

SEQUENCE LISTING

<110> UCB Biopharma SPRL

<120> Method for the treatment of immune thrombocytopenia

<130> PF0119

<150> GB1709554.8

<151> 2017-06-15

<150> GB1718589.3

<151> 2017-11-10

<160> 95

<170> PatentIn version 3.5

<210> 1

<211> 10

<212> PRT

<213> Artificial

<220>

<223> CA170_1519 CDRH1

<400> 1

Gly	Phe	Thr	Phe	Ser	Asn	Tyr	Gly	Met	Val
1				5				10	

<210> 2

<211> 17

<212> PRT

<213> Artificial

<220>

<223> CA170_1519 CDRH2

<400> 2

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

Gly

<210> 3

<211> 8

<212> PRT

<213> Artificial

<220>

<223> CA170_1519 CDRH3

<400> 3

Gly	Ile	Val	Arg	Pro	Phe	Leu	Tyr
1				5			

<210> 4
<211> 16
<212> PRT
<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
<211> 7
<212> PRT
<213> Artificial

<220>
<223> CA170_1519 CDRL2

<400> 5

Leu Val Ser Thr Leu Asp Ser
1 5

<210> 6
<211> 9
<212> PRT
<213> Artificial

<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 tgaccagac tccactgtct ttgtcggttg cccttggaca accagcctcc 60
 atctcttgca agtcaagtca gagcctcgta ggtgctagtg gaaagacata tttgtattgg 120
 ttatttcaga ggtccggcca gtctccaaag cgactaatct atctggtgtc cacactggac 180
 tctggaattc ctgatagggt 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

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 aaccagtgg 60
gatgttgtga tgaccagac tccactgtct ttgtcggttg cccttggaca accagcctcc 120
atctcttgca agtcaagtca gagcctcgta ggtgctagtg gaaagacata tttgtattgg 180
ttatttcaga ggtccggcca gtctccaaag cgactaatct atctggtgtc cacactggac 240
tctggaattc ctgatagggt cagtggcagt ggagcagaga cagattttac tcttaaaatc 300
cgcagagtgg aagccgatga tttgggagtt tattactgct tgcaaggtag 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 tgggtggagtc tggggggcggc tcagtgcagc ctgggaggtc catgaaactc 60
 tcctgtgtag tctcaggatt cactttcagt aattatggca tggctctgggt ccgccaggct 120
 ccaaagaagg gtctggagtg ggtcgcatat attgattctg atgggtgataa tacttactac 180
 cgagattccg tgaagggccg attcactatc tccagaaata atgcaaaaag caccctatat 240
 ttgcaaatgg acagtctgag gtctgaggac acggccactt attactgtac aacagggatt 300
 gtccggccct ttctctattg gggccaagga accacgggtca 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 ggcttttcctt gtcctttttca taaaagggtgt ccggtgtgag 60
gtgccgctgg tggagtctgg gggcggctca gtgcagcctg ggagggtccat gaaactctcc 120
tgtgtagtct caggattcac tttcagtaat tatggcatgg tctgggtccg ccaggctcca 180
aagaagggtc tggagtgggt cgcataatatt 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 gtccctgggtg ggtgcaagcg gcaaaaccta cctgtactgg 120
 ctcttccaga aaccgggcaa agctccgaaa cgcctgatct atctggtgtc taccctggat 180
 agcgggtattc 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 ggcacaaaaa cggctgatct atctggtgtc tacccttgac 180
 tctgggatac cgtcacgatt ttccggatct gggagcggaa ctgagttcac actcacgatt 240
 tcatacgtgc aacccgagga ctttgctacc tactactgcc tgcaaggcac tcattttccct 300

<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 gccttggtg gtttcgctac cgtagcgcaa 60

gctgatatcc agatgaccca gagtccaagc agtctctccg ccagcgtagg cgatcgtgtg 120

actattacct gtaaaagctc ccagtccttg gtgggtgcaa gcggcaaac ctacctgtac 180

tggtctcttcc 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
atgtctgtcc ccaccaagt cctcggactc ctgctactct ggcttacaga tgccagatgc      60
gatatccaga tgaccagag cccatctagc ttatccgctt ccgttggtga tcgcgtgaca      120
attacgtgta agagctccca atctctcgtg ggtgcaagtg gcaagaccta tctgtactgg      180
ctcttttcaga agcctggcaa ggcaccaaaa cggctgatct atctggtgtc tacccttgac      240
tctgggatac cgtcacgatt ttccggatct gggagcggaa ctgagttcac actcacgatt      300
tcatcgctgc aacccgagga ctttgctacc tactactgcc tgcaaggcac tcatttcctt      360
cacactttcg gccaggggac aaaactcgaa atcaaa                                396

```

```

<210> 22
<211> 219
<212> PRT
<213> Artificial

```

```

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

```

```

<400> 22

```

```

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 tgaccagag tccaagcagt ctctccgcca gcgtaggcga tcgtgtgact 60
attacctgta aaagctccca gtccctggtg ggtgcaagcg gcaaaaccta cctgtactgg 120
ctcttccaga aaccgggcaa agctccgaaa cgcctgatct atctggtgtc taccctggat 180
agcgggtattc 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
agcagcacc ctagcgtgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 600
gtcaccatc agggcctgag ctaccagta aaaaaagtt ttaatagagg ggagtgt 657

