

SEQUENCE LISTING

<110> BRISTOL-MYERS SQUIBB COMPANY

<120> ANTI-TREM-1 ANTIBODIES AND USES THEREOF

<130> 3338.0920002/ELE/C-K/DKC

<140> US 16/371,964

<141> 2019-04-01

<150> US 62/651,605

<151> 2018-04-02

<160> 85

<170> PatentIn version 3.5

<210> 1

<211> 234

<212> PRT

<213> homo sapiens

<400> 1

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

Glu Leu Arg Ala Ala Thr Lys Leu Thr Glu Glu Lys Tyr Glu Leu Lys
20 25 30

Glu Gly Gln Thr Leu Asp Val Lys Cys Asp Tyr Thr Leu Glu Lys Phe
35 40 45

Ala Ser Ser Gln Lys Ala Trp Gln Ile Ile Arg Asp Gly Glu Met Pro
50 55 60

Lys Thr Leu Ala Cys Thr Glu Arg Pro Ser Lys Asn Ser His Pro Val
65 70 75 80

Gln Val Gly Arg Ile Ile Leu Glu Asp Tyr His Asp His Gly Leu Leu
85 90 95

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

Cys Val Ile Tyr Gln Pro Pro Lys Glu Pro His Met Leu Phe Asp Arg
 115 120 125

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

Glu Asn Ser Thr Gln Asn Val Tyr Lys Ile Pro Pro Thr Thr Thr Lys
 145 150 155 160

Ala Leu Cys Pro Leu Tyr Thr Ser Pro Arg Thr Val Thr Gln Ala Pro
 165 170 175

Pro Lys Ser Thr Ala Asp Val Ser Thr Pro Asp Ser Glu Ile Asn Leu
 180 185 190

Thr Asn Val Thr Asp Ile Ile Arg Val Pro Val Phe Asn Ile Val Ile
 195 200 205

Leu Leu Ala Gly Gly Phe Leu Ser Lys Ser Leu Val Phe Ser Val Leu
 210 215 220

Phe Ala Val Thr Leu Arg Ser Phe Val Pro
 225 230

<210> 2
 <211> 225
 <212> PRT
 <213> homo sapiens

<400> 2

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

Glu Leu Arg Ala Ala Thr Lys Leu Thr Glu Glu Lys Tyr Glu Leu Lys
 20 25 30

Glu Gly Gln Thr Leu Asp Val Lys Cys Asp Tyr Thr Leu Glu Lys Phe
 35 40 45

Ala Ser Ser Gln Lys Ala Trp Gln Ile Ile Arg Asp Gly Glu Met Pro
 50 55 60

Lys Thr Leu Ala Cys Thr Glu Arg Pro Ser Lys Asn Ser His Pro Val
 65 70 75 80

Gln Val Gly Arg Ile Ile Leu Glu Asp Tyr His Asp His Gly Leu Leu
 85 90 95

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

Cys Val Ile Tyr Gln Pro Pro Lys Glu Pro His Met Leu Phe Asp Arg
 115 120 125

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

Glu Asn Ser Thr Gln Asn Val Tyr Lys Ile Pro Pro Thr Thr Thr Lys
 145 150 155 160

Ala Leu Cys Pro Leu Tyr Thr Ser Pro Arg Thr Val Thr Gln Ala Pro
 165 170 175

Pro Lys Ser Thr Ala Asp Val Ser Thr Pro Asp Ser Glu Ile Asn Leu
 180 185 190

Thr Asn Val Thr Asp Ile Ile Arg Tyr Ser Phe Gln Val Pro Gly Pro
 195 200 205

Leu Val Trp Thr Leu Ser Pro Leu Phe Pro Ser Leu Cys Ala Glu Arg
 210 215 220

Met
 225

<210> 3

<211> 150
 <212> PRT
 <213> homo sapiens

<400> 3

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

Glu Leu Arg Ala Ala Thr Lys Leu Thr Glu Glu Lys Tyr Glu Leu Lys
 20 25 30

Glu Gly Gln Thr Leu Asp Val Lys Cys Asp Tyr Thr Leu Glu Lys Phe
 35 40 45

Ala Ser Ser Gln Lys Ala Trp Gln Ile Ile Arg Asp Gly Glu Met Pro
 50 55 60

Lys Thr Leu Ala Cys Thr Glu Arg Pro Ser Lys Asn Ser His Pro Val
 65 70 75 80

Gln Val Gly Arg Ile Ile Leu Glu Asp Tyr His Asp His Gly Leu Leu
 85 90 95

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

Cys Val Ile Tyr Gln Pro Pro Lys Glu Pro His Met Leu Phe Asp Arg
 115 120 125

Ile Arg Leu Val Val Thr Lys Gly Phe Arg Cys Ser Thr Leu Ser Phe
 130 135 140

Ser Trp Leu Val Asp Ser
 145 150

<210> 4
 <211> 3333
 <212> DNA
 <213> Homo sapiens

<400> 4
 gtgcaacttt ccgaagcctc taggtcattg tggcgccttg tagctgtccc gggagccctc 60
 agcagcagtt ggagctgggtg cacaggaagg atgaggaaga ccaggctctg ggggctgctg 120
 tggatgctct ttgtctcaga actccgagct gcaactaaat taactgagga aaagtatgaa 180
 ctgaaagagg ggcagaccct ggatgtgaaa tgtgactaca cgctagagaa gtttgccagc 240
 agccagaaaag cttggcagat aataagggac ggagagatgc ccaagaccct ggcatgcaca 300
 gagaggcctt caaagaattc ccatccagtc caagtgggga ggatcatact agaagactac 360
 catgatcatg gtttactgcg cgtccgaatg gtcaaccttc aagtgggaaga ttctggactg 420
 tatcagtgtg tgatctacca gcctcccaag gagcctcaca tgctgttcga tcgcatccgc 480
 ttgggtgggtga ccaagggttt ttcaggggacc cctggctcca atgagaattc taccagaat 540
 gtgtataaga ttctcctac caccactaag gccttgtgcc cactctatac cagccccaga 600
 actgtgaccc aagctccacc caagtcaact gccgatgtct ccactcctga ctctgaaatc 660
 aaccttaca atgtgacaga tatcatcagg gttccgggtg tcaacattgt cattctcctg 720
 gctgggtggat tcctgagtaa gagcctgggtc ttctctgtcc tgtttgctgt cacgctgagg 780
 tcatttgtac cctaggccca cgaaccacg agaatgtcct ctgacttcca gccacatcca 840
 tctggcagtt gtgccaaggg aggagggagg aggtaaaagg caggaggtta ataacatgaa 900
 ttaaatctgt aatcaccggc tatttctaaa gtcagcgtct caccttcctg cccactgccc 960
 tcgttcctct aataatcttg ggtgggcatt tgtgcctcag aaaagaagtt acagcccaa 1020
 acatgcttgg tccttcattc caccagccac ttgggggttg catgaaatac agacagctca 1080
 atgcttttca ccgtaattct cttgtggggg ctgtgacatg cagaaggcac acctgatact 1140
 tctcctgctc agttttgccc tggaccatac aattttggcc tgacctggac agagctccca 1200
 ctacagaagc atcctgctcg ccccatgctg ggacttcctc tttctagcat cagacacttg 1260
 ggtttcatgc ttatgtgtgg ttctttccaa cactcccaga aaagggtggt gaagattgtg 1320
 gaacctggag aaataagaca tcgtgggtgag aaagtgcac cttctcagag aaaagagtta 1380
 aactgagtat cttcttctgg ggaaatactg gcaggccgag atgggatcca taggagagca 1440
 acaacagacc atgtcagaca tcctgtgtgc atttatcgct ggatcctgaa aatagccccg 1500

