SEQUENCE LISTING

<110> UCB Biopharma SPRL

<120> FcRn Antibody

<130> G0191

<150> GB1320066.2
<151> 2013-11-13

<160> 74

<170> PatentIn version 3.5

<210> 1
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<223> CDRH2

<400> 2

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1 5 10 15

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

<220>
<223> CDRH3

<400> 3

Thr Pro Ala Tyr Tyr Gly Ser His Pro Pro Phe Asp Tyr
1 5 10

<210> 4
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL1

<400> 4

Arg Thr Ser Glu Asp Ile Tyr Thr Asn Leu Ala

1 5 10

<210> 5
<211> 7
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<220>
<223> CDRL2

<400> 5

Val Ala Lys Thr Leu Gln Asp
1 5

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

<400> 6

Leu Gln Gly Phe Lys Phe Pro Trp Thr
1 5

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

<220>
<223> CDRL2 VARIANT

<400> 7

Val Ala Lys Thr Leu Gln Glu
1 5

<210> 8
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Rat Ab 1638 VL region

<400> 8

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

Glu Thr Ile Ser Ile Glu Cys Arg Thr Ser Glu Asp Ile Tyr Thr Asn
20 25 30

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

Tyr Val Ala Lys Thr Leu Gln Asp Gly Val Pro Ser Arg Phe Ser Gly

eolf-seql

50 55 60

Ser Gly Ser Gly Thr His Tyr Ser Leu Lys Ile Ser Gly Met Gln Pro
65 70 75 80

Glu Asp Glu Gly Asp Tyr Phe Cys Leu Gln Gly Phe Lys Phe Pro Trp
85 90 95

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

<210> 9
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Rat Ab 1638 VL region

<400> 9
gacatcctga tgacacagtc tccagcttcc ctgtctgcat ctctgggaga aactatctcc 60

atcgaatgtc gaacaagtga agacatttac actaatttag cgtggtacca gcagaagtca 120

gggaaatctc ctcaactcct gatctatgtt gcaaagacgt tgcaagatgg ggtcccatca 180

cggttcagtg gcagtggatc tggcacgcat tattctctca agatcagcgg catgcaacct 240

gaagatgaag gggattattt ctgtctgcag ggtttcaagt ttccgtggac gttcggtgga 300

ggcaccaagc tggaactgaa a 321

<210> 10
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> Rat Ab 1638 VL region with signal sequence underlined and italicised

<400> 10

Met Asn Val Pro Thr Gln Phe Leu Gly Leu Leu Leu Leu Trp Ile Thr
1 5 10 15

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

Ala Ser Leu Gly Glu Thr Ile Ser Ile Glu Cys Arg Thr Ser Glu Asp
35 40 45

Ile Tyr Thr Asn Leu Ala Trp Tyr Gln Gln Lys Ser Gly Lys Ser Pro
50 55 60

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

Arg Phe Ser Gly Ser Gly Ser Gly Thr His Tyr Ser Leu Lys Ile Ser
85 90 95

Gly Met Gln Pro Glu Asp Glu Gly Asp Tyr Phe Cys Leu Gln Gly Phe
100 105 110

Lys Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys
115 120 125

<210> 11
<211> 381
<212> DNA
<213> Artificial Sequence

<220>
<223> Rat Ab 1638 VL region with signal sequence underlined and italicised

<400> 11
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gacatcctga tgacacagtc tccagcttcc ctgtctgcat ctctgggaga aactatctcc 120

atcgaatgtc gaacaagtga agacatttac actaatttag cgtggtacca gcagaagtca 180

gggaaatctc ctcaactcct gatctatgtt gcaaagacgt tgcaagatgg ggtcccatca 240

cggttcagtg gcagtggatc tggcacgcat tattctctca agatcagcgg catgcaacct 300

gaagatgaag gggattattt ctgtctgcag ggtttcaagt ttccgtggac gttcggtgga 360

ggcaccaagc tggaactgaa a 381

<210> 12
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Rat Ab 1638 VH region

<400> 12

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

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

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

Trp Leu Ala Asn Ile Trp Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ser
50 55 60

