SEQUENCE LISTING

<110> UCB Pharma S.A.

<120> Anti-FcRn Antibodies

<130> G0165

<150> GB1208370.5
<151> 2012-05-14

<160> 94

<170> PatentIn version 3.5

<210> 1
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<220>
<223> CA170_1519 CDRH1

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<220>
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<400> 2

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1 5 10 15

Gly

<210> 3
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<400> 3

Gly Ile Val Arg Pro Phe Leu Tyr
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<213> Artificial

<220>
<223> CA170_1519 CDRL1

<400> 4

Lys Ser Ser Gln Ser Leu Val Gly Ala Ser Gly Lys Thr Tyr Leu Tyr
1 5 10 15

<210> 5
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<212> PRT
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<220>
<223> CA170_1519 CDRL2

<400> 5

Leu Val Ser Thr Leu Asp Ser
1 5

<210> 6
<211> 9
<212> PRT
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<220>
<223> CA170_1519 CDRL3

<400> 6

Leu Gln Gly Thr His Phe Pro His Thr
1 5

<210> 7
<211> 112
<212> PRT
<213> Artificial

<220>
<223> Rat Ab 1519 VL region

<400> 7

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Val Gly Ala
20 25 30

Ser Gly Lys Thr Tyr Leu Tyr Trp Leu Phe Gln Arg Ser Gly Gln Ser
35 40 45

Pro Lys Arg Leu Ile Tyr Leu Val Ser Thr Leu Asp Ser Gly Ile Pro
50 55 60

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

Arg Arg Val Glu Ala Asp Asp Leu Gly Val Tyr Tyr Cys Leu Gln Gly
85 90 95

```
Thr His Phe Pro His Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
            100                 105                 110


<210>  8
<211>  336
<212>  DNA
<213>  Artificial

<220>
<223>  Rat Ab 1519 VL region

<400>  8
gatgttgtga tgacccagac tccactgtct ttgtcggttg cccttggaca accagcctcc       60

atctcttgca agtcaagtca gagcctcgta ggtgctagtg gaaagacata tttgtattgg      120

ttatttcaga ggtccggcca gtctccaaag cgactaatct atctggtgtc cacactggac      180

tctggaattc ctgataggtt cagtggcagt ggagcagaga cagattttac tcttaaaatc      240

cgcagagtgg aagccgatga tttgggagtt tattactgct tgcaaggtac acattttcct      300

cacacgtttg gagctgggac caagctggaa ttgaaa                                336


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

<220>
<223>  Rat Ab 1519 VL region with signal sequence

<400>  9

Met Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Met Leu Trp Ile Gln
1               5                   10                  15


Gly Thr Ser Gly Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Ser
            20                  25                  30


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


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


Ser Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Thr Leu Asp
65                  70                  75                  80


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


Thr Leu Lys Ile Arg Arg Val Glu Ala Asp Asp Leu Gly Val Tyr Tyr
            100                 105                 110


Cys Leu Gln Gly Thr His Phe Pro His Thr Phe Gly Ala Gly Thr Lys
        115                 120                 125
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Leu Glu Leu Lys
130

<210> 10
<211> 396
<212> DNA
<213> Artificial

<220>
<223> Rat Ab 1519 VL region with signal sequence

<400> 10
atgatgagtc ctgcccagtt cctgtttctg ctgatgctct ggattcaggg aaccagtggt 60

gatgttgtga tgacccagac tccactgtct ttgtcggttg cccttggaca accagcctcc 120

atctcttgca agtcaagtca gagcctcgta ggtgctagtg gaaagacata tttgtattgg 180

ttatttcaga ggtccggcca gtctccaaag cgactaatct atctggtgtc cacactggac 240

tctggaattc ctgataggtt cagtggcagt ggagcagaga cagattttac tcttaaaatc 300

cgcagagtgg aagccgatga tttgggagtt tattactgct tgcaaggtac acattttcct 360

cacacgtttg gagctgggac caagctggaa ttgaaa 396

<210> 11
<211> 116
<212> PRT
<213> Artificial

<220>
<223> Rat Ab 1519 VH region

<400> 11

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

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

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

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

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

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

Thr Thr Gly Ile Val Arg Pro Phe Leu Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser

115

<210> 12
<211> 348
<212> DNA
<213> Artificial

<220>
<223> Rat Ab 1519 VH region

<400> 12
gaggtgccgc tggtggagtc tgggggcggc tcagtgcagc ctgggaggtc catgaaactc 60

tcctgtgtag tctcaggatt cactttcagt aattatggca tggtctgggt ccgccaggct 120

ccaaagaagg gtctggagtg ggtcgcatat attgattctg atggtgataa tacttactac 180

cgagattccg tgaagggccg attcactatc tccagaaata atgcaaaaag caccctatat 240

ttgcaaatgg acagtctgag gtctgaggac acggccactt attactgtac aacagggatt 300

gtccggccct ttctctattg gggccaagga accacggtca ccgtctcg 348

<210> 13
<211> 135
<212> PRT
<213> Artificial

<220>
<223> Rat Ab 1519 VH region with signal sequence

<400> 13

Met Asp Ile Ser Leu Ser Leu Ala Phe Leu Val Leu Phe Ile Lys Gly
1 5 10 15

Val Arg Cys Glu Val Pro Leu Val Glu Ser Gly Gly Gly Ser Val Gln
20 25 30

Pro Gly Arg Ser Met Lys Leu Ser Cys Val Val Ser Gly Phe Thr Phe
35 40 45

Ser Asn Tyr Gly Met Val Trp Val Arg Gln Ala Pro Lys Lys Gly Leu
50 55 60

Glu Trp Val Ala Tyr Ile Asp Ser Asp Gly Asp Asn Thr Tyr Tyr Arg
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asn Asn Ala Lys Ser
85 90 95

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

Tyr Tyr Cys Thr Thr Gly Ile Val Arg Pro Phe Leu Tyr Trp Gly Gln
115 120 125

Gly Thr Thr Val Thr Val Ser

130 135

<210> 14
<211> 405
<212> DNA
<213> Artificial

<220>
<223> Rat Ab 1519 VH region with signal sequence

<400> 14
atggacatca gtctcagctt ggctttcctt gtcctttca taaaaggtgt ccggtgtgag 60

gtgccgctgg tggagtctgg gggcggctca gtgcagcctg ggaggtccat gaaactctcc 120

tgtgtagtct caggattcac tttcagtaat tatggcatgg tctgggtccg ccaggctcca 180

aagaagggtc tggagtgggt cgcatatatt gattctgatg gtgataatac ttactaccga 240

gattccgtga agggccgatt cactatctcc agaaataatg caaaaagcac cctatatttg 300

caaatggaca gtctgaggtc tgaggacacg gccacttatt actgtacaac agggattgtc 360

cggccctttc tctattgggg ccaaggaacc acggtcaccg tctcg 405

<210> 15
<211> 112
<212> PRT
<213> Artificial

<220>
<223> 1519 gL20 V-region

<400> 15

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 Ser Ser Gln Ser Leu Val Gly Ala
20 25 30

Ser Gly Lys Thr Tyr Leu Tyr Trp Leu Phe Gln Lys Pro Gly Lys Ala
35 40 45

Pro Lys Arg Leu Ile Tyr Leu Val Ser Thr Leu Asp Ser Gly Ile Pro
50 55 60

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

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

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

<210> 16
<211> 336
<212> DNA

<213> Artificial

<220>
<223> 1519 gL20 V-region (E. coli expression)

<400> 16
gatatccaga tgacccagag tccaagcagt ctctccgcca gcgtaggcga tcgtgtgact 60

attacctgta aaagctccca gtccctggtg ggtgcaagcg gcaaaaccta cctgtactgg 120

ctcttccaga aaccgggcaa agctccgaaa cgcctgatct atctggtgtc taccctggat 180

agcggtattc cgtctcgttt ctccggtagc ggtagcggta ccgaattcac gctgaccatt 240

agctccctcc agccggagga ctttgctacc tattactgcc tccagggcac tcattttccg 300

cacactttcg gccagggtac caaactggaa atcaaa 336

<210> 17
<211> 336
<212> DNA
<213> Artificial

<220>
<223> 1519 gL20 V-region (mammalian expression)

<400> 17
gatatccaga tgacccagag cccatctagc ttatccgctt ccgttggtga tcgcgtgaca 60

attacgtgta agagctccca atctctcgtg ggtgcaagtg gcaagaccta tctgtactgg 120

ctctttcaga agcctggcaa ggcaccaaaa cggctgatct atctggtgtc taccccttgac 180

tctgggatac cgtcacgatt ttccggatct gggagcggaa ctgagttcac actcacgatt 240

tcatcgctgc aacccgagga ctttgctacc tactactgcc tgcaaggcac tcatttccct 300

cacactttcg gccaggggac aaaactcgaa atcaaa 336

<210> 18
<211> 133
<212> PRT
<213> Artificial

<220>
<223> 1519 gL20 V-region with signal sequence (E. coli expression)

<400> 18

Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
1 5 10 15

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

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

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

Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Leu Val Ser Thr Leu

65 70 75 80

Asp Ser Gly Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu
85 90 95

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
100 105 110

Tyr Cys Leu Gln Gly Thr His Phe Pro His Thr Phe Gly Gln Gly Thr
115 120 125

Lys Leu Glu Ile Lys
130

<210> 19
<211> 399
<212> DNA
<213> Artificial

<220>
<223> 1519 gL20 V-region with signal sequence (E. coli expression)

<400> 19
atgaaaaaga cagctatcgc aattgcagtg gccttggctg gtttcgctac cgtagcgcaa 60

gctgatatcc agatgaccca gagtccaagc agtctctccg ccagcgtagg cgatcgtgtg 120

actattacct gtaaaagctc ccagtccctg gtgggtgcaa gcggcaaaac ctacctgtac 180

tggctcttcc agaaaccggg caaagctccg aaacgcctga tctatctggt gtctaccctg 240

gatagcggta ttccgtctcg tttctccggt agcggtagcg gtaccgaatt cacgctgacc 300

attagctccc tccagccgga ggactttgct acctattact gcctccaggg cactcatttt 360

ccgcacactt tcggccaggg taccaaactg gaaatcaaa 399

<210> 20
<211> 132
<212> PRT
<213> Artificial

<220>
<223> 1519 gL20 V-region with signal sequence (mammalian expression)

<400> 20

Met Ser Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr
1 5 10 15

Asp Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
20 25 30

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

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

```
Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Leu Val Ser Thr Leu Asp
65                  70                  75                  80

Ser Gly Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe
                85                  90                  95

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
            100                 105                 110

Cys Leu Gln Gly Thr His Phe Pro His Thr Phe Gly Gln Gly Thr Lys
        115                 120                 125

Leu Glu Ile Lys
    130
```

<210> 21
<211> 396
<212> DNA
<213> Artificial

<220>
<223> 1519 gL20 V-region with signal sequence (mammalian expression)

<400> 21

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atgtctgtcc ccacccaagt cctcggactc ctgctactct ggcttacaga tgccagatgc       60

gatatccaga tgacccagag cccatctagc ttatccgctt ccgttggtga tcgcgtgaca      120

attacgtgta agagctccca atctctcgtg ggtgcaagtg gcaagaccta tctgtactgg      180

ctctttcaga agcctggcaa ggcaccaaaa cggctgatct atctggtgtc taccttgac       240

tctgggatac cgtcacgatt ttccggatct gggagcggaa ctgagttcac actcacgatt      300

tcatcgctgc aacccgagga ctttgctacc tactactgcc tgcaaggcac tcatttccct      360

cacactttcg gccaggggac aaaactcgaa atcaaa                                 396
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<210> 22
<211> 219
<212> PRT
<213> Artificial

<220>
<223> 1519 gL20 light chain (V + constant)

<400> 22

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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 Ser Ser Gln Ser Leu Val Gly Ala
            20                  25                  30

Ser Gly Lys Thr Tyr Leu Tyr Trp Leu Phe Gln Lys Pro Gly Lys Ala
        35                  40                  45

Pro Lys Arg Leu Ile Tyr Leu Val Ser Thr Leu Asp Ser Gly Ile Pro
```