tgaaggcaga aatgtatgtg actagaacga ggccacatga ataagccact gcccactggc	1560
aggagtgaaa actgaagcgc tccttacctg aaggacccca aaaccatata gaatagaata	1620
accaggagtt ccgcctgtgt ctaaatgcct cttttcctgt atcacacaag ggtcagggat	1680
ggtggagtaa aagctctccc cctgggaggc ttctggaggc tgtcccatg tgcttgccata	1740
gttccccact ctgcccctct cctcttctct cagtctgctc ctggaacacc tgcctcagtt	1800
tccatgctct ctccagtgcc ctccccgggtg aagcaggtag gtgttcaggc caccacagag	1860
acaatctctg tgggagattg tcttgcaatc tcccacagat ttcaatcagg attttgttat	1920
ttcctacttt gagctttaaa gggaaatggg cctcatgggt ggggaaagga tgggtgggtcc	1980
ttccagccca atttagtgat gcccagggca gatattatcc tcagttccca agagcaatca	2040
tacttttcca cacataccgt gtgtctcatg ttaggtaaat gtatttttac aatgagcacc	2100
acttctgtgg aaaaagttcc ctgcacgggg aggtccagct tccagactgc tccatcgcat	2160
aaggacttcc ccattcccct aaatgctgct ctgtcagaac ctgcccaggt aatggtaatg	2220
accctagaga gatgatttct gaaccgcaat tttgagccca ttagaagggtg tgtgggtgggc	2280
atttatttca tcctgatgct ctggtgagaa tctttgcaga cgcactagat ccagaagctg	2340
ttaatcttgg tgcatttatt ttctaccta aaagaaccaa gcagctcaga ggcagtgact	2400
gtacaggatg cagtgtttat aataatgctg agcttgctgg tctggaaccc cacactttag	2460
caatcccagc attgttcctg tttatgaagt tgacaaagt accagggcaa gggggtatta	2520
tcattaaata cactctagga gaggcagaac acatgagggc aatgtttttc agaggctttt	2580
aggccaccgc atcagattct cctggagcat aaagcaaagc ctttatgagt ccagggcccc	2640
tgcagaccta ctgtatacta gtatacagct ccctcttagt ggatctcaag cttgtttcca	2700
aaaagtcatt acactcctta ccaaagccca tgacacattc atacagattc atccagacat	2760
aaccactgc atgggtccagt gcatgcttgt gtgcttaact tattatagat caagtgttat	2820
ttaagtccaa catattaaac gtgactgaaa tattatatgc actaaatcgg aagacaaatg	2880
gccgtgctgg atactctccc atttgcactt acaggccacg ccatgctcca tcctccccat	2940
cctgcctggg aacctgacca atgtggctaa accagcaggc tccctggctg ccagcttctg	3000
gctggttgag ccaatgggaa gcatgagagg agagccgagg gtggggagac agtcagatca	3060

```

gggttttctgt cctcagggct ccctccctgg caggtggtgg caggagtggc tgcattcccc 3120
tctgaaggct ccttcaagcc tctcagcaaa cagctcccat ctccaagtcc agccacctgt 3180
tccatcctct cctctgtagg cccagcagtg ggaatgaccc accactattg ccagcctcag 3240
catactgaag cacccttac tggattccct aaattctatg cacatgttta ttaaagtctc 3300
ctcaattacc cagttaaaaa aaaaaaaaaa aaa 3333

```

```

<210> 5
<211> 2102
<212> DNA
<213> homo sapiens

```

```

<400> 5
attgtggtgc cttgtagctg tcccgggagc cctcagcagc agttggagct ggtgcacagg 60
aaggatgagg aagaccaggc tctgggggct gctgtggatg ctctttgtct cagaactccg 120
agctgcaact aaattaactg aggaaaagta tgaactgaaa gaggggcaga ccctggatgt 180
gaaatgtgac tacacgctag agaagtttgc cagcagccag aaagcttggc agataataag 240
ggacggagag atgccaaga ccctggcatg cacagagagg cttcaaaga attcccatcc 300
agtccaagtg gggaggatca tactagaaga ctacatgat catggtttac tgcgcgtccg 360
aatggtcaac cttcaagtgg aagattctgg actgtatcag tgtgtgatct accagcctcc 420
caaggagcct cacatgctgt tcgatcgcat ccgcttggtg gtgaccaagg gtttttcagg 480
gaccctggc tccaatgaga attctacca gaatgtgtat aagattcctc ctaccaccac 540
taaggccttg tgccactct ataccagccc cagaactgtg acccaagctc cacccaagtc 600
aactgccgat gtctccactc ctgactctga aatcaacctt acaaatgtga cagatatcat 660
caggtatagt ttccagggtc ctgggcccct ggtttggaca ctgagccctt tgtttcccag 720
tctgtgtgct gagaggatgt gaaagtgagg gaaaggggag ggtggggcag gagaagactt 780
gagtcacatt agtctgggta gaaatgtcca ggggaagaag gaagtggatg tggagaatag 840
gggaggctct cagccaggct gtccttctcc ccagttcacc ttctttgttt ccttgcaacc 900
tgagtattaa agagagggaa atggcatctt cccaagtgc cagtggagct catccaaccc 960
caggggcctg atgggcagtg ggaaagcact ctgagtgagg ggccctggat ctagtggttg 1020

