SEQUENCE LISTING

<110> F. Hoffmann-La Roche AG

<120> Bispecific antigen binding molecules comprising anti-4-1BB clone 20H4.9

<130> P34053-WO

<150> EP17164224.2
<151> 2017-03-31

<150> EP17150150.5
<151> 2017-01-03

<160> 217

<170> PatentIn version 3.5

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<400> 1

Gly Tyr Tyr Trp Ser
1 5

<210> 2
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<220>
<223> 4-1BB (20H4.9) CDR-H2

<400> 2

Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu Ser
1 5 10 15

<210> 3
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<212> PRT

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<220>
<223> 4-1BB (20H4.9) CDR-H3

<400> 3

Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu
1 5 10

<210> 4
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<212> PRT
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<220>
<223> 4-1BB (20H4.9) CDR-L1

<400> 4

Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala
1 5 10

<210> 5
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<220>
<223> 4-1BB (20H4.9) CDR-L2

<400> 5

Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 6
<211> 11
<212> PRT
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<220>
<223> 4-1BB (20H4.9) CDR-L3

<400> 6

Gln Gln Arg Ser Asn Trp Pro Pro Ala Leu Thr

1 5 10

<210> 7
<211> 121
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<213> Artificial Sequence

<220>
<223> 4-1BB (20H4.9) VH

<400> 7

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

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

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

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
50 55 60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 8
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-1BB (20H4.9) VL

<400> 8

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
            20   25   30

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

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

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

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

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

<210> 9
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> FAP(28H1) CDR-H1

<400> 9

Ser His Ala Met Ser
1   5

<210> 10
<211> 16
<212> PRT

<213> Artificial Sequence

<220>
<223> FAP(28H1) CDR-H2

<400> 10

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

<210> 11
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> FAP(28H1) CDR-H3

<400> 11

Gly Trp Leu Gly Asn Phe Asp Tyr
1 5

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

<220>
<223> FAP(28H1) CDR-L1

<400> 12

Arg Ala Ser Gln Ser Val Ser Arg Ser Tyr Leu Ala
1 5 10

<210> 13
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> FAP(28H1) CDR-L2

<400> 13

Gly Ala Ser Thr Arg Ala Thr

1 5

<210> 14
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> FAP(28H1) CDR-L3

<400> 14

Gln Gln Gly Gln Val Ile Pro Pro Thr
1 5

<210> 15
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> FAP(4B9) CDR-H1

<400> 15

Ser Tyr Ala Met Ser
1 5

<210> 16
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> FAP(4B9) CDR-H2

<400> 16

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

Gly

<210> 17

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

<220>
<223> FAP(4B9) CDR-H3

<400> 17

Gly Trp Phe Gly Gly Phe Asn Tyr
1 5

<210> 18
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> FAP(4B9) CDR-L1

<400> 18

Arg Ala Ser Gln Ser Val Thr Ser Ser Tyr Leu Ala
1 5 10

<210> 19
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> FAP(4B9) CDR-L2

<400> 19

Val Gly Ser Arg Arg Ala Thr
1 5

<210> 20
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> FAP(4B9) CDR-L3

<400> 20

Gln Gln Gly Ile Met Leu Pro Pro Thr
1   5

<210> 21
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> FAP(28H1) VH

<400> 21

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

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

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

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

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

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

Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100   105   110

Thr Val Ser Ser
        115

<210> 22
<211> 108
<212> PRT

<213> Artificial Sequence

<220>
<223> FAP(28H1) VL

<400> 22

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Arg Ser
20 25 30

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

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

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

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

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

<210> 23
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> FAP(4B9) VH

<400> 23

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

```
            20                  25                  30

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

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

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

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

Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110

Val Thr Val Ser Ser
        115


<210>  24
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  FAP(4B9) VL

<400>  24

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Ser Ser
            20                  25                  30

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

Ile Asn Val Gly Ser Arg Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
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50 55 60

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

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Gly Ile Met Leu Pro
85 90 95

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

<210> 25
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA (T84.66-LCHA)- CDR-H1

<400> 25

Asp Thr Tyr Met His
1 5

<210> 26
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA (T84.66-LCHA)- CDR-H2

<400> 26

Arg Ile Asp Pro Ala Asn Gly Asn Ser Lys Tyr Val Pro Lys Phe Gln
1 5 10 15

Gly

<210> 27
<211> 12
<212> PRT

<213> Artificial Sequence

<220>
<223> CEA (T84.66-LCHA)- CDR-H3

<400> 27

Phe Gly Tyr Tyr Val Ser Asp Tyr Ala Met Ala Tyr
1 5 10

<210> 28
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA (T84.66-LCHA)- CDR-L1

<400> 28

Arg Ala Gly Glu Ser Val Asp Ile Phe Gly Val Gly Phe Leu His
1 5 10 15

<210> 29
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA (T84.66-LCHA)- CDR-L2

<400> 29

Arg Ala Ser Asn Arg Ala Thr
1 5

<210> 30
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA (T84.66-LCHA)- CDR-L3

<400> 30

Gln Gln Thr Asn Glu Asp Pro Tyr Thr

1 5

<210> 31
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA (T84.66-LCHA) VH

<400> 31

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Thr
20 25 30

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

Gly Arg Ile Asp Pro Ala Asn Gly Asn Ser Lys Tyr Val Pro Lys Phe
50 55 60

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

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

Ala Pro Phe Gly Tyr Tyr Val Ser Asp Tyr Ala Met Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 32
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA (T84.66-LCHA) VL

<400> 32

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

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

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

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

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

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

Glu Asp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100   105   110

<210> 33
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA (A5B7)- CDR-H1

<400> 33

Ser Tyr Trp Met His
1   5

<210> 34
<211> 16
<212> PRT

<213> Artificial Sequence

<220>
<223> CEA (A5B7)- CDR-H2

<400> 34

Phe Ile Arg Asn Lys Ala Asn Gly Gly Thr Thr Glu Tyr Ala Ala Ser
1 5 10 15

<210> 35
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA (A5B7)- CDR-H3

<400> 35

Asp Arg Gly Leu Arg Phe Tyr Phe Asp Tyr
1 5 10

<210> 36
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA (A5B7)- CDR-L1

<400> 36

Thr Leu Arg Arg Gly Ile Asn Val Gly Ala Tyr Ser Ile Tyr
1 5 10

<210> 37
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA (A5B7)- CDR-L2

<400> 37

Tyr Lys Ser Asp Ser Asp Lys Gln Gln Gly Ser

1 5 10

<210> 38
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA (A5B7)- CDR-L3

<400> 38

Met Ile Trp His Ser Gly Ala Ser Ala Val
1 5 10

<210> 39
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA (A5B7) VH

<400> 39

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

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

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

Gly Phe Ile Arg Asn Lys Ala Asn Gly Gly Thr Thr Glu Tyr Ala Ala
50 55 60

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

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

Tyr Cys Ala Arg Asp Arg Gly Leu Arg Phe Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 40
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA (A5B7) VL

<400> 40

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

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

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

Leu Leu Arg Tyr Lys Ser Asp Ser Asp Lys Gln Gln Gly Ser Gly Val
50 55 60

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

Leu Leu Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys
85 90 95

Met Ile Trp His Ser Gly Ala Ser Ala Val Phe Gly Gly Gly Thr Lys
100 105 110

Leu Thr Val Leu
115

<210> 41
<211> 1734
<212> DNA
<213> Artificial Sequence

<220>
<223> VHCH1 (20H4.9)-Heavy chain hole-VL (4B9) (nucleotide sequence)

<400> 41
caggtgcagc tgcagcagtg gggagccgga ctgctgaagc ctagcgagac actgagcctg 60

acctgcgccg tgtacggcgg cagcttcagc ggctactact ggtcctggat cagacagagc 120

cccgagaagg gcctggaatg gatcggcgag atcaaccacg gcggctacgt gacctacaac 180

cccagcctgg aaagcagagt gaccatcagc gtggacacca gcaagaacca gttcagcctg 240

aagctgagca gcgtgacagc cgccgacaca gccgtgtact actgcgccag agattacggc 300

cctggcaact acgactggta cttcgacctg tggggcagag gcaccctcgt gaccgtgtct 360

agcgctagca 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 gaaagttgag 660

cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 720

ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 780

cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 840

tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 900

aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960

aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg cccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtgca ccctgccccc atcccgggat 1080

gagctgacca agaaccaggt cagcctctcg tgcgcagtca aaggcttcta tcccagcgac 1140

atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1200

gtgctggact ccgacggctc cttcttcctc gtgagcaagc tcaccgtgga caagagcagg 1260

tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1320

acgcagaaga gcctctccct gtctccgggt ggaggcggcg gaagcggagg aggaggatcc 1380

ggcggcggag gttccggagg cggaggatcc gagatcgtgc tgacccagtc tcccggcacc 1440

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tcctcctacc tcgcctggta tcagcagaag cccggccagg cccctcggct gctgatcaac 1560

gtgggcagtc ggagagccac cggcatccct gaccggttct ccggctctgg ctccggcacc 1620

gacttcaccc tgaccatctc ccggctggaa cccgaggact tcgccgtgta ctactgccag 1680

cagggcatca tgctgccccc cacctttggc cagggcacca aggtggaaat caag 1734

<210> 42
<211> 1761
<212> DNA
<213> Artificial Sequence

<220>
<223> VHCH1 (20H4.9)-Heavy chain knob-VH (4B9) (nucleotide sequence)

<400> 42
caggtgcagc tgcagcagtg gggagccgga ctgctgaagc ctagcgagac actgagcctg 60

acctgcgccg tgtacggcgg cagcttcagc ggctactact ggtcctggat cagacagagc 120

cccgagaagg gcctggaatg gatcggcgag atcaaccacg gcggctacgt gacctacaac 180

cccagcctgg aaagcagagt gaccatcagc gtggacacca gcaagaacca gttcagcctg 240

aagctgagca gcgtgacagc cgccgacaca gccgtgtact actgcgccag agattacggc 300

cctggcaact acgactggta cttcgacctg tggggcagag gcaccctcgt gaccgtgtct 360

agcgctagca 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 gaaagttgag 660

cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 720

ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 780

cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 840

tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 900

aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960

aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg cccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc ctgcagagat 1080

gagctgacca agaaccaggt gtccctgtgg tgtctggtca agggcttcta ccccagcgat 1140

atcgccgtgg agtgggagag caacggccag cctgagaaca actacaagac cacccccct 1200

gtgctggaca gcgacggcag cttcttcctg tactccaaac tgaccgtgga caagagccgg 1260

tggcagcagg gcaacgtgtt cagctgcagc gtgatgcacg aggccctgca caaccactac 1320

acccagaagt ccctgagcct gagccccggc ggaggcggcg gaagcggagg aggaggatct 1380

gggggcggag gttccggagg cggtggatct gaggtgcagc tgctcgaaag cggcggagga 1440

ctggtgcagc ctggcggcag cctgagactg tcttgcgccg ccagcggctt caccttcagc 1500

agctacgcca tgagctgggt ccgccaggcc cctggcaagg gactggaatg ggtgtccgcc 1560

atcatcggct ctggcgccag cacctactac gccgacagcg tgaagggccg gttcaccatc 1620

agccgggaca acagcaagaa caccctgtac ctgcagatga acagcctgcg ggccgaggac 1680

accgccgtgt actactgcgc caagggatgg ttcggcggct tcaactactg gggacagggc 1740

accctggtca ccgtgtccag c 1761

<210> 43
<211> 648
<212> DNA
<213> Artificial Sequence

<220>
<223> VLCL-Light chain (20H4.9) (nucleotide sequence)

<400> 43
gagatcgtgc tgacccagag ccccgccacc ctgtctctga gccctggcga gagagccacc 60

ctgagctgca gagccagcca gagcgtgtcc agctacctgg cttggtatca gcagaagccc 120

ggccaggccc ccagactgct gatctacgac gccagcaacc gggccaccgg catccctgcc 180

agattttctg gcagcggcag cggcaccgac ttcaccctga ccatcagcag cctggaaccc 240

gaggacttcg ccgtgtacta ctgccagcag cggagcaact ggccccctgc cctgaccttc 300

ggcggcggca ccaaggtgga aatcaagcgt acggtggctg 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 gagagtgt 648

<210> 44
<211> 578
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1 (20H4.9)-Heavy chain hole-VL (4B9)

<400> 44

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

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

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

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
50 55 60

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

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Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110

Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gly 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

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Ser Cys Ala 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 Val 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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    450                 455                 460

Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr
465                 470                 475                 480
```

```
Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser
                485                 490                 495


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


Gln Ala Pro Arg Leu Leu Ile Asn Val Gly Ser Arg Arg Ala Thr Gly
        515                 520                 525


Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
    530                 535                 540


Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln
545                 550                 555                 560


Gln Gly Ile Met Leu Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu
                565                 570                 575


Ile Lys
```

<210> 45
<211> 587
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1 (20H4.9)-Heavy chain knob-VH (4B9)

<400> 45

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


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


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

```
Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110

Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gly 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 Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Trp 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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    450                 455                 460

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly
465                 470                 475                 480

Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
                485                 490                 495

Phe Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly
            500                 505                 510

Lys Gly Leu Glu Trp Val Ser Ala Ile Ile Gly Ser Gly Ala Ser Thr
        515                 520                 525

Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
    530                 535                 540

Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
545                 550                 555                 560

Thr Ala Val Tyr Tyr Cys Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr
                565                 570                 575

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
            580                 585
```

<210> 46
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> VLCL-Light chain (20H4.9)

<400> 46

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

```
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
            20                  25                  30

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

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

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

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

Ala Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile 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> 47
<211> 1761
<212> DNA
<213> Artificial Sequence

<220>
<223> VHCH1 (20H4.9)-Heavy chain hole-VH (4B9) (nucleotide sequence)

<400> 47
caggtgcagc tgcagcagtg gggagccggc ctgctgaagc ccagcgagac actgagcctg 60

acctgcgccg tgtacggcgg cagcttcagc ggctactact ggtcctggat ccggcagagc 120

cccgagaagg gcctggaatg gatcggcgag atcaaccacg gcggctacgt gacctacaac 180

cccagcctgg aaagcagagt gaccatcagc gtggacacca gcaagaacca gttcagcctg 240

aagctgagca gcgtgacagc cgccgacacc gccgtgtact actgcgccag agactacggc 300

cctggcaact acgactggta cttcgacctg tggggcagag gcaccctggt gacagtgtcc 360

agcgctagca 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 gaaagttgag 660

cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 720

ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 780

cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 840

tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 900

aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960

aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg cccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtgca ccctgccccc atcccgggat 1080

gagctgacca agaaccaggt cagcctctcg tgcgcagtca aaggcttcta tcccagcgac 1140

atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1200

gtgctggact ccgacggctc cttcttcctc gtgagcaagc tcaccgtgga caagagcagg 1260

tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1320

acgcagaaga gcctctccct gtctccgggt ggaggcggcg gaagcggagg aggaggatcc 1380

ggcggcggag gttccggagg cggaggatcc gaggtgcagc tgctcgaaag cggcggagga 1440

ctggtgcagc ctggcggcag cctgagactg tcttgcgccg ccagcggctt caccttcagc 1500

agctacgcca tgagctgggt ccgccaggcc cctggcaagg gactggaatg ggtgtccgcc 1560

atcatcggct ctggcgccag cacctactac gccgacagcg tgaagggccg gttcaccatc 1620

agccgggaca acagcaagaa caccctgtac ctgcagatga acagcctgcg ggccgaggac 1680

accgccgtgt actactgcgc caagggatgg ttcggcggct tcaactactg gggacagggc 1740

accctggtca ccgtgtccag c 1761

<210> 48
<211> 1733
<212> DNA
<213> Artificial Sequence

<220>
<223> VHCH1 (20H4.9)-Heavy chain knob-VL (4B9) (nucleotide sequence)

<400> 48
aggtgcagct gcagcagtgg ggagccggcc tgctgaagcc cagcgagaca ctgagcctga 60

cctgcgccgt gtacggcggc agcttcagcg gctactactg gtcctggatc cggcagagcc 120

ccgagaaggg cctggaatgg atcggcgaga tcaaccacgg cggctacgtg acctacaacc 180

ccagcctgga aagcagagtg accatcagcg tggacaccag caagaaccag ttcagcctga 240

agctgagcag cgtgacagcc gccgacaccg ccgtgtacta ctgcgccaga gactacggcc 300

ctggcaacta cgactggtac ttcgacctgt ggggcagagg caccctggtg acagtgtcca 360

gcgctagcac caagggccca tcggtcttcc ccctggcacc ctcctccaag agcacctctg 420

ggggcacagc ggccctgggc tgcctggtca aggactactt ccccgaaccg gtgacggtgt 480

cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc ctacagtcct 540

caggactcta ctccctcagc agcgtggtga ccgtgccctc cagcagcttg ggcacccaga 600

cctacatctg caacgtgaat cacaagccca gcaacaccaa ggtggacaag aaagttgagc 660

ccaaatcttg tgacaaaact cacacatgcc caccgtgccc agcacctgaa gctgcagggg 720

gaccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgatc tcccggaccc 780

ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc aagttcaact 840

ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag gagcagtaca 900

acagcacgta ccgtgtggtc agcgtcctca ccgtcctgca ccaggactgg ctgaatggca 960

aggagtacaa gtgcaaggtc tccaacaaag ccctcggcgc ccccatcgag aaaaccatct 1020

ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgcccccc tgcagagatg 1080

agctgaccaa gaaccaggtg tccctgtggt gtctggtcaa gggcttctac cccagcgata 1140

tcgccgtgga gtgggagagc aacggccagc ctgagaacaa ctacaagacc acccccccctg 1200

tgctggacag cgacggcagc ttcttcctgt actccaaact gaccgtggac aagagccggt 1260

ggcagcaggg caacgtgttc agctgcagcg tgatgcacga ggccctgcac aaccactaca 1320

cccagaagtc cctgagcctg agccccggcg gaggcggcgg aagcggagga ggaggatctg 1380

ggggcggagg ttccggaggc ggtggatctg agatcgtgct gacccagtct cccggcaccc 1440

tgtctctgag ccctggcgag agagccaccc tgtcctgcag agcctcccag tccgtgacct 1500

cctcctacct cgcctggtat cagcagaagc ccggccaggc ccctcggctg ctgatcaacg 1560

tgggcagtcg gagagccacc ggcatccctg accggttctc cggctctggc tccggcaccg 1620

acttcaccct gaccatctcc cggctggaac ccgaggactt cgccgtgtac tactgccagc 1680

agggcatcat gctgcccccc acctttggcc agggcaccaa ggtggaaatc aag 1733

<210> 49
<211> 587
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1 (20H4.9)-Heavy chain hole-VH (4B9)

<400> 49

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

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

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

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110

Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gly 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

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Ser Cys Ala 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 Val 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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    450                 455                 460

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly
465                 470                 475                 480

Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
                485                 490                 495

Phe Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly
            500                 505                 510

Lys Gly Leu Glu Trp Val Ser Ala Ile Ile Gly Ser Gly Ala Ser Thr
        515                 520                 525

Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
    530                 535                 540

Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
545                 550                 555                 560

Thr Ala Val Tyr Tyr Cys Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr
                565                 570                 575

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
            580                 585
```

<210> 50

<211> 578
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1 (20H4.9)-Heavy chain knob-VL (4B9)

<400> 50

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

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

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

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
50 55 60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
100 105 110

Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gly 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 Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365
```

```
Leu Trp 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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    450                 455                 460

Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr
465                 470                 475                 480

Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser
                485                 490                 495

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

Gln Ala Pro Arg Leu Leu Ile Asn Val Gly Ser Arg Arg Ala Thr Gly
        515                 520                 525

Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
    530                 535                 540

Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln
545                 550                 555                 560

Gln Gly Ile Met Leu Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu
```

565 570 575

Ile Lys

<210> 51
<211> 681
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence Fc hole chain

<400> 51
gacaaaactc acacatgccc accgtgccca gcacctgaac tcctgggggg accgtcagtc 60

ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 120

tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 180

ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac 240

cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 300

tgcaaggtct ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa 360

gggcagcccc gagaaccaca ggtgtgcacc ctgcccccat cccgggatga gctgaccaag 420

aaccaggtca gcctctcgtg cgcagtcaaa ggcttctatc ccagcgacat cgccgtggag 480

tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 540

gacggctcct tcttcctcgt gagcaagctc accgtggaca agagcaggtg gcagcagggg 600

aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 660

ctctccctgt ctccgggtaa a 681

<210> 52
<211> 1266
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence human 4-1BB antigen Fc knob chain

<400> 52

ctgcaggacc cctgcagcaa ctgccctgcc ggcaccttct gcgacaacaa ccggaaccag 60

atctgcagcc cctgcccccc caacagcttc agctctgccg gcggacagcg gacctgcgac 120

atctgcagac agtgcaaggg cgtgttcaga acccggaaag agtgcagcag caccagcaac 180

gccgagtgcg actgcacccc cggcttccat tgtctgggag ccggctgcag catgtgcgag 240

caggactgca agcagggcca ggaactgacc aagaagggct gcaaggactg ctgcttcggc 300

accttcaacg accagaagcg gggcatctgc cggccctgga ccaactgtag cctggacggc 360

aagagcgtgc tggtcaacgg caccaaagaa cgggacgtcg tgtgcggccc cagccctgct 420

gatctgtctc ctggggccag cagcgtgacc cctcctgccc ctgccagaga gcctggccac 480

tctcctcagg tcgacgaaca gttatatttt cagggcggct cacccaaatc tgcagacaaa 540

actcacacat gcccaccgtg cccagcacct gaactcctgg ggggaccgtc agtcttcctc 600

ttcccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg 660

gtggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg 720

gaggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg 780

gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcaag 840

gtctccaaca aagccctccc agcccccatc gagaaaacca tctccaaagc caaagggcag 900

ccccgagaac cacaggtgta caccctgccc ccatgccggg atgagctgac caagaaccag 960

gtcagcctgt ggtgcctggt caaaggcttc tatcccagcg acatcgccgt ggagtgggag 1020

agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc 1080

tccttcttcc tctacagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc 1140

ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc 1200

ctgtctccgg gtaaatccgg aggcctgaac gacatcttcg aggcccagaa gattgaatgg 1260

cacgag 1266

<210> 53
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> Fc hole chain

<400> 53

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1               5                  10                  15


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


Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45


Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60


His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65                  70                  75                  80


Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95


Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110


Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125


Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140


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


Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175


Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
```

180 185 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220

Pro Gly Lys
225

<210> 54
<211> 422
<212> PRT
<213> Artificial Sequence

<220>
<223> human 4-1BB antigen Fc knob chain

<400> 54

Leu Gln Asp Pro Cys Ser Asn Cys Pro Ala Gly Thr Phe Cys Asp Asn
1 5 10 15

Asn Arg Asn Gln Ile Cys Ser Pro Cys Pro Pro Asn Ser Phe Ser Ser
20 25 30

Ala Gly Gly Gln Arg Thr Cys Asp Ile Cys Arg Gln Cys Lys Gly Val
35 40 45

Phe Arg Thr Arg Lys Glu Cys Ser Ser Thr Ser Asn Ala Glu Cys Asp
50 55 60

Cys Thr Pro Gly Phe His Cys Leu Gly Ala Gly Cys Ser Met Cys Glu
65 70 75 80

Gln Asp Cys Lys Gln Gly Gln Glu Leu Thr Lys Lys Gly Cys Lys Asp
85 90 95

Cys Cys Phe Gly Thr Phe Asn Asp Gln Lys Arg Gly Ile Cys Arg Pro

```
            100                 105                 110

Trp Thr Asn Cys Ser Leu Asp Gly Lys Ser Val Leu Val Asn Gly Thr
        115                 120                 125

Lys Glu Arg Asp Val Val Cys Gly Pro Ser Pro Ala Asp Leu Ser Pro
    130                 135                 140

Gly Ala Ser Ser Val Thr Pro Pro Ala Pro Ala Arg Glu Pro Gly His
145                 150                 155                 160

Ser Pro Gln Val Asp Glu Gln Leu Tyr Phe Gln Gly Gly Ser Pro Lys
                165                 170                 175

Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
            180                 185                 190

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
        195                 200                 205

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
    210                 215                 220

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
225                 230                 235                 240

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
                245                 250                 255

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
            260                 265                 270

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
        275                 280                 285

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
    290                 295                 300
```

```
Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln
305                 310                 315                 320


Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
                325                 330                 335


Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
            340                 345                 350


Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
        355                 360                 365


Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
    370                 375                 380


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


Leu Ser Pro Gly Lys Ser Gly Gly Leu Asn Asp Ile Phe Glu Ala Gln
                405                 410                 415


Lys Ile Glu Trp His Glu
            420
```

<210> 55
<211> 2439
<212> DNA
<213> Artificial Sequence

<220>
<223> VHCH1-VHCH1 (20H4.9)-Heavy chain hole-VL(4B9) (nucleotide sequence)

<400> 55
caggtgcagc tgcagcagtg gggagccgga ctgctgaagc ctagcgagac actgagcctg 60

acctgcgccg tgtacggcgg cagcttcagc ggctactact ggtcctggat cagacagagc 120

cccgagaagg gcctggaatg gatcggcgag atcaaccacg gcggctacgt gacctacaac 180

cccagcctgg aaagcagagt gaccatcagc gtggacacca gcaagaacca gttcagcctg 240

aagctgagca gcgtgacagc cgccgacaca gccgtgtact actgcgccag agattacggc 300

cctggcaact acgactggta cttcgacctg tggggcagag gcaccctcgt gaccgtgtct 360

agcgcttcta ccaagggccc cagcgtgttc cctctggccc ctagcagcaa gagcacatct 420

ggcggaacag ccgccctggg ctgcctcgtg aaggactact ttcccgagcc cgtgacagtg 480

tcctggaact ctggcgccct gacaagcggc gtgcacacct ttccagccgt gctgcagagc 540

agcggcctgt actctctgag cagcgtcgtg actgtgccca gcagcagcct gggaacccag 600

acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggaa 660

cccaagagct gcgacggcgg aggcggatct ggcggcggag gatcccaggt gcagctgcag 720

cagtggggcg ctggcctgct gaaaccctct gagactctgt ccctgacatg tgctgtgtat 780

ggcggctcct tctccggcta ctattggagc tggattcggc agtcccctga gaaaggactg 840

gaatggattg gggaaatcaa tcatggggga tatgtgacat acaatccctc actggaatcc 900

cgcgtgacca tctccgtgga tacctctaag aatcagttct ctctgaagct gtcctccgtg 960

accgccgctg ataccgctgt gtattactgt gcccgggact acggacccgg caattatgat 1020

tggtattttg atctgtgggg acggggcaca ctcgtgactg tgtcctctgc tagcaccaag 1080

ggcccatcgg tcttcccccc ggcaccctcc tccaagagca cctctggggg cacagcggcc 1140

ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 1200

gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc 1260

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 1320

gtgaatcaca agcccagcaa caccaaggtg gacaagaaag ttgagcccaa atcttgtgac 1380

aaaactcaca catgcccacc gtgcccagca cctgaagctg caggggggacc gtcagtcttc 1440

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 1500

gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 1560

gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt 1620

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 1680

aaggtctcca acaaagccct cggcgccccc atcgagaaaa ccatctccaa agccaaaggg 1740

cagccccgag aaccacaggt gtgcaccctg cccccatccc gggatgagct gaccaagaac 1800

caggtcagcc tctcgtgcgc agtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1860

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1920

ggctccttct tcctcgtgag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1980

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 2040

tccctgtctc cgggtggagg cggcggaagc ggaggaggag gatccggcgg cggaggttcc 2100

ggaggcggtg gatctgagat cgtgctgacc cagtctcccg gcaccctgtc tctgagccct 2160

ggcgagagag ccaccctgtc ctgcagagcc tcccagtccg tgacctcctc ctacctcgcc 2220

tggtatcagc agaagcccgg ccaggccct cggctgctga tcaacgtggg cagtcggaga 2280

gccaccggca tccctgaccg gttctccggc tctggctccg gcaccgactt caccctgacc 2340

atctcccggc tggaacccga ggacttcgcc gtgtactact gccagcaggg catcatgctg 2400

ccccccacct ttggccaggg caccaaggtg gaaatcaag 2439

<210> 56
<211> 2466
<212> DNA
<213> Artificial Sequence

<220>
<223> VHCH1-VHCH1 (20H4.9)-Heavy chain knob-VH(4B9) (nucleotide sequence)

<400> 56
caggtgcagc tgcagcagtg gggagccgga ctgctgaagc ctagcgagac actgagcctg 60

acctgcgccg tgtacggcgg cagcttcagc ggctactact ggtcctggat cagacagagc 120

cccgagaagg gcctggaatg gatcggcgag atcaaccacg gcggctacgt gacctacaac 180

cccagcctgg aaagcagagt gaccatcagc gtggacacca gcaagaacca gttcagcctg 240

aagctgagca gcgtgacagc cgccgacaca gccgtgtact actgcgccag agattacggc 300

cctggcaact acgactggta cttcgacctg tggggcagag gcaccctcgt gaccgtgtct 360

agcgcttcta ccaagggccc cagcgtgttc cctctggccc ctagcagcaa gagcacatct 420

ggcggaacag ccgccctggg ctgcctcgtg aaggactact ttcccgagcc cgtgacagtg 480

tcctggaact ctggcgccct gacaagcggc gtgcacacct ttccagccgt gctgcagagc 540

agcggcctgt actctctgag cagcgtcgtg actgtgccca gcagcagcct gggaacccag 600

acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggaa 660

cccaagagct gcgacggcgg aggcggatct ggcggcggag gatcccaggt gcagctgcag 720

cagtggggcg ctggcctgct gaaaccctct gagactctgt ccctgacatg tgctgtgtat 780

ggcggctcct tctccggcta ctattggagc tggattcggc agtcccctga gaaaggactg 840

gaatggattg gggaaatcaa tcatggggga tatgtgacat acaatccctc actggaatcc 900

cgcgtgacca tctccgtgga tacctctaag aatcagttct ctctgaagct gtcctccgtg 960

accgccgctg ataccgctgt gtattactgt gcccgggact acggacccgg caattatgat 1020

tggtattttg atctgtgggg acggggcaca ctcgtgactg tgtcctctgc tagcaccaag 1080

ggcccatcgg tcttcccccc ggcaccctcc tccaagagca cctctggggg cacagcggcc 1140

ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 1200

gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc 1260

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 1320

gtgaatcaca agcccagcaa caccaaggtg gacaagaaag ttgagcccaa atcttgtgac 1380

aaaactcaca catgcccacc gtgcccagca cctgaagctg caggggggacc gtcagtcttc 1440

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 1500

gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 1560

gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt 1620

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 1680

aaggtctcca acaaagccct cggcgccccc atcgagaaaa ccatctccaa agccaaaggg 1740

cagccccgag aaccacaggt gtacaccctg cccccctgca gagatgagct gaccaagaac 1800

caggtgtccc tgtggtgtct ggtcaagggc ttctacccca gcgatatcgc cgtggagtgg 1860

gagagcaacg gccagcctga gaacaactac aagaccaccc cccctgtgct ggacagcgac 1920

ggcagcttct tcctgtactc caaactgacc gtggacaaga gccggtggca gcagggcaac 1980

gtgttcagct gcagcgtgat gcacgaggcc ctgcacaacc actacaccca gaagtccctg 2040

agcctgagcc ccggcggagg cggcggaagc ggaggaggag gatctggggg cggaggttcc 2100

ggaggcggag gatccgaggt gcagctgctc gaaagcggcg gaggactggt gcagcctggc 2160

ggcagcctga gactgtcttg cgccgccagc ggcttcacct tcagcagcta cgccatgagc 2220

tgggtccgcc aggcccctgg caagggactg gaatgggtgt ccgccatcat cggctctggc 2280

gccagcacct actacgccga cagcgtgaag ggccggttca ccatcagccg ggacaacagc 2340

aagaacaccc tgtacctgca gatgaacagc ctgcgggccg aggacaccgc cgtgtactac 2400

tgcgccaagg gatggttcgg cggcttcaac tactggggac agggcaccct ggtcaccgtg 2460

tccagc 2466

<210> 57
<211> 813
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1-VHCH1 (20H4.9)-Heavy chain hole-VL (4B9)