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

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

<400> 24
gatatccaga tgaccagag tccaagcagt ctctccgcca gcgtaggcga tcgtgtgact 60
attacctgta aaagctccca gtccctggtg ggtgcaagcg gcaaaaccta cctgtactgg 120
ctcttccaga aaccgggcaa agctccgaaa cgcctgatct atctggtgtc taccctggat 180

```

agcgggtattc 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
agcagcaccg tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcttgcgaa      600
gtcaccatc agggcctgag ctgcgccgtc 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
atgaaaaaga cagctatcgc aattgcagtg gccttggctg gtttcgctac cgtagcgcaa 60
gctgatatcc agatgaccca gagtccaagc agtctctccg ccagcgtagg cgatcgtgtg 120
actattacct gtaaaagctc ccagtccctg gtgggtgcaa gcggcaaaac ctacctgtac 180
tggtcttcc 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
caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 600
ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 660
gaagtcaccc atcagggcct gagctcacca gtaacaaaaa gttttaatag aggggagtg 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

<210> 28
<211> 717
<212> DNA
<213> Artificial

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

<400> 28
atgtctgtcc ccaccaagt cctcggactc ctgctactct ggcttacaga tgccagatgc 60
gatatccaga tgaccagag cccatctagc ttatccgctt ccgttggtga tcgcgtgaca 120
attacgtgta agagctccca atctctcgtg ggtgcaagtg gcaagaccta tctgtactgg 180
ctcttttcaga agcctggcaa ggcaccaaaa cggctgatct atctggtgtc tacccttgac 240
tctgggatac cgtcacgatt ttccggatct gggagcggaa ctgagttcac actcacgatt 300
tcatcgctgc aaccgagga ctttgctacc tactactgcc tgcaaggcac tcatttcctt 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
agcagcacc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 660
gtcaccatc agggcctgag ctgcgccgtc acaaagagct tcaacagggg agagtgt 717

<210> 29
<211> 116
<212> PRT
<213> Artificial

<220>
<223> 1519 gH20 V-region

<400> 29
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
gagggttccgc tggtcgagtc tggaggcggg cttgtccagc ctggagggag cctgcgtctc 60
tcttgtgcag tatctggctt cacgttctcc aactacggta tgggtgtgggt tcgtcaggct 120
ccaggtaaag gtctggaatg ggtggcgtat attgactccg acggcgacaa cacctactat 180
cgcgactctg tgaaaggtcg cttcaccatt tcccgcgata acgccaatc cagcctgtac 240
ctgcagatga acagcctgcg tgctgaagat actgcggtgt actattgcac cactggcatc 300
gtgcgtccgt ttctgtattg gggtcagggt accctcggtta ctgtctcg 348

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

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

<400> 31
gagggtaccac ttgtggaaag cggaggaggt cttgtgcagc ctggaggaag tttacgtctc 60
tcttgtgctg tgtctggctt caccttctcc aattacggaa tgggtctgggt cagacaagca 120
cctggaaagg gtcttgaatg ggtggcctat attgactctg acggggacaa cacctactat 180
cgggattccg tgaaaggacg cttcacaatc tcccagata acgccaagag ctactgtac 240
ctgcagatga atagcctgag agccgaggat actgccgtgt actattgcac aacgggaatc 300
gttaggcctt ttctgtactg gggacagggc accttgggtta 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
gctgagggttc cgctggtcga gtctggaggc gggcttgctc agcctggagg gagcctgcgt 120
ctctcttggtg cagtatctgg cttcacgttc tccaactacg gtatggtgtg ggttcgtcag 180
gctccaggta aaggctctgga atgggtggcg tatattgact ccgacggcga caacacctac 240
tatcgcgact ctgtgaaagg tcgcttcacc atttcccgcg ataacgcaa 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 gggaatcggt	360

aggccttttc tgtactgggg acagggcacc ttggttactg tctcg

405

<210> 36

<211> 228

<212> PRT

<213> Artificial

<220>

<223> 1519gH20 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 tgggtgtgggt tcgtcaggct 120
ccaggtaaag gtctggaatg ggtggcgtat attgactccg acggcgacaa cacctactat 180
cgcgactctg tgaaaggctg cttcaccatt tcccgcgata acgccaatc cagcctgtac 240
ctgcagatga acagcctgcg tgctgaagat actgcggtgt actattgcac cactggcatc 300
gtgcgtccgt ttctgtattg gggtcagggt accctcgtaa ctgtctcgag cgcttctaca 360
aagggcccat cggctcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 420
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca 480
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540
tccctcagca gcgtgggtgac 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 tgggtctgggt cagacaagca 120
cctggaaagg gtcttgaatg ggtggcctat attgactctg acggggacaa cacctactat 180
cgggattccg tgaaaggacg cttcacaatc tcccagagata acgccaagag ctactgtac 240
ctgcagatga atagcctgag agccgaggat actgccgtgt actattgcac aacgggaatc 300

gttaggcctt ttctgtactg gggacagggc accttggtta ctgtctcgag cgcttctaca 360
 aagggcccat cggctcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 420
 gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca 480
 ggcgccctga ccagcggcgt gcacaccttc cgggctgtcc tacagtcctc aggactctac 540
 tccctcagca gcgtgggtgac 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 gH20 Fab' heavy chain with signal sequence (E. coli expression)

<400> 40

atgaagaaga ctgctatagc aattgcagtg gcgctagctg gtttcgccac cgtggcgcaa	60
gctgaggttc cgctggtcga gtctggaggc gggcttgctc agcctggagg gagcctgcgt	120
ctctcttggt cagtatctgg cttcacgttc tccaactacg gtatggtgtg ggttcgtcag	180
gctccaggta aaggtctgga atgggtggcg tatattgact ccgacggcga caacacctac	240
tatcgcgact ctgtgaaagg tcgcttcacc atttcccgcg ataacgcaa atccagcctg	300
tacctgcaga tgaacagcct gcgtgctgaa gatactgcgg tgtactattg caccactggc	360
atcgtgcgtc cgtttctgta ttggggtcag ggtaccctcg ttactgtctc gagcgcttct	420
acaaagggcc catcggctctt ccccctggca cctcctcca agagcacctc tgggggcaca	480
gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac	540
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc	600
tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc	660
tgcaacgtga atcacaagcc cagcaacacc aaggtcgaca agaaagttga gcccaaattct	720
tgtgacaaaa ctcacacatg cgccgcg	747

<210> 41

<211> 247