50 55 60

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

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

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

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

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

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

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

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

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

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

<210> 23
<211> 657
<212> DNA
<213> Artificial

<220>
<223> 1519 gL20 light chain (V + constant, E. coli expression)

<400> 23
gatatccaga tgacccagag tccaagcagt ctctccgcca gcgtaggcga tcgtgtgact 60

attacctgta aaagctccca gtccctggtg ggtgcaagcg gcaaaaccta cctgtactgg 120

ctcttccaga aaccgggcaa agctccgaaa cgcctgatct atctggtgtc taccctggat 180

agcggtattc cgtctcgttt ctccggtagc ggtagcggta ccgaattcac gctgaccatt 240

agctccctcc agccggagga ctttgctacc tattactgcc tccagggcac tcattttccg 300

cacactttcg gccagggtac caaactggaa atcaaacgta cggtagcggc cccatctgtc 360

ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg 420

ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa 480

tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc 540

agcagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 600

gtcacccatc agggcctgag ctcaccagta acaaaaagtt ttaatagagg ggagtgt 657

<210> 24
<211> 657
<212> DNA
<213> Artificial

<220>
<223> 1519 gL20 light chain (V + constant, mammalian expression)

<400> 24
gatatccaga tgacccagag tccaagcagt ctctccgcca gcgtaggcga tcgtgtgact 60

attacctgta aaagctccca gtccctggtg ggtgcaagcg gcaaaaccta cctgtactgg 120

ctcttccaga aaccgggcaa agctccgaaa cgcctgatct atctggtgtc taccctggat 180

agcggtattc cgtctcgttt ctccggtagc ggtagcggta ccgaattcac gctgaccatt 240

agctccctcc agccggagga ctttgctacc tattactgcc tccagggcac tcattttccg 300

cacactttcg gccagggtac caaactggaa atcaaacgta cggtagcggc cccatctgtc 360

ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg 420

ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa 480

tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc 540

agcagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 600

gtcacccatc agggcctgag ctcgcccgtc acaaagagct tcaacagggg agagtgt 657

<210> 25
<211> 240
<212> PRT
<213> Artificial

<220>
<223> 1519 gL20 light chain with signal sequence (E. coli expression)

<400> 25

Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
1 5 10 15

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

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

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

Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Leu Val Ser Thr Leu
65 70 75 80

```
Asp Ser Gly Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu
                85                  90                  95

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
            100                 105                 110

Tyr Cys Leu Gln Gly Thr His Phe Pro His Thr Phe Gly Gln Gly Thr
        115                 120                 125

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

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

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

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

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

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His
    210                 215                 220

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235                 240
```

<210> 26
<211> 720
<212> DNA
<213> Artificial

<220>
<223> 1519 gL20 light chain with signal sequence (E. coli expression)

<400> 26

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atgaaaaaga cagctatcgc aattgcagtg gccttggctg gtttcgctac cgtagcgcaa       60

gctgatatcc agatgaccca gagtccaagc agtctctccg ccagcgtagg cgatcgtgtg      120

actattacct gtaaaagctc ccagtccctg gtgggtgcaa gcggcaaaac ctacctgtac      180

tggctcttcc agaaaccggg caaagctccg aaacgcctga tctatctggt gtctaccctg      240

gatagcggta ttccgtctcg tttctccggt agcggtagcg gtaccgaatt cacgctgacc      300

attagctccc tccagccgga ggactttgct acctattact gcctccaggg cactcatttt      360

ccgcacactt tcggccaggg taccaaactg gaaatcaaac gtacggtagc ggccccatct      420

gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc      480

ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgccctc      540
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caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 600

ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 660

gaagtcaccc atcagggcct gagctcacca gtaacaaaaa gttttaatag aggggagtgt 720

<210> 27
<211> 239
<212> PRT
<213> Artificial

<220>
<223> 1519 gL20 light chain with signal sequence (mammalian expression)

<400> 27

Met Ser Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr
1 5 10 15

Asp Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
20 25 30

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

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

Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Leu Val Ser Thr Leu Asp
65 70 75 80

Ser Gly Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe
85 90 95

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
100 105 110

Cys Leu Gln Gly Thr His Phe Pro His Thr Phe Gly Gln Gly Thr Lys
115 120 125

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

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

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

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

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

```
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
    210                 215                 220

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235
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<210> 28
<211> 717
<212> DNA
<213> Artificial

<220>
<223> 1519 gL20 light chain with signal sequence (mammalian expression)

<400> 28

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atgtctgtcc ccacccaagt cctcggactc ctgctactct ggcttacaga tgccagatgc       60

gatatccaga tgacccagag cccatctagc ttatccgctt ccgttggtga tcgcgtgaca      120

attacgtgta agagctccca atctctcgtg ggtgcaagtg gcaagaccta tctgtactgg      180

ctctttcaga agcctggcaa ggcaccaaaa cggctgatct atctggtgtc taccttgac       240

tctgggatac cgtcacgatt ttccggatct gggagcggaa ctgagttcac actcacgatt      300

tcatcgctgc aacccgagga ctttgctacc tactactgcc tgcaaggcac tcatttccct      360

cacactttcg gccaggggac aaaactcgaa atcaaacgta cggtagcggc cccatctgtc      420

ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg      480

ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa      540

tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc      600

agcagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa      660

gtcacccatc agggcctgag ctcgcccgtc acaaagagct tcaacagggg agagtgt         717
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<210> 29
<211> 116
<212> PRT
<213> Artificial

<220>
<223> 1519 gH20 V-region

<400> 29

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

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

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

Ala Tyr Ile Asp Ser Asp Gly Asp Asn Thr Tyr Tyr Arg Asp Ser Val
    50                  55                  60
```

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

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

Thr Thr Gly Ile Val Arg Pro Phe Leu Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser
115

<210> 30
<211> 348
<212> DNA
<213> Artificial

<220>
<223> 1519 gH20 V-region (E. coli expression)

<400> 30
gaggttccgc tggtcgagtc tggaggcggg cttgtccagc ctggagggag cctgcgtctc 60

tcttgtgcag tatctggctt cacgttctcc aactacggta tggtgtgggt tcgtcaggct 120

ccaggtaaag gtctggaatg ggtggcgtat attgactccg acggcgacaa cacctactat 180

cgcgactctg tgaaaggtcg cttcaccatt tcccgcgata acgccaaatc agcctgtac 240

ctgcagatga acagcctgcg tgctgaagat actgcggtgt actattgcac cactggcatc 300

gtgcgtccgt ttctgtattg gggtcagggt accctcgtta ctgtctcg 348

<210> 31
<211> 348
<212> DNA
<213> Artificial

<220>
<223> 1519 gH20 V-region (mammalian expression)

<400> 31
gaggtaccac ttgtggaaag cggaggaggt cttgtgcagc ctggaggaag tttacgtctc 60

tcttgtgctg tgtctggctt caccttctcc aattacggaa tggtctgggt cagacaagca 120

cctggaaagg gtcttgaatg ggtggcctat attgactctg acggggacaa cacctactat 180

cgggattccg tgaaaggacg cttcacaatc tcccgagata acgccaagag ctcactgtac 240

ctgcagatga atagcctgag agccgaggat actgccgtgt actattgcac aacgggaatc 300

gttaggcctt ttctgtactg gggacagggc accttggtta ctgtctcg 348

<210> 32
<211> 137
<212> PRT
<213> Artificial

<220>
<223> 1519 gH20 V-region (E. coli expression)

<400> 32

Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
1 5 10 15

Thr Val Ala Gln Ala Glu Val Pro Leu Val Glu Ser Gly Gly Gly Leu
20 25 30

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe
35 40 45

Thr Phe Ser Asn Tyr Gly Met Val Trp Val Arg Gln Ala Pro Gly Lys
50 55 60

Gly Leu Glu Trp Val Ala Tyr Ile Asp Ser Asp Gly Asp Asn Thr Tyr
65 70 75 80

Tyr Arg Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
85 90 95

Lys Ser Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Thr Thr Gly Ile Val Arg Pro Phe Leu Tyr Trp
115 120 125

Gly Gln Gly Thr Leu Val Thr Val Ser
130 135

<210> 33
<211> 411
<212> DNA
<213> Artificial

<220>
<223> 1519 gH20 V-region (E. coli expression)

<400> 33
atgaagaaga ctgctatagc aattgcagtg gcgctagctg gtttcgccac cgtggcgcaa 60

gctgaggttc cgctggtcga gtctggaggc gggcttgtcc agcctggagg gagcctgcgt 120

ctctcttgtg cagtatctgg cttcacgttc tccaactacg gtatggtgtg ggttcgtcag 180

gctccaggta aaggtctgga atgggtggcg tatattgact ccgacggcga caacacctac 240

tatcgcgact ctgtgaaagg tcgcttcacc atttcccgcg ataacgccaa atccagcctg 300

tacctgcaga tgaacagcct gcgtgctgaa gatactgcgg tgtactattg caccactggc 360

atcgtgcgtc cgtttctgta ttggggtcag ggtaccctcg ttactgtctc g 411

<210> 34
<211> 135
<212> PRT
<213> Artificial

<220>
<223> 1519 gH20 V-region (mammalian expression)

<400> 34

Met Glu Trp Ser Trp Val Phe Leu Phe Phe Leu Ser Val Thr Thr Gly
1 5 10 15

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

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Thr Phe
35 40 45

Ser Asn Tyr Gly Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Ala Tyr Ile Asp Ser Asp Gly Asp Asn Thr Tyr Tyr Arg
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Ser
85 90 95

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

Tyr Tyr Cys Thr Thr Gly Ile Val Arg Pro Phe Leu Tyr Trp Gly Gln
115 120 125

Gly Thr Leu Val Thr Val Ser
130 135

<210> 35
<211> 405
<212> DNA
<213> Artificial

<220>
<223> 1519 gH20 V-region with signal sequence (mammalian expression)

<400> 35
atggaatgga gctgggtctt tctcttcttc ctgtcagtaa ctacaggagt ccattctgag 60

gtaccacttg tggaaagcgg aggaggtctt gtgcagcctg gaggaagttt acgtctctct 120

tgtgctgtgt ctggcttcac cttctccaat tacggaatgg tctgggtcag acaagcacct 180

ggaaagggtc ttgaatgggt ggcctatatt gactctgacg gggacaacac ctactatcgg 240

gattccgtga aaggacgctt cacaatctcc cgagataacg ccaagagctc actgtacctg 300

cagatgaata gcctgagagc cgaggatact gccgtgtact attgcacaac gggaatcgtt 360

aggccttttc tgtactgggg acagggcacc ttggttactg tctcg 405

<210> 36
<211> 228
<212> PRT

<213> Artificial

<220>
<223> 1519gH2O Fab' heavy chain (V + human gamma-1 CH1 + hinge)

<400> 36

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

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

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

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

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

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

Thr Thr Gly Ile Val Arg Pro Phe Leu Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110

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

Ala Pro 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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
    210                 215                 220

