tyr Tyr Gln Thr Ser
 1   5

<210> 246
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> A16b4 VH chain

<400> 246
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1   5   10   15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
            20   25   30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35   40   45
Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys His Tyr Asn Pro Ser
    50   55   60
Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65   70   75   80
Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
                85   90   95
Cys Ala Arg Asp Met Ile Phe Asn Trp Tyr Phe Asp Val Trp Gly Gln
            100   105   110
Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115   120   125
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130   135   140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145   150   155   160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165   170   175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180   185   190
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195   200   205
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
    210   215   220
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225   230   235   240
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245   250   255
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260   265   270
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275   280   285
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290   295   300
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305   310   315   320
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325   330   335
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340   345   350
Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
        355   360   365
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370   375   380
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385   390   395   400
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405   410   415
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His

```
            420                 425                 430
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445
Gly Lys
    450


<210> 247
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> A16b4 VH domain

<400> 247
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1               5                  10                  15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
            20                  25                  30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35                  40                  45
Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys His Tyr Asn Pro Ser
    50                  55                  60
Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65                  70                  75                  80
Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
                85                  90                  95
Cys Ala Arg Asp Met Ile Phe Asn Trp Tyr Phe Asp Val Trp Gly Gln
            100                 105                 110
Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210> 248
<211> 197
<212> PRT
<213> Artificial Sequence

<220>
<223> A16b4 VL chain

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

195

<210> 249
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> A16b4 VL domain

<400> 249
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Leu Leu Ser Ser Arg Val Gly Tyr Met
            20   25   30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
        35   40   45
Asp Thr Met Tyr Gln Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50   55   60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65   70   75   80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
                85   90   95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 250
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> A16b4 VL CDR1

<400> 250
Leu Leu Ser Ser Arg Val Gly Tyr Met His
 1   5   10

<210> 251
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> A16b4 VL CDR2

<400> 251
Asp Thr Met Tyr Gln Ala Ser
 1   5

<210> 252
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> A17b5 VH chain

<400> 252
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1   5   10   15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
            20   25   30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu

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


<210> 253
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> A17b5 VH domain

<400> 253
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1               5                  10                  15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
            20                  25                  30
```

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


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

<220>
<223> A17b5 VL chain

<400> 254
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1                  5                  10                  15
Asp Arg Val Thr Ile Thr Cys Ser Leu Ser Ser Arg Val Gly Tyr Met
            20                  25                  30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
        35                  40                  45
Asp Thr Tyr Tyr Leu Pro Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50                  55                  60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65                  70                  75                  80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
                85                  90                  95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
            100                 105                 110
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
        115                 120                 125
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
    130                 135                 140
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145                 150                 155                 160
Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
                165                 170                 175
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
            180                 185                 190
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
        195                 200                 205
Asn Arg Gly Glu Cys
    210


<210> 255
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> A17b5 VL domain

<400> 255
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1                  5                  10                  15
Asp Arg Val Thr Ile Thr Cys Ser Leu Ser Ser Arg Val Gly Tyr Met
            20                  25                  30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
        35                  40                  45
```

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


<210> 256
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> A17b5 VLCDR2

<400> 256
Asp Thr Tyr Tyr Leu Pro Ser
 1               5


<210> 257
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> A17f5 VH chain

<400> 257
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1               5                  10                  15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
            20                  25                  30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35                  40                  45
Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser
    50                  55                  60
Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65                  70                  75                  80
Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
                85                  90                  95
Cys Ala Arg Asp Met Ile Phe Asn Trp Tyr Phe Asp Val Trp Gly Gln
            100                 105                 110
Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
    210                 215                 220
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285
```

```
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350
Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
        355                 360                 365
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445
Gly Lys
    450
```

<210> 258
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> A17f5 VH domain

<400> 258
```
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1               5                  10                  15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
            20                  25                  30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35                  40                  45
Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser
    50                  55                  60
Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65                  70                  75                  80
Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
                85                  90                  95
Cys Ala Arg Asp Met Ile Phe Asn Trp Tyr Phe Asp Val Trp Gly Gln
            100                 105                 110
Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 259
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> A17f5 VH CDR2

<400> 259
```
Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser Leu Lys Asp
 1               5                  10                  15
```

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

<220>
<223> A17f5 VL chain

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

<210> 261
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> A17f5 VL domain

<400> 261
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Ser Leu Ser Ser Arg Val Gly Tyr Met
            20   25   30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
        35   40   45
Asp Thr Phe Arg His Thr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50   55   60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65   70   75   80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
                85   90   95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 262
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> A17f5 VL CDR2

<400> 262
Asp Thr Phe Arg His Thr Ser
 1   5

<210> 263
<211> 213
<212> PRT
<213> Artificial Sequence

<220>
<223> A17h4 VL chain

<400> 263
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Ser Pro Ser Ser Ser Val Gly Tyr Met
            20   25   30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
        35   40   45
Asp Thr Tyr Tyr Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50   55   60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65   70   75   80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
                85   90   95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
            100   105   110
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
        115   120   125
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
    130   135   140
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145   150   155   160
Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
                165   170   175
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
            180   185   190
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
        195   200   205
Asn Arg Gly Glu Cys
    210

<210> 264
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> A17h4 VL domain

<400> 264
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Ser Pro Ser Ser Ser Val Gly Tyr Met
            20   25   30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
        35   40   45
Asp Thr Tyr Tyr Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50   55   60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65   70   75   80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
                85   90   95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 265
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> A17h4 VL CDR1

<400> 265
Ser Pro Ser Ser Ser Val Gly Tyr Met His
 1   5   10

<210> 266
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> A17h4 VL CDR2

<400> 266
Asp Thr Tyr Tyr Leu Ala Ser
 1   5

<210> 267
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 267
Gly Gly Ser Ser Arg Ser Ser Ser Ser Gly Gly Gly Gly Ser Gly Gly
 1   5   10   15
Gly Gly

<210> 268
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 268
Gly Ser Gly Arg Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1   5   10   15

<210> 269
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 269
Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr
 1   5   10

<210> 270
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 270
Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr Gln
 1   5   10   15

<210> 271
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 271
Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Val Asp
 1   5   10

<210> 272
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 272
Gly Ser Thr Ser Gly Ser Gly Lys Ser Ser Glu Gly Lys Gly
 1   5   10

<210> 273
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 273
Lys Glu Ser Gly Ser Val Ser Ser Glu Gln Leu Ala Gln Phe Arg Ser
 1   5   10   15
Leu Asp

<210> 274
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 274
Glu Ser Gly Ser Val Ser Ser Glu Glu Leu Ala Phe Arg Ser Leu Asp
 1   5   10   15

<210> 275

<211> 298
<212> PRT
<213> Human respiratory syncytial virus

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

<210> 276
<211> 2165
<212> PRT
<213> Human respiratory syncytial virus

<400> 276
Met Asp Pro Ile Ile Asn Gly Asn Ser Ala Asn Val Tyr Leu Thr Asp
 1   5   10   15
Ser Tyr Leu Lys Gly Val Ile Ser Phe Ser Glu Cys Asn Ala Leu Gly
            20   25   30
Ser Tyr Ile Phe Asn Gly Pro Tyr Leu Lys Asn Asp Tyr Thr Asn Leu
        35   40   45
Ile Ser Arg Gln Asn Pro Leu Ile Glu His Met Asn Leu Lys Lys Leu
    50   55   60
Asn Ile Thr Gln Ser Leu Ile Ser Lys Tyr His Lys Gly Glu Ile Lys
65   70   75   80
Leu Glu Glu Pro Thr Tyr Phe Gln Ser Leu Leu Met Thr Tyr Lys Ser
                85   90   95
Met Thr Ser Ser Glu Gln Ile Ala Thr Thr Asn Leu Leu Lys Lys Ile
            100   105   110
Ile Arg Arg Ala Ile Glu Ile Ser Asp Val Lys Val Tyr Ala Ile Leu
        115   120   125
Asn Lys Leu Gly Leu Lys Glu Lys Asp Lys Ile Lys Ser Asn Asn Gly

```
    130                 135                 140
Gln Asp Glu Asp Asn Ser Val Ile Thr Thr Ile Ile Lys Asp Asp Ile
145                 150                 155                 160
Leu Ser Ala Val Lys Asp Asn Gln Ser His Leu Lys Ala Asp Lys Asn
                165                 170                 175
His Ser Thr Lys Gln Lys Asp Thr Ile Lys Thr Thr Leu Leu Lys Lys
            180                 185                 190
Leu Met Cys Ser Met Gln His Pro Pro Ser Trp Leu Ile His Trp Phe
        195                 200                 205
Asn Leu Tyr Thr Lys Leu Asn Asn Ile Leu Thr Gln Tyr Arg Ser Asn
    210                 215                 220
Glu Val Lys Asn His Gly Phe Thr Leu Ile Asp Asn Gln Thr Leu Ser
225                 230                 235                 240
Gly Phe Gln Phe Ile Leu Asn Gln Tyr Gly Cys Ile Val Tyr His Lys
                245                 250                 255
Glu Leu Lys Arg Ile Thr Val Thr Thr Tyr Asn Gln Phe Leu Thr Trp
            260                 265                 270
Lys Asp Ile Ser Leu Ser Arg Leu Asn Val Cys Leu Ile Thr Trp Ile
        275                 280                 285
Ser Asn Cys Leu Asn Thr Leu Asn Lys Ser Leu Gly Leu Arg Cys Gly
    290                 295                 300
Phe Asn Asn Val Ile Leu Thr Gln Leu Phe Leu Tyr Gly Asp Cys Ile
305                 310                 315                 320
Leu Lys Leu Phe His Asn Glu Gly Phe Tyr Ile Ile Lys Glu Val Glu
                325                 330                 335
Gly Phe Ile Met Ser Leu Ile Leu Asn Ile Thr Glu Glu Asp Gln Phe
            340                 345                 350
Arg Lys Arg Phe Tyr Asn Ser Met Leu Asn Asn Ile Thr Asp Ala Ala
        355                 360                 365
Asn Lys Ala Gln Lys Asn Leu Leu Ser Arg Val Cys His Thr Leu Leu
    370                 375                 380
Asp Lys Thr Val Ser Asp Asn Ile Ile Asn Gly Arg Trp Ile Ile Leu
385                 390                 395                 400
Leu Ser Lys Phe Leu Lys Leu Ile Lys Leu Ala Gly Asp Asn Asn Leu
                405                 410                 415
Asn Asn Leu Ser Glu Leu Tyr Phe Leu Phe Arg Ile Phe Gly His Pro
            420                 425                 430
Met Val Asp Glu Arg Gln Ala Met Asp Ala Val Lys Ile Asn Cys Asn
        435                 440                 445
Glu Thr Lys Phe Tyr Leu Leu Ser Ser Leu Ser Met Leu Arg Gly Ala
    450                 455                 460
Phe Ile Tyr Arg Ile Ile Lys Gly Phe Val Asn Asn Tyr Asn Arg Trp
465                 470                 475                 480
Pro Thr Leu Arg Asn Ala Ile Val Leu Pro Leu Arg Trp Leu Thr Tyr
                485                 490                 495
Tyr Lys Leu Asn Thr Tyr Pro Ser Leu Leu Glu Leu Thr Glu Arg Asp
            500                 505                 510
Leu Ile Val Leu Ser Gly Leu Arg Phe Tyr Arg Glu Phe Arg Leu Pro
        515                 520                 525
Lys Lys Val Asp Leu Glu Met Ile Ile Asn Asp Lys Ala Ile Ser Pro
    530                 535                 540
Pro Lys Asn Leu Ile Trp Thr Ser Phe Pro Arg Asn Tyr Met Pro Ser
545                 550                 555                 560
His Ile Gln Asn Tyr Ile Glu His Glu Lys Leu Lys Phe Ser Glu Ser
                565                 570                 575
Asp Lys Ser Arg Arg Val Leu Glu Tyr Tyr Leu Arg Asp Asn Lys Phe
            580                 585                 590
Asn Glu Cys Asp Leu Tyr Asn Cys Val Val Asn Gln Ser Tyr Leu Asn
        595                 600                 605
Asn Pro Asn His Val Val Ser Leu Thr Gly Lys Glu Arg Glu Leu Ser
    610                 615                 620
Val Gly Arg Met Phe Ala Met Gln Pro Gly Met Phe Arg Gln Val Gln
625                 630                 635                 640
Ile Leu Ala Glu Lys Met Ile Ala Glu Asn Ile Leu Gln Phe Phe Pro
                645                 650                 655
Glu Ser Leu Thr Arg Tyr Gly Asp Leu Glu Leu Gln Lys Ile Leu Glu
            660                 665                 670
Leu Lys Ala Gly Ile Ser Asn Lys Ser Asn Arg Tyr Asn Asp Asn Tyr
```

```
        675                 680                 685
Asn Asn Tyr Ile Ser Lys Cys Ser Ile Ile Thr Asp Leu Ser Lys Phe
    690                 695                 700
Asn Gln Ala Phe Arg Tyr Glu Thr Ser Cys Ile Cys Ser Asp Val Leu
705                 710                 715                 720
Asp Glu Leu His Gly Val Gln Ser Leu Phe Ser Trp Leu His Leu Thr
                725                 730                 735
Ile Pro His Val Thr Ile Ile Cys Thr Tyr Arg His Ala Pro Pro Tyr
            740                 745                 750
Ile Gly Asp His Ile Val Asp Leu Asn Asn Val Asp Glu Gln Ser Gly
        755                 760                 765
Leu Tyr Arg Tyr His Met Gly Gly Ile Glu Gly Trp Cys Gln Lys Leu
    770                 775                 780
Trp Thr Ile Glu Ala Ile Ser Leu Leu Asp Leu Ile Ser Leu Lys Gly
785                 790                 795                 800
Lys Phe Ser Ile Thr Ala Leu Ile Asn Gly Asp Asn Gln Ser Ile Asp
                805                 810                 815
Ile Ser Lys Pro Ile Arg Leu Met Glu Gly Gln Thr His Ala Gln Ala
            820                 825                 830
Asp Tyr Leu Leu Ala Leu Asn Ser Leu Lys Leu Leu Tyr Lys Glu Tyr
        835                 840                 845
Ala Gly Ile Gly His Lys Leu Lys Gly Thr Glu Thr Tyr Ile Ser Arg
    850                 855                 860
Asp Met Gln Phe Met Ser Lys Thr Ile Gln His Asn Gly Val Tyr Tyr
865                 870                 875                 880
Pro Ala Ser Ile Lys Lys Val Leu Arg Val Gly Pro Trp Ile Asn Thr
                885                 890                 895
Ile Leu Asp Asp Phe Lys Val Ser Leu Glu Ser Ile Gly Ser Leu Thr
            900                 905                 910
Gln Glu Leu Glu Tyr Arg Gly Glu Ser Leu Leu Cys Ser Leu Ile Phe
        915                 920                 925
Arg Asn Val Trp Leu Tyr Asn Gln Ile Ala Leu Gln Leu Lys Asn His
    930                 935                 940
Ala Leu Cys Asn Asn Lys Leu Tyr Leu Asp Ile Leu Lys Val Leu Lys
945                 950                 955                 960
His Leu Lys Thr Phe Phe Asn Leu Asp Asn Ile Asp Thr Ala Leu Thr
                965                 970                 975
Leu Tyr Met Asn Leu Pro Met Leu Phe Gly Gly Gly Asp Pro Asn Leu
            980                 985                 990
Leu Tyr Arg Ser Phe Tyr Arg Arg Thr Pro Asp Phe Leu Thr Glu Ala
        995                 1000                1005
Ile Val His Ser Val Phe Ile Leu Ser Tyr Tyr Thr Asn His Asp Leu
    1010                1015                1020
Lys Asp Lys Leu Gln Asp Leu Ser Asp Asp Arg Leu Asn Lys Phe Leu
1025                1030                1035                1040
Thr Cys Ile Ile Thr Phe Asp Lys Asn Pro Asn Ala Glu Phe Val Thr
                1045                1050                1055
Leu Met Arg Asp Pro Gln Ala Leu Gly Ser Glu Arg Gln Ala Lys Ile
            1060                1065                1070
Thr Ser Glu Ile Asn Arg Leu Ala Val Thr Glu Val Leu Ser Thr Ala
        1075                1080                1085
Pro Asn Lys Ile Phe Ser Lys Ser Ala Gln His Tyr Thr Thr Thr Glu
    1090                1095                1100
Ile Asp Leu Asn Asp Ile Met Gln Asn Ile Glu Pro Thr Tyr Pro His
1105                1110                1115                1120
Gly Leu Arg Val Val Tyr Glu Ser Leu Pro Phe Tyr Lys Ala Glu Lys
                1125                1130                1135
Ile Val Asn Leu Ile Ser Gly Thr Lys Ser Ile Thr Asn Ile Leu Glu
            1140                1145                1150
Lys Thr Ser Ala Ile Asp Leu Thr Asp Ile Asp Arg Ala Thr Glu Met
        1155                1160                1165
Met Arg Lys Asn Ile Thr Leu Leu Ile Arg Ile Leu Pro Leu Asp Cys
    1170                1175                1180
Asn Arg Asp Lys Arg Glu Ile Leu Ser Met Glu Asn Leu Ser Ile Thr
1185                1190                1195                1200
Glu Leu Ser Lys Tyr Val Arg Glu Arg Ser Trp Ser Leu Ser Asn Ile
                1205                1210                1215
Val Gly Val Thr Ser Pro Ser Ile Met Tyr Thr Met Asp Ile Lys Tyr
```