```

cctgactaac tgaatgtgac tttgggtgag tcaggaaccc tctctggcctt tagcttcttt	1080
gacaattcag taggcatggg agaaacccaa agctggaaga cattgtccac ctaataactc	1140
tcagcaggag ctggagctgg ggctaaatgc agtattgggtt tttgccttat tgtttttttaa	1200
ataacattgt tgcatgtgcc caattataga taaatagaat cagaattttt gcagatgagg	1260
tccctctcag tattttttaat aagatgttta ggagatttct aatgtgtagg caaacttaag	1320
aaccactaac ttagcaattt cacacctctt tacagttatt aaatgttgat ttatattaga	1380
atgtgtttat cattaaatac tgaattatca ggatggaaat acttttccac atcaccacta	1440
gtctaacatg tcttttttct catattctct tctagtcttt attcatgttt atacatattt	1500
taatatggca gtaagtctaa ttatacatgt ttttattctt ttccttgctg aaattattct	1560
ttgatgctgc tacctaaatt tcataaatat aatttcaatg agtgcattt tttctatcaa	1620
ttgggaaagc cataacttac ataaccattg gcctgttctt agacattgat atagtgttga	1680
taactctgag ataaacatat tcttgcatg atatttttct tcttttaaat aattaactcg	1740
aaatttccat gagataattt aaacactgat atcattttgt atacaaatag catctaccaa	1800
tggtcttcca aaagattgga aacaatttgc agtgtgatcc attaagcata aataaagcag	1860
tgtcatggca ggcttacaga cacggattta gtcttttaaa tcattaaata gtgtgagtta	1920
aatcacattc ctgctaaaac aaatgtgaac tggcgcctgc tctaatttct ctatgagtgt	1980
agactccacc tccatatggg tagtggcagt gcctttttcc ccattatgtt gtttggggaa	2040
caaagtgctc attaaacttc tgtggaataa atcaaacgaa tgatcaaaaa aaaaaaaaaa	2100
aa	2102

<210> 6
 <211> 3140
 <212> DNA
 <213> homo sapiens

<400> 6	
gtgcaacttt ccgaagcctc taggtcattg tggcgccttg tagctgtccc gggagccctc	60
agcagcagtt ggagctgggtg cacaggaagg atgaggaaga ccaggctctg ggggctgctg	120
tggatgctct ttgtctcaga actccgagct gcaactaaat taactgagga aaagtatgaa	180

ctgaaagagg ggcagaccct ggatgtgaaa tgtgactaca cgctagagaa gtttgccagc	240
agccagaaaag cttggcagat aataagggac ggagagatgc ccaagaccct ggcatgcaca	300
gagaggcctt caaagaattc ccatccagtc caagtgggga ggatcatact agaagactac	360
catgatcatg gtttactgcg cgtccgaatg gtcaaccttc aagtggaaga ttctggactg	420
tatcagtgtg tgatctacca gcctcccaag gagcctcaca tgctgttcga tcgcatccgc	480
ttggtggtga ccaagggggt ccggtgttca acattgtcat tctcctggct ggtggattcc	540
tgagtaagag cctggctcttc tctgtcctgt ttgctgtcac gctgaggta tttgtaccct	600
aggccacga acccacgaga atgtcctctg acttccagcc acatccatct ggcagttgtg	660
ccaagggagg agggaggagg taaaaggcag ggagttaata acatgaatta aatctgtaat	720
caccggctat ttctaaagtc agcgtctcac cttcctgccc actgccctcg ttcctctaata	780
aatcttgggt gggcatttgt gcctcagaaa agaagttaca gcccacaaaca tgcttggtcc	840
ttcattccac cagccacttg ggggtggcat gaaatacaga cagctcaatg cttttcaccg	900
taattctctt gtgggggctg tgacatgcag aaggcacacc tgatacttct cctgctcagt	960
tttgccctgg accatacaat tttggcctga cctggacaga gctcccacta cagaagcatc	1020
ctgctcgccc catgctggga cttcctcttt ctagcatcag acacttgggt ttcattgctta	1080
tgtgtggttc tttccaacac tcccagaaaa ggggtgtgaa gattgtggaa cctggagaaa	1140
taagacatcg tggtgagaaa gtgcatcctt ctcagagaaa agagttaaac tgagtatctt	1200
cttctgggga aatactggca ggccgagatg ggatccatag gagagcaaca acagaccatg	1260
tcagacatcc tgtgtgcatt tatcgctgga tcctgaaaat agccccgtga aggcagaaat	1320
gtatgtgact agaacgaggc cacatgaata agccactgcc cactggcagg agtgaaaact	1380
gaagcgctcc ttacctgaag gacccccaaa ccatatagaa tagaataacc aggagttccg	1440
cctgtgtcta aatgcctctt ttcctgtatc acacaagggt cagggatggg ggagtaaaag	1500
ctctccccct gggaggcttc tggaggctgt ccccatgtgc ttgcctagtt cccactctg	1560
ccctcctcct cttctctcag tctgtcctg gaacacctgc ctcagtttcc atgctctctc	1620
cagtgccctc cccggtgaag caggtaggtg ttcaggccac cacagagaca atctctgtgg	1680

gagattgtct tgcaatctcc cacagatttc aatcaggatt ttgttatttc ctactttgag	1740
ctttaaaggg aaatgggcct catgggtggg gaaaggatgg tgggtccttc cagcccaatt	1800
tagtgatgcc cagggcagat attatcctca gttcccaaga gcaatcatac ttttccacac	1860
ataccgtgtg tctcatgtta ggtaaatgta tttttacaat gagcaccact tctgtggaaa	1920
aagttccctg cacggggagg tccagcttcc agactgctcc atcgcataag gacttcccca	1980
ttcccctaaa tgctgctctg tcagaacctg cccaggtaat ggtaatgacc ctagagagat	2040
gatttctgaa ccgcaatttt gagcccatta gaagggtgtg ggtgggcatt tatttcatcc	2100
tgatgctctg gtgagaatct ttgcagacgc actagatcca gaagctgtta atcttggtgc	2160
atttattttc ctacctaaaa gaaccaagca gctcagaggc agtgactgta caggatgcag	2220
tgtttataat aatgctgagc ttgctggtct ggaacccac acttttagcaa tcccagcatt	2280
gttcctgttt atgaagttga caaagtgacc agggcaaggg ggtattatca ttaaatacac	2340
tctaggagag gcagaacaca tgagggaat gtttttcaga ggtctttagg ccaccgcatc	2400
agattctcct ggagcataaa gcaaatgctt tatgagtcca gggcccctgc agacctactg	2460
tatactagta tacagctccc tcttagtgga tctcaagctt gtttccaaaa agtcattaca	2520
ctccttacca aagcccatga cacattcata cagattcatc cagacataac cactgcatg	2580
gtccagtgca tgcttggtg ctttaacttat tatagatcaa gtgttattta agtccaacat	2640
attaaacgtg actgaaatat tatatgcact aaatcggaag acaaatggcc gtgctggata	2700
ctctcccatt tgcaattaca ggccacgcca tgctccatcc tccccatcct gcctgggaac	2760
ctgaccaatg tggctaaacc agcaggctcc ctggctgcca gcttctggct ggttgagcca	2820
atgggaagca tgagaggaga gccgagggtg gggagacagt cagatcaggg tttctgtcct	2880
cagggctccc tccctggcag gtggtggcag gagtggctgc attccccctt gaaggctcct	2940
tcaagcctct cagcaaacag ctcccatctc caagtccagc cacctgttcc atcctctcct	3000
ctgtaggccc agcagtggga atgaccacc actattgcca gcctcagcat actgaagcac	3060
cccttactgg attcccctaaa ttctatgcac atgtttatta aatgctcctc aattaccag	3120
ttaaaaaaaa aaaaaaaaaa	3140