Leu Glu Asn Arg Leu Thr Ile Ser Lys Asp Thr Ser Asn Asn Gln Ala
65 70 75 80

Phe Leu Lys Ile Thr Asn Val Asp Thr Ala Asp Ser Ala Thr Tyr Phe

eolf-seql

85 90 95

Cys Val Arg Thr Pro Ala Tyr Tyr Gly Ser His Pro Pro Phe Asp Tyr
100 105 110

Trp Gly Gln Gly Val Met Val Thr Val Ser
115 120

<210> 13
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Rat Ab 1638 VH region

<400> 13
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cagccttcag ggaagggtct ggagtggctg gcaaacattt ggtgggatga tgataagcgc 180

tacaatccat ctctggaaaa ccgactcact atctccaagg acacctccaa caaccaagca 240

ttcctcaaga tcaccaatgt ggacactgca gatagcgcca catacttctg tgttcggacc 300

ccggcttact atggcagcca tccccctttt gactactggg gccaaggagt catggtcaca 360

gtctcg 366

<210> 14
<211> 141
<212> PRT
<213> Artificial Sequence

<220>
<223> Rat Ab 1638 VH region with signal sequence underlined and italicised

<400> 14

Met Asp Arg Leu Thr Ser Ser Phe Leu Leu Leu Ile Val Pro Ala Tyr
1 5 10 15

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

Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu
35 40 45

Ser Thr Tyr Gly Val Gly Val Gly Trp Ile Arg Gln Pro Ser Gly Lys
50 55 60

Gly Leu Glu Trp Leu Ala Asn Ile Trp Trp Asp Asp Asp Lys Arg Tyr
65 70 75 80

Asn Pro Ser Leu Glu Asn Arg Leu Thr Ile Ser Lys Asp Thr Ser Asn
85 90 95

Asn Gln Ala Phe Leu Lys Ile Thr Asn Val Asp Thr Ala Asp Ser Ala
100 105 110

Thr Tyr Phe Cys Val Arg Thr Pro Ala Tyr Tyr Gly Ser His Pro Pro
115 120 125

Phe Asp Tyr Trp Gly Gln Gly Val Met Val Thr Val Ser
130 135 140

<210> 15
<211> 423
<212> DNA
<213> Artificial Sequence

<220>
<223> Rat Ab 1638 VH region with signal sequence underlined and italicised

<400> 15
atggacaggc taacttcctc attcctactg ctgattgtcc ctgcatatgt cctgtctcag 60

gttactctga aagagtctgg ccctgggata ttgcagccct cccagaccct cagtctgact 120

tgcactttct ctgggttttc actgagtact tatggtgtgg gtgtgggctg gattcgtcag 180

ccttcaggga agggtctgga gtggctggca aacatttggt gggatgatga taagcgctac 240

aatccatctc tggaaaaccg actcactatc tccaaggaca cctccaacaa ccaagcattc 300

ctcaagatca ccaatgtgga cactgcagat agcgccacat acttctgtgt tcggaccccg 360

gcttactatg gcagccatcc ccttttgac tactggggcc aaggagtcat ggtcacagtc 420

tcg 423

<210> 16
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> 1638 gL7 V-region

<400> 16

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 Thr Ser Glu Asp Ile Tyr Thr Asn
20 25 30

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

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

Ser Gly Ser Gly Thr His Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro

eolf-seql

65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gln Gly Phe Lys Phe Pro Trp
85 90 95

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

<210> 17
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> 1638 gL7 V-region

<400> 17
gatatccaga tgacccagag tccaagcagt ctctccgcca gcgtaggcga tcgtgtgact 60

attacctgtc gcactagcga ggacatctac accaacctgg cgtggtatca gcagaaacca 120

ggcaaagtgc cgaaactgct gatctacgtc gcgaaaaccc tccaggaagg tgtaccgtct 180

cgcttttccg gctctggtag cggtactcac tacaccctga ccatctcttc cctccagccg 240

gaagatgttg ctacctacta ttgcctccag ggcttcaaat tcccgtggac tttcggtggc 300

ggcacgaaag tggaaatcaa a 321

<210> 18
<211> 128
<212> PRT
<213> Artificial Sequence

<220>
<223> 1638 gL7 V-region (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 Arg Thr Ser Glu
35 40 45