```
            1220                1225                1230
Thr Thr Ser Thr Ile Ser Ser Gly Ile Ile Ile Glu Lys Tyr Asn Val
        1235                1240                1245
Asn Ser Leu Thr Arg Gly Glu Arg Gly Pro Thr Lys Pro Trp Val Gly
    1250                1255                1260
Ser Ser Thr Gln Glu Lys Lys Thr Met Pro Val Tyr Asn Arg Gln Val
1265                1270                1275                1280
Leu Thr Lys Lys Gln Arg Asp Gln Ile Asp Leu Leu Ala Lys Leu Asp
                1285                1290                1295
Trp Val Tyr Ala Ser Ile Asp Asn Lys Asp Glu Phe Met Glu Glu Leu
            1300                1305                1310
Ser Ile Gly Thr Leu Gly Leu Thr Tyr Glu Lys Ala Lys Lys Leu Phe
        1315                1320                1325
Pro Gln Tyr Leu Ser Val Asn Tyr Leu His Arg Leu Thr Val Ser Ser
    1330                1335                1340
Arg Pro Cys Glu Phe Pro Ala Ser Ile Pro Ala Tyr Arg Thr Thr Asn
1345                1350                1355                1360
Tyr His Phe Asp Thr Ser Pro Ile Asn Arg Ile Leu Thr Glu Lys Tyr
                1365                1370                1375
Gly Asp Glu Asp Ile Asp Ile Val Phe Gln Asn Cys Ile Ser Phe Gly
            1380                1385                1390
Leu Ser Leu Met Ser Val Val Glu Gln Phe Thr Asn Val Cys Pro Asn
        1395                1400                1405
Arg Ile Ile Leu Ile Pro Lys Leu Asn Glu Ile His Leu Met Lys Pro
    1410                1415                1420
Pro Ile Phe Thr Gly Asp Val Asp Ile His Lys Leu Lys Gln Val Ile
1425                1430                1435                1440
Gln Lys Gln His Met Phe Leu Pro Asp Lys Ile Ser Leu Thr Gln Tyr
                1445                1450                1455
Val Glu Leu Phe Leu Ser Asn Lys Thr Leu Lys Ser Gly Ser His Val
            1460                1465                1470
Asn Ser Asn Leu Ile Leu Ala His Lys Ile Ser Asp Tyr Phe His Asn
        1475                1480                1485
Thr Tyr Ile Leu Ser Thr Asn Leu Ala Gly His Trp Ile Leu Ile Ile
    1490                1495                1500
Gln Leu Met Lys Asp Ser Lys Gly Ile Phe Glu Lys Asp Trp Gly Glu
1505                1510                1515                1520
Gly Tyr Ile Thr Asp His Met Phe Ile Asn Leu Lys Val Phe Phe Asn
                1525                1530                1535
Ala Tyr Lys Thr Tyr Leu Leu Cys Phe His Lys Gly Tyr Gly Lys Ala
            1540                1545                1550
Lys Leu Glu Cys Asp Met Asn Thr Ser Asp Leu Leu Cys Val Leu Glu
        1555                1560                1565
Leu Ile Asp Ser Ser Tyr Trp Lys Ser Met Ser Lys Val Phe Leu Glu
    1570                1575                1580
Gln Lys Val Ile Lys Tyr Ile Leu Ser Gln Asp Ala Ser Leu His Arg
1585                1590                1595                1600
Val Lys Gly Cys His Ser Phe Lys Leu Trp Phe Leu Lys Arg Leu Asn
                1605                1610                1615
Val Ala Glu Phe Thr Val Cys Pro Trp Val Val Asn Ile Asp Tyr His
            1620                1625                1630
Pro Thr His Met Lys Ala Ile Leu Thr Tyr Ile Asp Leu Val Arg Met
        1635                1640                1645
Gly Leu Ile Asn Ile Asp Arg Ile His Ile Lys Asn Lys His Lys Phe
    1650                1655                1660
Asn Asp Glu Phe Tyr Thr Ser Asn Leu Phe Tyr Ile Asn Tyr Asn Phe
1665                1670                1675                1680
Ser Asp Asn Thr His Leu Leu Thr Lys His Ile Arg Ile Ala Asn Ser
                1685                1690                1695
Glu Leu Glu Asn Asn Tyr Asn Lys Leu Tyr His Pro Thr Pro Glu Thr
            1700                1705                1710
Leu Glu Asn Ile Leu Ala Asn Pro Ile Lys Ser Asn Asp Lys Lys Thr
        1715                1720                1725
Leu Asn Asp Tyr Cys Ile Gly Lys Asn Val Asp Ser Ile Met Leu Pro
    1730                1735                1740
Leu Leu Ser Asn Lys Lys Leu Ile Lys Ser Ser Ala Met Ile Arg Thr
1745                1750                1755                1760
Asn Tyr Ser Lys Gln Asp Leu Tyr Asn Leu Phe Pro Met Val Val Ile
```

```
                1765                1770                1775
Asp Arg Ile Ile Asp His Ser Gly Asn Thr Ala Lys Ser Asn Gln Leu
            1780                1785                1790
Tyr Thr Thr Thr Ser His Gln Ile Ser Leu Val His Asn Ser Thr Ser
        1795                1800                1805
Leu Tyr Cys Met Leu Pro Trp His His Ile Asn Arg Phe Asn Phe Val
    1810                1815                1820
Phe Ser Ser Thr Gly Cys Lys Ile Ser Ile Glu Tyr Ile Leu Lys Asp
1825                1830                1835                1840
Leu Lys Ile Lys Asp Pro Asn Cys Ile Ala Phe Ile Gly Glu Gly Ala
                1845                1850                1855
Gly Asn Leu Leu Leu Arg Thr Val Val Glu Leu His Pro Asp Ile Arg
            1860                1865                1870
Tyr Ile Tyr Arg Ser Leu Lys Asp Cys Asn Asp His Ser Leu Pro Ile
        1875                1880                1885
Glu Phe Leu Arg Leu Tyr Asn Gly His Ile Asn Ile Asp Tyr Gly Glu
    1890                1895                1900
Asn Leu Thr Ile Pro Ala Thr Asp Ala Thr Asn Asn Ile His Trp Ser
1905                1910                1915                1920
Tyr Leu His Ile Lys Phe Ala Glu Pro Ile Ser Leu Phe Val Cys Asp
                1925                1930                1935
Ala Glu Leu Ser Val Thr Val Asn Trp Ser Lys Ile Ile Ile Glu Trp
            1940                1945                1950
Ser Lys His Val Arg Lys Cys Lys Tyr Cys Ser Ser Val Asn Lys Cys
        1955                1960                1965
Met Leu Ile Val Lys Tyr His Ala Gln Asp Asp Ile Asp Phe Lys Leu
    1970                1975                1980
Asp Asn Ile Thr Ile Leu Lys Thr Tyr Val Cys Leu Gly Ser Lys Leu
1985                1990                1995                2000
Lys Gly Ser Glu Val Tyr Leu Val Leu Thr Ile Gly Pro Ala Asn Ile
                2005                2010                2015
Phe Pro Val Phe Asn Val Val Gln Asn Ala Lys Leu Ile Leu Ser Arg
            2020                2025                2030
Thr Lys Asn Phe Ile Met Pro Lys Lys Ala Asp Lys Glu Ser Ile Asp
        2035                2040                2045
Ala Asn Ile Lys Ser Leu Ile Pro Phe Leu Cys Tyr Pro Ile Thr Lys
    2050                2055                2060
Lys Gly Ile Asn Thr Ala Leu Ser Lys Leu Lys Ser Val Val Ser Gly
2065                2070                2075                2080
Asp Ile Leu Ser Tyr Ser Ile Ala Gly Arg Asn Glu Val Phe Ser Asn
                2085                2090                2095
Lys Leu Ile Asn His Lys His Met Asn Ile Leu Lys Trp Phe Asn His
            2100                2105                2110
Val Leu Asn Phe Arg Ser Thr Glu Leu Asn Tyr Asn His Leu Tyr Met
        2115                2120                2125
Val Glu Ser Thr Tyr Pro Tyr Leu Ser Glu Leu Leu Asn Ser Leu Thr
    2130                2135                2140
Thr Asn Glu Leu Lys Lys Leu Ile Lys Ile Thr Gly Ser Leu Leu Tyr
2145                2150                2155                2160
Asn Phe His Asn Glu
                2165


<210> 277
<211> 391
<212> PRT
<213> Human respiratory syncytial virus

<400> 277
Met Ala Leu Ser Lys Val Lys Leu Asn Asp Thr Leu Asn Lys Asp Gln
 1               5                  10                  15
Leu Leu Ser Ser Ser Lys Tyr Thr Ile Gln Arg Ser Thr Gly Asp Asn
            20                  25                  30
Ile Asp Thr Pro Asn Tyr Asp Val Gln Lys His Leu Asn Lys Leu Cys
        35                  40                  45
Gly Met Leu Leu Ile Thr Glu Asp Ala Asn His Lys Phe Thr Gly Leu
    50                  55                  60
Ile Gly Met Leu Tyr Ala Met Ser Arg Leu Gly Arg Glu Asp Thr Ile
```

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

<210> 278
<211> 391
<212> PRT
<213> Human respiratory syncytial virus

<400> 278
Met Ala Leu Ser Lys Val Lys Leu Asn Asp Thr Leu Asn Lys Asp Gln
1 5 10 15
Leu Leu Ser Ser Ser Lys Tyr Thr Ile Gln Arg Ser Thr Gly Asp Ser
20 25 30
Ile Asp Thr Pro Asn Tyr Asp Val Gln Lys His Ile Asn Lys Leu Cys
35 40 45
Gly Met Leu Leu Ile Thr Glu Asp Ala Asn His Lys Phe Thr Gly Leu
50 55 60
Ile Gly Met Leu Tyr Ala Met Ser Arg Leu Gly Arg Glu Asp Thr Ile
65 70 75 80
Lys Ile Leu Arg Asp Ala Gly Tyr His Val Lys Ala Asn Gly Val Asp
85 90 95
Val Thr Thr His Arg Gln Asp Ile Asn Gly Lys Glu Met Lys Phe Glu
100 105 110
Val Leu Thr Leu Ser Ser Leu Thr Thr Glu Ile Gln Ile Asn Ile Glu
115 120 125
Ile Glu Ser Arg Lys Ser Tyr Lys Lys Met Leu Lys Glu Met Gly Glu
130 135 140
Val Ala Pro Glu Tyr Arg His Asp Ser Pro Asp Cys Gly Met Ile Ile

145 150 155 160
Leu Cys Ile Ala Ala Leu Val Ile Thr Lys Leu Ala Ala Gly Asp Arg
165 170 175
Ser Gly Leu Thr Ala Val Ile Arg Arg Ala Asn Asn Val Leu Lys Asn
180 185 190
Glu Met Lys Arg Tyr Lys Gly Leu Leu Pro Lys Asp Ile Ala Asn Ser
195 200 205
Phe Tyr Glu Val Phe Glu Lys Tyr Pro His Phe Ile Asp Val Phe Val
210 215 220
His Phe Gly Ile Ala Gln Ser Ser Thr Arg Gly Gly Ser Arg Val Glu
225 230 235 240
Gly Ile Phe Ala Gly Leu Phe Met Asn Ala Tyr Gly Ala Gly Gln Val
245 250 255
Met Leu Arg Trp Gly Val Leu Ala Lys Ser Val Lys Asn Ile Met Leu
260 265 270
Gly His Ala Ser Val Gln Ala Glu Met Glu Gln Val Val Glu Val Tyr
275 280 285
Glu Tyr Ala Gln Lys Leu Gly Gly Glu Ala Gly Phe Tyr His Ile Leu
290 295 300
Asn Asn Pro Lys Ala Ser Leu Leu Ser Leu Thr Gln Phe Pro His Phe
305 310 315 320
Ser Ser Val Val Leu Gly Asn Ala Ala Gly Leu Gly Ile Met Gly Glu
325 330 335
Tyr Arg Gly Thr Pro Arg Asn Gln Asp Leu Tyr Asp Ala Ala Lys Ala
340 345 350
Tyr Ala Glu Gln Leu Lys Glu Asn Gly Val Ile Asn Tyr Ser Val Leu
355 360 365
Asp Leu Thr Ala Glu Glu Leu Glu Ala Ile Lys His Gln Leu Asn Pro
370 375 380
Lys Asp Asn Asp Val Glu Leu
385 390

<210> 279
<211> 241
<212> PRT
<213> Human respiratory syncytial virus

<400> 279
Met Glu Lys Phe Ala Pro Glu Phe His Gly Glu Asp Ala Asn Asn Arg
1 5 10 15
Ala Thr Lys Phe Leu Glu Ser Ile Lys Gly Lys Phe Thr Ser Pro Lys
20 25 30
Asp Pro Lys Lys Lys Asp Ser Ile Ile Ser Val Asn Ser Ile Asp Ile
35 40 45
Glu Val Thr Lys Glu Ser Pro Ile Thr Ser Asn Ser Thr Ile Met Asn
50 55 60
Pro Thr Asn Glu Thr Asp Asp Thr Val Gly Asn Lys Pro Asn Tyr Gln
65 70 75 80
Arg Lys Pro Leu Val Ser Phe Lys Glu Asp Pro Met Leu Ser Asp Asn
85 90 95
Pro Phe Ser Lys Leu Tyr Lys Glu Thr Ile Glu Thr Phe Asp Asn Asn
100 105 110
Glu Glu Glu Ser Ser Tyr Ser Tyr Glu Glu Ile Asn Asp Gln Thr Asn
115 120 125
Asp Asn Ile Thr Ala Arg Leu Asp Arg Ile Asp Glu Lys Leu Ser Glu
130 135 140
Ile Leu Gly Met Leu His Thr Leu Val Val Ala Ser Ala Gly Pro Thr
145 150 155 160
Ser Ala Arg Asp Gly Ile Arg Asp Ala Met Val Gly Leu Arg Glu Glu
165 170 175
Met Ile Glu Lys Ile Arg Thr Glu Ala Leu Met Thr Asn Asn Arg Leu
180 185 190
Glu Ala Met Ala Arg Leu Arg Asn Glu Glu Ser Glu Lys Met Ala Lys
195 200 205
Asp Thr Ser Asp Glu Val Ser Leu Asn Pro Thr Ser Glu Lys Leu Asn
210 215 220
Asn Leu Leu Glu Gly Asn Asp Ser Asp Asp Asp Leu Ser Leu Glu Asp

225 230 235 240
Phe

<210> 280
<211> 256
<212> PRT
<213> Human respiratory synctial virus

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

<210> 281
<211> 64
<212> PRT
<213> Human respiratory syncytial virus

<400> 281
Met Glu Asn Thr Ser Ile Thr Ile Glu Phe Ser Ser Lys Phe Trp Pro
1 5 10 15
Tyr Phe Thr Leu Ile His Met Ile Thr Thr Ile Ile Ser Leu Leu Ile
20 25 30
Ile Ile Ser Ile Met Ile Ala Ile Leu Asn Lys Leu Cys Glu Tyr Asn
35 40 45
Ala Phe His Asn Lys Thr Phe Glu Leu Pro Arg Ala Arg Ile Asn Thr
50 55 60

<210> 282
<211> 574
<212> PRT
<213> Human respiratory syncytial virus

<220>

<400> 282
Met Glu Leu Pro Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Ala
 1   5   10   15
Ala Val Thr Leu Cys Phe Val Ser Ser Gln Asn Ile Thr Glu Glu Phe
            20   25   30
Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
        35   40   45
Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
    50   55   60
Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
65   70   75   80
Gln Glu Leu Asp Lys Tyr Lys Asn Ala Val Thr Glu Leu Gln Leu Leu
                85   90   95
Met Gln Ser Thr Pro Ala Ala Asn Asn Arg Ala Arg Arg Glu Leu Pro
            100   105   110
Arg Phe Met Asn Tyr Thr Leu Asn Asn Thr Lys Asn Thr Asn Val Thr
        115   120   125
Leu Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val
    130   135   140
Gly Ser Ala Ile Ala Ser Gly Ile Ala Val Ser Lys Val Leu His Leu
145   150   155   160
Glu Gly Glu Val Asn Lys Ile Lys Ser Ala Leu Leu Ser Thr Asn Lys
                165   170   175
Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Ser Lys Val
            180   185   190
Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Val Asn
        195   200   205
Lys Gln Ser Cys Ser Ile Ser Asn Ile Glu Thr Val Ile Glu Phe Gln
    210   215   220
Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn
225   230   235   240
Ala Gly Val Thr Thr Pro Val Ser Thr Tyr Met Leu Thr Asn Ser Glu
                245   250   255
Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys
            260   265   270
Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile
        275   280   285
Met Ser Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro
    290   295   300
Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
305   310   315   320
Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg
                325   330   335
Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe
            340   345   350
Pro Gln Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp
        355   360   365
Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Val Asn Leu Cys Asn Val
    370   375   380
Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr
385   390   395   400
Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys
                405   410   415
Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile
            420   425   430
Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp
        435   440   445
Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly
    450   455   460
Lys Asn Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro
465   470   475   480
Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn
                485   490   495
Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Lys Ser Asp Glu Leu
            500   505   510
Leu His Asn Val Asn Ala Gly Lys Ser Thr Thr Asn Ile Met Ile Thr
        515   520   525
Thr Ile Ile Ile Val Ile Ile Val Ile Leu Leu Ser Leu Ile Ala Val

