SEQUENCE LISTING

<110> ONCOMED PHARMACEUTICALS, INC.
GURNEY, Austin L.
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<120> RSPO3 BINDING AGENTS AND USES THEREOF

<130> 2293.093PC04/PAC/KBK

<140> To be assigned
<141> Herewith

<150> US 61/826,747
<151> 2013-05-23

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<160> 95

<170> PatentIn version 3.5

<210> 1
<211> 263
<212> PRT
<213> Homo sapiens

<400> 1

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Met Arg Leu Gly Leu Cys Val Val Ala Leu Val Leu Ser Trp Thr His
1               5                  10                  15

Leu Thr Ile Ser Ser Arg Gly Ile Lys Gly Lys Arg Gln Arg Arg Ile
            20                  25                  30

Ser Ala Glu Gly Ser Gln Ala Cys Ala Lys Gly Cys Glu Leu Cys Ser
        35                  40                  45

Glu Val Asn Gly Cys Leu Lys Cys Ser Pro Lys Leu Phe Ile Leu Leu
    50                  55                  60

Glu Arg Asn Asp Ile Arg Gln Val Gly Val Cys Leu Pro Ser Cys Pro
65                  70                  75                  80

Pro Gly Tyr Phe Asp Ala Arg Asn Pro Asp Met Asn Lys Cys Ile Lys
                85                  90                  95

Cys Lys Ile Glu His Cys Glu Ala Cys Phe Ser His Asn Phe Cys Thr
            100                 105                 110

Lys Cys Lys Glu Gly Leu Tyr Leu His Lys Gly Arg Cys Tyr Pro Ala
        115                 120                 125
```

```
Cys Pro Glu Gly Ser Ser Ala Ala Asn Gly Thr Met Glu Cys Ser Ser
    130                 135                 140

Pro Ala Gln Cys Glu Met Ser Glu Trp Ser Pro Trp Gly Pro Cys Ser
145                 150                 155                 160

Lys Lys Gln Gln Leu Cys Gly Phe Arg Arg Gly Ser Glu Glu Arg Thr
                165                 170                 175

Arg Arg Val Leu His Ala Pro Val Gly Asp His Ala Ala Cys Ser Asp
            180                 185                 190

Thr Lys Glu Thr Arg Arg Cys Thr Val Arg Arg Val Pro Cys Pro Glu
        195                 200                 205

Gly Gln Lys Arg Arg Lys Gly Gly Gln Gly Arg Arg Glu Asn Ala Asn
    210                 215                 220

Arg Asn Leu Ala Arg Lys Glu Ser Lys Glu Ala Gly Ala Gly Ser Arg
225                 230                 235                 240

Arg Arg Lys Gly Gln Gln Gln Gln Gln Gln Gln Gly Thr Val Gly Pro
                245                 250                 255

Leu Thr Ser Ala Gly Pro Ala
            260
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<210> 2
<211> 243
<212> PRT
<213> Homo sapiens

<400> 2

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Met Gln Phe Arg Leu Phe Ser Phe Ala Leu Ile Ile Leu Asn Cys Met
1               5                   10                  15

Asp Tyr Ser His Cys Gln Gly Asn Arg Trp Arg Arg Ser Lys Arg Ala
            20                  25                  30

Ser Tyr Val Ser Asn Pro Ile Cys Lys Gly Cys Leu Ser Cys Ser Lys
        35                  40                  45

Asp Asn Gly Cys Ser Arg Cys Gln Gln Lys Leu Phe Phe Phe Leu Arg
    50                  55                  60

Arg Glu Gly Met Arg Gln Tyr Gly Glu Cys Leu His Ser Cys Pro Ser
65                  70                  75                  80

Gly Tyr Tyr Gly His Arg Ala Pro Asp Met Asn Arg Cys Ala Arg Cys
                85                  90                  95

Arg Ile Glu Asn Cys Asp Ser Cys Phe Ser Lys Asp Phe Cys Thr Lys
```

100 105 110

Cys Lys Val Gly Phe Tyr Leu His Arg Gly Arg Cys Phe Asp Glu Cys
115 120 125

Pro Asp Gly Phe Ala Pro Leu Glu Glu Thr Met Glu Cys Val Glu Gly
130 135 140

Cys Glu Val Gly His Trp Ser Glu Trp Gly Thr Cys Ser Arg Asn Asn
145 150 155 160

Arg Thr Cys Gly Phe Lys Trp Gly Leu Glu Thr Arg Thr Arg Gln Ile
165 170 175

Val Lys Lys Pro Val Lys Asp Thr Ile Pro Cys Pro Thr Ile Ala Glu
180 185 190

Ser Arg Arg Cys Lys Met Thr Met Arg His Cys Pro Gly Gly Lys Arg
195 200 205

Thr Pro Lys Ala Lys Glu Lys Arg Asn Lys Lys Lys Lys Arg Lys Leu
210 215 220

Ile Glu Arg Ala Gln Glu Gln His Ser Val Phe Leu Ala Thr Asp Arg
225 230 235 240

Ala Asn Gln

<210> 3
<211> 272
<212> PRT
<213> Homo sapiens

<400> 3

Met His Leu Arg Leu Ile Ser Trp Leu Phe Ile Ile Leu Asn Phe Met
1 5 10 15

Glu Tyr Ile Gly Ser Gln Asn Ala Ser Arg Gly Arg Arg Gln Arg Arg
20 25 30

Met His Pro Asn Val Ser Gln Gly Cys Gln Gly Gly Cys Ala Thr Cys
35 40 45

Ser Asp Tyr Asn Gly Cys Leu Ser Cys Lys Pro Arg Leu Phe Phe Ala
50 55 60

Leu Glu Arg Ile Gly Met Lys Gln Ile Gly Val Cys Leu Ser Ser Cys
65 70 75 80

Pro Ser Gly Tyr Tyr Gly Thr Arg Tyr Pro Asp Ile Asn Lys Cys Thr
85 90 95

```
Lys Cys Lys Ala Asp Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys Thr
            100                 105                 110

Lys Cys Lys Ser Gly Phe Tyr Leu His Leu Gly Lys Cys Leu Asp Asn
        115                 120                 125

Cys Pro Glu Gly Leu Glu Ala Asn Asn His Thr Met Glu Cys Val Ser
    130                 135                 140

Ile Val His Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro Cys Thr
145                 150                 155                 160

Lys Lys Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg Val
                165                 170                 175

Arg Glu Ile Ile Gln His Pro Ser Ala Lys Gly Asn Leu Cys Pro Pro
            180                 185                 190

Thr Asn Glu Thr Arg Lys Cys Thr Val Gln Arg Lys Lys Cys Gln Lys
        195                 200                 205

Gly Glu Arg Gly Lys Lys Gly Arg Glu Arg Lys Arg Lys Lys Pro Asn
    210                 215                 220

Lys Gly Glu Ser Lys Glu Ala Ile Pro Asp Ser Lys Ser Leu Glu Ser
225                 230                 235                 240

Ser Lys Glu Ile Pro Glu Gln Arg Glu Asn Lys Gln Gln Gln Lys Lys
                245                 250                 255

Arg Lys Val Gln Asp Lys Gln Lys Ser Val Ser Val Ser Thr Val His
            260                 265                 270
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<210> 4
<211> 272
<212> PRT
<213> Homo sapiens

<400> 4

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Met His Leu Arg Leu Ile Ser Trp Leu Phe Ile Ile Leu Asn Phe Met
1               5                   10                  15

Glu Tyr Ile Gly Ser Gln Asn Ala Ser Arg Gly Arg Arg Gln Arg Arg
            20                  25                  30

Met His Pro Asn Val Ser Gln Gly Cys Gln Gly Gly Cys Ala Thr Cys
        35                  40                  45

Ser Asp Tyr Asn Gly Cys Leu Ser Cys Lys Pro Arg Leu Phe Phe Ala
    50                  55                  60
```

```
Leu Glu Arg Ile Gly Met Lys Gln Ile Gly Val Cys Leu Ser Ser Cys
65                  70                  75                  80

Pro Ser Gly Tyr Tyr Gly Thr Arg Tyr Pro Asp Ile Asn Lys Cys Thr
                85                  90                  95

Lys Cys Lys Ala Asp Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys Thr
            100                 105                 110

Lys Cys Lys Ser Gly Phe Tyr Leu His Leu Gly Lys Cys Leu Asp Asn
        115                 120                 125

Cys Pro Glu Gly Leu Glu Ala Asn Asn His Thr Met Glu Cys Val Ser
    130                 135                 140

Ile Val His Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro Cys Thr
145                 150                 155                 160

Lys Lys Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg Val
                165                 170                 175

Arg Glu Ile Ile Gln His Pro Ser Ala Lys Gly Asn Leu Cys Pro Pro
            180                 185                 190

Thr Asn Glu Thr Arg Lys Cys Thr Val Gln Arg Lys Lys Cys Gln Lys
        195                 200                 205

Gly Glu Arg Gly Lys Lys Gly Arg Glu Arg Lys Arg Lys Lys Pro Asn
    210                 215                 220

Lys Gly Glu Ser Lys Glu Ala Ile Pro Asp Ser Lys Ser Leu Glu Ser
225                 230                 235                 240

Ser Lys Glu Ile Pro Glu Gln Arg Glu Asn Lys Gln Gln Gln Lys Lys
                245                 250                 255

Arg Lys Val Gln Asp Lys Gln Lys Ser Val Ser Val Ser Thr Val His
            260                 265                 270
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<210> 5
<211> 251
<212> PRT
<213> Homo sapiens

<400> 5

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Gln Asn Ala Ser Arg Gly Arg Arg Gln Arg Arg Met His Pro Asn Val
1               5                   10                  15

Ser Gln Gly Cys Gln Gly Gly Cys Ala Thr Cys Ser Asp Tyr Asn Gly
            20                  25                  30
```

```
Cys Leu Ser Cys Lys Pro Arg Leu Phe Phe Ala Leu Glu Arg Ile Gly
        35                  40                  45

Met Lys Gln Ile Gly Val Cys Leu Ser Ser Cys Pro Ser Gly Tyr Tyr
    50                  55                  60

Gly Thr Arg Tyr Pro Asp Ile Asn Lys Cys Thr Lys Cys Lys Ala Asp
65                  70                  75                  80

Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys Thr Lys Cys Lys Ser Gly
                85                  90                  95

Phe Tyr Leu His Leu Gly Lys Cys Leu Asp Asn Cys Pro Glu Gly Leu
            100                 105                 110

Glu Ala Asn Asn His Thr Met Glu Cys Val Ser Ile Val His Cys Glu
        115                 120                 125

Val Ser Glu Trp Asn Pro Trp Ser Pro Cys Thr Lys Lys Gly Lys Thr
    130                 135                 140

Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg Val Arg Glu Ile Ile Gln
145                 150                 155                 160

His Pro Ser Ala Lys Gly Asn Leu Cys Pro Pro Thr Asn Glu Thr Arg
                165                 170                 175

Lys Cys Thr Val Gln Arg Lys Lys Cys Gln Lys Gly Glu Arg Gly Lys
            180                 185                 190

Lys Gly Arg Glu Arg Lys Arg Lys Lys Pro Asn Lys Gly Glu Ser Lys
        195                 200                 205

Glu Ala Ile Pro Asp Ser Lys Ser Leu Glu Ser Ser Lys Glu Ile Pro
    210                 215                 220

Glu Gln Arg Glu Asn Lys Gln Gln Gln Lys Lys Arg Lys Val Gln Asp
225                 230                 235                 240

Lys Gln Lys Ser Val Ser Val Ser Thr Val His
                245                 250
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<210> 6
<211> 52
<212> PRT
<213> Homo sapiens