<210> 7
 <211> 233
 <212> PRT
 <213> *Macaca fascicularis*

<400> 7

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

Glu Leu Arg Ala Thr Thr Glu Leu Thr Glu Glu Lys Tyr Glu Tyr Lys
 20 25 30

Glu Gly Gln Thr Leu Glu Val Lys Cys Asp Tyr Ala Leu Glu Lys Tyr
 35 40 45

Ala Asn Ser Arg Lys Ala Trp Gln Lys Met Glu Gly Lys Met Pro Lys
 50 55 60

Ile Leu Ala Lys Thr Glu Arg Pro Ser Glu Asn Ser His Pro Val Gln
 65 70 75 80

Val Gly Arg Ile Thr Leu Glu Asp Tyr Pro Asp His Gly Leu Leu Gln
 85 90 95

Val Gln Met Thr Asn Leu Gln Val Glu Asp Ser Gly Leu Tyr Gln Cys
 100 105 110

Val Ile Tyr Gln His Pro Lys Glu Ser His Val Leu Phe Asn Pro Ile
 115 120 125

Cys Leu Val Val Thr Lys Gly Ser Ser Gly Thr Pro Gly Ser Ser Glu
 130 135 140

Asn Ser Thr Gln Asn Val Tyr Arg Thr Pro Ser Thr Thr Ala Lys Ala
 145 150 155 160

Leu Gly Pro Arg Tyr Thr Ser Pro Arg Thr Val Thr Gln Ala Pro Pro
 165 170 175

Glu Ser Thr Val Val Val Ser Thr Pro Gly Ser Glu Ile Asn Leu Thr
 180 185 190

Asn Val Thr Asp Ile Ile Arg Val Pro Val Phe Asn Ile Val Ile Ile
 195 200 205

Val Ala Gly Gly Phe Leu Ser Lys Ser Leu Val Phe Ser Val Leu Phe
 210 215 220

Ala Val Thr Leu Arg Ser Phe Gly Pro
 225 230

<210> 8
 <211> 196
 <212> PRT
 <213> homo sapiens

<400> 8

Met Ser Arg Arg Ser Met Leu Leu Ala Trp Ala Leu Pro Ser Leu Leu
 1 5 10 15

Arg Leu Gly Ala Ala Gln Glu Thr Glu Asp Pro Ala Cys Cys Ser Pro
 20 25 30

Ile Val Pro Arg Asn Glu Trp Lys Ala Leu Ala Ser Glu Cys Ala Gln
 35 40 45

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

Ser Ser Cys Asn Thr Pro Ala Ser Cys Gln Gln Gln Ala Arg Asn Val
 65 70 75 80

Gln His Tyr His Met Lys Thr Leu Gly Trp Cys Asp Val Gly Tyr Asn
 85 90 95

Phe Leu Ile Gly Glu Asp Gly Leu Val Tyr Glu Gly Arg Gly Trp Asn
 100 105 110

Phe Thr Gly Ala His Ser Gly His Leu Trp Asn Pro Met Ser Ile Gly
 115 120 125

Ile Ser Phe Met Gly Asn Tyr Met Asp Arg Val Pro Thr Pro Gln Ala
 130 135 140

Ile Arg Ala Ala Gln Gly Leu Leu Ala Cys Gly Val Ala Gln Gly Ala
 145 150 155 160

Leu Arg Ser Asn Tyr Val Leu Lys Gly His Arg Asp Val Gln Arg Thr
 165 170 175

Leu Ser Pro Gly Asn Gln Leu Tyr His Leu Ile Gln Asn Trp Pro His
 180 185 190

Tyr Arg Ser Pro
 195

<210> 9
 <211> 330
 <212> PRT
 <213> homo sapiens

<400> 9

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 10
 <211> 327
 <212> PRT
 <213> homo sapiens

<400> 10

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Leu Ser Leu Ser Leu Gly Lys
 325

<210> 11
 <211> 330
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IgG1-Aba Heavy Chain Constant Region

<400> 11

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 12

<211> 330

<212> PRT

<213> Artificial Sequence

<220>

<223> IgG4-Aba Heavy Chain Constant Region

<400> 12

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 13
 <211> 107
 <212> PRT
 <213> homo sapiens

<400> 13

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
 1 5 10 15

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

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
 35 40 45

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
 50 55 60

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
 65 70 75 80

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
 85 90 95

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 100 105

<210> 14
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> mAb 0318 VH

<400> 14

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

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

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

Gly Arg Ile Arg Thr Lys Ser Ser Asn Tyr Ala Thr Tyr Tyr Ala Ala
 50 55 60

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

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

Tyr Cys Thr Arg Asp Met Gly Ile Arg Arg Gln Phe Ala Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 15
 <211> 218
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> mAb 0318 VL

<400> 15

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

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

Asp Tyr Ser Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45

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

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

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

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

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln

115

120

125

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

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

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

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

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

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

<210> 16
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318-IgG1.3f VH

<400> 16

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

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

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

Gly Arg Ile Arg Thr Lys Ser Ser Asn Tyr Ala Thr Tyr Tyr Ala Ala
 50 55 60

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

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

Tyr Cys Thr Arg Asp Met Gly Ile Arg Arg Gln Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 17
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> 0318-IgG1.3f VL

<400> 17

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

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

Asp Tyr Ser Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

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

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

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

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

<210> 18
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318-IgG1.1f VH

<400> 18

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

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

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

Gly Arg Ile Arg Thr Lys Ser Ser Asn Tyr Ala Thr Tyr Tyr Ala Ala
 50 55 60

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

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

Tyr Cys Thr Arg Asp Met Gly Ile Arg Arg Gln Phe Ala Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 19
 <211> 111
 <212> PRT
 <213> Artificial Sequence

<220>

<223> 0318-IgG1.1f VL

<400> 19

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

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

Asp Tyr Ser Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45

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

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

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

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

<210> 20

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> 0318-IgG1-Aba VH

<400> 20

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

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

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

Gly Arg Ile Arg Thr Lys Ser Ser Asn Tyr Ala Thr Tyr Tyr Ala Ala
50 55 60

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

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

Tyr Cys Thr Arg Asp Met Gly Ile Arg Arg Gln Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

$\langle 210 \rangle$	21
$\langle 211 \rangle$	111
$\langle 212 \rangle$	PRT
$\langle 213 \rangle$	Artificial Sequence