```
    530                 535                 540
Gly Leu Leu Leu Tyr Cys Lys Ala Arg Ser Thr Pro Val Thr Leu Ser
545                 550                 555                 560
Lys Asp Gln Leu Ser Gly Ile Asn Asn Ile Ala Phe Ser Ser
                565                 570
```

<210> 283
<211> 83
<212> PRT
<213> Human respiratory syncytial virus

<400> 283

```
Lys Arg Asp Pro Lys Thr Pro Ala Lys Met Leu Asn Lys Glu Thr Thr
 1               5                  10                  15
Thr Asn Pro Thr Lys Asn Leu Thr Leu Lys Thr Thr Glu Arg Asp Thr
            20                  25                  30
Ser Thr Ser Gln Ser Thr Val Leu Asp Thr Ser Thr Ser Lys His Ile
        35                  40                  45
Ile Leu Gln Gln Ser Leu His Ser Thr Thr Pro Glu Asn Thr Pro Asn
    50                  55                  60
Phe Thr Gln Thr Pro Thr Ala Ser Glu Pro Ser Thr Ser Asn Ser Thr
65                  70                  75                  80
Gln Lys Thr
```

<210> 284
<211> 21
<212> PRT
<213> Bufo gargarizans

<220>
<223> Asian toad Buforin II

<400> 284

```
Thr Arg Ser Ser Arg Ala Gly Leu Gln Phe Pro Val Gly Arg Val His
 1               5                  10                  15
Arg Leu Leu Arg Lys
            20
```

<210> 285
<211> 16
<212> PRT
<213> Homo sapiens

<220>
<223> DPV3

<400> 285

```
Arg Lys Lys Arg Arg Arg Glu Ser Arg Lys Lys Arg Arg Arg Glu Ser
 1               5                  10                  15
```

<210> 286
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<223> DPV6

<400> 286

```
Gly Arg Pro Arg Glu Ser Gly Lys Lys Arg Lys Arg Lys Arg Leu Lys
 1               5                  10                  15
Pro
```

<210> 287
<211> 15
<212> PRT
<213> Homo sapiens

<220>
<223> DPV7

<400> 287
Gly Lys Arg Lys Lys Lys Gly Lys Leu Gly Lys Lys Arg Asp Pro
 1   5   10   15

<210> 288
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<223> DPV7b

<400> 288
Gly Lys Arg Lys Lys Lys Gly Lys Leu Gly Lys Lys Arg Pro Arg Ser
 1   5   10   15
Arg

<210> 289
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> DPV3/10

<400> 289
Arg Lys Lys Arg Arg Arg Glu Ser Arg Arg Ala Arg Arg Ser Pro Arg
 1   5   10   15
His Leu

<210> 290
<211> 19
<212> PRT
<213> Homo sapiens

<220>
<223> DPV10/6

<400> 290
Ser Arg Arg Ala Arg Arg Ser Pro Arg Glu Ser Gly Lys Lys Arg Lys
 1   5   10   15
Arg Lys Arg

<210> 291
<211> 19
<212> PRT
<213> Homo sapiens

<220>
<223> DPV1047

<400> 291
Val Lys Arg Gly Leu Lys Leu Arg His Val Arg Pro Arg Val Thr Arg
 1   5   10   15
Met Asp Val

<210> 292
<211> 18
<212> PRT
<213> Homo sapiens

<220>
<223> DPV1048

<400> 292
Val Lys Arg Gly Leu Lys Leu Arg His Val Arg Pro Arg Val Thr Arg
 1   5   10   15
Asp Val

<210> 293
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<223> DPV10

<400> 293
Ser Arg Arg Ala Arg Arg Ser Pro Arg His Leu Gly Ser Gly
 1   5   10

<210> 294
<211> 16
<212> PRT
<213> Homo sapiens

<220>
<223> DPV15

<400> 294
Leu Arg Arg Glu Arg Gln Ser Arg Leu Arg Arg Glu Arg Gln Ser Arg
 1   5   10   15

<210> 295
<211> 22
<212> PRT
<213> Homo sapiens

<220>
<223> DPV15b

<400> 295
Gly Ala Tyr Asp Leu Arg Arg Arg Glu Arg Gln Ser Arg Leu Arg Arg
 1   5   10   15
Arg Glu Arg Gln Ser Arg
            20

<210> 296
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> GALA

<400> 296
Trp Glu Ala Ala Leu Ala Glu Ala Leu Ala Glu Ala Leu Ala Glu His
 1   5   10   15
Leu Ala Glu Ala Leu Ala Glu Ala Leu Glu Ala Leu Ala Ala
            20   25   30

<210> 297
<211> 21
<212> PRT
<213> Homo sapiens

<220>
<223> Human fibrinogen beta chain

<400> 297
Lys Gly Ser Trp Tyr Ser Met Arg Lys Met Ser Met Lys Ile Arg Pro
 1   5   10   15
Phe Phe Pro Gln Gln
            20

<210> 298
<211> 20
<212> PRT
<213> Homo sapiens

<220>
<223> Human fibrinogen gamma chain precursor

<400> 298
Lys Thr Arg Tyr Tyr Ser Met Lys Lys Thr Thr Met Lys Ile Ile Pro
 1   5   10   15
Phe Asn Arg Leu
            20

<210> 299
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Human fibrinogen alpha chain

<400> 299
Arg Gly Ala Asp Tyr Ser Leu Arg Ala Val Arg Met Lys Ile Arg Pro
 1   5   10   15
Leu Val Thr Gln
            20

<210> 300
<211> 24
<212> PRT
<213> Homo sapiens

<220>
<223> Human hCT (9-32)

<400> 300
Leu Gly Thr Tyr Thr Gln Asp Phe Asn Lys Phe His Thr Phe Pro Gln
 1   5   10   15
Thr Ala Ile Gly Val Gly Ala Pro
            20

<210> 301
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> HN-1

<400> 301
Thr Ser Pro Leu Asn Ile His Asn Gly Gln Lys Leu
 1   5   10

<210> 302
<211> 12
<212> PRT
<213> Influenza virus

<220>
<223> Influenza virus nucleoprotein (NLS)

<400> 302
Asn Ser Ala Ala Phe Glu Asp Leu Arg Val Leu Ser
 1   5   10

<210> 303
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> KALA

<400> 303
Trp Glu Ala Lys Leu Ala Lys Ala Leu Ala Lys Ala Leu Ala Lys His
 1   5   10   15
Leu Ala Lys Ala Leu Ala Lys Ala Leu Lys Ala Cys Glu Ala
            20   25   30

<210> 304
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Ku70

<400> 304
Val Pro Met Leu Lys Pro Met Leu Lys Glu
 1   5   10

<210> 305
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> MAP

<400> 305
Lys Leu Ala Leu Lys Leu Ala Leu Lys Ala Leu Lys Ala Ala Leu Lys
 1   5   10   15
Leu Ala

<210> 306
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> MPG

<400> 306
Gly Ala Leu Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser Thr Met Gly
 1   5   10   15
Ala Trp Ser Gln Pro Lys Lys Lys Arg Lys Val
            20   25

<210> 307
<211> 16
<212> PRT
<213> Homo sapiens

<220>
<223> Human Fibroblast growth factor 4

<400> 307
Ala Ala Val Ala Leu Leu Pro Ala Val Leu Leu Ala Leu Leu Ala Pro
 1   5   10   15

<210> 308
<211> 9
<212> PRT
<213> Homo sapiens

<220>
<223> Human N50 (NLS of NF-kB P50)

<400> 308
Val Gln Arg Lys Arg Gln Lys Leu Met
 1   5

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

<220>
<223> Pep-1

<400> 309
Lys Glu Thr Trp Trp Glu Thr Trp Trp Thr Glu Trp Ser Gln Pro Lys
 1   5   10   15
Lys Lys Arg Lys Val
            20

<210> 310
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Pep-7

<400> 310

Ser Asp Leu Trp Glu Met Met Met Val Ser Leu Ala Cys Gln Tyr
 1   5   10   15

<210> 311
<211> 16
<212> PRT
<213> Drosophila antennapedia

<220>
<223> Fruit Fly Penetratin

<400> 311
Arg Gln Ile Lys Ile Trp Phe Gln Asn Arg Arg Met Lys Trp Lys Lys
 1   5   10   15

<210> 312
<211> 17
<212> PRT
<213> Drosophila antennapedia

<220>
<223> Fruit Fly Penetratin variant

<400> 312
Gly Arg Gln Ile Lys Ile Trp Phe Gln Asn Arg Arg Met Lys Trp Lys
 1   5   10   15
Lys

<210> 313
<211> 7
<212> PRT
<213> Drosophila antennapedia

<220>
<223> Fruit Fly Short Penetratin

<400> 313
Arg Arg Met Lys Trp Lys Lys
 1   5

<210> 314
<211> 17
<212> PRT
<213> Drosophila antennapedia

<220>
<223> Fruit Fly Penetratin 42-58

<400> 314
Glu Arg Gln Ile Lys Ile Trp Phe Gln Asn Arg Arg Met Lys Trp Lys
 1   5   10   15
Lys

<210> 315
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Poly Arginine R7

<400> 315
Arg Arg Arg Arg Arg Arg Arg
 1   5

<210> 316
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Poly Arginine R9

<400> 316
Arg Arg Arg Arg Arg Arg Arg Arg Arg
 1   5

<210> 317
<211> 16
<212> PRT
<213> Rattus norvegicus

<220>
<223> Rat pISL

<400> 317
Arg Val Ile Arg Val Trp Phe Gln Asn Lys Arg Cys Lys Asp Lys Lys
 1   5   10   15

<210> 318
<211> 28
<212> PRT
<213> Mus musculus

<220>
<223> Prion mouse PrPc1-28

<400> 318
Met Ala Asn Leu Gly Tyr Trp Leu Leu Ala Leu Phe Val Thr Met Trp
 1   5   10   15
Thr Asp Val Gly Leu Cys Lys Lys Arg Pro Lys Pro
            20   25

<210> 319
<211> 18
<212> PRT
<213> Mus musculus

<220>
<223> Mouse pVEC

<400> 319
Leu Leu Ile Ile Leu Arg Arg Arg Ile Arg Lys Gln Ala His Ala His
 1   5   10   15
Ser Lys

<210> 320
<211> 16
<212> PRT
<213> Mus musculus

<220>
<223> Mouse pVEC variant

<400> 320
Leu Leu Ile Ile Leu Arg Arg Arg Ile Arg Lys Gln Ala His Ala His
 1   5   10   15

<210> 321
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> SAP

<400> 321
Val Arg Leu Pro Pro Pro Val Arg Leu Pro Pro Pro Val Arg Leu Pro
 1   5   10   15
Pro Pro

<210> 322
<211> 7
<212> PRT
<213> Simian virus

<220>
<223> SV-40 (NLS)

<400> 322
Pro Lys Lys Lys Arg Lys Val
 1   5

<210> 323
<211> 18
<212> PRT
<213> Sus scrofa

<220>
<223> Porcine SynB1

<400> 323
Arg Gly Gly Arg Leu Ser Tyr Ser Arg Arg Arg Phe Ser Thr Ser Thr
 1   5   10   15
Gly Arg

<210> 324
<211> 10
<212> PRT
<213> Sus scrofa

<220>
<223> Porcine SynB3

<400> 324
Arg Arg Leu Ser Tyr Ser Arg Arg Arg Phe
 1   5   10

<210> 325
<211> 17
<212> PRT
<213> Sus scrofa

<220>

<223> Porcine SynB4

<400> 325
Ala Trp Ser Phe Arg Val Ser Tyr Arg Gly Ile Ser Tyr Arg Arg Ser
 1   5   10   15
Arg

<210> 326
<211> 14
<212> PRT
<213> Human immunodeficiency virus

<220>
<223> HIV type I Tat 47-60

<400> 326
Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln
 1   5   10

<210> 327
<211> 11
<212> PRT
<213> Human immunodeficiency virus

<220>
<223> HIV type I Tat 47-57

<400> 327
Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg
 1   5   10

<210> 328
<211> 10
<212> PRT
<213> Human immunodeficiency virus

<220>
<223> HIV type I Tat 47-56

<400> 328
Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg
 1   5   10

<210> 329
<211> 9
<212> PRT
<213> Human immunodeficiency virus

<220>
<223> HIV type I Tat 48-56

<400> 329
Gly Arg Lys Lys Arg Arg Gln Arg Arg
 1   5

<210> 330
<211> 10
<212> PRT
<213> Human immundeficiency virus

<220>
<223> HIV type I Tat 48-57

<400> 330
Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg
 1   5   10

<210> 331
<211> 9
<212> PRT
<213> Human immundeficiency virus

<220>
<223> HIV type I Tat 49-57

<400> 331
Arg Lys Lys Arg Arg Gln Arg Arg Arg
 1   5

<210> 332
<211> 8
<212> PRT
<213> Human immundeficiency virus

<220>
<223> HIV type I Tat 49-56

<400> 332
Arg Lys Lys Arg Arg Gln Arg Arg
 1   5

<210> 333
<211> 13
<212> PRT
<213> Human immundeficiency virus

<220>
<223> HIV type I Tat 48-60

<400> 333
Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln
 1   5   10

<210> 334
<211> 5
<212> PRT
<213> Human immundeficiency virus

<220>
<223> HIV type I Tat 48-52

<400> 334
Gly Arg Lys Lys Arg
 1   5

<210> 335
<211> 36
<212> PRT
<213> Human immundeficiency virus

<220>
<223> HIV type I Tat 37-72

<400> 335
Cys Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr Gly Arg Lys Lys Arg

```
 1               5                   10                  15
Arg Gln Arg Arg Arg Pro Pro Gln Phe Ser Gln Thr His Gln Val Ser
            20                  25                  30
Leu Ser Lys Gln
        35


<210> 336
<211> 35
<212> PRT
<213> Human immundeficiency virus

<220>
<223> HIV type I Tat 38-72

<400> 336
Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr Gly Arg Lys Lys Arg Arg
 1               5                   10                  15
Gln Arg Arg Arg Pro Pro Gln Phe Ser Gln Thr His Gln Val Ser Leu
            20                  25                  30
Ser Lys Gln
        35


<210> 337
<211> 13
<212> PRT
<213> Human immundeficiency virus

<220>
<223> HIV type I Tat 47-59

<400> 337
Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro
 1               5                   10