<400> 57

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

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

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

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
50 55 60

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

```
Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110

Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
225                 230                 235                 240

Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr
                245                 250                 255

Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Ser Trp Ile
            260                 265                 270

Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His
```

```
        275                 280                 285

Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu Ser Arg Val Thr Ile
    290                 295                 300

Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val
305                 310                 315                 320

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Tyr Gly Pro
                325                 330                 335

Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val
            340                 345                 350

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
        355                 360                 365

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
    370                 375                 380

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
385                 390                 395                 400

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
                405                 410                 415

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
            420                 425                 430

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        435                 440                 445

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    450                 455                 460

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
465                 470                 475                 480
```

```
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                485                 490                 495

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            500                 505                 510

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        515                 520                 525

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    530                 535                 540

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
545                 550                 555                 560

Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
                565                 570                 575

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro
            580                 585                 590

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val
        595                 600                 605

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    610                 615                 620

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
625                 630                 635                 640

Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                645                 650                 655

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            660                 665                 670

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

```
        675                 680                 685

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    690                 695                 700

Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro
705                 710                 715                 720

Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Ser
                725                 730                 735

Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu
            740                 745                 750

Leu Ile Asn Val Gly Ser Arg Arg Ala Thr Gly Ile Pro Asp Arg Phe
        755                 760                 765

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu
    770                 775                 780

Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Gly Ile Met Leu
785                 790                 795                 800

Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
                805                 810


<210>  58
<211>  822
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  VHCH1-VHCH1 (20H4.9)-Heavy chain knob-VH (4B9)

<400>  58

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

Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr
```

```
            20                  25                  30

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

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110

Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220
```

```
Asp Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
225                 230                 235                 240


Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr
                245                 250                 255


Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Ser Trp Ile
            260                 265                 270


Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His
        275                 280                 285


Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu Ser Arg Val Thr Ile
    290                 295                 300


Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val
305                 310                 315                 320


Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Tyr Gly Pro
                325                 330                 335


Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val
            340                 345                 350


Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
        355                 360                 365


Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
    370                 375                 380


Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
385                 390                 395                 400


Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
                405                 410                 415


Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
```

```
            420                 425                 430

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        435                 440                 445

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    450                 455                 460

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
465                 470                 475                 480

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                485                 490                 495

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            500                 505                 510

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        515                 520                 525

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    530                 535                 540

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
545                 550                 555                 560

Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
                565                 570                 575

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            580                 585                 590

Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val
        595                 600                 605

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    610                 615                 620
```

```
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
625                 630                 635                 640


Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                645                 650                 655


Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            660                 665                 670


Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly
        675                 680                 685


Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    690                 695                 700


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


Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser
                725                 730                 735


Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
            740                 745                 750


Val Ser Ala Ile Ile Gly Ser Gly Ala Ser Thr Tyr Tyr Ala Asp Ser
        755                 760                 765


Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
    770                 775                 780


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


Cys Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln Gly Thr
                805                 810                 815


Leu Val Thr Val Ser Ser
```

820

<210> 59
<211> 2466
<212> DNA
<213> Artificial Sequence

<220>
<223> VHCH1-VHCH1 (20H4.9)-Heavy chain hole-VH (4B9) (nucleotide sequence)

<400> 59
caggtgcagc tgcagcagtg gggagccgga ctgctgaagc ctagcgagac actgagcctg 60

acctgcgccg tgtacggcgg cagcttcagc ggctactact ggtcctggat cagacagagc 120

cccgagaagg gcctggaatg gatcggcgag atcaaccacg gcggctacgt gacctacaac 180

cccagcctgg aaagcagagt gaccatcagc gtggacacca gcaagaacca gttcagcctg 240

aagctgagca gcgtgacagc cgccgacaca gccgtgtact actgcgccag agattacggc 300

cctggcaact acgactggta cttcgacctg tggggcagag gcaccctcgt gaccgtgtct 360

agcgcttcca caaagggccc cagcgtgttc cctctggccc ctagcagcaa gagcacatct 420

ggcggaacag ccgccctggg ctgcctcgtg aaggactact ttcccgagcc cgtgacagtg 480

tcctggaact ctggcgccct gacaagcggc gtgcacacct ttccagccgt gctgcagagc 540

agcggcctgt actctctgtc cagcgtcgtg actgtgccca gcagcagcct gggcacccag 600

acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggaa 660

cccaagagct gcgacggcgg aggcggatct ggcggcggag gatcccaggt gcagctgcag 720

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cgcgtgacca tctccgtgga tacctctaag aatcagttct ctctgaagct gtcctccgtg 960

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<210> 60
<211> 2439

<212> DNA
<213> Artificial Sequence

<220>
<223> VHCH1-VHCH1 (20H4.9)-Heavy chain knob-VL (4B9) (nucleotide sequence)

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cccgagaagg gcctggaatg gatcggcgag atcaaccacg gcggctacgt gacctacaac 180

cccagcctgg aaagcagagt gaccatcagc gtggacacca gcaagaacca gttcagcctg 240

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ggcggaacag ccgccctggg ctgcctcgtg aaggactact ttcccgagcc cgtgacagtg 480

tcctggaact ctggcgccct gacaagcggc gtgcacacct ttccagccgt gctgcagagc 540

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gagagcaacg gccagcctga gaacaactac aagaccaccc cccctgtgct ggacagcgac 1920

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gtgttcagct gcagcgtgat gcacgaggcc ctgcacaacc actacaccca gaagtccctg 2040

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gccaccggca tccctgaccg gttctccggc tctggctccg gcaccgactt caccctgacc 2340

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<210> 61
<211> 822
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1-VHCH1 (20H4.9)-Heavy chain hole-VH (4B9)

<400> 61

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

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

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110

Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
225                 230                 235                 240

Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr
                245                 250                 255

Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Ser Trp Ile
            260                 265                 270

Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His
        275                 280                 285

Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu Ser Arg Val Thr Ile
    290                 295                 300

Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val
305                 310                 315                 320

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Tyr Gly Pro
                325                 330                 335

Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val
            340                 345                 350

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
        355                 360                 365

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
    370                 375                 380

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
385                 390                 395                 400
```

```
Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
                405                 410                 415

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
            420                 425                 430

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        435                 440                 445

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    450                 455                 460

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
465                 470                 475                 480

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                485                 490                 495

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            500                 505                 510

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        515                 520                 525

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    530                 535                 540

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
545                 550                 555                 560

Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
                565                 570                 575

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro
            580                 585                 590

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val
```

```
        595                 600                 605

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    610                 615                 620

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
625                 630                 635                 640

Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                645                 650                 655

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            660                 665                 670

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly
        675                 680                 685

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    690                 695                 700

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

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser
                725                 730                 735

Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
            740                 745                 750

Val Ser Ala Ile Ile Gly Ser Gly Ala Ser Thr Tyr Tyr Ala Asp Ser
        755                 760                 765

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
    770                 775                 780

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

Cys Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln Gly Thr
805 810 815

Leu Val Thr Val Ser Ser
820

<210> 62
<211> 813
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1-VHCH1 (20H4.9)-Heavy chain knob-VL (4B9)

<400> 62

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

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

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

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
50 55 60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
100 105 110

Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
225                 230                 235                 240

Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr
                245                 250                 255

Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Ser Trp Ile
            260                 265                 270

Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His
        275                 280                 285

Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu Ser Arg Val Thr Ile
    290                 295                 300

Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val
305                 310                 315                 320

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Tyr Gly Pro
```

```
                325                 330                 335

Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val
            340                 345                 350

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
        355                 360                 365

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
    370                 375                 380

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
385                 390                 395                 400

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
                405                 410                 415

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
            420                 425                 430

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        435                 440                 445

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    450                 455                 460

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
465                 470                 475                 480

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                485                 490                 495

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            500                 505                 510

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        515                 520                 525
```

```
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    530                 535                 540

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
545                 550                 555                 560

Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
                565                 570                 575

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            580                 585                 590

Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val
        595                 600                 605

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    610                 615                 620

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
625                 630                 635                 640

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                645                 650                 655

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            660                 665                 670

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly
        675                 680                 685

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    690                 695                 700

Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro
705                 710                 715                 720

Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Ser
```

```
                725                 730                 735

Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu
            740                 745                 750

Leu Ile Asn Val Gly Ser Arg Arg Ala Thr Gly Ile Pro Asp Arg Phe
        755                 760                 765

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu
    770                 775                 780

Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Gly Ile Met Leu
785                 790                 795                 800

Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
                805                 810
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<210> 63
<211> 1743
<212> DNA
<213> Artificial Sequence

<220>
<223> VHCH1 (20H4.9)-Heavy chain hole-VL (T84.66-LCHA) (nucleotide sequence)

<400> 63

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cccagcctgg aaagcagagt gaccatcagc gtggacacca gcaagaacca gttcagcctg      240

aagctgagca gcgtgacagc cgccgacacc gccgtgtact actgcgccag agactacggc      300

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agcgctagca ccaagggccc atcggtcttc cccctggcac cctcctccaa gagcacctct      420

gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg      480

tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc      540
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aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg cccccatcga gaaaaccatc 1020

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atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1200

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<210> 64
<211> 1773
<212> DNA
<213> Artificial Sequence

<220>

<223> VHCH1 (20H4.9)-Heavy chain knob-VH (T84.66-LCHA) (nucleotide sequence)

<400> 64

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cctggcaact acgactggta cttcgacctg tggggcagag gcaccctggt gacagtgtcc 360

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tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 600

acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660

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acccagaagt ccctgagcct gagccccggc ggaggcggcg gaagcggagg aggaggatct 1380

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gggggcggag gttccggagg cggtggatct caggtgcagc tggtgcagtc tggcgccgaa     1440

gtgaagaaac ccggcagcag cgtgaaggtg tcctgcaagg ccagcggctt caacatcaag     1500

gacacctaca tgcactgggt gcgccaggcc cctggacagg gactggaatg gatgggcaga     1560

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accgccgtgt actactgtgc ccccttcggc tactacgtgt ccgactacgc catggcctat     1740

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<210> 65
<211> 581
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1 (20H4.9)-Heavy chain hole-VL (T84.66-LCHA)

<400> 65

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


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


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


Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60


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


Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95


Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
```

```
            100                 105                 110

Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gly 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

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Ser Cys Ala 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 Val 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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    450                 455                 460

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

Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Gly
                485                 490                 495

Glu Ser Val Asp Ile Phe Gly Val Gly Phe Leu His Trp Tyr Gln Gln
```

```
            500                 505                 510

Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Arg Ala Ser Asn Arg
        515                 520                 525

Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
    530                 535                 540

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

Tyr Cys Gln Gln Thr Asn Glu Asp Pro Tyr Thr Phe Gly Gln Gly Thr
                565                 570                 575

Lys Leu Glu Ile Lys
            580
```

<210> 66
<211> 591
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1 (20H4.9)-Heavy chain knob-VH (T84.66-LCHA)

<400> 66

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

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

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

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
```

```
65                  70                  75                  80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110

Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gly 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 Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Trp 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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    450                 455                 460

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu
```

```
465                 470                 475                 480

Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly
                485                 490                 495

Phe Asn Ile Lys Asp Thr Tyr Met His Trp Val Arg Gln Ala Pro Gly
            500                 505                 510

Gln Gly Leu Glu Trp Met Gly Arg Ile Asp Pro Ala Asn Gly Asn Ser
        515                 520                 525

Lys Tyr Val Pro Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Thr
    530                 535                 540

Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp
545                 550                 555                 560

Thr Ala Val Tyr Tyr Cys Ala Pro Phe Gly Tyr Tyr Val Ser Asp Tyr
                565                 570                 575

Ala Met Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
            580                 585                 590
```

<210> 67
<211> 1773
<212> DNA
<213> Artificial Sequence

<220>
<223> VHCH1 (20H4.9)-Heavy chain hole-VH (T84.66-LCHA) (nucleotide sequence)

<400> 67

```
caggtgcagc tgcagcagtg gggagccggc ctgctgaagc ccagcgagac actgagcctg       60

acctgcgccg tgtacggcgg cagcttcagc ggctactact ggtcctggat ccggcagagc      120

cccgagaagg gcctggaatg gatcggcgag atcaaccacg gcggctacgt gacctacaac      180

cccagcctgg aaagcagagt gaccatcagc gtggacacca gcaagaacca gttcagcctg      240

aagctgagca gcgtgacagc cgccgacacc gccgtgtact actgcgccag agactacggc      300
```

cctggcaact acgactggta cttcgacctg tggggcagag gcaccctggt gacagtgtcc 360

agcgctagca 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 gaaagttgag 660

cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 720

ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 780

cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 840

tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 900

aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960

aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg cccccatcga gaaaaccatc 1020

tccaaagcca aggggcagcc ccgagaacca caggtgtgca ccctgccccc atcccgggat 1080

gagctgacca agaaccaggt cagcctctcg tgcgcagtca aaggcttcta tcccagcgac 1140

atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1200

gtgctggact ccgacggctc cttcttcctc gtgagcaagc tcaccgtgga caagagcagg 1260

tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1320

acgcagaaga gcctctccct gtctccgggt ggaggcggcg gaagcggagg aggaggatcc 1380

ggcggcggag gttccggagg cggaggatcc caggtgcagc tggtgcagtc tggcgccgaa 1440

gtgaagaaac ccggcagcag cgtgaaggtg tcctgcaagg ccagcggctt caacatcaag 1500

gacacctaca tgcactgggt gcgccaggcc cctggacagg gactggaatg gatgggcaga 1560

atcgaccccg ccaacggcaa cagcaaatac gtgcccaagt tccagggcag agtgaccatc 1620

accgccgaca ccagcacctc caccgcctac atggaactga gcagcctgcg gagcgaggac 1680

accgccgtgt actactgtgc ccccttcggc tactacgtgt ccgactacgc catggcctat 1740

tggggccagg gcacactcgt gaccgtgtcc tct 1773

<210> 68
<211> 1743
<212> DNA
<213> Artificial Sequence

<220>
<223> VHCH1 (20H4.9)-Heavy chain knob-VL (T84.66-LCHA) (nucleotide sequence)

<400> 68
caggtgcagc tgcagcagtg gggagccggc ctgctgaagc ccagcgagac actgagcctg 60

acctgcgccg tgtacggcgg cagcttcagc ggctactact ggtcctggat ccggcagagc 120

cccgagaagg gcctggaatg gatcggcgag atcaaccacg gcggctacgt gacctacaac 180

cccagcctgg aaagcagagt gaccatcagc gtggacacca gcaagaacca gttcagcctg 240

aagctgagca gcgtgacagc cgccgacacc gccgtgtact actgcgccag agactacggc 300

cctggcaact acgactggta cttcgacctg tggggcagag gcaccctggt gacagtgtcc 360

agcgctagca 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 gaaagttgag 660

cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 720

ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 780

cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 840

tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 900

aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960

aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg cccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc ctgcagagat 1080

gagctgacca agaaccaggt gtccctgtgg tgtctggtca agggcttcta ccccagcgat 1140

atcgccgtgg agtgggagag caacggccag cctgagaaca actacaagac cacccccct 1200

gtgctggaca gcgacggcag cttcttcctg tactccaaac tgaccgtgga caagagccgg 1260

tggcagcagg gcaacgtgtt cagctgcagc gtgatgcacg aggccctgca caaccactac 1320

acccagaagt ccctgagcct gagccccggc ggaggcggcg gaagcggagg aggaggatct 1380

gggggcggag gttccggagg cggtggatct gagatcgtgc tgacccagag ccctgccacc 1440

ctgtcactgt ctccaggcga gagagccacc ctgagctgta gagccggcga gagcgtggac 1500

atcttcggcg tgggatttct gcactggtat cagcagaagc ccggccaggc ccccagactg 1560

ctgatctaca gagccagcaa ccgggccaca ggcatccccg ccagattttc tggctctggc 1620

agcggcaccg acttcaccct gacaatcagc agcctggaac ccgaggactt cgccgtgtac 1680

tactgccagc agaccaacga ggacccctac acctttggcc agggcaccaa gctggaaatc 1740

aag 1743

<210> 69
<211> 591
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1 (20H4.9)-Heavy chain hole-VH (T84.66-LCHA)

<400> 69

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

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

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

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu

```
65                  70                  75                  80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110

Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gly 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

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Ser Cys Ala 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 Val 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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    450                 455                 460

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu
```

```
465                 470                 475                 480

Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly
                485                 490                 495

Phe Asn Ile Lys Asp Thr Tyr Met His Trp Val Arg Gln Ala Pro Gly
            500                 505                 510

Gln Gly Leu Glu Trp Met Gly Arg Ile Asp Pro Ala Asn Gly Asn Ser
        515                 520                 525

Lys Tyr Val Pro Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Thr
    530                 535                 540

Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp
545                 550                 555                 560

Thr Ala Val Tyr Tyr Cys Ala Pro Phe Gly Tyr Tyr Val Ser Asp Tyr
                565                 570                 575

Ala Met Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
            580                 585                 590
```

<210> 70
<211> 581
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1 (20H4.9)-Heavy chain knob-VL (T84.66-LCHA)

<400> 70

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

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

Tyr Trp Ser Trp Ile Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Ile
```

```
        35                  40                  45

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110

Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gly 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 Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Trp 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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    450                 455                 460

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

Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Gly
                485                 490                 495

Glu Ser Val Asp Ile Phe Gly Val Gly Phe Leu His Trp Tyr Gln Gln
            500                 505                 510

Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Arg Ala Ser Asn Arg
        515                 520                 525

Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
    530                 535                 540

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

Tyr Cys Gln Gln Thr Asn Glu Asp Pro Tyr Thr Phe Gly Gln Gly Thr
                565                 570                 575

Lys Leu Glu Ile Lys
            580
```

<210> 71
<211> 1758
<212> DNA
<213> Artificial Sequence

<220>
<223> VHCH1 (20H4.9)-Heavy chain hole-VL (A5B7) (nucleotide sequence)

<400> 71
caggtgcagc tgcagcagtg gggagccggc ctgctgaagc ccagcgagac actgagcctg 60

acctgcgccg tgtacggcgg cagcttcagc ggctactact ggtcctggat ccggcagagc 120

cccgagaagg gcctggaatg gatcggcgag atcaaccacg gcggctacgt gacctacaac 180

cccagcctgg aaagcagagt gaccatcagc gtggacacca gcaagaacca gttcagcctg 240

aagctgagca gcgtgacagc cgccgacacc gccgtgtact actgcgccag agactacggc 300

cctggcaact acgactggta cttcgacctg tggggcagag gcaccctggt gacagtgtcc 360

agcgctagca 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 gaaagttgag 660

cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 720

ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 780

cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 840

tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 900

aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960

aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg cccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtgca ccctgccccc atcccgggat 1080

gagctgacca agaaccaggt cagcctctcg tgcgcagtca aaggcttcta tcccagcgac 1140

atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1200

gtgctggact ccgacggctc cttcttcctc gtgagcaagc tcaccgtgga caagagcagg 1260

tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1320

acgcagaaga gcctctccct gtctccgggt ggaggcggcg gaagcggagg aggaggatcc 1380

ggcggcggag gttccggagg cggaggatcc caggccgtgc tgacacagcc tgccagcctg 1440

tctgcttctc ctggcgcctc tgcctccctg acctgcacac tgagaagagg catcaacgtg 1500

ggcgcctaca gcatctactg gtatcagcag aagcccggca gccccctca gtacctgctg 1560

agatacaaga gcgacagcga caagcagcag ggcagcggcg tgtccagcag attcagcgcc 1620

agcaaggacg cctctgccaa cgccggaatc ctgctgatca gcggcctgca gtctgaggac 1680

gaggccgact actactgcat gatctggcac tctggcgcca gcgccgtgtt tggcggaggc 1740

acaaaactga ccgtgctg 1758

<210> 72
<211> 1773
<212> DNA
<213> Artificial Sequence

<220>
<223> VHCH1 (20H4.9)-Heavy chain knob-VH (A5B7) (nucleotide sequence)

<400> 72
caggtgcagc tgcagcagtg gggagccggc ctgctgaagc ccagcgagac actgagcctg 60

acctgcgccg tgtacggcgg cagcttcagc ggctactact ggtcctggat ccggcagagc 120

cccgagaagg gcctggaatg gatcggcgag atcaaccacg gcggctacgt gacctacaac 180

cccagcctgg aaagcagagt gaccatcagc gtggacacca gcaagaacca gttcagcctg 240

aagctgagca gcgtgacagc cgccgacacc gccgtgtact actgcgccag agactacggc 300

cctggcaact acgactggta cttcgacctg tggggcagag gcaccctggt gacagtgtcc 360

agcgctagca 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 gaaagttgag 660

cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 720

ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 780

cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 840

tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 900

aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960

```
aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg cccccatcga gaaaaccatc     1020

tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc ctgcagagat     1080

gagctgacca agaaccaggt gtccctgtgg tgtctggtca agggcttcta ccccagcgat     1140

atcgccgtgg agtgggagag caacggccag cctgagaaca actacaagac cacccccccct     1200

gtgctggaca gcgacggcag cttcttcctg tactccaaac tgaccgtgga caagagccgg     1260

tggcagcagg gcaacgtgtt cagctgcagc gtgatgcacg aggccctgca caaccactac     1320

acccagaagt ccctgagcct gagccccggc ggaggcggcg gaagcggagg aggaggatct     1380

gggggcggag gttccggagg cggtggatct gaagtgcagc tggtggaatc tggcggcgga     1440

ctggtgcagc ctggcagaag cctgagactg agctgtgccg ccagcggctt taccgtgtcc     1500

agctactgga tgcactgggt ccgacaggcc cctggcaagg gactggaatg ggtcggattc     1560

atcagaaaca aggccaacgg cggcaccacc gagtacgccg cctctgtgaa gggccggttc     1620

accatcagcc gggacgacag caagaacacc ctgtacctgc agatgaacag cctgcgggcc     1680

gaggacaccg ccgtgtacta ctgcgccaga gacagaggcc tgcggttcta cttcgactac     1740

tggggccagg gcaccaccgt gacagtctct tcc                                  1773
```

<210> 73
<211> 586
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1 (20H4.9)-Heavy chain hole-VL (A5B7)

<400> 73

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


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


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

```
Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110

Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gly 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

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Ser Cys Ala 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 Val 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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    450                 455                 460

Ser Gly Gly Gly Gly Ser Gln Ala Val Leu Thr Gln Pro Ala Ser Leu
465                 470                 475                 480

Ser Ala Ser Pro Gly Ala Ser Ala Ser Leu Thr Cys Thr Leu Arg Arg
                485                 490                 495

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

Gly Ser Pro Pro Gln Tyr Leu Leu Arg Tyr Lys Ser Asp Ser Asp Lys
        515                 520                 525

Gln Gln Gly Ser Gly Val Ser Ser Arg Phe Ser Ala Ser Lys Asp Ala
    530                 535                 540

Ser Ala Asn Ala Gly Ile Leu Leu Ile Ser Gly Leu Gln Ser Glu Asp
545                 550                 555                 560

Glu Ala Asp Tyr Tyr Cys Met Ile Trp His Ser Gly Ala Ser Ala Val
                565                 570                 575

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            580                 585
```

<210> 74
<211> 591
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1 (20H4.9)-Heavy chain knob-VH (A5B7)

<400> 74

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

```
Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr
            20                  25                  30

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

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110

Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
```

```
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gly 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 Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Trp 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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    450                 455                 460

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
465                 470                 475                 480

Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
                485                 490                 495

Phe Thr Val Ser Ser Tyr Trp Met His Trp Val Arg Gln Ala Pro Gly
            500                 505                 510

Lys Gly Leu Glu Trp Val Gly Phe Ile Arg Asn Lys Ala Asn Gly Gly
        515                 520                 525

Thr Thr Glu Tyr Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
    530                 535                 540

Asp Asp Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala
545                 550                 555                 560

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Arg Gly Leu Arg Phe
                565                 570                 575

Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
            580                 585                 590
```

<210> 75
<211> 1773
<212> DNA
<213> Artificial Sequence

<220>
<223> VHCH1 (20H4.9)-Heavy chain hole-VH (A5B7) (nucleotide sequence)

<400> 75
caggtgcagc tgcagcagtg gggagccggc ctgctgaagc ccagcgagac actgagcctg 60

acctgcgccg tgtacggcgg cagcttcagc ggctactact ggtcctggat ccggcagagc 120

cccgagaagg gcctggaatg gatcggcgag atcaaccacg gcggctacgt gacctacaac 180

cccagcctgg aaagcagagt gaccatcagc gtggacacca gcaagaacca gttcagcctg 240

aagctgagca gcgtgacagc cgccgacacc gccgtgtact actgcgccag agactacggc 300

cctggcaact acgactggta cttcgacctg tggggcagag gcaccctggt gacagtgtcc 360

agcgctagca 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 gaaagttgag 660

cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 720

ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 780

cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 840

tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 900

aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960

aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg cccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtgca ccctgccccc atcccgggat 1080

gagctgacca agaaccaggt cagcctctcg tgcgcagtca aaggcttcta tcccagcgac 1140

atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1200

gtgctggact ccgacggctc cttcttcctc gtgagcaagc tcaccgtgga caagagcagg 1260

tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1320

acgcagaaga gcctctccct gtctccgggt ggaggcggcg gaagcggagg aggaggatcc 1380

ggcggcggag gttccggagg cggaggatcc gaagtgcagc tggtggaatc tggcggcgga 1440

ctggtgcagc ctggcagaag cctgagactg agctgtgccg ccagcggctt taccgtgtcc 1500

agctactgga tgcactgggt ccgacaggcc cctggcaagg gactggaatg ggtcggattc 1560

atcagaaaca aggccaacgg cggcaccacc gagtacgccg cctctgtgaa gggccggttc 1620

accatcagcc gggacgacag caagaacacc ctgtacctgc agatgaacag cctgcgggcc 1680

gaggacaccg ccgtgtacta ctgcgccaga gacagaggcc tgcggttcta cttcgactac 1740

tggggccagg gcaccaccgt gacagtctct tcc 1773

<210> 76
<211> 1758
<212> DNA
<213> Artificial Sequence

<220>
<223> VHCH1 (20H4.9)-Heavy chain knob-VL (A5B7) (nucleotide sequence)

<400> 76
caggtgcagc tgcagcagtg gggagccggc ctgctgaagc ccagcgagac actgagcctg 60

acctgcgccg tgtacggcgg cagcttcagc ggctactact ggtcctggat ccggcagagc 120

cccgagaagg gcctggaatg gatcggcgag atcaaccacg gcggctacgt gacctacaac 180

cccagcctgg aaagcagagt gaccatcagc gtggacacca gcaagaacca gttcagcctg 240

aagctgagca gcgtgacagc cgccgacacc gccgtgtact actgcgccag agactacggc 300

cctggcaact acgactggta cttcgacctg tggggcagag gcaccctggt gacagtgtcc 360

agcgctagca 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 gaaagttgag 660

cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 720

ggaccgtcag tcttcctctt cccccccaaaa cccaaggaca ccctcatgat ctcccggacc 780

cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 840

tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 900

aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960

aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg cccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc ctgcagagat 1080

gagctgacca agaaccaggt gtccctgtgg tgtctggtca agggcttcta ccccagcgat 1140

atcgccgtgg agtgggagag caacggccag cctgagaaca actacaagac cacccccct 1200

gtgctggaca gcgacggcag cttcttcctg tactccaaac tgaccgtgga caagagccgg 1260

tggcagcagg gcaacgtgtt cagctgcagc gtgatgcacg aggccctgca caaccactac 1320

acccagaagt ccctgagcct gagccccggc ggaggcggcg gaagcggagg aggaggatct 1380

gggggcggag gttccggagg cggtggatct caggccgtgc tgacacagcc tgccagcctg 1440

tctgcttctc ctggcgcctc tgcctccctg acctgcacac tgagaagagg catcaacgtg 1500

ggcgcctaca gcatctactg gtatcagcag aagcccggca gccccctca gtacctgctg 1560

agatacaaga gcgacagcga caagcagcag ggcagcggcg tgtccagcag attcagcgcc 1620

agcaaggacg cctctgccaa cgccggaatc ctgctgatca gcggcctgca gtctgaggac 1680

gaggccgact actactgcat gatctggcac tctggcgcca gcgccgtgtt tggcggaggc 1740

acaaaactga ccgtgctg 1758

<210> 77
<211> 591
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1 (20H4.9)-Heavy chain hole-VH (A5B7)

<400> 77

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

Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr

```
            20                  25                  30

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

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110

Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220
```

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gly 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

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Ser Cys Ala 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 Val 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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    450                 455                 460

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
465                 470                 475                 480

Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
                485                 490                 495

Phe Thr Val Ser Ser Tyr Trp Met His Trp Val Arg Gln Ala Pro Gly
            500                 505                 510

Lys Gly Leu Glu Trp Val Gly Phe Ile Arg Asn Lys Ala Asn Gly Gly
        515                 520                 525

Thr Thr Glu Tyr Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
    530                 535                 540

Asp Asp Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala
545                 550                 555                 560

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Arg Gly Leu Arg Phe
                565                 570                 575

Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
            580                 585                 590
```

<210> 78
<211> 586
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1 (20H4.9)-Heavy chain knob-VL (A5B7)

<400> 78

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


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


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


Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60


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


Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95


Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110


Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gly 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 Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Trp 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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    450                 455                 460

Ser Gly Gly Gly Gly Ser Gln Ala Val Leu Thr Gln Pro Ala Ser Leu
465                 470                 475                 480

Ser Ala Ser Pro Gly Ala Ser Ala Ser Leu Thr Cys Thr Leu Arg Arg
                485                 490                 495

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

Gly Ser Pro Pro Gln Tyr Leu Leu Arg Tyr Lys Ser Asp Ser Asp Lys
        515                 520                 525

Gln Gln Gly Ser Gly Val Ser Ser Arg Phe Ser Ala Ser Lys Asp Ala
    530                 535                 540

Ser Ala Asn Ala Gly Ile Leu Leu Ile Ser Gly Leu Gln Ser Glu Asp
545                 550                 555                 560

Glu Ala Asp Tyr Tyr Cys Met Ile Trp His Ser Gly Ala Ser Ala Val
                565                 570                 575

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            580                 585
```

<210> 79
<211> 2448
<212> DNA
<213> Artificial Sequence

<220>
<223> VHCH1-VHCH1 (20H4.9)-Heavy chain hole-VL(T84.66-LCHA) (nucleotide sequence)

<400> 79
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cccgagaagg gcctggaatg gatcggcgag atcaaccacg gcggctacgt gacctacaac 180

cccagcctgg aaagcagagt gaccatcagc gtggacacca gcaagaacca gttcagcctg 240

aagctgagca gcgtgacagc cgccgacacc gccgtgtact actgcgccag agactacggc 300

cctggcaact acgactggta cttcgacctg tggggcagag gcaccctggt gacagtgtcc 360

agcgcttcta ccaagggccc cagcgtgttc cctctggccc ctagcagcaa gagcacatct 420

ggcggaacag ccgccctggg ctgcctcgtg aaggactact ttcccgagcc cgtgacagtg 480

tcctggaact ctggcgccct gacaagcggc gtgcacacct ttccagccgt gctgcagagc 540

agcggcctgt actctctgag cagcgtcgtg actgtgccca gcagcagcct gggaacccag 600

acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggaa 660

cccaagagct gcgacggcgg aggcggatct ggcggcggag gatcccaggt gcagctgcag 720

cagtggggag ccggcctgct gaagcccagc gagacactga gcctgacctg cgccgtgtac 780

ggcggcagct tcagcggcta ctactggtcc tggatccggc agagccccga gaagggcctg 840

gaatggatcg gcgagatcaa ccacggcggc tacgtgacct acaaccccag cctggaaagc 900

agagtgacca tcagcgtgga caccagcaag aaccagttca gcctgaagct gagcagcgtg 960

acagccgccg acaccgccgt gtactactgc gccagagact acggccctgg caactacgac 1020

tggtacttcg acctgtgggg cagaggcacc ctggtgacag tgtccagcgc tagcaccaag 1080

ggcccatcgg tcttcccccc ggcaccctcc tccaagagca cctctggggg cacagcggcc 1140

ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 1200

gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc 1260

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ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 1500

gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 1560

gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt 1620

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 1680

aaggtctcca acaaagccct cggcgccccc atcgagaaaa ccatctccaa agccaaaggg 1740

cagccccgag aaccacaggt gtgcaccctg cccccatccc gggatgagct gaccaagaac 1800

caggtcagcc tctcgtgcgc agtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1860

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1920

ggctccttct tcctcgtgag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1980

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 2040

tccctgtctc cgggtggagg cggcggaagc ggaggaggag gatccggcgg cggaggttcc 2100

ggaggcggag gatccgagat cgtgctgacc cagagccctg ccaccctgtc actgtctcca 2160

ggcgagagag ccaccctgag ctgtagagcc ggcgagagcg tggacatctt cggcgtggga 2220

tttctgcact ggtatcagca gaagcccggc caggccccca gactgctgat ctacagagcc 2280

agcaaccggg ccacaggcat ccccgccaga ttttctggct ctggcagcgg caccgacttc 2340

accctgacaa tcagcagcct ggaacccgag gacttcgccg tgtactactg ccagcagacc 2400

aacgaggacc cctacacctt tggccagggc accaagctgg aaatcaag 2448

<210> 80
<211> 2478
<212> DNA
<213> Artificial Sequence

<220>

<223> VHCH1-VHCH1 (20H4.9)-Heavy chain knob-VH(T84.66-LCHA) (nucleotide sequence)

<400> 80

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acctgcgccg tgtacggcgg cagcttcagc ggctactact ggtcctggat ccggcagagc 120

cccgagaagg gcctggaatg gatcggcgag atcaaccacg gcggctacgt gacctacaac 180

cccagcctgg aaagcagagt gaccatcagc gtggacacca gcaagaacca gttcagcctg 240

aagctgagca gcgtgacagc cgccgacacc gccgtgtact actgcgccag agactacggc 300

cctggcaact acgactggta cttcgacctg tggggcagag gcaccctggt gacagtgtcc 360

agcgcttcta ccaagggccc cagcgtgttc cctctggccc ctagcagcaa gagcacatct 420

ggcggaacag ccgccctggg ctgcctcgtg aaggactact ttcccgagcc cgtgacagtg 480

tcctggaact ctggcgccct gacaagcggc gtgcacacct ttccagccgt gctgcagagc 540

agcggcctgt actctctgag cagcgtcgtg actgtgccca gcagcagcct gggaacccag 600

acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggaa 660

cccaagagct gcgacggcgg aggcggatct ggcggcggag gatcccaggt gcagctgcag 720

cagtggggag ccggcctgct gaagcccagc gagacactga gcctgacctg cgccgtgtac 780

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gaatggatcg gcgagatcaa ccacggcggc tacgtgacct acaaccccag cctggaaagc 900

agagtgacca tcagcgtgga caccagcaag aaccagttca gcctgaagct gagcagcgtg 960

acagccgccg acaccgccgt gtactactgc gccagagact acggccctgg caactacgac 1020

tggtacttcg acctgtgggg cagaggcacc ctggtgacag tgtccagcgc tagcaccaag 1080

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gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 1680

aaggtctcca acaaagccct cggcgccccc atcgagaaaa ccatctccaa agccaaaggg 1740

cagccccgag aaccacaggt gtacaccctg cccccctgca gagatgagct gaccaagaac 1800

caggtgtccc tgtggtgtct ggtcaagggc ttctacccca gcgatatcgc cgtggagtgg 1860

gagagcaacg gccagcctga gaacaactac aagaccaccc cccctgtgct ggacagcgac 1920

ggcagcttct tcctgtactc caaactgacc gtggacaaga gccggtggca gcagggcaac 1980

gtgttcagct gcagcgtgat gcacgaggcc ctgcacaacc actacaccca gaagtccctg 2040

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tgggtgcgcc aggcccctgg acagggactg gaatggatgg gcagaatcga ccccgccaac 2280

ggcaacagca aatacgtgcc caagttccag ggcagagtga ccatcaccgc cgacaccagc 2340

acctccaccg cctacatgga actgagcagc ctgcggagcg aggacaccgc cgtgtactac 2400

tgtgcccccc tcggctacta cgtgtccgac tacgccatgg cctattgggg ccagggcaca 2460

ctcgtgaccg tgtcctct 2478

<210> 81
<211> 816
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1-VHCH1 (20H4.9)-Heavy chain hole-VL (T84.66-LCHA)

<400> 81

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu

```
1               5                   10                  15

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

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

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110

Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
225                 230                 235                 240

Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr
                245                 250                 255

Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Ser Trp Ile
            260                 265                 270

Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His
        275                 280                 285

Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu Ser Arg Val Thr Ile
    290                 295                 300

Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val
305                 310                 315                 320

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Tyr Gly Pro
                325                 330                 335

Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val
            340                 345                 350

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
        355                 360                 365

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
    370                 375                 380

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
385                 390                 395                 400

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
```

```
                405                 410                 415

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
            420                 425                 430

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        435                 440                 445

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    450                 455                 460

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
465                 470                 475                 480

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                485                 490                 495

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            500                 505                 510

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        515                 520                 525

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    530                 535                 540

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
545                 550                 555                 560

Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
                565                 570                 575

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro
            580                 585                 590

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val
        595                 600                 605
```

```
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    610                 615                 620

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
625                 630                 635                 640

Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                645                 650                 655

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            660                 665                 670

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly
        675                 680                 685

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    690                 695                 700

Ser Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro
705                 710                 715                 720

Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Gly Glu Ser Val Asp Ile
                725                 730                 735

Phe Gly Val Gly Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Ala
            740                 745                 750

Pro Arg Leu Leu Ile Tyr Arg Ala Ser Asn Arg Ala Thr Gly Ile Pro
        755                 760                 765

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
    770                 775                 780

Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Thr
785                 790                 795                 800

Asn Glu Asp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
```

805 810 815

<210> 82
<211> 826
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1-VHCH1 (20H4.9)-Heavy chain knob-VH (T84.66-LCHA)

<400> 82

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

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

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

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
50 55 60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
100 105 110

Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
225                 230                 235                 240

Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr
                245                 250                 255

Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Ser Trp Ile
            260                 265                 270

Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His
        275                 280                 285

Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu Ser Arg Val Thr Ile
    290                 295                 300

Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val
305                 310                 315                 320

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Tyr Gly Pro
                325                 330                 335

Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val
            340                 345                 350
```

```
Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
        355                 360                 365

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
    370                 375                 380

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
385                 390                 395                 400

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
                405                 410                 415

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
            420                 425                 430

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        435                 440                 445

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    450                 455                 460

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
465                 470                 475                 480

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                485                 490                 495

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            500                 505                 510

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        515                 520                 525

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    530                 535                 540

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
```

```
545                 550                 555                 560

Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
                565                 570                 575

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            580                 585                 590

Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val
        595                 600                 605

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    610                 615                 620

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
625                 630                 635                 640

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                645                 650                 655

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            660                 665                 670

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly
        675                 680                 685

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    690                 695                 700

Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
705                 710                 715                 720

Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp
                725                 730                 735

Thr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp
            740                 745                 750
```

```
Met Gly Arg Ile Asp Pro Ala Asn Gly Asn Ser Lys Tyr Val Pro Lys
        755                 760                 765

Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Ser Thr Ala
    770                 775                 780

Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr
785                 790                 795                 800

Cys Ala Pro Phe Gly Tyr Tyr Val Ser Asp Tyr Ala Met Ala Tyr Trp
                805                 810                 815

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
            820                 825
```

<210> 83
<211> 2478
<212> DNA
<213> Artificial Sequence

<220>
<223> VHCH1-VHCH1 (20H4.9)-Heavy chain hole-VH (T84.66-LCHA)
(nucleotide sequence)

<400> 83

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acctgcgccg tgtacggcgg cagcttcagc ggctactact ggtcctggat ccggcagagc      120

cccgagaagg gcctggaatg gatcggcgag atcaaccacg gcggctacgt gacctacaac      180

cccagcctgg aaagcagagt gaccatcagc gtggacacca gcaagaacca gttcagcctg      240

aagctgagca gcgtgacagc cgccgacacc gccgtgtact actgcgccag agactacggc      300

cctggcaact acgactggta cttcgacctg tggggcagag gcaccctggt gacagtgtcc      360

agcgcttcca caaagggccc cagcgtgttc cctctggccc ctagcagcaa gagcacatct      420

ggcggaacag ccgccctggg ctgcctcgtg aaggactact ttcccgagcc cgtgacagtg      480

tcctggaact ctggcgccct gacaagcggc gtgcacacct ttccagccgt gctgcagagc      540

agcggcctgt actctctgtc cagcgtcgtg actgtgccca gcagcagcct gggcacccag      600
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cccaagagct gcgacggcgg aggcggatct ggcggcggag gatcccaggt gcagctgcag 720

cagtggggag ccggcctgct gaagcccagc gagacactga gcctgacctg cgccgtgtac 780

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gaatggatcg gcgagatcaa ccacggcggc tacgtgacct acaaccccag cctggaaagc 900

agagtgacca tcagcgtgga caccagcaag aaccagttca gcctgaagct gagcagcgtg 960

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tggtacttcg acctgtgggg cagaggcacc ctggtgacag tgtccagcgc tagcaccaag 1080

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tgggtgcgcc aggcccctgg acagggactg gaatggatgg gcagaatcga ccccgccaac 2280

ggcaacagca aatacgtgcc caagttccag ggcagagtga ccatcaccgc cgacaccagc 2340

acctccaccg cctacatgga actgagcagc ctgcggagcg aggacaccgc cgtgtactac 2400

tgtgcccccct tcggctacta cgtgtccgac tacgccatgg cctattgggg ccagggcaca 2460

ctcgtgaccg tgtcctct 2478

<210> 84
<211> 2448
<212> DNA
<213> Artificial Sequence

<220>
<223> VHCH1-VHCH1 (20H4.9)-Heavy chain knob-VL (T84.66-LCHA)
(nucleotide sequence)

<400> 84
caggtgcagc tgcagcagtg gggagccggc ctgctgaagc ccagcgagac actgagcctg 60

acctgcgccg tgtacggcgg cagcttcagc ggctactact ggtcctggat ccggcagagc 120

cccgagaagg gcctggaatg gatcggcgag atcaaccacg gcggctacgt gacctacaac 180

cccagcctgg aaagcagagt gaccatcagc gtggacacca gcaagaacca gttcagcctg 240

aagctgagca gcgtgacagc cgccgacacc gccgtgtact actgcgccag agactacggc 300

cctggcaact acgactggta cttcgacctg tggggcagag gcaccctggt gacagtgtcc 360

agcgcttcca caaagggccc cagcgtgttc cctctggccc ctagcagcaa gagcacatct 420

ggcggaacag ccgccctggg ctgcctcgtg aaggactact ttcccgagcc cgtgacagtg 480

tcctggaact ctggcgccct gacaagcggc gtgcacacct ttccagccgt gctgcagagc 540

agcggcctgt actctctgtc cagcgtcgtg actgtgccca gcagcagcct gggcacccag 600

acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggaa 660

cccaagagct gcgacggcgg aggcggatct ggcggcggag gatcccaggt gcagctgcag 720

cagtggggag ccggcctgct gaagcccagc gagacactga gcctgacctg cgccgtgtac 780

ggcggcagct tcagcggcta ctactggtcc tggatccggc agagccccga gaagggcctg 840

gaatggatcg gcgagatcaa ccacggcggc tacgtgacct acaaccccag cctggaaagc 900

agagtgacca tcagcgtgga caccagcaag aaccagttca gcctgaagct gagcagcgtg 960

acagccgccg acaccgccgt gtactactgc gccagagact acggccctgg caactacgac 1020

tggtacttcg acctgtgggg cagaggcacc ctggtgacag tgtccagcgc tagcaccaag 1080

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cagccccgag aaccacaggt gtacaccctg cccccctgca gagatgagct gaccaagaac 1800

caggtgtccc tgtggtgtct ggtcaagggc ttctacccca gcgatatcgc cgtggagtgg 1860

gagagcaacg gccagcctga gaacaactac aagaccaccc cccctgtgct ggacagcgac 1920

ggcagcttct tcctgtactc caaactgacc gtggacaaga gccggtggca gcagggcaac 1980

gtgttcagct gcagcgtgat gcacgaggcc ctgcacaacc actacaccca gaagtccctg 2040

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tttctgcact ggtatcagca gaagcccggc caggccccca gactgctgat ctacagagcc 2280

agcaaccggg ccacaggcat ccccgccaga ttttctggct ctggcagcgg caccgacttc 2340

accctgacaa tcagcagcct ggaacccgag gacttcgccg tgtactactg ccagcagacc 2400

aacgaggacc cctacacctt tggccagggc accaagctgg aaatcaag 2448

<210> 85
<211> 826
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1-VHCH1 (20H4.9)-Heavy chain hole-VH (T84.66-LCHA)

<400> 85

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

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

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

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
50 55 60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
100 105 110

Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
225                 230                 235                 240

Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr
                245                 250                 255

Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Ser Trp Ile
            260                 265                 270

Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His
        275                 280                 285

Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu Ser Arg Val Thr Ile
    290                 295                 300

Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val
305                 310                 315                 320

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Tyr Gly Pro
```

```
                325                 330                 335

Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val
            340                 345                 350

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
        355                 360                 365

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
    370                 375                 380

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
385                 390                 395                 400

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
                405                 410                 415

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
            420                 425                 430

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        435                 440                 445

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    450                 455                 460

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
465                 470                 475                 480

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                485                 490                 495

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            500                 505                 510

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        515                 520                 525
```

```
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    530                 535                 540

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
545                 550                 555                 560

Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
                565                 570                 575

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro
            580                 585                 590

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val
        595                 600                 605

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    610                 615                 620

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
625                 630                 635                 640

Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                645                 650                 655

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            660                 665                 670

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly
        675                 680                 685

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    690                 695                 700

Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
705                 710                 715                 720

Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp
```

```
                725                 730                 735

Thr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp
            740                 745                 750

Met Gly Arg Ile Asp Pro Ala Asn Gly Asn Ser Lys Tyr Val Pro Lys
        755                 760                 765

Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Ser Thr Ala
    770                 775                 780

Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr
785                 790                 795                 800

Cys Ala Pro Phe Gly Tyr Tyr Val Ser Asp Tyr Ala Met Ala Tyr Trp
                805                 810                 815

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
            820                 825
```

<210> 86
<211> 816
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1-VHCH1 (20H4.9)-Heavy chain knob-VL (T84.66-LCHA)

<400> 86

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

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

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

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
```

```
    50                  55                  60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110

Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
225                 230                 235                 240

Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr
                245                 250                 255
```

```
Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Ser Trp Ile
            260                 265                 270

Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His
        275                 280                 285

Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu Ser Arg Val Thr Ile
    290                 295                 300

Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val
305                 310                 315                 320

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Tyr Gly Pro
                325                 330                 335

Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val
            340                 345                 350

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
        355                 360                 365

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
    370                 375                 380

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
385                 390                 395                 400

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
                405                 410                 415

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
            420                 425                 430

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        435                 440                 445

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
```

```
    450                 455                 460

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
465                 470                 475                 480

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                485                 490                 495

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            500                 505                 510

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        515                 520                 525

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    530                 535                 540

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
545                 550                 555                 560

Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
                565                 570                 575

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            580                 585                 590

Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val
        595                 600                 605

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    610                 615                 620

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
625                 630                 635                 640

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                645                 650                 655
```

```
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            660                 665                 670

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly
        675                 680                 685

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    690                 695                 700

Ser Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro
705                 710                 715                 720

Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Gly Glu Ser Val Asp Ile
                725                 730                 735

Phe Gly Val Gly Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Ala
            740                 745                 750

Pro Arg Leu Leu Ile Tyr Arg Ala Ser Asn Arg Ala Thr Gly Ile Pro
        755                 760                 765

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
    770                 775                 780

Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Thr
785                 790                 795                 800

Asn Glu Asp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
                805                 810                 815
```

<210> 87
<211> 2463
<212> DNA
<213> Artificial Sequence

<220>
<223> VHCH1-VHCH1 (20H4.9)-Heavy chain hole-VL(A5B7) (nucleotide sequence)

<400> 87
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acctgcgccg tgtacggcgg cagcttcagc ggctactact ggtcctggat ccggcagagc 120

cccgagaagg gcctggaatg gatcggcgag atcaaccacg gcggctacgt gacctacaac 180

cccagcctgg aaagcagagt gaccatcagc gtggacacca gcaagaacca gttcagcctg 240

aagctgagca gcgtgacagc cgccgacacc gccgtgtact actgcgccag agactacggc 300

cctggcaact acgactggta cttcgacctg tggggcagag gcaccctggt gacagtgtcc 360

agcgcttcta ccaagggccc cagcgtgttc cctctggccc ctagcagcaa gagcacatct 420

ggcggaacag ccgccctggg ctgcctcgtg aaggactact ttcccgagcc cgtgacagtg 480

tcctggaact ctggcgccct gacaagcggc gtgcacacct ttccagccgt gctgcagagc 540

agcggcctgt actctctgag cagcgtcgtg actgtgccca gcagcagcct gggaacccag 600

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cccaagagct gcgacggcgg aggcggatct ggcggcggag gatcccaggt gcagctgcag 720

cagtggggag ccggcctgct gaagcccagc gagacactga gcctgacctg cgccgtgtac 780

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gaatggatcg gcgagatcaa ccacggcggc tacgtgacct acaaccccag cctggaaagc 900

agagtgacca tcagcgtgga caccagcaag aaccagttca gcctgaagct gagcagcgtg 960

acagccgccg acaccgccgt gtactactgc gccagagact acggccctgg caactacgac 1020

tggtacttcg acctgtgggg cagaggcacc ctggtgacag tgtccagcgc tagcaccaag 1080

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gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 1560

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aaggtctcca acaaagccct cggcgccccc atcgagaaaa ccatctccaa agccaaaggg 1740

cagccccgag aaccacaggt gtgcaccctg cccccatccc gggatgagct gaccaagaac 1800

caggtcagcc tctcgtgcgc agtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1860

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1920

ggctccttct tcctcgtgag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1980

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 2040

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agcgacaagc agcagggcag cggcgtgtcc agcagattca gcgccagcaa ggacgcctct 2340

gccaacgccg gaatcctgct gatcagcggc ctgcagtctg aggacgaggc cgactactac 2400

tgcatgatct ggcactctgg cgccagcgcc gtgtttggcg gaggcacaaa actgaccgtg 2460

ctg 2463

<210> 88
<211> 2478
<212> DNA
<213> Artificial Sequence

<220>
<223> VHCH1-VHCH1 (20H4.9)-Heavy chain knob-VH(A5B7) (nucleotide sequence)

<400> 88
caggtgcagc tgcagcagtg gggagccggc ctgctgaagc ccagcgagac actgagcctg 60

acctgcgccg tgtacggcgg cagcttcagc ggctactact ggtcctggat ccggcagagc 120

cccgagaagg gcctggaatg gatcggcgag atcaaccacg gcggctacgt gacctacaac 180

cccagcctgg aaagcagagt gaccatcagc gtggacacca gcaagaacca gttcagcctg 240

aagctgagca gcgtgacagc cgccgacacc gccgtgtact actgcgccag agactacggc 300

cctggcaact acgactggta cttcgacctg tggggcagag gcaccctggt gacagtgtcc 360

agcgcttcta ccaagggccc cagcgtgttc cctctggccc ctagcagcaa gagcacatct 420

ggcggaacag ccgccctggg ctgcctcgtg aaggactact ttcccgagcc cgtgacagtg 480

tcctggaact ctggcgccct gacaagcggc gtgcacacct ttccagccgt gctgcagagc 540

agcggcctgt actctctgag cagcgtcgtg actgtgccca gcagcagcct gggaacccag 600

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gaatggatcg gcgagatcaa ccacggcggc tacgtgacct acaaccccag cctggaaagc 900

agagtgacca tcagcgtgga caccagcaag aaccagttca gcctgaagct gagcagcgtg 960

acagccgccg acaccgccgt gtactactgc gccagagact acggccctgg caactacgac 1020

tggtacttcg acctgtgggg cagaggcacc ctggtgacag tgtccagcgc tagcaccaag 1080

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aaggtctcca acaaagccct cggcgccccc atcgagaaaa ccatctccaa agccaaaggg 1740

cagccccgag aaccacaggt gtacaccctg ccccccctgca gagatgagct gaccaagaac 1800

caggtgtccc tgtggtgtct ggtcaagggc ttctacccca gcgatatcgc cgtggagtgg 1860

gagagcaacg gccagcctga gaacaactac aagaccaccc cccctgtgct ggacagcgac 1920

ggcagcttct tcctgtactc caaactgacc gtggacaaga gccggtggca gcagggcaac 1980

gtgttcagct gcagcgtgat gcacgaggcc ctgcacaacc actacaccca gaagtccctg 2040

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aacggcggca ccaccgagta cgccgcctct gtgaagggcc ggttcaccat cagccgggac 2340

gacagcaaga acaccctgta cctgcagatg aacagcctgc gggccgagga caccgccgtg 2400

tactactgcg ccagagacag aggcctgcgg ttctacttcg actactgggg ccagggcacc 2460

accgtgacag tctcttcc 2478

<210> 89
<211> 821
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1-VHCH1 (20H4.9)-Heavy chain hole-VL (A5B7)

<400> 89

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

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

Tyr Trp Ser Trp Ile Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Ile

```
        35                  40                  45

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110

Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
225                 230                 235                 240
```

```
Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr
               245                 250                 255

Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Ser Trp Ile
            260                 265                 270

Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His
        275                 280                 285

Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu Ser Arg Val Thr Ile
    290                 295                 300

Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val
305                 310                 315                 320

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Tyr Gly Pro
               325                 330                 335

Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val
            340                 345                 350

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
        355                 360                 365

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
    370                 375                 380

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
385                 390                 395                 400

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
               405                 410                 415

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
            420                 425                 430

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
```

```
        435                 440                 445

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    450                 455                 460

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
465                 470                 475                 480

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                485                 490                 495

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            500                 505                 510

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        515                 520                 525

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    530                 535                 540

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
545                 550                 555                 560

Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
                565                 570                 575

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro
            580                 585                 590

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val
        595                 600                 605

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    610                 615                 620

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
625                 630                 635                 640
```

```
Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                645                 650                 655

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            660                 665                 670

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly
        675                 680                 685

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    690                 695                 700

Ser Gln Ala Val Leu Thr Gln Pro Ala Ser Leu Ser Ala Ser Pro Gly
705                 710                 715                 720

Ala Ser Ala Ser Leu Thr Cys Thr Leu Arg Arg Gly Ile Asn Val Gly
                725                 730                 735

Ala Tyr Ser Ile Tyr Trp Tyr Gln Gln Lys Pro Gly Ser Pro Pro Gln
            740                 745                 750

Tyr Leu Leu Arg Tyr Lys Ser Asp Ser Asp Lys Gln Gln Gly Ser Gly
        755                 760                 765

Val Ser Ser Arg Phe Ser Ala Ser Lys Asp Ala Ser Ala Asn Ala Gly
    770                 775                 780

Ile Leu Leu Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr
785                 790                 795                 800

Cys Met Ile Trp His Ser Gly Ala Ser Ala Val Phe Gly Gly Gly Thr
                805                 810                 815

Lys Leu Thr Val Leu
            820
```

<210> 90

<211> 826
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1-VHCH1 (20H4.9)-Heavy chain knob-VH (A5B7)

<400> 90

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

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

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

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
50 55 60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
100 105 110

Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
225                 230                 235                 240

Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr
                245                 250                 255

Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Ser Trp Ile
            260                 265                 270

Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His
        275                 280                 285

Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu Ser Arg Val Thr Ile
    290                 295                 300

Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val
305                 310                 315                 320

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Tyr Gly Pro
                325                 330                 335

Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val
            340                 345                 350

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
        355                 360                 365
```

```
Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
    370                 375                 380

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
385                 390                 395                 400

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
                405                 410                 415

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
            420                 425                 430

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        435                 440                 445

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    450                 455                 460

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
465                 470                 475                 480

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                485                 490                 495

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            500                 505                 510

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        515                 520                 525

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    530                 535                 540

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
545                 550                 555                 560

Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
```

```
                565                 570                 575

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            580                 585                 590

Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val
        595                 600                 605

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    610                 615                 620

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
625                 630                 635                 640

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                645                 650                 655

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            660                 665                 670

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly
        675                 680                 685

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    690                 695                 700

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

Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Val Ser Ser
                725                 730                 735

Tyr Trp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
            740                 745                 750

Val Gly Phe Ile Arg Asn Lys Ala Asn Gly Gly Thr Thr Glu Tyr Ala
        755                 760                 765
```

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


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


Tyr Tyr Cys Ala Arg Asp Arg Gly Leu Arg Phe Tyr Phe Asp Tyr Trp
                805                 810                 815


Gly Gln Gly Thr Thr Val Thr Val Ser Ser
            820                 825
```

<210> 91
<211> 2478
<212> DNA
<213> Artificial Sequence

<220>
<223> VHCH1-VHCH1 (20H4.9)-Heavy chain hole-VH (A5B7) (nucleotide sequence)

<400> 91

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caggtgcagc tgcagcagtg gggagccggc ctgctgaagc ccagcgagac actgagcctg       60

acctgcgccg tgtacggcgg cagcttcagc ggctactact ggtcctggat ccggcagagc      120

cccgagaagg gcctggaatg gatcggcgag atcaaccacg gcggctacgt gacctacaac      180

cccagcctgg aaagcagagt gaccatcagc gtggacacca gcaagaacca gttcagcctg      240

aagctgagca gcgtgacagc cgccgacacc gccgtgtact actgcgccag agactacggc      300

cctggcaact acgactggta cttcgacctg tggggcagag gcaccctggt gacagtgtcc      360

agcgcttcca caaagggccc cagcgtgttc cctctggccc ctagcagcaa gagcacatct      420

ggcggaacag ccgccctggg ctgcctcgtg aaggactact ttcccgagcc cgtgacagtg      480

tcctggaact ctggcgccct gacaagcggc gtgcacacct ttccagccgt gctgcagagc      540

agcggcctgt actctctgtc cagcgtcgtg actgtgccca gcagcagcct gggcacccag      600

acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggaa      660

cccaagagct gcgacggcgg aggcggatct ggcggcggag gatcccaggt gcagctgcag      720
```

cagtggggag ccggcctgct gaagcccagc gagacactga gcctgacctg cgccgtgtac 780

ggcggcagct tcagcggcta ctactggtcc tggatccggc agagccccga gaagggcctg 840

gaatggatcg gcgagatcaa ccacggcggc tacgtgacct acaaccccag cctggaaagc 900

agagtgacca tcagcgtgga caccagcaag aaccagttca gcctgaagct gagcagcgtg 960

acagccgccg acaccgccgt gtactactgc gccagagact acggccctgg caactacgac 1020

tggtacttcg acctgtgggg cagaggcacc ctggtgacag tgtccagcgc tagcaccaag 1080

ggcccatcgg tcttcccccc ggcaccctcc tccaagagca cctctggggg cacagcggcc 1140

ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 1200

gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc 1260

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 1320

gtgaatcaca agcccagcaa caccaaggtg gacaagaaag ttgagcccaa atcttgtgac 1380

aaaactcaca catgcccacc gtgcccagca cctgaagctg caggggggacc gtcagtcttc 1440

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 1500

gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 1560

gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt 1620

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 1680

aaggtctcca acaaagccct cggcgccccc atcgagaaaa ccatctccaa agccaaaggg 1740

cagccccgag aaccacaggt gtgcaccctg cccccatccc gggatgagct gaccaagaac 1800

caggtcagcc tctcgtgcgc agtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1860

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1920

ggctccttct tcctcgtgag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1980

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 2040

tccctgtctc cgggtggagg cggcggaagc ggaggaggag gatccggcgg cggaggttcc 2100

ggaggcggag gatccgaagt gcagctggtg gaatctggcg gcggactggt gcagcctggc 2160

agaagcctga gactgagctg tgccgccagc ggctttaccg tgtccagcta ctggatgcac 2220

tgggtccgac aggcccctgg caagggactg gaatgggtcg gattcatcag aaacaaggcc 2280

aacggcggca ccaccgagta cgccgcctct gtgaagggcc ggttcaccat cagccgggac 2340

gacagcaaga acaccctgta cctgcagatg aacagcctgc gggccgagga caccgccgtg 2400

tactactgcg ccagagacag aggcctgcgg ttctacttcg actactgggg ccagggcacc 2460

accgtgacag tctcttcc 2478

<210> 92
<211> 2463
<212> DNA
<213> Artificial Sequence

<220>
<223> VHCH1-VHCH1 (20H4.9)-Heavy chain knob-VL (A5B7) (nucleotide sequence)