```

<212>  PRT
<213>  Artificial

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

<400> 42
 atggaatgga gctgggtctt tctcttcttc ctgtcagtaa ctacaggagt ccattctgag 60
 gtaccacttg tggaagcgg aggaggtctt gtgcagcctg gaggaagttt acgtctctct 120
 tgtgctgtgt ctggcttcac cttctccaat tacggaatgg tctgggtcag acaagcacct 180
 ggaaagggtc ttgaatgggt ggcctatatatt gactctgacg gggacaacac ctactatcgg 240
 gattccgtga aaggacgctt cacaatctcc cgagataacg ccaagagctc actgtacctg 300
 cagatgaata gcctgagagc cgaggatact gccgtgtact attgcacaac gggaatcgtt 360
 aggcccttttc tgtactgggg acagggcacc ttgggttactg tctcgagcgc ttctacaaag 420
 ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 480
 ctgggctgcc tgggtcaagga ctacttcccc gaaccggtga cgggtgctgt gaactcaggc 540
 gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc 600
 ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 660
 gtgaatcaca agcccagcaa caccaaggct 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
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
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
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 tggctctgggt cagacaagca 120
 cctggaaagg gtcttgaatg ggtggcctat attgactctg acggggacaa cacctactat 180
 cgggattccg tgaaaggacg cttcacaatc tcccagata acgccaagag ctactgtac 240
 ctgcagatga atagcctgag agccgaggat actgccgtgt actattgcac aacgggaatc 300
 gttaggcctt ttctgtactg gggacagggc accttggtta ctgtctcgag cgcttctaca 360
 aagggcccat ccgtcttccc cctggcgccc tgctccagga gcacctccga gagcacagcc 420
 gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca 480
 ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacgaagac ctacacctgc	600
aacgtagatc acaagcccag caacaccaag gtggacaaga gagttggtga gaggccagca	660
cagggaggga ggggtgtctgc tggaagccag gctcagccct cctgcctgga cgcaccccg	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 tgacctaaag ccaccccaaa	960
ggccaaactc tccactccct cagctcagac accttctctc ctcccagatc tgagtaactc	1020
ccaatcttct ctctgcagag tccaaatatg gtcccccattg cccaccatgc ccaggtaagc	1080
caaccagggc ctgcacctcc agctcaaggc gggacaggtg ccctagagta gcctgcatcc	1140
agggacaggc cccagccggg tgctgacgca tccacctcca tctcttcctc agcacctgag	1200
ttcctggggg gaccatcagt cttcctgttc cccccaaaac ccaaggacac tctcatgac	1260
tcccggaacc 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 cacgggggtgc gagggccaca tggacagagg	1560
tcagctcggc ccacctctg ccctgggagt gaccgctgtg ccaacctctg tccctacagg	1620
gcagccccga gagccacagg tgtacaccct gccccatcc caggaggaga tgaccaagaa	1680
ccaggtcagc ctgacctgcc tgggtcaaagg 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	ggcctatat	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	tcttccccct	ggcgccctgc	tccaggagca	cctccgagag	cacagccgcc	480
ctgggctgcc	tggatcaagg	ctacttcccc	gaaccggtga	cggtgtcgtg	gaactcaggc	540
gccctgacca	gcggcgtgca	caccttcccc	gctgtcctac	agtcctcagg	actctactcc	600
ctcagcagcg	tggtgaccgt	gccctccagc	agcttgggca	cgaagaccta	cacctgcaac	660
gtagatcaca	agcccagcaa	caccaagggt	gacaagagag	ttggtgagag	gccagcacag	720
ggagggaggg	tgtctgctgg	aagccaggct	cagccctcct	gcctggacgc	accccggctg	780
tgcagcccca	gcccagggca	gcaaggcatg	ccccatctgt	ctcctcacc	ggaggcctct	840
gaccacccca	ctcatgcccc	gggagagggg	cttctggatt	tttccaccag	gctccgggca	900
gccacaggct	ggatgcccct	accccaggcc	ctgcgcatac	aggggcagg	gctgcgctca	960
gacctgcca	gagccatata	cgggaggacc	ctgcccctga	cctaagccca	ccccaaaggc	1020
caaactctcc	actccctcag	ctcagacacc	ttctctcctc	ccagatctga	gtaactccca	1080
atcttctctc	tgcagagtcc	aaatatgggt	ccccatgccc	accatgcccc	ggtaagccaa	1140
cccaggcctc	gccctccagc	tcaaggcggg	acaggtgccc	tagagtagcc	tgcattccagg	1200
gacaggcccc	agccgggtgc	tgacgcatcc	acctccatct	cttcctcagc	acctgagttc	1260
ctgggggggac	catcagtctt	cctgttcccc	ccaaaaccca	aggacactct	catgatctcc	1320
cggaccccctg	aggtcacgtg	cgtgggtggtg	gacgtgagcc	aggaagaccc	cgagggtccag	1380
ttcaactggt	acgtggatgg	cgtggagggtg	cataatgcca	agacaaagcc	gcgggaggag	1440
cagttcaaca	gcacgtaccg	tgtgggtcagc	gtcctcaccg	tcctgcacca	ggactggctg	1500
aacggcaagg	agtacaagtg	caagggtctcc	aacaaaggcc	tcccgtcctc	catcgagaaa	1560
accatctcca	aagccaaagg	tgggaccac	ggggtgcgag	ggccacatgg	acagagggtca	1620
gctcggccca	ccctctgccc	tgggagtgc	cgctgtgcca	acctctgtcc	ctacagggca	1680
gccccgagag	ccacagggtg	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 tgaccagag cccatctagc ttatccgctt ccgttggtga tcgcgtgaca 60
 attacgtgta agagctccca atctctcgtg ggtgcaagtg gcaagaccta tctgtactgg 120
 ctcttttcaga agcctggcaa ggcacaaaaa cggctgatct atctggtgtc tacccttgac 180
 tctgggatac cgtcacgatt ttccggatct gggagcggaa ctgagttcac actcacgatt 240
 tcatcgctgc aaccgagga 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
 agcagcacc tgacgctgtc taaagcagac tacgagaaac acaaagtgtg cgccctgcga 600