<220>
<223> 0318-IgG1-Aba VL

<400> 21

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

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

Asp Tyr Ser Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

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

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

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

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

<210> 22

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> 0318-IgG4-Aba VH

<400> 22

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

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

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

Gly Arg Ile Arg Thr Lys Ser Ser Asn Tyr Ala Thr Tyr Tyr Ala Ala
 50 55 60

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

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

Tyr Cys Thr Arg Asp Met Gly Ile Arg Arg Gln Phe Ala Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 23
 <211> 111
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318-IgG4-Aba VL

<400> 23

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

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

Asp Tyr Ser Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45

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

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

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

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

<210> 24
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318-IgG1.3f VH CDR1

<400> 24

Thr Tyr Ala Met His
1 5

<210> 25
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> 0318-IgG1.3f VH CDR2

<400> 25

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

Val Lys Gly

<210> 26
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 0318-IgG1.3f VH CDR3

<400> 26

Asp Met Gly Ile Arg Arg Gln Phe Ala Tyr
1 5 10

<210> 27
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 0318-IgG1.3f VL CDR1

<400> 27

Arg Ala Ser Gln Ser Val Asp Thr Phe Asp Tyr Ser Phe Leu His
1 5 10 15

<210> 28

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

<220>
 <223> 0318-IgG1.3f VL CDR2

<400> 28

Arg Ala Ser Asn Leu Glu Ser
 1 5

<210> 29
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318-IgG1.3f VL CDR3

<400> 29

Gln Gln Ser Asn Gln Asp Pro Tyr Thr
 1 5

<210> 30
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318-IgG1.1f VH CDR1

<400> 30

Thr Tyr Ala Met His
 1 5

<210> 31
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318-IgG1.1f VH CDR2

<400> 31

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

Val Lys Gly

<210> 32
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318-IgG1.1f VH CDR3

<400> 32

Asp Met Gly Ile Arg Arg Gln Phe Ala Tyr
 1 5 10

<210> 33
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318-IgG1.1f VL CDR1

<400> 33

Arg Ala Ser Gln Ser Val Asp Thr Phe Asp Tyr Ser Phe Leu His
 1 5 10 15

<210> 34
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318-IgG1.1f VL CDR2

<400> 34

Arg Ala Ser Asn Leu Glu Ser
 1 5

<210> 35

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

<220>
 <223> 0318-IgG1.1f VL CDR3

<400> 35

Gln Gln Ser Asn Gln Asp Pro Tyr Thr
 1 5

<210> 36
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318-IgG1-Aba VH CDR1

<400> 36

Thr Tyr Ala Met His
 1 5

<210> 37
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318-IgG1-Aba VH CDR2

<400> 37

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

Val Lys Gly

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

<220>

<223> 0318-IgG1-Aba VH CDR3

<400> 38

Asp	Met	Gly	Ile	Arg	Arg	Gln	Phe	Ala	Tyr
1				5					10

<210> 39

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> 0318-IgG1-Aba VL CDR1

<400> 39

Arg	Ala	Ser	Gln	Ser	Val	Asp	Thr	Phe	Asp	Tyr	Ser	Phe	Leu	His
1				5					10					15

<210> 40

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> 0318-IgG1-Aba VL CDR2

<400> 40

Arg	Ala	Ser	Asn	Leu	Glu	Ser
1				5		

<210> 41

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> 0318-IgG1-Aba VL CDR3

<400> 41

Gln	Gln	Ser	Asn	Gln	Asp	Pro	Tyr	Thr
1				5				

<210> 42

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

<220>
 <223> 0318-IgG4-Aba VH CDR1

<400> 42

Thr Tyr Ala Met His
 1 5

<210> 43
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318-IgG4-Aba VH CDR2

<400> 43

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

Val Lys Gly

<210> 44
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318-IgG4-Aba VH CDR3

<400> 44

Asp Met Gly Ile Arg Arg Gln Phe Ala Tyr
 1 5 10

<210> 45
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>

<223> 0318-IgG4-Aba VL CDR1

<400> 45

Arg	Ala	Ser	Gln	Ser	Val	Asp	Thr	Phe	Asp	Tyr	Ser	Phe	Leu	His
1				5					10					15

<210> 46

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> 0318-IgG4-Aba VL CDR2

<400> 46

Arg	Ala	Ser	Asn	Leu	Glu	Ser
1				5		

<210> 47

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> 0318-IgG4-Aba VL CDR3

<400> 47

Gln	Gln	Ser	Asn	Gln	Asp	Pro	Tyr	Thr
1				5				

<210> 48

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> LSPGK (C-terminal end of heavy chain)

<400> 48

Leu	Ser	Pro	Gly	Lys
1				5

<210> 49

<211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> LSPG (C-terminal end of heavy chain)

<400> 49

Leu Ser Pro Gly
 1

<210> 50
 <211> 451
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318-IgG1.3f HC

<400> 50

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

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

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

Gly Arg Ile Arg Thr Lys Ser Ser Asn Tyr Ala Thr Tyr Tyr Ala Ala
 50 55 60

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

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

Tyr Cys Thr Arg Asp Met Gly Ile Arg Arg Gln Phe Ala Tyr Trp Gly
 100 105 110

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

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

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

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

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

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
 195 200 205

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

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly
 225 230 235 240

Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
 355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 385 390 395 400

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

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 435 440 445

Pro Gly Lys
 450

<210> 51
 <211> 450
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318-IgG1.1f HC

<400> 51

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

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

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

Gly Arg Ile Arg Thr Lys Ser Ser Asn Tyr Ala Thr Tyr Tyr Ala Ala
 50 55 60

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

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

Tyr Cys Thr Arg Asp Met Gly Ile Arg Arg Gln Phe Ala Tyr Trp Gly
 100 105 110

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

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

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

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

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

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
 195 200 205

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

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly
 225 230 235 240

Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ser Ser Ile
 325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
 355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 385 390 395 400

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

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 435 440 445

Pro Gly
 450

<210> 52
 <211> 451
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318-IgG1-Aba HC

<400> 52

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

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

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

Gly Arg Ile Arg Thr Lys Ser Ser Asn Tyr Ala Thr Tyr Tyr Ala Ala
 50 55 60

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

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

Tyr Cys Thr Arg Asp Met Gly Ile Arg Arg Gln Phe Ala Tyr Trp Gly
 100 105 110

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

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

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

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

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

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
 195 200 205

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

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

Gly Ser Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 340 345 350

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

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 385 390 395 400

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

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 435 440 445

Pro Gly Lys
 450

<210> 53
 <211> 451
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318-IgG4-Aba HC

<400> 53

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

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

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

Gly Arg Ile Arg Thr Lys Ser Ser Asn Tyr Ala Thr Tyr Tyr Ala Ala
 50 55 60

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

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

Tyr Cys Thr Arg Asp Met Gly Ile Arg Arg Gln Phe Ala Tyr Trp Gly
 100 105 110

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

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

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

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

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

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

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

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

Gly Ser Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 340 345 350

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

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 385 390 395 400

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

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser

435

440

445

Pro Gly Lys
450

<210> 54
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> 0318-IgG1.3f LC

<400> 54

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

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

Asp Tyr Ser Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

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

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

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

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

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

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

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

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

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

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

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

<210> 55
 <211> 218
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318-IgG1.1f LC