Asp Ile Tyr Thr Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val
50 55 60

Pro Lys Leu Leu Ile Tyr Val Ala Lys Thr Leu Gln Glu Gly Val Pro
65 70 75 80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr His Tyr Thr Leu Thr Ile
85 90 95

Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gln Gly

eolf-seql

100 105 110

Phe Lys Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
115 120 125

<210> 19
<211> 384
<212> DNA
<213> Artificial Sequence

<220>
<223> 1638 gL7 V-region (E. coli expression)

<400> 19
atgaaaaaga cagctatcgc aattgcagtg gccttggctg gtttcgctac cgtagcgcaa 60

gctgatatcc agatgaccca gagtccaagc agtctctccg ccagcgtagg cgatcgtgtg 120

actattacct gtcgcactag cgaggacatc tacaccaacc tggcgtggta tcagcagaaa 180

ccaggcaaag tgccgaaact gctgatctac gtcgcgaaaa ccctccagga aggtgtaccg 240

tctcgctttt ccggctctgg tagcggtact cactacaccc tgaccatctc ttccctccag 300

ccggaagatg ttgctaccta ctattgcctc cagggcttca aattcccgtg gactttcggt 360

ggcggcacga aagtggaaat caaa 384

<210> 20
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> 1638 gL7 light chain (V + constant)

<400> 20

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 Thr Ser Glu Asp Ile Tyr Thr Asn
20 25 30

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

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

Ser Gly Ser Gly Thr His Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gln Gly Phe Lys Phe Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

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

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

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

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

Phe Asn Arg Gly Glu Cys
210

<210> 21
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> 1638 gL7 light chain (V + constant, E. coli expression)

<400> 21
gatatccaga tgacccagag tccaagcagt ctctccgcca gcgtaggcga tcgtgtgact 60

attacctgtc gcactagcga ggacatctac accaacctgg cgtggtatca gcagaaacca 120

ggcaaagtgc cgaaactgct gatctacgtc gcgaaaaccc tccaggaagg tgtaccgtct 180

cgcttttccg gctctggtag cggtactcac tacaccctga ccatctcttc cctccagccg 240

gaagatgttg ctacctacta ttgcctccag ggcttcaaat tcccgtggac tttcggtggc 300

ggcacgaaag tggaaatcaa acgtacggta gcggccccat ctgtcttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcac cagtaacaaa aagttttaat agaggggagt gt 642

<210> 22
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> 1638 gL7 light chain (V + constant, mammalian expression)

<400> 22
gatatccaga tgacccagag tccaagcagt ctctccgcca gcgtaggcga tcgtgtgact 60

attacctgtc gcactagcga ggacatctac accaacctgg cgtggtatca gcagaaacca 120

ggcaaagtgc cgaaactgct gatctacgtc gcgaaaaccc tccaggaagg tgtaccgtct 180

cgcttttccg gctctggtag cggtactcac tacaccctga ccatctcttc cctccagccg 240

gaagatgttg ctacctacta ttgcctccag ggcttcaaat tcccgtggac tttcggtggc 300

ggcacgaaag tggaaatcaa acggaccgtg gccgctccct ccgtgttcat cttcccaccc 360

tccgacgagc agctgaagtc cggcaccgcc tccgtcgtgt gcctgctgaa caacttctac 420

ccccgcgagg ccaaggtgca gtggaaggtg gacaacgccc tgcagtccgg caactcccag 480

gaatccgtca ccgagcagga ctccaaggac agcacctact ccctgtcctc caccctgacc 540

ctgtccaagg ccgactacga gaagcacaag gtgtacgcct gcgaagtgac ccaccagggc 600

ctgtccagcc ccgtgaccaa gtccttcaac cggggcgagt gc 642

<210> 23
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> 1638 gL7 light chain (E. coli expression)

<400> 23

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 Arg Thr Ser Glu
35 40 45

Asp Ile Tyr Thr Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val
50 55 60

Pro Lys Leu Leu Ile Tyr Val Ala Lys Thr Leu Gln Glu Gly Val Pro
65 70 75 80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr His Tyr Thr Leu Thr Ile
85 90 95

Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gln Gly
100 105 110

Phe Lys Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
115 120 125

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

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130 135 140

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

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

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

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

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

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

<210> 24
<211> 705
<212> DNA
<213> Artificial Sequence

<220>
<223> 1638 gL7 light chain (E. coli expression)