<210> 338
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Transportan

<400> 338
Gly Trp Thr Leu Asn Ser Ala Gly Tyr Leu Leu Gly Lys Ile Asn Leu
 1               5                   10                  15
Lys Ala Leu Ala Ala Leu Ala Lys Lys Ile Leu
            20                  25


<210> 339
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Transportan 10

<400> 339
Ala Gly Tyr Leu Leu Gly Lys Ile Asn Leu Lys Ala Leu Ala Ala Leu
 1               5                   10                  15
Ala Lys Lys Ile Leu
            20


<210> 340
```

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

<220>
<223> Transportan derivative

<400> 340
Gly Trp Thr Leu Asn Ser Ala Gly Tyr Leu Leu Gly
 1   5   10

<210> 341
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Transportan derivative

<400> 341
Ile Asn Leu Lys Ala Leu Ala Ala Leu Ala Lys Lys Ile Leu
 1   5   10

<210> 342
<211> 34
<212> PRT
<213> Herpes simplex virus

<220>
<223> Herpes simplex virus 1 VP22

<400> 342
Asp Ala Ala Thr Ala Thr Arg Gly Arg Ser Ala Ala Ser Arg Pro Thr
 1   5   10   15
Glu Arg Pro Arg Ala Pro Ala Arg Ser Ala Ser Arg Pro Arg Arg Pro
            20   25   30
Val Asp

<210> 343
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> VT5

<400> 343
Asp Pro Lys Gly Asp Pro Lys Gly Val Thr Val Thr Val Thr Val Thr
 1   5   10   15
Val Thr Gly Lys Gly Asp Pro Lys Pro Asp
            20   25

<210> 344
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Signal sequence-based peptide

<400> 344
Gly Ala Leu Phe Leu Gly Trp Leu Gly Ala Ala Gly Ser Thr Met Gly
 1   5   10   15

Ala Trp Ser Gln Pro Lys Lys Lys Arg Lys Val
            20   25

<210> 345
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Amphiphilic model peptide

<400> 345
Lys Leu Ala Leu Lys Leu Ala Leu Lys Ala Leu Lys Ala Ala Leu Lys
 1   5   10   15
Leu Ala

<210> 346
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Bacterial cell wall permeating

<400> 346
Lys Phe Phe Lys Phe Phe Lys Phe Phe Lys
 1   5   10

<210> 347
<211> 37
<212> PRT
<213> Homo sapiens

<220>
<223> Human LL-37

<400> 347
Leu Leu Gly Asp Phe Phe Arg Lys Ser Lys Glu Lys Ile Gly Lys Glu
 1   5   10   15
Phe Lys Arg Ile Val Gln Arg Ile Lys Asp Phe Leu Arg Asn Leu Val
            20   25   30
Pro Arg Thr Glu Ser
        35

<210> 348
<211> 31
<212> PRT
<213> Sus scrofa

<220>
<223> Porcine cecropin P1

<400> 348
Ser Trp Leu Ser Lys Thr Ala Lys Lys Leu Glu Asn Ser Ala Lys Lys
 1   5   10   15
Arg Ile Ser Glu Gly Ile Ala Ile Ala Ile Gln Gly Gly Pro Arg
            20   25   30

<210> 349
<211> 30
<212> PRT
<213> Homo sapiens

<220>
<223> Human alpha defensin

<400> 349
Ala Cys Tyr Cys Arg Ile Pro Ala Cys Ile Ala Gly Glu Arg Arg Tyr
 1   5   10   15
Gly Thr Cys Ile Tyr Gln Gly Arg Leu Trp Ala Phe Cys Cys
            20   25   30

<210> 350
<211> 36
<212> PRT
<213> Homo sapiens

<220>
<223> Human beta defensin

<400> 350
Asp His Tyr Asn Cys Val Ser Ser Gly Gly Gln Cys Leu Tyr Ser Ala
 1   5   10   15
Cys Pro Ile Phe Thr Lys Ile Gln Gly Thr Cys Tyr Arg Gly Lys Ala
            20   25   30
Lys Cys Cys Lys
        35

<210> 351
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Bactenecin

<400> 351
Arg Lys Cys Arg Ile Trp Ile Arg Val Cys Arg
 1   5   10

<210> 352
<211> 42
<212> PRT
<213> Sus scrofa

<220>
<223> Porcine PR-39

<400> 352
Arg Arg Arg Pro Arg Pro Pro Tyr Leu Pro Arg Pro Arg Pro Pro Pro
 1   5   10   15
Phe Phe Pro Pro Arg Leu Pro Pro Arg Ile Pro Pro Gly Phe Pro Pro
            20   25   30
Arg Phe Pro Pro Arg Phe Pro Gly Lys Arg
        35   40

<210> 353
<211> 13
<212> PRT
<213> Bos taurus

<220>
<223> Bovine Indolicidin

<400> 353
Ile Leu Pro Trp Lys Trp Pro Trp Trp Pro Trp Arg Arg

```
 1               5                   10


<210> 354
<211> 27
<212> PRT
<213> Simian immunodeficiency virus

<220>
<223> SIV MPS

<400> 354
Gly Ala Leu Phe Leu Gly Trp Leu Gly Ala Ala Gly Ser Thr Met Gly
 1               5                   10                  15
Ala Trp Ser Gln Pro Lys Lys Lys Arg Lys Val
            20                  25


<210> 355
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> pIs1

<400> 355
Pro Val Ile Arg Arg Val Trp Phe Gln Asn Lys Arg Cys Lys Asp Lys
 1               5                   10                  15
Lys



<210> 356
<211> 330
<212> PRT
<213> Homo sapiens

<220>
<223> hIgG1 heavy chain constant

<400> 356
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
 1               5                   10                  15
Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20                  25                  30
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35                  40                  45
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50                  55                  60
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65                  70                  75                  80
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95
Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
            100                 105                 110
Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
        115                 120                 125
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
    130                 135                 140
Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145                 150                 155                 160
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
                165                 170                 175
Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
            180                 185                 190
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
        195                 200                 205
```

```
Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
    210                 215                 220
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225                 230                 235                 240
Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
                245                 250                 255
Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
            260                 265                 270
Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
        275                 280                 285
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
    290                 295                 300
Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305                 310                 315                 320
Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330


<210> 357
<211> 326
<212> PRT
<213> Homo sapiens

<220>
<223> hIgG2 heavy chain constant

<400> 357
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
 1               5                  10                  15
Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20                  25                  30
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35                  40                  45
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50                  55                  60
Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr
65                  70                  75                  80
Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95
Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
            100                 105                 110
Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
        115                 120                 125
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
    130                 135                 140
Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
145                 150                 155                 160
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
                165                 170                 175
Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp
            180                 185                 190
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
        195                 200                 205
Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu
    210                 215                 220
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
225                 230                 235                 240
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
                245                 250                 255
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
            260                 265                 270
Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
        275                 280                 285
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
    290                 295                 300
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
305                 310                 315                 320
Ser Leu Ser Pro Gly Lys
```

325

<210> 358
<211> 377
<212> PRT
<213> Homo sapiens

<220>
<223> hIgG3 heavy chain constant

<400> 358
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
 1   5   10   15
Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20   25   30
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35   40   45
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50   55   60
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65   70   75   80
Tyr Thr Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85   90   95
Arg Val Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro
            100   105   110
Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg
        115   120   125
Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys
    130   135   140
Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
145   150   155   160
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                165   170   175
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            180   185   190
Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Lys Trp Tyr
        195   200   205
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    210   215   220
Gln Tyr Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Leu His
225   230   235   240
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                245   250   255
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln
            260   265   270
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
        275   280   285
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    290   295   300
Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu Asn Asn
305   310   315   320
Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
                325   330   335
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile
            340   345   350
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln
        355   360   365
Lys Ser Leu Ser Leu Ser Pro Gly Lys
    370   375

<210> 359
<211> 327
<212> PRT
<213> Artificial Sequence

<220>

<223> hIgG4 heavy chain constant

<400> 359
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
 1   5   10   15
Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20   25   30
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35   40   45
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50   55   60
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
65   70   75   80
Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85   90   95
Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro
            100   105   110
Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
        115   120   125
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
    130   135   140
Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145   150   155   160
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
                165   170   175
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
            180   185   190
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
        195   200   205
Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
    210   215   220
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
225   230   235   240
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
                245   250   255
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
            260   265   270
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
        275   280   285
Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
    290   295   300
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
305   310   315   320
Leu Ser Leu Ser Leu Gly Lys
                325

<210> 360
<211> 231
<212> PRT
<213> Artificial Sequence

<220>
<223> hIgG1 Fc

<400> 360
Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
 1   5   10   15
Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
            20   25   30
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
        35   40   45
Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
    50   55   60
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
65   70   75   80
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
                85   90   95

```
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
            100                 105                 110
Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
        115                 120                 125
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
    130                 135                 140
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
145                 150                 155                 160
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
                165                 170                 175
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
            180                 185                 190
Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
        195                 200                 205
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
    210                 215                 220
Leu Ser Leu Ser Pro Gly Lys
225                 230
```

<210> 361
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> hIgG1 Fc

<400> 361

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

<210> 362
<211> 129
<212> PRT
<213> Artificial Sequence

<220>
<223> Rsv6/11/21/22/23 Heavy chain

<400> 362
Gln Val Lys Leu Leu Glu Gln Ser Gly Gly Gly Leu Val Gln Pro Gly
 1   5   10   15
Gly Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Val Thr Phe Ser Ala
            20   25   30
Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
        35   40   45
Val Ser Gly Ile Ser Gly Ser Gly Asp Ser Thr Asp Tyr Ala Asp Ser
    50   55   60
Val Lys Gly Arg Leu Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
65   70   75   80
Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr
                85   90   95
Cys Ala Ser His Leu Pro Asp Tyr Trp Asn Leu Asp Tyr Thr Arg Phe
            100   105   110
Phe Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser
        115   120   125
Ser

<210> 363
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Rsv6/11/21/22/23 Heavy CDR1

<400> 363
Ala Tyr Ala Met Ser
 1   5

<210> 364
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Rsv6/11/21/22/23 Heavy CDR2

<400> 364
Gly Ile Ser Gly Ser Gly Asp Ser Thr Asp Tyr Ala Asp Ser Val Lys
 1   5   10   15
Gly

<210> 365
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Rsv6/11/21/22/23 Heavy CDR3

<400> 365
His Leu Pro Asp Tyr Trp Asn Leu Asp Tyr Thr Arg Phe Phe Tyr Tyr
 1   5   10   15
Met Asp Val

<210> 366
<211> 120
<212> PRT

<213> Artificial Sequence

<220>
<223> Rsv13/19H Heavy chain

<400> 366
Gln Val Lys Leu Leu Glu Glu Ser Gly Gly Gly Leu Val Arg Leu Ala
 1   5   10   15
Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Thr Thr Leu Ser Gly
            20   25   30
Tyr Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
        35   40   45
Val Ser Ser Ile Thr Gly Gly Ser Asn Phe Ile Asn Tyr Ser Asp Ser
    50   55   60
Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu
65   70   75   80
Tyr Leu Gln Met Asn Ser Leu Thr Ala Glu Asp Thr Ala Val Tyr Tyr
                85   90   95
Cys Ala Thr Ala Pro Ile Ala Pro Pro Tyr Phe Asp His Trp Gly Gln
            100   105   110
Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 367
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Rsv13/19H Heavy CDR1

<400> 367
Gly Tyr Thr Met His
 1   5

<210> 368
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Rsv13/19H Heavy CDR2

<400> 368
Ser Ile Thr Gly Gly Ser Asn Phe Ile Asn Tyr Ser Asp Ser Val Lys
 1   5   10   15
Gly

<210> 369
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Rsv13/19H Heavy CDR3

<400> 369
Ala Pro Ile Ala Pro Pro Tyr Phe Asp His
 1   5   10

<210> 370
<211> 109
<212> PRT

<213> Artificial Sequence

<220>
<223> Rsv 6/11/21/22 Light chain

<400> 370
Met Ala Glu 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 Thr Gln Ser Ile Ser Ser Asn
            20   25   30
Tyr Leu Ala Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu
        35   40   45
Ile Tyr Gly Ala Ser Asn Arg Ala Thr Asp 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 Met Tyr Tyr Cys Gln Gln Tyr Asp Ile Ser Pro
                85   90   95
Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
            100   105

<210> 371
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Rsv 6/11/21/22 Light CDR1

<400> 371
Arg Ala Thr Gln Ser Ile Ser Ser Asn Tyr Leu Ala
 1   5   10

<210> 372
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Rsv 6/11/21/22 Light CDR2

<400> 372
Gly Ala Ser Asn Arg Ala Thr
 1   5

<210> 373
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Rsv 6/11/21/22 Light CDR3

<400> 373
Gln Gln Tyr Asp Ile Ser Pro Tyr Thr
 1   5

<210> 374
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Rsv23 Light Chain

<400> 374
Met Ala Glu Leu Thr Gln Ser Pro Val Thr Leu Ser Val Ser Pro Gly
 1   5   10   15
Glu Arg Val Ala Leu Ser Cys Lys Ala Ser Gln Asn Ile Asn Asp 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 Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Arg Leu Glu Pro
65   70   75   80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Gly Ser Pro Tyr
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr
            100   105

<210> 375
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Rsv23 Light CDR1

<400> 375
Lys Ala Ser Gln Asn Ile Asn Asp Asn Leu Ala
 1   5   10

<210> 376
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Rsv23 Light CDR2

<400> 376
Gly Ala Ser Ser Arg Ala Thr
 1   5

<210> 377
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Rsv23 Light CDR3

<400> 377
Gln Gln Tyr Gly Gly Ser Pro Tyr Thr
 1   5

<210> 378
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Rsv13/19 Light Chain

<400> 378
Met Ala Glu Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15

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


<210> 379
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Rsv13/19 Light CDR1

<400> 379
Arg Ala Thr Gln Ser Val Ser Asn Phe Leu Asn
 1               5                  10


<210> 380
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Rsv13/19 Light CDR2

<400> 380
Asp Ala Ser Thr Ser Gln Ser
 1               5


<210> 381
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Rsv13/19 Light CDR3

<400> 381
Gln Ala Ser Ile Asn Thr Pro Leu
 1               5


<210> 382
<211> 574
<212> PRT
<213> Artificial Sequence

<220>
<223> Respiratory Syncytial Virus Strain A2 F protein

<400> 382
Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
 1               5                  10                  15
Ala Val Thr Phe Cys Phe Ala Ser Gly Gln Asn Ile Thr Glu Glu Phe
            20                  25                  30
Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
        35                  40                  45
```

```
Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
    50                  55                  60
Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
65                  70                  75                  80
Gln Glu Leu Asp Lys Tyr Lys Asn Ala Val Thr Glu Leu Gln Leu Leu
                85                  90                  95
Met Gln Ser Thr Pro Pro Thr Asn Asn Arg Ala Arg Arg Glu Leu Pro
            100                 105                 110
Arg Phe Met Asn Tyr Thr Leu Asn Asn Ala Lys Lys Thr Asn Val Thr
        115                 120                 125
Leu Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val
    130                 135                 140
Gly Ser Ala Ile Ala Ser Gly Val Ala Val Ser Lys Val Leu His Leu
145                 150                 155                 160
Glu Gly Glu Val Asn Lys Ile Lys Ser Ala Leu Leu Ser Thr Asn Lys
                165                 170                 175
Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Ser Lys Val
            180                 185                 190
Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Val Asn
        195                 200                 205
Lys Gln Ser Cys Ser Ile Ser Asn Ile Glu Thr Val Ile Glu Phe Gln
    210                 215                 220
Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn
225                 230                 235                 240
Ala Gly Val Thr Thr Pro Val Ser Thr Tyr Met Leu Thr Asn Ser Glu
                245                 250                 255
Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys
            260                 265                 270
Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile
        275                 280                 285
Met Ser Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro
    290                 295                 300
Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
305                 310                 315                 320
Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg
                325                 330                 335
Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe
            340                 345                 350
Pro Gln Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp
        355                 360                 365
Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Ile Asn Leu Cys Asn Val
    370                 375                 380
Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr
385                 390                 395                 400
Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys
                405                 410                 415
Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile
            420                 425                 430
Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Met Asp
        435                 440                 445
Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly
    450                 455                 460
Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro
465                 470                 475                 480
Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn
                485                 490                 495
Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Lys Ser Asp Glu Leu
            500                 505                 510
Leu His Asn Val Asn Ala Gly Lys Ser Thr Thr Asn Ile Met Ile Thr
        515                 520                 525
Thr Ile Ile Ile Val Ile Ile Val Ile Leu Leu Ser Leu Ile Ala Val
    530                 535                 540
Gly Leu Leu Leu Tyr Cys Lys Ala Arg Ser Thr Pro Val Thr Leu Ser
545                 550                 555                 560
Lys Asp Gln Leu Ser Gly Ile Asn Asn Ile Ala Phe Ser Asn
                565                 570
```