Thr Cys Ala Ala
225
```

<210> 37

<211> 684
<212> DNA
<213> Artificial

<220>
<223> 1519gH20 Fab' heavy chain (V + human gamma-1 CH1 + hinge, E.coli expression)

<400> 37
gaggttccgc tggtcgagtc tggaggcggg cttgtccagc ctggagggag cctgcgtctc 60

tcttgtgcag tatctggctt cacgttctcc aactacggta tggtgtgggt tcgtcaggct 120

ccaggtaaag gtctggaatg ggtggcgtat attgactccg acggcgacaa cacctactat 180

cgcgactctg tgaaaggtcg cttcaccatt tcccgcgata acgccaaatc agcctgtac 240

ctgcagatga acagcctgcg tgctgaagat actgcggtgt actattgcac cactggcatc 300

gtgcgtccgt ttctgtattg gggtcagggt accctcgtta ctgtctcgag cgcttctaca 360

aagggcccat cggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 600

aacgtgaatc acaagcccag caacaccaag gtcgacaaga aagttgagcc caaatcttgt 660

gacaaaactc acacatgcgc cgcg 684

<210> 38
<211> 684
<212> DNA
<213> Artificial

<220>
<223> 1519gH20 Fab' heavy chain (V + human gamma-1 CH1 + hinge, mammalian expression)

<400> 38
gaggtaccac ttgtggaaag cggaggaggt cttgtgcagc ctggaggaag tttacgtctc 60

tcttgtgctg tgtctggctt caccttctcc aattacggaa tggtctgggt cagacaagca 120

cctggaaagg gtcttgaatg ggtggcctat attgactctg acggggacaa cacctactat 180

cgggattccg tgaaaggacg cttcacaatc tcccgagata acgccaagag ctcactgtac 240

ctgcagatga atagcctgag agccgaggat actgccgtgt actattgcac aacgggaatc 300

gttaggcctt ttctgtactg gggacagggc accttggtta ctgtctcgag cgcttctaca 360

aagggcccat cggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 600

aacgtgaatc acaagcccag caacaccaag gtcgacaaga aagttgagcc caaatcttgt 660

gacaaaactc acacatgcgc cgcg 684

<210> 39
<211> 249
<212> PRT
<213> Artificial

<220>
<223> 1519 gH20 Fab' heavy chain with signal sequence (E. coli expression)

<400> 39

```
Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
1               5                   10                  15

Thr Val Ala Gln Ala Glu Val Pro Leu Val Glu Ser Gly Gly Gly Leu
            20                  25                  30

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe
        35                  40                  45

Thr Phe Ser Asn Tyr Gly Met Val Trp Val Arg Gln Ala Pro Gly Lys
    50                  55                  60

Gly Leu Glu Trp Val Ala Tyr Ile Asp Ser Asp Gly Asp Asn Thr Tyr
65                  70                  75                  80

Tyr Arg Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
                85                  90                  95

Lys Ser Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
            100                 105                 110

Ala Val Tyr Tyr Cys Thr Thr Gly Ile Val Arg Pro Phe Leu Tyr Trp
        115                 120                 125

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

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
145                 150                 155                 160

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

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

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

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
    210                 215                 220

His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
```

225 230 235 240

Cys Asp Lys Thr His Thr Cys Ala Ala
245

<210> 40
<211> 747
<212> DNA
<213> Artificial

<220>
<223> 1519 gH2O Fab' heavy chain with signal sequence (E. coli expression)

<400> 40
atgaagaaga ctgctatagc aattgcagtg gcgctagctg gtttcgccac cgtggcgcaa 60

gctgaggttc cgctggtcga gtctggaggc gggcttgtcc agcctggagg gagcctgcgt 120

ctctcttgtg cagtatctgg cttcacgttc tccaactacg gtatggtgtg ggttcgtcag 180

gctccaggta aaggtctgga atgggtggcg tatattgact ccgacggcga caacacctac 240

tatcgcgact ctgtgaaagg tcgcttcacc atttcccgcg ataacgccaa atccagcctg 300

tacctgcaga tgaacagcct gcgtgctgaa gatactgcgg tgtactattg caccactggc 360

atcgtgcgtc cgtttctgta ttggggtcag ggtaccctcg ttactgtctc gagcgcttct 420

acaaagggcc catcggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca 480

gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 540

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 600

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 660

tgcaacgtga atcacaagcc cagcaacacc aaggtcgaca agaaagttga gcccaaatct 720

tgtgacaaaa ctcacacatg cgccgcg 747

<210> 41
<211> 247
<212> PRT
<213> Artificial

<220>
<223> 1519 gH2O Fab' heavy chain with signal sequence (mammalian expression)

<400> 41

Met Glu Trp Ser Trp Val Phe Leu Phe Phe Leu Ser Val Thr Thr Gly
1 5 10 15

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

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Thr Phe
35 40 45

Ser Asn Tyr Gly Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

```
Glu Trp Val Ala Tyr Ile Asp Ser Asp Gly Asp Asn Thr Tyr Tyr Arg
65                  70                  75                  80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Ser
                85                  90                  95

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

Tyr Tyr Cys Thr Thr Gly Ile Val Arg Pro Phe Leu Tyr Trp Gly Gln
        115                 120                 125

Gly Thr Leu Val 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 Lys Val Glu Pro Lys Ser Cys Asp
225                 230                 235                 240

Lys Thr His Thr Cys Ala Ala
                245
```

<210> 42
<211> 741
<212> DNA
<213> Artificial

<220>
<223> 1519 gH2O Fab' heavy chain with signal sequence (mammalian expression)

<400> 42

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atggaatgga gctgggtctt tctcttcttc ctgtcagtaa ctacaggagt ccattctgag       60

gtaccacttg tggaaagcgg aggaggtctt gtgcagcctg gaggaagttt acgtctctct      120

tgtgctgtgt ctggcttcac cttctccaat tacggaatgg tctgggtcag acaagcacct      180

ggaaagggtc ttgaatgggt ggcctatatt gactctgacg gggacaacac ctactatcgg      240

gattccgtga aaggacgctt cacaatctcc cgagataacg ccaagagctc actgtacctg      300
```

cagatgaata gcctgagagc cgaggatact gccgtgtact attgcacaac gggaatcgtt 360

aggccttttc tgtactgggg acagggcacc ttggttactg tctcgagcgc ttctacaaag 420

ggcccatcgg tcttcccccc ggcaccctcc tccaagagca cctctggggg cacagcggcc 480

ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 540

gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc 600

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 660

gtgaatcaca agcccagcaa caccaaggtc gacaagaaag ttgagcccaa atcttgtgac 720

aaaactcaca catgcgccgc g 741

<210> 43
<211> 444
<212> PRT
<213> Artificial

<220>
<223> 1519gH20 IgG4 heavy chain (V + human gamma-4P constant)

<400> 43

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

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

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

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

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

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

Thr Thr Gly Ile Val Arg Pro Phe Leu Tyr Trp Gly Gln Gly Thr Leu
100 105 110

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

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

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

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

```
                165                 170                 175

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

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

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

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

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

Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
            260                 265                 270

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

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

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

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

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

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

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

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

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

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

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
```

435 440

<210> 44
<211> 1939
<212> DNA
<213> Artificial

<220>
<223> 1519gH20 IgG4 heavy chain (V + human gamma-4P constant with exons)

<400> 44
gaggtaccac ttgtggaaag cggaggaggt cttgtgcagc ctggaggaag tttacgtctc 60

tcttgtgctg tgtctggctt caccttctcc aattacggaa tggtctgggt cagacaagca 120

cctggaaagg gtcttgaatg ggtggcctat attgactctg acggggacaa cacctactat 180

cgggattccg tgaaaggacg cttcacaatc tcccgagata acgccaagag ctcactgtac 240

ctgcagatga atagcctgag agccgaggat actgccgtgt actattgcac aacgggaatc 300

gttaggcctt ttctgtactg gggacagggc accttggtta ctgtctcgag cgcttctaca 360

aagggcccat ccgtcttccc cctggcgccc tgctccagga gcacctccga gagcacagcc 420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacgaagac ctacacctgc 600

aacgtagatc acaagcccag caacaccaag gtggacaaga gagttggtga gaggccagca 660

cagggaggga gggtgtctgc tggaagccag gctcagccct cctgcctgga cgcaccccgg 720

ctgtgcagcc ccagcccagg gcagcaaggc atgccccatc tgtctcctca cccggaggcc 780

tctgaccacc ccactcatgc ccagggagag ggtcttctgg atttttccac caggctccgg 840

gcagccacag gctggatgcc cctaccccag gccctgcgca tacaggggca ggtgctgcgc 900

tcagacctgc caagagccat atccgggagg accctgcccc tgacctaagc ccaccccaaa 960

ggccaaactc tccactccct cagctcagac accttctctc ctcccagatc tgagtaactc 1020

ccaatcttct ctctgcagag tccaaatatg gtcccccatg cccaccatgc ccaggtaagc 1080

caacccaggc ctcgccctcc agctcaaggc gggacaggtg ccctagagta gcctgcatcc 1140

agggacaggc cccagccggg tgctgacgca tccacctcca tctcttcctc agcacctgag 1200

ttcctggggg gaccatcagt cttcctgttc cccccaaaac ccaaggacac tctcatgatc 1260

tcccggaccc ctgaggtcac gtgcgtggtg gtggacgtga gccaggaaga ccccgaggtc 1320

cagttcaact ggtacgtgga tggcgtggag gtgcataatg ccaagacaaa gccgcgggag 1380

gagcagttca acagcacgta ccgtgtggtc agcgtcctca ccgtcctgca ccaggactgg 1440

ctgaacggca aggagtacaa gtgcaaggtc tccaacaaag gcctcccgtc ctccatcgag 1500

aaaaccatct ccaaagccaa aggtgggacc cacggggtgc gagggccaca tggacagagg 1560

tcagctcggc ccaccctctg ccctgggagt gaccgctgtg ccaacctctg tccctacagg 1620

gcagccccga gagccacagg tgtacaccct gcccccatcc caggaggaga tgaccaagaa 1680

ccaggtcagc ctgacctgcc tggtcaaagg cttctacccc agcgacatcg ccgtggagtg 1740

ggagagcaat gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga 1800

cggctccttc ttcctctaca gcaggctaac cgtggacaag agcaggtggc aggaggggaa 1860

tgtcttctca tgctccgtga tgcatgaggc tctgcacaac cactacacac agaagagcct 1920

ctccctgtct ctgggtaaa 1939

<210> 45
<211> 1996
<212> DNA
<213> Artificial

<220>
<223> 1519gH20 IgG4 heavy chain (V + human gamma-4P constant) with signal sequence

<400> 45
atggaatgga gctgggtctt tctcttcttc ctgtcagtaa ctacaggagt ccattctgag 60

gtaccacttg tggaaagcgg aggaggtctt gtgcagcctg gaggaagttt acgtctctct 120

tgtgctgtgt ctggcttcac cttctccaat tacggaatgg tctgggtcag acaagcacct 180

ggaaagggtc ttgaatgggt ggcctatatt gactctgacg gggacaacac ctactatcgg 240

gattccgtga aaggacgctt cacaatctcc cgagataacg ccaagagctc actgtacctg 300

cagatgaata gcctgagagc cgaggatact gccgtgtact attgcacaac gggaatcgtt 360

aggccttttc tgtactgggg acagggcacc ttggttactg tctcgagcgc ttctacaaag 420

ggcccatccg tcttcccccc ggcgccctgc tccaggagca cctccgagag cacagccgcc 480

ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 540

gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc 600

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cgaagaccta cacctgcaac 660

gtagatcaca agcccagcaa caccaaggtg gacaagagag ttggtgagag gccagcacag 720

ggagggaggg tgtctgctgg aagccaggct cagccctcct gcctggacgc accccggctg 780

tgcagcccca gcccagggca gcaaggcatg ccccatctgt ctcctcaccc ggaggcctct 840

gaccacccca ctcatgccca gggagagggt cttctggatt tttccaccag gctccgggca 900

gccacaggct ggatgcccct accccaggcc ctgcgcatac aggggcaggt gctgcgctca 960

gacctgccaa gagccatatc cgggaggacc ctgcccctga cctaagccca ccccaaaggc 1020

caaactctcc actccctcag ctcagacacc ttctctcctc ccagatctga gtaactccca 1080

atcttctctc tgcagagtcc aaatatggtc ccccatgccc accatgccca ggtaagccaa 1140

cccaggcctc gccctccagc tcaaggcggg acaggtgccc tagagtagcc tgcatccagg 1200

gacaggcccc agccgggtgc tgacgcatcc acctccatct cttcctcagc acctgagttc 1260

ctgggggggac catcagtctt cctgttcccc ccaaaaccca aggacactct catgatctcc 1320

cggacccctg aggtcacgtg cgtggtggtg gacgtgagcc aggaagaccc cgaggtccag 1380

ttcaactggt acgtggatgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 1440

cagttcaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 1500

aacggcaagg agtacaagtg caaggtctcc aacaaaggcc tcccgtcctc catcgagaaa 1560

accatctcca aagccaaagg tgggacccac ggggtgcgag ggccacatgg acagaggtca 1620

gctcggccca ccctctgccc tgggagtgac cgctgtgcca acctctgtcc ctacagggca 1680

gccccgagag ccacaggtgt acaccctgcc cccatcccag gaggagatga ccaagaacca 1740

ggtcagcctg acctgcctgg tcaaaggctt ctaccccagc gacatcgccg tggagtggga 1800

gagcaatggg cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg 1860

ctccttcttc ctctacagca ggctaaccgt ggacaagagc aggtggcagg aggggaatgt 1920

cttctcatgc tccgtgatgc atgaggctct gcacaaccac tacacacaga agagcctctc 1980

cctgtctctg ggtaaa 1996

<210> 46
<211> 347
<212> PRT
<213> Artificial

<220>
<223> 1519gL20 FabFv light chain

<400> 46

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 Ser Ser Gln Ser Leu Val Gly Ala
20 25 30