<400> 24
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gctgatatcc agatgaccca gagtccaagc agtctctccg ccagcgtagg cgatcgtgtg 120

actattacct gtcgcactag cgaggacatc tacaccaacc tggcgtggta tcagcagaaa 180

ccaggcaaag tgccgaaact gctgatctac gtcgcgaaaa ccctccagga aggtgtaccg 240

tctcgctttt ccggctctgg tagcggtact cactacaccc tgaccatctc ttccctccag 300

ccggaagatg ttgctaccta ctattgcctc cagggcttca aattcccgtg gactttcggt 360

ggcggcacga aagtggaaat caaacgtacg gtagcggccc catctgtctt catcttcccg 420

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 480

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 540

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 600

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 660

ggcctgagct caccagtaac aaaaagtttt aatagagggg agtgt 705

<210> 25
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> 1638 gH33 V-region

<400> 25

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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 Ser Leu Ser Thr Tyr
            20                  25                  30

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

Trp Leu Ala Asn Ile Trp Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ser
    50                  55                  60

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

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

Cys Ala Arg Thr Pro Ala Tyr Tyr Gly Ser His Pro Pro Phe Asp Tyr
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser
        115                 120
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<210> 26
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> 1638 gH33 V-region

<400> 26

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gaggttcagc tggtcgagtc tggaggcggg cttgtccagc ctggagggag cctgcgtctc       60

tcttgtgcag cgtccggctt ctctctgtct acctacggcg ttggtgttgg ttgggtacgt      120

caggctccag gtaaaggtct ggaatggctc gcaaacatct ggtgggacga cgataaacgc      180

tacaacccgt ccctggagaa ccgcttcacc attagccgtg ataacgcgaa aaactccgcg      240

tatctccaga tgaactccct gcgtgccgaa gacacggctg tgtactattg cgcgcgcact      300

ccggcgtact atggctctca cccaccgttt gattactggg gtcagggtac aatggttacc      360

gtctcg                                                                 366
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<210> 27
<211> 143
<212> PRT
<213> Artificial Sequence

<220>
<223> 1638 gH33 V-region (E. coli expression)

<400> 27

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

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

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

Gly Lys Gly Leu Glu Trp Leu Ala Asn Ile Trp Trp Asp Asp Asp Lys
65                  70                  75                  80

Arg Tyr Asn Pro Ser Leu Glu Asn Arg Phe Thr Ile Ser Arg Asp Asn
                85                  90                  95

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

Thr Ala Val Tyr Tyr Cys Ala Arg Thr Pro Ala Tyr Tyr Gly Ser His
        115                 120                 125