<400> 6

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

Tyr Asn Gly Cys Leu Ser Cys Lys Pro Arg Leu Phe Phe Ala Leu Glu
```

20 25 30

Arg Ile Gly Met Lys Gln Ile Gly Val Cys Leu Ser Ser Cys Pro Ser
35 40 45

Gly Tyr Tyr Gly
50

<210> 7
<211> 44
<212> PRT
<213> Homo sapiens

<400> 7

Ile Asn Lys Cys Thr Lys Cys Lys Ala Asp Cys Asp Thr Cys Phe Asn
1 5 10 15

Lys Asn Phe Cys Thr Lys Cys Lys Ser Gly Phe Tyr Leu His Leu Gly
20 25 30

Lys Cys Leu Asp Asn Cys Pro Glu Gly Leu Glu Ala
35 40

<210> 8
<211> 61
<212> PRT
<213> Homo sapiens

<400> 8

His Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro Cys Thr Lys Lys
1 5 10 15

Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg Val Arg Glu
20 25 30

Ile Ile Gln His Pro Ser Ala Lys Gly Asn Leu Cys Pro Pro Thr Asn
35 40 45

Glu Thr Arg Lys Cys Thr Val Gln Arg Lys Lys Cys Gln
50 55 60

<210> 9
<211> 11
<212> PRT
<213> Artificial sequence

<220>
<223> 131R002/131R003 Heavy chain CDR1

<400> 9

Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Ser
1 5 10

<210> 10

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

<220>
<223> 131R002/131R003 Heavy chain CDR2

<400> 10

Ile Tyr Pro Ser Asn Gly Asp Ser
1 5

<210> 11
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> 131R002/131R003 Heavy chain CDR3

<400> 11

Ala Thr Tyr Phe Ala Asn Tyr Phe Asp Tyr
1 5 10

<210> 12
<211> 11
<212> PRT
<213> Artificial sequence

<220>
<223> 131R002/131R003 Light chain CDR1

<400> 12

Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Met
1 5 10

<210> 13
<211> 3
<212> PRT
<213> Artificial sequence

<220>
<223> 131R002/131R003 Light chain CDR2

<400> 13

Ala Ala Ser
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<210> 14
<211> 9
<212> PRT
<213> Artificial sequence

<220>
<223> 131R002/131R003 Light chain CDR3

<400> 14

Gln Gln Ser Asn Glu Asp Pro Leu Thr
1 5

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

<220>
<223> 131R002 Heavy chain variable region

<400> 15

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

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

Ser Ile His Trp Val Lys Gln Asn His Gly Lys Ser Leu Asp Trp Ile
35 40 45

Gly Tyr Ile Tyr Pro Ser Asn Gly Asp Ser Gly Tyr Asn Gln Lys Phe
50 55 60

Lys Asn Arg Ala Thr Leu Thr Val Asp Thr Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Ala Thr Tyr Phe Ala Asn Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Leu Thr Val Ser Ser Ala Ser Thr
115 120

<210> 16
<211> 120
<212> PRT
<213> Artificial sequence

<220>
<223> 131R003 Heavy chain variable region

<400> 16

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

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

Ser Ile His Trp Val Lys Gln Asn His Gly Lys Ser Leu Asp Trp Ile
35 40 45

Gly Tyr Ile Tyr Pro Ser Asn Gly Asp Ser Gly Tyr Asn Gln Lys Phe
50 55 60

Lys Asn Arg Ala Thr Leu Thr Val Asp Thr Ser Tyr Ser Thr Ala Tyr
65 70 75 80

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

Ala Thr Tyr Phe Ala Asn Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Leu Thr Val Ser Ser Ala Ser Thr
115 120

<210> 17
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> 131R002/131R003 Light chain variable region

<400> 17

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

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

Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala
50 55 60

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

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

Glu Asp Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
100 105 110

<210> 18
<211> 360
<212> DNA
<213> Artificial sequence

<220>
<223> 131R002 Heavy chain variable region nucleotide sequence

<400> 18
caggtacaat tgcaagaatc cggacccgaa cttgtgaagc ccggagcgtc agtcaagatc 60

tcgtgtaagg ccagcgggta cacctttacg gattattcga tccattgggt aaaacagaat 120

cacgggaagt cgctcgactg gattggttat atctacccgt ccaacggtga ttcgggatac 180

aaccagaagt tcaaaaatcg ggccacactt acagtggaca catcgtcgtc aactgcatat 240

ctcgaggtcc gcagactgac gtttgaggac tcagctgtct actattgcgc gacttatttc 300

gccaactact tcgattactg gggccagggg acgacactga cggtcagctc cgcgagcacc 360

<210> 19
<211> 360
<212> DNA
<213> Artificial sequence

<220>
<223> 131R003 Heavy chain variable region nucleotide sequence

<400> 19
caggtgcaac ttaaacagtc ggggcctgag ttggtcaaac caggagcctc agtaaagatt 60

agctgcaaag catcaggtta tacctttacg gattactcga tccactgggt gaagcagaac 120

cacggaaagt cactggattg gatcgggtac atctacccct cgaatggaga ttcggggtat 180

aaccaaaagt tcaaaaaccg ggccacgctg actgtggaca cgtcgtattc caccgcatat 240

ttggaagtcc gcagactcac gttcgaggac tccgcggtat actattgtgc cacatacttt 300

gcgaattact ttgactactg gggtcagggc acaacgctta ctgtctccag cgcgtcaaca 360

<210> 20
<211> 336
<212> DNA
<213> Artificial sequence

<220>
<223> 131R002/131R003 Light chain variable region nucleotide sequence

<400> 20
gacatcgtgc tcacacagag ccctgcatcg ctcgcagtat cgcttggtca gcgagcgacc 60

atttcatgca aagcgtcaca atcggtagat tacgacggag actcctacat gaactggtat 120

cagcagaaac cagggcagcc cccgaagttg ctcatctacg ccgcgtccaa tctggagtca 180

ggcattcccg ccagattcag cgggagcggg tcaggaacgg attttaccct caatatccat 240

ccggtagagg aggaagatgc ggcgacttac tattgtcagc agtcgaatga ggacccactc 300

acgttcgggg ctggaacaaa actggaactt aaacgg 336

<210> 21
<211> 462
<212> PRT
<213> Artificial sequence

<220>
<223> 131R002 Heavy chain amino acid sequence

<400> 21

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

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

```
            20                  25                  30

Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45

Thr Asp Tyr Ser Ile His Trp Val Lys Gln Asn His Gly Lys Ser Leu
    50                  55                  60

Asp Trp Ile Gly Tyr Ile Tyr Pro Ser Asn Gly Asp Ser Gly Tyr Asn
65                  70                  75                  80

Gln Lys Phe Lys Asn Arg Ala Thr Leu Thr Val Asp Thr Ser Ser Ser
                85                  90                  95

Thr Ala Tyr Leu Glu Val Arg Arg Leu Thr Phe Glu Asp Ser Ala Val
            100                 105                 110

Tyr Tyr Cys Ala Thr Tyr Phe Ala Asn Tyr Phe Asp Tyr Trp Gly Gln
        115                 120                 125

Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
    130                 135                 140

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

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

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
            180                 185                 190

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
        195                 200                 205

Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys
    210                 215                 220

Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val
225                 230                 235                 240

Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe
                245                 250                 255

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
            260                 265                 270

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
        275                 280                 285

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
```

290 295 300

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val
305 310 315 320

Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
325 330 335

Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
340 345 350

Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
355 360 365

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
370 375 380

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

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp
405 410 415

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
420 425 430

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
435 440 445

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

<210> 22
<211> 462
<212> PRT
<213> Artificial sequence

<220>
<223> 131R003 Heavy chain amino acid sequence

<400> 22

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Glu Leu Val Lys
20 25 30

Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

Thr Asp Tyr Ser Ile His Trp Val Lys Gln Asn His Gly Lys Ser Leu
50 55 60

```
Asp Trp Ile Gly Tyr Ile Tyr Pro Ser Asn Gly Asp Ser Gly Tyr Asn
65                  70                  75                  80

Gln Lys Phe Lys Asn Arg Ala Thr Leu Thr Val Asp Thr Ser Tyr Ser
                85                  90                  95

Thr Ala Tyr Leu Glu Val Arg Arg Leu Thr Phe Glu Asp Ser Ala Val
            100                 105                 110

Tyr Tyr Cys Ala Thr Tyr Phe Ala Asn Tyr Phe Asp Tyr Trp Gly Gln
        115                 120                 125

Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
    130                 135                 140

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

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

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
            180                 185                 190

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
        195                 200                 205

Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys
    210                 215                 220

Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val
225                 230                 235                 240

Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe
                245                 250                 255

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
            260                 265                 270

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
        275                 280                 285

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
    290                 295                 300

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val
305                 310                 315                 320

Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
                325                 330                 335
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```
Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
            340                 345                 350

Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
        355                 360                 365

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
    370                 375                 380

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

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp
                405                 410                 415

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
            420                 425                 430

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
        435                 440                 445

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455                 460
```

<210> 23
<211> 237
<212> PRT
<213> Artificial sequence

<220>
<223> 131R002/131R003 Light chain amino acid sequence

<400> 23

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Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

Val Leu Ser Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val
            20                  25                  30

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

Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly
    50                  55                  60

Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly
65                  70                  75                  80

Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
                85                  90                  95

Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
```

100 105 110

Gln Ser Asn Glu Asp Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu
115 120 125

Leu Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
130 135 140

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
145 150 155 160

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
165 170 175

Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
180 185 190

Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp
195 200 205

Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
210 215 220

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 24
<211> 1389
<212> DNA
<213> Artificial sequence