<400> 92
caggtgcagc tgcagcagtg gggagccggc ctgctgaagc ccagcgagac actgagcctg 60

acctgcgccg tgtacggcgg cagcttcagc ggctactact ggtcctggat ccggcagagc 120

cccgagaagg gcctggaatg gatcggcgag atcaaccacg gcggctacgt gacctacaac 180

cccagcctgg aaagcagagt gaccatcagc gtggacacca gcaagaacca gttcagcctg 240

aagctgagca gcgtgacagc cgccgacacc gccgtgtact actgcgccag agactacggc 300

cctggcaact acgactggta cttcgacctg tggggcagag gcaccctggt gacagtgtcc 360

agcgcttcca caaagggccc cagcgtgttc cctctggccc ctagcagcaa gagcacatct 420

ggcggaacag ccgccctggg ctgcctcgtg aaggactact ttcccgagcc cgtgacagtg 480

tcctggaact ctggcgccct gacaagcggc gtgcacacct ttccagccgt gctgcagagc 540

agcggcctgt actctctgtc cagcgtcgtg actgtgccca gcagcagcct gggcacccag 600

acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggaa 660

cccaagagct gcgacggcgg aggcggatct ggcggcggag gatcccaggt gcagctgcag 720

cagtggggag ccggcctgct gaagcccagc gagacactga gcctgacctg cgccgtgtac 780

ggcggcagct tcagcggcta ctactggtcc tggatccggc agagccccga gaagggcctg 840

gaatggatcg gcgagatcaa ccacggcggc tacgtgacct acaaccccag cctggaaagc 900

agagtgacca tcagcgtgga caccagcaag aaccagttca gcctgaagct gagcagcgtg 960

acagccgccg acaccgccgt gtactactgc gccagagact acggccctgg caactacgac 1020

tggtacttcg acctgtgggg cagaggcacc ctggtgacag tgtccagcgc tagcaccaag 1080

ggcccatcgg tcttcccccc ggcaccctcc tccaagagca cctctggggg cacagcggcc 1140

ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 1200

gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc 1260

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aaaactcaca catgcccacc gtgcccagca cctgaagctg caggggggacc gtcagtcttc 1440

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 1500

gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 1560

gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt 1620

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 1680

aaggtctcca acaaagccct cggcgccccc atcgagaaaa ccatctccaa agccaaaggg 1740

cagccccgag aaccacaggt gtacaccctg cccccctgca gagatgagct gaccaagaac 1800

caggtgtccc tgtggtgtct ggtcaagggc ttctacccca gcgatatcgc cgtggagtgg 1860

gagagcaacg gccagcctga gaacaactac aagaccaccc cccctgtgct ggacagcgac 1920

ggcagcttct tcctgtactc caaactgacc gtggacaaga gccggtggca gcagggcaac 1980

gtgttcagct gcagcgtgat gcacgaggcc ctgcacaacc actacaccca gaagtccctg 2040

agcctgagcc ccggcggagg cggcggaagc ggaggaggag gatctggggg cggaggttcc 2100

ggaggcggtg gatctcaggc cgtgctgaca cagcctgcca gcctgtctgc ttctcctggc 2160

gcctctgcct ccctgacctg cacactgaga agaggcatca acgtgggcgc ctacagcatc 2220

tactggtatc agcagaagcc cggcagcccc cctcagtacc tgctgagata caagagcgac 2280

agcgacaagc agcagggcag cggcgtgtcc agcagattca gcgccagcaa ggacgcctct 2340

gccaacgccg gaatcctgct gatcagcggc ctgcagtctg aggacgaggc cgactactac 2400

tgcatgatct ggcactctgg cgccagcgcc gtgtttggcg gaggcacaaa actgaccgtg 2460

ctg 2463

<210> 93
<211> 826
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1-VHCH1 (20H4.9)-Heavy chain hole-VH (A5B7)

<400> 93

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

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

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

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
50 55 60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
100 105 110

Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
225                 230                 235                 240

Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr
                245                 250                 255

Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Ser Trp Ile
            260                 265                 270

Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His
        275                 280                 285

Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu Ser Arg Val Thr Ile
    290                 295                 300

Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val
305                 310                 315                 320

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Tyr Gly Pro
                325                 330                 335
```

```
Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val
            340                 345                 350

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
        355                 360                 365

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
    370                 375                 380

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
385                 390                 395                 400

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
                405                 410                 415

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
            420                 425                 430

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        435                 440                 445

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    450                 455                 460

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
465                 470                 475                 480

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                485                 490                 495

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            500                 505                 510

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        515                 520                 525

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
```

```
    530                 535                 540

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
545                 550                 555                 560

Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
                565                 570                 575

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro
            580                 585                 590

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val
        595                 600                 605

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    610                 615                 620

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
625                 630                 635                 640

Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                645                 650                 655

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            660                 665                 670

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly
        675                 680                 685

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    690                 695                 700

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

Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Val Ser Ser
                725                 730                 735
```

```
Tyr Trp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
            740                 745                 750

Val Gly Phe Ile Arg Asn Lys Ala Asn Gly Gly Thr Thr Glu Tyr Ala
        755                 760                 765

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

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

Tyr Tyr Cys Ala Arg Asp Arg Gly Leu Arg Phe Tyr Phe Asp Tyr Trp
                805                 810                 815

Gly Gln Gly Thr Thr Val Thr Val Ser Ser
            820                 825
```

<210> 94
<211> 821
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1-VHCH1 (20H4.9)-Heavy chain knob-VL (A5B7)

<400> 94

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

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

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

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60
```

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110

Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
225                 230                 235                 240

Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr
                245                 250                 255

Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Ser Trp Ile
```

```
            260                 265                 270

Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His
        275                 280                 285

Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu Ser Arg Val Thr Ile
    290                 295                 300

Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val
305                 310                 315                 320

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Tyr Gly Pro
                325                 330                 335

Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val
            340                 345                 350

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
        355                 360                 365

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
    370                 375                 380

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
385                 390                 395                 400

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
                405                 410                 415

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
            420                 425                 430

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        435                 440                 445

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    450                 455                 460
```

```
Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
465                 470                 475                 480

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                485                 490                 495

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            500                 505                 510

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        515                 520                 525

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    530                 535                 540

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
545                 550                 555                 560

Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
                565                 570                 575

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            580                 585                 590

Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val
        595                 600                 605

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    610                 615                 620

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
625                 630                 635                 640

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                645                 650                 655

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
```

```
            660                 665                 670

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly
        675                 680                 685

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    690                 695                 700

Ser Gln Ala Val Leu Thr Gln Pro Ala Ser Leu Ser Ala Ser Pro Gly
705                 710                 715                 720

Ala Ser Ala Ser Leu Thr Cys Thr Leu Arg Arg Gly Ile Asn Val Gly
                725                 730                 735

Ala Tyr Ser Ile Tyr Trp Tyr Gln Gln Lys Pro Gly Ser Pro Pro Gln
            740                 745                 750

Tyr Leu Leu Arg Tyr Lys Ser Asp Ser Asp Lys Gln Gln Gly Ser Gly
        755                 760                 765

Val Ser Ser Arg Phe Ser Ala Ser Lys Asp Ala Ser Ala Asn Ala Gly
    770                 775                 780

Ile Leu Leu Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr
785                 790                 795                 800

Cys Met Ile Trp His Ser Gly Ala Ser Ala Val Phe Gly Gly Gly Thr
                805                 810                 815

Lys Leu Thr Val Leu
            820
```

<210> 95
<211> 760
<212> PRT
<213> Homo sapiens

<400> 95

```
Met Lys Thr Trp Val Lys Ile Val Phe Gly Val Ala Thr Ser Ala Val
1               5                   10                  15

Leu Ala Leu Leu Val Met Cys Ile Val Leu Arg Pro Ser Arg Val His
            20                  25                  30

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

Asn Gly Thr Phe Ser Tyr Lys Thr Phe Phe Pro Asn Trp Ile Ser Gly
    50                  55                  60

Gln Glu Tyr Leu His Gln Ser Ala Asp Asn Asn Ile Val Leu Tyr Asn
65                  70                  75                  80

Ile Glu Thr Gly Gln Ser Tyr Thr Ile Leu Ser Asn Arg Thr Met Lys
                85                  90                  95

Ser Val Asn Ala Ser Asn Tyr Gly Leu Ser Pro Asp Arg Gln Phe Val
            100                 105                 110

Tyr Leu Glu Ser Asp Tyr Ser Lys Leu Trp Arg Tyr Ser Tyr Thr Ala
        115                 120                 125

Thr Tyr Tyr Ile Tyr Asp Leu Ser Asn Gly Glu Phe Val Arg Gly Asn
    130                 135                 140

Glu Leu Pro Arg Pro Ile Gln Tyr Leu Cys Trp Ser Pro Val Gly Ser
145                 150                 155                 160

Lys Leu Ala Tyr Val Tyr Gln Asn Asn Ile Tyr Leu Lys Gln Arg Pro
                165                 170                 175

Gly Asp Pro Pro Phe Gln Ile Thr Phe Asn Gly Arg Glu Asn Lys Ile
            180                 185                 190

Phe Asn Gly Ile Pro Asp Trp Val Tyr Glu Glu Glu Met Leu Ala Thr
        195                 200                 205
```

```
Lys Tyr Ala Leu Trp Trp Ser Pro Asn Gly Lys Phe Leu Ala Tyr Ala
    210                 215                 220

Glu Phe Asn Asp Thr Asp Ile Pro Val Ile Ala Tyr Ser Tyr Tyr Gly
225                 230                 235                 240

Asp Glu Gln Tyr Pro Arg Thr Ile Asn Ile Pro Tyr Pro Lys Ala Gly
                245                 250                 255

Ala Lys Asn Pro Val Val Arg Ile Phe Ile Ile Asp Thr Thr Tyr Pro
            260                 265                 270

Ala Tyr Val Gly Pro Gln Glu Val Pro Val Pro Ala Met Ile Ala Ser
        275                 280                 285

Ser Asp Tyr Tyr Phe Ser Trp Leu Thr Trp Val Thr Asp Glu Arg Val
    290                 295                 300

Cys Leu Gln Trp Leu Lys Arg Val Gln Asn Val Ser Val Leu Ser Ile
305                 310                 315                 320

Cys Asp Phe Arg Glu Asp Trp Gln Thr Trp Asp Cys Pro Lys Thr Gln
                325                 330                 335

Glu His Ile Glu Glu Ser Arg Thr Gly Trp Ala Gly Gly Phe Phe Val
            340                 345                 350

Ser Thr Pro Val Phe Ser Tyr Asp Ala Ile Ser Tyr Tyr Lys Ile Phe
        355                 360                 365

Ser Asp Lys Asp Gly Tyr Lys His Ile His Tyr Ile Lys Asp Thr Val
    370                 375                 380

Glu Asn Ala Ile Gln Ile Thr Ser Gly Lys Trp Glu Ala Ile Asn Ile
385                 390                 395                 400
```

```
Phe Arg Val Thr Gln Asp Ser Leu Phe Tyr Ser Ser Asn Glu Phe Glu
                405                 410                 415

Glu Tyr Pro Gly Arg Arg Asn Ile Tyr Arg Ile Ser Ile Gly Ser Tyr
            420                 425                 430

Pro Pro Ser Lys Lys Cys Val Thr Cys His Leu Arg Lys Glu Arg Cys
        435                 440                 445

Gln Tyr Tyr Thr Ala Ser Phe Ser Asp Tyr Ala Lys Tyr Tyr Ala Leu
    450                 455                 460

Val Cys Tyr Gly Pro Gly Ile Pro Ile Ser Thr Leu His Asp Gly Arg
465                 470                 475                 480

Thr Asp Gln Glu Ile Lys Ile Leu Glu Glu Asn Lys Glu Leu Glu Asn
                485                 490                 495

Ala Leu Lys Asn Ile Gln Leu Pro Lys Glu Glu Ile Lys Lys Leu Glu
            500                 505                 510

Val Asp Glu Ile Thr Leu Trp Tyr Lys Met Ile Leu Pro Pro Gln Phe
        515                 520                 525

Asp Arg Ser Lys Lys Tyr Pro Leu Leu Ile Gln Val Tyr Gly Gly Pro
    530                 535                 540

Cys Ser Gln Ser Val Arg Ser Val Phe Ala Val Asn Trp Ile Ser Tyr
545                 550                 555                 560

Leu Ala Ser Lys Glu Gly Met Val Ile Ala Leu Val Asp Gly Arg Gly
                565                 570                 575

Thr Ala Phe Gln Gly Asp Lys Leu Leu Tyr Ala Val Tyr Arg Lys Leu
            580                 585                 590

Gly Val Tyr Glu Val Glu Asp Gln Ile Thr Ala Val Arg Lys Phe Ile
        595                 600                 605
```

```
Glu Met Gly Phe Ile Asp Glu Lys Arg Ile Ala Ile Trp Gly Trp Ser
    610                 615                 620

Tyr Gly Gly Tyr Val Ser Ser Leu Ala Leu Ala Ser Gly Thr Gly Leu
625                 630                 635                 640

Phe Lys Cys Gly Ile Ala Val Ala Pro Val Ser Ser Trp Glu Tyr Tyr
                645                 650                 655

Ala Ser Val Tyr Thr Glu Arg Phe Met Gly Leu Pro Thr Lys Asp Asp
            660                 665                 670

Asn Leu Glu His Tyr Lys Asn Ser Thr Val Met Ala Arg Ala Glu Tyr
        675                 680                 685

Phe Arg Asn Val Asp Tyr Leu Leu Ile His Gly Thr Ala Asp Asp Asn
    690                 695                 700

Val His Phe Gln Asn Ser Ala Gln Ile Ala Lys Ala Leu Val Asn Ala
705                 710                 715                 720

Gln Val Asp Phe Gln Ala Met Trp Tyr Ser Asp Gln Asn His Gly Leu
                725                 730                 735

Ser Gly Leu Ser Thr Asn His Leu Tyr Thr His Met Thr His Phe Leu
            740                 745                 750

Lys Gln Cys Phe Ser Leu Ser Asp
        755                 760
```

<210> 96
<211> 748
<212> PRT
<213> Artificial Sequence

<220>
<223> hu FAP ectodomain+poly-lys-tag+his6-tag

<400> 96

```
Arg Pro Ser Arg Val His Asn Ser Glu Glu Asn Thr Met Arg Ala Leu
1               5                   10                  15


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


Pro Asn Trp Ile Ser Gly Gln Glu Tyr Leu His Gln Ser Ala Asp Asn
        35                  40                  45


Asn Ile Val Leu Tyr Asn Ile Glu Thr Gly Gln Ser Tyr Thr Ile Leu
    50                  55                  60


Ser Asn Arg Thr Met Lys Ser Val Asn Ala Ser Asn Tyr Gly Leu Ser
65                  70                  75                  80


Pro Asp Arg Gln Phe Val Tyr Leu Glu Ser Asp Tyr Ser Lys Leu Trp
                85                  90                  95


Arg Tyr Ser Tyr Thr Ala Thr Tyr Tyr Ile Tyr Asp Leu Ser Asn Gly
            100                 105                 110


Glu Phe Val Arg Gly Asn Glu Leu Pro Arg Pro Ile Gln Tyr Leu Cys
        115                 120                 125


Trp Ser Pro Val Gly Ser Lys Leu Ala Tyr Val Tyr Gln Asn Asn Ile
    130                 135                 140


Tyr Leu Lys Gln Arg Pro Gly Asp Pro Pro Phe Gln Ile Thr Phe Asn
145                 150                 155                 160


Gly Arg Glu Asn Lys Ile Phe Asn Gly Ile Pro Asp Trp Val Tyr Glu
                165                 170                 175


Glu Glu Met Leu Ala Thr Lys Tyr Ala Leu Trp Trp Ser Pro Asn Gly
            180                 185                 190
```

```
Lys Phe Leu Ala Tyr Ala Glu Phe Asn Asp Thr Asp Ile Pro Val Ile
        195                 200                 205

Ala Tyr Ser Tyr Tyr Gly Asp Glu Gln Tyr Pro Arg Thr Ile Asn Ile
    210                 215                 220

Pro Tyr Pro Lys Ala Gly Ala Lys Asn Pro Val Val Arg Ile Phe Ile
225                 230                 235                 240

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

Pro Ala Met Ile Ala Ser Ser Asp Tyr Tyr Phe Ser Trp Leu Thr Trp
            260                 265                 270

Val Thr Asp Glu Arg Val Cys Leu Gln Trp Leu Lys Arg Val Gln Asn
        275                 280                 285

Val Ser Val Leu Ser Ile Cys Asp Phe Arg Glu Asp Trp Gln Thr Trp
    290                 295                 300

Asp Cys Pro Lys Thr Gln Glu His Ile Glu Glu Ser Arg Thr Gly Trp
305                 310                 315                 320

Ala Gly Gly Phe Phe Val Ser Thr Pro Val Phe Ser Tyr Asp Ala Ile
                325                 330                 335

Ser Tyr Tyr Lys Ile Phe Ser Asp Lys Asp Gly Tyr Lys His Ile His
            340                 345                 350

Tyr Ile Lys Asp Thr Val Glu Asn Ala Ile Gln Ile Thr Ser Gly Lys
        355                 360                 365

Trp Glu Ala Ile Asn Ile Phe Arg Val Thr Gln Asp Ser Leu Phe Tyr
    370                 375                 380

Ser Ser Asn Glu Phe Glu Glu Tyr Pro Gly Arg Arg Asn Ile Tyr Arg
385                 390                 395                 400
```

```
Ile Ser Ile Gly Ser Tyr Pro Pro Ser Lys Lys Cys Val Thr Cys His
                405                 410                 415

Leu Arg Lys Glu Arg Cys Gln Tyr Tyr Thr Ala Ser Phe Ser Asp Tyr
            420                 425                 430

Ala Lys Tyr Tyr Ala Leu Val Cys Tyr Gly Pro Gly Ile Pro Ile Ser
        435                 440                 445

Thr Leu His Asp Gly Arg Thr Asp Gln Glu Ile Lys Ile Leu Glu Glu
    450                 455                 460

Asn Lys Glu Leu Glu Asn Ala Leu Lys Asn Ile Gln Leu Pro Lys Glu
465                 470                 475                 480

Glu Ile Lys Lys Leu Glu Val Asp Glu Ile Thr Leu Trp Tyr Lys Met
                485                 490                 495

Ile Leu Pro Pro Gln Phe Asp Arg Ser Lys Lys Tyr Pro Leu Leu Ile
            500                 505                 510

Gln Val Tyr Gly Gly Pro Cys Ser Gln Ser Val Arg Ser Val Phe Ala
        515                 520                 525

Val Asn Trp Ile Ser Tyr Leu Ala Ser Lys Glu Gly Met Val Ile Ala
    530                 535                 540

Leu Val Asp Gly Arg Gly Thr Ala Phe Gln Gly Asp Lys Leu Leu Tyr
545                 550                 555                 560

Ala Val Tyr Arg Lys Leu Gly Val Tyr Glu Val Glu Asp Gln Ile Thr
                565                 570                 575

Ala Val Arg Lys Phe Ile Glu Met Gly Phe Ile Asp Glu Lys Arg Ile
            580                 585                 590
```

```
Ala Ile Trp Gly Trp Ser Tyr Gly Gly Tyr Val Ser Ser Leu Ala Leu
        595                 600                 605

Ala Ser Gly Thr Gly Leu Phe Lys Cys Gly Ile Ala Val Ala Pro Val
    610                 615                 620

Ser Ser Trp Glu Tyr Tyr Ala Ser Val Tyr Thr Glu Arg Phe Met Gly
625                 630                 635                 640

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

Met Ala Arg Ala Glu Tyr Phe Arg Asn Val Asp Tyr Leu Leu Ile His
            660                 665                 670

Gly Thr Ala Asp Asp Asn Val His Phe Gln Asn Ser Ala Gln Ile Ala
        675                 680                 685

Lys Ala Leu Val Asn Ala Gln Val Asp Phe Gln Ala Met Trp Tyr Ser
    690                 695                 700

Asp Gln Asn His Gly Leu Ser Gly Leu Ser Thr Asn His Leu Tyr Thr
705                 710                 715                 720

His Met Thr His Phe Leu Lys Gln Cys Phe Ser Leu Ser Asp Gly Lys
                725                 730                 735

Lys Lys Lys Lys Lys Gly His His His His His His
            740                 745
```

<210> 97
<211> 761
<212> PRT
<213> Mus musculus

<400> 97

```
Met Lys Thr Trp Leu Lys Thr Val Phe Gly Val Thr Thr Leu Ala Ala
1               5                   10                  15
```

```
Leu Ala Leu Val Val Ile Cys Ile Val Leu Arg Pro Ser Arg Val Tyr
            20                  25                  30

Lys Pro Glu Gly Asn Thr Lys Arg Ala Leu Thr Leu Lys Asp Ile Leu
        35                  40                  45

Asn Gly Thr Phe Ser Tyr Lys Thr Tyr Phe Pro Asn Trp Ile Ser Glu
    50                  55                  60

Gln Glu Tyr Leu His Gln Ser Glu Asp Asp Asn Ile Val Phe Tyr Asn
65                  70                  75                  80

Ile Glu Thr Arg Glu Ser Tyr Ile Ile Leu Ser Asn Ser Thr Met Lys
                85                  90                  95

Ser Val Asn Ala Thr Asp Tyr Gly Leu Ser Pro Asp Arg Gln Phe Val
            100                 105                 110

Tyr Leu Glu Ser Asp Tyr Ser Lys Leu Trp Arg Tyr Ser Tyr Thr Ala
        115                 120                 125

Thr Tyr Tyr Ile Tyr Asp Leu Gln Asn Gly Glu Phe Val Arg Gly Tyr
    130                 135                 140

Glu Leu Pro Arg Pro Ile Gln Tyr Leu Cys Trp Ser Pro Val Gly Ser
145                 150                 155                 160

Lys Leu Ala Tyr Val Tyr Gln Asn Asn Ile Tyr Leu Lys Gln Arg Pro
                165                 170                 175

Gly Asp Pro Pro Phe Gln Ile Thr Tyr Thr Gly Arg Glu Asn Arg Ile
            180                 185                 190

Phe Asn Gly Ile Pro Asp Trp Val Tyr Glu Glu Glu Met Leu Ala Thr
        195                 200                 205

Lys Tyr Ala Leu Trp Trp Ser Pro Asp Gly Lys Phe Leu Ala Tyr Val
```

```
    210                 215                 220

Glu Phe Asn Asp Ser Asp Ile Pro Ile Ile Ala Tyr Ser Tyr Tyr Gly
225                 230                 235                 240

Asp Gly Gln Tyr Pro Arg Thr Ile Asn Ile Pro Tyr Pro Lys Ala Gly
                245                 250                 255

Ala Lys Asn Pro Val Val Arg Val Phe Ile Val Asp Thr Thr Tyr Pro
            260                 265                 270

His His Val Gly Pro Met Glu Val Pro Val Pro Glu Met Ile Ala Ser
        275                 280                 285

Ser Asp Tyr Tyr Phe Ser Trp Leu Thr Trp Val Ser Ser Glu Arg Val
    290                 295                 300

Cys Leu Gln Trp Leu Lys Arg Val Gln Asn Val Ser Val Leu Ser Ile
305                 310                 315                 320

Cys Asp Phe Arg Glu Asp Trp His Ala Trp Glu Cys Pro Lys Asn Gln
                325                 330                 335

Glu His Val Glu Glu Ser Arg Thr Gly Trp Ala Gly Gly Phe Phe Val
            340                 345                 350

Ser Thr Pro Ala Phe Ser Gln Asp Ala Thr Ser Tyr Tyr Lys Ile Phe
        355                 360                 365

Ser Asp Lys Asp Gly Tyr Lys His Ile His Tyr Ile Lys Asp Thr Val
    370                 375                 380

Glu Asn Ala Ile Gln Ile Thr Ser Gly Lys Trp Glu Ala Ile Tyr Ile
385                 390                 395                 400

Phe Arg Val Thr Gln Asp Ser Leu Phe Tyr Ser Ser Asn Glu Phe Glu
                405                 410                 415
```

```
Gly Tyr Pro Gly Arg Arg Asn Ile Tyr Arg Ile Ser Ile Gly Asn Ser
            420                 425                 430

Pro Pro Ser Lys Lys Cys Val Thr Cys His Leu Arg Lys Glu Arg Cys
        435                 440                 445

Gln Tyr Tyr Thr Ala Ser Phe Ser Tyr Lys Ala Lys Tyr Tyr Ala Leu
    450                 455                 460

Val Cys Tyr Gly Pro Gly Leu Pro Ile Ser Thr Leu His Asp Gly Arg
465                 470                 475                 480

Thr Asp Gln Glu Ile Gln Val Leu Glu Glu Asn Lys Glu Leu Glu Asn
                485                 490                 495

Ser Leu Arg Asn Ile Gln Leu Pro Lys Val Glu Ile Lys Lys Leu Lys
            500                 505                 510

Asp Gly Gly Leu Thr Phe Trp Tyr Lys Met Ile Leu Pro Pro Gln Phe
        515                 520                 525

Asp Arg Ser Lys Lys Tyr Pro Leu Leu Ile Gln Val Tyr Gly Gly Pro
    530                 535                 540

Cys Ser Gln Ser Val Lys Ser Val Phe Ala Val Asn Trp Ile Thr Tyr
545                 550                 555                 560

Leu Ala Ser Lys Glu Gly Ile Val Ile Ala Leu Val Asp Gly Arg Gly
                565                 570                 575

Thr Ala Phe Gln Gly Asp Lys Phe Leu His Ala Val Tyr Arg Lys Leu
            580                 585                 590

Gly Val Tyr Glu Val Glu Asp Gln Leu Thr Ala Val Arg Lys Phe Ile
        595                 600                 605

Glu Met Gly Phe Ile Asp Glu Glu Arg Ile Ala Ile Trp Gly Trp Ser
```

```
    610                 615                 620

Tyr Gly Gly Tyr Val Ser Ser Leu Ala Leu Ala Ser Gly Thr Gly Leu
625                 630                 635                 640

Phe Lys Cys Gly Ile Ala Val Ala Pro Val Ser Ser Trp Glu Tyr Tyr
                645                 650                 655

Ala Ser Ile Tyr Ser Glu Arg Phe Met Gly Leu Pro Thr Lys Asp Asp
            660                 665                 670

Asn Leu Glu His Tyr Lys Asn Ser Thr Val Met Ala Arg Ala Glu Tyr
        675                 680                 685

Phe Arg Asn Val Asp Tyr Leu Leu Ile His Gly Thr Ala Asp Asp Asn
    690                 695                 700

Val His Phe Gln Asn Ser Ala Gln Ile Ala Lys Ala Leu Val Asn Ala
705                 710                 715                 720

Gln Val Asp Phe Gln Ala Met Trp Tyr Ser Asp Gln Asn His Gly Ile
                725                 730                 735

Ser Ser Gly Arg Ser Gln Asn His Leu Tyr Thr His Met Thr His Phe
            740                 745                 750

Leu Lys Gln Cys Phe Ser Leu Ser Asp
        755                 760


<210>  98
<211>  749
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Murine FAP ectodomain+poly-lys-tag+his6-tag

<400>  98

Arg Pro Ser Arg Val Tyr Lys Pro Glu Gly Asn Thr Lys Arg Ala Leu
```

```
1               5                   10                  15

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

Pro Asn Trp Ile Ser Glu Gln Glu Tyr Leu His Gln Ser Glu Asp Asp
        35                  40                  45

Asn Ile Val Phe Tyr Asn Ile Glu Thr Arg Glu Ser Tyr Ile Ile Leu
    50                  55                  60

Ser Asn Ser Thr Met Lys Ser Val Asn Ala Thr Asp Tyr Gly Leu Ser
65                  70                  75                  80

Pro Asp Arg Gln Phe Val Tyr Leu Glu Ser Asp Tyr Ser Lys Leu Trp
                85                  90                  95

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

Glu Phe Val Arg Gly Tyr Glu Leu Pro Arg Pro Ile Gln Tyr Leu Cys
        115                 120                 125

Trp Ser Pro Val Gly Ser Lys Leu Ala Tyr Val Tyr Gln Asn Asn Ile
    130                 135                 140

Tyr Leu Lys Gln Arg Pro Gly Asp Pro Pro Phe Gln Ile Thr Tyr Thr
145                 150                 155                 160

Gly Arg Glu Asn Arg Ile Phe Asn Gly Ile Pro Asp Trp Val Tyr Glu
                165                 170                 175

Glu Glu Met Leu Ala Thr Lys Tyr Ala Leu Trp Trp Ser Pro Asp Gly
            180                 185                 190

Lys Phe Leu Ala Tyr Val Glu Phe Asn Asp Ser Asp Ile Pro Ile Ile
        195                 200                 205
```

```
Ala Tyr Ser Tyr Tyr Gly Asp Gly Gln Tyr Pro Arg Thr Ile Asn Ile
    210                 215                 220

Pro Tyr Pro Lys Ala Gly Ala Lys Asn Pro Val Val Arg Val Phe Ile
225                 230                 235                 240

Val Asp Thr Thr Tyr Pro His His Val Gly Pro Met Glu Val Pro Val
                245                 250                 255

Pro Glu Met Ile Ala Ser Ser Asp Tyr Tyr Phe Ser Trp Leu Thr Trp
            260                 265                 270

Val Ser Ser Glu Arg Val Cys Leu Gln Trp Leu Lys Arg Val Gln Asn
        275                 280                 285

Val Ser Val Leu Ser Ile Cys Asp Phe Arg Glu Asp Trp His Ala Trp
    290                 295                 300

Glu Cys Pro Lys Asn Gln Glu His Val Glu Glu Ser Arg Thr Gly Trp
305                 310                 315                 320

Ala Gly Gly Phe Phe Val Ser Thr Pro Ala Phe Ser Gln Asp Ala Thr
                325                 330                 335

Ser Tyr Tyr Lys Ile Phe Ser Asp Lys Asp Gly Tyr Lys His Ile His
            340                 345                 350

Tyr Ile Lys Asp Thr Val Glu Asn Ala Ile Gln Ile Thr Ser Gly Lys
        355                 360                 365

Trp Glu Ala Ile Tyr Ile Phe Arg Val Thr Gln Asp Ser Leu Phe Tyr
    370                 375                 380