<400> 55

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

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

Asp Tyr Ser Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45

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

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

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

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

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

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

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

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

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

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

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

<210> 56

<211> 218

<212> PRT

<213> Artificial Sequence

<220>

<223> 0318-IgG1-Aba LC

<400> 56

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

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

Asp Tyr Ser Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45

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

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

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

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

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

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

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

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

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

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

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

<210> 57
 <211> 218
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318-IgG4-Aba LC

<400> 57

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

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

Asp Tyr Ser Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45

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

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

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

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

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

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

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

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

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

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

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

<210> 58
 <211> 1407
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 0318-IgG1.3f HC

<400> 58
 atgagggctt ggatcttctt tctgctctgc ctggccgggc ggccttggc cgaagtgcag 60
 ctcgtggagt ccggcggagg actggtccaa cctggcggct ccctgaagct gtcctgcgct 120
 gcctccggct tcaccttctc cacctacgcc atgcactggg tcaggcaggc ctccggaaag 180
 ggcttggaaat gggtcggccg gattaggacc aagtccagca actacgctac ctactacgcc 240
 gccagcgtca agggccgggt cacaatctcc cgggacgact ccaagaacac cgcctatctc 300
 cagatgaaca gcctgaagac agaggacacc gccgtgtact attgcacccg ggatatgggc 360
 attcggaggc agttcgcta ttggggccag ggcaccctgg tgacagtcag ctccgccagc 420
 acaaaaggac ctagcgtgtt ccccttggcc cctagcagca agtccacaag cggcggcacc 480
 gctgccctgg gctgtctggt gaaagactac tttcccagac ccgtgacagt gagctggaac 540
 tctggcgcgc tgacatccgg agtgcacacc ttccctgccg tgctccagtc cagcggcctg 600
 tacagcctga gcagcgtcgt gaccgtccct agcagcagcc tgggaacca gacctacatc 660
 tgcaacgtga accacaagcc ctccaacacc aaggtggaca agagggtgga gccaagtcc 720
 tgtgacaaga cccatacctg cccccctgt cctgctcctg aagctgaggg cgcccccttc 780

gtcttcctgt tccctcctaa gccaagagac accctgatga tctccaggac ccccgagggtg	840
acctgtgtgg tgggtggatgt gtccacagag gaccccgagg tgaagttcaa ttggtacgtc	900
gacggcgtgg aggtgcacaa cgccaagacc aaaccccggg aggagcagta taacagcacc	960
taccgggtgg tgtccgtgct caccgtgctg caccaggact ggctgaacgg caaggagtac	1020
aagtgttaagg tcagcaataa ggccctgcct gcccctatcg agaagaccat tagcaaggct	1080
aagggccagc ccagggaacc ccagggtgtat accctcccc ctagccggga ggagatgacc	1140
aagaaccagg tcagcctgac ctgcctgggtg aaaggattct accctagcga catcgctgtg	1200
gagtgggaga gcaatggaca gcccgagaac aactacaaaa ccacccctcc cgtcctggac	1260
tccgatggca gcttctttct gtactccaag ctcaccgtcg acaagagccg gtggcagcag	1320
ggcaatgtgt ttagctgtc cgtgatgcac gaggctctgc acaaccacta tacccaaaag	1380
tccctgtccc tcagccccgg caagtga	1407

<210> 59

<211> 1404

<212> DNA

<213> Artificial Sequence

<220>

<223> 0318-IgG1.1f HC

<400> 59

atgagggctt ggatcttctt tctgctctgc ctggccgggc gcgccttggc cgaagtgcag	60
ctgggtggaaa gcggcggagg actggtgcag ccaggcggca gcctgaagct gtcttgcgcc	120
gccagcggct tcaccttcag cacctacgcc atgcactggg tccgccaggc cagcggcaag	180
ggcctggaat gggtcggacg gatccggacc aagagcagca actacgccac ctactacgcc	240
gcctccgtga agggccggtt caccatcagc cgggacgaca gcaagaacac cgcctacctg	300
cagatgaaca gcctgaaaac cgaggacacc gccgtgtact actgcacccg ggacatgggc	360
atccggcggc agtttgccta ctggggccag ggcaccctgg tcacagtgtc cagcgcgtcg	420
accaagggcc catcgttctt cccctggca ccctcctcca agagcacctc tgggggcaca	480
gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac	540
tcaggcgcgc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc	600

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc	660
tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agagagttga gcccaaattct	720
tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagccgaagg ggccccgtca	780
gtcttcctct tcccccaaaa acccaaggac accctcatga tctcccggac ccctgaggtc	840
acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg	900
gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg	960
taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac	1020
aagtgcagg tctccaacaa agccctccca agcagcatcg agaaaaccat ctcaaagcc	1080
aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc	1140
aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg	1200
gagtgggaga gcaatgggca gccggagAAC aactacaaga ccacgcctcc cgtgctggac	1260
tccgacggct ccttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag	1320
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag	1380
agcctctccc tgtccccggg ttga	1404

<210> 60
 <211> 1407
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 0318-IgG1-Aba HC

<400> 60	
atgagggctt ggatcttctt tctgctctgc ctggccgggc gcgccttggc cgaggtccag	60
ctggtggaga gcgaggagg actcgtgcag cctggaggat ccctgaagct gtcctgcgct	120
gcctccggct ttaccttctc cacctacgcc atgcattggg tgaggcaggc ctccggcaag	180
ggcctggaat ggggtgggcag gatcaggaca aagagctcca actacgccac ctactacgcc	240
gccagcgtga aaggacggtt caccatctcc cgggacgatt ccaaaaacac cgcttacctc	300
cagatgaata gcctgaagac cgaggacacc gccgtctact actgcaccag ggatatgggc	360

atccggcggc agtttgccta ctggggccag ggcaccctgg tgacagtgtc cagcgctagc	420
accaaaggcc cctccgtgtt cccctggct ccctccagca agtccacatc cggcggaacc	480
gccgctctgg gatgtctggt gaaggactac ttccccgagc ccgtgacagt gagctggaac	540
tctggcgctc tgacctccgg cgtgcacacc tttcctgctg tgctgcagtc ctccggcctc	600
tacagcctgt cctccgtcgt gacagtgtcc tcctccagcc tgggcaccca gacctacatc	660
tgcaacgtga accacaagcc ttccaacacc aagggtggata agcgggtcga acccaagagc	720
tgcgacaaga cccacaccag ccccccttcc cctgctcccg agctcctggg aggcagctcc	780
gtgtttctgt ttcccccaa gcctaaggac accctgatga tcagcaggac ccccgaaagt	840
acatgcgtgg tggctgacgt gtccacgag gaccccgagg tcaagttcaa ctggtacgtg	900
gatggagtgg aggtccataa tgccaagacc aagccccggg aggagcagta caattccacc	960
taccgggtgg tgtccgtgct gacagtcctg catcaggact ggctcaacgg caaggagtac	1020
aaatgcaagg tgtccaacaa ggctctgtccc gccccatcg agaagacaat cagcaaggct	1080
aagggccagc ctagggagcc ccaggtgtac accctgtccc cttccaggga cgagctcacc	1140
aagaaccagg tgtccctgac atgcctcgtg aagggtttt accctagcga catcgctgtg	1200
gagtgggagt ccaacggaca gcccgagaac aactacaaga caacaccccc tgtgctggac	1260
tccgacggct ctttcttctt gtacagcaag ctcaccgtgg acaaattccc gtggcagcag	1320
ggaaacgtgt tcagctgtc cgtgatgcat gaggccctgc acaaccatta caccagaaa	1380
tccctgtccc tgtcccccg caagtga	1407