<210> 383
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> VH-g1(a/b)-REV primer

<400> 383
acaagatttg ggctcaacty tcttgtcc 28

<210> 384
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> 5'L VLambda 1 primer

<400> 384
ggtcctgggc ccagtctgtg ctg 23

<210> 385
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> 5'L VLambda 2 primer

<400> 385
ggtcctgggc ccagtctgcc ctg 23

<210> 386
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> 5'L VLambda 3 primer

<400> 386
gctctgtgac ctcctatgag ctg 23

<210> 387
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> 5'L VLambda 4/5 primer

<400> 387
ggtctctctc scagcytgtg ctg 23

<210> 388
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> 5'L VLambda 6 primer

<400> 388
gttcttgggc caattttatg ctg 23

<210> 389
<211> 23

<212> DNA
<213> Artificial Sequence

<220>
<223> 5'L VLambda 7 primer

<400> 389
ggtccaattc ycaggctgtg gtg 23

<210> 390
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> 5'L VLambda 8 primer

<400> 390
gagtggattc tcagactgtg gtg 23

<210> 391
<211> 6822
<212> DNA
<213> Artificial Sequence

<220>
<223> 28d11/pCAL vector

<400> 391
atgcattagt tattaatagt aatcaattac ggggtcatta gttcatagcc catatatgga 60
gttccgcgtt acataactta cggtaaatgg cccgcctggc tgaccgccca acgacccccg 120
cccattgacg tcaataatga cgtatgttcc catagtaacg ccaataggga ctttccattg 180
acgtcaatgg gtggagtatt tacggtaaac tgcccacttg gcagtacatc aagtgtatca 240
tatgccaagt acgcccccta ttgacgtcaa tgacggtaaa tggcccgcct ggcattatgc 300
ccagtacatg accttatggg actttcctac ttggcagtac atctacgtat tagtcatcgc 360
tattaccatg gtgatgcggt tttggcagta catcaatggg cgtggatagc ggtttgactc 420
acggggattt ccaagtctcc accccattga cgtcaatggg agtttgtttt ggcaccaaaa 480
tcaacgggac tttccaaaat gtcgtaacaa ctccgcccca ttgacgcaaa tgggcggtag 540
gcgtgtacgg tgggaggtct atataagcag agctggttta gtgaaccgtc agatccgcta 600
gcgattacgc caagctcgaa attaaccctc actaaaggga acaaaagctg gagctccacc 660
gcggtggcgg ccgcccacca tggactggac ctggcggatc ctgttcctgg tggccgcggc 720
caccggggcc cacagccagc tgcagctgca ggagtcgggc ccaggactgg tgaaggtttc 780
ggacaccctg tccctcagct gcactgtctc tggtgactcc atcaatagtt attcctggag 840
ttggatccgg cagcccccag ggaagggact tgagtggatt ggatatctct attacagtgg 900
gagctccaat tatagtccct ccctcaaggg ccgagtcacc atgtcgctag acacgtccaa 960
gaaccagttt tccctgaagc ttcactctct gaccgctgcg gacacggccg tctattactg 1020
tgcgagagga tcttgtggta gaaccacctg ctactgggaa aaccactact acatggacgt 1080
ctggggcaaa gggaccgcgg tcaccgtctc ctcacagctg cagctgcagg agtcgggccc 1140
aggactggtg aaggtttcgg acaccctgtc cctcagctgc actgtctctg gtgactccat 1200
caatagttat tcctggagtt ggatccggca gcccccaggg aagggacttg agtggattgg 1260
atatctctat tacagtggga gctccaatta tagtccctcc ctcaagggcc gagtcaccat 1320
gtcgctagac acgtccaaga accagttttc cctgaagctt cactctctga ccgctgcgga 1380
cacggccgtc tattactgtg cgagaggatc ttgtggtaga accacctgct actgggaaaa 1440
ccactactac atggacgtct ggggcaaagg gaccgcggtc accgtctcct cagctagcac 1500
caagggcccc agcgtgttcc ccctggcccc cagcagcaag agcaccagcg gcggcaccgc 1560
cgccctgggc tgcctggtga aggactactt ccccgagccc gtgaccgtga gctggaacag 1620
cggcgccctg accagcggcg tgcacacctt ccccgccgtg ctgcagagca gcggcctgta 1680
cagcctgagc agcgtggtga ccgtgcccag cagcagcctg ggcacccaga cctacatctg 1740
caacgtgaac cacaagccca gcaacaccaa ggtggacaag aaggtggagc ccaagagctg 1800
cgacaaaact cacacatgcc caccgtgccc agcacctgaa ctcctggggg gaccgtcagt 1860
cttcctcttc cccccaaaac ccaaggacac cctcatgatc tcccggaccc ctgaggtcac 1920
atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc aagttcaact ggtacgtgga 1980
cggcgtggag gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta 2040
ccgggtggtc agcgtcctca ccgtcctgca ccaggactgg ctgaatggca aggagtacaa 2100
gtgcaaggtc tccaacaaag ccctcccagc ccccatcgag aaaaccatct ccaaagccaa 2160
agggcagccc cgagaaccac aggtgtacac cctgccccca tcccgggatg agctgaccaa 2220
gaaccaggtc agcctgacct gcctggtcaa aggcttctat cccagcgaca tcgccgtgga 2280
gtgggagagc aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc 2340

cgacggctcc ttcttcctct acagcaagct caccgtggac aagagcaggt ggcagcaggg 2400
gaacgtcttc tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag 2460
cctctccctg tctccgggta aacgggccaa gcgggcaccc gtgaagcaga ccctgaactt 2520
cgacctgctg aagctggccg gcgacgtgga gagcaacccc ggccccatga ggctccctgc 2580
tcagctcctg gggctgctaa tgctctgggt ccctggctcg agtgaggttc tgcctgtgct 2640
gactcagcca ccctcagcgt ctgcgacccc cgggcagagg gtcaccatct cttgttctgg 2700
aagcagctcc aacatcgggc gtaatactgt aaactggtac cagcgtctcc caggaacggc 2760
ccccaaactc ctcatctata atactaatca gcggccctca ggggtccctg accgattctc 2820
tggctccaag tctggcacct cagccgccct ggccatcagt ggactccagt ctgaggatga 2880
ggctgagtat tactgtgcag cctgggatga cagcctgaat ggcctttctt gggtgttcgg 2940
cggagggacc aagctgaccg tcctaagtca gcccaaggct gccccctcgg tcactctgtt 3000
cccgccctcc tctgaggagc ttcaagccaa caaggccaca ctggtgtgtc tcataagtga 3060
cttctacccg ggagccgtga cagcctggaa ggcagatagc agccacgtca aggcgggagt 3120
ggagaccacc acaccctcca aacaaagcaa caacaagtac gcggccagca gctacctgag 3180
cctgacgcct gagcagtgga agtcccacaa aagctacagc tgccaggtca cgcatgaagg 3240
gagcaccgtg gagaagacaa ttgcccctac agaatgctca taaggccggg acggccggta 3300
ccaggtaagt gtacccaatt cgccctatag tgagtcgtat tacaattcac tcgatcgccc 3360
ttcccaacag ttgcgcagcc tgaatggcga atggagatcc aatttttaag tgtataatgt 3420
gttaaactac tgattctaat tgtttgtgta ttttagattc acagtcccaa ggctcatttc 3480
aggcccctca gtcctcacag tctgttcatg atcataatca gccataccac atttgtagag 3540
gttttacttg ctttaaaaaa cctcccacac ctccccctga acctgaaaca taaaatgaat 3600
gcaattgttg ttgttaactt gtttattgca gcttataatg gttacaaata aagcaatagc 3660
atcacaaatt tcacaaataa agcatttttt tcactgcatt ctagttgtgg tttgtccaaa 3720
ctcatcaatg tatcttaacg cgtaaattgt aagcgttaat attttgttaa aattcgcgtt 3780
aaatttttgt taaatcagct catttttaa ccaataggcc gaaatcggca aaatccctta 3840
taaatcaaaa gaatagaccg agatagggtt gagtgttgtt ccagtttgga acaagagtcc 3900
actattaaag aacgtggact ccaacgtcaa agggcgaaaa accgtctatc agggcgatgg 3960
cccactacgt gaaccatcac cctaatcaag ttttttgggg tcgaggtgcc gtaaagcact 4020
aaatcggaac cctaaaggga gcccccgatt tagagcttga cggggaaagc cggcgaacgt 4080
ggcgagaaag gaagggaaga aagcgaaagg agcgggcgct agggcgctgg caagtgtagc 4140
ggtcacgctg cgcgtaacca ccacacccgc cgcgcttaat gcgccgctac agggcgcgtc 4200
aggtggcact tttcggggaa atgtgcgcgg aacccctatt tgtttatttt tctaaataca 4260
ttcaaatatg tatccgctca tgagacaata accctgataa atgcttcaat aatattgaaa 4320
aaggaagaat cctgaggcgg aaagaaccag ctgtggaatg tgtgtcagtt agggtgtgga 4380
aagtccccag gctccccagc aggcagaagt atgcaaagca tgcatctcaa ttagtcagca 4440
accaggtgtg gaaagtcccc aggctcccca gcaggcagaa gtatgcaaag catgcatctc 4500
aattagtcag caaccatagt cccgccccta actccgccca tcccgccccc aactccgccc 4560
agttccgccc attctccgcc ccatggctga ctaatttttt ttatttatgc agaggccgag 4620
gccgcctccg cctctgagct attccagaag tagtgaggag gctttttggg aggcctaggc 4680
ttttgcaaag atcgatcaag agacaggatg aggatcgttt cgcatgattg aacaagatgg 4740
attgcacgca ggttctccgg ccgcttgggt ggagaggcta ttcggctatg actgggcaca 4800
acagacaatc ggctgctctg atgccgccgt gttccggctg tcagcgcagg ggcgcccggt 4860
tctttttgtc aagaccgacc tgtccggtgc cctgaatgaa ctgcaagacg aggcagcgcg 4920
gctatcgtgg ctggccacga cgggcgttcc ttgcgcagct gtgctcgacg ttgtcactga 4980
agcgggaagg gactggctgc tattgggcga agtgccgggg caggatctcc tgtcatctca 5040
ccttgctcct gccgagaaag tatccatcat ggctgatgca atgcggcggc tgcatacgct 5100
tgatccggct acctgcccat tcgaccacca agcgaaacat cgcatcgagc gagcacgtac 5160
tcggatggaa gccggtcttg tcgatcagga tgatctggac gaagaacatc aggggctcgc 5220
gccagccgaa ctgttcgcca ggctcaaggc gagcatgccc gacggcgagg atctcgtcgt 5280
gacccatggc gatgcctgct tgccgaatat catggtggaa aatggccgct tttctggatt 5340
catcgactgt ggccggctgg gtgtggcgga ccgctatcag gacatagcgt tggctacccg 5400
tgatattgct gaagaacttg gcggcgaatg ggctgaccgc ttcctcgtgc tttacggtat 5460
cgccgctccc gattcgcagc gcatcgcctt ctatcgcctt cttgacgagt tcttctgagc 5520
gggactctgg ggttcgaaat gaccgaccaa gcgacgccca acctgccatc acgagatttc 5580
gattccaccg ccgccttcta tgaaaggttg ggcttcggaa tcgttttccg ggacgccggc 5640
tggatgatcc tccagcgcgg ggatctcatg ctggagttct tcgcccaccc taggggggagg 5700
ctaactgaaa cacggaagga gacaataccg gaaggaaccc gcgctatgac ggcaataaaa 5760
agacagaata aaacgcacgg tgttgggtcg tttgttcata aacgcggggt tcggtcccag 5820
ggctggcact ctgtcgatac cccaccgaga ccccattggg gccaatacgc ccgcgtttct 5880
tccttttccc caccccaccc cccaagttcg ggtgaaggcc cagggctcgc agccaacgtc 5940
ggggcggcag gccctgccat agcctcaggt tactcatata tactttagat tgatttaaaa 6000
cttcattttt aatttaaaag gatctaggtg aagatccttt ttgataatct catgaccaaa 6060
atcccttaac gtgagttttc gttccactga gcgtcagacc ccgtagaaaa gatcaaagga 6120
tcttcttgag atccttttttt tctgcgcgta atctgctgct tgcaaacaaa aaaaccaccg 6180
ctaccagcgg tggtttgttt gccggatcaa gagctaccaa ctctttttcc gaaggtaact 6240
ggcttcagca gagcgcagat accaaatact gtccttctag tgtagccgta gttaggccac 6300
cacttcaaga actctgtagc accgcctaca tacctcgctc tgctaatcct gttaccagtg 6360
gctgctgcca gtggcgataa gtcgtgtctt accgggttgg actcaagacg atagttaccg 6420

gataaggcgc agcggtcggg ctgaacgggg ggttcgtgca cacagcccag cttggagcga 6480
acgacctaca ccgaactgag atacctacag cgtgagctat gagaaagcgc cacgcttccc 6540
gaagggagaa aggcggacag gtatccggta agcggcaggg tcggaacagg agagcgcacg 6600
agggagcttc cagggggaaa cgcctggtat ctttatagtc ctgtcgggtt tcgccacctc 6660
tgacttgagc gtcgattttt gtgatgctcg tcaggggggc ggagcctatg gaaaaacgcc 6720
agcaacgcgg cctttttacg gttcctggcc ttttgctggc cttttgctca catgttcttt 6780
cctgcgttat cccctgattc tgtggataac cgtattaccg cc 6822

<210> 392
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> FabLinkerCLambda-Fwd

<400> 392
gacartkgcc cmtrcagaat gctcataatt aattaataag gaggatataa ttatgaaaaa 60
g 61

<210> 393
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> FabLinker-Rev-IT*