Ser Ser Asn Glu Phe Glu Gly Tyr Pro Gly Arg Arg Asn Ile Tyr Arg
385                 390                 395                 400

Ile Ser Ile Gly Asn Ser Pro Pro Ser Lys Lys Cys Val Thr Cys His
```

```
                405                 410                 415

Leu Arg Lys Glu Arg Cys Gln Tyr Tyr Thr Ala Ser Phe Ser Tyr Lys
            420                 425                 430

Ala Lys Tyr Tyr Ala Leu Val Cys Tyr Gly Pro Gly Leu Pro Ile Ser
        435                 440                 445

Thr Leu His Asp Gly Arg Thr Asp Gln Glu Ile Gln Val Leu Glu Glu
    450                 455                 460

Asn Lys Glu Leu Glu Asn Ser Leu Arg Asn Ile Gln Leu Pro Lys Val
465                 470                 475                 480

Glu Ile Lys Lys Leu Lys Asp Gly Gly Leu Thr Phe Trp Tyr Lys Met
                485                 490                 495

Ile Leu Pro Pro Gln Phe Asp Arg Ser Lys Lys Tyr Pro Leu Leu Ile
            500                 505                 510

Gln Val Tyr Gly Gly Pro Cys Ser Gln Ser Val Lys Ser Val Phe Ala
        515                 520                 525

Val Asn Trp Ile Thr Tyr Leu Ala Ser Lys Glu Gly Ile Val Ile Ala
    530                 535                 540

Leu Val Asp Gly Arg Gly Thr Ala Phe Gln Gly Asp Lys Phe Leu His
545                 550                 555                 560

Ala Val Tyr Arg Lys Leu Gly Val Tyr Glu Val Glu Asp Gln Leu Thr
                565                 570                 575

Ala Val Arg Lys Phe Ile Glu Met Gly Phe Ile Asp Glu Glu Arg Ile
            580                 585                 590

Ala Ile Trp Gly Trp Ser Tyr Gly Gly Tyr Val Ser Ser Leu Ala Leu
        595                 600                 605
```

```
Ala Ser Gly Thr Gly Leu Phe Lys Cys Gly Ile Ala Val Ala Pro Val
    610                 615                 620

Ser Ser Trp Glu Tyr Tyr Ala Ser Ile Tyr Ser Glu Arg Phe Met Gly
625                 630                 635                 640

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

Met Ala Arg Ala Glu Tyr Phe Arg Asn Val Asp Tyr Leu Leu Ile His
            660                 665                 670

Gly Thr Ala Asp Asp Asn Val His Phe Gln Asn Ser Ala Gln Ile Ala
        675                 680                 685

Lys Ala Leu Val Asn Ala Gln Val Asp Phe Gln Ala Met Trp Tyr Ser
    690                 695                 700

Asp Gln Asn His Gly Ile Leu Ser Gly Arg Ser Gln Asn His Leu Tyr
705                 710                 715                 720

Thr His Met Thr His Phe Leu Lys Gln Cys Phe Ser Leu Ser Asp Gly
                725                 730                 735

Lys Lys Lys Lys Lys Lys Gly His His His His His His
            740                 745
```

<210> 99
<211> 748
<212> PRT
<213> Artificial Sequence

<220>
<223> Cynomolgus FAP ectodomain+poly-lys-tag+his6-tag

<400> 99

```
Arg Pro Pro Arg Val His Asn Ser Glu Glu Asn Thr Met Arg Ala Leu
1               5                   10                  15
```

```
Thr Leu Lys Asp Ile Leu Asn Gly Thr Phe Ser Tyr Lys Thr Phe Phe
            20                  25                  30

Pro Asn Trp Ile Ser Gly Gln Glu Tyr Leu His Gln Ser Ala Asp Asn
        35                  40                  45

Asn Ile Val Leu Tyr Asn Ile Glu Thr Gly Gln Ser Tyr Thr Ile Leu
    50                  55                  60

Ser Asn Arg Thr Met Lys Ser Val Asn Ala Ser Asn Tyr Gly Leu Ser
65                  70                  75                  80

Pro Asp Arg Gln Phe Val Tyr Leu Glu Ser Asp Tyr Ser Lys Leu Trp
                85                  90                  95

Arg Tyr Ser Tyr Thr Ala Thr Tyr Tyr Ile Tyr Asp Leu Ser Asn Gly
            100                 105                 110

Glu Phe Val Arg Gly Asn Glu Leu Pro Arg Pro Ile Gln Tyr Leu Cys
        115                 120                 125

Trp Ser Pro Val Gly Ser Lys Leu Ala Tyr Val Tyr Gln Asn Asn Ile
    130                 135                 140

Tyr Leu Lys Gln Arg Pro Gly Asp Pro Pro Phe Gln Ile Thr Phe Asn
145                 150                 155                 160

Gly Arg Glu Asn Lys Ile Phe Asn Gly Ile Pro Asp Trp Val Tyr Glu
                165                 170                 175

Glu Glu Met Leu Ala Thr Lys Tyr Ala Leu Trp Trp Ser Pro Asn Gly
            180                 185                 190

Lys Phe Leu Ala Tyr Ala Glu Phe Asn Asp Thr Asp Ile Pro Val Ile
        195                 200                 205

Ala Tyr Ser Tyr Tyr Gly Asp Glu Gln Tyr Pro Arg Thr Ile Asn Ile
```

```
    210                 215                 220

Pro Tyr Pro Lys Ala Gly Ala Lys Asn Pro Phe Val Arg Ile Phe Ile
225                 230                 235                 240

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

Pro Ala Met Ile Ala Ser Ser Asp Tyr Tyr Phe Ser Trp Leu Thr Trp
            260                 265                 270

Val Thr Asp Glu Arg Val Cys Leu Gln Trp Leu Lys Arg Val Gln Asn
        275                 280                 285

Val Ser Val Leu Ser Ile Cys Asp Phe Arg Glu Asp Trp Gln Thr Trp
    290                 295                 300

Asp Cys Pro Lys Thr Gln Glu His Ile Glu Glu Ser Arg Thr Gly Trp
305                 310                 315                 320

Ala Gly Gly Phe Phe Val Ser Thr Pro Val Phe Ser Tyr Asp Ala Ile
                325                 330                 335

Ser Tyr Tyr Lys Ile Phe Ser Asp Lys Asp Gly Tyr Lys His Ile His
            340                 345                 350

Tyr Ile Lys Asp Thr Val Glu Asn Ala Ile Gln Ile Thr Ser Gly Lys
        355                 360                 365

Trp Glu Ala Ile Asn Ile Phe Arg Val Thr Gln Asp Ser Leu Phe Tyr
    370                 375                 380

Ser Ser Asn Glu Phe Glu Asp Tyr Pro Gly Arg Arg Asn Ile Tyr Arg
385                 390                 395                 400

Ile Ser Ile Gly Ser Tyr Pro Pro Ser Lys Lys Cys Val Thr Cys His
                405                 410                 415
```

```
Leu Arg Lys Glu Arg Cys Gln Tyr Tyr Thr Ala Ser Phe Ser Asp Tyr
            420                 425                 430

Ala Lys Tyr Tyr Ala Leu Val Cys Tyr Gly Pro Gly Ile Pro Ile Ser
        435                 440                 445

Thr Leu His Asp Gly Arg Thr Asp Gln Glu Ile Lys Ile Leu Glu Glu
    450                 455                 460

Asn Lys Glu Leu Glu Asn Ala Leu Lys Asn Ile Gln Leu Pro Lys Glu
465                 470                 475                 480

Glu Ile Lys Lys Leu Glu Val Asp Glu Ile Thr Leu Trp Tyr Lys Met
                485                 490                 495

Ile Leu Pro Pro Gln Phe Asp Arg Ser Lys Lys Tyr Pro Leu Leu Ile
            500                 505                 510

Gln Val Tyr Gly Gly Pro Cys Ser Gln Ser Val Arg Ser Val Phe Ala
        515                 520                 525

Val Asn Trp Ile Ser Tyr Leu Ala Ser Lys Glu Gly Met Val Ile Ala
    530                 535                 540

Leu Val Asp Gly Arg Gly Thr Ala Phe Gln Gly Asp Lys Leu Leu Tyr
545                 550                 555                 560

Ala Val Tyr Arg Lys Leu Gly Val Tyr Glu Val Glu Asp Gln Ile Thr
                565                 570                 575

Ala Val Arg Lys Phe Ile Glu Met Gly Phe Ile Asp Glu Lys Arg Ile
            580                 585                 590

Ala Ile Trp Gly Trp Ser Tyr Gly Gly Tyr Val Ser Ser Leu Ala Leu
        595                 600                 605

Ala Ser Gly Thr Gly Leu Phe Lys Cys Gly Ile Ala Val Ala Pro Val
```

610 615 620

Ser Ser Trp Glu Tyr Tyr Ala Ser Val Tyr Thr Glu Arg Phe Met Gly
625 630 635 640

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

Met Ala Arg Ala Glu Tyr Phe Arg Asn Val Asp Tyr Leu Leu Ile His
660 665 670

Gly Thr Ala Asp Asp Asn Val His Phe Gln Asn Ser Ala Gln Ile Ala
675 680 685

Lys Ala Leu Val Asn Ala Gln Val Asp Phe Gln Ala Met Trp Tyr Ser
690 695 700

Asp Gln Asn His Gly Leu Ser Gly Leu Ser Thr Asn His Leu Tyr Thr
705 710 715 720

His Met Thr His Phe Leu Lys Gln Cys Phe Ser Leu Ser Asp Gly Lys
725 730 735

Lys Lys Lys Lys Lys Gly His His His His His His
740 745

<210> 100
<211> 702
<212> PRT
<213> Homo sapiens

<400> 100

Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile Pro Trp Gln
1 5 10 15

Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
20 25 30

```
Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
        35                  40                  45

Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
    50                  55                  60

Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
65                  70                  75                  80

Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
                85                  90                  95

Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
            100                 105                 110

Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
        115                 120                 125

Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
    130                 135                 140

Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
145                 150                 155                 160

Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
                165                 170                 175

Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
            180                 185                 190

Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
        195                 200                 205

Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
    210                 215                 220

Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
225                 230                 235                 240
```

```
Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
                245                 250                 255

Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
            260                 265                 270

Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
        275                 280                 285

Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser
    290                 295                 300

Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala
305                 310                 315                 320

Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu
                325                 330                 335

Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr
            340                 345                 350

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

Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr
    370                 375                 380

Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Lys Leu Ser
385                 390                 395                 400

Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp
                405                 410                 415

Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn
            420                 425                 430
```

```
Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser
        435                 440                 445

Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
    450                 455                 460

Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn
465                 470                 475                 480

Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val
                485                 490                 495

Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro
            500                 505                 510

Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln
        515                 520                 525

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

Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn
545                 550                 555                 560

Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser
                565                 570                 575

Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly
            580                 585                 590

Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly
        595                 600                 605

Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln
    610                 615                 620

Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
625                 630                 635                 640
```

```
Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
                645                 650                 655


Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile
            660                 665                 670


Thr Val Ser Ala Ser Gly Thr Ser Pro Gly Leu Ser Ala Gly Ala Thr
        675                 680                 685


Val Gly Ile Met Ile Gly Val Leu Val Gly Val Ala Leu Ile
    690                 695                 700
```

<210> 101
<211> 2322
<212> PRT
<213> Homo sapiens

<400> 101

```
Met Gln Ser Gly Pro Arg Pro Pro Leu Pro Ala Pro Gly Leu Ala Leu
1               5                   10                  15


Ala Leu Thr Leu Thr Met Leu Ala Arg Leu Ala Ser Ala Ala Ser Phe
            20                  25                  30


Phe Gly Glu Asn His Leu Glu Val Pro Val Ala Thr Ala Leu Thr Asp
        35                  40                  45


Ile Asp Leu Gln Leu Gln Phe Ser Thr Ser Gln Pro Glu Ala Leu Leu
    50                  55                  60


Leu Leu Ala Ala Gly Pro Ala Asp His Leu Leu Leu Gln Leu Tyr Ser
65                  70                  75                  80


Gly Arg Leu Gln Val Arg Leu Val Leu Gly Gln Glu Glu Leu Arg Leu
                85                  90                  95


Gln Thr Pro Ala Glu Thr Leu Leu Ser Asp Ser Ile Pro His Thr Val
```

```
            100                 105                 110

Val Leu Thr Val Val Glu Gly Trp Ala Thr Leu Ser Val Asp Gly Phe
        115                 120                 125

Leu Asn Ala Ser Ser Ala Val Pro Gly Ala Pro Leu Glu Val Pro Tyr
    130                 135                 140

Gly Leu Phe Val Gly Gly Thr Gly Thr Leu Gly Leu Pro Tyr Leu Arg
145                 150                 155                 160

Gly Thr Ser Arg Pro Leu Arg Gly Cys Leu His Ala Ala Thr Leu Asn
                165                 170                 175

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

Ala Glu Glu Phe Ser Ala Ser Asp Asp Val Ala Leu Gly Phe Ser Gly
        195                 200                 205

Pro His Ser Leu Ala Ala Phe Pro Ala Trp Gly Thr Gln Asp Glu Gly
    210                 215                 220

Thr Leu Glu Phe Thr Leu Thr Thr Gln Ser Arg Gln Ala Pro Leu Ala
225                 230                 235                 240

Phe Gln Ala Gly Gly Arg Arg Gly Asp Phe Ile Tyr Val Asp Ile Phe
                245                 250                 255

Glu Gly His Leu Arg Ala Val Val Glu Lys Gly Gln Gly Thr Val Leu
            260                 265                 270

Leu His Asn Ser Val Pro Val Ala Asp Gly Gln Pro His Glu Val Ser
        275                 280                 285

Val His Ile Asn Ala His Arg Leu Glu Ile Ser Val Asp Gln Tyr Pro
    290                 295                 300
```

```
Thr His Thr Ser Asn Arg Gly Val Leu Ser Tyr Leu Glu Pro Arg Gly
305                 310                 315                 320

Ser Leu Leu Leu Gly Gly Leu Asp Ala Glu Ala Ser Arg His Leu Gln
                325                 330                 335

Glu His Arg Leu Gly Leu Thr Pro Glu Ala Thr Asn Ala Ser Leu Leu
            340                 345                 350

Gly Cys Met Glu Asp Leu Ser Val Asn Gly Gln Arg Arg Gly Leu Arg
        355                 360                 365

Glu Ala Leu Leu Thr Arg Asn Met Ala Ala Gly Cys Arg Leu Glu Glu
    370                 375                 380

Glu Glu Tyr Glu Asp Asp Ala Tyr Gly His Tyr Glu Ala Phe Ser Thr
385                 390                 395                 400

Leu Ala Pro Glu Ala Trp Pro Ala Met Glu Leu Pro Glu Pro Cys Val
                405                 410                 415

Pro Glu Pro Gly Leu Pro Pro Val Phe Ala Asn Phe Thr Gln Leu Leu
            420                 425                 430

Thr Ile Ser Pro Leu Val Val Ala Glu Gly Gly Thr Ala Trp Leu Glu
        435                 440                 445

Trp Arg His Val Gln Pro Thr Leu Asp Leu Met Glu Ala Glu Leu Arg
    450                 455                 460

Lys Ser Gln Val Leu Phe Ser Val Thr Arg Gly Ala Arg His Gly Glu
465                 470                 475                 480

Leu Glu Leu Asp Ile Pro Gly Ala Gln Ala Arg Lys Met Phe Thr Leu
                485                 490                 495

Leu Asp Val Val Asn Arg Lys Ala Arg Phe Ile His Asp Gly Ser Glu
```

```
            500                 505                 510

Asp Thr Ser Asp Gln Leu Val Leu Glu Val Ser Val Thr Ala Arg Val
        515                 520                 525

Pro Met Pro Ser Cys Leu Arg Arg Gly Gln Thr Tyr Leu Leu Pro Ile
    530                 535                 540

Gln Val Asn Pro Val Asn Asp Pro Pro His Ile Ile Phe Pro His Gly
545                 550                 555                 560

Ser Leu Met Val Ile Leu Glu His Thr Gln Lys Pro Leu Gly Pro Glu
                565                 570                 575

Val Phe Gln Ala Tyr Asp Pro Asp Ser Ala Cys Glu Gly Leu Thr Phe
            580                 585                 590

Gln Val Leu Gly Thr Ser Ser Gly Leu Pro Val Glu Arg Arg Asp Gln
        595                 600                 605

Pro Gly Glu Pro Ala Thr Glu Phe Ser Cys Arg Glu Leu Glu Ala Gly
    610                 615                 620

Ser Leu Val Tyr Val His Arg Gly Gly Pro Ala Gln Asp Leu Thr Phe
625                 630                 635                 640

Arg Val Ser Asp Gly Leu Gln Ala Ser Pro Pro Ala Thr Leu Lys Val
                645                 650                 655

Val Ala Ile Arg Pro Ala Ile Gln Ile His Arg Ser Thr Gly Leu Arg
            660                 665                 670

Leu Ala Gln Gly Ser Ala Met Pro Ile Leu Pro Ala Asn Leu Ser Val
        675                 680                 685

Glu Thr Asn Ala Val Gly Gln Asp Val Ser Val Leu Phe Arg Val Thr
    690                 695                 700
```

```
Gly Ala Leu Gln Phe Gly Glu Leu Gln Lys Gln Gly Ala Gly Gly Val
705                 710                 715                 720


Glu Gly Ala Glu Trp Trp Ala Thr Gln Ala Phe His Gln Arg Asp Val
                725                 730                 735


Glu Gln Gly Arg Val Arg Tyr Leu Ser Thr Asp Pro Gln His His Ala
            740                 745                 750


Tyr Asp Thr Val Glu Asn Leu Ala Leu Glu Val Gln Val Gly Gln Glu
        755                 760                 765


Ile Leu Ser Asn Leu Ser Phe Pro Val Thr Ile Gln Arg Ala Thr Val
    770                 775                 780


Trp Met Leu Arg Leu Glu Pro Leu His Thr Gln Asn Thr Gln Gln Glu
785                 790                 795                 800


Thr Leu Thr Thr Ala His Leu Glu Ala Thr Leu Glu Glu Ala Gly Pro
                805                 810                 815


Ser Pro Pro Thr Phe His Tyr Glu Val Val Gln Ala Pro Arg Lys Gly
            820                 825                 830


Asn Leu Gln Leu Gln Gly Thr Arg Leu Ser Asp Gly Gln Gly Phe Thr
        835                 840                 845


Gln Asp Asp Ile Gln Ala Gly Arg Val Thr Tyr Gly Ala Thr Ala Arg
    850                 855                 860


Ala Ser Glu Ala Val Glu Asp Thr Phe Arg Phe Arg Val Thr Ala Pro
865                 870                 875                 880


Pro Tyr Phe Ser Pro Leu Tyr Thr Phe Pro Ile His Ile Gly Gly Asp
                885                 890                 895


Pro Asp Ala Pro Val Leu Thr Asn Val Leu Leu Val Val Pro Glu Gly
```

```
            900                 905                 910

Gly Glu Gly Val Leu Ser Ala Asp His Leu Phe Val Lys Ser Leu Asn
        915                 920                 925

Ser Ala Ser Tyr Leu Tyr Glu Val Met Glu Arg Pro Arg His Gly Arg
    930                 935                 940

Leu Ala Trp Arg Gly Thr Gln Asp Lys Thr Thr Met Val Thr Ser Phe
945                 950                 955                 960

Thr Asn Glu Asp Leu Leu Arg Gly Arg Leu Val Tyr Gln His Asp Asp
                965                 970                 975

Ser Glu Thr Thr Glu Asp Asp Ile Pro Phe Val Ala Thr Arg Gln Gly
            980                 985                 990

Glu Ser Ser Gly Asp Met Ala Trp  Glu Glu Val Arg Gly  Val Phe Arg
        995                 1000                1005

Val Ala  Ile Gln Pro Val Asn  Asp His Ala Pro Val  Gln Thr Ile
    1010                1015                1020

Ser Arg  Ile Phe His Val Ala  Arg Gly Gly Arg Arg  Leu Leu Thr
    1025                1030                1035

Thr Asp  Asp Val Ala Phe Ser  Asp Ala Asp Ser Gly  Phe Ala Asp
    1040                1045                1050

Ala Gln  Leu Val Leu Thr Arg  Lys Asp Leu Leu Phe  Gly Ser Ile
    1055                1060                1065

Val Ala  Val Asp Glu Pro Thr  Arg Pro Ile Tyr Arg  Phe Thr Gln
    1070                1075                1080

Glu Asp  Leu Arg Lys Arg Arg  Val Leu Phe Val His  Ser Gly Ala
    1085                1090                1095
```

```
Asp Arg  Gly Trp Ile Gln Leu  Gln Val Ser Asp Gly  Gln His Gln
    1100                1105                1110

Ala Thr  Ala Leu Leu Glu Val  Gln Ala Ser Glu Pro  Tyr Leu Arg
    1115                1120                1125

Val Ala  Asn Gly Ser Ser Leu  Val Val Pro Gln Gly  Gly Gln Gly
    1130                1135                1140

Thr Ile  Asp Thr Ala Val Leu  His Leu Asp Thr Asn  Leu Asp Ile
    1145                1150                1155

Arg Ser  Gly Asp Glu Val His  Tyr His Val Thr Ala  Gly Pro Arg
    1160                1165                1170

Trp Gly  Gln Leu Val Arg Ala  Gly Gln Pro Ala Thr  Ala Phe Ser
    1175                1180                1185

Gln Gln  Asp Leu Leu Asp Gly  Ala Val Leu Tyr Ser  His Asn Gly
    1190                1195                1200

Ser Leu  Ser Pro Arg Asp Thr  Met Ala Phe Ser Val  Glu Ala Gly
    1205                1210                1215

Pro Val  His Thr Asp Ala Thr  Leu Gln Val Thr Ile  Ala Leu Glu
    1220                1225                1230

Gly Pro  Leu Ala Pro Leu Lys  Leu Val Arg His Lys  Lys Ile Tyr
    1235                1240                1245

Val Phe  Gln Gly Glu Ala Ala  Glu Ile Arg Arg Asp  Gln Leu Glu
    1250                1255                1260

Ala Ala  Gln Glu Ala Val Pro  Pro Ala Asp Ile Val  Phe Ser Val
    1265                1270                1275

Lys Ser  Pro Pro Ser Ala Gly  Tyr Leu Val Met Val  Ser Arg Gly
```

```
    1280                1285                1290

Ala Leu  Ala Asp Glu Pro Pro  Ser Leu Asp Pro Val  Gln Ser Phe
    1295                1300                1305

Ser Gln  Glu Ala Val Asp Thr  Gly Arg Val Leu Tyr  Leu His Ser
    1310                1315                1320

Arg Pro  Glu Ala Trp Ser Asp  Ala Phe Ser Leu Asp  Val Ala Ser
    1325                1330                1335

Gly Leu  Gly Ala Pro Leu Glu  Gly Val Leu Val Glu  Leu Glu Val
    1340                1345                1350

Leu Pro  Ala Ala Ile Pro Leu  Glu Ala Gln Asn Phe  Ser Val Pro
    1355                1360                1365

Glu Gly  Gly Ser Leu Thr Leu  Ala Pro Pro Leu Leu  Arg Val Ser
    1370                1375                1380

Gly Pro  Tyr Phe Pro Thr Leu  Leu Gly Leu Ser Leu  Gln Val Leu
    1385                1390                1395

Glu Pro  Pro Gln His Gly Ala  Leu Gln Lys Glu Asp  Gly Pro Gln
    1400                1405                1410

Ala Arg  Thr Leu Ser Ala Phe  Ser Trp Arg Met Val  Glu Glu Gln
    1415                1420                1425

Leu Ile  Arg Tyr Val His Asp  Gly Ser Glu Thr Leu  Thr Asp Ser
    1430                1435                1440

Phe Val  Leu Met Ala Asn Ala  Ser Glu Met Asp Arg  Gln Ser His
    1445                1450                1455

Pro Val  Ala Phe Thr Val Thr  Val Leu Pro Val Asn  Asp Gln Pro
    1460                1465                1470
```

```
Pro Ile  Leu Thr Thr Asn Thr  Gly Leu Gln Met Trp  Glu Gly Ala
    1475                1480                1485

Thr Ala  Pro Ile Pro Ala Glu  Ala Leu Arg Ser Thr  Asp Gly Asp
    1490                1495                1500

Ser Gly  Ser Glu Asp Leu Val  Tyr Thr Ile Glu Gln  Pro Ser Asn
    1505                1510                1515

Gly Arg  Val Val Leu Arg Gly  Ala Pro Gly Thr Glu  Val Arg Ser
    1520                1525                1530

Phe Thr  Gln Ala Gln Leu Asp  Gly Gly Leu Val Leu  Phe Ser His
    1535                1540                1545

Arg Gly  Thr Leu Asp Gly Gly  Phe Arg Phe Arg Leu  Ser Asp Gly
    1550                1555                1560

Glu His  Thr Ser Pro Gly His  Phe Phe Arg Val Thr  Ala Gln Lys
    1565                1570                1575

Gln Val  Leu Leu Ser Leu Lys  Gly Ser Gln Thr Leu  Thr Val Cys
    1580                1585                1590

Pro Gly  Ser Val Gln Pro Leu  Ser Ser Gln Thr Leu  Arg Ala Ser
    1595                1600                1605

Ser Ser  Ala Gly Thr Asp Pro  Gln Leu Leu Leu Tyr  Arg Val Val
    1610                1615                1620

Arg Gly  Pro Gln Leu Gly Arg  Leu Phe His Ala Gln  Gln Asp Ser
    1625                1630                1635

Thr Gly  Glu Ala Leu Val Asn  Phe Thr Gln Ala Glu  Val Tyr Ala
    1640                1645                1650

Gly Asn  Ile Leu Tyr Glu His  Glu Met Pro Pro Glu  Pro Phe Trp
```

```
    1655                1660                1665

Glu Ala  His Asp Thr Leu Glu  Leu Gln Leu Ser Ser  Pro Pro Ala
    1670                1675                1680

Arg Asp  Val Ala Ala Thr Leu  Ala Val Ala Val Ser  Phe Glu Ala
    1685                1690                1695

Ala Cys  Pro Gln Arg Pro Ser  His Leu Trp Lys Asn  Lys Gly Leu
    1700                1705                1710

Trp Val  Pro Glu Gly Gln Arg  Ala Arg Ile Thr Val  Ala Ala Leu
    1715                1720                1725

Asp Ala  Ser Asn Leu Leu Ala  Ser Val Pro Ser Pro  Gln Arg Ser
    1730                1735                1740

Glu His  Asp Val Leu Phe Gln  Val Thr Gln Phe Pro  Ser Arg Gly
    1745                1750                1755

Gln Leu  Leu Val Ser Glu Glu  Pro Leu His Ala Gly  Gln Pro His
    1760                1765                1770

Phe Leu  Gln Ser Gln Leu Ala  Ala Gly Gln Leu Val  Tyr Ala His
    1775                1780                1785

Gly Gly  Gly Gly Thr Gln Gln  Asp Gly Phe His Phe  Arg Ala His
    1790                1795                1800

Leu Gln  Gly Pro Ala Gly Ala  Ser Val Ala Gly Pro  Gln Thr Ser
    1805                1810                1815

Glu Ala  Phe Ala Ile Thr Val  Arg Asp Val Asn Glu  Arg Pro Pro
    1820                1825                1830

Gln Pro  Gln Ala Ser Val Pro  Leu Arg Leu Thr Arg  Gly Ser Arg
    1835                1840                1845
```

```
Ala Pro  Ile Ser Arg Ala Gln  Leu Ser Val Val Asp  Pro Asp Ser
    1850                1855                1860

Ala Pro  Gly Glu Ile Glu Tyr  Glu Val Gln Arg Ala  Pro His Asn
    1865                1870                1875

Gly Phe  Leu Ser Leu Val Gly  Gly Gly Leu Gly Pro  Val Thr Arg
    1880                1885                1890

Phe Thr  Gln Ala Asp Val Asp  Ser Gly Arg Leu Ala  Phe Val Ala
    1895                1900                1905

Asn Gly  Ser Ser Val Ala Gly  Ile Phe Gln Leu Ser  Met Ser Asp
    1910                1915                1920

Gly Ala  Ser Pro Pro Leu Pro  Met Ser Leu Ala Val  Asp Ile Leu
    1925                1930                1935

Pro Ser  Ala Ile Glu Val Gln  Leu Arg Ala Pro Leu  Glu Val Pro
    1940                1945                1950

Gln Ala  Leu Gly Arg Ser Ser  Leu Ser Gln Gln Gln  Leu Arg Val
    1955                1960                1965

Val Ser  Asp Arg Glu Glu Pro  Glu Ala Ala Tyr Arg  Leu Ile Gln
    1970                1975                1980

Gly Pro  Gln Tyr Gly His Leu  Leu Val Gly Gly Arg  Pro Thr Ser
    1985                1990                1995

Ala Phe  Ser Gln Phe Gln Ile  Asp Gln Gly Glu Val  Val Phe Ala
    2000                2005                2010

Phe Thr  Asn Phe Ser Ser Ser  His Asp His Phe Arg  Val Leu Ala
    2015                2020                2025

Leu Ala  Arg Gly Val Asn Ala  Ser Ala Val Val Asn  Val Thr Val
```

```
    2030                2035                2040

Arg Ala  Leu Leu His Val Trp  Ala Gly Gly Pro Trp  Pro Gln Gly
    2045                2050                2055

Ala Thr  Leu Arg Leu Asp Pro  Thr Val Leu Asp Ala  Gly Glu Leu
    2060                2065                2070

Ala Asn  Arg Thr Gly Ser Val  Pro Arg Phe Arg Leu  Leu Glu Gly
    2075                2080                2085

Pro Arg  His Gly Arg Val Val  Arg Val Pro Arg Ala  Arg Thr Glu
    2090                2095                2100

Pro Gly  Gly Ser Gln Leu Val  Glu Gln Phe Thr Gln  Gln Asp Leu
    2105                2110                2115

Glu Asp  Gly Arg Leu Gly Leu  Glu Val Gly Arg Pro  Glu Gly Arg
    2120                2125                2130

Ala Pro  Gly Pro Ala Gly Asp  Ser Leu Thr Leu Glu  Leu Trp Ala
    2135                2140                2145

Gln Gly  Val Pro Pro Ala Val  Ala Ser Leu Asp Phe  Ala Thr Glu
    2150                2155                2160

Pro Tyr  Asn Ala Ala Arg Pro  Tyr Ser Val Ala Leu  Leu Ser Val
    2165                2170                2175

Pro Glu  Ala Ala Arg Thr Glu  Ala Gly Lys Pro Glu  Ser Ser Thr
    2180                2185                2190

Pro Thr  Gly Glu Pro Gly Pro  Met Ala Ser Ser Pro  Glu Pro Ala
    2195                2200                2205