gtcaccatc agggcctgag ctcaccagta acaaaaagtt ttaatagagg ggagtgtagc 660
 ggtggcgggtg gcagtgggtgg gggagggtcc ggaggtggcg gttcagacat acaaagacc 720
 cagagtcctt catcggtatc cgcgtccgtt ggcgataggg tgactattac atgtcaaagc 780
 tctccttagcg tctggagcaa ttttctatcc tggtatcaac agaaaccggg gaaggctcca 840
 aaactttctga tttatgaagc ctcgaaactc accagtggag ttccgtcaag attcagtggc 900
 tctggatcag ggacagactt cacgttgaca atcagttcgc tgcaaccaga ggactttgcg 960
 acctactatt gtggtggagg ttacagtagc ataagtata 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 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 ccaccaagt cctcggactc ctgctactct ggcttacaga tgccagatgc      60
gatatccaga tgaccagag cccatctagc ttatccgctt ccgttggtga tcgcgtgaca      120
attacgtgta agagctccca atctctcgtg ggtgcaagtg gcaagaccta tctgtactgg      180
ctcttttcaga agcctggcaa ggcaccaaaa cggctgatct atctggtgtc tacccttgac      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
agcagcacc tgacgctgtc taaagcagac tacgagaaac acaaagtgtg cgcctgcgaa      660
gtcaccatc agggcctgag ctcaccagta aaaaaagtt ttaatagagg ggagtgtagc      720
ggtggcggtg gcagtgggtg gggaggctcc ggaggtggcg gttcagacat acaaatgacc      780
cagagtcctt catcgggtatc cgcgtccgtt ggcgataggg tgactattac atgtcaaagc      840
tctcctagcg tctggagcaa ttttctatcc tggatatcaac agaaaccggg gaaggctcca      900
aaactttctga 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 tgtctggcct cacccttctcc aattacggaa tggctctgggt cagacaagca 120
 cctggaaagg gtcttgaatg ggtggcctat attgactctg acggggacaa cacctactat 180
 cgggattccg tgaaaggacg cttcacaaatc tcccagagata acgccaagag ctactgttac 240
 ctgcagatga atagcctgag agccgaggat actgccgtgt actattgcac aacgggaatc 300
 gttaggcctt ttctgtactg gggacagggc accttggtta ctgtctcgag cgcgtccaca 360
 aagggcccat cggctcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 420
 gccctgggct gcctgggtcaa ggactacttc cccgaaccag tgacgggtgtc gtggaactca 480
 ggtgccctga ccagcggcgt tcacaccttc ccggctgtcc tacagtcttc aggactctac 540
 tccctgagca gcgtgggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 600
 aacgtgaatc acaagcccag caacaccaag gtcgataaga aagttgagcc caaatcttgt 660
 agtggaggtg ggggctcagg tggaggcggg accggtggag gtggcagcga ggttcaactg 720
 cttgagtctg gaggaggcct agtccagcct ggaggagacc tgcgtctctc ttgtgcagta 780
 agcggcatcg acctgagcaa ttacgccatc aactgggtga gacaagctcc ggggaagtgt 840
 ttagaatgga tcggtataat atgggccagt gggacgacct tttatgctac atgggcgaaa 900
 ggaagggttta caattagccg ggacaatagc aaaaacaccg tgtatctcca aatgaactoc 960
 ttgcgagcag aggacacggc ggtgtactat tgtgctcgca ctgtcccagg ttatagcaact 1020
 gcaccctact tcgatctgtg gggacaaggg accctgggtga 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 gctgggtcctt tctcttcttc ctgtcagtaa ctacaggagt ccattctgag 60
gtaccacttg tggaagcgg aggaggtcct 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 gggaatcggt 360
aggccttttc tgtactgggg acagggcacc ttgggttactg tctcgagcgc gtccacaaag 420
ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 480
ctgggctgcc tgggtcaagga ctacttcccc gaaccagtga cggtgtcgtg gaactcaggt 540

gccctgacca gcggcggttca caccttcccc 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
 ggcacgcacc tgagcaatta cgccatcaac tgggtgagac aagctccggg gaagtgttta 900
 gaatggatcg gtataatatg ggccagtggg acgacctttt atgctacatg ggcgaaagga 960
 aggtttacaa ttagccggga caatagcaaa aacaccgtgt atctccaaat gaactccttg 1020
 cgagcagagg acacggcggt gtactattgt gctcgcactg tcccagggtta 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 gctggatatca 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	ctgggggggtc	cctgagactc	60
tcctgtgcag	cctctggatt	cacctttagt	agctattgga	tgagctgggt	ccgccaggct	120
ccaggaag	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

gatgtttgtga tgacccagac tccactgtct ttgtcggttg cccttgga accagcctcc 60
atctcttgca agtcaagtca gagcctcgta ggtgctagtq gaaagacata tttgtattgg 120

ttattttcaga	ggtccggcca	gtctccaaag	cgactaatct	atctgggtgc	cacactggac	180
tctggaattc	ctgatagggt	cagtggcagt	ggagcagaga	cagattttac	tcttaaaatc	240
cgcagagtgg	aagccgatga	tttgggagtt	tattactgct	tgcaaggtac	acatttttct	300
cacacgtttg	gagctgggac	caagctggaa	ataaaa			336

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

```
<220>
<223> Rat Ab 1548 VH region
```