<220>
<223> 131R002 Heavy chain nucleotide sequence

<400> 24

atgaaacact tgtggttctt tcttttgctg gtggcagcgc ctaggtgggt gctcagccag 60

gtacaattgc aagaatccgg acccgaactt gtgaagcccg gagcgtcagt caagatctcg 120

tgtaaggcca gcgggtacac ctttacggat tattcgatcc attgggtaaa acagaatcac 180

gggaagtcgc tcgactggat tggttatatc tacccgtcca acggtgattc gggatacaac 240

cagaagttca aaaatcgggc cacacttaca gtggacacat cgtcgtcaac tgcatatctc 300

gaggtccgca gactgacgtt tgaggactca gctgtctact attgcgcgac ttatttcgcc 360

aactacttcg attactgggg ccaggggacg acactgacgg tcagctccgc gagcaccaag 420

ggcccctccg tgttccctct ggcccccttgc tcccggtcca cctctgagtc taccgccgct 480

ctgggctgcc tggtgaagga ctacttccct gagcctgtga ccgtgtcctg gaactctggc 540

gccctgacct ctggcgtgca caccttccct gccgtgctgc agtcctccgg cctgtactcc 600

ctgtcctccg tggtgaccgt gccttcctcc aacttcggca cccagaccta cacctgcaac 660

gtggaccaca agccttccaa caccaaggtg gacaagaccg tggagcggaa gtgctgcgtg 720

gagtgccctc cttgtcctgc tcctcctgtg gctggccctt ctgtgttcct gttccctcct 780

aagcctaagg acaccctgat gatctcccgg acccctgaag tgacctgcgt ggtggtggac 840

gtgtcccacg aggaccctga ggtgcagttc aattggtacg tggacggcgt ggaggtgcac 900

aacgccaaga ccaagcctcg ggaggaacag ttcaactcca ccttccgggt ggtgtctgtg 960

ctgaccgtgg tgcaccagga ctggctgaac ggcaaagaat acaagtgcaa ggtgtccaac 1020

aagggcctgc ctgcccctat cgaaaagacc atctctaaga ccaagggcca gcctcgcgag 1080

cctcaggtct acaccctgcc tcctagccgg gaggaaatga ccaagaacca ggtgtccctg 1140

acctgtctgg tgaagggctt ctacccttcc gatatcgccg tggagtggga gtctaacggc 1200

cagcctgaga acaactacaa gaccacccct cctatgctgg actccgacgg ctccttcttc 1260

ctgtactcca agctgacagt ggacaagtcc cggtggcagc agggcaacgt gttctcctgc 1320

tccgtgatgc acgaggccct gcacaaccac tacacccaga agtccctgtc cctgtctcct 1380

ggcaagtga 1389

<210> 25
<211> 1389
<212> DNA
<213> Artificial sequence

<220>
<223> 131R003 Heavy chain nucleotide sequence

<400> 25

atgaagcatc tttggttctt cctgctcttg gtggctgcgc cgaggtgggt gctcagccag 60

gtgcaactta aacagtcggg gcctgagttg gtcaaaccag gagcctcagt aaagattagc 120

tgcaaagcat caggttatac ctttacggat tactcgatcc actgggtgaa gcagaaccac 180

ggaaagtcac tggattggat cgggtacatc tacccctcga atggagattc ggggtataac 240

caaaagttca aaaaccgggc cacgctgact gtggacacgt cgtattccac cgcatatttg 300

gaagtccgca gactcacgtt cgaggactcc gcggtatact attgtgccac atactttgcg 360

aattactttg actactgggg tcagggcaca acgcttactg tctccagcgc gtcaacaaag 420

ggcccctccg tgttcctct ggccccttgc tcccggtcca cctctgagtc taccgccgct 480

ctgggctgcc tggtgaagga ctacttccct gagcctgtga ccgtgtcctg gaactctggc 540

gccctgacct ctggcgtgca caccttccct gccgtgctgc agtcctccgg cctgtactcc 600

ctgtcctccg tggtgaccgt gccttcctcc aacttcggca cccagaccta cacctgcaac 660

gtggaccaca agccttccaa caccaaggtg gacaagaccg tggagcggaa gtgctgcgtg 720

gagtgccctc cttgtcctgc tcctcctgtg gctggccctt ctgtgttcct gttccctcct 780

aagcctaagg acaccctgat gatctcccgg acccctgaag tgacctgcgt ggtggtggac 840

gtgtcccacg aggaccctga ggtgcagttc aattggtacg tggacggcgt ggaggtgcac 900

aacgccaaga ccaagcctcg ggaggaacag ttcaactcca ccttccgggt ggtgtctgtg 960

ctgaccgtgg tgcaccagga ctggctgaac ggcaaagaat acaagtgcaa ggtgtccaac 1020

aagggcctgc ctgcccctat cgaaaagacc atctctaaga ccaagggcca gcctcgcgag 1080

cctcaggtct acaccctgcc tcctagccgg gaggaaatga ccaagaacca ggtgtccctg 1140

acctgtctgg tgaagggctt ctacccttcc gatatcgccg tggagtggga gtctaacggc 1200

cagcctgaga acaactacaa gaccacccct cctatgctgg actccgacgg ctccttcttc 1260

ctgtactcca agctgacagt ggacaagtcc cggtggcagc agggcaacgt gttctcctgc 1320

tccgtgatgc acgaggccct gcacaaccac tacacccaga agtccctgtc cctgtctcct 1380

ggcaagtga 1389

<210> 26
<211> 714
<212> DNA
<213> Artificial sequence

<220>
<223> 131R002/131R003 Light chain nucleotide sequence

<400> 26

atgaagcacc tctggttctt tcttcttctg gtcgcagcgc cgagatgggt acttagcgac 60

atcgtgctca cacagagccc tgcatcgctc gcagtatcgc ttggtcagcg agcgaccatt 120

tcatgcaaag cgtcacaatc ggtagattac gacggagact cctacatgaa ctggtatcag 180

cagaaaccag ggcagccccc gaagttgctc atctacgccg cgtccaatct ggagtcaggc 240

attcccgcca gattcagcgg gagcgggtca ggaacggatt ttaccctcaa tatccatccg 300

gtagaggagg aagatgcggc gacttactat tgtcagcagt cgaatgagga cccactcacg 360

ttcggggctg gaacaaaact ggaacttaaa cggactgtgg cggctccctc agtgttcatc 420

ttccctccct ccgacgaaca attgaagtcg ggtactgcct ccgtcgtctg tttgttgaac 480

aacttttatc cgagggaagc caaggtgcag tggaaggtgg ataatgcgct gcagagcggt 540

aactcgcaag agtcagtcac agagcaagac tcgaaggatt cgacgtattc gctcagcagc 600

acattgacgc tgtcgaaggc agattacgag aaacacaagg tgtacgcgtg cgaggtcacc 660

catcagggat tgtcgtcacc cgtgacgaaa tcctttaacc gcggagaatg ctga 714

<210> 27
<211> 443
<212> PRT
<213> Artificial sequence

<220>
<223> 131R002 Heavy chain amino acid sequence

<400> 27

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

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

```
Ser Ile His Trp Val Lys Gln Asn His Gly Lys Ser Leu Asp Trp Ile
        35                  40                  45

Gly Tyr Ile Tyr Pro Ser Asn Gly Asp Ser Gly Tyr Asn Gln Lys Phe
    50                  55                  60

Lys Asn Arg Ala Thr Leu Thr Val Asp Thr Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80

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

Ala Thr Tyr Phe Ala Asn Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
            100                 105                 110

Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
        115                 120                 125

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
    130                 135                 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145                 150                 155                 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
                165                 170                 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn
            180                 185                 190

Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
        195                 200                 205

Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro
    210                 215                 220

Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro
225                 230                 235                 240

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
                245                 250                 255

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn
            260                 265                 270

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
        275                 280                 285

Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val
    290                 295                 300
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Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
305                 310                 315                 320

Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys
                325                 330                 335

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
            340                 345                 350

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
        355                 360                 365

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
    370                 375                 380

Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe
385                 390                 395                 400

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
                405                 410                 415

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
            420                 425                 430

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440
```

<210> 28
<211> 443
<212> PRT
<213> Artificial sequence

<220>
<223> 131R003 Heavy chain amino acid sequence

<400> 28

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

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

Ser Ile His Trp Val Lys Gln Asn His Gly Lys Ser Leu Asp Trp Ile
        35                  40                  45

Gly Tyr Ile Tyr Pro Ser Asn Gly Asp Ser Gly Tyr Asn Gln Lys Phe
    50                  55                  60

Lys Asn Arg Ala Thr Leu Thr Val Asp Thr Ser Tyr Ser Thr Ala Tyr
65                  70                  75                  80
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Leu Glu Val Arg Arg Leu Thr Phe Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Thr Tyr Phe Ala Asn Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
            100                 105                 110

Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
        115                 120                 125

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
    130                 135                 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145                 150                 155                 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
                165                 170                 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn
            180                 185                 190

Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
        195                 200                 205

Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro
    210                 215                 220

Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro
225                 230                 235                 240

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
                245                 250                 255

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn
            260                 265                 270

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
        275                 280                 285

Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val
    290                 295                 300

Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
305                 310                 315                 320

Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys
                325                 330                 335

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
            340                 345                 350
```

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
355 360 365

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
370 375 380

Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe
385 390 395 400

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
405 410 415

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
420 425 430

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 29
<211> 218
<212> PRT
<213> Artificial sequence

<220>
<223> 131R002/131R003 Light chain amino acid sequence

<400> 29

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

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

Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala
50 55 60

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

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

Glu Asp Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
100 105 110

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

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

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

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

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

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

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

<210> 30
<211> 1332
<212> DNA
<213> Artificial sequence

<220>
<223> 131R002 Heavy chain nucleic acid sequence

<400> 30

caggtacaat tgcaagaatc cggacccgaa cttgtgaagc ccggagcgtc agtcaagatc 60

tcgtgtaagg ccagcgggta cacctttacg gattattcga tccattgggt aaaacagaat 120

cacgggaagt cgctcgactg gattggttat atctacccgt ccaacggtga ttcgggatac 180

aaccagaagt tcaaaaatcg ggccacactt acagtggaca catcgtcgtc aactgcatat 240

ctcgaggtcc gcagactgac gtttgaggac tcagctgtct actattgcgc gacttatttc 300

gccaactact tcgattactg gggccagggg acgacactga cggtcagctc cgcgagcacc 360

aagggcccct ccgtgttccc tctggccct tgctcccggt ccacctctga gtctaccgcc 420

gctctgggct gcctggtgaa ggactacttc cctgagcctg tgaccgtgtc ctggaactct 480

ggcgccctga cctctggcgt gcacaccttc cctgccgtgc tgcagtcctc cggcctgtac 540

tccctgtcct ccgtggtgac cgtgccttcc tccaacttcg gcacccagac ctacacctgc 600

aacgtggacc acaagccttc caacaccaag gtggacaaga ccgtggagcg gaagtgctgc 660

gtggagtgcc ctccttgtcc tgctcctcct gtggctggcc cttctgtgtt cctgttccct 720

cctaagccta aggacaccct gatgatctcc cggacccctg aagtgacctg cgtggtggtg 780

gacgtgtccc acgaggaccc tgaggtgcag ttcaattggt acgtggacgg cgtggaggtg 840

cacaacgcca agaccaagcc tcgggaggaa cagttcaact ccaccttccg ggtggtgtct 900

gtgctgaccg tggtgcacca ggactggctg aacggcaaag aatacaagtg caaggtgtcc 960

aacaagggcc tgcctgcccc tatcgaaaag accatctcta agaccaaggg ccagcctcgc 1020

gagcctcagg tctacaccct gcctcctagc cgggaggaaa tgaccaagaa ccaggtgtcc 1080

ctgacctgtc tggtgaaggg cttctaccct tccgatatcg ccgtggagtg ggagtctaac 1140

ggccagcctg agaacaacta caagaccacc cctcctatgc tggactccga cggctccttc 1200

ttcctgtact ccaagctgac agtggacaag tcccggtggc agcagggcaa cgtgttctcc 1260

tgctccgtga tgcacgaggc cctgcacaac cactacaccc agaagtccct gtccctgtct 1320

cctggcaagt ga 1332

<210> 31
<211> 1332
<212> DNA
<213> Artificial sequence

<220>
<223> 131R003 Heavy chain nucleic acid sequence

<400> 31

caggtgcaac ttaaacagtc ggggcctgag ttggtcaaac caggagcctc agtaaagatt 60

agctgcaaag catcaggtta tacctttacg gattactcga tccactgggt gaagcagaac 120

cacggaaagt cactggattg gatcgggtac atctacccct cgaatggaga ttcggggtat 180

aaccaaaagt tcaaaaaccg ggccacgctg actgtggaca cgtcgtattc caccgcatat 240

ttggaagtcc gcagactcac gttcgaggac tccgcggtat actattgtgc cacatacttt 300

gcgaattact ttgactactg gggtcagggc acaacgctta ctgtctccag cgcgtcaaca 360

aagggcccct ccgtgttccc tctggccct tgctcccggt ccacctctga gtctaccgcc 420

gctctgggct gcctggtgaa ggactacttc cctgagcctg tgaccgtgtc ctggaactct 480

ggcgccctga cctctggcgt gcacaccttc cctgccgtgc tgcagtcctc cggcctgtac 540

tccctgtcct ccgtggtgac cgtgccttcc tccaacttcg gcacccagac ctacacctgc 600

aacgtggacc acaagccttc caacaccaag gtggacaaga ccgtggagcg gaagtgctgc 660

gtggagtgcc ctccttgtcc tgctcctcct gtggctggcc cttctgtgtt cctgttccct 720

cctaagccta aggacaccct gatgatctcc cggacccctg aagtgacctg cgtggtggtg 780

gacgtgtccc acgaggaccc tgaggtgcag ttcaattggt acgtggacgg cgtggaggtg 840

cacaacgcca agaccaagcc tcgggaggaa cagttcaact ccaccttccg ggtggtgtct 900

gtgctgaccg tggtgcacca ggactggctg aacggcaaag aatacaagtg caaggtgtcc 960

aacaagggcc tgcctgcccc tatcgaaaag accatctcta agaccaaggg ccagcctcgc 1020

gagcctcagg tctacaccct gcctcctagc cgggaggaaa tgaccaagaa ccaggtgtcc 1080

ctgacctgtc tggtgaaggg cttctaccct tccgatatcg ccgtggagtg ggagtctaac 1140

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ttcctgtact ccaagctgac agtggacaag tcccggtggc agcagggcaa cgtgttctcc 1260

tgctccgtga tgcacgaggc cctgcacaac cactacaccc agaagtccct gtccctgtct 1320

cctggcaagt ga 1332

<210> 32
<211> 657
<212> DNA
<213> Artificial sequence

<220>
<223> 131R002/131R003 Light chain nucleic acid sequence

<400> 32

gacatcgtgc tcacacagag ccctgcatcg ctcgcagtat cgcttggtca gcgagcgacc 60

atttcatgca aagcgtcaca atcggtagat tacgacggag actcctacat gaactggtat 120

cagcagaaac cagggcagcc cccgaagttg ctcatctacg ccgcgtccaa tctggagtca 180

ggcattcccg ccagattcag cgggagcggg tcaggaacgg attttaccct caatatccat 240

ccggtagagg aggaagatgc ggcgacttac tattgtcagc agtcgaatga ggacccactc 300

acgttcgggg ctggaacaaa actggaactt aaacggactg tggcggctcc ctcagtgttc 360

atcttccctc cctccgacga acaattgaag tcgggtactg cctccgtcgt ctgtttgttg 420

aacaactttt atccgaggga agccaaggtg cagtggaagg tggataatgc gctgcagagc 480

ggtaactcgc aagagtcagt cacagagcaa gactcgaagg attcgacgta ttcgctcagc 540

agcacattga cgctgtcgaa ggcagattac gagaaacaca aggtgtacgc gtgcgaggtc 600

acccatcagg gattgtcgtc acccgtgacg aaatccttta accgcggaga atgctga 657

<210> 33
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> FLAG Tag

<400> 33

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 34
<211> 12
<212> PRT
<213> Artificial sequence

<220>
<223> 131R003 Heavy chain CDR1 variant

<400> 34

Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Thr Phe
1 5 10

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

<220>
<223> 131R003 Heavy chain CDR3 variant

<400> 35

Ala Thr Tyr Phe Ala Asn Asn Phe Asp Tyr
1 5 10

<210> 36
<211> 117
<212> PRT
<213> Artificial sequence

<220>
<223> 131R003 Heavy chain variable region - Variant 1

<400> 36

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

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

Ser Ile His Trp Val Lys Gln Asn His Gly Lys Ser Leu Asp Trp Ile
35 40 45

Gly Tyr Ile Tyr Pro Ser Asn Gly Asp Ser Gly Tyr Asn Gln Lys Phe
50 55 60

Lys Asn Arg Ala Thr Leu Thr Val Asp Thr Ser Tyr Ser Thr Ala Tyr
65 70 75 80

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

Ala Thr Tyr Phe Ala Asn Asn Phe Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Leu Thr Val Ser Ser
115

<210> 37
<211> 117
<212> PRT
<213> Artificial sequence

<220>
<223> 131R003 Heavy chain variable region - Variant 2

<400> 37

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

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

Thr Phe His Trp Val Lys Gln Asn His Gly Lys Ser Leu Asp Trp Ile

35 40 45

Gly Tyr Ile Tyr Pro Ser Asn Gly Asp Ser Gly Tyr Asn Gln Lys Phe
50 55 60

Lys Asn Arg Ala Thr Leu Thr Val Asp Thr Ser Tyr Ser Thr Ala Tyr
65 70 75 80

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

Ala Thr Tyr Phe Ala Asn Asn Phe Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Leu Thr Val Ser Ser
115

<210> 38
<211> 462
<212> PRT
<213> Artificial sequence

<220>
<223> 131R003 Heavy chain - Variant 1

<400> 38

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Glu Leu Val Lys
20 25 30

Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

Thr Asp Tyr Ser Ile His Trp Val Lys Gln Asn His Gly Lys Ser Leu
50 55 60

Asp Trp Ile Gly Tyr Ile Tyr Pro Ser Asn Gly Asp Ser Gly Tyr Asn
65 70 75 80

Gln Lys Phe Lys Asn Arg Ala Thr Leu Thr Val Asp Thr Ser Tyr Ser
85 90 95

Thr Ala Tyr Leu Glu Val Arg Arg Leu Thr Phe Glu Asp Ser Ala Val
100 105 110

Tyr Tyr Cys Ala Thr Tyr Phe Ala Asn Asn Phe Asp Tyr Trp Gly Gln
115 120 125

Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
130 135 140

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

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

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
            180                 185                 190

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
        195                 200                 205

Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys
    210                 215                 220

Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val
225                 230                 235                 240

Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe
                245                 250                 255

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
            260                 265                 270

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
        275                 280                 285

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
    290                 295                 300

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val
305                 310                 315                 320

Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
                325                 330                 335

Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
            340                 345                 350

Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
        355                 360                 365

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
    370                 375                 380

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

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp
                405                 410                 415
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Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
            420                 425                 430


Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
        435                 440                 445


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


<210>  39
<211>  443
<212>  PRT
<213>  Artificial sequence

<220>
<223>  131R003  Heavy chain - Variant 1 without predicted signal
       sequence

<400>  39

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


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


Ser Ile His Trp Val Lys Gln Asn His Gly Lys Ser Leu Asp Trp Ile
        35                  40                  45


Gly Tyr Ile Tyr Pro Ser Asn Gly Asp Ser Gly Tyr Asn Gln Lys Phe
    50                  55                  60


Lys Asn Arg Ala Thr Leu Thr Val Asp Thr Ser Tyr Ser Thr Ala Tyr
65                  70                  75                  80


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


Ala Thr Tyr Phe Ala Asn Asn Phe Asp Tyr Trp Gly Gln Gly Thr Thr
            100                 105                 110


Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
        115                 120                 125


Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
    130                 135                 140


Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145                 150                 155                 160


Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
                165                 170                 175
```

```
Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn
            180                 185                 190

Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
        195                 200                 205

Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro
    210                 215                 220

Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro
225                 230                 235                 240

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
                245                 250                 255

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn
            260                 265                 270

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
        275                 280                 285

Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val
    290                 295                 300

Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
305                 310                 315                 320

Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys
                325                 330                 335

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
            340                 345                 350

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
        355                 360                 365

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
    370                 375                 380

Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe
385                 390                 395                 400

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
                405                 410                 415

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
            420                 425                 430

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440
```