Val Ala  Lys Gly Gly Phe Leu  Ser Phe Leu Glu Ala  Asn Met Phe
    2210                2215                2220
```

```
Ser Val  Ile Ile Pro Met Cys  Leu Val Leu Leu Leu  Leu Ala Leu
    2225                2230                2235


Ile Leu  Pro Leu Leu Phe Tyr  Leu Arg Lys Arg Asn  Lys Thr Gly
    2240                2245                2250


Lys His  Asp Val Gln Val Leu  Thr Ala Lys Pro Arg  Asn Gly Leu
    2255                2260                2265


Ala Gly  Asp Thr Glu Thr Phe  Arg Lys Val Glu Pro  Gly Gln Ala
    2270                2275                2280


Ile Pro  Leu Thr Ala Val Pro  Gly Gln Gly Pro Pro  Pro Gly Gly
    2285                2290                2295


Gln Pro  Asp Pro Glu Leu Leu  Gln Phe Cys Arg Thr  Pro Asn Pro
    2300                2305                2310


Ala Leu  Lys Asn Gly Gln Tyr  Trp Val
    2315                2320
```

<210> 102
<211> 1210
<212> PRT
<213> Homo sapiens

<400> 102

```
Met Arg Pro Ser Gly Thr Ala Gly Ala Ala Leu Leu Ala Leu Leu Ala
1               5                  10                  15


Ala Leu Cys Pro Ala Ser Arg Ala Leu Glu Glu Lys Lys Val Cys Gln
            20                  25                  30


Gly Thr Ser Asn Lys Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe
        35                  40                  45


Leu Ser Leu Gln Arg Met Phe Asn Asn Cys Glu Val Val Leu Gly Asn
    50                  55                  60
```

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

Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val
                85                  90                  95

Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Met Tyr
            100                 105                 110

Tyr Glu Asn Ser Tyr Ala Leu Ala Val Leu Ser Asn Tyr Asp Ala Asn
        115                 120                 125

Lys Thr Gly Leu Lys Glu Leu Pro Met Arg Asn Leu Gln Glu Ile Leu
    130                 135                 140

His Gly Ala Val Arg Phe Ser Asn Asn Pro Ala Leu Cys Asn Val Glu
145                 150                 155                 160

Ser Ile Gln Trp Arg Asp Ile Val Ser Ser Asp Phe Leu Ser Asn Met
                165                 170                 175

Ser Met Asp Phe Gln Asn His Leu Gly Ser Cys Gln Lys Cys Asp Pro
            180                 185                 190

Ser Cys Pro Asn Gly Ser Cys Trp Gly Ala Gly Glu Glu Asn Cys Gln
        195                 200                 205

Lys Leu Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser Gly Arg Cys Arg
    210                 215                 220

Gly Lys Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys
225                 230                 235                 240

Thr Gly Pro Arg Glu Ser Asp Cys Leu Val Cys Arg Lys Phe Arg Asp
                245                 250                 255
```

```
Glu Ala Thr Cys Lys Asp Thr Cys Pro Pro Leu Met Leu Tyr Asn Pro
            260                 265                 270

Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys Tyr Ser Phe Gly
        275                 280                 285

Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val Val Thr Asp His
    290                 295                 300

Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu
305                 310                 315                 320

Asp Gly Val Arg Lys Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val
                325                 330                 335

Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn
            340                 345                 350

Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp
        355                 360                 365

Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr
    370                 375                 380

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

Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp
                405                 410                 415

Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln
            420                 425                 430

His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu
        435                 440                 445

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

```
Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu
465                 470                 475                 480

Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu
                485                 490                 495

Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro
            500                 505                 510

Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn
        515                 520                 525

Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu Leu Glu Gly
    530                 535                 540

Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro
545                 550                 555                 560

Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro
                565                 570                 575

Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val
            580                 585                 590

Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp
        595                 600                 605

Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys
    610                 615                 620

Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro Thr Asn Gly
625                 630                 635                 640

Pro Lys Ile Pro Ser Ile Ala Thr Gly Met Val Gly Ala Leu Leu Leu
                645                 650                 655
```

```
Leu Leu Val Val Ala Leu Gly Ile Gly Leu Phe Met Arg Arg Arg His
            660                 665                 670

Ile Val Arg Lys Arg Thr Leu Arg Arg Leu Leu Gln Glu Arg Glu Leu
        675                 680                 685

Val Glu Pro Leu Thr Pro Ser Gly Glu Ala Pro Asn Gln Ala Leu Leu
    690                 695                 700

Arg Ile Leu Lys Glu Thr Glu Phe Lys Lys Ile Lys Val Leu Gly Ser
705                 710                 715                 720

Gly Ala Phe Gly Thr Val Tyr Lys Gly Leu Trp Ile Pro Glu Gly Glu
                725                 730                 735

Lys Val Lys Ile Pro Val Ala Ile Lys Glu Leu Arg Glu Ala Thr Ser
            740                 745                 750

Pro Lys Ala Asn Lys Glu Ile Leu Asp Glu Ala Tyr Val Met Ala Ser
        755                 760                 765

Val Asp Asn Pro His Val Cys Arg Leu Leu Gly Ile Cys Leu Thr Ser
    770                 775                 780

Thr Val Gln Leu Ile Thr Gln Leu Met Pro Phe Gly Cys Leu Leu Asp
785                 790                 795                 800

Tyr Val Arg Glu His Lys Asp Asn Ile Gly Ser Gln Tyr Leu Leu Asn
                805                 810                 815

Trp Cys Val Gln Ile Ala Lys Gly Met Asn Tyr Leu Glu Asp Arg Arg
            820                 825                 830

Leu Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Lys Thr Pro
        835                 840                 845

Gln His Val Lys Ile Thr Asp Phe Gly Leu Ala Lys Leu Leu Gly Ala
    850                 855                 860
```

```
Glu Glu Lys Glu Tyr His Ala Glu Gly Gly Lys Val Pro Ile Lys Trp
865                 870                 875                 880

Met Ala Leu Glu Ser Ile Leu His Arg Ile Tyr Thr His Gln Ser Asp
                885                 890                 895

Val Trp Ser Tyr Gly Val Thr Val Trp Glu Leu Met Thr Phe Gly Ser
            900                 905                 910

Lys Pro Tyr Asp Gly Ile Pro Ala Ser Glu Ile Ser Ser Ile Leu Glu
        915                 920                 925

Lys Gly Glu Arg Leu Pro Gln Pro Pro Ile Cys Thr Ile Asp Val Tyr
    930                 935                 940

Met Ile Met Val Lys Cys Trp Met Ile Asp Ala Asp Ser Arg Pro Lys
945                 950                 955                 960

Phe Arg Glu Leu Ile Ile Glu Phe Ser Lys Met Ala Arg Asp Pro Gln
                965                 970                 975

Arg Tyr Leu Val Ile Gln Gly Asp Glu Arg Met His Leu Pro Ser Pro
            980                 985                 990

Thr Asp Ser Asn Phe Tyr Arg Ala  Leu Met Asp Glu Glu  Asp Met Asp
        995                 1000                1005

Asp Val  Val Asp Ala Asp Glu  Tyr Leu Ile Pro Gln  Gln Gly Phe
    1010                1015                1020

Phe Ser  Ser Pro Ser Thr Ser  Arg Thr Pro Leu Leu  Ser Ser Leu
    1025                1030                1035

Ser Ala  Thr Ser Asn Asn Ser  Thr Val Ala Cys Ile  Asp Arg Asn
    1040                1045                1050
```

```
Gly Leu  Gln Ser Cys Pro Ile  Lys Glu Asp Ser Phe  Leu Gln Arg
    1055                1060                1065

Tyr Ser  Ser Asp Pro Thr Gly  Ala Leu Thr Glu Asp  Ser Ile Asp
    1070                1075                1080

Asp Thr  Phe Leu Pro Val Pro  Glu Tyr Ile Asn Gln  Ser Val Pro
    1085                1090                1095

Lys Arg  Pro Ala Gly Ser Val  Gln Asn Pro Val Tyr  His Asn Gln
    1100                1105                1110

Pro Leu  Asn Pro Ala Pro Ser  Arg Asp Pro His Tyr  Gln Asp Pro
    1115                1120                1125

His Ser  Thr Ala Val Gly Asn  Pro Glu Tyr Leu Asn  Thr Val Gln
    1130                1135                1140

Pro Thr  Cys Val Asn Ser Thr  Phe Asp Ser Pro Ala  His Trp Ala
    1145                1150                1155

Gln Lys  Gly Ser His Gln Ile  Ser Leu Asp Asn Pro  Asp Tyr Gln
    1160                1165                1170

Gln Asp  Phe Phe Pro Lys Glu  Ala Lys Pro Asn Gly  Ile Phe Lys
    1175                1180                1185

Gly Ser  Thr Ala Glu Asn Ala  Glu Tyr Leu Arg Val  Ala Pro Gln
    1190                1195                1200

Ser Ser  Glu Phe Ile Gly Ala
    1205                1210
```

<210> 103
<211> 556
<212> PRT
<213> Homo sapiens

<400> 103

```
Met Pro Pro Pro Arg Leu Leu Phe Phe Leu Leu Phe Leu Thr Pro Met
1               5                  10                  15

Glu Val Arg Pro Glu Glu Pro Leu Val Val Lys Val Glu Glu Gly Asp
            20                  25                  30

Asn Ala Val Leu Gln Cys Leu Lys Gly Thr Ser Asp Gly Pro Thr Gln
        35                  40                  45

Gln Leu Thr Trp Ser Arg Glu Ser Pro Leu Lys Pro Phe Leu Lys Leu
    50                  55                  60

Ser Leu Gly Leu Pro Gly Leu Gly Ile His Met Arg Pro Leu Ala Ile
65                  70                  75                  80

Trp Leu Phe Ile Phe Asn Val Ser Gln Gln Met Gly Gly Phe Tyr Leu
                85                  90                  95

Cys Gln Pro Gly Pro Pro Ser Glu Lys Ala Trp Gln Pro Gly Trp Thr
            100                 105                 110

Val Asn Val Glu Gly Ser Gly Glu Leu Phe Arg Trp Asn Val Ser Asp
        115                 120                 125

Leu Gly Gly Leu Gly Cys Gly Leu Lys Asn Arg Ser Ser Glu Gly Pro
    130                 135                 140

Ser Ser Pro Ser Gly Lys Leu Met Ser Pro Lys Leu Tyr Val Trp Ala
145                 150                 155                 160

Lys Asp Arg Pro Glu Ile Trp Glu Gly Glu Pro Pro Cys Leu Pro Pro
                165                 170                 175

Arg Asp Ser Leu Asn Gln Ser Leu Ser Gln Asp Leu Thr Met Ala Pro
            180                 185                 190

Gly Ser Thr Leu Trp Leu Ser Cys Gly Val Pro Pro Asp Ser Val Ser
```

```
        195                 200                 205

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

Leu Leu Ser Leu Glu Leu Lys Asp Asp Arg Pro Ala Arg Asp Met Trp
225                 230                 235                 240

Val Met Glu Thr Gly Leu Leu Leu Pro Arg Ala Thr Ala Gln Asp Ala
                245                 250                 255

Gly Lys Tyr Tyr Cys His Arg Gly Asn Leu Thr Met Ser Phe His Leu
            260                 265                 270

Glu Ile Thr Ala Arg Pro Val Leu Trp His Trp Leu Leu Arg Thr Gly
        275                 280                 285

Gly Trp Lys Val Ser Ala Val Thr Leu Ala Tyr Leu Ile Phe Cys Leu
    290                 295                 300

Cys Ser Leu Val Gly Ile Leu His Leu Gln Arg Ala Leu Val Leu Arg
305                 310                 315                 320

Arg Lys Arg Lys Arg Met Thr Asp Pro Thr Arg Arg Phe Phe Lys Val
                325                 330                 335

Thr Pro Pro Pro Gly Ser Gly Pro Gln Asn Gln Tyr Gly Asn Val Leu
            340                 345                 350

Ser Leu Pro Thr Pro Thr Ser Gly Leu Gly Arg Ala Gln Arg Trp Ala
        355                 360                 365

Ala Gly Leu Gly Gly Thr Ala Pro Ser Tyr Gly Asn Pro Ser Ser Asp
    370                 375                 380

Val Gln Ala Asp Gly Ala Leu Gly Ser Arg Ser Pro Pro Gly Val Gly
385                 390                 395                 400
```

```
Pro Glu Glu Glu Glu Gly Glu Gly Tyr Glu Glu Pro Asp Ser Glu Glu
                405                 410                 415

Asp Ser Glu Phe Tyr Glu Asn Asp Ser Asn Leu Gly Gln Asp Gln Leu
            420                 425                 430

Ser Gln Asp Gly Ser Gly Tyr Glu Asn Pro Glu Asp Glu Pro Leu Gly
        435                 440                 445

Pro Glu Asp Glu Asp Ser Phe Ser Asn Ala Glu Ser Tyr Glu Asn Glu
    450                 455                 460

Asp Glu Glu Leu Thr Gln Pro Val Ala Arg Thr Met Asp Phe Leu Ser
465                 470                 475                 480

Pro His Gly Ser Ala Trp Asp Pro Ser Arg Glu Ala Thr Ser Leu Gly
                485                 490                 495

Ser Gln Ser Tyr Glu Asp Met Arg Gly Ile Leu Tyr Ala Ala Pro Gln
            500                 505                 510

Leu Arg Ser Ile Arg Gly Gln Pro Gly Pro Asn His Glu Glu Asp Ala
        515                 520                 525

Asp Ser Tyr Glu Asn Met Asp Asn Pro Asp Gly Pro Asp Pro Ala Trp
    530                 535                 540

Gly Gly Gly Gly Arg Met Gly Thr Trp Ser Thr Arg
545                 550                 555


<210>  104
<211>  297
<212>  PRT
<213>  Homo sapiens

<400>  104

Met Thr Thr Pro Arg Asn Ser Val Asn Gly Thr Phe Pro Ala Glu Pro
1               5                   10                  15
```

```
Met Lys Gly Pro Ile Ala Met Gln Ser Gly Pro Lys Pro Leu Phe Arg
            20                  25                  30

Arg Met Ser Ser Leu Val Gly Pro Thr Gln Ser Phe Phe Met Arg Glu
        35                  40                  45

Ser Lys Thr Leu Gly Ala Val Gln Ile Met Asn Gly Leu Phe His Ile
    50                  55                  60

Ala Leu Gly Gly Leu Leu Met Ile Pro Ala Gly Ile Tyr Ala Pro Ile
65                  70                  75                  80

Cys Val Thr Val Trp Tyr Pro Leu Trp Gly Gly Ile Met Tyr Ile Ile
                85                  90                  95

Ser Gly Ser Leu Leu Ala Ala Thr Glu Lys Asn Ser Arg Lys Cys Leu
            100                 105                 110

Val Lys Gly Lys Met Ile Met Asn Ser Leu Ser Leu Phe Ala Ala Ile
        115                 120                 125

Ser Gly Met Ile Leu Ser Ile Met Asp Ile Leu Asn Ile Lys Ile Ser
    130                 135                 140

His Phe Leu Lys Met Glu Ser Leu Asn Phe Ile Arg Ala His Thr Pro
145                 150                 155                 160

Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn
                165                 170                 175

Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe Leu Gly
            180                 185                 190

Ile Leu Ser Val Met Leu Ile Phe Ala Phe Phe Gln Glu Leu Val Ile
        195                 200                 205
```

```
Ala Gly Ile Val Glu Asn Glu Trp Lys Arg Thr Cys Ser Arg Pro Lys
    210                 215                 220

Ser Asn Ile Val Leu Leu Ser Ala Glu Glu Lys Lys Glu Gln Thr Ile
225                 230                 235                 240

Glu Ile Lys Glu Glu Val Val Gly Leu Thr Glu Thr Ser Ser Gln Pro
                245                 250                 255

Lys Asn Glu Glu Asp Ile Glu Ile Ile Pro Ile Gln Glu Glu Glu Glu
            260                 265                 270

Glu Glu Thr Glu Thr Asn Phe Pro Glu Pro Pro Gln Asp Gln Glu Ser
        275                 280                 285

Ser Pro Ile Glu Asn Asp Ser Ser Pro
    290                 295
```

<210> 105
<211> 364
<212> PRT
<213> Homo sapiens

<400> 105

```
Met Pro Leu Leu Leu Leu Leu Pro Leu Leu Trp Ala Gly Ala Leu Ala
1               5                   10                  15

Met Asp Pro Asn Phe Trp Leu Gln Val Gln Glu Ser Val Thr Val Gln
            20                  25                  30

Glu Gly Leu Cys Val Leu Val Pro Cys Thr Phe Phe His Pro Ile Pro
        35                  40                  45

Tyr Tyr Asp Lys Asn Ser Pro Val His Gly Tyr Trp Phe Arg Glu Gly
    50                  55                  60

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

```
Glu Val Gln Glu Glu Thr Gln Gly Arg Phe Arg Leu Leu Gly Asp Pro
                85                  90                  95

Ser Arg Asn Asn Cys Ser Leu Ser Ile Val Asp Ala Arg Arg Arg Asp
            100                 105                 110

Asn Gly Ser Tyr Phe Phe Arg Met Glu Arg Gly Ser Thr Lys Tyr Ser
        115                 120                 125

Tyr Lys Ser Pro Gln Leu Ser Val His Val Thr Asp Leu Thr His Arg
    130                 135                 140

Pro Lys Ile Leu Ile Pro Gly Thr Leu Glu Pro Gly His Ser Lys Asn
145                 150                 155                 160

Leu Thr Cys Ser Val Ser Trp Ala Cys Glu Gln Gly Thr Pro Pro Ile
                165                 170                 175

Phe Ser Trp Leu Ser Ala Ala Pro Thr Ser Leu Gly Pro Arg Thr Thr
            180                 185                 190

His Ser Ser Val Leu Ile Ile Thr Pro Arg Pro Gln Asp His Gly Thr
        195                 200                 205

Asn Leu Thr Cys Gln Val Lys Phe Ala Gly Ala Gly Val Thr Thr Glu
    210                 215                 220

Arg Thr Ile Gln Leu Asn Val Thr Tyr Val Pro Gln Asn Pro Thr Thr
225                 230                 235                 240

Gly Ile Phe Pro Gly Asp Gly Ser Gly Lys Gln Glu Thr Arg Ala Gly
                245                 250                 255

Val Val His Gly Ala Ile Gly Gly Ala Gly Val Thr Ala Leu Leu Ala
            260                 265                 270

Leu Cys Leu Cys Leu Ile Phe Phe Ile Val Lys Thr His Arg Arg Lys
```

```
        275                 280                 285

Ala Ala Arg Thr Ala Val Gly Arg Asn Asp Thr His Pro Thr Thr Gly
    290                 295                 300

Ser Ala Ser Pro Lys His Gln Lys Lys Ser Lys Leu His Gly Pro Thr
305                 310                 315                 320

Glu Thr Ser Ser Cys Ser Gly Ala Ala Pro Thr Val Glu Met Asp Glu
                325                 330                 335

Glu Leu His Tyr Ala Ser Leu Asn Phe His Gly Met Asn Pro Ser Lys
            340                 345                 350

Asp Thr Ser Thr Glu Tyr Ser Glu Val Arg Thr Gln
        355                 360
```

<210> 106
<211> 255
<212> PRT
<213> Homo sapiens

<400> 106

```
Met Gly Asn Ser Cys Tyr Asn Ile Val Ala Thr Leu Leu Leu Val Leu
1               5                   10                  15

Asn Phe Glu Arg Thr Arg Ser Leu Gln Asp Pro Cys Ser Asn Cys Pro
            20                  25                  30

Ala Gly Thr Phe Cys Asp Asn Asn Arg Asn Gln Ile Cys Ser Pro Cys
        35                  40                  45

Pro Pro Asn Ser Phe Ser Ser Ala Gly Gly Gln Arg Thr Cys Asp Ile
    50                  55                  60

Cys Arg Gln Cys Lys Gly Val Phe Arg Thr Arg Lys Glu Cys Ser Ser
65                  70                  75                  80
```

```
Thr Ser Asn Ala Glu Cys Asp Cys Thr Pro Gly Phe His Cys Leu Gly
                85                  90                  95

Ala Gly Cys Ser Met Cys Glu Gln Asp Cys Lys Gln Gly Gln Glu Leu
            100                 105                 110

Thr Lys Lys Gly Cys Lys Asp Cys Cys Phe Gly Thr Phe Asn Asp Gln
        115                 120                 125

Lys Arg Gly Ile Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Lys
    130                 135                 140

Ser Val Leu Val Asn Gly Thr Lys Glu Arg Asp Val Val Cys Gly Pro
145                 150                 155                 160

Ser Pro Ala Asp Leu Ser Pro Gly Ala Ser Ser Val Thr Pro Pro Ala
                165                 170                 175

Pro Ala Arg Glu Pro Gly His Ser Pro Gln Ile Ile Ser Phe Phe Leu
            180                 185                 190

Ala Leu Thr Ser Thr Ala Leu Leu Phe Leu Leu Phe Phe Leu Thr Leu
        195                 200                 205

Arg Phe Ser Val Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
    210                 215                 220

Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
225                 230                 235                 240

Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
                245                 250                 255
```

<210> 107
<211> 256
<212> PRT
<213> Mus musculus

<400> 107

```
Met Gly Asn Asn Cys Tyr Asn Val Val Val Ile Val Leu Leu Leu Val
1               5                  10                  15

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

Pro Gly Thr Phe Cys Arg Lys Tyr Asn Pro Val Cys Lys Ser Cys Pro
        35                  40                  45

Pro Ser Thr Phe Ser Ser Ile Gly Gly Gln Pro Asn Cys Asn Ile Cys
    50                  55                  60

Arg Val Cys Ala Gly Tyr Phe Arg Phe Lys Lys Phe Cys Ser Ser Thr
65                  70                  75                  80

His Asn Ala Glu Cys Glu Cys Ile Glu Gly Phe His Cys Leu Gly Pro
                85                  90                  95

Gln Cys Thr Arg Cys Glu Lys Asp Cys Arg Pro Gly Gln Glu Leu Thr
            100                 105                 110

Lys Gln Gly Cys Lys Thr Cys Ser Leu Gly Thr Phe Asn Asp Gln Asn
        115                 120                 125

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

Ser Val Leu Lys Thr Gly Thr Thr Glu Lys Asp Val Val Cys Gly Pro
145                 150                 155                 160

Pro Val Val Ser Phe Ser Pro Ser Thr Thr Ile Ser Val Thr Pro Glu
                165                 170                 175

Gly Gly Pro Gly Gly His Ser Leu Gln Val Leu Thr Leu Phe Leu Ala
            180                 185                 190

Leu Thr Ser Ala Leu Leu Leu Ala Leu Ile Phe Ile Thr Leu Leu Phe
```

```
        195                 200                 205

Ser Val Leu Lys Trp Ile Arg Lys Lys Phe Pro His Ile Phe Lys Gln
    210                 215                 220

Pro Phe Lys Lys Thr Thr Gly Ala Ala Gln Glu Glu Asp Ala Cys Ser
225                 230                 235                 240

Cys Arg Cys Pro Gln Glu Glu Glu Gly Gly Gly Gly Gly Tyr Glu Leu
                245                 250                 255
```

<210> 108
<211> 254
<212> PRT
<213> Macaca fascicularis

<400> 108

```
Met Gly Asn Ser Cys Tyr Asn Ile Val Ala Thr Leu Leu Leu Val Leu
1               5                   10                  15

Asn Phe Glu Arg Thr Arg Ser Leu Gln Asp Leu Cys Ser Asn Cys Pro
            20                  25                  30

Ala Gly Thr Phe Cys Asp Asn Asn Arg Ser Gln Ile Cys Ser Pro Cys
        35                  40                  45

Pro Pro Asn Ser Phe Ser Ser Ala Gly Gly Gln Arg Thr Cys Asp Ile
    50                  55                  60

Cys Arg Gln Cys Lys Gly Val Phe Lys Thr Arg Lys Glu Cys Ser Ser
65                  70                  75                  80

Thr Ser Asn Ala Glu Cys Asp Cys Ile Ser Gly Tyr His Cys Leu Gly
                85                  90                  95

Ala Glu Cys Ser Met Cys Glu Gln Asp Cys Lys Gln Gly Gln Glu Leu
            100                 105                 110
```

```
Thr Lys Lys Gly Cys Lys Asp Cys Cys Phe Gly Thr Phe Asn Asp Gln
        115                 120                 125

Lys Arg Gly Ile Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Lys
    130                 135                 140

Ser Val Leu Val Asn Gly Thr Lys Glu Arg Asp Val Val Cys Gly Pro
145                 150                 155                 160

Ser Pro Ala Asp Leu Ser Pro Gly Ala Ser Ser Ala Thr Pro Pro Ala
                165                 170                 175

Pro Ala Arg Glu Pro Gly His Ser Pro Gln Ile Ile Phe Phe Leu Ala
            180                 185                 190

Leu Thr Ser Thr Val Val Leu Phe Leu Leu Phe Phe Leu Val Leu Arg
        195                 200                 205

Phe Ser Val Val Lys Arg Ser Arg Lys Lys Leu Leu Tyr Ile Phe Lys
    210                 215                 220

Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys
225                 230                 235                 240

Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
                245                 250
```

<210> 109
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> Peptide linker

<400> 109

```
Gly Gly Gly Gly Ser
1               5
```

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

<220>
<223> Peptide linker

<400> 110

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

<210> 111
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Peptide linker

<400> 111

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

<210> 112
<211> 14
<212> PRT
<213> Artificial sequence

<220>
<223> Peptide linker

<400> 112

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

<210> 113
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Peptide linker

<400> 113

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

<210> 114
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Peptide linker

<400> 114

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

<210> 115
<211> 20
<212> PRT
<213> Artificial sequence

<220>
<223> Peptide linker

<400> 115

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

Gly Gly Gly Ser
20

<210> 116
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Peptide linker

<400> 116

Gly Ser Gly Ser Gly Ser Gly Ser
1 5

<210> 117
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Peptide linker

<400> 117

Gly Ser Gly Ser Gly Asn Gly Ser
1 5

<210> 118
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Peptide linker

<400> 118

Gly Gly Ser Gly Ser Gly Ser Gly
1 5

<210> 119
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> Peptide linker

<400> 119

Gly Gly Ser Gly Ser Gly
1 5

<210> 120
<211> 4
<212> PRT
<213> Artificial sequence

<220>

<223> Peptide linker

<400> 120

Gly Gly Ser Gly
1

<210> 121
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Peptide linker

<400> 121

Gly Gly Ser Gly Asn Gly Ser Gly
1   5

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

<220>
<223> Peptide linker

<400> 122

Gly Gly Asn Gly Ser Gly Ser Gly
1   5

<210> 123
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> Peptide linker

<400> 123

Gly Gly Asn Gly Ser Gly
1   5

<210> 124
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1(EE) 4-1BB(20H4.9)-Heavy chain knob

<400> 124

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

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

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

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
50 55 60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
100 105 110

Arg Gly Thr Leu 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 Glu 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 Glu Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gly 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 Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365
```

```
Leu Trp 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> 125
<211> 440
<212> PRT
<213> Artificial Sequence

<220>
<223> VLCH1 FAP (4B9)-Heavy chain hole

<400> 125

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Ser Ser
            20                  25                  30

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

Ile Asn Val Gly Ser Arg Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60
```

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

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Gly Ile Met Leu Pro
                85                  90                  95

Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Ser Ser Ala Ser
            100                 105                 110

Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr
        115                 120                 125

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

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

His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
                165                 170                 175

Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile
            180                 185                 190

Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val
        195                 200                 205

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
    210                 215                 220

Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
225                 230                 235                 240

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
                245                 250                 255
```

```
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
            260                 265                 270

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
        275                 280                 285

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
    290                 295                 300

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
305                 310                 315                 320

Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
                325                 330                 335

Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
            340                 345                 350

Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser
        355                 360                 365

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
    370                 375                 380

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

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
                405                 410                 415

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
            420                 425                 430

Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440
```

<210> 126
<211> 216

<212> PRT
<213> Artificial Sequence

<220>
<223> VLCL(RK)-Light chain 4-1BB (20H4.9)

<400> 126

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


Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
            20                  25                  30


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


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


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


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


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


Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Arg Lys 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>  127
<211>  224
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  VHCL-Light chain FAP(4B9)

<400>  127

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


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


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


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


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


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


Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110
```

```
Val Thr Val Ser Ser Ala Ser Val Ala Ala Pro Ser Val Phe Ile Phe
        115                 120                 125


Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys
    130                 135                 140


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


Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln
                165                 170                 175


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


Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His
        195                 200                 205


Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215                 220


<210>  128
<211>  568
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  VHCH1 (20H4.9)-Heavy chain hole-VL (DP47)

<400>  128

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


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


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

```
Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110

Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gly 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

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Ser Cys Ala 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 Val 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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu
    450                 455                 460


Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr
465                 470                 475                 480


Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser Tyr Leu Ala Trp
                485                 490                 495


Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala
            500                 505                 510


Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser
        515                 520                 525


Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe
    530                 535                 540


Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Leu Thr Phe Gly
545                 550                 555                 560


Gln Gly Thr Lys Val Glu Ile Lys
                565


<210>  129
<211>  585
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  VHCH1 (20H4.9)-Heavy chain knob-VH (DP47)

<400>  129

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


Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr
            20                  25                  30
```

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

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110

Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220
```

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gly 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 Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Trp 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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    450                 455                 460

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly
465                 470                 475                 480

Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
                485                 490                 495

Phe Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly
            500                 505                 510

Lys Gly Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr
        515                 520                 525

Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
    530                 535                 540

Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
545                 550                 555                 560

Thr Ala Val Tyr Tyr Cys Ala Lys Gly Ser Gly Phe Asp Tyr Trp Gly
                565                 570                 575

Gln Gly Thr Leu Val Thr Val Ser Ser
            580                 585
```

<210> 130
<211> 575
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1 (20H4.9)-Heavy chain hole-VH (DP47)

<400> 130

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


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


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


Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60


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


Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95


Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110


Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gly 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

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Ser Cys Ala 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 Val 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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
    450                 455                 460

Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu
465                 470                 475                 480

Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met Ser Trp
                485                 490                 495

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Ser
            500                 505                 510

Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe
        515                 520                 525

Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn
    530                 535                 540

Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Gly Ser
545                 550                 555                 560

Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
                565                 570                 575
```

<210> 131
<211> 578
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1 (20H4.9)-Heavy chain knob-VL (DP47)

<400> 131

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


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


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


Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60


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


Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95


Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110


Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gly 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 Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Trp 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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    450                 455                 460

Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr
465                 470                 475                 480

Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser
                485                 490                 495

Gln Ser Val Ser Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly
            500                 505                 510

Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly
        515                 520                 525

Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
    530                 535                 540

Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln
545                 550                 555                 560

Gln Tyr Gly Ser Ser Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu
                565                 570                 575
```