Ser Gly Lys Thr Tyr Leu Tyr Trp Leu Phe Gln Lys Pro Gly Lys Ala
35 40 45

Pro Lys Arg Leu Ile Tyr Leu Val Ser Thr Leu Asp Ser Gly Ile Pro
50 55 60

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

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

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

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

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

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

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

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

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

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

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr
225                 230                 235                 240

Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly Asp Arg Val Thr Ile
                245                 250                 255

Thr Cys Gln Ser Ser Pro Ser Val Trp Ser Asn Phe Leu Ser Trp Tyr
            260                 265                 270

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Glu Ala Ser
        275                 280                 285

Lys Leu Thr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
    290                 295                 300

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
305                 310                 315                 320

Thr Tyr Tyr Cys Gly Gly Gly Tyr Ser Ser Ile Ser Asp Thr Thr Phe
                325                 330                 335

Gly Cys Gly Thr Lys Val Glu Ile Lys Arg Thr
            340                 345
```

<210> 47
<211> 1041
<212> DNA
<213> Artificial

<220>
<223> 1519gL20 FabFv light chain

<400> 47

```
gatatccaga tgacccagag cccatctagc ttatccgctt ccgttggtga tcgcgtgaca       60

attacgtgta agagctccca atctctcgtg ggtgcaagtg gcaagaccta tctgtactgg      120

ctctttcaga agcctggcaa ggcaccaaaa cggctgatct atctggtgtc taccttgac       180

tctgggatac cgtcacgatt ttccggatct gggagcggaa ctgagttcac actcacgatt      240
```

tcatcgctgc aacccgagga ctttgctacc tactactgcc tgcaaggcac tcatttccct 300

cacactttcg gccaggggac aaaactcgaa atcaaacgta cggtagcggc cccatctgtc 360

ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg 420

ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa 480

tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctg 540

agcagcaccc tgacgctgtc taaagcagac tacgagaaac acaaagtgta cgcctgcgaa 600

gtcacccatc agggcctgag ctcaccagta acaaaaagtt ttaatagagg ggagtgtagc 660

ggtggcggtg gcagtggtgg gggaggctcc ggaggtggcg gttcagacat acaaatgacc 720

cagagtcctt catcggtatc cgcgtccgtt ggcgataggg tgactattac atgtcaaagc 780

tctcctagcg tctggagcaa ttttctatcc tggtatcaac agaaaccggg gaaggctcca 840

aaacttctga tttatgaagc ctcgaaactc accagtggag ttccgtcaag attcagtggc 900

tctggatcag ggacagactt cacgttgaca atcagttcgc tgcaaccaga ggactttgcg 960

acctactatt gtggtggagg ttacagtagc ataagtgata cgacatttgg gtgcggtact 1020

aaggtggaaa tcaaacgtac c 1041

<210> 48
<211> 367
<212> PRT
<213> Artificial

<220>
<223> 1519gL20 FabFv light chain with signal sequence

<400> 48

Met Ser Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr
1 5 10 15

Asp Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
20 25 30

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

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

Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Leu Val Ser Thr Leu Asp
65 70 75 80

Ser Gly Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe
85 90 95

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
100 105 110

```
Cys Leu Gln Gly Thr His Phe Pro His Thr Phe Gly Gln Gly Thr Lys
        115                 120                 125

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

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

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

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

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

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

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Ser
225                 230                 235                 240

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
                245                 250                 255

Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly Asp
            260                 265                 270

Arg Val Thr Ile Thr Cys Gln Ser Ser Pro Ser Val Trp Ser Asn Phe
        275                 280                 285

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
    290                 295                 300

Tyr Glu Ala Ser Lys Leu Thr Ser Gly Val Pro Ser Arg Phe Ser Gly
305                 310                 315                 320

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
                325                 330                 335

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gly Gly Tyr Ser Ser Ile Ser
            340                 345                 350

Asp Thr Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys Arg Thr
        355                 360                 365


<210>  49
<211>  1101
<212>  DNA
<213>  Artificial
```

<220>
<223> 1519gL20 FabFv light chain with signal sequence

<400> 49
atgtctgtcc ccacccaagt cctcggactc ctgctactct ggcttacaga tgccagatgc 60

gatatccaga tgacccagag cccatctagc ttatccgctt ccgttggtga tcgcgtgaca 120

attacgtgta agagctccca atctctcgtg ggtgcaagtg gcaagaccta tctgtactgg 180

ctctttcaga agcctggcaa ggcaccaaaa cggctgatct atctggtgtc taccttgac 240

tctgggatac cgtcacgatt ttccggatct gggagcggaa ctgagttcac actcacgatt 300

tcatcgctgc aacccgagga ctttgctacc tactactgcc tgcaaggcac tcatttccct 360

cacactttcg gccaggggac aaaactcgaa atcaaacgta cggtagcggc cccatctgtc 420

ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg 480

ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa 540

tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctg 600

agcagcaccc tgacgctgtc taaagcagac tacgagaaac acaaagtgta cgcctgcgaa 660

gtcacccatc agggcctgag ctcaccagta acaaaaagtt ttaatagagg ggagtgtagc 720

ggtggcggtg gcagtggtgg gggaggctcc ggaggtggcg gttcagacat acaaatgacc 780

cagagtcctt catcggtatc cgcgtccgtt ggcgataggg tgactattac atgtcaaagc 840

tctcctagcg tctggagcaa ttttctatcc tggtatcaac agaaaccggg gaaggctcca 900

aaacttctga tttatgaagc ctcgaaactc accagtggag ttccgtcaag attcagtggc 960

tctggatcag ggacagactt cacgttgaca atcagttcgc tgcaaccaga ggactttgcg 1020

acctactatt gtggtggagg ttacagtagc ataagtgata cgacatttgg gtgcggtact 1080

aaggtggaaa tcaaacgtac c 1101

<210> 50
<211> 357
<212> PRT
<213> Artificial

<220>
<223> 1519gH20 FabFv heavy chain

<400> 50

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

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

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

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

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

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

Thr Thr Gly Ile Val Arg Pro Phe Leu Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110

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

Ala Pro 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 Lys Val Glu Pro Lys Ser Cys Ser Gly Gly Gly
    210                 215                 220

Gly Ser Gly Gly Gly Gly Thr Gly Gly Gly Gly Ser Glu Val Gln Leu
225                 230                 235                 240

Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu
                245                 250                 255

Ser Cys Ala Val Ser Gly Ile Asp Leu Ser Asn Tyr Ala Ile Asn Trp
            260                 265                 270

Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Ile Gly Ile Ile Trp
        275                 280                 285

Ala Ser Gly Thr Thr Phe Tyr Ala Thr Trp Ala Lys Gly Arg Phe Thr
    290                 295                 300

Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr Leu Gln Met Asn Ser
305                 310                 315                 320

Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Thr Val Pro
                325                 330                 335
```

Gly Tyr Ser Thr Ala Pro Tyr Phe Asp Leu Trp Gly Gln Gly Thr Leu
340 345 350

Val Thr Val Ser Ser
355

<210> 51
<211> 1071
<212> DNA
<213> Artificial

<220>
<223> 1519gH20 FabFv heavy chain

<400> 51
gaggtaccac ttgtggaaag cggaggaggt cttgtgcagc ctggaggaag tttacgtctc 60

tcttgtgctg tgtctggctt caccttctcc aattacggaa tggtctgggt cagacaagca 120

cctggaaagg gtcttgaatg ggtggcctat attgactctg acggggacaa cacctactat 180

cgggattccg tgaaaggacg cttcacaatc tcccgagata acgccaagag ctcactgtac 240

ctgcagatga atagcctgag agccgaggat actgccgtgt actattgcac aacgggaatc 300

gttaggcctt ttctgtactg gggacagggc accttggtta ctgtctcgag cgcgtccaca 360

aagggcccat cggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 420

gccctgggct gcctggtcaa ggactacttc cccgaaccag tgacggtgtc gtggaactca 480

ggtgccctga ccagcggcgt tcacaccttc ccggctgtcc tacagtcttc aggactctac 540

tccctgagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 600

aacgtgaatc acaagcccag caacaccaag gtcgataaga aagttgagcc caaatcttgt 660

agtggaggtg ggggctcagg tggaggcggg accggtggag gtggcagcga ggttcaactg 720

cttgagtctg gaggaggcct agtccagcct ggagggagcc tgcgtctctc ttgtgcagta 780

agcggcatcg acctgagcaa ttacgccatc aactgggtga gacaagctcc ggggaagtgt 840

ttagaatgga tcggtataat atgggccagt gggacgacct tttatgctac atgggcgaaa 900

ggaaggttta caattagccg ggacaatagc aaaaacaccg tgtatctcca aatgaactcc 960

ttgcgagcag aggacacggc ggtgtactat tgtgctcgca ctgtcccagg ttatagcact 1020

gcaccctact tcgatctgtg gggacaaggg accctggtga ctgtttcaag t 1071

<210> 52
<211> 376
<212> PRT
<213> Artificial

<220>
<223> 1519gH20 FabFv heavy chain with signal sequence

<400> 52

Met Glu Trp Ser Trp Val Phe Leu Phe Phe Leu Ser Val Thr Thr Gly
1 5 10 15

```
Val His Ser Glu Val Pro Leu Val Glu Ser Gly Gly Gly Leu Val Gln
            20                  25                  30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Thr Phe
        35                  40                  45

Ser Asn Tyr Gly Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
    50                  55                  60

Glu Trp Val Ala Tyr Ile Asp Ser Asp Gly Asp Asn Thr Tyr Tyr Arg
65                  70                  75                  80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Ser
                85                  90                  95

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

Tyr Tyr Cys Thr Thr Gly Ile Val Arg Pro Phe Leu Tyr Trp Gly Gln
        115                 120                 125

Gly Thr Leu Val 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 Lys Val Glu Pro Lys Ser Cys Ser
225                 230                 235                 240

Gly Gly Gly Gly Ser Gly Gly Gly Gly Thr Gly Gly Gly Gly Ser Glu
                245                 250                 255

Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
            260                 265                 270

Leu Arg Leu Ser Cys Ala Val Ser Gly Ile Asp Leu Ser Asn Tyr Ala
        275                 280                 285
```

```
Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Ile Gly
    290                 295                 300

Ile Ile Trp Ala Ser Gly Thr Thr Phe Tyr Ala Thr Trp Ala Lys Gly
305                 310                 315                 320

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr Leu Gln
                325                 330                 335

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
            340                 345                 350

Thr Val Pro Gly Tyr Ser Thr Ala Pro Tyr Phe Asp Leu Trp Gly Gln
        355                 360                 365

Gly Thr Leu Val Thr Val Ser Ser
    370                 375
```