<210> 40
<211> 1389
<212> DNA
<213> Artificial sequence

<220>
<223> 131R003 Heavy chain - Variant 1 nucleic acid

<400> 40

atgaagcatc tttggttctt cctgctcttg gtggctgcgc cgaggtgggt gctcagccag 60

gtgcaactta aacagtcggg gcctgagttg gtcaaaccag gagcctcagt aaagattagc 120

tgcaaagcat caggttatac ctttacggat tactcgatcc actgggtgaa gcagaaccac 180

ggaaagtcac tggattggat cgggtacatc tacccctcga atggagattc ggggtataac 240

caaaagttca aaaaccgggc cacgctgact gtggacacgt cgtattccac cgcatatttg 300

gaagtccgca gactcacgtt cgaggactcc gcggtatact attgtgccac atactttgcg 360

aataactttg actactgggg tcagggcaca acgcttactg tctccagcgc gtcaacaaag 420

ggcccctccg tgttccctct ggcccccttgc tcccggtcca cctctgagtc taccgccgct 480

ctgggctgcc tggtgaagga ctacttccct gagcctgtga ccgtgtcctg gaactctggc 540

gccctgacct ctggcgtgca caccttccct gccgtgctgc agtcctccgg cctgtactcc 600

ctgtcctccg tggtgaccgt gccttcctcc aacttcggca cccagaccta cacctgcaac 660

gtggaccaca agccttccaa caccaaggtg gacaagaccg tggagcggaa gtgctgcgtg 720

gagtgccctc cttgtcctgc tcctcctgtg gctggccctt ctgtgttcct gttccctcct 780

aagcctaagg acaccctgat gatctcccgg acccctgaag tgacctgcgt ggtggtggac 840

gtgtcccacg aggaccctga ggtgcagttc aattggtacg tggacggcgt ggaggtgcac 900

aacgccaaga ccaagcctcg ggaggaacag ttcaactcca ccttccgggt ggtgtctgtg 960

ctgaccgtgg tgcaccagga ctggctgaac ggcaaagaat acaagtgcaa ggtgtccaac 1020

aagggcctgc ctgcccctat cgaaaagacc atctctaaga ccaagggcca gcctcgcgag 1080

cctcaggtct acaccctgcc tcctagccgg gaggaaatga ccaagaacca ggtgtccctg 1140

acctgtctgg tgaagggctt ctacccttcc gatatcgccg tggagtggga gtctaacggc 1200

cagcctgaga acaactacaa gaccacccct cctatgctgg actccgacgg ctccttcttc 1260

ctgtactcca agctgacagt ggacaagtcc cggtggcagc agggcaacgt gttctcctgc 1320

tccgtgatgc acgaggccct gcacaaccac tacacccaga agtccctgtc cctgtctcct 1380

ggcaagtga 1389

<210> 41
<211> 462
<212> PRT
<213> Artificial sequence

<220>
<223> 131R003 Heavy chain - Variant 2

<400> 41

```
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                  10                  15

Val Leu Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Glu Leu Val Lys
            20                  25                  30

Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45

Thr Ser Tyr Thr Phe His Trp Val Lys Gln Asn His Gly Lys Ser Leu
    50                  55                  60

Asp Trp Ile Gly Tyr Ile Tyr Pro Ser Asn Gly Asp Ser Gly Tyr Asn
65                  70                  75                  80

Gln Lys Phe Lys Asn Arg Ala Thr Leu Thr Val Asp Thr Ser Tyr Ser
                85                  90                  95

Thr Ala Tyr Leu Glu Val Arg Arg Leu Thr Phe Glu Asp Ser Ala Val
            100                 105                 110

Tyr Tyr Cys Ala Thr Tyr Phe Ala Asn Asn Phe Asp Tyr Trp Gly Gln
        115                 120                 125

Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
    130                 135                 140

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

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

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
            180                 185                 190

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
        195                 200                 205

Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys
    210                 215                 220

Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val
225                 230                 235                 240

Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe
                245                 250                 255

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
            260                 265                 270
```

```
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
        275                 280                 285

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
    290                 295                 300

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val
305                 310                 315                 320

Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
                325                 330                 335

Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
            340                 345                 350

Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
        355                 360                 365

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
    370                 375                 380

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

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp
                405                 410                 415

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
            420                 425                 430

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
        435                 440                 445

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


<210>  42
<211>  443
<212>  PRT
<213>  Artificial sequence

<220>
<223>  131R003  Heavy chain - Variant 2

<400>  42

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

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

Thr Phe His Trp Val Lys Gln Asn His Gly Lys Ser Leu Asp Trp Ile
```

```
        35                  40                  45

Gly Tyr Ile Tyr Pro Ser Asn Gly Asp Ser Gly Tyr Asn Gln Lys Phe
    50                  55                  60

Lys Asn Arg Ala Thr Leu Thr Val Asp Thr Ser Tyr Ser Thr Ala Tyr
65                  70                  75                  80

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

Ala Thr Tyr Phe Ala Asn Asn Phe Asp Tyr Trp Gly Gln Gly Thr Thr
            100                 105                 110

Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
        115                 120                 125

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
    130                 135                 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145                 150                 155                 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
                165                 170                 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn
            180                 185                 190

Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
        195                 200                 205

Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro
    210                 215                 220

Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro
225                 230                 235                 240

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
                245                 250                 255

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn
            260                 265                 270

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
        275                 280                 285

Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val
    290                 295                 300

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

305 310 315 320

Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys
325 330 335

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
340 345 350

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
355 360 365

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
370 375 380

Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe
385 390 395 400

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
405 410 415

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
420 425 430

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 43
<211> 1389
<212> DNA
<213> Artificial sequence

<220>
<223> 131R003 Heavy chain - Variant 2 nucleic acid

<400> 43

atgaagcatc tttggttctt cctgctcttg gtggctgcgc cgaggtgggt gctcagccag 60

gtgcaactta aacagtcggg gcctgagttg gtcaaaccag gagcctcagt aaagattagc 120

tgcaaagcat caggatacac cttcactagc tatacattcc actgggtgaa gcagaaccac 180

ggaaagtcac tggattggat cgggtacatc tacccctcga atggagattc ggggtataac 240

caaaagttca aaaaccgggc cacgctgact gtggacacgt cgtattccac cgcatatttg 300

gaagtccgca gactcacgtt cgaggactcc gcggtatact attgtgccac atactttgcg 360

aataactttg actactgggg tcagggcaca acgcttactg tctccagcgc gtcaacaaag 420

ggcccctccg tgttccctct ggcccccttgc tcccggtcca cctctgagtc taccgccgct 480

ctgggctgcc tggtgaagga ctacttccct gagcctgtga ccgtgtcctg gaactctggc 540

gccctgacct ctggcgtgca caccttccct gccgtgctgc agtcctccgg cctgtactcc 600

ctgtcctccg tggtgaccgt gccttcctcc aacttcggca cccagaccta cacctgcaac 660

gtggaccaca agccttccaa caccaaggtg gacaagaccg tggagcggaa gtgctgcgtg 720

gagtgccctc cttgtcctgc tcctcctgtg gctggccctt ctgtgttcct gttccctcct 780

aagcctaagg acaccctgat gatctcccgg acccctgaag tgacctgcgt ggtggtggac 840

gtgtcccacg aggaccctga ggtgcagttc aattggtacg tggacggcgt ggaggtgcac 900

aacgccaaga ccaagcctcg ggaggaacag ttcaactcca ccttccgggt ggtgtctgtg 960

ctgaccgtgg tgcaccagga ctggctgaac ggcaaagaat acaagtgcaa ggtgtccaac 1020

aagggcctgc ctgcccctat cgaaaagacc atctctaaga ccaagggcca gcctcgcgag 1080

cctcaggtct acaccctgcc tcctagccgg gaggaaatga ccaagaacca ggtgtccctg 1140

acctgtctgg tgaagggctt ctacccttcc gatatcgccg tggagtggga gtctaacggc 1200

cagcctgaga acaactacaa gaccacccct cctatgctgg actccgacgg ctccttcttc 1260

ctgtactcca agctgacagt ggacaagtcc cggtggcagc agggcaacgt gttctcctgc 1320

tccgtgatgc acgaggccct gcacaaccac tacacccaga agtccctgtc cctgtctcct 1380

ggcaagtga 1389

<210> 44
<211> 117
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized 131R005/131R007/131R008/131R010/131R011 Heavy chain variable region

<400> 44

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

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

Gly Tyr Ile Tyr Pro Ser Asn Gly Asp Ser Gly Tyr Asn Gln Lys Phe
50 55 60

Lys Asn Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ala Thr Tyr Phe Ala Asn Asn Phe Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Leu Thr Val Ser Ser
115

<210> 45
<211> 117
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized 131R006A Heavy chain variable region

<400> 45

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 Ser Tyr
20 25 30

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

Gly Tyr Ile Tyr Pro Ser Asn Gly Asp Ser Gly Tyr Asn Gln Lys Phe
50 55 60

Lys Asn Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ala Thr Tyr Phe Ala Asn Asn Phe Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Leu Thr Val Ser Ser
115

<210> 46
<211> 462
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized 131R005/131R007/131R011 Heavy chain (IgG2)

<400> 46

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

Thr Asp Tyr Ser Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

```
Glu Trp Ile Gly Tyr Ile Tyr Pro Ser Asn Gly Asp Ser Gly Tyr Asn
65                  70                  75                  80

Gln Lys Phe Lys Asn Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser
                85                  90                  95

Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

Tyr Tyr Cys Ala Thr Tyr Phe Ala Asn Asn Phe Asp Tyr Trp Gly Gln
        115                 120                 125

Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
    130                 135                 140

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

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

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
            180                 185                 190

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
        195                 200                 205

Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys
    210                 215                 220

Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val
225                 230                 235                 240

Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe
                245                 250                 255

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
            260                 265                 270

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
        275                 280                 285

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
    290                 295                 300

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val
305                 310                 315                 320

Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
                325                 330                 335
```

```
Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
            340                 345                 350

Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
        355                 360                 365

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
    370                 375                 380

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

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp
                405                 410                 415

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
            420                 425                 430

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
        435                 440                 445

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


<210>  47
<211>  462
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Humanized 131RO06A  Heavy chain

<400>  47

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45

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

Glu Trp Ile Gly Tyr Ile Tyr Pro Ser Asn Gly Asp Ser Gly Tyr Asn
65                  70                  75                  80

Gln Lys Phe Lys Asn Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser
                85                  90                  95

Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser Glu Asp Thr Ala Val
```

```
            100                 105                 110

Tyr Tyr Cys Ala Thr Tyr Phe Ala Asn Asn Phe Asp Tyr Trp Gly Gln
        115                 120                 125

Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
    130                 135                 140

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

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

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
            180                 185                 190

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
        195                 200                 205

Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys
    210                 215                 220

Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val
225                 230                 235                 240

Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe
                245                 250                 255

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
            260                 265                 270

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
        275                 280                 285

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
    290                 295                 300

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val
305                 310                 315                 320

Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
                325                 330                 335

Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
            340                 345                 350

Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
        355                 360                 365

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
```

370 375 380

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

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp
405 410 415

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
420 425 430

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
435 440 445

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

<210> 48
<211> 443
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized 131R005/131R007/131R011 Heavy chain (IgG2)

<400> 48

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

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

Gly Tyr Ile Tyr Pro Ser Asn Gly Asp Ser Gly Tyr Asn Gln Lys Phe
50 55 60

Lys Asn Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ala Thr Tyr Phe Ala Asn Asn Phe Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
115 120 125

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
130 135 140

```
Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145                 150                 155                 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
                165                 170                 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn
            180                 185                 190

Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
        195                 200                 205

Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro
    210                 215                 220

Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro
225                 230                 235                 240

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
                245                 250                 255

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn
            260                 265                 270

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
        275                 280                 285

Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val
    290                 295                 300

Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
305                 310                 315                 320

Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys
                325                 330                 335

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
            340                 345                 350

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
        355                 360                 365

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
    370                 375                 380

Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe
385                 390                 395                 400

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
                405                 410                 415
```

```
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
            420                 425                 430

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440
```

<210> 49
<211> 443
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized 131R006A Heavy chain
<400> 49

```
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 Ser Tyr
            20                  25                  30

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

Gly Tyr Ile Tyr Pro Ser Asn Gly Asp Ser Gly Tyr Asn Gln Lys Phe
    50                  55                  60

Lys Asn Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

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

Ala Thr Tyr Phe Ala Asn Asn Phe Asp Tyr Trp Gly Gln Gly Thr Thr
            100                 105                 110

Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
        115                 120                 125

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
    130                 135                 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145                 150                 155                 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
                165                 170                 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn
            180                 185                 190

Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
        195                 200                 205
```

```
Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro
    210                 215                 220

Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro
225                 230                 235                 240

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
                245                 250                 255

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn
            260                 265                 270

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
        275                 280                 285

Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val
    290                 295                 300

Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
305                 310                 315                 320

Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys
                325                 330                 335

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
            340                 345                 350

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
        355                 360                 365

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
    370                 375                 380

Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe
385                 390                 395                 400

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
                405                 410                 415

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
            420                 425                 430

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440
```

<210> 50
<211> 351
<212> DNA
<213> Artificial sequence

<220>

<223> Humanized 131R005/131R007 Heavy chain variable region nucleic acid

<400> 50
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agctgcaagg cttctggata caccttcact gactattcaa tccactgggt gagacaggca 120

cctggtcagg gactggagtg gattggatac atctacccct caaatgggga ctctggctac 180

aaccaaaagt tcaagaaccg ggtgactatg accagagata cctcaacatc tactgcctac 240

atggaactca gcaggctgcg ctcagaggac accgcagtgt attactgtgc cacctacttc 300

gctaataact tcgactattg ggggcagggc accaccctga ctgtcagctc a 351

<210> 51
<211> 351
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized 131R006A Heavy chain variable region nucleic acid

<400> 51
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cctggtcagg gactggagtg gattggatac atctacccct caaatgggga ctctggctac 180

aaccaaaagt tcaagaaccg ggtgactatg accagagata cctcaacatc tactgcctac 240

atggaactca gcaggctgcg ctcagaggac accgcagtgt attactgtgc cacctacttc 300

gctaataact tcgactattg ggggcagggc accaccctga ctgtcagctc a 351

<210> 52
<211> 1389
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized 131R005/131R007 Heavy chain nucleic acid

<400> 52
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tgcaaggctt ctggatacac cttcactgac tattcaatcc actgggtgag acaggcacct 180

ggtcagggac tggagtggat tggatacatc tacccctcaa atggggactc tggctacaac 240

caaaagttca agaaccgggt gactatgacc agagatacct caacatctac tgcctacatg 300

gaactcagca ggctgcgctc agaggacacc gcagtgtatt actgtgccac ctacttcgct 360

aataacttcg actattgggg gcagggcacc accctgactg tcagctcagc ctcaaccaag 420

ggcccctccg tgttccctct ggcccccttgc tcccggtcca cctctgagtc taccgccgct 480

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gccctgacct ctggcgtgca caccttcccct gccgtgctgc agtcctccgg cctgtactcc 600

ctgtcctccg tggtgaccgt gccttcctcc aacttcggca cccagaccta cacctgcaac 660

gtggaccaca agccttccaa caccaaggtg gacaagaccg tggagcggaa gtgctgcgtg 720

gagtgccctc cttgtcctgc tcctcctgtg gctggccctt ctgtgttcct gttccctcct 780

aagcctaagg acaccctgat gatctcccgg acccctgaag tgacctgcgt ggtggtggac 840

gtgtcccacg aggaccctga ggtgcagttc aattggtacg tggacggcgt ggaggtgcac 900

aacgccaaga ccaagcctcg ggaggaacag ttcaactcca ccttccgggt ggtgtctgtg 960

ctgaccgtgg tgcaccagga ctggctgaac ggcaaagaat acaagtgcaa ggtgtccaac 1020

aagggcctgc ctgcccctat cgaaaagacc atctctaaga ccaagggcca gcctcgcgag 1080

cctcaggtct acaccctgcc tcctagccgg gaggaaatga ccaagaacca ggtgtccctg 1140

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cagcctgaga acaactacaa gaccacccct cctatgctgg actccgacgg ctccttcttc 1260

ctgtactcca agctgacagt ggacaagtcc cggtggcagc agggcaacgt gttctcctgc 1320

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ggcaagtga 1389

<210> 53
<211> 1389
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized 131RO06A Heavy chain nucleic acid

<400> 53
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gtccaattgg tccagagcgg tgccgaagtg aagaaaccgg gagcttccgt gaaagtgagc 120

tgcaaggctt ctggatacac cttcactagc tatacattcc actgggtgag acaggcacct 180

ggtcagggac tggagtggat tggatacatc tacccctcaa atggggactc tggctacaac 240

caaaagttca agaaccgggt gactatgacc agagatacct caacatctac tgcctacatg 300

gaactcagca ggctgcgctc agaggacacc gcagtgtatt actgtgccac ctacttcgct 360

aataacttcg actattgggg gcagggcacc accctgactg tcagctcagc ctcaaccaag 420

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gccctgacct ctggcgtgca caccttccct gccgtgctgc agtcctccgg cctgtactcc 600

ctgtcctccg tggtgaccgt gccttcctcc aacttcggca cccagaccta cacctgcaac 660

gtggaccaca agccttccaa caccaaggtg gacaagaccg tggagcggaa gtgctgcgtg 720

gagtgccctc cttgtcctgc tcctcctgtg gctggccctt ctgtgttcct gttccctcct 780

aagcctaagg acaccctgat gatctcccgg acccctgaag tgacctgcgt ggtggtggac 840

gtgtcccacg aggaccctga ggtgcagttc aattggtacg tggacggcgt ggaggtgcac 900

aacgccaaga ccaagcctcg ggaggaacag ttcaactcca ccttccgggt ggtgtctgtg 960

ctgaccgtgg tgcaccagga ctggctgaac ggcaaagaat acaagtgcaa ggtgtccaac 1020

aagggcctgc ctgcccctat cgaaaagacc atctctaaga ccaagggcca gcctcgcgag 1080

cctcaggtct acaccctgcc tcctagccgg gaggaaatga ccaagaacca ggtgtccctg 1140

acctgtctgg tgaagggctt ctacccttcc gatatcgccg tggagtggga gtctaacggc 1200

cagcctgaga acaactacaa gaccacccct cctatgctgg actccgacgg ctccttcttc 1260

ctgtactcca agctgacagt ggacaagtcc cggtggcagc agggcaacgt gttctcctgc 1320

tccgtgatgc acgaggccct gcacaaccac tacacccaga agtccctgtc cctgtctcct 1380

ggcaagtga 1389

<210> 54
<211> 1332
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized 131R005/131R007 Heavy chain nucleic acid

<400> 54
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cctggtcagg gactggagtg gattggatac atctacccct caaatgggga ctctggctac 180

aaccaaaagt tcaagaaccg ggtgactatg accagagata cctcaacatc tactgcctac 240

atggaactca gcaggctgcg ctcagaggac accgcagtgt attactgtgc cacctacttc 300

gctaataact tcgactattg ggggcagggc accaccctga ctgtcagctc agcctcaacc 360

aagggcccct ccgtgttccc tctggccccc tgctcccggt ccacctctga gtctaccgcc 420

gctctgggct gcctggtgaa ggactacttc cctgagcctg tgaccgtgtc ctggaactct 480

ggcgccctga cctctggcgt gcacaccttc cctgccgtgc tgcagtcctc cggcctgtac 540

tccctgtcct ccgtggtgac cgtgccttcc tccaacttcg gcacccagac ctacacctgc 600

aacgtggacc acaagccttc caacaccaag gtggacaaga ccgtggagcg gaagtgctgc 660

gtggagtgcc ctccttgtcc tgctcctcct gtggctggcc cttctgtgtt cctgttccct 720

cctaagccta aggacaccct gatgatctcc cggacccctg aagtgacctg cgtggtggtg 780

gacgtgtccc acgaggaccc tgaggtgcag ttcaattggt acgtggacgg cgtggaggtg 840

cacaacgcca agaccaagcc tcgggaggaa cagttcaact ccaccttccg ggtggtgtct 900

gtgctgaccg tggtgcacca ggactggctg aacggcaaag aatacaagtg caaggtgtcc 960

aacaagggcc tgcctgcccc tatcgaaaag accatctcta agaccaaggg ccagcctcgc 1020

gagcctcagg tctacaccct gcctcctagc cgggaggaaa tgaccaagaa ccaggtgtcc 1080

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tgctccgtga tgcacgaggc cctgcacaac cactacaccc agaagtccct gtccctgtct 1320

cctggcaagt ga 1332

<210> 55
<211> 1332
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized 131RO06A Heavy chain - nucleic acid

<400> 55
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cctggtcagg gactggagtg gattggatac atctacccct caaatgggga ctctggctac 180

aaccaaaagt tcaagaaccg ggtgactatg accagagata cctcaacatc tactgcctac 240

atggaactca gcaggctgcg ctcagaggac accgcagtgt attactgtgc cacctacttc 300

gctaataact tcgactattg ggggcagggc accaccctga ctgtcagctc agcctcaacc 360

aagggcccct ccgtgttccc tctggccccc tgctcccggt ccacctctga gtctaccgcc 420

gctctgggct gcctggtgaa ggactacttc cctgagcctg tgaccgtgtc ctggaactct 480

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aacgtggacc acaagccttc caacaccaag gtggacaaga ccgtggagcg gaagtgctgc 660

gtggagtgcc ctccttgtcc tgctcctcct gtggctggcc cttctgtgtt cctgttccct 720

cctaagccta aggacaccct gatgatctcc cggacccctg aagtgacctg cgtggtggtg 780

gacgtgtccc acgaggaccc tgaggtgcag ttcaattggt acgtggacgg cgtggaggtg 840

cacaacgcca agaccaagcc tcgggaggaa cagttcaact ccaccttccg ggtggtgtct 900

gtgctgaccg tggtgcacca ggactggctg aacggcaaag aatacaagtg caaggtgtcc 960

aacaagggcc tgcctgcccc tatcgaaaag accatctcta agaccaaggg ccagcctcgc 1020

gagcctcagg tctacaccct gcctcctagc cgggaggaaa tgaccaagaa ccaggtgtcc 1080

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ttcctgtact ccaagctgac agtggacaag tcccggtggc agcagggcaa cgtgttctcc 1260

tgctccgtga tgcacgaggc cctgcacaac cactacaccc agaagtccct gtccctgtct 1320

cctggcaagt ga 1332

<210> 56
<211> 330
<212> PRT
<213> Artificial sequence

<220>
<223> Human IgG1 Heavy chain constant region

<400> 56

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

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

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

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

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

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

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

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

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

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145                 150                 155                 160

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

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

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

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

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

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

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

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

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

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

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330
```

<210> 57
<211> 326
<212> PRT
<213> Artificial sequence

<220>
<223> Human IgG2 Heavy chain constant region

<400> 57

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

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

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

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

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

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

Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
            100                 105                 110

Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
        115                 120                 125