$\langle 400 \rangle$ 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 tgggtggagtc tggggggcggc tcagtgcagc ctgggaggtc catgaaactc 60

tcctgtgtag tctcaggatt cactttcagt aattatggca tggtctgggt ccgccaggct 120

ccaaagaagg gtctggagtg ggtcgcataat attgattctg atggtgataa tacttactac	180
cgagattccg tgaagggccg attcactatc tccagaaata atgcaaaaag caccctatat	240
ttgcaaatgg acagtctgag gtctgaggac acggccactt attactgtac aacagggatt	300
gtccggccct ttctctattg gggccaagga gtcatgggtca 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

gatgttgatga tgaccagac tccactgtct ttgtcggttg ccattggaca accagcctcc	60
atctcttgca agtcaagtca gagcctcgta ggtgctagtg gaaagacata tttgtattgg	120
ttatttcaga ggtccggcca gtctccaaag cgactaatct atctgggtgtc cactactggac	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 tgggtggagtc tggggggcggc tcagtgcagc ctgggaggtc cacgaaactc 60

tcctgtgtag tctcaggatt cactttcagt aactatggca tgggtctgggt ccgccaggct 120

ccaaagaagg gtctggagtg ggtcgcatat attggttctg atgggtgataa tatttactac 180

cgagattccg tgaagggtcg attcactatc tccagaaata atgcaaaaag caccctatat 240

ttgcaaattgg acagtctgag gtctgaggac acggccactt attactgtac aacagggatt	300
gtccggccct ttctctactg gggccaagga accacgggtca 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 tgaccagac tccactgtct ttgtcggttg cccttggaca accagcctcc	60
atctcttgca agtcaagtca gagcctcgta ggtgctagtg gaaagacata tttgtattgg	120
ttatttcaga ggtccggcca gtctccaaag cgactaatct atctggtgtc cacactggac	180
tctggaattc ctgatagggt 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 tgggtggagtc tggggggcggc tcagtgcagc ctgggaggtc catgaaactc	60
tctgtgtag tctcaggatt cactttcagt aattatggca tggctctgggt 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 accatgggtca 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> 1519gH20 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 tggctctgggt cagacaagca	120
cctggaaagg gtcttgaatg ggtggcctat attgactctg acggggacaa cacctactat	180
cgggattccg tgaaaggacg cttcacaatc tcccagata acgccaagag ctactgtac	240
ctgcagatga atagcctgag agccgaggat actgccgtgt actattgcac aacgggaatc	300
gttaggcctt ttctgtactg gggacagggc accttggtta ctgtctcgag cgcttctaca	360
aagggcccat cggcttctcc cctggcacc cctccaaga gcacctctgg gggcacagcg	420
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca	480
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac	540
tccctcagca gcgtggtgac cgtgccctcc agcagcttggt gcaccagac ctacatctgc	600
aacgtgaatc acaagcccag caacaccaag gtcgacaaga aagttggtga gaggccagca	660
cagggagggga ggggtgtctgc tggaagccag gctcagcgt cctgcctgga cgcacccgg	720
ctatgcagcc ccagtccagg gcagcaaggc agggcccgtc tgcctcttca cccggaggcc	780
tctgcccgcc cactcatgc tcaggagag ggtcttctgg ctttttcccc aggctctggg	840
caggcacagg ctaggtgccc ctaaccagg ccctgcacac aaaggggcag gtgctgggct	900
cagacctgcc aagagccata tccgggagga ccctgcccct gacctaaccc caccacaaag	960

gccaaactct ccactccctc agctcggaca ccttctctcc tcccagatct gagtaactcc	1020
caatctttctc tctgcagagc ccaaactcttg 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 ccggaccctt gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc	1320
ctgaggtcaa gttcaactgg tacgtggacg gcgtggaggt gcataatgcc aagacaaagc	1380
cgcgggagga gcagtacaac agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc	1440
aggactggct gaatggcaag gagtacaagt gcaagggtct caacaaagcc ctcccagccc	1500
ccatcgagaa aaccatctcc aaagccaaag gtgggacccg tgggggtgca gggccacatg	1560
gacagaggcc ggctcggccc accctctgcc ctgagagtga ccgctgtacc aacctctgtc	1620
cctacagggc agccccgaga accacagggtg tacaccctgc ccccatcccg ggatgagctg	1680
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc	1740
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg	1800
gactccgacg gtccttctt 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 tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc	480
ctgggctgcc tgggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc	540
gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc	600

ctcagcagcg	tgggtgaccgt	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
gcccgcacca	ctcatgctca	gggagagggg	cttctggctt	tttcccagag	ctctgggcag	900
gcacaggcta	ggtgccccta	acccaggccc	tgcacacaaa	ggggcaggtg	ctgggctcag	960
acctgccaag	agccatatcc	gggaggaccc	tgcccttgac	ctaagcccac	cccaaaggcc	1020
aaactctcca	ctccctcagc	tccgacacct	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	ggggggaccg	tcagtcttcc	tcttcccccc	aaaaccaag	gacaccctca	1320
tgatctcccg	gacccttgag	gtcacatgcg	tgggtggtgga	cgtgagccac	gaagaccctg	1380
aggtcaagtt	caactggtac	gtggacggcg	tggaggtgca	taatgccaag	acaagccgc	1440
gggaggagca	gtacaacagc	acgtaccgtg	tggtcagcgt	cctcaccgtc	ctgcaccagg	1500
actggctgaa	tggcaaggag	tacaagtgca	aggtctccaa	caaagccctc	ccagccccc	1560
tcgagaaaac	catctccaaa	gccaaagggt	ggaccctggt	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	ccttcttctc	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	tgaccagag 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
tcatacgctgc aacccgagga ctttgctacc tactactgcc tgcaaggcac tcatttcctt	300
cacacttttcg 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
agcagcaccg tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa	600
gtcaccatc agggcctgag ctgcgccgtc acaaagagct tcaacagggg agagtgt	657