<400> 393
tgcggccgcc tacgctacgg tagcaaagcc agccagtgcc ac 42

<210> 394
<211> 5882
<212> DNA
<213> Artificial Sequence

<220>
<223> 2G12 pCAL IT* vector

<400> 394
gtggcacttt tcggggaaat gtgcgcggaa cccctatttg tttatttttc taaatacatt 60
caaatatgta tccgctcatg agacaataac cctgataaat gcttcaataa tattgaaaaa 120
ggaagagtat gagtattcaa catttccgtg tcgcccttat tccctttttt gcggcatttt 180
gccttcctgt ttttgctcac ccagaaacgc tggtgaaagt aaaagatgct gaagatcagt 240
tgggtgcacg agtgggttac atcgaactgg atctcaacag cggtaagatc cttgagagtt 300
ttcgccccga agaacgtttt ccaatgatga gcacttttaa agttctgcta tgtggcgcgg 360
tattatcccg tattgacgcc gggcaagagc aactcggtcg ccgcatacac tattctcaga 420
atgacttggt tgagtactca ccagtcacag aaaagcatct tacggatggc atgacagtaa 480
gagaattatg cagtgctgcc ataaccatga gtgataacac tgcggccaac ttacttctga 540
caacgatcgg aggaccgaag gagctaaccg ctttttgca caacatgggg gatcatgtaa 600
ctcgccttga tcgttgggaa ccggagctga atgaagccat accaaacgac gagcgtgaca 660
ccacgatgcc tgtagcaatg gcaacaacgt tgcgcaaact attaactggc gaactactta 720
ctctagcttc ccggcaacaa ttaatagact ggatggaggc ggataaagtt gcaggaccac 780
ttctgcgctc ggcccttccg gctggctggt ttattgctga taaatctgga gccggtgagc 840
gtgggtctcg cggtatcatt gcagcactgg ggccagatgg taagccctcc cgtatcgtag 900
ttatctacac gacggggagt caggcaacta tggatgaacg aaatagacag atcgctgaga 960
taggtgcctc actgattaag cattggtaac tgtcagacca agtttactca tatatacttt 1020
agattgattt aaaacttcat ttttaattta aaaggatcta ggtgaagatc ctttttgata 1080
atctcatgac caaaatccct taacgtgagt tttcgttcca ctgagcgtca gaccccgtag 1140
aaaagatcaa aggatcttct tgagatcctt tttttctgcg cgtaatctgc tgcttgcaaa 1200
caaaaaaacc accgctacca gcggtggttt gtttgccgga tcaagagcta ccaactcttt 1260
ttccgaaggt aactggcttc agcagagcgc agataccaaa tactgtcctt ctagtgtagc 1320
cgtagttagg ccaccacttc aagaactctg tagcaccgcc tacatacctc gctctgctaa 1380
tcctgttacc agtggctgct gccagtggcg ataagtcgtg tcttaccggg ttggactcaa 1440
gacgatagtt accggataag gcgcagcggt cgggctgaac gggggttcg tgcacacagc 1500
ccagcttgga gcgaacgacc tacaccgaac tgagatacct acagcgtgag ctatgagaaa 1560

gcgccacgct tcccgaaggg agaaaggcgg acaggtatcc ggtaagcggc agggtcggaa 1620
caggagagcg cacgagggag cttccagggg gaaacgcctg gtatctttat agtcctgtcg 1680
ggtttcgcca cctctgactt gagcgtcgat ttttgtgatg ctcgtcaggg gggcggagcc 1740
tatggaaaaa cgccagcaac gcggcctttt tacggttcct ggccttttgc tggccttttg 1800
ctcacatgtt ctttcctgcg ttatcccctg attctgtgga taaccgtatt accgcctttg 1860
agtgagctga taccgctcgc cgcagccgaa cgaccgagcg cagcgagtca gtgagcgagg 1920
aagcgacacc atcgaatggc gcaaaacctt tcgcggtatg gcatgatagc gcccggaaga 1980
gagtcaattc agggtggtga atgtgaaacc agtaacgtta tacgatgtcg cagagtatgc 2040
cggtgtctct tatcagaccg tttcccgcgt ggtgaaccag gccagccacg tttctgcgaa 2100
aacgcgggaa aaagtggaag cggcgatggc ggagctgaat tacattccca accgcgtggc 2160
acaacaactg gcgggcaaac agtcgttgct gattggcgtt gccacctcca gtctggccct 2220
gcacgcgccg tcgcaaattg tcgcggcgat taaatctcgc gccgatcaac tgggtgccag 2280
cgtggtggtg tcgatggtag aacgaagcgg cgtcgaagcc tgtaaagcgg cggtgcacaa 2340
tcttctcgcg caacgcgtca gtgggctgat cattaactat ccgctggatg accaggatgc 2400
cattgctgtg gaagctgcct gcactaatgt tccggcgtta tttcttgatg tctctgacca 2460
gacacccatc aacagtatta ttttctccca tgaagacggt acgcgactgg gcgtggagca 2520
tctggtcgca ttgggtcacc agcaaatcgc gctgttagcg ggcccattaa gttctgtctc 2580
ggcgcgtctg cgtctggctg gctggcataa atatctcact cgcaatcaaa ttcagccgat 2640
agcggaacgg gaaggcgact ggagtgccat gtccggtttt caacaaacca tgcaaatgct 2700
gaatgagggc atcgttccca ctgcgatgct ggttgccaac gatcagatgg cgctgggcgc 2760
aatgcgcgcc attaccgagt ccgggctgcg cgttggtgcg gatatctcgg tagtgggata 2820
cgacgatacc gaagacagct catgttatat cccgccgtta accaccatca aacaggattt 2880
tcgcctgctg gggcaaacca gcgtggaccg cttgctgcaa ctctctcagg gccaggcggt 2940
gaagggcaat cagctgttgc ccgtctcact ggtgaaaaga aaaaccaccc tggcgcccaa 3000
tacgcaaacc gcctctcccc gcgcgttggc cgattcatta atgcagctgg cacgacaggt 3060
ttcccgactg gaaagcgggc agtgagcggt acccgataaa agcggcttcc tgacaggagg 3120
ccgttttgtt ttgcagccca cctcaacgca attaatgtga gttagctcac tcattaggca 3180
ccccaggctt tacactttat gcttccggct cgtatgttgt gtggaattgt gagcggataa 3240
caattgaatt aaggaggata taattatgaa atacctgctg ccgaccgcag ccgctggtct 3300
gctgctgctc gcggcctagc cggccatggc cgccggtgtt gttatgaccc agtctccgtc 3360
taccctgtct gcttctgttg gtgacaccat caccatcacc tgccgtgctt ctcagtctat 3420
cgaaacctgg ctggcttggt accagcagaa accgggtaaa gctccgaaac tgctgatcta 3480
caaggcttct accctgaaaa ccggtgttcc gtctcgtttc tctggttctg gttctggtac 3540
cgagttcacc ctgaccatct ctggtctgca gttcgacgac ttcgctacct accactgcca 3600
gcactacgct ggttactctg ctaccttcgg tcagggtacc cgtgttgaaa tcaaacgtac 3660
cgttgctgct ccgtctgttt tcatcttccc gccgtctgac gaacagctga aatctggtac 3720
cgcttctgtt gtttgcctgc tgaacaactt ctacccgcgt gaagctaaag ttcagtggaa 3780
agttgacaac gctctgcagt ctggtaactc tcaggaatct gttaccgaac aggactctaa 3840
agactctacc tactctctgt cttctaccct gaccctgtct aaagctgact acgaaaagca 3900
caaagtttac gcttgcgaag ttacccacca gggtctgtct tctccggtta ccaaatcttt 3960
caaccgtggt gaatgctaat taattaataa ggaggatata attatgaaaa agacagctat 4020
cgcgattgca gtggcactgg ctggtttcgc taccgtagcc taggcggccg cagaagttca 4080
gctggttgaa tctggtggtg gtctggttaa agctggtggt tctctgatcc tgtcttgcgg 4140
tgtttctaac ttccgtatct ctgctcacac catgaactgg gttcgtcgtg ttccgggtgg 4200
tggtctggaa tgggttgctt ctatctctac ctcttctacc taccgtgact acgctgacgc 4260
tgttaaaggt cgtttcaccg tttctcgtga cgacctggaa gacttcgttt acctgcagat 4320
gcataaaatg cgtgttgaag acaccgctat ctactactgc gctcgtaaag gttctgaccg 4380
tctgtctgac aacgacccgt tcgacgcttg gggtccgggt accgttgtta ccgtttctcc 4440
ggcgtcgacc aaaggtccgt ctgttttccc gctggctccg tcttctaaat ctacctctgg 4500
tggtaccgct gctctgggtt gcctggttaa agactacttc ccggaaccgg ttaccgtttc 4560
ttggaactct ggtgctctga cctctggtgt tcacaccttc ccggctgttc tgcagtcttc 4620
tggtctgtac tctctgtctt ctgttgttac cgttccgtct tcttctctgg gtacccagac 4680
ctacatctgc aacgttaacc acaaaccgtc taacaccaaa gttgacaaga aagttgaacc 4740
gaaatcttgc ctgcgatcgc ggccaggccg gccgcaccat caccatcacc atggcgcata 4800
cccgtacgac gttccggact acgcttctac tagttaggag ggtggtggct ctgagggtgg 4860
cggttctgag ggtggcggct ctgagggagg cggttccggt ggtggctctg gttccggtga 4920
ttttgattat gaaaagatgg caaacgctaa taaggggggct atgaccgaaa atgccgatga 4980
aaacgcgcta cagtctgacg ctaaaggcaa acttgattct gtcgctactg attacggtgc 5040
tgctatcgat ggtttcattg gtgacgtttc cggccttgct aatggtaatg gtgctactgg 5100
tgattttgct ggctctaatt cccaaatggc tcaagtcggt gacggtgata attcaccttt 5160
aatgaataat ttccgtcaat atttaccttc cctccctcaa tcggttgaat gtcgcccttt 5220
tgtctttggc gctggtaaac catatgaatt ttctattgat tgtgacaaaa taaacttatt 5280
ccgtggtgtc tttgcgtttc ttttatatgt tgccaccttt atgtatgtat tttctacgtt 5340
tgctaacata ctgcgtaata aggagtctta agctagctaa cgatcgccct tcccaacagt 5400
tgcgcagcct gaatggcgaa tgggacgcgc cctgtagcgg cgcattaagc gcggcgggtg 5460
tggtggttac gcgcagcgtg accgctacac ttgccagcgc cctagcgccc gctcctttcg 5520
ctttcttccc ttcctttctc gccacgttcg ccggctttcc ccgtcaagct ctaaatcggg 5580
ggctcccttt agggttccga tttagtgctt tacggcacct cgaccccaaa aaacttgatt 5640

```
agggtgatgg ttcacgtagt gggccatcgc cctgatagac ggtttttcgc cctttgacgt 5700
tggagtccac gttctttaat agtggactct tgttccaaac tggaacaaca ctcaacccta 5760
tctcggtcta ttcttttgat ttataaggga ttttgccgat ttcggcctat tggttaaaaa 5820
atgagctgat ttaacaaaaa tttaacgcga attttaacaa aatattaacg cttacaattt 5880
ag                                                                5882
```

<210> 395
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> 30D8 Light Chain

<400> 395

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

<210> 396
<211> 224
<212> PRT
<213> Artificial Sequence

<220>
<223> 30D8 Fab Heavy Chain

<400> 396

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

```
Ala Arg Glu Trp Leu Val Met Gly Gly Phe Ala Phe Asp His Trp Gly
            100                 105                 110
Gln Gly Thr Leu Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
        115                 120                 125
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
    130                 135                 140
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
    210                 215                 220


<210> 397
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> 104E5 Light Chain

<400> 397
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Pro Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Lys Thr Tyr
            20                  25                  30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Arg Ala Pro Lys Leu Leu Ile
        35                  40                  45
Ser Ala Val Ser Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Thr 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 Phe Ser Ile Pro Leu
                85                  90                  95
Thr Phe Gly Gly Gly Ala 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 Leu 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> 398
<211> 228
<212> PRT
<213> Artificial Sequence

<220>
<223> 104E5 Fab Heavy Chain

<400> 398
Gln Val Gln Leu Glu Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1               5                  10                  15
```

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


<210> 399
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> 38F10 Light Chain

<400> 399
Asp Ile Gln Leu Thr Gln Ser Pro Pro Thr Leu Ser Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Ser Met Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Trp
            20                  25                  30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45
Gln Lys Ala Ser Asn Leu Glu Asp Gly Val Pro Ser Arg Phe Thr Ala
    50                  55                  60
Ser Gly Phe Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Ser Gly
                85                  90                  95
Leu Ser Phe Gly Gly Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
            100                 105                 110
Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115                 120                 125
Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    130                 135                 140
Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160
Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
                165                 170                 175
Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
            180                 185                 190
Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
        195                 200                 205
Ser Phe Asn Arg Gly Glu Cys
    210                 215
```

<210> 400
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> 38F10 Fab Heavy Chain

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

<210> 401
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> 14G3 Light Chain

<400> 401
Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
 1   5   10   15
Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Asp Ser
            20   25   30
Asp Asp Gly Asn Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln
        35   40   45
Ser Pro Gln Leu Leu Ile Tyr Thr Leu Ser Tyr Arg Ala Ser Gly Val
    50   55   60
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys
65   70   75   80
Ile Ser Arg Val Glu Ala Asp Asp Val Gly Ile Tyr Tyr Cys Met Gln
                85   90   95
Arg Met Glu Phe Pro Phe Thr Phe Gly Gln Gly Thr Arg Leu Asp Ile
            100   105   110
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
        115   120   125
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn

```
    130                 135                 140
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145                 150                 155                 160
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
                165                 170                 175
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
            180                 185                 190
Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
        195                 200                 205
Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215                 220


<210> 402
<211> 228
<212> PRT
<213> Artificial Sequence

<220>
<223> 14G3 Fab Heavy Chain

<400> 402
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1               5                  10                  15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Ala Ser Ile Ser Ser Asp
            20                  25                  30
Asn His Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45
Trp Ile Ala Ser Ile Tyr Tyr Thr Gly Gly Thr Asn Tyr Asn Pro Ser
    50                  55                  60
Leu Lys Ser Arg Leu Ala Leu Ser Ile Asp Thr Ser Gly Asp Gln Phe
65                  70                  75                  80
Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95
Cys Val Arg Gly Leu Phe Phe Ile Thr Ala Arg Pro Tyr Trp Tyr Phe
            100                 105                 110
Asp Leu Trp Gly Arg Gly Thr Leu Val Ala Val Ser Ser Ala Ser Thr
        115                 120                 125
Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
    130                 135                 140
Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
145                 150                 155                 160
Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
                165                 170                 175
Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
            180                 185                 190
Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
        195                 200                 205
Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
    210                 215                 220
Pro Lys Ser Cys
225


<210> 403
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> 9OD3 Light Chain

<400> 403
Ala Ile Arg Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Ser Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Phe
            20                  25                  30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Arg Ala Pro Lys Leu Leu Ile
```

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


<210> 404
<211> 226
<212> PRT
<213> Artificial Sequence

<220>
<223> 9OD3 Fab Heavy Chain

<400> 404
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Val Gly Ser Gly Phe Thr Leu Lys Asn Tyr
            20                  25                  30
Glu Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Gln Tyr Ile
        35                  40                  45
Ser Tyr Ile Ser Ser Ser Gly Asn Val Val Lys Tyr Val Asp Ser Val
    50                  55                  60
Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Gly Asn Ser Leu Tyr
65                  70                  75                  80
Leu Gln Met Asn Asn Leu Arg Ala Glu Asp Thr Ala Thr Tyr Tyr Cys
                85                  90                  95
Val Arg Gly Phe Ser Ile Asp Lys Tyr Asp Ser Ser Val Asp Glu Tyr
            100                 105                 110
Trp Gly Gln Gly Ile Ala Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125
Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140
Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160
Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
    210                 215                 220
Ser Cys
225


<210> 405
<211> 10
```

<212> PRT
<213> Artificial Sequence

<220>
<223> 30D8 VH CDR1

<400> 405
Gly Phe Thr Phe Ser Gly His Thr Ile Ala
 1   5   10

<210> 406
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 30D8 VH CDR2

<400> 406
Trp Val Ser Thr Asn Asn Gly Asn Thr Glu Tyr Ala Gln Lys Ile Gln
 1   5   10   15
Gly

<210> 407
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> 30D8 VH CDR3

<400> 407
Glu Trp Leu Val Met Gly Gly Phe Ala Phe Asp His
 1   5   10

<210> 408
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 30D8 VL CDR1

<400> 408
Gly Ala Asn Asn Ile Gly Ser Gln Asn Val His
 1   5   10

<210> 409
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 30D8 VL CDR2

<400> 409
Asp Asp Arg Asp Arg Pro Ser
 1   5

<210> 410
<211> 12
<212> PRT

<213> Artificial Sequence

<220>
<223> 30D8 VL CDR3

<400> 410
Gln Val Trp Asp Ser Ser Arg Asp Gln Ala Val Ile
 1   5   10

<210> 411
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 104E5 VH CDR1

<400> 411
Gly Gly Thr Phe Asp Thr Tyr Thr Ile Ser
 1   5   10

<210> 412
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 104E5 VH CDR2

<400> 412
Arg Ile Ile Pro Ser Leu Gly Glu Thr Asn Tyr Ala His Lys Leu Gln
 1   5   10   15
Gly

<210> 413
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> 104E5 VH CDR3

<400> 413
Arg Ile Thr Gly Pro Val Asp Trp Val Trp Asp Tyr Gly Met Asp Val
 1   5   10   15

<210> 414
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 104E5 VL CDR1

<400> 414
Arg Ala Ser Gln Asn Ile Lys Thr Tyr Leu Asn
 1   5   10

<210> 415
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 104E5 VL CDR2

<400> 415
Ala Val Ser Asn Leu Gln Ser
 1   5

<210> 416
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 104E5 VL CDR3

<400> 416
Gln Gln Ser Phe Ser Ile Pro Leu Thr
 1   5

<210> 417
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 38F10 VH CDR1

<400> 417
Gly Phe Ser Ile Thr Asp Phe Gly Ile His
 1   5   10

<210> 418
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 38F10 VH CDR2

<400> 418
Leu Ile Ser Tyr Asn Glu Val Asn Ile His Tyr Gly Glu Ser Val Arg
 1   5   10   15
Gly

<210> 419
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 38F10 VH CDR3

<400> 419
Asp Val Trp Glu Asp Ser Trp Leu Ser Leu Ala Cys Phe Gln Glu
 1   5   10   15