Pro Pro Phe Asp Tyr Trp Gly Gln Gly Thr Met Val Thr Val Ser
    130                 135                 140
```

<210> 28
<211> 429
<212> DNA
<213> Artificial Sequence

<220>
<223> 1638 gH33 V-region (E.coli expression)

<400> 28

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atgaagaaga ctgctatagc aattgcagtg gcgctagctg gtttcgccac cgtggcgcaa       60

gctgaggttc agctggtcga gtctggaggc gggcttgtcc agcctggagg gagcctgcgt      120

ctctcttgtg cagcgtccgg cttctctctg tctacctacg gcgttggtgt tggttgggta      180

cgtcaggctc caggtaaagg tctggaatgg ctcgcaaaca tctggtggga cgacgataaa      240

cgctacaacc cgtccctgga gaaccgcttc accattagcc gtgataacgc gaaaaactcc      300

gcgtatctcc agatgaactc cctgcgtgcc gaagacacgg ctgtgtacta ttgcgcgcgc      360

actccggcgt actatggctc tcacccaccg tttgattact ggggtcaggg taccatggtt      420

accgtctcg                                                              429
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<210> 29
<211> 226
<212> PRT
<213> Artificial Sequence

<220>
<223> 1638 gH33 Fab heavy chain (V + human gamma-1 CH1)

<400> 29

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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 Ser Leu Ser Thr Tyr
            20                  25                  30

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

Trp Leu Ala Asn Ile Trp Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ser
    50                  55                  60

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

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

Cys Ala Arg Thr Pro Ala Tyr Tyr Gly Ser His Pro Pro Phe Asp Tyr
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

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

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

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

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

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

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
    210                 215                 220

Ser Cys
225
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<210> 30
<211> 678
<212> DNA

<213> Artificial Sequence

<220>
<223> 1638 gH33 Fab heavy chain (V + human gamma-1 CH1)

<400> 30
gaggttcagc tggtcgagtc tggaggcggg cttgtccagc ctggagggag cctgcgtctc 60

tcttgtgcag cgtccggctt ctctctgtct acctacggcg ttggtgttgg ttgggtacgt 120

caggctccag gtaaaggtct ggaatggctc gcaaacatct ggtgggacga cgataaacgc 180

tacaacccgt ccctggagaa ccgcttcacc attagccgtg ataacgcgaa aaactccgcg 240

tatctccaga tgaactccct gcgtgccgaa gacacggctg tgtactattg cgcgcgcact 300

ccggcgtact atggctctca cccaccgttt gattactggg gtcagggtac catggttacc 360

gtctcgagcg cttctacaaa gggcccatcg gtcttccccc tggcaccctc ctccaagagc 420

acctctgggg gcacagcggc cctgggctgc ctggtcaagg actacttccc cgaaccggtg 480

acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta 540

cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc 600

acccagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt cgacaagaaa 660

gttgagccca aatcttgt 678

<210> 31
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> 1638 gH33 Fab heavy chain with (E. coli expression)

<400> 31

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

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

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

Gly Lys Gly Leu Glu Trp Leu Ala Asn Ile Trp Trp Asp Asp Asp Lys
65 70 75 80

Arg Tyr Asn Pro Ser Leu Glu Asn Arg Phe Thr Ile Ser Arg Asp Asn
85 90 95

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

```
Thr Ala Val Tyr Tyr Cys Ala Arg Thr Pro Ala Tyr Tyr Gly Ser His
        115                 120                 125

Pro Pro Phe Asp Tyr Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
    130                 135                 140

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

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
                165                 170                 175

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

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
        195                 200                 205

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
    210                 215                 220

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
225                 230                 235                 240

Lys Val Glu Pro Lys Ser Cys
                245
```

<210> 32
<211> 741
<212> DNA
<213> Artificial Sequence

<220>
<223> 1638 gH33 Fab heavy chain (E. coli expression)

<400> 32

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atgaagaaga ctgctatagc aattgcagtg gcgctagctg gtttcgccac cgtggcgcaa       60

gctgaggttc agctggtcga gtctggaggc gggcttgtcc agcctggagg gagcctgcgt      120

ctctcttgtg cagcgtccgg cttctctctg tctacctacg gcgttggtgt tggttgggta      180

cgtcaggctc caggtaaagg tctggaatgg ctcgcaaaca tctggtggga cgacgataaa      240

cgctacaacc cgtccctgga gaaccgcttc accattagcc gtgataacgc gaaaaactcc      300

gcgtatctcc agatgaactc cctgcgtgcc gaagacacgg ctgtgtacta ttgcgcgcgc      360

actccggcgt actatggctc tcacccaccg tttgattact ggggtcaggg taccatggtt      420

accgtctcga gcgcttctac aaagggccca tcggtcttcc ccctggcacc ctcctccaag      480

agcacctctg ggggcacagc ggccctgggc tgcctggtca aggactactt ccccgaaccg      540

gtgacggtgt cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc      600

ctacagtcct caggactcta ctccctcagc agcgtggtga ccgtgccctc cagcagcttg      660
```

ggcacccaga cctacatctg caacgtgaat cacaagccca gcaacaccaa ggtcgacaag 720

aaagttgagc ccaaatcttg t 741

<210> 33
<211> 234
<212> PRT
<213> Artificial Sequence

<220>
<223> 1638 gH33 Fab' heavy chain (V + human gamma-1 CH1 + hinge)

<400> 33

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 Ser Leu Ser Thr Tyr
20 25 30

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

Trp Leu Ala Asn Ile Trp Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ser
50 55 60

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

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

Cys Ala Arg Thr Pro Ala Tyr Tyr Gly Ser His Pro Pro Phe Asp Tyr
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125