Ile Lys

<210> 132
<211> 571
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1 (MU137-1)-Heavy chain Fc-DD-VL (28H1)

<400> 132

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


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


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


Ala Ser Ile Ser Pro Ser Gly Asp Ile Pro Tyr Tyr Arg Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Val Ser Arg Glu Asn Ala Lys Ser Ser Leu Tyr
65                  70                  75                  80


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


Ala Arg Arg Ser Tyr Gly Gly Tyr Ser Glu Leu Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Val Met Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val
        115                 120                 125


Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr
    130                 135                 140
```

```
Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr
145                 150                 155                 160


Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175


Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser
            180                 185                 190


Ser Thr Trp Pro Ser Gln Thr Val Thr Cys Asn Val Ala His Pro Ala
        195                 200                 205


Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Cys
    210                 215                 220


Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe
225                 230                 235                 240


Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val
                245                 250                 255


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


Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Lys Pro
        275                 280                 285


Arg Glu Glu Gln Ile Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro
    290                 295                 300


Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val
305                 310                 315                 320


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


Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro Lys
            340                 345                 350
```

```
Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asn
        355                 360                 365

Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro
    370                 375                 380

Ala Glu Asn Tyr Asp Asn Thr Gln Pro Ile Met Asp Thr Asp Gly Ser
385                 390                 395                 400

Tyr Phe Val Tyr Ser Asp Leu Asn Val Gln Lys Ser Asn Trp Glu Ala
                405                 410                 415

Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His
            420                 425                 430

His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Gly Gly Gly Gly Ser
        435                 440                 445

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
    450                 455                 460

Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu
465                 470                 475                 480

Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Arg Ser Tyr
                485                 490                 495

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
            500                 505                 510

Ile Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly
        515                 520                 525

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
    530                 535                 540
```

```
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Gly Gln Val Ile Pro Pro
545                 550                 555                 560


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
                565                 570


<210>  133
<211>  579
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  VHCH1 (20H4.9)-Heavy chain Fc-KK-VH (28H1)

<400>  133

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


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


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


Ala Ser Ile Ser Pro Ser Gly Asp Ile Pro Tyr Tyr Arg Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Val Ser Arg Glu Asn Ala Lys Ser Ser Leu Tyr
65                  70                  75                  80


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


Ala Arg Arg Ser Tyr Gly Gly Tyr Ser Glu Leu Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Val Met Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val
        115                 120                 125
```

```
Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr
    130                 135                 140

Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr
145                 150                 155                 160

Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser
            180                 185                 190

Ser Thr Trp Pro Ser Gln Thr Val Thr Cys Asn Val Ala His Pro Ala
        195                 200                 205

Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Cys
    210                 215                 220

Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe
225                 230                 235                 240

Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val
                245                 250                 255

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

Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Lys Pro
        275                 280                 285

Arg Glu Glu Gln Ile Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro
    290                 295                 300

Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val
305                 310                 315                 320

Asn Ser Ala Ala Phe Gly Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr
                325                 330                 335
```

```
Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro Lys
            340                 345                 350

Lys Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asn
        355                 360                 365

Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro
    370                 375                 380

Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Lys Thr Asp Gly Ser
385                 390                 395                 400

Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala
                405                 410                 415

Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His
            420                 425                 430

His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Gly Gly Gly Gly Ser
        435                 440                 445

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
    450                 455                 460

Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
465                 470                 475                 480

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser His Ala
                485                 490                 495

Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
            500                 505                 510

Ala Ile Trp Ala Ser Gly Glu Gln Tyr Tyr Ala Asp Ser Val Lys Gly
        515                 520                 525
```

```
Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
    530                 535                 540

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys
545                 550                 555                 560

Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
                565                 570                 575

Val Ser Ser
```

<210> 134
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> VLCL-Light chain (MU137-1)

<400> 134

```
Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Leu Glu
1               5                   10                  15

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

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

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

Ser Ser Ser Gly Ser Gln Tyr Ser Leu Lys Ile Ser Arg Leu Gln Val
65                  70                  75                  80

Glu Asp Ile Gly Ile Tyr Tyr Cys Leu Gln Ala Tyr Gly Ala Pro Trp
                85                  90                  95
```

```
Thr Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys Arg Ala Asp Ala Ala
            100                 105                 110


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


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


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


Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser
                165                 170                 175


Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr
            180                 185                 190


Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser
        195                 200                 205


Phe Asn Arg Asn Glu Cys
    210


<210>  135
<211>  579
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  VHCH1 (MU137-1)-Heavy chain Fc-DD-VH (28H1)

<400>  135

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


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

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

Ala Ser Ile Ser Pro Ser Gly Asp Ile Pro Tyr Tyr Arg Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Val Ser Arg Glu Asn Ala Lys Ser Ser Leu Tyr
65                  70                  75                  80

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

Ala Arg Arg Ser Tyr Gly Gly Tyr Ser Glu Leu Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Val Met Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val
        115                 120                 125

Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr
    130                 135                 140

Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr
145                 150                 155                 160

Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser
            180                 185                 190

Ser Thr Trp Pro Ser Gln Thr Val Thr Cys Asn Val Ala His Pro Ala
        195                 200                 205

Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Cys
    210                 215                 220

Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe
225                 230                 235                 240
```

```
Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val
                245                 250                 255

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

Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Lys Pro
        275                 280                 285

Arg Glu Glu Gln Ile Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro
    290                 295                 300

Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val
305                 310                 315                 320

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

Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro Lys
            340                 345                 350

Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asn
        355                 360                 365

Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro
    370                 375                 380

Ala Glu Asn Tyr Asp Asn Thr Gln Pro Ile Met Asp Thr Asp Gly Ser
385                 390                 395                 400

Tyr Phe Val Tyr Ser Asp Leu Asn Val Gln Lys Ser Asn Trp Glu Ala
                405                 410                 415

Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His
            420                 425                 430
```

```
His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Gly Gly Gly Gly Ser
        435                 440                 445

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
    450                 455                 460

Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
465                 470                 475                 480

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser His Ala
                485                 490                 495

Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
            500                 505                 510

Ala Ile Trp Ala Ser Gly Glu Gln Tyr Tyr Ala Asp Ser Val Lys Gly
        515                 520                 525

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
    530                 535                 540

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys
545                 550                 555                 560

Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
                565                 570                 575

Val Ser Ser
```

<210> 136
<211> 571
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1 (MU137-1)-Heavy chain Fc-KK-VL (28H1)

<400> 136

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


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


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


Ala Ser Ile Ser Pro Ser Gly Asp Ile Pro Tyr Tyr Arg Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Val Ser Arg Glu Asn Ala Lys Ser Ser Leu Tyr
65                  70                  75                  80


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


Ala Arg Arg Ser Tyr Gly Gly Tyr Ser Glu Leu Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Val Met Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val
        115                 120                 125


Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr
    130                 135                 140


Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr
145                 150                 155                 160


Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175


Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser
            180                 185                 190


Ser Thr Trp Pro Ser Gln Thr Val Thr Cys Asn Val Ala His Pro Ala
        195                 200                 205
```

```
Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Cys
    210                 215                 220

Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe
225                 230                 235                 240

Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val
                245                 250                 255

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

Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Lys Pro
        275                 280                 285

Arg Glu Glu Gln Ile Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro
    290                 295                 300

Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val
305                 310                 315                 320

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

Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro Lys
            340                 345                 350

Lys Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asn
        355                 360                 365

Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro
    370                 375                 380

Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Lys Thr Asp Gly Ser
385                 390                 395                 400
```

```
Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala
                405                 410                 415

Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His
            420                 425                 430

His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Gly Gly Gly Gly Ser
        435                 440                 445

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
    450                 455                 460

Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu
465                 470                 475                 480

Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Arg Ser Tyr
                485                 490                 495

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
            500                 505                 510

Ile Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly
        515                 520                 525

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
    530                 535                 540

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Gly Gln Val Ile Pro Pro
545                 550                 555                 560

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
                565                 570
```

<210> 137
<211> 576
<212> PRT
<213> Artificial Sequence

<220>

<223> VHCH1 (20H4.9)-Heavy chain hole-VL (A5B7) (G4S)2

<400> 137

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


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


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


Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60


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


Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95


Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110


Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gly 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

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Ser Cys Ala 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 Val 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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ala Val Leu
    450                 455                 460

Thr Gln Pro Ala Ser Leu Ser Ala Ser Pro Gly Ala Ser Ala Ser Leu
465                 470                 475                 480

Thr Cys Thr Leu Arg Arg Gly Ile Asn Val Gly Ala Tyr Ser Ile Tyr
                485                 490                 495

Trp Tyr Gln Gln Lys Pro Gly Ser Pro Pro Gln Tyr Leu Leu Arg Tyr
            500                 505                 510

Lys Ser Asp Ser Asp Lys Gln Gln Gly Ser Gly Val Ser Ser Arg Phe
        515                 520                 525

Ser Ala Ser Lys Asp Ala Ser Ala Asn Ala Gly Ile Leu Leu Ile Ser
    530                 535                 540

Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Met Ile Trp His
545                 550                 555                 560

Ser Gly Ala Ser Ala Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
                565                 570                 575
```

<210> 138
<211> 581

<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1 (20H4.9)-Heavy chain hole-VH (A5B7) (G4S)2

<400> 138

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


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


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


Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60


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


Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95


Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110


Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gly 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

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365
```

```
Leu Ser Cys Ala 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 Val 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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
    450                 455                 460

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg Ser Leu Arg Leu
465                 470                 475                 480

Ser Cys Ala Ala Ser Gly Phe Thr Val Ser Ser Tyr Trp Met His Trp
                485                 490                 495

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Phe Ile Arg
            500                 505                 510

Asn Lys Ala Asn Gly Gly Thr Thr Glu Tyr Ala Ala Ser Val Lys Gly
        515                 520                 525

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr Leu Gln
    530                 535                 540

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
545                 550                 555                 560

Asp Arg Gly Leu Arg Phe Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
                565                 570                 575
```

Val Thr Val Ser Ser
            580

<210> 139
<211> 582
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1 (20H4.9)-Heavy chain hole-VL (2B11)

<400> 139

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

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

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

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50   55   60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85   90   95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100   105   110

Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gly 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

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Ser Cys Ala 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 Val 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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    450                 455                 460

Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Thr Pro Leu Ser
465                 470                 475                 480

Leu Ser Val Thr Pro Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser
                485                 490                 495

Gln Ser Leu Glu Thr Ser Thr Gly Thr Thr Tyr Leu Asn Trp Tyr Leu
            500                 505                 510

Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Arg Val Ser Lys
        515                 520                 525

Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
    530                 535                 540
```

```
Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val
545                 550                 555                 560


Tyr Tyr Cys Leu Gln Leu Leu Glu Asp Pro Tyr Thr Phe Gly Gln Gly
                565                 570                 575


Thr Lys Leu Glu Ile Lys
            580
```

<210> 140
<211> 591
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1 (20H4.9)-Heavy chain knob-VH (2B11)

<400> 140

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


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


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


Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60


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


Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95


Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110
```

```
Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gly 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 Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Trp 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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    450                 455                 460

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu
465                 470                 475                 480

Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly
                485                 490                 495

Tyr Thr Phe Thr Asp Tyr Ile Met His Trp Val Arg Gln Ala Pro Gly
            500                 505                 510
```

```
Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Ser
        515                 520                 525


Lys Tyr Thr Glu Lys Phe Gln Gly Arg Val Thr Met Thr Ser Asp Thr
    530                 535                 540


Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser Asp Asp
545                 550                 555                 560


Thr Ala Val Tyr Tyr Cys Ala Arg Gly Thr Tyr Tyr Tyr Gly Pro Gln
                565                 570                 575


Leu Phe Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
            580                 585                 590


<210>  141
<211>  591
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  VHCH1 (20H4.9)-Heavy chain hole-VH (2B11)

<400>  141

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


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


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


Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60


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

```
Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110

Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gly 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

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Ser Cys Ala 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 Val 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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    450                 455                 460

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu
465                 470                 475                 480
```

```
Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly
                485                 490                 495


Tyr Thr Phe Thr Asp Tyr Ile Met His Trp Val Arg Gln Ala Pro Gly
            500                 505                 510


Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Ser
        515                 520                 525


Lys Tyr Thr Glu Lys Phe Gln Gly Arg Val Thr Met Thr Ser Asp Thr
    530                 535                 540


Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser Asp Asp
545                 550                 555                 560


Thr Ala Val Tyr Tyr Cys Ala Arg Gly Thr Tyr Tyr Tyr Gly Pro Gln
                565                 570                 575


Leu Phe Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
            580                 585                 590


<210>  142
<211>  582
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  VHCH1 (20H4.9)-Heavy chain knob-VL (2B11)

<400>  142

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


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


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

```
Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110

Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gly 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 Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Trp 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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    450                 455                 460

Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Thr Pro Leu Ser
465                 470                 475                 480

Leu Ser Val Thr Pro Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser
                485                 490                 495

Gln Ser Leu Glu Thr Ser Thr Gly Thr Thr Tyr Leu Asn Trp Tyr Leu
            500                 505                 510

Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Arg Val Ser Lys
        515                 520                 525

Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
    530                 535                 540

Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val
545                 550                 555                 560

Tyr Tyr Cys Leu Gln Leu Leu Glu Asp Pro Tyr Thr Phe Gly Gln Gly
                565                 570                 575

Thr Lys Leu Glu Ile Lys
            580
```

<210> 143
<211> 582
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1 (20H4.9)-Heavy chain hole-VL (8B8-018)

<400> 143

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

```
Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr
            20                  25                  30

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

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110

Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gly 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

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Ser Cys Ala 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 Val 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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    450                 455                 460

Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Thr Pro Leu Ser
465                 470                 475                 480

Leu Ser Val Thr Pro Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser
                485                 490                 495

Gln Ser Leu Glu Asn Pro Asn Gly Asn Thr Tyr Leu Asn Trp Tyr Leu
            500                 505                 510

Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Arg Val Ser Lys
        515                 520                 525

Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
    530                 535                 540

Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val
545                 550                 555                 560

Tyr Tyr Cys Leu Gln Leu Thr His Val Pro Tyr Thr Phe Gly Gln Gly
                565                 570                 575

Thr Lys Leu Glu Ile Lys
            580
```

<210> 144
<211> 591
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1 (20H4.9)-Heavy chain knob-VH (8B8-018)

<400> 144

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


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


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


Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60


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


Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95


Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110


Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gly 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 Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Trp 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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    450                 455                 460

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu
465                 470                 475                 480

Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly
                485                 490                 495

Tyr Thr Phe Thr Asp Tyr Ile Met His Trp Val Arg Gln Ala Pro Gly
            500                 505                 510

Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Ser
        515                 520                 525

Lys Tyr Thr Glu Lys Phe Gln Gly Arg Val Thr Met Thr Ser Asp Thr
    530                 535                 540

Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser Asp Asp
545                 550                 555                 560

Thr Ala Val Tyr Tyr Cys Ala Arg Gly Thr Tyr Tyr Tyr Gly Ser Ala
                565                 570                 575
```

Leu Phe Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
580 585 590

<210> 145
<211> 591
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1 (20H4.9)-Heavy chain hole-VH (8B8-018)

<400> 145

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

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

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

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
50 55 60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
100 105 110

Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220


Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gly 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
```

```
Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Ser Cys Ala 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 Val 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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    450                 455                 460

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu
465                 470                 475                 480

Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly
                485                 490                 495

Tyr Thr Phe Thr Asp Tyr Ile Met His Trp Val Arg Gln Ala Pro Gly
            500                 505                 510

Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Ser
        515                 520                 525

Lys Tyr Thr Glu Lys Phe Gln Gly Arg Val Thr Met Thr Ser Asp Thr
    530                 535                 540
```

```
Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser Asp Asp
545                 550                 555                 560


Thr Ala Val Tyr Tyr Cys Ala Arg Gly Thr Tyr Tyr Tyr Gly Ser Ala
                565                 570                 575


Leu Phe Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
            580                 585                 590


<210>  146
<211>  582
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  VHCH1 (20H4.9)-Heavy chain knob-VL (8B8-018)

<400>  146

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


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


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


Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60


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


Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95


Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110
```

```
Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gly 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 Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Trp 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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    450                 455                 460

Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Thr Pro Leu Ser
465                 470                 475                 480

Leu Ser Val Thr Pro Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser
               485                 490                 495

Gln Ser Leu Glu Asn Pro Asn Gly Asn Thr Tyr Leu Asn Trp Tyr Leu
            500                 505                 510
```

```
Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Arg Val Ser Lys
        515                 520                 525

Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
    530                 535                 540

Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val
545                 550                 555                 560

Tyr Tyr Cys Leu Gln Leu Thr His Val Pro Tyr Thr Phe Gly Gln Gly
                565                 570                 575

Thr Lys Leu Glu Ile Lys
            580
```

<210> 147
<211> 817
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1-VHCH1 (20H4.9)-Heavy chain Fc hole-VL (2B11)

<400> 147

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

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

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

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60

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

```
Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110

Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
225                 230                 235                 240

Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr
                245                 250                 255

Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Ser Trp Ile
            260                 265                 270

Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His
        275                 280                 285
```

```
Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu Ser Arg Val Thr Ile
    290                 295                 300

Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val
305                 310                 315                 320

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Tyr Gly Pro
                325                 330                 335

Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val
            340                 345                 350

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
        355                 360                 365

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
    370                 375                 380

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
385                 390                 395                 400

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
                405                 410                 415

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
            420                 425                 430

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        435                 440                 445

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    450                 455                 460

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
465                 470                 475                 480
```

```
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                485                 490                 495

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            500                 505                 510

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        515                 520                 525

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    530                 535                 540

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
545                 550                 555                 560

Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
                565                 570                 575

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro
            580                 585                 590

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val
        595                 600                 605

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    610                 615                 620

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
625                 630                 635                 640

Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                645                 650                 655

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            660                 665                 670

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly
        675                 680                 685
```

```
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    690                 695                 700

Ser Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro
705                 710                 715                 720

Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Glu Thr
                725                 730                 735

Ser Thr Gly Thr Thr Tyr Leu Asn Trp Tyr Leu Gln Lys Pro Gly Gln
            740                 745                 750

Ser Pro Gln Leu Leu Ile Tyr Arg Val Ser Lys Arg Phe Ser Gly Val
        755                 760                 765

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys
    770                 775                 780

Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Leu Gln
785                 790                 795                 800

Leu Leu Glu Asp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
                805                 810                 815

Lys
```

<210> 148
<211> 826
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1-VHCH1 (20H4.9)-Heavy chain Fc knob-VH (2B11)

<400> 148

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

```
Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr
            20                  25                  30

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

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110

Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
225                 230                 235                 240

Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr
                245                 250                 255

Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Ser Trp Ile
            260                 265                 270

Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His
        275                 280                 285

Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu Ser Arg Val Thr Ile
    290                 295                 300

Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val
305                 310                 315                 320

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Tyr Gly Pro
                325                 330                 335

Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val
            340                 345                 350

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
        355                 360                 365

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
    370                 375                 380

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
385                 390                 395                 400

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
                405                 410                 415
```

```
Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
            420                 425                 430

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        435                 440                 445

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    450                 455                 460

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
465                 470                 475                 480

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                485                 490                 495

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            500                 505                 510

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        515                 520                 525

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    530                 535                 540

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
545                 550                 555                 560

Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
                565                 570                 575

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            580                 585                 590

Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val
        595                 600                 605
```

```
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    610                 615                 620

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
625                 630                 635                 640

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                645                 650                 655

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            660                 665                 670

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly
        675                 680                 685

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    690                 695                 700

Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
705                 710                 715                 720

Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp
                725                 730                 735

Tyr Ile Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp
            740                 745                 750

Met Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Ser Lys Tyr Thr Glu Lys
        755                 760                 765

Phe Gln Gly Arg Val Thr Met Thr Ser Asp Thr Ser Ile Ser Thr Ala
    770                 775                 780

Tyr Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr
785                 790                 795                 800

Cys Ala Arg Gly Thr Tyr Tyr Tyr Gly Pro Gln Leu Phe Asp Tyr Trp
                805                 810                 815
```

Gly Gln Gly Thr Thr Val Thr Val Ser Ser
820 825

<210> 149
<211> 826
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1-VHCH1 (20H4.9)-Heavy chain hole-VH (2B11)

<400> 149

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

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

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

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
50 55 60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
100 105 110

Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
225                 230                 235                 240

Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr
                245                 250                 255

Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Ser Trp Ile
            260                 265                 270

Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His
        275                 280                 285

Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu Ser Arg Val Thr Ile
    290                 295                 300

Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val
305                 310                 315                 320

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Tyr Gly Pro
                325                 330                 335
```

```
Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val
            340                 345                 350

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
        355                 360                 365

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
    370                 375                 380

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
385                 390                 395                 400

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
                405                 410                 415

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
            420                 425                 430

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        435                 440                 445

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    450                 455                 460

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
465                 470                 475                 480

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                485                 490                 495

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            500                 505                 510

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        515                 520                 525

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    530                 535                 540
```

```
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
545                 550                 555                 560


Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
                565                 570                 575


Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro
            580                 585                 590


Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val
        595                 600                 605


Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    610                 615                 620


Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
625                 630                 635                 640


Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                645                 650                 655


Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            660                 665                 670


Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly
        675                 680                 685


Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    690                 695                 700


Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
705                 710                 715                 720


Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp
                725                 730                 735
```

```
Tyr Ile Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp
            740                 745                 750

Met Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Ser Lys Tyr Thr Glu Lys
        755                 760                 765

Phe Gln Gly Arg Val Thr Met Thr Ser Asp Thr Ser Ile Ser Thr Ala
    770                 775                 780

Tyr Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr
785                 790                 795                 800

Cys Ala Arg Gly Thr Tyr Tyr Tyr Gly Pro Gln Leu Phe Asp Tyr Trp
                805                 810                 815

Gly Gln Gly Thr Thr Val Thr Val Ser Ser
            820                 825
```

<210> 150
<211> 817
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1-VHCH1 (20H4.9)-Heavy chain knob-VL (2B11)

<400> 150

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

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

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

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60
```

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110

Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
225                 230                 235                 240

Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr
                245                 250                 255

Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Ser Trp Ile
            260                 265                 270
```

```
Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His
        275                 280                 285

Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu Ser Arg Val Thr Ile
    290                 295                 300

Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val
305                 310                 315                 320

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Tyr Gly Pro
                325                 330                 335

Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val
            340                 345                 350

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
        355                 360                 365

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
    370                 375                 380

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
385                 390                 395                 400

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
                405                 410                 415

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
            420                 425                 430

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        435                 440                 445

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    450                 455                 460
```

```
Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
465                 470                 475                 480


Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                485                 490                 495


Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            500                 505                 510


Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        515                 520                 525


Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    530                 535                 540


Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
545                 550                 555                 560


Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
                565                 570                 575


Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            580                 585                 590


Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val
        595                 600                 605


Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    610                 615                 620


Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
625                 630                 635                 640


Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                645                 650                 655


Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            660                 665                 670
```

```
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly
        675                 680                 685

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    690                 695                 700

Ser Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro
705                 710                 715                 720

Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Glu Thr
                725                 730                 735

Ser Thr Gly Thr Thr Tyr Leu Asn Trp Tyr Leu Gln Lys Pro Gly Gln
            740                 745                 750

Ser Pro Gln Leu Leu Ile Tyr Arg Val Ser Lys Arg Phe Ser Gly Val
        755                 760                 765

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys
    770                 775                 780

Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Leu Gln
785                 790                 795                 800

Leu Leu Glu Asp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
                805                 810                 815

Lys
```

<210> 151
<211> 817
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1-VHCH1 (20H4.9)-Heavy chain Fc hole-VL (8B8-018)

<400> 151

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


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


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


Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60


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


Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95


Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110


Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
225                 230                 235                 240

Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr
                245                 250                 255

Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Ser Trp Ile
            260                 265                 270

Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His
        275                 280                 285

Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu Ser Arg Val Thr Ile
    290                 295                 300

Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val
305                 310                 315                 320

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Tyr Gly Pro
                325                 330                 335

Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val
            340                 345                 350

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
        355                 360                 365

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
    370                 375                 380

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
385                 390                 395                 400
```

```
Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
                405                 410                 415

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
            420                 425                 430

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        435                 440                 445

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    450                 455                 460

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
465                 470                 475                 480

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                485                 490                 495

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            500                 505                 510

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        515                 520                 525

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    530                 535                 540

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
545                 550                 555                 560

Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
                565                 570                 575

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro
            580                 585                 590
```

```
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val
        595                 600                 605

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    610                 615                 620

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
625                 630                 635                 640

Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                645                 650                 655

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            660                 665                 670

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly
        675                 680                 685

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    690                 695                 700

Ser Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro
705                 710                 715                 720

Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Glu Asn
                725                 730                 735

Pro Asn Gly Asn Thr Tyr Leu Asn Trp Tyr Leu Gln Lys Pro Gly Gln
            740                 745                 750

Ser Pro Gln Leu Leu Ile Tyr Arg Val Ser Lys Arg Phe Ser Gly Val
        755                 760                 765

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys
    770                 775                 780

Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Leu Gln
785                 790                 795                 800
```

```
Leu Thr His Val Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
                805                 810                 815


Lys
```

<210> 152
<211> 826
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1-VHCH1 (20H4.9)-Heavy chain Fc knob-VH (8B8-018)

<400> 152

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


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


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


Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60


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


Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95


Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110


Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
225                 230                 235                 240

Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr
                245                 250                 255

Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Ser Trp Ile
            260                 265                 270

Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His
        275                 280                 285

Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu Ser Arg Val Thr Ile
    290                 295                 300

Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val
305                 310                 315                 320
```

```
Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Tyr Gly Pro
                325                 330                 335

Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val
            340                 345                 350

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
        355                 360                 365

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
    370                 375                 380

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
385                 390                 395                 400

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
                405                 410                 415

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
            420                 425                 430

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        435                 440                 445

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    450                 455                 460

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
465                 470                 475                 480

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                485                 490                 495

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            500                 505                 510

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        515                 520                 525
```

```
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    530                 535                 540

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
545                 550                 555                 560

Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
                565                 570                 575

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            580                 585                 590

Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val
        595                 600                 605

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    610                 615                 620

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
625                 630                 635                 640

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                645                 650                 655

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            660                 665                 670

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly
        675                 680                 685

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    690                 695                 700

Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
705                 710                 715                 720
```

```
Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp
                725                 730                 735


Tyr Ile Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp
            740                 745                 750


Met Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Ser Lys Tyr Thr Glu Lys
        755                 760                 765


Phe Gln Gly Arg Val Thr Met Thr Ser Asp Thr Ser Ile Ser Thr Ala
    770                 775                 780


Tyr Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr
785                 790                 795                 800


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


Gly Gln Gly Thr Thr Val Thr Val Ser Ser
            820                 825
```

<210> 153
<211> 826
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1-VHCH1 (20H4.9)-Heavy chain hole-VH (8B8-018)

<400> 153

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


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


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

```
Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110

Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
225                 230                 235                 240

Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr
                245                 250                 255
```

```
Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Ser Trp Ile
            260                 265                 270

Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His
        275                 280                 285

Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu Ser Arg Val Thr Ile
    290                 295                 300

Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val
305                 310                 315                 320

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Tyr Gly Pro
                325                 330                 335

Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val
            340                 345                 350

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
        355                 360                 365

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
    370                 375                 380

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
385                 390                 395                 400

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
                405                 410                 415

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
            420                 425                 430

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        435                 440                 445
```

```
Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    450                 455                 460

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
465                 470                 475                 480

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                485                 490                 495

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            500                 505                 510

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        515                 520                 525

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    530                 535                 540

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
545                 550                 555                 560

Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
                565                 570                 575

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro
            580                 585                 590

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val
        595                 600                 605

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    610                 615                 620

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
625                 630                 635                 640

Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                645                 650                 655
```

```
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            660                 665                 670

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly
        675                 680                 685

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    690                 695                 700

Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
705                 710                 715                 720

Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp
                725                 730                 735

Tyr Ile Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp
            740                 745                 750

Met Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Ser Lys Tyr Thr Glu Lys
        755                 760                 765

Phe Gln Gly Arg Val Thr Met Thr Ser Asp Thr Ser Ile Ser Thr Ala
    770                 775                 780

Tyr Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr
785                 790                 795                 800

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

Gly Gln Gly Thr Thr Val Thr Val Ser Ser
            820                 825
```

<210> 154
<211> 817
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1-VHCH1 (20H4.9)-Heavy chain knob-VL (8B8-018)

<400> 154

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


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


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


Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60


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


Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95


Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110


Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
225                 230                 235                 240

Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr
                245                 250                 255

Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Ser Trp Ile
            260                 265                 270

Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His
        275                 280                 285

Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu Ser Arg Val Thr Ile
    290                 295                 300

Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val
305                 310                 315                 320

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Tyr Gly Pro
                325                 330                 335

Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val
            340                 345                 350

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
        355                 360                 365

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
    370                 375                 380
```

```
Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
385                 390                 395                 400

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
                405                 410                 415

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
            420                 425                 430

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        435                 440                 445

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    450                 455                 460

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
465                 470                 475                 480

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                485                 490                 495

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            500                 505                 510

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        515                 520                 525

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    530                 535                 540

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
545                 550                 555                 560

Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
                565                 570                 575
```

```
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            580                 585                 590

Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val
        595                 600                 605

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    610                 615                 620

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
625                 630                 635                 640

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                645                 650                 655

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            660                 665                 670

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly
        675                 680                 685

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    690                 695                 700

Ser Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro
705                 710                 715                 720

Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Glu Asn
                725                 730                 735

Pro Asn Gly Asn Thr Tyr Leu Asn Trp Tyr Leu Gln Lys Pro Gly Gln
            740                 745                 750

Ser Pro Gln Leu Leu Ile Tyr Arg Val Ser Lys Arg Phe Ser Gly Val
        755                 760                 765

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys
    770                 775                 780
```

Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Leu Gln
785 790 795 800

Leu Thr His Val Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
805 810 815

Lys

<210> 155
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-2B11) CDR-H1

<400> 155

Asp Tyr Ile Met His
1 5

<210> 156
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-2B11) CDR-H2

<400> 156

Tyr Ile Asn Pro Tyr Asn Asp Gly Ser Lys Tyr Thr Glu Lys Phe Gln
1 5 10 15

Gly

<210> 157
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-2B11) CDR-H3

<400> 157

Gly Thr Tyr Tyr Tyr Gly Pro Gln Leu Phe Asp Tyr
1   5   10

<210> 158
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-2B11) CDR-L1

<400> 158

Lys Ser Ser Gln Ser Leu Glu Thr Ser Thr Gly Thr Thr Tyr Leu Asn
1   5   10   15

<210> 159
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-2B11) CDR-L2

<400> 159

Arg Val Ser Lys Arg Phe Ser
1   5

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

<220>
<223> CD19 (8B8-2B11) CDR-L3

<400> 160

Leu Gln Leu Leu Glu Asp Pro Tyr Thr
1   5

<210> 161
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-2B11) VH

<400> 161

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

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

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

Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Ser Lys Tyr Thr Glu Lys Phe
    50   55   60

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

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

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

Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 162
<211> 112
<212> PRT
<213> Artificial Sequence