<210> 53
<211> 1128
<212> DNA
<213> Artificial

<220>
<223> 1519gH20 FabFv heavy chain with signal sequence

<400> 53

```
atggaatgga gctgggtctt tctcttcttc ctgtcagtaa ctacaggagt ccattctgag       60

gtaccacttg tggaaagcgg aggaggtctt gtgcagcctg gaggaagttt acgtctctct      120

tgtgctgtgt ctggcttcac cttctccaat tacggaatgg tctgggtcag acaagcacct      180

ggaaagggtc ttgaatgggt ggcctatatt gactctgacg gggacaacac ctactatcgg      240

gattccgtga aaggacgctt cacaatctcc cgagataacg ccaagagctc actgtacctg      300

cagatgaata gcctgagagc cgaggatact gccgtgtact attgcacaac gggaatcgtt      360

aggccttttc tgtactgggg acagggcacc ttggttactg tctcgagcgc gtccacaaag      420

ggcccatcgg tcttcccccc ggcaccctcc tccaagagca cctctggggg cacagcggcc      480

ctgggctgcc tggtcaagga ctacttcccc gaaccagtga cggtgtcgtg gaactcaggt      540

gccctgacca gcggcgttca caccttcccg gctgtcctac agtcttcagg actctactcc      600

ctgagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac      660

gtgaatcaca agcccagcaa caccaaggtc gataagaaag ttgagcccaa atcttgtagt      720

ggaggtgggg gctcaggtgg aggcgggacc ggtggaggtg gcagcgaggt tcaactgctt      780

gagtctggag gaggcctagt ccagcctgga gggagcctgc gtctctcttg tgcagtaagc      840

ggcatcgacc tgagcaatta cgccatcaac tgggtgagac aagctccggg gaagtgttta      900

gaatggatcg gtataatatg ggccagtggg acgacctttt atgctacatg ggcgaaagga      960

aggtttacaa ttagccggga caatagcaaa aacaccgtgt atctccaaat gaactccttg     1020
```

cgagcagagg acacggcggt gtactattgt gctcgcactg tcccaggtta tagcactgca 1080

ccctacttcg atctgtgggg acaagggacc ctggtgactg tttcaagt 1128

<210> 54
<211> 107
<212> PRT
<213> Artificial

<220>
<223> Human VK1 2-1-(1) A30 JK2 acceptor framework

<400> 54

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

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

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

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

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

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

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

<210> 55
<211> 321
<212> DNA
<213> Artificial

<220>
<223> Human VK1 2-1-(1) A30 JK2 acceptor framework

<400> 55
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gggcattaga aatgatttag gctggtatca gcagaaacca 120

gggaaagccc ctaagcgcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240

gaagattttg caacttatta ctgtctacag cataatagtt acccttacac ttttggccag 300

gggaccaagc tggagatcaa a 321

<210> 56
<211> 112

<212> PRT
<213> Artificial

<220>
<223> Human VH3 1-3 3-07 JH4 acceptor framework

<400> 56

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

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

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

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

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

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

Ala Arg Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
100 105 110

<210> 57
<211> 336
<212> DNA
<213> Artificial

<220>
<223> Human VH3 1-3 3-07 JH4 acceptor framework

<400> 57
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagt agctattgga tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtggccaac ataaagcaag atggaagtga gaaatactat 180

gtggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctcactgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagatacttt 300

gactactggg gccagggaac cctggtcacc gtctcc 336

<210> 58
<211> 112
<212> PRT
<213> Artificial

<220>
<223> Rat Ab 1548 VL region

<400> 58

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Val Gly Ala
20 25 30

Ser Gly Lys Thr Tyr Leu Tyr Trp Leu Phe Gln Arg Ser Gly Gln Ser
35 40 45

Pro Lys Arg Leu Ile Tyr Leu Val Ser Thr Leu Asp Ser Gly Ile Pro
50 55 60

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

Arg Arg Val Glu Ala Asp Asp Leu Gly Val Tyr Tyr Cys Leu Gln Gly
85 90 95

Thr His Phe Pro His Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 59
<211> 336
<212> DNA
<213> Artificial

<220>
<223> Rat Ab 1548 VL region

<400> 59
gatgttgtga tgacccagac tccactgtct ttgtcggttg cccttggaca accagcctcc 60

atctcttgca agtcaagtca gagcctcgta ggtgctagtg gaaagacata tttgtattgg 120

ttatttcaga ggtccggcca gtctccaaag cgactaatct atctggtgtc cacactggac 180

tctggaattc ctgataggtt cagtggcagt ggagcagaga cagattttac tcttaaaatc 240

cgcagagtgg aagccgatga tttgggagtt tattactgct tgcaaggtac acattttcct 300

cacacgtttg gagctgggac caagctggaa ataaaa 336

<210> 60
<211> 116
<212> PRT
<213> Artificial

<220>
<223> Rat Ab 1548 VH region

<400> 60

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

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

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

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

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

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

Thr Thr Gly Ile Val Arg Pro Phe Leu Tyr Trp Gly Gln Gly Val Met
            100                 105                 110

Val Thr Val Ser
        115
```

<210> 61
<211> 348
<212> DNA
<213> Artificial

<220>
<223> Rat Ab 1548 VH region

<400> 61

```
gaggtgccgc tggtggagtc tgggggcggc tcagtgcagc ctgggaggtc catgaaactc       60

tcctgtgtag tctcaggatt cactttcagt aattatggca tggtctgggt ccgccaggct      120

ccaaagaagg gtctggagtg ggtcgcatat attgattctg atggtgataa tacttactac      180

cgagattccg tgaagggccg attcactatc tccagaaata atgcaaaaag cacctatat       240

ttgcaaatgg acagtctgag gtctgaggac acggccactt attactgtac aacagggatt      300

gtccggccct ttctctattg gggccaagga gtcatggtca cagtctcg                   348
```

<210> 62
<211> 112
<212> PRT
<213> Artificial

<220>
<223> Rat Ab 1644 VL region

<400> 62

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Val Gly Ala
            20                  25                  30

Ser Gly Lys Thr Tyr Leu Tyr Trp Leu Phe Gln Arg Ser Gly Gln Ser
        35                  40                  45
```

```
Pro Lys Arg Leu Ile Tyr Leu Val Ser Thr Leu Asp Ser Gly Ile Pro
    50                  55                  60

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

Arg Arg Val Glu Ala Asp Asp Leu Gly Val Tyr Tyr Cys Leu Gln Gly
                85                  90                  95

Thr His Phe Pro His Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
            100                 105                 110
```

<210> 63
<211> 336
<212> DNA
<213> Artificial

<220>
<223> Rat Ab 1644 VL region

<400> 63

```
gatgttgtga tgacccagac tccactgtct ttgtcggttg ccattggaca accagcctcc       60

atctcttgca agtcaagtca gagcctcgta ggtgctagtg gaaagacata tttgtattgg      120

ttatttcaga ggtccggcca gtctccaaag cgactaatct atctggtgtc cacactggac      180

tctggaattc ctgataggtt cagtggcagt ggagcagaga cagattttac tcttaaaatc      240

cgcagagtgg aagccgatga tttgggagtt tattactgct tgcaaggtac acattttcct      300

cacacgtttg gagctgggac caagctggaa ctgaaa                                336
```

<210> 64
<211> 116
<212> PRT
<213> Artificial

<220>
<223> Rat Ab 1644 VH region

<400> 64

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

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

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

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

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

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

Thr Thr Gly Ile Val Arg Pro Phe Leu Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser
115

<210> 65
<211> 348
<212> DNA
<213> Artificial

<220>
<223> Rat Ab 1644 VH region

<400> 65
gaggtgccgc tggtggagtc tgggggcggc tcagtgcagc ctgggaggtc cacgaaactc 60

tcctgtgtag tctcaggatt cactttcagt aactatggca tggtctgggt ccgccaggct 120

ccaaagaagg gtctggagtg ggtcgcatat attggttctg atggtgataa tatttactac 180

cgagattccg tgaagggtcg attcactatc tccagaaata atgcaaaaag cacctatat 240

ttgcaaatgg acagtctgag gtctgaggac acggccactt attactgtac aacagggatt 300

gtccggccct ttctctactg gggccaagga accacggtca ccgtctcg 348

<210> 66
<211> 112
<212> PRT
<213> Artificial

<220>
<223> Rat Ab 1496 VK region

<400> 66

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Val Gly Ala
20 25 30

Ser Gly Lys Thr Tyr Leu Tyr Trp Leu Phe Gln Arg Ser Gly Gln Ser
35 40 45

Pro Lys Arg Leu Ile Tyr Leu Val Ser Thr Leu Asp Ser Gly Ile Pro
50 55 60

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

Arg Arg Val Glu Ala Asp Asp Leu Gly Val Tyr Tyr Cys Leu Gln Gly
85 90 95

Thr His Phe Pro His Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105 110

<210> 67
<211> 336
<212> DNA
<213> Artificial

<220>
<223> Rat Ab 1496 VK region

<400> 67
gatgttgtga tgacccagac tccactgtct ttgtcggttg cccttggaca accagcctcc 60

atctcttgca agtcaagtca gagcctcgta ggtgctagtg gaaagacata tttgtattgg 120

ttatttcaga ggtccggcca gtctccaaag cgactaatct atctggtgtc cacactggac 180

tctggaattc ctgataggtt cagtggcagt ggagcagaga cagattttac tcttaaaatc 240

cgcagagtgg aagccgatga tttgggagtt tattactgct tgcaaggtac acattttcct 300

cacacgtttg gagctgggac caagctggaa ctgaaa 336

<210> 68
<211> 116
<212> PRT
<213> Artificial

<220>
<223> Rat Ab 1496 VH region

<400> 68

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

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

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

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

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

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

Thr Thr Gly Ile Val Arg Pro Phe Leu Tyr Trp Gly Gln Gly Thr Met
100 105 110

Val Thr Val Ser
115

<210> 69
<211> 348
<212> DNA
<213> Artificial

<220>
<223> Rat Ab 1496 VH region

<400> 69
gaggtgctgc tggtggagtc tgggggcggc tcagtgcagc ctgggaggtc catgaaactc 60

tcctgtgtag tctcaggatt cactttcagt aattatggca tggtctgggt ccgccaggct 120

ccaaagaagg gtctggagtg ggtcgcatat attgattctg atggtgataa tacttactac 180

cgagattccg tgaagggccg attcactatc tccagaaata atgcaaaaag caccctatat 240

ttgcaaatgg acagtctgag gtctgaggac acggccactt attactgtac aacagggatt 300

gtccggccct ttctctattg gggccaagga accatggtca ccgtctcg 348

<210> 70
<211> 14
<212> PRT
<213> Artificial

<220>
<223> framework

<400> 70

Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
1 5 10

<210> 71
<211> 12
<212> PRT
<213> Artificial

<220>
<223> framework

<400> 71

Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
1 5 10

<210> 72
<211> 447
<212> PRT
<213> Artificial

<220>
<223> 1519gH2O IgG1 heavy chain (V + human gamma-1 constant)

<400> 72

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

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

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

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

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

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

Thr Thr Gly Ile Val Arg Pro Phe Leu Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110

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

Ala Pro 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 Lys 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 Asp Glu Leu 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>  73
<211>  1947
<212>  DNA
<213>  Artificial

<220>
<223>  1519gH20 IgG1 heavy chain (V + human gamma-1 constant with exons)