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

<220>
 <223> 1519gH20 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 tggctctgggt cagacaagca	120
cctggaaagg gtcttgaatg ggtggcctat attgactctg acggggacaa cacctactat	180
cgggattccg tgaaaggacg cttcacaatc tcccagata acgccaagag ctactgtac	240
ctgcagatga atagcctgag agccgaggat actgccgtgt actattgcac aacgggaatc	300
gttaggcctt ttctgtactg gggacagggc accttggtta ctgtctcgag cgcttctaca	360
aagggcccat cggctttccc cctggcaccg tcctccaaga gcacctctgg gggcacagcg	420
gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca	480
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac	540
tcctcagca gcgtggtgac cgtgccctcc agcagcttgg gcaccagac ctacatctgc	600
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt	660
gacaaaactc acacatgcgc cgcg	684

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

<220>
 <223> 1519 gH20 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 tggaagcgaggagggtctt gtgcagcctg gaggaagttt acgtctctct      120
tgtgctgtgt ctggcttcac cttctccaat tacggaatgg tctgggtcag acaagcacct      180
ggaaagggtc ttgaatgggt ggcctatatatt gactctgacg gggacaacac ctactatcgg      240
gattccgtga aaggacgctt cacaatctcc cgagataacg ccaagagctc actgtacctg      300
cagatgaata gcctgagagc cgaggatact gccgtgtact attgcacaac gggaatcggt      360
aggccttttc tgtactgggg acagggcacc ttgggttactg tctcgagcgc ttctacaaag      420
ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc      480
ctgggctgcc tgggtcaagga ctacttcccc gaaccgggtga cggtgtcgtg gaactcaggc      540
gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc      600
ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac      660
gtgaatcaca agcccagcaa caccaagggtg 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 cctcccgggt ctccggctct ggctctggca ccgagttcac cctgaccatc	240
tccagcctgc agcccagga 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
tccggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc	540
agcagcacc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcttgcgaa	600
gtcaccatc agggcctgag ctgcgccgtc acaaagagct tcaacagggg agagtgtggt	660
ggaggtggct ctggcgggtg tggtccgga ggcggaggaa gcgacatcca gatgaccag	720
agcccttcct ctgtaagcgc cagtgtcgga gacagagtga ctattacctg ccaaagctcc	780
ccttcagtct ggtccaattt tctatcctgg tatcagcaaa agcccggaaa ggctcctaaa	840
ttgctgatct acgaagcaag caaactcacc agcggcgtgc ccagcagggt cagcggcagt	900
gggtctggaa ctgactttac cctgacaatc tcctcactcc agcccagga cttcgccacc	960
tattactgcg gtggagggtta cagtagcata agtgatacga catttggtg cggcactaaa	1020
gtggaaatca agcgtacc	1038

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

<220>

<223> 1519gH20 FabFv heavy chain (alternative sequence to SEQ ID NO: 51)

<400> 80

gaggtgcccc tgggtggaatc tggcggcgga ctggtgcagc ctggcggctc cctgagactg	60
tcttgcgccg tgtccggctt caccttctcc aactacggca tgggtctgggt 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 accctgggtca ccgtgtcctc tgcttctaca      360
aagggcccat cgggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg      420
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca      480
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtccctc tggactctac      540
tccctcagca gcgtgggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc      600
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt      660
tccggagggtg gcggttccgg aggtggcggg acaggtggcg gtgggtccga agtccagctg      720
cttgaatccg gaggcggact cgtgcagccc ggaggcagtc ttcgcttgctc 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 actctgggtca 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
gatgttgatga tgacccagac tccactgtct ttgtcgggtg ccattggaca accagcctcc 60
atctcttcta agtcaagtca gagcctcgta ggtgctggtg gaaagacata tttgtattgg 120
ttattacaga ggtccggcca gtctccaaag cgactaatct atctggtgtc cacactggac 180
tctggaattc ctgatagggt 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 tgggtggagtc tggggggcggc tcagtgcagc ctgggaggtc catgaaactc 60
tcctgtgtag tctcaggatt cacttttcagt aactatggca tgggtctgggt ccgccaggct 120
ccaaagaagg gtctggagtg ggtcgcataat attggttctg atggtgataa tacttactac 180
cgagattccg tgaagggccg attcactatc tccagaaata atgcaaaaag caccctatat 240
ttgcaaatgg acagtctgag gtctgaggac acggccactt attactgtac aacagggatt 300
gtccggccct ttctctactg gggccaagga gtcattggtca 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 tgggtctgggt cagacaagca 120
cctggaaaagg gtcttgaatg ggtggcctat attgactctg acggggacaa cacctactat 180
cgggattccg tgaaaggacg cttcacaatc tcccagata acgccaagag ctactgtac 240
ctgcagatga atagcctgag agccgaggat actgccgtgt actattgcac aacgggaatc 300
gttaggcctt ttctgtactg gggacagggc accttggtta ctgtctcgag cgcttctaca 360
aagggcccat cggctcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 420
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca 480
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540
tccctcagca gcgtgggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 600
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttggtga gaggccagca 660
cagggaggga ggggtgtctgc tggaagccag gctcagcgct cctgcctgga cgcattcccg 720
ctatgcagcc ccagtccagg gcagcaaggc agggccccgtc tgcctcttca cccggaggcc 780
tctgccccgc cactcatgc tcaggagag ggtcttctgg ctttttcccc aggctctggg 840
caggcacagg ctaggtgccc ctaaccagg ccctgcacac aaaggggcag gtgctgggct 900