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

Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
```

145 150 155 160

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
165 170 175

Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp
180 185 190

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
195 200 205

Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu
210 215 220

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
225 230 235 240

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
245 250 255

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
260 265 270

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

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

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
305 310 315 320

Ser Leu Ser Pro Gly Lys
325

<210> 58
<211> 377
<212> PRT
<213> Artificial sequence

<220>
<223> Human IgG3 Heavy chain constant region

<400> 58

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

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

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

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

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

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

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

Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg
        115                 120                 125

Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys
    130                 135                 140

Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
145                 150                 155                 160

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                165                 170                 175

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            180                 185                 190

Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Lys Trp Tyr
        195                 200                 205

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    210                 215                 220

Gln Tyr Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Leu His
225                 230                 235                 240

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                245                 250                 255

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln
            260                 265                 270

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
        275                 280                 285

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    290                 295                 300

Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu Asn Asn
305                 310                 315                 320
```

Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
325 330 335

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile
340 345 350

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln
355 360 365

Lys Ser Leu Ser Leu Ser Pro Gly Lys
370 375

<210> 59
<211> 327
<212> PRT
<213> Artificial sequence

<220>
<223> Human IgG4 Heavy chain constant region

<400> 59

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

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

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

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

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

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

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro
100 105 110

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

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

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145 150 155 160

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe

165 170 175

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
180 185 190

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
195 200 205

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
210 215 220

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
225 230 235 240

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

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

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

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

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

Leu Ser Leu Ser Leu Gly Lys
325

<210> 60
<211> 326
<212> PRT
<213> Artificial sequence

<220>
<223> Human IgG2 Heavy chain constant region (13A Chain variant)

<400> 60

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

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

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

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

```
Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr
65                  70                  75                  80

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

Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
            100                 105                 110

Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
        115                 120                 125

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

Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
145                 150                 155                 160

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
                165                 170                 175

Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp
            180                 185                 190

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
        195                 200                 205

Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu
    210                 215                 220

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Lys Met Thr Lys Asn
225                 230                 235                 240

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
                245                 250                 255

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
            260                 265                 270

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

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

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
305                 310                 315                 320

Ser Leu Ser Pro Gly Lys
                325
```

<210> 61
<211> 326
<212> PRT
<213> Artificial sequence

<220>
<223> Human IgG2 Heavy chain constant region (13B Chain variant)

<400> 61

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


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


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


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


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


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


Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
            100                 105                 110


Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
        115                 120                 125


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


Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
145                 150                 155                 160


Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
                165                 170                 175


Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp
            180                 185                 190


Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
        195                 200                 205


Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu
    210                 215                 220


Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
```

225 230 235 240

Gln Val Ser Leu Thr Cys Leu Val Glu Gly Phe Tyr Pro Ser Asp Ile
245 250 255

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
260 265 270

Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Glu
275 280 285

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

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
305 310 315 320

Ser Leu Ser Pro Gly Lys
325

<210> 62
<211> 117
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized 131RO06B Heavy chain variable region

<400> 62

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

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

Gly Tyr Ile Tyr Pro Ser Asn Gly Asp Ser Gly Tyr Asn Gln Lys Phe
50 55 60

Lys Asn Arg Val Thr Met Thr Val Asp Thr Ser Tyr Ser Thr Ala Tyr
65 70 75 80

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

Ala Thr Tyr Phe Ala Asn Asn Phe Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Leu Thr Val Ser Ser
115

<210> 63
<211> 462
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized 131R006B Heavy chain

<400> 63

```
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45

Thr Asp Tyr Ser Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
    50                  55                  60

Glu Trp Ile Gly Tyr Ile Tyr Pro Ser Asn Gly Asp Ser Gly Tyr Asn
65                  70                  75                  80

Gln Lys Phe Lys Asn Arg Val Thr Met Thr Val Asp Thr Ser Tyr Ser
                85                  90                  95

Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

Tyr Tyr Cys Ala Thr Tyr Phe Ala Asn Asn Phe Asp Tyr Trp Gly Gln
        115                 120                 125

Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
    130                 135                 140

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

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

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
            180                 185                 190

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
        195                 200                 205

Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys
    210                 215                 220

Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val
```

225 230 235 240

Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe
245 250 255

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
260 265 270

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
275 280 285

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
290 295 300

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val
305 310 315 320

Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
325 330 335

Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
340 345 350

Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
355 360 365

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
370 375 380

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

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp
405 410 415

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
420 425 430

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
435 440 445

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

<210> 64
<211> 443
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized 131RO06B Heavy chain

<400> 64

```
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

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

Gly Tyr Ile Tyr Pro Ser Asn Gly Asp Ser Gly Tyr Asn Gln Lys Phe
    50                  55                  60

Lys Asn Arg Val Thr Met Thr Val Asp Thr Ser Tyr Ser Thr Ala Tyr
65                  70                  75                  80

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

Ala Thr Tyr Phe Ala Asn Asn Phe Asp Tyr Trp Gly Gln Gly Thr Thr
            100                 105                 110

Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
        115                 120                 125

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
    130                 135                 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145                 150                 155                 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
                165                 170                 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn
            180                 185                 190

Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
        195                 200                 205

Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro
    210                 215                 220

Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro
225                 230                 235                 240

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
                245                 250                 255

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn
            260                 265                 270
```

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
275 280 285

Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val
290 295 300

Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
305 310 315 320

Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys
325 330 335

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
340 345 350

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
355 360 365

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
370 375 380

Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe
385 390 395 400

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
405 410 415

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
420 425 430

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 65
<211> 351
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized 131RO06B Heavy chain variable region nucleic acid

<400> 65
caagtccaat tggtccagag cggtgccgaa gtgaagaaac cgggagcttc cgtgaaagtg 60

agctgcaagg cttctggata caccttcact gactattcaa tccactgggt gagacaggca 120

cctggtcagg gactggagtg gattggatac atctacccct caaatgggga ctctggctac 180

aaccaaaagt tcaagaaccg ggtgactatg accgtggata cctcatactc tactgcctac 240

atggaactca gcaggctgcg ctcagaggac accgcagtgt attactgtgc cacctacttc 300

gctaataact tcgactattg ggggcagggc accaccctga ctgtcagctc a 351

<210> 66

<211> 1389
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized 131R006B Heavy chain nucleic acid

<400> 66
atgaagcatc tgtggttttt cctcctcctt gtcgccgctc cacgctgggt gctttcccaa 60

gtccaattgg tccagagcgg tgccgaagtg aagaaaccgg gagcttccgt gaaagtgagc 120

tgcaaggctt ctggatacac cttcactgac tattcaatcc actgggtgag acaggcacct 180

ggtcagggac tggagtggat tggatacatc tacccctcaa atggggactc tggctacaac 240

caaaagttca agaaccgggt gactatgacc gtggatacct catactctac tgcctacatg 300

gaactcagca ggctgcgctc agaggacacc gcagtgtatt actgtgccac ctacttcgct 360

aataacttcg actattgggg gcagggcacc accctgactg tcagctcagc ctcaaccaag 420

ggcccctccg tgttccctct ggcccccttgc tcccggtcca cctctgagtc taccgccgct 480

ctgggctgcc tggtgaagga ctacttccct gagcctgtga ccgtgtcctg gaactctggc 540

gccctgacct ctggcgtgca caccttccct gccgtgctgc agtcctccgg cctgtactcc 600

ctgtcctccg tggtgaccgt gccttcctcc aacttcggca cccagaccta cacctgcaac 660

gtggaccaca agccttccaa caccaaggtg gacaagaccg tggagcggaa gtgctgcgtg 720

gagtgccctc cttgtcctgc tcctcctgtg gctggccctt ctgtgttcct gttccctcct 780

aagcctaagg acaccctgat gatctcccgg acccctgaag tgacctgcgt ggtggtggac 840

gtgtcccacg aggaccctga ggtgcagttc aattggtacg tggacggcgt ggaggtgcac 900

aacgccaaga ccaagcctcg ggaggaacag ttcaactcca ccttccgggt ggtgtctgtg 960

ctgaccgtgg tgcaccagga ctggctgaac ggcaaagaat acaagtgcaa ggtgtccaac 1020

aagggcctgc ctgcccctat cgaaaagacc atctctaaga ccaagggcca gcctcgcgag 1080

cctcaggtct acaccctgcc tcctagccgg gaggaaatga ccaagaacca ggtgtccctg 1140

acctgtctgg tgaagggctt ctacccttcc gatatcgccg tggagtggga gtctaacggc 1200

cagcctgaga acaactacaa gaccacccct cctatgctgg actccgacgg ctccttcttc 1260

ctgtactcca agctgacagt ggacaagtcc cggtggcagc agggcaacgt gttctcctgc 1320

tccgtgatgc acgaggccct gcacaaccac tacacccaga agtccctgtc cctgtctcct 1380

ggcaagtga 1389

<210> 67
<211> 1332
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized 131R006B Heavy chain nucleic acid

<400> 67
caagtccaat tggtccagag cggtgccgaa gtgaagaaac cgggagcttc cgtgaaagtg 60

agctgcaagg cttctggata caccttcact gactattcaa tccactgggt gagacaggca 120

cctggtcagg gactggagtg gattggatac atctacccct caaatgggga ctctggctac 180

aaccaaaagt tcaagaaccg ggtgactatg accgtggata cctcatactc tactgcctac 240

atggaactca gcaggctgcg ctcagaggac accgcagtgt attactgtgc cacctacttc 300

gctaataact tcgactattg ggggcagggc accaccctga ctgtcagctc agcctcaacc 360

aagggcccct ccgtgttccc tctggccct tgctcccggt ccacctctga gtctaccgcc 420

gctctgggct gcctggtgaa ggactacttc cctgagcctg tgaccgtgtc ctggaactct 480

ggcgccctga cctctggcgt gcacaccttc cctgccgtgc tgcagtcctc cggcctgtac 540

tccctgtcct ccgtggtgac cgtgccttcc tccaacttcg gcacccagac ctacacctgc 600

aacgtggacc acaagccttc caacaccaag gtggacaaga ccgtggagcg gaagtgctgc 660

gtggagtgcc ctccttgtcc tgctcctcct gtggctggcc cttctgtgtt cctgttccct 720

cctaagccta aggacaccct gatgatctcc cggacccctg aagtgacctg cgtggtggtg 780

gacgtgtccc acgaggaccc tgaggtgcag ttcaattggt acgtggacgg cgtggaggtg 840

cacaacgcca agaccaagcc tcgggaggaa cagttcaact ccaccttccg ggtggtgtct 900

gtgctgaccg tggtgcacca ggactggctg aacggcaaag aatacaagtg caaggtgtcc 960

aacaagggcc tgcctgcccc tatcgaaaag accatctcta agaccaaggg ccagcctcgc 1020

gagcctcagg tctacaccct gcctcctagc cgggaggaaa tgaccaagaa ccaggtgtcc 1080

ctgacctgtc tggtgaaggg cttctaccct tccgatatcg ccgtggagtg ggagtctaac 1140

ggccagcctg agaacaacta caagaccacc cctcctatgc tggactccga cggctccttc 1200

ttcctgtact ccaagctgac agtggacaag tcccggtggc agcagggcaa cgtgttctcc 1260

tgctccgtga tgcacgaggc cctgcacaac cactacaccc agaagtccct gtccctgtct 1320

cctggcaagt ga 1332

<210> 68
<211> 466
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized 131RO08/131RO10 Heavy chain (IgG1)

<400> 68

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

Thr Asp Tyr Ser Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu

50 55 60

Glu Trp Ile Gly Tyr Ile Tyr Pro Ser Asn Gly Asp Ser Gly Tyr Asn
65 70 75 80

Gln Lys Phe Lys Asn Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser
85 90 95

Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Thr Tyr Phe Ala Asn Asn Phe Asp Tyr Trp Gly Gln
115 120 125

Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
130 135 140

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
145 150 155 160

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

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
180 185 190

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
195 200 205

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
210 215 220

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
225 230 235 240

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
245 250 255

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
260 265 270

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
275 280 285

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
290 295 300

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
305 310 315 320

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys

325 330 335

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
340 345 350

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
355 360 365

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
370 375 380

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
385 390 395 400

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
405 410 415

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
420 425 430

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
435 440 445

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
450 455 460

Gly Lys
465

<210> 69
<211> 447
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized 131R008/131R010 Heavy chain (IgG1)

<400> 69

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

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

Gly Tyr Ile Tyr Pro Ser Asn Gly Asp Ser Gly Tyr Asn Gln Lys Phe
50 55 60

Lys Asn Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ala Thr Tyr Phe Ala Asn Asn Phe Asp Tyr Trp Gly Gln Gly Thr Thr
            100                 105                 110

Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
        115                 120                 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
    130                 135                 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145                 150                 155                 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
                165                 170                 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
            180                 185                 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
        195                 200                 205

Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His
    210                 215                 220

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
225                 230                 235                 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
                245                 250                 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
            260                 265                 270

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
        275                 280                 285

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
    290                 295                 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305                 310                 315                 320

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
                325                 330                 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
            340                 345                 350
```

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

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

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

<210> 70
<211> 1401
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized 131RO08 Heavy chain (IgG1)