<400>  73
gaggtaccac ttgtggaaag cggaggaggt cttgtgcagc ctggaggaag tttacgtctc       60

tcttgtgctg tgtctggctt caccttctcc aattacggaa tggtctgggt cagacaagca      120

cctggaaagg gtcttgaatg ggtggcctat attgactctg acggggacaa cacctactat      180

cgggattccg tgaaaggacg cttcacaatc tcccgagata acgccaagag ctcactgtac      240

ctgcagatga atagcctgag agccgaggat actgccgtgt actattgcac aacgggaatc      300

gttaggcctt ttctgtactg gggacagggc accttggtta ctgtctcgag cgcttctaca      360

aagggcccat cggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg      420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca      480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac      540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc      600

aacgtgaatc acaagcccag caacaccaag gtcgacaaga aagttggtga gaggccagca      660

cagggaggga gggtgtctgc tggaagccag gctcagcgct cctgcctgga cgcatcccgg      720
```

ctatgcagcc ccagtccagg gcagcaaggc aggccccgtc tgcctcttca cccggaggcc 780

tctgcccgcc ccactcatgc tcagggagag ggtcttctgg ctttttcccc aggctctggg 840

caggcacagg ctaggtgccc ctaacccagg ccctgcacac aaaggggcag gtgctgggct 900

cagacctgcc aagagccata tccgggagga ccctgcccct gacctaagcc caccccaaag 960

gccaaactct ccactccctc agctcggaca ccttctctcc tcccagatct gagtaactcc 1020

caatcttctc tctgcagagc ccaaatcttg tgacaaaact cacacatgcc caccgtgccc 1080

aggtaagcca gcccaggcct cgccctccag ctcaaggcgg gacaggtgcc ctagagtagc 1140

ctgcatccag ggacaggccc cagccgggtg ctgacacgtc cacctccatc tcttcctcag 1200

cacctgaact cctgggggga ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc 1260

tcatgatctc ccggacccct gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc 1320

ctgaggtcaa gttcaactgg tacgtggacg gcgtggaggt gcataatgcc aagacaaagc 1380

cgcgggagga gcagtacaac agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc 1440

aggactggct gaatggcaag gagtacaagt gcaaggtctc caacaaagcc ctcccagccc 1500

ccatcgagaa aaccatctcc aaagccaaag gtgggacccg tggggtgcga gggccacatg 1560

gacagaggcc ggctcggccc accctctgcc ctgagagtga ccgctgtacc aacctctgtc 1620

cctacagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1680

accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1740

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1800

gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1860

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1920

aagagcctct ccctgtctcc gggtaaa 1947

<210> 74
<211> 2004
<212> DNA
<213> Artificial

<220>
<223> 1519gH20 IgG1 heavy chain (V + human gamma-1 constant) with signal sequence

<400> 74
atggaatgga gctgggtctt tctcttcttc ctgtcagtaa ctacaggagt ccattctgag 60

gtaccacttg tggaaagcgg aggaggtctt gtgcagcctg gaggaagttt acgtctctct 120

tgtgctgtgt ctggcttcac cttctccaat tacggaatgg tctgggtcag acaagcacct 180

ggaaagggtc ttgaatgggt ggcctatatt gactctgacg gggacaacac ctactatcgg 240

gattccgtga aaggacgctt cacaatctcc cgagataacg ccaagagctc actgtacctg 300

cagatgaata gcctgagagc cgaggatact gccgtgtact attgcacaac gggaatcgtt 360

aggccttttc tgtactgggg acagggcacc ttggttactg tctcgagcgc ttctacaaag 420

ggcccatcgg tcttcccccc ggcaccctcc tccaagagca cctctggggg cacagcggcc 480

ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 540

gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc 600

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 660

gtgaatcaca agcccagcaa caccaaggtc gacaagaaag ttggtgagag gccagcacag 720

ggagggaggg tgtctgctgg aagccaggct cagcgctcct gcctggacgc atcccggcta 780

tgcagcccca gtccagggca gcaaggcagg ccccgtctgc ctcttcaccc ggaggcctct 840

gcccgcccca ctcatgctca gggagagggt cttctggctt tttccccagg ctctgggcag 900

gcacaggcta ggtgccccta acccaggccc tgcacacaaa ggggcaggtg ctgggctcag 960

acctgccaag agccatatcc gggaggaccc tgcccctgac ctaagcccac cccaaaggcc 1020

aaactctcca ctccctcagc tcggacacct tctctcctcc cagatctgag taactcccaa 1080

tcttctctct gcagagccca aatcttgtga caaaactcac acatgcccac cgtgcccagg 1140

taagccagcc caggcctcgc cctccagctc aaggcgggac aggtgcccta gagtagcctg 1200

catccaggga caggccccag ccgggtgctg acacgtccac ctccatctct tcctcagcac 1260

ctgaactcct gggggggaccg tcagtcttcc tcttcccccc aaaacccaag gacaccctca 1320

tgatctcccg gacccctgag gtcacatgcg tggtggtgga cgtgagccac gaagaccctg 1380

aggtcaagtt caactggtac gtggacggcg tggaggtgca taatgccaag acaaagccgc 1440

gggaggagca gtacaacagc acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg 1500

actggctgaa tggcaaggag tacaagtgca aggtctccaa caaagccctc ccagccccca 1560

tcgagaaaac catctccaaa gccaaaggtg ggacccgtgg ggtgcgaggg ccacatggac 1620

agaggccggc tcggcccacc ctctgccctg agagtgaccg ctgtaccaac ctctgtccct 1680

acagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc 1740

aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1800

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1860

tccgacggct ccttcttcct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag 1920

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1980

agcctctccc tgtctccggg taaa 2004

<210> 75
<211> 657
<212> DNA
<213> Artificial

<220>
<223> 1519 gL20 light chain (V + constant, mammalian expression alternative)

<400> 75
gatatccaga tgacccagag cccatctagc ttatccgctt ccgttggtga tcgcgtgaca 60

attacgtgta agagctccca atctctcgtg ggtgcaagtg gcaagaccta tctgtactgg 120

ctctttcaga agcctggcaa ggcaccaaaa cggctgatct atctggtgtc tacccttgac 180

tctgggatac cgtcacgatt ttccggatct gggagcggaa ctgagttcac actcacgatt 240

tcatcgctgc aacccgagga ctttgctacc tactactgcc tgcaaggcac tcatttccct 300

cacactttcg gccaggggac aaaactcgaa atcaaacgta cggtagcggc cccatctgtc 360

ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg 420

ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa 480

tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc 540

agcagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 600

gtcacccatc agggcctgag ctcgcccgtc acaaagagct tcaacagggg agagtgt 657

<210> 76
<211> 684
<212> DNA
<213> Artificial

<220>
<223> 1519gH2O Fab' heavy chain (V + human gamma-1 CH1 + hinge, mammalian expression one base change from SEQ ID NO: 38)

<400> 76
gaggtaccac ttgtggaaag cggaggaggt cttgtgcagc ctggaggaag tttacgtctc 60

tcttgtgctg tgtctggctt caccttctcc aattacggaa tggtctgggt cagacaagca 120

cctggaaagg gtcttgaatg ggtggcctat attgactctg acggggacaa cacctactat 180

cgggattccg tgaaaggacg cttcacaatc tcccgagata acgccaagag ctcactgtac 240

ctgcagatga atagcctgag agccgaggat actgccgtgt actattgcac aacgggaatc 300

gttaggcctt ttctgtactg gggacagggc accttggtta ctgtctcgag cgcttctaca 360

aagggcccat cggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 600

aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 660

gacaaaactc acacatgcgc cgcg 684

<210> 77
<211> 741
<212> DNA
<213> Artificial

<220>
<223> 1519 gH2O Fab' heavy chain with signal sequence (mammalian expression one base changed from SEQ ID NO: 42)

<400> 77
atggaatgga gctgggtctt tctcttcttc ctgtcagtaa ctacaggagt ccattctgag 60

gtaccacttg tggaaagcgg aggaggtctt gtgcagcctg gaggaagttt acgtctctct 120

tgtgctgtgt ctggcttcac cttctccaat tacggaatgg tctgggtcag acaagcacct 180

ggaaagggtc ttgaatgggt ggcctatatt gactctgacg gggacaacac ctactatcgg 240

gattccgtga aaggacgctt cacaatctcc cgagataacg ccaagagctc actgtacctg 300

cagatgaata gcctgagagc cgaggatact gccgtgtact attgcacaac gggaatcgtt 360

aggccttttc tgtactgggg acagggcacc ttggttactg tctcgagcgc ttctacaaag 420

ggcccatcgg tcttcccccc ggcaccctcc tccaagagca cctctggggg cacagcggcc 480

ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 540

gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc 600

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 660

gtgaatcaca agcccagcaa caccaaggtg gacaagaaag ttgagcccaa atcttgtgac 720

aaaactcaca catgcgccgc g 741

<210> 78
<211> 346
<212> PRT
<213> Artificial

<220>
<223> 1519gL20 FabFv light chain (alternative sequence to SEQ ID NO: 46)

<400> 78

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 Ser Ser Gln Ser Leu Val Gly Ala
20 25 30

Ser Gly Lys Thr Tyr Leu Tyr Trp Leu Phe Gln Lys Pro Gly Lys Ala
35 40 45

Pro Lys Arg Leu Ile Tyr Leu Val Ser Thr Leu Asp Ser Gly Ile Pro
50 55 60

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

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

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

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

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe

130 135 140

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

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

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

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

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

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln
225 230 235 240

Ser Pro Ser Ser Val Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
245 250 255

Cys Gln Ser Ser Pro Ser Val Trp Ser Asn Phe Leu Ser Trp Tyr Gln
260 265 270

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Glu Ala Ser Lys
275 280 285

Leu Thr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
290 295 300

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
305 310 315 320

Tyr Tyr Cys Gly Gly Gly Tyr Ser Ser Ile Ser Asp Thr Thr Phe Gly
325 330 335

Cys Gly Thr Lys Val Glu Ile Lys Arg Thr
340 345

<210> 79
<211> 1038
<212> DNA
<213> Artificial

<220>
<223> 1519gL20 FabFv light chain (alternative sequence to SEQ ID NO: 47)

<400> 79
gacatccaga tgacccagtc cccctccagc ctgtccgcct ccgtgggcga cagagtgacc 60

atcacatgca agtcctccca gtccctggtc ggagcctccg gcaagaccta cctgtactgg 120

ctgttccaga agcccggcaa ggcccccaag cggctgatct acctggtgtc taccctggac 180

tccggcatcc cctcccggtt ctccggctct ggctctggca ccgagttcac cctgaccatc 240

tccagcctgc agcccgagga cttcgccacc tactactgtc tgcaaggcac ccacttcccc 300

cacaccttcg gccagggcac caagctggaa atcaagcgga ccgtagcggc cccatctgtc 360

ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg 420

ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa 480

tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc 540

agcagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 600

gtcacccatc agggcctgag ctcgcccgtc acaaagagct tcaacagggg agagtgtggt 660

ggaggtggct ctggcggtgg tggctccgga ggcggaggaa gcgacatcca gatgacccag 720

agcccttcct ctgtaagcgc cagtgtcgga gacagagtga ctattacctg ccaaagctcc 780

ccttcagtct ggtccaattt tctatcctgg tatcagcaaa agcccggaaa ggctcctaaa 840

ttgctgatct acgaagcaag caaactcacc agcggcgtgc ccagcaggtt cagcggcagt 900

gggtctggaa ctgactttac cctgacaatc tcctcactcc agcccgagga cttcgccacc 960

tattactgcg gtggaggtta cagtagcata agtgatacga catttggatg cggcactaaa 1020

gtggaaatca agcgtacc 1038

<210> 80
<211> 1071
<212> DNA
<213> Artificial

<220>
<223> 1519gH2O FabFv heavy chain (alternative sequence to SEQ ID NO: 51)

<400> 80
gaggtgcccc tggtggaatc tggcggcgga ctggtgcagc ctggcggctc cctgagactg 60

tcttgcgccg tgtccggctt caccttctcc aactacggca tggtctgggt ccgacaggct 120

cctggcaagg gactggaatg ggtggcctac atcgactccg acggcgacaa cacctactac 180

cgggactccg tgaagggccg gttcaccatc tcccgggaca acgccaagtc ctccctgtac 240

ctgcagatga actccctgcg ggccgaggac accgccgtgt actactgcac caccggcatc 300

gtgcggccct ttctgtactg gggccagggc accctggtca ccgtgtcctc tgcttctaca 360

aagggcccat cggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc tggactctac 540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 600

aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 660

tccggaggtg gcggttccgg aggtggcggt acaggtggcg gtgggtccga agtccagctg 720

cttgaatccg gaggcggact cgtgcagccc ggaggcagtc ttcgcttgtc ctgcgctgta 780

tctggaatcg acctgagcaa ttacgccatc aactgggtga gacaggcacc tgggaaatgc 840

ctcgaatgga tcggcattat atgggctagt gggacgacct tttatgctac atgggcgaag 900

ggtagattca caatctcacg ggataatagt aagaacacag tgtacctgca gatgaactcc 960

ctgcgagcag aggataccgc cgtttactat tgtgctcgca ctgtcccagg ttatagcact 1020

gcaccctact ttgatctgtg ggggcagggc actctggtca ccgtctcgtc c 1071

<210> 81
<211> 112
<212> PRT
<213> Artificial

<220>
<223> Rat Ab 1548 VL region (alternative sequence to SEQ ID NO: 58)

<400> 81

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

Gln Pro Ala Ser Ile Ser Ser Lys Ser Ser Gln Ser Leu Val Gly Ala
20 25 30

Gly Gly Lys Thr Tyr Leu Tyr Trp Leu Leu Gln Arg Ser Gly Gln Ser
35 40 45

Pro Lys Arg Leu Ile Tyr Leu Val Ser Thr Leu Asp Ser Gly Ile Pro
50 55 60

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

Arg Arg Val Glu Ala Asp Asp Leu Gly Val Tyr Tyr Cys Leu Gln Gly
85 90 95

Thr His Phe Pro His Thr Phe Gly Ala Gly Thr Asn Leu Glu Ile Lys
100 105 110

<210> 82
<211> 336
<212> DNA
<213> Artificial

<220>
<223> Rat Ab 1548 VL region (alternative sequence to SEQ ID NO: 59)

<400> 82
gatgttgtga tgacccagac tccactgtct ttgtcggttg ccattggaca accagcctcc 60

atctcttcta agtcaagtca gagcctcgta ggtgctggtg gaaagacata tttgtattgg 120

ttattacaga ggtccggcca gtctccaaag cgactaatct atctggtgtc cacactggac 180

tctggaattc ctgataggtt cagtggcagt ggagcagaga cagattttac tcttaaaatc 240

cgcagagtgg aagccgatga tttgggagtt tattactgct tgcaaggtac acattttcct 300

cacacgtttg gagctgggac caacctggaa ataaaa 336

<210> 83
<211> 116
<212> PRT
<213> Artificial

<220>
<223> Rat Ab 1548 VH region (alternative sequence to SEQ ID NO: 60)

<400> 83

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

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

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

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

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

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

Thr Thr Gly Ile Val Arg Pro Phe Leu Tyr Trp Gly Gln Gly Val Met
100 105 110

Val Thr Val Ser
115

<210> 84
<211> 348
<212> DNA
<213> Artificial

<220>
<223> Rat Ab 1548 VH region (alternative sequence to SEQ IS NO: 61)

<400> 84
gaggtgccgc tggtggagtc tgggggcggc tcagtgcagc ctgggaggtc catgaaactc 60

tcctgtgtag tctcaggatt cactttcagt aactatggca tggtctgggt ccgccaggct 120

ccaaagaagg gtctggagtg ggtcgcatat attggttctg atggtgataa tacttactac 180

cgagattccg tgaagggccg attcactatc tccagaaata atgcaaaaag caccctatat 240

ttgcaaatgg acagtctgag gtctgaggac acggccactt attactgtac aacagggatt 300

gtccggccct ttctctactg gggccaagga gtcatggtca cagtctcg 348

<210> 85
<211> 1947
<212> DNA
<213> Artificial

<220>
<223> 1519gH20 IgG1 heavy chain (V + human gamma-1 constant with exons one base change to SEQ ID NO: 71)

<400> 85
gaggtaccac ttgtggaaag cggaggaggt cttgtgcagc ctggaggaag tttacgtctc 60

tcttgtgctg tgtctggctt caccttctcc aattacggaa tggtctgggt cagacaagca 120

cctggaaagg gtcttgaatg ggtggcctat attgactctg acggggacaa cacctactat 180

cgggattccg tgaaaggacg cttcacaatc tcccgagata acgccaagag ctcactgtac 240

ctgcagatga atagcctgag agccgaggat actgccgtgt actattgcac aacgggaatc 300

gttaggcctt ttctgtactg gggacagggc accttggtta ctgtctcgag cgcttctaca 360

aagggcccat cggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 600

aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttggtga gaggccagca 660