cagacctgcc aagagccata tccgggagga ccctgcccct gacctaaagg caccccaag	960
gccaaactct ccactccctc agctcggaca ctttctctcc tcccagatct gagtaactcc	1020
caatcttctc tctgcagagc ccaaactcttg tgacaaaact cacacatgcc caccgtgccc	1080
aggtaagcca gccagggcct cgccctccag ctcaaggcgg gacaggtgcc ctagagtagc	1140
ctgcatccag ggacaggccc cagccgggtg ctgacacgtc cacctccatc tcttcctcag	1200
cacctgaact cctgggggga ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc	1260
tcatgatctc ccggaccctt gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc	1320
ctgaggtcaa gttcaactgg tacgtggacg gcgtggagggt gcataatgcc aagacaaagc	1380
cgcggggagga gcagtacaac agcacgtacc gtgtgggtcag cgtcctcacc gtcctgcacc	1440
aggactggct gaatggcaag gagtacaagt gcaagggtct caacaaagcc ctcccagccc	1500
ccatcgagaa aaccatctcc aaagccaaag gtgggacccg tggggtgcca gggccacatg	1560
gacagaggcc ggctcggccc accctctgcc ctgagagtga ccgctgtacc aacctctgtc	1620
cctacagggc agccccgaga accacagggtg tacaccctgc ccccatcccg ggatgagctg	1680
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc	1740
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg	1800
gactccgacg gtccttctt cctctacagc aagctcaccg tggacaagag cagggtggcag	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 gggaatcggt	360
aggccttttc tgtactgggg acagggcacc ttggttactg tctcgagcgc ttctacaaag	420
ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc	480
ctgggctgcc tggtaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc	540

gccctgacca	gcggcgtgca	caccttcccc	gctgtcctac	agtcctcagg	actctactcc	600
ctcagcagcg	tggtgaccgt	gccctccagc	agcttgggca	cccagaccta	catctgcaac	660
gtgaatcaca	agcccagcaa	caccaaggtg	gacaagaaag	ttggtgagag	gccagcacag	720
ggagggaggg	tgtctgctgg	aagccaggct	cagcgctcct	gcctggacgc	atccccggcta	780
tgcagcccca	gtccagggca	gcaaggcagg	ccccgtctgc	ctcttcaccc	ggaggcctct	840
gcccgccccca	ctcatgctca	gggagaggggt	cttctggctt	tttccccagg	ctctgggcag	900
gcacaggcta	ggtgccccta	acccaggccc	tgcacacaaa	ggggcagggtg	ctgggctcag	960
acctgccaag	agccatatcc	gggaggaccc	tgcccttgac	ctaagcccac	cccaaaggcc	1020
aaactctcca	ctccctcagc	tgggacacct	tctctcctcc	cagatctgag	taactcccaa	1080
tcttctctct	gcagagccca	aatcttgtag	caaaactcac	acatgcccac	cgtgcccagg	1140
taagccagcc	caggcctcgc	cctccagctc	aaggcgggac	aggtgcccta	gagtagcctg	1200
catccaggga	caggccccag	ccgggtgctg	acacgtccac	ctccatctct	tcctcagcac	1260
ctgaactcct	ggggggaccg	tcagtcttcc	tcttcccccc	aaaaccaag	gacaccctca	1320
tgatctcccg	gacccttgag	gtcacatgcg	tgggtggtgga	cgtgagccac	gaagaccctg	1380
aggtcaagtt	caactggtac	gtggacggcg	tggaggtgca	taatgccaag	acaagccgc	1440
gggaggagca	gtacaacagc	acgtaccgtg	tggtcagcgt	cctcaccgtc	ctgcaccagg	1500
actggctgaa	tggcaaggag	tacaagtgca	aggtctccaa	caaagccctc	ccagccccca	1560
tcgagaaaac	catctccaaa	gccaaagggtg	ggaccctgtg	ggtgcgagg	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
tccgacgggt	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								
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