<210> 61
 <211> 1407
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 0318-IgG4-Aba HC

<400> 61	
atgagggtt ggatcttctt tctgctctgc ctggccgggc gcgccttggc cgagggtccag	60
ctggctgaga gcggcggagg actggtccag cctggaggat ccctgaagct ctcctgtgcc	120
gctagcggat ttaccttcag cacctacgct atgcattggg tgaggcaggc ttccggcaag	180

```

ggactggagt ggggtgggacg gattcggacc aagagctcca attacgccac ctattacgcc      240
gcttccgtga agggccggtt caccatctcc agggacgact ccaagaacac cgcttacctg      300
cagatgaact ccctcaagac cgaggacacc gccgtgtatt actgcacccg ggacatgggc      360
atccggaggc agttcgctta ttggggacag ggcaccctgg tgaccgtgag ctccgcctcc      420
accaagggcc cttccgtgtt ccctctggcc ccctgtagca ggtccaccag cgagtccaca      480
gctgctctgg gctgtctggt gaaggattat ttccccgagc ccgtgacagt gtcctggaat      540
agcggcgccc tgacctccgg cgtgcatacc ttccctgccg tcctgcaaag cagcggcctg      600
tacagcctgt cctccgtggt gacagtccct tcctccagcc tgggaaccaa gacctacacc      660
tgcaatgtgg accacaagcc tagcaacacc aagggtggaca agagggtcga gccaagtcc      720
tgcgataaga cacacacctc ccctccttcc cctgctcctg agctgctcgg cggaagcagc      780
gtgttcctgt tccctcctaa gcctaaggac accctgatga tcagccggac ccctgaggtg      840
acctgtgtcg tgggtggacgt gtcccacgaa gaccccgagg tgaaattcaa ctggtacgtg      900
gacggcgctc aggtgcacaa cgctaagaca aaacccaggg aggagcagta caattccacc      960
taccgggtcg tgtccgtgct gaccgtgctg caccaggact ggctgaacgg caaagagtac     1020
aagtgttaagg tcagcaataa ggccctgcct gccccattg agaagaccat ttccaaggcc     1080
aagggccagc ccagggaacc tcaggtgtac accctgcctc cctcccggga cgagctgacc     1140
aagaaccagg tcagcctgac ctgcctcgtg aagggttctt accctagcga catcgccgtg     1200
gagtgggagt ccaacggcca gcctgagaac aattacaaga ccaccccccc tgcctggac      1260
tccgacggat ctttcttctt gtactccaag ctgacagtgg ataagtcccg gtggcagcag      1320
ggaaatgtgt tctcctgctc cgtcatgcac gaagccctgc ataaccacta cacacagaag      1380
agcctgtccc tgagccctgg caagtga                                           1407

```

```

<210> 62
<211> 708
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> 0318-IgG1.3f LC

```

<400> 62
 atgagggcctt ggatccttctt tctgctctgc ctggccgggc gcgccttggc cgatatcgtg 60
 ctgacccaga gccccgatag cctggctgtg agcctgggcg agagagccac catcaactgc 120
 agggcctccc agagcgtcga caccttcgac tacagcttcc tccactggta ccagcagaag 180
 cctggccagc cccccaagct gctgatctac agggccagca acctggagag cggagtgtccc 240
 gataggttca gcggcagcgg ctccggaacc gactttaccc tcaccatcag ctccctgcag 300
 gccgaggatg tggccgtcta ctactgccag cagagcaacc aggaccccta cacctttggc 360
 cagggcacca agctggagat caagaggacc gtggccgccc cctccgtgtt catcttcctt 420
 cccagcgacg agcagctgaa gagcgggaacc gccagcgtgg tgtgcctgct gaacaacttc 480
 taccacaggg agggcaaggt gcagtggaaag gtcgacaacg ccctgcagag cggcaatagc 540
 caggagagcg tgaccgaaca ggacagcaag gactccacct actccctgag cagcaccctg 600
 accctgagca aggccgacta cgagaagcac aaggtgtacg cctgtgaggt gaccaccag 660
 ggactgagca gccccgtgac aaagagcttt aacaggggcg agtgctga 708

<210> 63
 <211> 708
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 0318-IgG1.1f LC

<400> 63
 atgagggcctt ggatccttctt tctgctctgc ctggccgggc gcgccttggc cgatatcgtg 60
 ctgacccaga gccccgatag cctggctgtg agcctgggcg agagagccac catcaactgc 120
 agggcctccc agagcgtcga caccttcgac tacagcttcc tccactggta ccagcagaag 180
 cctggccagc cccccaagct gctgatctac agggccagca acctggagag cggagtgtccc 240
 gataggttca gcggcagcgg ctccggaacc gactttaccc tcaccatcag ctccctgcag 300
 gccgaggatg tggccgtcta ctactgccag cagagcaacc aggaccccta cacctttggc 360
 cagggcacca agctggagat caagaggacc gtggccgccc cctccgtgtt catcttcctt 420
 cccagcgacg agcagctgaa gagcgggaacc gccagcgtgg tgtgcctgct gaacaacttc 480

taccccaggg aggccaaggt gcagtggaag gtcgacaacg ccctgcagag cggcaatagc 540
 caggagagcg tgaccgaaca ggacagcaag gactccacct actccctgag cagcaccctg 600
 accctgagca aggccgacta cgagaagcac aaggtgtacg cctgtgaggt gacccaccag 660
 ggactgagca gccccgtgac aaagagcttt aacaggggcg agtgctga 708

<210> 64
 <211> 708
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 0318-IgG1-Aba LC