cagggaggga gggtgtctgc tggaagccag gctcagcgct cctgcctgga cgcatcccgg 720

ctatgcagcc ccagtccagg gcagcaaggc aggccccgtc tgcctcttca cccggaggcc 780

tctgcccgcc ccactcatgc tcagggagag ggtcttctgg ctttttcccc aggctctggg 840

caggcacagg ctaggtgccc ctaacccagg ccctgcacac aaaggggcag gtgctgggct 900

cagacctgcc aagagccata tccgggagga ccctgcccct gacctaagcc caccccaaag 960

gccaaactct ccactccctc agctcggaca ccttctctcc tcccagatct gagtaactcc 1020

caatcttctc tctgcagagc ccaaatcttg tgacaaaact cacacatgcc caccgtgccc 1080

aggtaagcca gcccaggcct cgccctccag ctcaaggcgg gacaggtgcc ctagagtagc 1140

ctgcatccag ggacaggccc cagccgggtg ctgacacgtc cacctccatc tcttcctcag 1200

cacctgaact cctgggggga ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc 1260

tcatgatctc ccggacccct gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc 1320

ctgaggtcaa gttcaactgg tacgtggacg gcgtggaggt gcataatgcc aagacaaagc 1380

cgcgggagga gcagtacaac agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc 1440

aggactggct gaatggcaag gagtacaagt gcaaggtctc caacaaagcc ctcccagccc 1500

ccatcgagaa aaccatctcc aaagccaaag gtgggacccg tggggtgcga gggccacatg 1560

gacagaggcc ggctcggccc accctctgcc ctgagagtga ccgctgtacc aacctctgtc 1620

cctacagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1680

accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1740

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1800

gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1860

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1920

aagagcctct ccctgtctcc gggtaaa 1947

<210> 86
<211> 2004
<212> DNA
<213> Artificial

<220>
<223> 1519gH20 IgG1 heavy chain (V + human gamma-1 constant) with signal sequence (one base change from SEQ ID NO:72)

<400> 86
atggaatgga gctgggtctt tctcttcttc ctgtcagtaa ctacaggagt ccattctgag 60

gtaccacttg tggaaagcgg aggaggtctt gtgcagcctg gaggaagttt acgtctctct 120

tgtgctgtgt ctggcttcac cttctccaat tacggaatgg tctgggtcag acaagcacct 180

ggaaagggtc ttgaatgggt ggcctatatt gactctgacg gggacaacac ctactatcgg 240

gattccgtga aaggacgctt cacaatctcc cgagataacg ccaagagctc actgtacctg 300

cagatgaata gcctgagagc cgaggatact gccgtgtact attgcacaac gggaatcgtt 360

aggccttttc tgtactgggg acagggcacc ttggttactg tctcgagcgc ttctacaaag 420

ggcccatcgg tcttcccccc ggcaccctcc tccaagagca cctctggggg cacagcggcc 480

ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 540

gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc 600

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 660

gtgaatcaca agcccagcaa caccaaggtg gacaagaaag ttggtgagag gccagcacag 720

ggagggaggg tgtctgctgg aagccaggct cagcgctcct gcctggacgc atcccggcta 780

tgcagcccca gtccagggca gcaaggcagg ccccgtctgc ctcttcaccc ggaggcctct 840

gcccgcccca ctcatgctca gggagagggt cttctggctt tttccccagg ctctgggcag 900

gcacaggcta ggtgccccta acccaggccc tgcacacaaa ggggcaggtg ctgggctcag 960

acctgccaag agccatatcc gggaggaccc tgcccctgac ctaagcccac cccaaaggcc 1020

aaactctcca ctccctcagc tcggacacct tctctcctcc cagatctgag taactcccaa 1080

tcttctctct gcagagccca aatcttgtga caaaactcac acatgcccac cgtgcccagg 1140

taagccagcc caggcctcgc cctccagctc aaggcgggac aggtgcccta gagtagcctg 1200

catccaggga caggccccag ccgggtgctg acacgtccac ctccatctct tcctcagcac 1260

ctgaactcct gggggggaccg tcagtcttcc tcttcccccc aaaacccaag gacaccctca 1320

tgatctcccg gacccctgag gtcacatgcg tggtggtgga cgtgagccac gaagaccctg 1380

aggtcaagtt caactggtac gtggacggcg tggaggtgca taatgccaag acaaagccgc 1440

gggaggagca gtacaacagc acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg 1500

actggctgaa tggcaaggag tacaagtgca aggtctccaa caaagccctc ccagccccca 1560

tcgagaaaac catctccaaa gccaaaggtg ggacccgtgg ggtgcgaggg ccacatggac 1620

agaggccggc tcggcccacc ctctgccctg agagtgaccg ctgtaccaac ctctgtccct 1680

acagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc 1740

aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1800

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1860

tccgacggct ccttcttcct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag 1920

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1980

agcctctccc tgtctccggg taaa 2004

<210> 87
<211> 444
<212> PRT
<213> Artificial

<220>
<223> 1519gH20 IgG4 heavy chain (V + human gamma-4 constant no P mutations)

<400> 87

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

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

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

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

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

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

Thr Thr Gly Ile Val Arg Pro Phe Leu Tyr Trp Gly Gln Gly Thr Leu
100 105 110

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

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

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

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

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

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

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

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

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

Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
            260                 265                 270

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

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

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

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

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

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

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

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

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

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

<210> 88
<211> 1939
<212> DNA
<213> Artificial

<220>
<223> 1519gH20 IgG4 heavy chain (V + human gamma-4 constant with exons no P mutations)

<400> 88
gaggtaccac ttgtggaaag cggaggaggt cttgtgcagc ctggaggaag tttacgtctc 60

tcttgtgctg tgtctggctt caccttctcc aattacggaa tggtctgggt cagacaagca 120

cctggaaagg gtcttgaatg ggtggcctat attgactctg acggggacaa cacctactat 180

cgggattccg tgaaaggacg cttcacaatc tcccgagata acgccaagag ctcactgtac 240

ctgcagatga atagcctgag agccgaggat actgccgtgt actattgcac aacgggaatc 300

gttaggcctt ttctgtactg gggacagggc accttggtta ctgtctcgag cgcttctaca 360

aagggcccat ccgtcttccc cctggcgccc tgctccagga gcacctccga gagcacagcc 420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacgaagac ctacacctgc 600

aacgtagatc acaagcccag caacaccaag gtggacaaga gagttggtga gaggccagca 660

cagggaggga gggtgtctgc tggaagccag gctcagccct cctgcctgga cgcaccccgg 720

ctgtgcagcc ccagcccagg gcagcaaggc atgccccatc tgtctcctca cccggaggcc 780

tctgaccacc ccactcatgc ccagggagag ggtcttctgg atttttccac caggctccgg 840

gcagccacag gctggatgcc cctaccccag gccctgcgca tacaggggca ggtgctgcgc 900

tcagacctgc caagagccat atccgggagg accctgcccc tgacctaagc ccaccccaaa 960

ggccaaactc tccactccct cagctcagac accttctctc ctcccagatc tgagtaactc 1020

ccaatcttct ctctgcagag tccaaatatg gtcccccatg cccatcatgc ccaggtaagc 1080

caacccaggc ctcgccctcc agctcaaggc gggacaggtg ccctagagta gcctgcatcc 1140

agggacaggc cccagccggg tgctgacgca tccacctcca tctcttcctc agcacctgag 1200

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tcccggaccc ctgaggtcac gtgcgtggtg gtggacgtga gccaggaaga ccccgaggtc 1320

cagttcaact ggtacgtgga tggcgtggag gtgcataatg ccaagacaaa gccgcgggag 1380

gagcagttca acagcacgta ccgtgtggtc agcgtcctca ccgtcctgca ccaggactgg 1440

ctgaacggca aggagtacaa gtgcaaggtc tccaacaaag gcctcccgtc ctccatcgag 1500

aaaaccatct ccaaagccaa aggtgggacc cacggggtgc gagggccaca tggacagagg 1560

tcagctcggc ccaccctctg ccctgggagt gaccgctgtg ccaacctctg tccctacagg 1620

gcagccccga gagccacagg tgtacaccct gcccccatcc caggaggaga tgaccaagaa 1680

ccaggtcagc ctgacctgcc tggtcaaagg cttctacccc agcgacatcg ccgtggagtg 1740

ggagagcaat gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga 1800

cggctccttc ttcctctaca gcaggctaac cgtggacaag agcaggtggc aggaggggaa 1860

tgtcttctca tgctccgtga tgcatgaggc tctgcacaac cactacacac agaagagcct 1920

ctccctgtct ctgggtaaa 1939

<210> 89
<211> 1996
<212> DNA
<213> Artificial

<220>
<223> 1519gH2O IgG4 heavy chain (V + human gamma-4 constant) with signal sequence - no P mutation

<400> 89
atggaatgga gctgggtctt tctcttcttc ctgtcagtaa ctacaggagt ccattctgag 60

gtaccacttg tggaaagcgg aggaggtctt gtgcagcctg gaggaagttt acgtctctct 120

tgtgctgtgt ctggcttcac cttctccaat tacggaatgg tctgggtcag acaagcacct 180

ggaaagggtc ttgaatgggt ggcctatatt gactctgacg gggacaacac ctactatcgg 240

gattccgtga aaggacgctt cacaatctcc cgagataacg ccaagagctc actgtacctg 300

cagatgaata gcctgagagc cgaggatact gccgtgtact attgcacaac gggaatcgtt 360

aggccttttc tgtactgggg acagggcacc ttggttactg tctcgagcgc ttctacaaag 420

ggcccatccg tcttcccccc ggcgccctgc tccaggagca cctccgagag cacagccgcc 480

ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 540

gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc 600

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cgaagaccta cacctgcaac 660

gtagatcaca agcccagcaa caccaaggtg gacaagagag ttggtgagag gccagcacag 720

ggagggaggg tgtctgctgg aagccaggct cagccctcct gcctggacgc accccggctg 780

tgcagcccca gcccagggca gcaaggcatg ccccatctgt ctcctcaccc ggaggcctct 840

gaccacccca ctcatgccca gggagagggt cttctggatt tttccaccag gctccgggca 900

gccacaggct ggatgcccct accccaggcc ctgcgcatac aggggcaggt gctgcgctca 960

gacctgccaa gagccatatc cgggaggacc ctgcccctga cctaagccca ccccaaaggc 1020

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atcttctctc tgcagagtcc aaatatggtc ccccatgccc atcatgccca ggtaagccaa 1140

cccaggcctc gccctccagc tcaaggcggg acaggtgccc tagagtagcc tgcatccagg 1200

gacaggcccc agccgggtgc tgacgcatcc acctccatct cttcctcagc acctgagttc 1260

ctggggggac catcagtctt cctgttcccc ccaaaaccca aggacactct catgatctcc 1320

cggacccctg aggtcacgtg cgtggtggtg gacgtgagcc aggaagaccc cgaggtccag 1380

ttcaactggt acgtggatgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 1440

cagttcaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 1500

aacggcaagg agtacaagtg caaggtctcc aacaaaggcc tcccgtcctc catcgagaaa 1560

accatctcca aagccaaagg tgggacccac ggggtgcgag ggccacatgg acagaggtca 1620

gctcggccca ccctctgccc tgggagtgac cgctgtgcca acctctgtcc ctacagggca 1680

gccccgagag ccacaggtgt acaccctgcc cccatcccag gaggagatga ccaagaacca 1740

ggtcagcctg acctgcctgg tcaaaggctt ctaccccagc gacatcgccg tggagtggga 1800

gagcaatggg cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg 1860

ctccttcttc ctctacagca ggctaaccgt ggacaagagc aggtggcagg aggggaatgt 1920

cttctcatgc tccgtgatgc atgaggctct gcacaaccac tacacacaga agagcctctc 1980

cctgtctctg ggtaaa 1996

<210> 90
<211> 336
<212> DNA
<213> Artificial

<220>
<223> 1519 gL20 V-region (mammalian expression alternative to SEQ ID NO: 17)

<400> 90
gacatccaga tgacccagtc cccctccagc ctgtccgcct ccgtgggcga cagagtgacc 60

atcacatgca agtcctccca gtccctggtc ggagcctccg gcaagaccta cctgtactgg 120

ctgttccaga agcccggcaa ggcccccaag cggctgatct acctggtgtc taccctggac 180

tccggcatcc cctcccggtt ctccggctct ggctctggca ccgagttcac cctgaccatc 240

tccagcctgc agcccgagga cttcgccacc tactactgtc tgcaaggcac ccacttcccc 300

cacaccttcg gccagggcac caagctggaa atcaag 336

<210> 91
<211> 657
<212> DNA
<213> Artificial

<220>
<223> 1519 gL20 light chain (V + constant, mammalian expression) alternative to SEQ ID NO: 24)

<400> 91
gacatccaga tgacccagtc cccctccagc ctgtccgcct ccgtgggcga cagagtgacc 60

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ctgttccaga agcccggcaa ggcccccaag cggctgatct acctggtgtc taccctggac 180

tccggcatcc cctcccggtt ctccggctct ggctctggca ccgagttcac cctgaccatc 240

tccagcctgc agcccgagga cttcgccacc tactactgtc tgcaaggcac ccacttcccc 300

cacaccttcg gccagggcac caagctggaa atcaagcgga ccgtggccgc tccctccgtg 360

ttcatcttcc caccctccga cgagcagctg aagtccggca ccgcctccgt cgtgtgcctg 420

ctgaacaact tctacccccg cgaggccaag gtgcagtgga aggtggacaa cgccctgcag 480

tccggcaact cccaggaatc cgtcaccgag caggactcca aggacagcac ctactccctg 540

tcctccaccc tgaccctgtc caaggccgac tacgagaagc acaaggtgta cgcctgcgaa 600

gtgacccacc agggcctgtc agccccgtg accaagtcct tcaaccgggg cgagtgc 657

<210> 92
<211> 348
<212> DNA
<213> Artificial

<220>
<223> 1519 gH20 V-region (mammalian expression alternative to SEQ ID NO: 31)

<400> 92
gaggtgcccc tggtggaatc tggcggcgga ctggtgcagc ctggcggctc cctgagactg 60

tcttgcgccg tgtccggctt caccttctcc aactacggca tggtctgggt ccgacaggct 120

cctggcaagg gactggaatg ggtggcctac atcgactccg acggcgacaa cacctactac 180

cgggactccg tgaagggccg gttcaccatc tcccgggaca acgccaagtc ctccctgtac 240

ctgcagatga actccctgcg ggccgaggac accgccgtgt actactgcac caccggcatc 300

gtgcggccct ttctgtactg gggccagggc accctggtca ccgtgtcc 348

<210> 93
<211> 1332
<212> DNA
<213> Artificial

<220>
<223> 1519gH20 IgG4 heavy chain (V + human gamma-4P constant alternative to SEQ ID NO: 44)

<400> 93
gaggtgcccc tggtggaatc tggcggcgga ctggtgcagc ctggcggctc cctgagactg 60

tcttgcgccg tgtccggctt caccttctcc aactacggca tggtctgggt ccgacaggct 120

cctggcaagg gactggaatg ggtggcctac atcgactccg acggcgacaa cacctactac 180

cgggactccg tgaagggccg gttcaccatc tcccgggaca acgccaagtc ctccctgtac 240

ctgcagatga actccctgcg ggccgaggac accgccgtgt actactgcac caccggcatc 300

gtgcggccct ttctgtactg gggccagggc accctggtca ccgtgtcctc tgcctccacc 360

aagggcccct ccgtgttccc tctggccccc tgctcccggt ccacctccga gtctaccgcc 420

gctctgggct gcctggtcaa ggactacttc cccgagcccg tgacagtgtc ctggaactct 480

ggcgccctga cctccggcgt gcacaccttc cctgccgtgc tgcagtcctc cggcctgtac 540

tccctgtcct ccgtcgtgac cgtgccctcc tccagcctgg gcaccaagac ctacacctgt 600

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tccgtgctga ccgtgctgca ccaggactgg ctgaacggca aagagtacaa gtgcaaggtg 960

tccaacaagg gcctgccctc cagcatcgaa aagaccatct ccaaggccaa gggccagccc 1020

cgcgagcccc aggtgtacac cctgcccccc agccaggaag agatgaccaa gaaccaggtg 1080

tccctgacct gtctggtcaa gggcttctac ccctccgaca ttgccgtgga atgggagtcc 1140

aacggccagc ccgagaacaa ctacaagacc acccccccctg tgctggacag cgacggctcc 1200

ttcttcctgt actctcggct gaccgtggac aagtcccggt ggcaggaagg caacgtcttc 1260

tcctgctccg tgatgcacga ggccctgcac aaccactaca cccagaagtc cctgtccctg 1320

agcctgggca ag 1332

<210> 94
<211> 267
<212> PRT
<213> Artificial

<220>
<223> FcRn alpha chain extracellular sequence

<400> 94

Ala Glu Ser His Leu Ser Leu Leu Tyr His Leu Thr Ala Val Ser Ser
1 5 10 15

Pro Ala Pro Gly Thr Pro Ala Phe Trp Val Ser Gly Trp Leu Gly Pro
20 25 30

Gln Gln Tyr Leu Ser Tyr Asn Ser Leu Arg Gly Glu Ala Glu Pro Cys
35 40 45

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

Thr Thr Asp Leu Arg Ile Lys Glu Lys Leu Phe Leu Glu Ala Phe Lys
65 70 75 80

Ala Leu Gly Gly Lys Gly Pro Tyr Thr Leu Gln Gly Leu Leu Gly Cys
85 90 95

Glu Leu Gly Pro Asp Asn Thr Ser Val Pro Thr Ala Lys Phe Ala Leu
100 105 110