<400> 70
atgaagcatc tgtggttttt cctcctcctt gtcgccgctc cacgctgggt gctttcccaa 60

gtccaattgg tccagagcgg tgccgaagtg aagaaaccgg gagcttccgt gaaagtgagc 120

tgcaaggctt ctggatacac cttcactgac tattcaatcc actgggtgag acaggcacct 180

ggtcagggac tggagtggat tggatacatc tacccctcaa atggggactc tggctacaac 240

caaaagttca agaaccgggt gactatgacc agagatacct caacatctac tgcctacatg 300

gaactcagca ggctgcgctc agaggacacc gcagtgtatt actgtgccac ctacttcgct 360

aataacttcg actattgggg gcagggcacc accctgactg tcagctcagc ctcaaccaag 420

ggcccctccg tgttccctct ggcccccttcc tccaagtcca cctccggcgg caccgccgct 480

ctgggctgcc tggtgaagga ctacttccct gagcctgtga ccgtgtcctg gaactctggc 540

gccctgacct ctggcgtgca caccttccca gccgtgctgc agtcctccgg cctgtactcc 600

ctgtcctccg tggtgaccgt gccttcctcc tccctgggca cccagaccta catctgcaac 660

gtgaaccaca agccttccaa caccaaggtg gacaagcggg tggagcctaa gtcctgcgac 720

aagacccaca cctgccctcc ctgccctgcc cctgagctgc tgggcggacc ttccgtgttc 780

ctgttccctc ctaagcctaa ggacaccctg atgatctccc ggacccctga ggtgacctgc 840

gtggtggtgg acgtgtccca cgaggatcct gaggtgaagt tcaattggta cgtggacggc 900

gtggaggtgc acaacgctaa gaccaagcca agggaggagc agtacaactc cacctaccgg 960

gtggtgtctg tgctgaccgt gctgcaccag gactggctga acggcaaaga atacaagtgc 1020

aaggtctcca acaaggccct gcccgctccc atcgagaaaa ccatctccaa ggccaagggc 1080

cagcctcgcg agcctcaggt gtacaccctg ccacccagcc gggaggagat gaccaagaac 1140

caggtgtccc tgacctgtct ggtgaagggc ttctaccctt ccgatatcgc cgtggagtgg 1200

gagtctaacg gccagcccga gaacaactac aagaccaccc ctcctgtgct ggactccgac 1260

ggctccttct tcctgtactc caagctgacc gtggacaagt cccggtggca gcagggcaac 1320

gtgttctcct gctccgtgat gcacgaggcc ctgcacaacc actacaccca gaagagcctg 1380

tctctgtctc ctggcaagtg a 1401

<210> 71
<211> 1344
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized 131RO08 Heavy chain (IgG1)

<400> 71
caagtccaat tggtccagag cggtgccgaa gtgaagaaac cgggagcttc cgtgaaagtg 60

agctgcaagg cttctggata caccttcact gactattcaa tccactgggt gagacaggca 120

cctggtcagg gactggagtg gattggatac atctacccct caaatgggga ctctggctac 180

aaccaaaagt tcaagaaccg ggtgactatg accagagata cctcaacatc tactgcctac 240

atggaactca gcaggctgcg ctcagaggac accgcagtgt attactgtgc cacctacttc 300

gctaataact tcgactattg ggggcagggc accaccctga ctgtcagctc agcctcaacc 360

aagggcccct ccgtgttccc tctggccccc tcctccaagt ccacctccgg cggcaccgcc 420

gctctgggct gcctggtgaa ggactacttc cctgagcctg tgaccgtgtc ctggaactct 480

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aacgtgaacc acaagccttc caacaccaag gtggacaagc gggtggagcc taagtcctgc 660

gacaagaccc acacctgccc tccctgccct gcccctgagc tgctgggcgg accttccgtg 720

ttcctgttcc ctcctaagcc taaggacacc ctgatgatct cccggacccc tgaggtgacc 780

tgcgtggtgg tggacgtgtc ccacgaggat cctgaggtga agttcaattg gtacgtggac 840

ggcgtggagg tgcacaacgc taagaccaag ccaagggagg agcagtacaa ctccacctac 900

cgggtggtgt ctgtgctgac cgtgctgcac caggactggc tgaacggcaa agaatacaag 960

tgcaaggtct ccaacaaggc cctgcccgct cccatcgaga aaaccatctc caaggccaag 1020

ggccagcctc gcgagcctca ggtgtacacc ctgccaccca gccgggagga gatgaccaag 1080

aaccaggtgt ccctgacctg tctggtgaag ggcttctacc cttccgatat cgccgtggag 1140

tgggagtcta acggccagcc cgagaacaac tacaagacca cccctcctgt gctggactcc 1200

gacggctcct tcttcctgta ctccaagctg accgtggaca agtcccggtg gcagcagggc 1260

aacgtgttct cctgctccgt gatgcacgag gccctgcaca accactacac ccagaagagc 1320

ctgtctctgt ctcctggcaa gtga 1344

<210> 72
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized 131R005/131R007/131R008 Light chain variable region

<400> 72

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

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

Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala
50 55 60

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

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

Glu Asp Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
100 105 110

<210> 73
<211> 237
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized 131R005/131R007/131R008 Light chain

<400> 73

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val
20 25 30

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

Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly
50 55 60

Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly

65 70 75 80

Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
85 90 95

Thr Ile Asn Pro Val Glu Ala Glu Asp Val Ala Thr Tyr Tyr Cys Gln
100 105 110

Gln Ser Asn Glu Asp Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu
115 120 125

Leu Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
130 135 140

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
145 150 155 160

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
165 170 175

Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
180 185 190

Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp
195 200 205

Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
210 215 220

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 74
<211> 218
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized 131R005/131R007/131R008 Light chain

<400> 74

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

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

Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala
50 55 60

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

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

Glu Asp Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
100 105 110

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

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

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

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

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

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

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

<210> 75
<211> 336
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized 131R005/131R007/131R008 Light chain

<400> 75
gatatcgtcc tgacccaaag ccctgcttca cttgctgtga gcctggggca acgcgccacc 60

atcacttgca aggcatctca gagcgtggac tatgatggag actcttacat gaattggtat 120

caacagaagc caggtcaacc tcccaaactg ctgatctacg ccgcatctaa tcttgaaagc 180

ggcatcccgg ctcggttctc tggttctgga tcaggaaccg acttcaccct caccattaac 240

ccagtggagg ccgaggacgt ggctacttac tactgccagc agtcaaacga ggacccccctg 300

actttcggag ccgggaccaa gctggagctt aagcgt 336

<210> 76
<211> 714
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized 131R005/131R007/131R008 Light chain
<400> 76
atgaaacatc tttggttctt ccttctgctg gtcgctgctc ctcggtgggt gcttagcgat 60

atcgtcctga cccaaagccc tgcttcactt gctgtgagcc tggggcaacg cgccaccatc 120

acttgcaagg catctcagag cgtggactat gatggagact cttacatgaa ttggtatcaa 180

cagaagccag gtcaacctcc caaactgctg atctacgccg catctaatct tgaaagcggc 240

atcccggctc ggttctctgg ttctggatca ggaaccgact tcaccctcac cattaaccca 300

gtggaggccg aggacgtggc tacttactac tgccagcagt caaacgagga ccccctgact 360

ttcggagccg ggaccaagct ggagcttaag cgtacggtgg ccgcaccgtc agtctttatc 420

tttccaccct ccgacgaaca gcttaagtca ggcactgcct cagtcgtgtg tctcctcaat 480

aacttctacc ccagggaggc caaggtgcag tggaaagtgg acaacgccct ccagtccggg 540

aactctcaag aaagcgtcac cgagcaggac agcaaggact ccacctactc actgtcaagc 600

actctcaccc tctcaaaggc cgattatgag aagcacaagg tgtacgcatg cgaagtgacc 660

catcagggtc tgtcctctcc tgtcaccaag tccttcaata gaggagaatg ttga 714

<210> 77
<211> 657
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized 131R005/131R007/131R008 Light chain

<400> 77
gatatcgtcc tgacccaaag ccctgcttca cttgctgtga gcctggggca acgcgccacc 60

atcacttgca aggcatctca gagcgtggac tatgatggag actcttacat gaattggtat 120

caacagaagc caggtcaacc tcccaaactg ctgatctacg ccgcatctaa tcttgaaagc 180

ggcatcccgg ctcggttctc tggttctgga tcaggaaccg acttcaccct caccattaac 240

ccagtggagg ccgaggacgt ggctacttac tactgccagc agtcaaacga ggacccccctg 300

actttcggag ccgggaccaa gctggagctt aagcgtacgg tggccgcacc gtcagtcttt 360

atctttccac cctccgacga acagcttaag tcaggcactg cctcagtcgt gtgtctcctc 420

aataacttct accccaggga ggccaaggtg cagtggaaag tggacaacgc cctccagtcc 480

gggaactctc aagaaagcgt caccgagcag gacagcaagg actccaccta ctcactgtca 540

agcactctca ccctctcaaa ggccgattat gagaagcaca aggtgtacgc atgcgaagtg 600

acccatcagg gtctgtcctc tcctgtcacc aagtccttca atagaggaga atgttga 657

<210> 78
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> Variant Heavy chain CDR1

<400> 78

Asp Tyr Ser Ile His
1 5

<210> 79
<211> 16
<212> PRT
<213> Artificial sequence

<220>
<223> Variant Heavy chain CDR2

<400> 79

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

<210> 80
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Variant Heavy chain CDR3

<400> 80

Thr Tyr Phe Ala Asn Asn Phe Asp
1 5

<210> 81
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Variant Light chain CDR1

<400> 81

Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn
1 5 10 15

<210> 82
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> Variant Light chain CDR2

<400> 82

Ala Ala Ser Asn Leu Glu Ser
1 5

<210> 83
<211> 10
<212> PRT
<213> Artificial sequence

<220>

<223> Variant Light chain CDR3

<400> 83

Gln Gln Ser Asn Glu Asp Pro Leu Thr Phe
1 5 10

<210> 84
<211> 1404
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized 131R010 Heavy chain (IgG1)

<400> 84
atgaaacact tgtggttctt tctgctcctt gtcgcagcac cacggtgggt gctgtcgcaa 60

gtgcaattgg tgcagtccgg agcggaagtg aagaagcctg gtgcctcggt caaagtctca 120

tgcaaggcca gcggatacac tttcaccgac tactccatcc attgggtgag gcaggctccg 180

ggccagggcc tggagtggat tgggtacatc tacccgtcga acggagattc ggggtacaat 240

cagaagttca agaaccgcgt gaccatgact cgggacacct caacttccac ggcttatatg 300

gaactgagcc gcctgagatc cgaggacact gcggtgtact actgtgccac ctactttgcg 360

aacaatttcg attactgggg acaaggaacc acgctcactg tcagctcagc cagcaccaag 420

ggcccctccg tgttccctct ggcccccttcc tccaagtcca cctccggcgg caccgccgct 480

ctgggctgcc tggtgaagga ctacttccct gagcctgtga ccgtgtcctg gaactctggc 540

gccctgacct ctggcgtgca caccttccca gccgtgctgc agtcctccgg cctgtactcc 600

ctgtcctccg tggtgaccgt gccttcctcc tccctgggca cccagaccta catctgcaac 660

gtgaaccaca agccttccaa caccaaggtg gacaagcggg tggagcctaa gtcctgcgac 720

aagacccaca cctgccctcc ctgccctgcc cctgagctgc tgggcggacc ttccgtgttc 780

ctgttccctc ctaagcctaa ggacaccctg atgatctccc ggacccctga ggtgacctgc 840

gtggtggtgg acgtgtccca cgaggatcct gaggtgaagt tcaattggta cgtggacggc 900

gtggaggtgc acaacgctaa gaccaagcca agggaggagc agtacaactc cacctaccgg 960

gtggtgtctg tgctgaccgt gctgcaccag gactggctga acggcaaaga atacaagtgc 1020

aaggtctcca acaaggccct gcccgctccc atcgagaaaa ccatctccaa ggccaagggc 1080

cagcctcgcg agcctcaggt gtacaccctg ccacccagcc gggaggagat gaccaagaac 1140

caggtgtccc tgacctgtct ggtgaagggc ttctaccctt ccgatatcgc cgtggagtgg 1200

gagtctaacg gccagcccga gaacaactac aagaccaccc ctcctgtgct ggactccgac 1260

ggctccttct tcctgtactc caagctgacc gtggacaagt cccggtggca gcagggcaac 1320

gtgttctcct gctccgtgat gcacgaggcc ctgcacaacc actacaccca gaagagcctg 1380

tctctgtctc ctggcaagtg ataa 1404

<210> 85
<211> 1347

<212> DNA
<213> Artificial sequence

<220>
<223> Humanized 131R010 Heavy chain (IgG1)