<210> 420
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 38F10 VL CDR1

<400> 420
Arg Ala Ser Gln Ser Ile Ser Asn Trp Leu Ala
 1   5   10

<210> 421
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 38F10 VL CDR2

<400> 421
Lys Ala Ser Asn Leu Glu Asp
 1   5

<210> 422
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 38F10 VL CDR3

<400> 422
Gln Gln Tyr Asn Ser Tyr Ser Gly Leu Ser
 1   5   10

<210> 423
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> 14G3 VH CDR1

<400> 423
Gly Ala Ser Ile Ser Ser Asp Asn His Tyr Trp Ser
 1   5   10

<210> 424
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> 14G3 VH CDR2

<400> 424
Ser Ile Tyr Tyr Thr Gly Gly Thr Asn Tyr Asn Pro Ser Leu Lys Ser
 1   5   10   15

<210> 425
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 14G3 VH CDR3

<400> 425
Gly Leu Phe Phe Ile Thr Ala Arg Pro Tyr Trp Tyr Phe Asp Leu
 1   5   10   15

<210> 426
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 14G3 VL CDR1

<400> 426
Arg Ser Ser Gln Ser Leu Leu Asp Ser Asp Asp Gly Asn Thr Tyr Leu
 1   5   10   15
Asp

<210> 427
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 14G3 VL CDR2

<400> 427
Thr Leu Ser Tyr Arg Ala Ser
 1   5

<210> 428
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 14G3 VL CDR3

<400> 428
Met Gln Arg Met Glu Phe Pro Phe Thr
 1   5

<210> 429
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 9OD3 VH CDR1

<400> 429
Gly Phe Thr Leu Lys Asn Tyr Glu Met Asn
 1   5   10

<210> 430
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 9OD3 VH CDR2

<400> 430

Tyr Ile Ser Ser Ser Gly Asn Val Val Lys Tyr Val Asp Ser Val Gln
 1   5   10   15
Gly

<210> 431
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 9OD3 VH CDR3

<400> 431
Gly Phe Ser Ile Asp Lys Tyr Asp Ser Ser Val Asp Glu Tyr
 1   5   10

<210> 432
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 9OD3 VL CDR1

<400> 432
Arg Ala Ser Gln Ser Ile Ser Asn Phe Leu Asn
 1   5   10

<210> 433
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 9OD3 VL CDR2

<400> 433
Ala Ala Ser Ser Leu Gln Gly
 1   5

<210> 434
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 9OD3 VL CDR3

<400> 434
Gln Gln Thr Tyr Ile Ser Leu Tyr Thr
 1   5

<210> 435
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 58c5 VH CDR1

<400> 435
Ser Asp Asn Tyr Tyr Trp Thr

1 5

<210> 436
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> sc5 VH CDR1

<400> 436
Gly Ser Asn Trp Trp Asn
1 5

<210> 437
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> 30D8 VH CDR1

<400> 437
Gly His Thr Ile Ala
1 5

<210> 438
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> 104E5 VH CDR1

<400> 438
Thr Tyr Thr Ile Ser
1 5

<210> 439
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> 38F10 VH CDR1

<400> 439
Asp Phe Gly Ile His
1 5

<210> 440
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 14G3 VH CDR1

<400> 440
Ser Asp Asn His Tyr Trp Ser
1 5

<210> 441
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> 9OD3 VH CDR1

<400> 441
Asn Tyr Glu Met Asn
 1   5

<210> 442
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> 3OD8 Light Chain

<400> 442
cagtctgtgc tgacgcaggc atcctcggtg tcagtggccc caggacagac ggccagaatt 60
acctgtgggg caaacaacat tggaagtcaa aatgttcact ggtaccagca gaagccaggc 120
caggcccctg ttttggtcgt ctatgatgat cgcgaccggc cctcagggat ccctgaccga 180
ttctctggct ccaactctgg gaatacggcc accctgacca tcagcagggt cgaggccggg 240
gatgaggccg actattactg tcaggtgtgg gatagtagtc gtgatcaggc cgtaattttt 300
ggcggaggga ccaagctgac cgtcctaggt cagcccaagg ctgcccctc ggtcactctg 360
ttcccgccct cctctgagga gcttcaagcc aacaaggcca cactggtgtg tctcataagt 420
gacttctacc cgggagccgt gacagtggcc tggaaggcag atagcagccc cgtcaaggcg 480
ggagtggaga ccaccacacc ctccaaacaa agcaacaaca agtacgcggc cagcagctac 540
ctgagcctga cgcctgagca gtggaagtcc cacagaagct acagctgcca ggtcacgcat 600
gaagggagca ccgtggagaa gacaattgcc cctacagaat gctca   645

<210> 443
<211> 672
<212> DNA
<213> Artificial Sequence

<220>
<223> 3OD8 Fab Heavy Chain

<400> 443
gaggtgcagc tgttgcagtc tggagcagag ttgaagaagc ctggggcctc agtgaagatc 60
tcctgcaaga cttctggttt cacctttagc ggtcatacta tcgcctgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatgggctgg gtcagcacta ataatggaaa cacagagtat 180
gcacagaaga tccagggcag agtcaccatg actatggaca catcaacgag cacagtctac 240
atggagttga ggagcctgac atctgacgac acggccgtgt atttctgtgc gagagagtgg 300
ctggtcatgg ggggcttcgc ctttgaccac tggggccagg gaaccctgct caccgtctcc 360
tcagcctcca ccaagggccc atcggtcttc cccctggcac cctcctccaa gagcacctct 420
gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540
tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 600
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gagagttgag 660
cccaaatctt gt   672

<210> 444
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> 1O4E5 Light Chain

<400> 444
gacatccaga tgacccagtc tccatcctcc ctgcctgcat ctgtgggaga cagagtcacc 60
atcacttgcc gggcaagtca gaacattaag acctatttaa attggtatca gcagaaacca 120
gggagagccc ctaaactcct gatctctgct gtgtccaatt tacaaagtgg ggtcccgtca 180

aggttcagtg gcaccggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcagcag agtttcagta ttccgctcac tttcggcgga 300
ggggccaagg tggagatcaa acgaactgtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa ctctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gctaa 645

<210> 445
<211> 684
<212> DNA
<213> Artificial Sequence

<220>
<223> 104E5 Fab Heavy Chain

<400> 445
caggtccaat tggaacagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
tcctgcaagc cttctggagg caccttcgac acatacacta tcagctgggt gcgacaggcc 120
cctggacaac gtcttgagtg gctgggaagg atcatccctt cacttggtga aacaaactat 180
gcacacaaac tccagggcag agtcacgatt accgcggaca aagccacgag tgtcgtctat 240
atggacctga gcgacctgac atccgaggac gcggccgtct attactgtgc atttcgtata 300
actggacctg tcgactgggt ctgggactat gggatggacg tctggggcca agggaccacg 360
gtcagcgtct cgtcagcctc cagcaagggc ccatcggtct tcccctggc accctcctcc 420
aagagcacct ctgggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa 480
ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct 540
gtcctacagt cctcaggact ctactccctc agcagcgtgg tgaccgtgcc ctccagcagc 600
ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac 660
aagagagttg agcccaaatc ttgt 684

<210> 446
<211> 684
<212> DNA
<213> Artificial Sequence

<220>
<223> 38F10 Light Chain

<400> 446
ccggccatgg ccgccggtga catccagttg acccagtctc cccccaccct gtctgcgtct 60
gtgggagaca gagtctccat gacttgccgg gccagtcaga gtattagtaa ctggttggcc 120
tggtatcagc aaaaaccagg gaaagccccct aaactcctca tccagaaggc gtccaattta 180
gaagatggcg tcccctcacg gttcaccgcc agtggatttg ggacagaatt cactctcacc 240
atcagcagcc tacagcctga tgatttcgca acttattact gtcaacagta taatagttac 300
tcaggcctca gtttcggcgg agggaccaag gtggacatca aacgaactgt ggctgcacca 360
tctgtcttca tcttcccgcc atctgatgag cagttgaaat ctggaactgc ctctgttgtg 420
tgcctgctga ataacttcta tcccagagag gccaaagtac agtggaaggt ggataacgcc 480
ctccaatcgg gtaactccca ggagagtgtc acagagcagg acagcaagga cagcacctac 540
agcctcagca gcaccctgac gctgagcaaa gcagactacg agaaacacaa agtctacgcc 600
tgcgaagtca cccatcaggg cctgagctcg cccgtcacaa agagcttcaa caggggagag 660
tgctaattaa ttaataagga ggat 684

<210> 447
<211> 726
<212> DNA
<213> Artificial Sequence

<220>
<223> 38F10 Fab Heavy Chain

<400> 447
gcggccgcag aggtgcagct gttggagtct gggggagacg tggtccagcc tgggaagtcc 60
ctgagactct cctgcacagc ctctggattc agcatcactg actttggcat ccactgggtc 120
cgccaggctc caggcaaggg gctggagtgg gtggccctta tttcatataa cgaagtaaat 180
atacactatg gcgagtccgt gaggggccgc ttcaccatct ccagagacat tgccaagaac 240
acagtatatc tgcagatgaa tggcctgaga cctgaagaca cgggtgtgta tttttgtgcg 300
agggatgtct gggaggactc gtggctgtca cttgcgtgct tccaggaatg gggccagggc 360

tccctggtcg tcgtctcatc agcctccacc aagggcccat cggtcttccc cctggcaccc 420
tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctggtcaa ggactacttc 480
cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 540
ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc 600
agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 660
gtggacaaga aagttgagcc caaatcttgt ggtcggccag gccggccgca ccatcaccat 720
caccat 726

<210> 448
<211> 663
<212> DNA
<213> Artificial Sequence

<220>
<223> 14G3 Light Chain

<400> 448
gatgttgtga tgacccagac tccactctcc ctgtccgtca cccctggaga gccggcctcc 60
atctcctgca ggtctagtca gagcctcttg gatagtgatg atggaaacac ctatttggac 120
tggtacctgc agaagccagg gcagtctcca cagctcctga tctatacact ttcctatcgg 180
gcctctggag tcccagacag gttcagtggc agtgggtcag gcactgattt cacactgaaa 240
atcagcaggg tggaggctga cgatgttgga atttattact gcatgcaacg tatggagttt 300
cccttcacct tcggccaagg gacacgactg gacattaaac gaactgtggc tgcaccatct 360
gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc 420
ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgccctc 480
caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 540
ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600
gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgc 660
taa 663

<210> 449
<211> 684
<212> DNA
<213> Artificial Sequence

<220>
<223> 14G3 Fab Heavy Chain

<400> 449
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60
acctgcactg tctctggtgc ctccatcagc agtgataatc actactggag ttggattcga 120
cagccccccg ggaagggcct ggagtggatt gcttccatct attacactgg tggcaccaac 180
tacaacccgt ccctcaagag tcgactcgcc ttatcaatag acacgtccgg ggaccagttc 240
tccttgaagc tgagctctgt gactgccgca gacacggccg tctattactg tgtcaggggc 300
ttgtttttca taacagctcg tccctactgg tacttcgatc tctggggccg tggcaccctg 360
gtcgctgtct cctcagcctc caccaagggc ccatcggtct tccccctggc accctcctcc 420
aagagcacct ctgggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa 480
ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct 540
gtcctacagt cctcaggact ctactccctc agcagcgtgg tgaccgtgcc ctccagcagc 600
ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac 660
aagagagttg agcccaaatc ttgt 684

<210> 450
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> 90D3 Light Chain

<400> 450
gccatccggt tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcagc 60
atcacttgcc gggcaagtca gagtattagc aacttttaa attggtatca gcagaaacca 120
gggagagccc cgaaactcct gatctctgct gcatccagtt tgcaaggtgg ggtcccatca 180
agattcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag acttacattt ccctgtacac ctttggccag 300
gggaccaaac tggagatcaa acgaactgtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

```
cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gc                    642

<210> 451
<211> 723
<212> DNA
<213> Artificial Sequence

<220>
<223> 9OD3 Fab Light Chain

<400> 451
gcggccgcac aggtgcagct ggtggagtcg gggggaggcc tggtaaagcc tggagggtcc 60
ctgagactct cgtgtgtagg ctctggattc accctcaaga attatgagat gaattgggtc 120
cgccaggctc cagggcaggg gctacaatat atttcataca tcagtagcag tggcaatgtc 180
gttaagtacg tagactctgt gcagggccga ttcaccatct ccagagacaa cgccgggaat 240
tcgctgtatc tccaaatgaa caacctgagg gccgaggaca cggccactta ttactgtgtg 300
agaggttttt cgatcgataa gtatgatagc agtgttgatg aatactgggg ccagggaatc 360
gcggtcaccg tctcctcagc ctccaccaag ggcccatcgg tcttcccccc ggcaccctcc 420
tccaagagca cctctggggg cacagcggcc ctgggctgcc tggtcaagga ctacttcccc 480
gaaccggtga cggtgtcgtg gaactcaggc gccctgacca gcggcgtgca caccttcccg 540
gctgtcctac agtcctcagg actctactcc ctcagcagcg tggtgaccgt gccctccagc 600
agcttgggca cccagaccta catctgcaac gtgaatcaca agcccagcaa caccaaggtg 660
gacaagaaag ttgagcccaa atcttgtggt cggccaggcc ggccgcacca tcaccatcac 720
cat                                                              723

<210> 452
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> 56E11 Heavy Chain

<400> 452
Glu 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 Ser Val Ser Gly Val Ser Ile Asn Ser Asn
            20                  25                  30
Asn Tyr Phe Trp Ala Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45
Trp Ile Gly Asn Ile Tyr Tyr Gly Gly Ser Thr His Tyr Asn Ala Ser
    50                  55                  60
Leu Gln Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Ser Gln Phe
65                  70                  75                  80
Ser Leu Lys Leu Asn Ser Val Thr Ser Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95
Cys Ala Ala Ser Glu Ser Ile Phe Trp Asp Tyr Tyr Tyr Gly Leu Asp
            100                 105                 110
Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys
        115                 120                 125
Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
    130                 135                 140
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
145                 150                 155                 160
Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
                165                 170                 175
Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
            180                 185                 190
Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
        195                 200                 205
Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
    210                 215                 220
Lys Ser Cys
225
```

<210> 453
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> 56E11 Light Chain

<400> 453
Gln Ala Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Ser Pro Gly Gln
 1   5   10   15
Ser Val Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
            20   25   30
Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Arg Leu
        35   40   45
Ile Ile Ser Glu Val Thr Lys Arg Pro Ser Gly Val Pro Gly Arg Phe
    50   55   60
Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Val Ser Gly Leu
65   70   75   80
Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Ala Gly Ser
                85   90   95
Arg His Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
            100   105   110
Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
        115   120   125
Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
    130   135   140
Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
145   150   155   160
Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
                165   170   175
Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
            180   185   190
Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
        195   200   205
Thr Ile Ala Pro Ala Glu Cys Ser
    210   215

<210> 454
<211> 236
<212> PRT
<213> Artificial Sequence

<220>
<223> 17C9 Heavy Chain

<400> 454
Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Val Arg Pro Ser Glu
 1   5   10   15
Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Asp Ser Phe Asn Asp Tyr
            20   25   30
Phe Trp Thr Trp Ile Arg Gln Thr Pro Gly Lys Gly Leu Glu Trp Ile
        35   40   45
Gly Glu Ile Ser His Ser Gly Ser Thr Asn Tyr Ser Pro Ser Leu Lys
    50   55   60
Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65   70   75   80
Lys Leu Ser Ala Val Thr Ala Ala Asp Thr Thr Val Tyr Phe Cys Ala
                85   90   95
Arg Gly Val Arg Ser Arg Pro Pro Pro Ser Tyr Arg Gly Ser Gly Ser
            100   105   110
Pro Pro Tyr Tyr His Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr
        115   120   125
Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
    130   135   140
Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys

145 150 155 160
Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
165 170 175
Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
180 185 190
Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
195 200 205
Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
210 215 220
Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225 230 235

<210> 455
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> 17C9 Light Chain

<400> 455
Glu Ile Val Leu Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Asn Thr Trp
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Ala Ala Ser Phe 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 Asn Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Ala Asn Ser Phe Pro Arg
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Val 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> 456
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> 69F6 Heavy Chain

<400> 456
Gln Met Gln Leu Val Gln Ser Gly Ala Glu Val Arg Lys Pro Gly Glu
1 5 10 15
Ser Leu Lys Ile Ala Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30
Trp Ile Ala Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45
Gly Ile Ile Phe Pro Asn Asp Ser Asp Ala Thr Tyr Ser Pro Ser Phe

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


<210> 457
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> 69F6 Light Chain