```
Asn Gly Glu Glu Phe Met Asn Phe Asp Leu Lys Gln Gly Thr Trp Gly
        115                 120                 125

Gly Asp Trp Pro Glu Ala Leu Ala Ile Ser Gln Arg Trp Gln Gln Gln
    130                 135                 140

Asp Lys Ala Ala Asn Lys Glu Leu Thr Phe Leu Leu Phe Ser Cys Pro
145                 150                 155                 160

His Arg Leu Arg Glu His Leu Glu Arg Gly Arg Gly Asn Leu Glu Trp
                165                 170                 175

Lys Glu Pro Pro Ser Met Arg Leu Lys Ala Arg Pro Ser Ser Pro Gly
            180                 185                 190

Phe Ser Val Leu Thr Cys Ser Ala Phe Ser Phe Tyr Pro Pro Glu Leu
        195                 200                 205

Gln Leu Arg Phe Leu Arg Asn Gly Leu Ala Ala Gly Thr Gly Gln Gly
    210                 215                 220

Asp Phe Gly Pro Asn Ser Asp Gly Ser Phe His Ala Ser Ser Ser Leu
225                 230                 235                 240

Thr Val Lys Ser Gly Asp Glu His His Tyr Cys Cys Ile Val Gln His
                245                 250                 255

Ala Gly Leu Ala Gln Pro Leu Arg Val Glu Leu Glu Ser Pro Ala Lys
            260                 265                 270

Ser Ser
```

<210> 95
<211> 99
<212> PRT
<213> Homo sapiens

<400> 95

```
Ile Gln Lys Thr Pro Gln Ile Gln Val Tyr Ser Arg His Pro Pro Glu
1               5                   10                  15

Asn Gly Lys Pro Asn Phe Leu Asn Cys Tyr Val Ser Gln Phe His Pro
            20                  25                  30

Pro Gln Ile Glu Ile Glu Leu Leu Lys Asn Gly Lys Lys Ile Pro Asn
        35                  40                  45

Ile Glu Met Ser Asp Leu Ser Phe Ser Lys Asp Trp Ser Phe Tyr Ile
    50                  55                  60
```

```
Leu Ala His Thr Glu Phe Thr Pro Thr Glu Thr Asp Val Tyr Ala Cys
65                  70                  75                  80

Arg Val Lys His Val Thr Leu Lys Glu Pro Lys Thr Val Thr Trp Asp
                85                  90                  95

Arg Asp Met
```