<220>

<223> CD19 (8B8-2B11) VL

<400> 162

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Glu Thr Ser
20 25 30

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

Pro Gln Leu Leu Ile Tyr Arg Val Ser Lys Arg Phe Ser Gly Val Pro
50 55 60

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

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

Leu Glu Asp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 163
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-018) CDR-H1

<400> 163

Asp Tyr Ile Met His
1 5

<210> 164
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-018) CDR-H2

<400> 164

Tyr Ile Asn Pro Tyr Asn Asp Gly Ser Lys Tyr Thr Glu Lys Phe Gln
1   5   10   15

Gly

<210> 165
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-018) CDR-H3

<400> 165

Gly Thr Tyr Tyr Tyr Gly Ser Ala Leu Phe Asp Tyr
1   5   10

<210> 166
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-018) CDR-L1

<400> 166

Lys Ser Ser Gln Ser Leu Glu Asn Pro Asn Gly Asn Thr Tyr Leu Asn
1   5   10   15

<210> 167
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-018) CDR-L2

<400> 167

Arg Val Ser Lys Arg Phe Ser
1 5

<210> 168
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-018) CDR-L3

<400> 168

Leu Gln Leu Thr His Val Pro Tyr Thr
1 5

<210> 169
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-018) VH

<400> 169

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

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

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

Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Ser Lys Tyr Thr Glu Lys Phe
50 55 60

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

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

Ala Arg Gly Thr Tyr Tyr Tyr Gly Ser Ala Leu Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 170
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-018) VL

<400> 170

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Glu Asn Pro
20 25 30

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

Pro Gln Leu Leu Ile Tyr Arg Val Ser Lys Arg Phe Ser Gly Val Pro
50 55 60

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

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

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

<210> 171
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-1BB (MU137-1) CDR-H1

<400> 171

Tyr Phe Asp Met Ala
1 5

<210> 172
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-1BB (MU137-1) CDR-H2

<400> 172

Ser Ile Ser Pro Ser Gly Asp Ile Pro Tyr Tyr Arg Asp Ser Val Lys
1 5 10 15

Gly

<210> 173
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-1BB (MU137-1) CDR-H3

<400> 173

Arg Ser Tyr Gly Gly Tyr Ser Glu Leu Asp Tyr
1 5 10

<210> 174
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-1BB (MU137-1) CDR-L1

<400> 174

Gln Ala Ser Gln Asp Ile Gly Asn Trp Leu Ala
1   5   10

<210> 175
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-1BB (MU137-1) CDR-L2

<400> 175

Gly Thr Ser Ser Leu Ala Asp
1   5

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

<220>
<223> 4-1BB (MU137-1) CDR-L3

<400> 176

Leu Gln Ala Tyr Gly Ala Pro Trp Thr
1   5

<210> 177
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-1BB (MU137-1) VH

<400> 177

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

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

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

Ala Ser Ile Ser Pro Ser Gly Asp Ile Pro Tyr Tyr Arg Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Val Ser Arg Glu Asn Ala Lys Ser Ser Leu Tyr
65                  70                  75                  80

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

Ala Arg Arg Ser Tyr Gly Gly Tyr Ser Glu Leu Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Val Met Val Thr Val Ser Ser
        115                 120
```

<210> 178
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-1BB (MU137-1) VL

<400> 178

```
Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Leu Glu
1               5                   10                  15

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

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

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


Ser Ser Ser Gly Ser Gln Tyr Ser Leu Lys Ile Ser Arg Leu Gln Val
65                  70                  75                  80


Glu Asp Ile Gly Ile Tyr Tyr Cys Leu Gln Ala Tyr Gly Ala Pro Trp
                85                  90                  95


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


<210>  179
<211>  5
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CEA (A5B7P)- CDR-H1

<400>  179

Asp Tyr Tyr Met Asn
1               5


<210>  180
<211>  19
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CEA (A5B7P)- CDR-H2

<400>  180

Phe Ile Gly Asn Lys Ala Asn Gly Tyr Thr Thr Glu Tyr Ser Ala Ser
1               5                   10                  15


Val Lys Gly
```

<210> 181
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA (A5B7P)- CDR-H3

<400> 181

Asp Arg Gly Leu Arg Phe Tyr Phe Asp Tyr
1 5 10

<210> 182
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA (A5B7P)- CDR-L1

<400> 182

Arg Ala Ser Ser Ser Val Thr Tyr Ile His
1 5 10

<210> 183
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA (A5B7P)- CDR-L2

<400> 183

Ala Thr Ser Asn Leu Ala Ser
1 5

<210> 184
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA (A5B7P)- CDR-L3

<400> 184

Gln His Trp Ser Ser Lys Pro Pro Thr
1 5

<210> 185
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA (A5B7P) VH

<400> 185

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

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

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

Gly Phe Ile Gly Asn Lys Ala Asn Gly Tyr Thr Thr Glu Tyr Ser Ala
50 55 60

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

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

Tyr Cys Thr Arg Asp Arg Gly Leu Arg Phe Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Leu Thr Val Ser Ser
115 120

<210> 186
<211> 106

<212> PRT
<213> Artificial Sequence

<220>
<223> CEA (A5B7P) VL

<400> 186

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

Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Thr Tyr Ile
            20   25   30

His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Ser Trp Ile Tyr
        35   40   45

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

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

Asp Ala Ala Thr Tyr Tyr Cys Gln His Trp Ser Ser Lys Pro Pro Thr
                85   90   95

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

<210> 187
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA (431/26)- CDR-H1

<400> 187

Ser Gly Tyr Ser Trp His
1   5

<210> 188
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA (431/26)- CDR-H2

<400> 188

Tyr Ile Gln Tyr Ser Gly Ile Thr Asn Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

<210> 189
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA (431/26)- CDR-H3

<400> 189

Glu Asp Tyr Asp Tyr His Trp Tyr Phe Asp Val
1 5 10

<210> 190
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA (431/26)- CDR-L1

<400> 190

Ser Thr Ser Ser Ser Val Ser Tyr Met His
1 5 10

<210> 191
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA (431/26)- CDR-L2

<400> 191

Ser Thr Ser Asn Leu Ala Ser
1 5

<210> 192
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA (431/26)- CDR-L3

<400> 192

His Gln Trp Ser Ser Tyr Pro Thr
1 5

<210> 193
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA (431/26) VH

<400> 193

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Thr Ile Ser Ser Gly
20 25 30

Tyr Ser Trp His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp
35 40 45

Ile Gly Tyr Ile Gln Tyr Ser Gly Ile Thr Asn Tyr Asn Pro Ser Leu
50 55 60

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

```
Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Glu Asp Tyr Asp Tyr His Trp Tyr Phe Asp Val Trp Gly Gln
            100                 105                 110


Gly Ser Leu Val Thr Val Ser Ser
        115                 120
```

<210> 194
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA (431/26) VL

<400> 194

```
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 Ser Thr Ser Ser Ser Val Ser Tyr Met
            20                  25                  30


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


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


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


Asp Ile Ala Thr Tyr Tyr Cys His Gln Trp Ser Ser Tyr Pro Thr Phe
                85                  90                  95


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

<210> 195
<211> 576
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1 (20H4.9)-Heavy chain hole-VL (A5B7P)

<400> 195

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


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


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


Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60


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


Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95


Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110


Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gly 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

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365
```

```
Leu Ser Cys Ala 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 Val 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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    450                 455                 460

Ser Gly Gly Gly Gly Ser Gln Thr Val Leu Ser Gln Ser Pro Ala Ile
465                 470                 475                 480

Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
                485                 490                 495

Ser Ser Val Thr Tyr Ile His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
            500                 505                 510

Pro Lys Ser Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro
        515                 520                 525

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
    530                 535                 540

Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Trp
545                 550                 555                 560
```

Ser Ser Lys Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
565 570 575

<210> 196
<211> 591
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1 (20H4.9)-Heavy chain knob-VH (A5B7P)

<400> 196

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

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

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

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
50 55 60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
100 105 110

Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220


Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gly 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 Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Trp 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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    450                 455                 460

Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Val Glu Ser Gly Gly Gly
465                 470                 475                 480

Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly
                485                 490                 495

Phe Thr Phe Thr Asp Tyr Tyr Met Asn Trp Val Arg Gln Pro Pro Gly
            500                 505                 510

Lys Ala Leu Glu Trp Leu Gly Phe Ile Gly Asn Lys Ala Asn Gly Tyr
        515                 520                 525

Thr Thr Glu Tyr Ser Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
    530                 535                 540
```

```
Asp Lys Ser Gln Ser Ile Leu Tyr Leu Gln Met Asn Thr Leu Arg Ala
545                 550                 555                 560


Glu Asp Ser Ala Thr Tyr Tyr Cys Thr Arg Asp Arg Gly Leu Arg Phe
                565                 570                 575


Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
            580                 585                 590


<210>  197
<211>  591
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  VHCH1 (20H4.9)-Heavy chain hole-VH (A5B7P)

<400>  197

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


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


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


Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60


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


Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95


Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110
```

```
Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gly 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

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Ser Cys Ala 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 Val 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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    450                 455                 460

Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Val Glu Ser Gly Gly Gly
465                 470                 475                 480

Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly
                485                 490                 495

Phe Thr Phe Thr Asp Tyr Tyr Met Asn Trp Val Arg Gln Pro Pro Gly
            500                 505                 510
```

```
Lys Ala Leu Glu Trp Leu Gly Phe Ile Gly Asn Lys Ala Asn Gly Tyr
        515                 520                 525

Thr Thr Glu Tyr Ser Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
    530                 535                 540

Asp Lys Ser Gln Ser Ile Leu Tyr Leu Gln Met Asn Thr Leu Arg Ala
545                 550                 555                 560

Glu Asp Ser Ala Thr Tyr Tyr Cys Thr Arg Asp Arg Gly Leu Arg Phe
                565                 570                 575

Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
            580                 585                 590
```

<210> 198
<211> 576
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1 (20H4.9)-Heavy chain knob-VL (A5B7P)

<400> 198

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

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

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

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60

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

```
Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110

Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gly 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 Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Trp 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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    450                 455                 460

Ser Gly Gly Gly Gly Ser Gln Thr Val Leu Ser Gln Ser Pro Ala Ile
465                 470                 475                 480
```

```
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
                485                 490                 495


Ser Ser Val Thr Tyr Ile His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
            500                 505                 510


Pro Lys Ser Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro
        515                 520                 525


Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
    530                 535                 540


Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Trp
545                 550                 555                 560


Ser Ser Lys Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
                565                 570                 575


<210>  199
<211>  575
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  VHCH1 (20H4.9)-Heavy chain hole-VL (431/26)

<400>  199

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


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


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


Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60
```

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110

Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gly 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

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Ser Cys Ala 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 Val 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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    450                 455                 460
```

```
Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
465                 470                 475                 480


Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Thr Ser
                485                 490                 495


Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala
            500                 505                 510


Pro Lys Leu Leu Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro
        515                 520                 525


Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile
    530                 535                 540


Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys His Gln Trp
545                 550                 555                 560


Ser Ser Tyr Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
                565                 570                 575


<210>  200
<211>  590
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  VHCH1 (20H4.9)-Heavy chain knob-VH (431/26)

<400>  200

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


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


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

```
Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110

Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gly 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 Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Trp 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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    450                 455                 460

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly
465                 470                 475                 480

Leu Val Arg Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly
                485                 490                 495

Phe Thr Ile Ser Ser Gly Tyr Ser Trp His Trp Val Arg Gln Pro Pro
            500                 505                 510

Gly Arg Gly Leu Glu Trp Ile Gly Tyr Ile Gln Tyr Ser Gly Ile Thr
        515                 520                 525

Asn Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Met Leu Val Asp Thr
    530                 535                 540

Ser Lys Asn Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp
545                 550                 555                 560

Thr Ala Val Tyr Tyr Cys Ala Arg Glu Asp Tyr Asp Tyr His Trp Tyr
                565                 570                 575

Phe Asp Val Trp Gly Gln Gly Ser Leu Val Thr Val Ser Ser
            580                 585                 590
```

<210> 201
<211> 590
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1 (20H4.9)-Heavy chain hole-VH (431/26)

<400> 201

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

```
Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr
            20                  25                  30

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

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110

Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220
```

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gly 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

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Ser Cys Ala 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 Val 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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    450                 455                 460

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly
465                 470                 475                 480

Leu Val Arg Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly
                485                 490                 495

Phe Thr Ile Ser Ser Gly Tyr Ser Trp His Trp Val Arg Gln Pro Pro
            500                 505                 510

Gly Arg Gly Leu Glu Trp Ile Gly Tyr Ile Gln Tyr Ser Gly Ile Thr
        515                 520                 525

Asn Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Met Leu Val Asp Thr
    530                 535                 540

Ser Lys Asn Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp
545                 550                 555                 560

Thr Ala Val Tyr Tyr Cys Ala Arg Glu Asp Tyr Asp Tyr His Trp Tyr
                565                 570                 575

Phe Asp Val Trp Gly Gln Gly Ser Leu Val Thr Val Ser Ser
            580                 585                 590
```

<210> 202
<211> 575
<212> PRT
<213> Artificial Sequence

<220>

<223> VHCH1 (20H4.9)-Heavy chain knob-VL (431/26)

<400> 202

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


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


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


Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60


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


Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95


Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110


Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gly 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 Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Trp 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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    450                 455                 460


Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
465                 470                 475                 480


Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Thr Ser
                485                 490                 495


Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala
            500                 505                 510


Pro Lys Leu Leu Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro
        515                 520                 525


Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile
    530                 535                 540


Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys His Gln Trp
545                 550                 555                 560


Ser Ser Tyr Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
                565                 570                 575


<210>  203
<211>  811
```

<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1-VHCH1 (20H4.9)-Heavy chain hole-VL (A5B7P)

<400> 203

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


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


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


Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60


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


Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95


Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110


Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
225                 230                 235                 240

Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr
                245                 250                 255

Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Ser Trp Ile
            260                 265                 270

Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His
        275                 280                 285

Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu Ser Arg Val Thr Ile
    290                 295                 300

Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val
305                 310                 315                 320

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Tyr Gly Pro
                325                 330                 335

Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val
            340                 345                 350

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
        355                 360                 365
```

```
Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
    370                 375                 380

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
385                 390                 395                 400

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
                405                 410                 415

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
            420                 425                 430

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        435                 440                 445

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    450                 455                 460

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
465                 470                 475                 480

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                485                 490                 495

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            500                 505                 510

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        515                 520                 525

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    530                 535                 540

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
545                 550                 555                 560

Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
                565                 570                 575
```

```
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro
            580                 585                 590

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val
        595                 600                 605

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    610                 615                 620

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
625                 630                 635                 640

Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                645                 650                 655

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            660                 665                 670

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly
        675                 680                 685

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    690                 695                 700

Ser Gln Thr Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro
705                 710                 715                 720

Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Thr Tyr
                725                 730                 735

Ile His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Ser Trp Ile
            740                 745                 750

Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly
        755                 760                 765
```

```
Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala
    770                 775                 780

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Trp Ser Ser Lys Pro Pro
785                 790                 795                 800

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
                805                 810
```

<210> 204
<211> 826
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1-VHCH1 (20H4.9)-Heavy chain knob-VH (A5B7P)

<400> 204

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

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

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

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110
```

```
Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
225                 230                 235                 240

Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr
                245                 250                 255

Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Ser Trp Ile
            260                 265                 270

Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His
        275                 280                 285

Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu Ser Arg Val Thr Ile
    290                 295                 300

Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val
305                 310                 315                 320
```

```
Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Tyr Gly Pro
                325                 330                 335

Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val
            340                 345                 350

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
        355                 360                 365

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
    370                 375                 380

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
385                 390                 395                 400

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
                405                 410                 415

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
            420                 425                 430

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        435                 440                 445

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    450                 455                 460

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
465                 470                 475                 480

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                485                 490                 495

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            500                 505                 510
```

```
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        515                 520                 525

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    530                 535                 540

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
545                 550                 555                 560

Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
                565                 570                 575

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            580                 585                 590

Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val
        595                 600                 605

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    610                 615                 620

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
625                 630                 635                 640

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                645                 650                 655

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            660                 665                 670

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly
        675                 680                 685

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    690                 695                 700

Ser Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
705                 710                 715                 720
```

```
Gly Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Thr Asp
                725                 730                 735


Tyr Tyr Met Asn Trp Val Arg Gln Pro Pro Gly Lys Ala Leu Glu Trp
            740                 745                 750


Leu Gly Phe Ile Gly Asn Lys Ala Asn Gly Tyr Thr Thr Glu Tyr Ser
        755                 760                 765


Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Lys Ser Gln Ser
    770                 775                 780


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


Tyr Tyr Cys Thr Arg Asp Arg Gly Leu Arg Phe Tyr Phe Asp Tyr Trp
                805                 810                 815


Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
            820                 825


<210>  205
<211>  826
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  VHCH1-VHCH1 (20H4.9)-Heavy chain hole-VH (A5B7P)

<400>  205

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


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


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

```
Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110

Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
225                 230                 235                 240
```

```
Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr
                245                 250                 255

Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Ser Trp Ile
            260                 265                 270

Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His
        275                 280                 285

Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu Ser Arg Val Thr Ile
    290                 295                 300

Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val
305                 310                 315                 320

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Tyr Gly Pro
                325                 330                 335

Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val
            340                 345                 350

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
        355                 360                 365

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
    370                 375                 380

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
385                 390                 395                 400

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
                405                 410                 415

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
            420                 425                 430

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        435                 440                 445
```

```
Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    450                 455                 460

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
465                 470                 475                 480

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                485                 490                 495

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            500                 505                 510

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        515                 520                 525

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    530                 535                 540

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
545                 550                 555                 560

Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
                565                 570                 575

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro
            580                 585                 590

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val
        595                 600                 605

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    610                 615                 620

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
625                 630                 635                 640
```

```
Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                645                 650                 655

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            660                 665                 670

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly
        675                 680                 685

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    690                 695                 700

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

Gly Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Thr Asp
                725                 730                 735

Tyr Tyr Met Asn Trp Val Arg Gln Pro Pro Gly Lys Ala Leu Glu Trp
            740                 745                 750

Leu Gly Phe Ile Gly Asn Lys Ala Asn Gly Tyr Thr Thr Glu Tyr Ser
        755                 760                 765

Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Lys Ser Gln Ser
    770                 775                 780

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

Tyr Tyr Cys Thr Arg Asp Arg Gly Leu Arg Phe Tyr Phe Asp Tyr Trp
                805                 810                 815

Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
            820                 825
```

<210> 206
<211> 811

<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1-VHCH1 (20H4.9)-Heavy chain knob-VL (A5B7 P)

<400> 206

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


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


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


Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60


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


Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95


Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110


Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
225                 230                 235                 240

Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr
                245                 250                 255

Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Ser Trp Ile
            260                 265                 270

Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His
        275                 280                 285

Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu Ser Arg Val Thr Ile
    290                 295                 300

Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val
305                 310                 315                 320

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Tyr Gly Pro
                325                 330                 335

Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val
            340                 345                 350

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
        355                 360                 365
```

```
Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
    370                 375                 380

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
385                 390                 395                 400

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
                405                 410                 415

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
            420                 425                 430

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        435                 440                 445

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    450                 455                 460

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
465                 470                 475                 480

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                485                 490                 495

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            500                 505                 510

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        515                 520                 525

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    530                 535                 540

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
545                 550                 555                 560

Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
                565                 570                 575
```

```
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            580                 585                 590

Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val
        595                 600                 605

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    610                 615                 620

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
625                 630                 635                 640

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                645                 650                 655

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            660                 665                 670

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly
        675                 680                 685

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    690                 695                 700

Ser Gln Thr Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro
705                 710                 715                 720

Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Thr Tyr
                725                 730                 735

Ile His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Ser Trp Ile
            740                 745                 750

Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly
        755                 760                 765
```

```
Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala
    770                 775                 780

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Trp Ser Ser Lys Pro Pro
785                 790                 795                 800

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
                805                 810
```

<210> 207
<211> 810
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1-VHCH1 (20H4.9)-Heavy chain hole-VL (431/26)

<400> 207

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

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

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

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110
```

```
Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
225                 230                 235                 240

Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr
                245                 250                 255

Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Ser Trp Ile
            260                 265                 270

Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His
        275                 280                 285

Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu Ser Arg Val Thr Ile
    290                 295                 300

Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val
305                 310                 315                 320
```

```
Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Tyr Gly Pro
                325                 330                 335

Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val
            340                 345                 350

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
        355                 360                 365

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
    370                 375                 380

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
385                 390                 395                 400

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
                405                 410                 415

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
            420                 425                 430

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        435                 440                 445

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    450                 455                 460

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
465                 470                 475                 480

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                485                 490                 495

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            500                 505                 510
```

```
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        515                 520                 525

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    530                 535                 540

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
545                 550                 555                 560

Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
                565                 570                 575

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro
            580                 585                 590

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val
        595                 600                 605

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    610                 615                 620

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
625                 630                 635                 640

Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                645                 650                 655

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            660                 665                 670

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly
        675                 680                 685

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    690                 695                 700

Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
705                 710                 715                 720
```

```
Gly Asp Arg Val Thr Ile Thr Cys Ser Thr Ser Ser Ser Val Ser Tyr
                725                 730                 735


Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
            740                 745                 750


Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
        755                 760                 765


Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
    770                 775                 780


Glu Asp Ile Ala Thr Tyr Tyr Cys His Gln Trp Ser Ser Tyr Pro Thr
785                 790                 795                 800


Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
                805                 810
```

<210> 208
<211> 825
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1-VHCH1 (20H4.9)-Heavy chain knob-VH (431/26)

<400> 208

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


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


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


Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60
```

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110

Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
225                 230                 235                 240

Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr
                245                 250                 255
```

```
Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Ser Trp Ile
            260                 265                 270

Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His
        275                 280                 285

Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu Ser Arg Val Thr Ile
    290                 295                 300

Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val
305                 310                 315                 320

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Tyr Gly Pro
                325                 330                 335

Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val
            340                 345                 350

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
        355                 360                 365

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
    370                 375                 380

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
385                 390                 395                 400

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
                405                 410                 415

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
            420                 425                 430

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        435                 440                 445

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    450                 455                 460
```

```
Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
465                 470                 475                 480

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                485                 490                 495

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            500                 505                 510

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        515                 520                 525

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    530                 535                 540

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
545                 550                 555                 560

Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
                565                 570                 575

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            580                 585                 590

Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val
        595                 600                 605

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    610                 615                 620

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
625                 630                 635                 640

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                645                 650                 655
```

```
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            660                 665                 670

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly
        675                 680                 685

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    690                 695                 700

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

Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Thr Ile Ser Ser
                725                 730                 735

Gly Tyr Ser Trp His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu
            740                 745                 750

Trp Ile Gly Tyr Ile Gln Tyr Ser Gly Ile Thr Asn Tyr Asn Pro Ser
        755                 760                 765

Leu Lys Ser Arg Val Thr Met Leu Val Asp Thr Ser Lys Asn Gln Phe
    770                 775                 780

Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
785                 790                 795                 800

Cys Ala Arg Glu Asp Tyr Asp Tyr His Trp Tyr Phe Asp Val Trp Gly
                805                 810                 815

Gln Gly Ser Leu Val Thr Val Ser Ser
            820                 825
```

<210> 209
<211> 825
<212> PRT
<213> Artificial Sequence

<220>

<223> VHCH1-VHCH1 (20H4.9)-Heavy chain hole-VH (431/26)

<400> 209

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


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


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


Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60


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


Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95


Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110


Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
225                 230                 235                 240

Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr
                245                 250                 255

Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Ser Trp Ile
            260                 265                 270

Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His
        275                 280                 285

Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu Ser Arg Val Thr Ile
    290                 295                 300

Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val
305                 310                 315                 320

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Tyr Gly Pro
                325                 330                 335

Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val
            340                 345                 350

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
        355                 360                 365

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
    370                 375                 380
```

```
Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
385                 390                 395                 400


Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
                405                 410                 415


Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
            420                 425                 430


Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        435                 440                 445


Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    450                 455                 460


Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
465                 470                 475                 480


Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                485                 490                 495


Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            500                 505                 510


Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        515                 520                 525


Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    530                 535                 540


Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
545                 550                 555                 560


Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
                565                 570                 575


Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro
            580                 585                 590
```

```
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val
        595                 600                 605

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    610                 615                 620

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
625                 630                 635                 640

Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                645                 650                 655

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            660                 665                 670

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly
        675                 680                 685

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    690                 695                 700

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

Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Thr Ile Ser Ser
                725                 730                 735

Gly Tyr Ser Trp His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu
            740                 745                 750

Trp Ile Gly Tyr Ile Gln Tyr Ser Gly Ile Thr Asn Tyr Asn Pro Ser
        755                 760                 765

Leu Lys Ser Arg Val Thr Met Leu Val Asp Thr Ser Lys Asn Gln Phe
    770                 775                 780
```

```
Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
785                 790                 795                 800


Cys Ala Arg Glu Asp Tyr Asp Tyr His Trp Tyr Phe Asp Val Trp Gly
                805                 810                 815


Gln Gly Ser Leu Val Thr Val Ser Ser
            820                 825


<210>  210
<211>  810
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  VHCH1-VHCH1 (20H4.9)-Heavy chain knob-VL (431/26)

<400>  210

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


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


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


Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60


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


Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95


Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110
```

```
Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
225                 230                 235                 240

Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr
                245                 250                 255

Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Ser Trp Ile
            260                 265                 270

Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His
        275                 280                 285

Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu Ser Arg Val Thr Ile
    290                 295                 300

Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val
305                 310                 315                 320
```

```
Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Tyr Gly Pro
                325                 330                 335

Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val
            340                 345                 350

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
        355                 360                 365

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
    370                 375                 380

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
385                 390                 395                 400

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
                405                 410                 415

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
            420                 425                 430

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        435                 440                 445

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    450                 455                 460

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
465                 470                 475                 480

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                485                 490                 495

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            500                 505                 510
```

```
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        515                 520                 525

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    530                 535                 540

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
545                 550                 555                 560

Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
                565                 570                 575

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            580                 585                 590

Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val
        595                 600                 605

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    610                 615                 620

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
625                 630                 635                 640

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                645                 650                 655

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            660                 665                 670

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly
        675                 680                 685

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    690                 695                 700

Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
705                 710                 715                 720
```

```
Gly Asp Arg Val Thr Ile Thr Cys Ser Thr Ser Ser Ser Val Ser Tyr
                725                 730                 735


Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
            740                 745                 750


Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
        755                 760                 765


Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
    770                 775                 780


Glu Asp Ile Ala Thr Tyr Tyr Cys His Gln Trp Ser Ser Tyr Pro Thr
785                 790                 795                 800


Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
                805                 810


<210>  211
<211>  698
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  VHCH1 (20H4.9)-Heavy chain knob-VHCL (A5B7P)

<400>  211

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


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


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


Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60
```

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110

Arg Gly Thr Leu 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 Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gly 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 Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Trp 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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    450                 455                 460
```

```
Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Val Glu Ser Gly Gly Gly
465                 470                 475                 480

Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly
                485                 490                 495

Phe Thr Phe Thr Asp Tyr Tyr Met Asn Trp Val Arg Gln Pro Pro Gly
            500                 505                 510

Lys Ala Leu Glu Trp Leu Gly Phe Ile Gly Asn Lys Ala Asn Gly Tyr
        515                 520                 525

Thr Thr Glu Tyr Ser Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
    530                 535                 540

Asp Lys Ser Gln Ser Ile Leu Tyr Leu Gln Met Asn Thr Leu Arg Ala
545                 550                 555                 560

Glu Asp Ser Ala Thr Tyr Tyr Cys Thr Arg Asp Arg Gly Leu Arg Phe
                565                 570                 575

Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala
            580                 585                 590

Ser Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
        595                 600                 605

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
    610                 615                 620

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
625                 630                 635                 640

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
                645                 650                 655
```

```
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
            660                 665                 670


His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
        675                 680                 685


Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    690                 695


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

<220>
<223>  VHCH1 (20H4.9)-Heavy chain hole

<400>  212

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


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


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


Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60


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


Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95


Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110
```

```
Arg Gly Thr Leu 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 Glu 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 Glu Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gly 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


Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365


Leu Ser Cys Ala 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 Val 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> 213
<211> 211
<212> PRT
<213> Artificial Sequence

<220>
<223> VLCH1-Light chain (A5B7P)

<400> 213

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

```
Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Thr Tyr Ile
            20                  25                  30

His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Ser Trp Ile Tyr
        35                  40                  45

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

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

Asp Ala Ala Thr Tyr Tyr Cys Gln His Trp Ser Ser Lys Pro Pro Thr
                85                  90                  95

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

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
        115                 120                 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
    130                 135                 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
145                 150                 155                 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
                165                 170                 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
            180                 185                 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
        195                 200                 205
```

Lys Ser Cys
    210

<210> 214
<211> 681
<212> PRT
<213> Artificial Sequence

<220>
<223> VHCH1 (20H4.9)-Heavy chain knob-VLCH (A5B7P)

<400> 214

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

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

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

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50   55   60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85   90   95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100   105   110

Arg Gly Thr Leu 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 Glu 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 Glu Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gly 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 Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Trp 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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    450                 455                 460

Ser Gly Gly Gly Gly Ser Gln Thr Val Leu Ser Gln Ser Pro Ala Ile
465                 470                 475                 480

Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
                485                 490                 495

Ser Ser Val Thr Tyr Ile His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
            500                 505                 510

Pro Lys Ser Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro
        515                 520                 525

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
    530                 535                 540
```

```
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Trp
545                 550                 555                 560


Ser Ser Lys Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
                565                 570                 575


Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
            580                 585                 590


Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
        595                 600                 605


Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
    610                 615                 620


Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
625                 630                 635                 640


Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
                645                 650                 655


Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
            660                 665                 670


Asp Lys Lys Val Glu Pro Lys Ser Cys
        675                 680


<210>  215
<211>  451
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  VHCH1 (20H4.9)-Heavy chain hole

<400>  215

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

```
Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr
            20                  25                  30

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

Gly Glu Ile Asn His Gly Gly Tyr Val Thr Tyr Asn Pro Ser Leu Glu
    50                  55                  60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110

Arg Gly Thr Leu 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 Glu 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 Glu Lys Val Glu Pro Lys Ser Cys
    210                 215                 220
```

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gly 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

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Ser Cys Ala 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 Val 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> 216
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> VLCL-Light chain (20H4.9) (RK mutations)

<400> 216

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


Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
            20                  25                  30


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


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


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


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


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

```
Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Arg Lys 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>  217
<211>  228
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  VHCL-Light chain (A5B7P)

<400>  217

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


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


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

```
Gly Phe Ile Gly Asn Lys Ala Asn Gly Tyr Thr Thr Glu Tyr Ser Ala
    50                  55                  60

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

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

Tyr Cys Thr Arg Asp Arg Gly Leu Arg Phe Tyr Phe Asp Tyr Trp Gly
            100                 105                 110

Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Val Ala Ala Pro Ser
        115                 120                 125

Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala
    130                 135                 140

Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val
145                 150                 155                 160

Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser
                165                 170                 175

Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr
            180                 185                 190

Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys
        195                 200                 205

Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn
    210                 215                 220

Arg Gly Glu Cys
225
```