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 tggctctgggt cagacaagca 120

cctggaaagg gtcttgaatg ggtggcctat attgactctg acggggacaa cacctactat 180

cgggattccg tgaaaggacg cttcacaatc tcccagagata acgccaagag ctactgtac 240

ctgcagatga atagcctgag agccgaggat actgccgtgt actattgcac aacgggaatc	300
gttaggcctt ttctgtactg gggacagggc accttggtta ctgtctcgag cgcttctaca	360
aagggcccat ccgtcttccc cctggcgccc tgctccagga gcacctccga gagcacagcc	420
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca	480
ggcgccctga ccagcggcgt gcacaccttc cgggctgtcc tacagtcctc aggactctac	540
tccctcagca gcgtgggtgac cgtgccctcc agcagcttgg gcacgaagac ctacacctgc	600
aacgtagatc acaagcccag caacaccaag gtggacaaga gagttggtga gaggccagca	660
cagggagggg ggggtgtctgc tgggaagccag gctcagccct cctgcctgga cgcaccccg	720
ctgtgcagcc ccagcccagg gcagcaaggc atgccccatc tgtctcctca cccggaggcc	780
tctgaccacc ccactcatgc ccagggagag ggtcttcttg atttttccac caggctccgg	840
gcagccacag gctggatgcc cctaccccag gccctgcgca tacaggggca ggtgctgcgc	900
tcagacctgc caagagccat atccgggagg accctgcccc tgacctaaagc ccaccccaaa	960
ggccaaactc tccactccct cagctcagac accttctctc ctcccagatc tgagtaactc	1020
ccaatcttct ctctgcagag tccaaatatg gtcccccatg cccatcatgc ccaggtaagc	1080
caaccacaggc ctcgccctcc agctcaaggc gggacagggtg ccctagagta gcctgcatcc	1140
agggacaggc cccagccggg tgctgacgca tccacctcca tctcttcctc agcacctgag	1200
ttcctggggg gaccatcagt cttcctgttc cccccaaaac ccaaggacac tctcatgac	1260
tcccggaacc ctgaggtcac gtgcgtgggtg 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 cacgggggtgc gagggccaca tggacagagg	1560
tcagctcggc ccacctctg ccctgggagt gaccgctgtg ccaacctctg tccctacagg	1620
gcagccccga gagccacagg tgtacacctt gccccatcc caggaggaga tgaccaagaa	1680
ccaggtcagc ctgacctgcc tgggtcaaagg cttctacccc agcgacatcg ccgtggagt	1740
ggagagcaat gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga	1800
cggctccttc ttctcttaca 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> 1519gH20 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 gggaatcggt	360
aggccttttc tgtactgggg acagggcacc ttgggttactg tctcgagcgc ttctacaaag	420
ggcccatccg tcttccccct ggcgccctgc tccaggagca cctccgagag cacagccgcc	480
ctgggctgcc tgggtcaagga ctacttcccc gaaccggtga cgggtgctgt gaactcaggc	540
gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc	600
ctcagcagcg tggtgaccgt gccctccagc agcttgggca cgaagaccta cacctgcaac	660
gtagatcaca agcccagcaa caccaagggtg gacaagagag ttggtgagag gccagcacag	720
ggaggggaggg tgtctgctgg aagccaggct cagccctcct gcctggacgc accccggctg	780
tgcagcccca gcccagggca gcaaggcatg ccccatctgt ctctcaccg ggaggcctct	840
gaccacccca ctcatgcca gggagagggt cttctggatt tttccaccag gctccgggca	900
gccacaggct ggatgcccct accccaggcc ctgcgcatac aggggcagggt gctgcgctca	960
gacctgccaa gagccatata cgggaggacc ctgcccctga cctaagccca ccccaaaggc	1020
caaaactctcc actccctcag ctacagacacc ttctctcctc ccagatctga gtaactccca	1080
atcttctctc tgcagagtcc aaatatggtc ccccatgccc atcatgcca ggtaagccaa	1140
cccaggcctc gccctccagc tcaaggcggg acagggtgcc tagagtagcc tgcattccagg	1200
gacaggcccc agccgggtgc tgacgcatcc acctccatct ctctctcagc acctgagttc	1260
ctgggggggac catcagtctt cctgttcccc ccaaaacca aggacactct catgatctcc	1320
cggacccctg aggtcacgtg cgtgggtggtg gacgtgagcc aggaagaccg cgagggtccag	1380
ttcaactggt acgtggatgg cgtggagggtg cataatgcca agacaaagcc gcgggaggag	1440
cagttcaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg	1500
aacggcaagg agtacaagtg caaggctctc aacaaaggcc tcccgtcctc catcgagaaa	1560
accatctcca aagccaaagg tgggaccac ggggtgcgag ggccacatgg acagagggtca	1620
gctcggccca ccctctgcc tgggagtgac cgctgtgcca acctctgtcc ctacagggca	1680
gccccgagag ccacagggtg acaccctgcc cccatcccag gaggagatga ccaagaacca	1740

ggtcagcctg acctgcctgg tcaaaggctt ctaccccgagc 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 tgaccagtc cccctccagc ctgtccgcct ccgtgggcga cagagtgacc	60
atcacatgca agtcctccca gtccctggtc ggagcctccg gcaagaccta cctgtactgg	120
ctgttccaga agcccggcaa ggcccccaag cggctgatct acctggtgtc taccctggac	180
tccggcatcc cctcccgggt ctccggctct ggctctggca ccgagttcac cctgaccatc	240
tccagcctgc agcccagga 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 tgaccagtc cccctccagc ctgtccgcct ccgtgggcga cagagtgacc	60
atcacatgca agtcctccca gtccctggtc ggagcctccg gcaagaccta cctgtactgg	120
ctgttccaga agcccggcaa ggcccccaag cggctgatct acctggtgtc taccctggac	180
tccggcatcc cctcccgggt ctccggctct ggctctggca ccgagttcac cctgaccatc	240
tccagcctgc agcccagga cttcgccacc tactactgtc tgcaaggcac ccacttcccc	300
cacaccttcg gccagggcac caagctggaa atcaagcggga 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 cgcttgcgaa	600

gtgacccacc agggcctgtc cagccccgtg 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 tgggtggaatc tggcggcgga ctggtgcagc ctggcggctc cctgagactg 60
tcttgcgccg tgtccggctt caccttctcc aactacggca tggctctgggt 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 accctgggtca 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 tgggtggaatc tggcggcgga ctggtgcagc ctggcggctc cctgagactg 60
tcttgcgccg tgtccggctt caccttctcc aactacggca tggctctgggt 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 accctgggtca ccgtgtcctc tgcctccacc 360
aagggcccct ccgtgttccc tctggcccct tgctcccgggt ccacctccga gtctaccgcc 420
gctctgggct gcctgggtcaa ggactacttc cccgagcccg tgacagtgtc ctggaactct 480
ggcgccctga cctccggcgt gcacaccttc cctgccgtgc tgcagtcctc cggcctgtac 540
tccctgtcct ccgtcgtgac cgtgccctcc tccagcctgg gcaccaagac ctacacctgt 600
aacgtggacc acaagccctc caacaccaag gtggacaagc ggggtggaatc taagtacggc 660
cctccctgcc ccccctgcc tgcccctgaa tttctgggag gaccttccgt gttcctgttc 720
cccccaaagc ccaaggacac cctgatgatc tcccggaccc ccgaagtgtc ctgcgtgggtg 780

gtggacgtgt cccaggaaga tcccagagtc cagttcaatt ggtacgtgga cggcgtggaa	840
gtgcacaatg ccaagaccaa gcccagagag gaacagttca actccaccta ccgggtggtg	900
tccgtgctga ccgtgctgca ccaggactgg ctgaacggca aagagtacaa gtgcaagggtg	960
tccaacaagg gcctgccctc cagcatcgaa aagaccatct ccaaggccaa gggccagccc	1020
cgcgagcccc aggtgtacac cctgccccct agccaggaag agatgaccaa gaaccagggtg	1080
tccctgacct gtctggtcaa gggcttctac ccctccgaca ttgccgtgga atgggagtcc	1140
aacggccagc ccgagaacaa ctacaagacc accccccctg tgctggacag cgacgggtcc	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