<400> 64
 atgagggctt ggatcttctt tctgctctgc ctggccgggc ggccttggc cgatatcgtg 60
 ctgaccacaga gccccgatag cctggctgtg agcctgggcg agagagccac catcaactgc 120
 agggcctccc agagcgtcga caccttcgac tacagcttcc tccactggta ccagcagaag 180
 cctggccagc cccccaagct gctgatctac agggccagca acctggagag cggagtgtccc 240
 gatagggttca gcggcagcgg ctccggaacc gactttaccc tcaccatcag ctccctgcag 300
 gccgaggatg tggccgtcta ctactgccag cagagcaacc aggacccta cacctttggc 360
 cagggcacca agctggagat caagaggacc gtggccgccc cctccgtgtt catcttccct 420
 cccagcgacg agcagctgaa gagcgggaacc gccagcgtgg tgtgcctgct gaacaacttc 480
 taccccaggg aggccaaggt gcagtggaag gtcgacaacg ccctgcagag cggcaatagc 540
 caggagagcg tgaccgaaca ggacagcaag gactccacct actccctgag cagcaccctg 600
 accctgagca aggccgacta cgagaagcac aaggtgtacg cctgtgaggt gacccaccag 660
 ggactgagca gccccgtgac aaagagcttt aacaggggcg agtgctga 708

<210> 65
 <211> 708
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 0318-IgG4-Aba LC

<400> 65
 atgagggctt ggatcttctt tctgctctgc ctggccgggc gcgccttggc cgatatcgtg 60
 ctgacccaga gccccgatag cctggctgtg agcctgggcg agagagccac catcaactgc 120
 agggcctccc agagcgtcga caccttcgac tacagcttcc tccactggta ccagcagaag 180
 cctggccagc cccccaagct gctgatctac agggccagca acctggagag cggagtgtccc 240
 gataggttca gcggcagcgg ctccggaacc gactttaccc tcaccatcag ctccctgcag 300
 gccgaggatg tggccgtcta ctactgccag cagagcaacc aggaccccta cacctttggc 360
 cagggcacca agctggagat caagaggacc gtggccgccc cctccgtgtt catcttcctt 420
 cccagcgacg agcagctgaa gagcgggaacc gccagcgtgg tgtgcctgct gaacaacttc 480
 taccacaggg agggccaaggt gcagtgggaag gtcgacaacg ccctgcagag cggcaatagc 540
 caggagagcg tgaccgaaca ggacagcaag gactccacct actccctgag cagcaccctg 600
 accctgagca aggccgacta cgagaagcac aaggtgtacg cctgtgaggt gaccaccag 660
 ggactgagca gccccgtgac aaagagcttt aacaggggcg agtgctga 708

<210> 66
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318 Ab - VH CDR1

<400> 66

Thr Tyr Ala Met His
 1 5

<210> 67
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318 Ab - VH CDR2

<400> 67

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

Val Lys Asp

<210> 68
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318 Ab - VH CDR3

<400> 68

Asp Met Gly Gln Arg Arg Gln Phe Ala Tyr
 1 5 10

<210> 69
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318 Ab - VL CDR1

<400> 69

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

<210> 70
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318 Ab - VL CDR2

<400> 70

Arg Ala Ser Asn Leu Glu Ser
 1 5

<210> 71

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

<220>
 <223> 0318 Ab - VL CDR3

<400> 71

Gln Gln Ser Asn Glu Asp Pro Tyr Thr
 1 5

<210> 72
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318 AB - VH CDR3 (mutant)

<400> 72

Asp Gln Gly Ile Arg Arg Gln Phe Ala Tyr
 1 5 10

<210> 73
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318 AB - VH CDR3 (mutant)

<400> 73

Asp Leu Gly Ile Arg Arg Gln Phe Ala Tyr
 1 5 10

<210> 74
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 0318 Ab - VH CDR1 (mutant)

<400> 74

Thr Tyr Ala Gln His
1 5

<210> 75
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> 0318 Ab - VH CDR1 (mutant)

<400> 75

Thr Tyr Ala Leu His
1 5

<210> 76
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> 0318 Ab - HC (IgG4)

<400> 76

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

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

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

Gly Arg Ile Arg Thr Lys Ser Ser Asn Tyr Ala Thr Tyr Tyr Ala Ala
50 55 60

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

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

Tyr Cys Thr Arg Asp Met Gly Ile Arg Arg Gln Phe Ala Tyr Trp Gly
 100 105 110

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

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

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

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

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

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

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

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

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

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

Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 275 280 285

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

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

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

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

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

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
 370 375 380

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

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

Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 420 425 430

Leu His Asn Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val
 435 440 445

Ser Leu Gly
 450

<210> 77
 <211> 330
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> WT IgG1 Constant Region (Allotypic Variant)

<400> 77

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 78

<211> 330

<212> PRT

<213> Artificial Sequence

<220>

<223> IgG1.1f HC Constant Region

<400> 78

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 79

<211> 330

<212> PRT

<213> Artificial Sequence

<220>

<223> IgG1.3f HC Constant Region

<400> 79

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 80
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Linker

<400> 80

Pro Val Gly Val Val
 1 5

<210> 81
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 318 Ab - Mutant

<400> 81

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

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

Ala Met His Trp Val Arg Gln Ala Ser Gly Lys Gly Leu Glu Trp Val

35

40

45

Gly Arg Ile Arg Thr Lys Ser Ser Asn Tyr Ala Thr Tyr Tyr Ala Ala
 50 55 60

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

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

Tyr Cys Thr Arg Asp Gln Gly Ile Arg Arg Gln Phe Ala Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 82
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 319 Ab - Mutant

<400> 82

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

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

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

Gly Arg Ile Arg Thr Lys Ser Ser Asn Tyr Ala Thr Tyr Tyr Ala Ala
 50 55 60

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

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

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

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 83
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 320 Ab - Mutant

<400> 83

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

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

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

Gly Arg Ile Arg Thr Lys Ser Ser Asn Tyr Ala Thr Tyr Tyr Ala Ala
 50 55 60

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

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

Tyr Cys Thr Arg Asp Met Gly Ile Arg Arg Gln Phe Ala Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 84
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 321 Ab - Mutant

<400> 84

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

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

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

Gly Arg Ile Arg Thr Lys Ser Ser Asn Tyr Ala Thr Tyr Tyr Ala Ala
 50 55 60

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

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

Tyr Cys Thr Arg Asp Met Gly Ile Arg Arg Gln Phe Ala Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 85
 <211> 450
 <212> PRT
 <213> Artificial Sequence

<220>

<223> 0318-IgG1.3f HC Kdel

<400> 85

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

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

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

Gly Arg Ile Arg Thr Lys Ser Ser Asn Tyr Ala Thr Tyr Tyr Ala Ala
 50 55 60

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

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

Tyr Cys Thr Arg Asp Met Gly Ile Arg Arg Gln Phe Ala Tyr Trp Gly
 100 105 110

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

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

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

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

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val

180

185

190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
 195 200 205

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

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly
 225 230 235 240

Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
 355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 370 375 380

Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro
385					390					395					400

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

Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met
			420					425					430		

His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser
		435					440					445			

Pro	Gly
	450