<400> 85
caagtgcaat tggtgcagtc cggagcggaa gtgaagaagc ctggtgcctc ggtcaaagtc 60

tcatgcaagg ccagcggata cactttcacc gactactcca tccattgggt gaggcaggct 120

ccgggccagg gcctggagtg gattgggtac atctacccgt cgaacggaga ttcggggtac 180

aatcagaagt tcaagaaccg cgtgaccatg actcgggaca cctcaacttc cacggcttat 240

atggaactga gccgcctgag atccgaggac actgcggtgt actactgtgc cacctacttt 300

gcgaacaatt tcgattactg gggacaagga accacgctca ctgtcagctc agccagcacc 360

aagggcccct ccgtgttccc tctggccccc tcctccaagt ccacctccgg cggcaccgcc 420

gctctgggct gcctggtgaa ggactacttc cctgagcctg tgaccgtgtc ctggaactct 480

ggcgccctga cctctggcgt gcacaccttc ccagccgtgc tgcagtcctc cggcctgtac 540

tccctgtcct ccgtggtgac cgtgccttcc tcctccctgg gcacccagac ctacatctgc 600

aacgtgaacc acaagccttc caacaccaag gtggacaagc gggtggagcc taagtcctgc 660

gacaagaccc acacctgccc tccctgccct gcccctgagc tgctgggcgg accttccgtg 720

ttcctgttcc ctcctaagcc taaggacacc ctgatgatct cccggacccc tgaggtgacc 780

tgcgtggtgg tggacgtgtc ccacgaggat cctgaggtga agttcaattg gtacgtggac 840

ggcgtggagg tgcacaacgc taagaccaag ccaagggagg agcagtacaa ctccacctac 900

cgggtggtgt ctgtgctgac cgtgctgcac caggactggc tgaacggcaa agaatacaag 960

tgcaaggtct ccaacaaggc cctgcccgct cccatcgaga aaaccatctc caaggccaag 1020

ggccagcctc gcgagcctca ggtgtacacc ctgccaccca gccgggagga gatgaccaag 1080

aaccaggtgt ccctgacctg tctggtgaag ggcttctacc cttccgatat cgccgtggag 1140

tgggagtcta acggccagcc cgagaacaac tacaagacca cccctcctgt gctggactcc 1200

gacggctcct tcttcctgta ctccaagctg accgtggaca agtcccggtg gcagcagggc 1260

aacgtgttct cctgctccgt gatgcacgag gccctgcaca accactacac ccagaagagc 1320

ctgtctctgt ctcctggcaa gtgataa 1347

<210> 86
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized 131R010/131R011 Light chain variable region

<400> 86

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 Lys Ala Ser Gln Ser Val Asp Tyr Asp
20 25 30

Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
35 40 45

Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly Val Pro Ser
50 55 60

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

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

Glu Asp Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
100 105 110

<210> 87
<211> 237
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized 131R010/131R011 Light chain

<400> 87

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
20 25 30

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

Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly
50 55 60

Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly
65 70 75 80

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
85 90 95

Thr Ile Ser Pro Val Gln Ala Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
100 105 110

Gln Ser Asn Glu Asp Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu
115 120 125

Leu Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
130 135 140

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Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
145                 150                 155                 160


Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
                165                 170                 175


Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
            180                 185                 190


Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp
        195                 200                 205


Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
    210                 215                 220


Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235


<210>  88
<211>  218
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Humanized 131RO10/131RO11  Light chain

<400>  88

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 Lys Ala Ser Gln Ser Val Asp Tyr Asp
            20                  25                  30


Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
        35                  40                  45


Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly Val Pro Ser
    50                  55                  60


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


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


Glu Asp Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
            100                 105                 110


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

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

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

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

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

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

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

<210> 89
<211> 336
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized 131R010/131R011 Light chain variable region nucleic acid

<400> 89
gatatccaga tgactcagtc gccctcatcg ttgagcgcct cggtcgggga tcgcgtgact 60

attacttgta aagcgtccca gagcgtggac tacgacggag attcctacat gaactggtat 120

cagcaaaaac cgggaaaggc tcctaaactt ctcatctacg cagcctcgaa tctggaatca 180

ggagtcccga gccggttcag cggatcaggc tccggtactg attttaccct cacgatctcg 240

ccagtgcaag ccgaggactt cgcgacctac tactgccaac agtccaacga ggacccgctg 300

accttcggcg cagggaccaa gctggaactg aagcgt 336

<210> 90
<211> 714
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized 131R010/131R011 Light chain

<400> 90
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt cctgtccgat 60

atccagatga ctcagtcgcc ctcatcgttg agcgcctcgg tcggggatcg cgtgactatt 120

acttgtaaag cgtcccagag cgtggactac gacggagatt cctacatgaa ctggtatcag 180

caaaaaccgg gaaaggctcc taaacttctc atctacgcag cctcgaatct ggaatcagga 240

gtcccgagcc ggttcagcgg atcaggctcc ggtactgatt ttaccctcac gatctcgcca 300

gtgcaagccg aggacttcgc gacctactac tgccaacagt ccaacgagga cccgctgacc 360

ttcggcgcag ggaccaagct ggaactgaag cgtacggtgg ccgctccatc cgtgtttatc 420

tttccgccgt ccgatgagca gctcaagtcg ggcactgcca gcgtggtctg cctgcttaac 480

aatttctacc ctagggaagc caaggtgcag tggaaggtgg ataacgcgct ccaatccggt 540

aactcgcaag agagcgtgac cgaacaggac tcaaaggact cgacgtacag cctgtcatcg 600

accttgactc tctcaaaggc cgactacgaa aagcacaagg tctacgcgtg cgaagtcacc 660

catcagggac tgtcctcgcc tgtgaccaag agcttcaatc gcggagagtg ctga 714

<210> 91
<211> 657
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized 131R010/131R011 Light chain

<400> 91
gatatccaga tgactcagtc gccctcatcg ttgagcgcct cggtcgggga tcgcgtgact 60

attacttgta aagcgtccca gagcgtggac tacgacggag attcctacat gaactggtat 120

cagcaaaaac cgggaaaggc tcctaaactt ctcatctacg cagcctcgaa tctggaatca 180

ggagtcccga gccggttcag cggatcaggc tccggtactg attttaccct cacgatctcg 240

ccagtgcaag ccgaggactt cgcgacctac tactgccaac agtccaacga ggacccgctg 300

accttcggcg cagggaccaa gctggaactg aagcgtacgg tggccgctcc atccgtgttt 360

atctttccgc cgtccgatga gcagctcaag tcgggcactg ccagcgtggt ctgcctgctt 420

aacaatttct accctaggga agccaaggtg cagtggaagg tggataacgc gctccaatcc 480

ggtaactcgc aagagagcgt gaccgaacag gactcaaagg actcgacgta cagcctgtca 540

tcgaccttga ctctctcaaa ggccgactac gaaaagcaca aggtctacgc gtgcgaagtc 600

acccatcagg gactgtcctc gcctgtgacc aagagcttca atcgcggaga gtgctga 657

<210> 92
<211> 351
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized 131R011 Heavy chain variable region nucleic acid

<400> 92
caagtgcaat tggtgcagtc cggagcggaa gtgaagaagc ctggtgcctc ggtcaaagtc 60

tcatgcaagg ccagcggata cactttcacc gactactcca tccattgggt gaggcaggct 120

ccgggccagg gcctggagtg gattgggtac atctacccgt cgaacggaga ttcggggtac 180

aatcagaagt tcaagaaccg cgtgaccatg actcgggaca cctcaacttc cacggcttat 240

atggaactga gccgcctgag atccgaggac actgcggtgt actactgtgc cacctacttt 300

gcgaacaatt tcgattactg gggacaagga accacgctca ctgtcagctc a 351

<210> 93

<211> 1392
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized 131R011 Heavy chain (IgG2)

<400> 93
atgaaacact tgtggttctt tctgctcctt gtcgcagcac cacggtgggt gctgtcgcaa 60

gtgcaattgg tgcagtccgg agcggaagtg aagaagcctg gtgcctcggt caaagtctca 120

tgcaaggcca gcggatacac tttcaccgac tactccatcc attgggtgag gcaggctccg 180

ggccagggcc tggagtggat tgggtacatc tacccgtcga acggagattc ggggtacaat 240

cagaagttca agaaccgcgt gaccatgact cgggacacct caacttccac ggcttatatg 300

gaactgagcc gcctgagatc cgaggacact gcggtgtact actgtgccac ctactttgcg 360

aacaatttcg attactgggg acaaggaacc acgctcactg tcagctcagc cagcaccaag 420

ggcccctccg tgttccctct ggcccccttgc tcccggtcca cctctgagtc taccgccgct 480

ctgggctgcc tggtgaagga ctacttccct gagcctgtga ccgtgtcctg gaactctggc 540

gccctgacct ctggcgtgca caccttccct gccgtgctgc agtcctccgg cctgtactcc 600

ctgtcctccg tggtgaccgt gccttcctcc aacttcggca cccagaccta cacctgcaac 660

gtggaccaca agccttccaa caccaaggtg gacaagaccg tggagcggaa gtgctgcgtg 720

gagtgccctc cttgtcctgc tcctcctgtg gctggccctt ctgtgttcct gttccctcct 780

aagcctaagg acaccctgat gatctcccgg acccctgaag tgacctgcgt ggtggtggac 840

gtgtcccacg aggaccctga ggtgcagttc aattggtacg tggacggcgt ggaggtgcac 900

aacgccaaga ccaagcctcg ggaggaacag ttcaactcca ccttccgggt ggtgtctgtg 960

ctgaccgtgg tgcaccagga ctggctgaac ggcaaagaat acaagtgcaa ggtgtccaac 1020

aagggcctgc ctgcccctat cgaaaagacc atctctaaga ccaagggcca gcctcgcgag 1080

cctcaggtct acaccctgcc tcctagccgg gaggaaatga ccaagaacca ggtgtccctg 1140

acctgtctgg tgaagggctt ctacccttcc gatatcgccg tggagtggga gtctaacggc 1200

cagcctgaga acaactacaa gaccacccct cctatgctgg actccgacgg ctccttcttc 1260

ctgtactcca agctgacagt ggacaagtcc cggtggcagc agggcaacgt gttctcctgc 1320

tccgtgatgc acgaggccct gcacaaccac tacacccaga agtccctgtc cctgtctcct 1380

ggcaagtgat aa 1392

<210> 94
<211> 1335
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized 131R011 Heavy chain (IgG2)

<400> 94
caagtgcaat tggtgcagtc cggagcggaa gtgaagaagc ctggtgcctc ggtcaaagtc 60

tcatgcaagg ccagcggata cactttcacc gactactcca tccattgggt gaggcaggct 120

ccgggccagg gcctggagtg gattgggtac atctacccgt cgaacggaga ttcggggtac 180

aatcagaagt tcaagaaccg cgtgaccatg actcgggaca cctcaacttc cacggcttat 240

atggaactga gccgcctgag atccgaggac actgcggtgt actactgtgc cacctacttt 300

gcgaacaatt tcgattactg gggacaagga accacgctca ctgtcagctc agccagcacc 360

aagggcccct ccgtgttccc tctggccccc tgctcccggt ccacctctga gtctaccgcc 420

gctctgggct gcctggtgaa ggactacttc cctgagcctg tgaccgtgtc ctggaactct 480

ggcgccctga cctctggcgt gcacaccttc cctgccgtgc tgcagtcctc cggcctgtac 540

tccctgtcct ccgtggtgac cgtgccttcc tccaacttcg gcacccagac ctacacctgc 600

aacgtggacc acaagccttc caacaccaag gtggacaaga ccgtggagcg gaagtgctgc 660

gtggagtgcc ctccttgtcc tgctcctcct gtggctggcc cttctgtgtt cctgttccct 720

cctaagccta aggacaccct gatgatctcc cggacccctg aagtgacctg cgtggtggtg 780

gacgtgtccc acgaggaccc tgaggtgcag ttcaattggt acgtggacgg cgtggaggtg 840

cacaacgcca agaccaagcc tcgggaggaa cagttcaact ccaccttccg ggtggtgtct 900

gtgctgaccg tggtgcacca ggactggctg aacggcaaag aatacaagtg caaggtgtcc 960

aacaagggcc tgcctgcccc tatcgaaaag accatctcta agaccaaggg ccagcctcgc 1020

gagcctcagg tctacaccct gcctcctagc cgggaggaaa tgaccaagaa ccaggtgtcc 1080

ctgacctgtc tggtgaaggg cttctaccct tccgatatcg ccgtggagtg ggagtctaac 1140

ggccagcctg agaacaacta caagaccacc cctcctatgc tggactccga cggctccttc 1200

ttcctgtact ccaagctgac agtggacaag tcccggtggc agcagggcaa cgtgttctcc 1260

tgctccgtga tgcacgaggc cctgcacaac cactacaccc agaagtccct gtccctgtct 1320

cctggcaagt gataa 1335

<210> 95
<211> 350
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized 131RO10 Heavy chain variable region

<400> 95
caagtgcaat tggtgcagtc cggagcggaa gtgaagaagc ctggtgcctc ggtcaaagtc 60

tcatgcaagg ccagcggata cactttcacc gactactcca tccattgggt gaggcaggct 120

ccgggccagg gcctggagtg gattgggtac atctacccgt cgaacggaga ttcggggtac 180

aatcagaagt tcaagaaccg cgtgaccatg actcgggaca cctcaacttc cacggcttat 240

atggaactga gccgcctgag atccgaggac actgcggtgt actactgtgc cacctacttt 300

gcgaacaatt tcgattactg gggacaagga accacgctca ctgtcagctc 350