<400> 457
Glu Ile Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1                  5                  10                  15
Asp Arg Val Thr Ile Ser Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
            20                  25                  30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
        35                  40                  45
Tyr Asp Ala Ser Tyr Leu Asp Thr Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asp Leu Arg Gly
                85                  90                  95
Gly Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Val Lys Arg Thr Val
            100                 105                 110
Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
        115                 120                 125
Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
    130                 135                 140
Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
145                 150                 155                 160
Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
                165                 170                 175
Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
            180                 185                 190
Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
        195                 200                 205
Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215


<210> 458
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
```

<223> 56E11 VH CDR1

<400> 458
Gly Val Ser Ile Asn Ser Asn Asn Tyr Phe Trp Ala
 1   5   10

<210> 459
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> 56E11 VH CDR2

<400> 459
Asn Ile Tyr Tyr Gly Gly Ser Thr His Tyr Asn Ala Ser Leu Gln Ser
 1   5   10   15

<210> 460
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 56E11 VH CDR3

<400> 460
Ser Glu Ser Ile Phe Trp Asp Tyr Tyr Tyr Gly Leu Asp Val
 1   5   10

<210> 461
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 56E11 VL CDR1

<400> 461
Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr Asn Tyr Val Ser
 1   5   10

<210> 462
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 56E11 VL CDR2

<400> 462
Glu Val Thr Lys Arg Pro Ser
 1   5

<210> 463
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 56E11 VL CDR3

<400> 463

Ser Ser Tyr Ala Gly Ser Arg His Val Val
 1   5   10

<210> 464
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 17C9 VH CDR1

<400> 464
Gly Asp Ser Phe Asn Asp Tyr Phe Trp Thr
 1   5   10

<210> 465
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> 17C9 VH CDR2

<400> 465
Glu Ile Ser His Ser Gly Ser Thr Asn Tyr Ser Pro Ser Leu Lys Ser
 1   5   10   15

<210> 466
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 17C9 VH CDR3

<400> 466
Gly Val Arg Ser Arg Pro Pro Pro Ser Tyr Arg Gly Ser Gly Ser Pro
 1   5   10   15
Pro Tyr Tyr His Tyr Gly Met Asp Val
            20   25

<210> 467
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 17C9 VL CDR1

<400> 467
Arg Ala Ser Gln Asn Ile Asn Thr Trp Leu Ala
 1   5   10

<210> 468
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 17C9 VL CDR2

<400> 468
Ala Ala Ser Phe Leu Gln Ser

1 5

<210> 469
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 17C9 VL CDR3

<400> 469
Gln Gln Ala Asn Ser Phe Pro Arg Thr
1 5

<210> 470
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 69F6 VH CDR1

<400> 470
Gly Tyr Ser Phe Thr Ser Tyr Trp Ile Ala
1 5 10

<210> 471
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 69F6 VH CDR2

<400> 471
Ile Ile Phe Pro Asn Asp Ser Asp Ala Thr Tyr Ser Pro Ser Phe Gln
1 5 10 15
Gly

<210> 472
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 69F6 VH CDR3

<400> 472
Gln Tyr Tyr Leu Gly Ser Phe Glu Ser
1 5

<210> 473
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 69F6 VL CDR1

<400> 473
Gln Ala Ser Asp Ile Ser Asn Tyr Leu Asn
1 5 10

<210> 474
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 69F6 VL CDR2

<400> 474
Asp Ala Ser Tyr Leu Asp Thr
 1   5

<210> 475
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 69F6 VL CDR3

<400> 475
Gln Gln Tyr Asp Asp Leu Arg Gly Gly Phe Thr
 1   5   10

<210> 476
<211> 648
<212> DNA
<213> Artificial Sequence

<220>
<223> 56E11 Light Chain

<400> 476
caggctgtgc tgactcagcc tccctccgcg tccgggtctc ctggacagtc agtcaccatc 60
tcctgcactg gaaccagcag tgacgttggt ggttataatt atgtctcctg gtaccaacaa 120
caccccggga aagcccccag actcataatt tctgaagtca ctaagcggcc ctcaggggtc 180
cctggtcgct tctccggctc caagtctggc aacacggcct ccctgaccgt ctctgggctc 240
caggctgagg atgaggctga ttattactgc agctcatatg caggcagcag gcatgtggtt 300
ttcggcggag ggaccaagtt gaccgtcctc ggtcagccca aggctgcccc ctcggtcact 360
ctgttcccgc cctcctctga ggagcttcaa gccaacaagg ccacactggt gtgtctcata 420
agtgacttct acccgggagc cgtgacagtg gcctggaagg cagatagcag ccccgtcaag 480
gcgggagtgg agaccaccac accctccaaa caaagcaaca acaagtacgc ggccagcagc 540
tacctgagcc tgacgcctga gcagtggaag tcccacagaa gctacagctg ccaggtcacg 600
catgaaggga gcaccgtgga gaagacaatt gcccctgcag aatgctca   648

<210> 477
<211> 681
<212> DNA
<213> Artificial Sequence

<220>
<223> 56E11 Heavy Chain

<400> 477
gaggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60
acctgcagtg tctctggtgt ctccatcaac agcaacaatt atttctgggc ctggatccgc 120
cagcccccag gcaaggggct ggagtggatt gggaatatct attatggtgg gagcacccac 180
tacaatgcgt ccctgcagag tcgagtcacc atatccgtag acacgtccaa gagccagttc 240
tccctgaagc tgaactctgt gacctccgcc gacacggctg tgtattactg tgcggcttcc 300
gagtctatct tttgggacta ctactacggc ctggacgtct ggggccaagg gaccacggtc 360
accgtctcct ctgcctccac caagggccca tcggtcttcc ccctggcacc ctcctccaag 420
agcacctctg ggggcacagc ggccctgggc tgcctggtca aggactactt ccccgaaccg 480
gtgacggtgt cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc 540
ctacagtcct caggactcta ctccctcagc agcgtggtga ccgtgccctc cagcagcttg 600

ggcacccaga cctacatctg caacgtgaat cacaagccca gcaacaccaa ggtggacaag 660
aaagttgagc ccaaatcttg t 681

<210> 478
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> 17C9 Light Chain

<400> 478
gaaattgtgt tgacccagtc tccttccacc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggccagtca gaatattaat acctggttgg cctggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatgct gcatcctttt tgcaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcaa cttgcagcct 240
gaagattttg caacttactt ttgtcaacag gctaacagtt tccctcggac cttcggccag 300
gggaccaagg tggaagtcaa acgaactgtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gc 642

<210> 479
<211> 708
<212> DNA
<213> Artificial Sequence

<220>
<223> 17C9 Heavy Chain

<400> 479
caggtacagc tgcagcagtg gggcgcagga ctggtgaggc cttcggagac cctgtccctc 60
acctgcgctg tctatggtga ctccttcaat gattacttct ggacgtggat ccgccagacc 120
ccaggaaagg ggctggagtg gattggggaa atcagtcata gtggaagcac caactacagc 180
ccgtccctca agagtcgagt caccatatca gttgacacgt ccaagaacca gttctccctg 240
aaactcagcg ctgtgaccgc cgcggacacg actgtgtatt tctgtgcgag aggtgtccgc 300
tcccgacccc ctccgagtta ccgtggctcg ggctcccccc cttactacca ttacggtatg 360
gacgtctggg gccaagggac cacggtcacc gtctcctcag cctccaccaa gggcccatcg 420
gtcttccccc tggcaccctc ctccaagagc acctctgggg gcacagcggc cctgggctgc 480
ctggtcaagg actacttccc cgaaccggtg acggtgtcgt ggaactcagg cgccctgacc 540
agcggcgtgc acaccttccc ggctgtccta cagtcctcag gactctactc cctcagcagc 600
gtggtgaccg tgccctccag cagcttgggc acccagacct acatctgcaa cgtgaatcac 660
aagcccagca acaccaaggt ggacaagaga gttgagccca aatcttgt 708

<210> 480
<211> 648
<212> DNA
<213> Artificial Sequence

<220>
<223> 69F6 Light Chain

<400> 480
gaaattgtgt tgacccagtc tccatcctcc ctgtctgcat ctgtcggaga cagagtcacc 60
atctcttgcc aggcgagtca ggacattagc aactatttaa attggtatca acagaaacca 120
gggaaagccc ctaggctcct gatctacgat gcatcctatt tggacacagg ggtcccatca 180
aggttcagtg gaagtggatc tgggacagat tttactttca ccatcagcag cctacagcct 240
gaagattttg caacatatta ctgtcaacaa tatgatgatc tccgggggg gttcactttc 300
ggccctggga ccaaagtgga cgtcaaacga actgtggctg caccatctgt cttcatcttc 360
ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 420
ttctatccca gagaggccaa agtacagtgg aaggtggata acgccctcca atcgggtaac 480
tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 540
ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 600
cagggcctga gctcgcccgt cacaaagagc ttcaacaggg gagagtgc 648

<210> 481

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

<220>
<223> 69F6 Heavy Chain

<400> 481
cagatgcagc tggtgcagtc tggagcagag gtgagaaagc cgggggagtc tctgaagatc 60
gcctgtaagg gttccggata cagttttacc agctactgga tcgcctgggt gcgccagatg 120
cccgggaaag gcctggaatg gctggggatc atctttccta atgactctga tgccacatac 180
agcccgtcct tccaaggcca ggtcaccatg tcagtcgaca agtccatcag caccgcctac 240
ctgcagtgga acagcctgaa ggcctcggac accgccgtgt atttttgtgc gagacagtat 300
tatcttggct cgtttgaatc ctggggccaa ggaaccacgg tcaccgtctc ctcagcctcc 360
accaagggcc catcggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca 420
gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540
tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600
tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagttga gcccaaatct 660
tgt 663

<210> 482
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 56E11 VH CDR1

<400> 482
Ser Asn Asn Tyr Phe Trp Ala
 1   5

<210> 483
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> 17C9 VH CDR1

<400> 483
Asp Tyr Phe Trp Thr
 1   5

<210> 484
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> 69F6 VH CDR1

<400> 484
Ser Tyr Trp Ile Ala
 1   5

<210> 485
<211> 574
<212> PRT
<213> Respiratory syncytial virus

<220>
<223> F Protein

<400> 485
Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
 1   5   10   15
Ala Val Thr Phe Cys Phe Ala Ser Gly Gln Asn Ile Thr Glu Glu Phe
            20   25   30
Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
        35   40   45
Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
    50   55   60
Lys Lys Asn Lys Cys Asn Gly Thr Asp Ala Lys Ala Lys Leu Ile Lys
65   70   75   80
Gln Glu Leu Asp Lys Tyr Lys Asn Ala Val Thr Glu Leu Gln Leu Leu
                85   90   95
Met Gln Ser Thr Gln Ala Thr Asn Asn Arg Ala Arg Arg Glu Leu Pro
            100   105   110
Arg Phe Met Asn Tyr Thr Leu Asn Asn Ala Lys Lys Thr Asn Val Thr
        115   120   125
Leu Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val
    130   135   140
Gly Ser Ala Ile Ala Ser Gly Val Ala Val Ser Lys Val Leu His Leu
145   150   155   160
Glu Gly Glu Val Asn Lys Ile Lys Ser Ala Leu Leu Ser Thr Asn Lys
                165   170   175
Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Ser Lys Val
            180   185   190
Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Val Asn
        195   200   205
Lys Gln Ser Cys Ser Ile Ser Asn Ile Glu Thr Val Ile Glu Phe Gln
    210   215   220
Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn
225   230   235   240
Ala Gly Val Thr Thr Pro Val Ser Thr Tyr Met Leu Thr Asn Ser Glu
                245   250   255
Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys
            260   265   270
Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile
        275   280   285
Met Ser Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro
    290   295   300
Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
305   310   315   320
Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg
                325   330   335
Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe
            340   345   350
Pro Gln Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp
        355   360   365
Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Val Asn Leu Cys Asn Val
    370   375   380
Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr
385   390   395   400
Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys
                405   410   415
Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile
            420   425   430
Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp
        435   440   445
Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly
    450   455   460
Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro
465   470   475   480
Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn
                485   490   495
Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Lys Ser Asp Glu Leu
            500   505   510
Leu His Asn Val Ile Ala Gly Lys Ser Thr Thr Asn Ile Met Ile Thr
        515   520   525
Thr Ile Ile Ile Val Ile Ile Val Ile Leu Leu Ser Leu Ile Ala Val

```
    530                 535                 540
Gly Leu Leu Leu Tyr Cys Lys Ala Arg Ser Thr Pro Val Thr Leu Ser
545                 550                 555                 560
Lys Asp Gln Leu Ser Gly Ile Asn Asn Ile Ala Phe Ser Asn
                565                 570


<210> 486
<211> 574
<212> PRT
<213> Artificial Sequence

<220>
<223> Motavizumab MARM F protein

<400> 486
Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
 1               5                  10                  15
Ala Val Thr Phe Cys Phe Ala Ser Gly Gln Asn Ile Thr Glu Glu Phe
            20                  25                  30
Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
        35                  40                  45
Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
    50                  55                  60
Lys Lys Asn Lys Cys Asn Gly Thr Asp Ala Lys Ala Lys Leu Ile Lys
65                  70                  75                  80
Gln Glu Leu Asp Lys Tyr Lys Asn Ala Val Thr Glu Leu Gln Leu Leu
                85                  90                  95
Met Gln Ser Thr Gln Ala Thr Asn Asn Arg Ala Arg Arg Glu Leu Pro
            100                 105                 110
Arg Phe Met Asn Tyr Thr Leu Asn Asn Ala Lys Lys Thr Asn Val Thr
        115                 120                 125
Leu Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val
    130                 135                 140
Gly Ser Ala Ile Ala Ser Gly Val Ala Val Ser Lys Val Leu His Leu
145                 150                 155                 160
Glu Gly Glu Val Asn Lys Ile Lys Ser Ala Leu Leu Ser Thr Asn Lys
                165                 170                 175
Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Ser Lys Val
            180                 185                 190
Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Val Asn
        195                 200                 205
Lys Gln Ser Cys Ser Ile Ser Asn Ile Glu Thr Val Ile Glu Phe Gln
    210                 215                 220
Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn
225                 230                 235                 240
Ala Gly Val Thr Thr Pro Val Ser Thr Tyr Met Leu Thr Asn Ser Glu
                245                 250                 255
Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Glu
            260                 265                 270
Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile
        275                 280                 285
Met Ser Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro
    290                 295                 300
Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
305                 310                 315                 320
Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg
                325                 330                 335
Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe
            340                 345                 350
Pro Gln Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp
        355                 360                 365
Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Val Asn Leu Cys Asn Val
    370                 375                 380
Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr
385                 390                 395                 400
Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys
                405                 410                 415
```

```
Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile
            420                 425                 430
Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp
        435                 440                 445
Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly
    450                 455                 460
Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro
465                 470                 475                 480
Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn
                485                 490                 495
Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Lys Ser Asp Glu Leu
            500                 505                 510
Leu His Asn Val Ile Ala Gly Lys Ser Thr Thr Asn Ile Met Ile Thr
        515                 520                 525
Thr Ile Ile Ile Val Ile Ile Val Ile Leu Leu Ser Leu Ile Ala Val
    530                 535                 540
Gly Leu Leu Leu Tyr Cys Lys Ala Arg Ser Thr Pro Val Thr Leu Ser
545                 550                 555                 560
Lys Asp Gln Leu Ser Gly Ile Asn Asn Ile Ala Phe Ser Asn
                565                 570
```

<210> 487
<211> 574
<212> PRT
<213> Artificial Sequence

<220>
<223> 58C5 MARM F protein

<400> 487

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

```
    290                 295                 300
Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
305                 310                 315                 320
Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg
                325                 330                 335
Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe
            340                 345                 350
Pro Gln Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp
        355                 360                 365
Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Val Asn Leu Cys Asn Val
    370                 375                 380
Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr
385                 390                 395                 400
Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys
                405                 410                 415
Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile
            420                 425                 430
Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp
        435                 440                 445
Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly
    450                 455                 460
Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro
465                 470                 475                 480
Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn
                485                 490                 495
Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Lys Ser Asp Glu Leu
            500                 505                 510
Leu His Asn Val Ile Ala Gly Lys Ser Thr Thr Asn Ile Met Ile Thr
        515                 520                 525
Thr Ile Ile Ile Val Ile Ile Val Ile Leu Leu Ser Leu Ile Ala Val
    530                 535                 540
Gly Leu Leu Leu Tyr Cys Lys Ala Arg Ser Thr Pro Val Thr Leu Ser
545                 550                 555                 560
Lys Asp Gln Leu Ser Gly Ile Asn Asn Ile Ala Phe Ser Asn
                565                 570
```