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

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

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

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
180 185 190

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

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

210 215 220

Ser Cys Asp Lys Thr His Thr Cys Ala Ala
225 230

<210> 34
<211> 702
<212> DNA
<213> Artificial Sequence

<220>
<223> 1638 gH33 Fab' heavy chain (V + human gamma-1 CH1 + hinge)

<400> 34
gaggttcagc tggtcgagtc tggaggcggg cttgtccagc ctggagggag cctgcgtctc 60

tcttgtgcag cgtccggctt ctctctgtct acctacggcg ttggtgttgg ttgggtacgt 120

caggctccag gtaaaggtct ggaatggctc gcaaacatct ggtgggacga cgataaacgc 180

tacaacccgt ccctggagaa ccgcttcacc attagccgtg ataacgcgaa aaactccgcg 240

tatctccaga tgaactccct gcgtgccgaa gacacggctg tgtactattg cgcgcgcact 300

ccggcgtact atggctctca cccaccgttt gattactggg gtcagggtac catggttacc 360

gtctcgagcg cttctacaaa gggcccatcg gtcttccccc tggcaccctc ctccaagagc 420

acctctgggg gcacagcggc cctgggctgc ctggtcaagg actacttccc cgaaccggtg 480

acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta 540

cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc 600

acccagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt cgacaagaaa 660

gttgagccca aatcttgtga caaaactcac acatgcgccg cg 702

<210> 35
<211> 255
<212> PRT
<213> Artificial Sequence

<220>
<223> 1638 gH33 Fab' heavy chain (E. coli expression)

<400> 35

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

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

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

Gly Lys Gly Leu Glu Trp Leu Ala Asn Ile Trp Trp Asp Asp Asp Lys

65 70 75 80

Arg Tyr Asn Pro Ser Leu Glu Asn Arg Phe Thr Ile Ser Arg Asp Asn
85 90 95

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

Thr Ala Val Tyr Tyr Cys Ala Arg Thr Pro Ala Tyr Tyr Gly Ser His
115 120 125

Pro Pro Phe Asp Tyr Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
130 135 140

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

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
165 170 175

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

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
195 200 205

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
210 215 220

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
225 230 235 240

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Ala Ala
245 250 255

<210> 36
<211> 765
<212> DNA
<213> Artificial Sequence

<220>
<223> 1638 gH33 Fab' heavy chain (E. coli expression)

<400> 36
atgaagaaga ctgctatagc aattgcagtg gcgctagctg gtttcgccac cgtggcgcaa 60

gctgaggttc agctggtcga gtctggaggc gggcttgtcc agcctggagg gagcctgcgt 120

ctctcttgtg cagcgtccgg cttctctctg tctacctacg gcgttggtgt tggttgggta 180

cgtcaggctc caggtaaagg tctggaatgg ctcgcaaaca tctggtggga cgacgataaa 240

cgctacaacc cgtccctgga gaaccgcttc accattagcc gtgataacgc gaaaaactcc 300

gcgtatctcc agatgaactc cctgcgtgcc gaagacacgg ctgtgtacta ttgcgcgcgc 360

actccggcgt actatggctc tcacccaccg tttgattact ggggtcaggg taccatggtt 420

accgtctcga gcgcttctac aaagggccca tcggtcttcc ccctggcacc ctcctccaag 480

agcacctctg ggggcacagc ggccctgggc tgcctggtca aggactactt ccccgaaccg 540

gtgacggtgt cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc 600

ctacagtcct caggactcta ctccctcagc agcgtggtga ccgtgccctc cagcagcttg 660

ggcacccaga cctacatctg caacgtgaat cacaagccca gcaacaccaa ggtcgacaag 720

aaagttgagc ccaaatcttg tgacaaaact cacacatgcg ccgcg 765

<210> 37
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> 1638 gH33 IgG4 heavy chain (V + human gamma-4P constant)

<400> 37

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 Ser Leu Ser Thr Tyr
20 25 30

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

Trp Leu Ala Asn Ile Trp Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ser
50 55 60

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

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

Cys Ala Arg Thr Pro Ala Tyr Tyr Gly Ser His Pro Pro Phe Asp Tyr
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125

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

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

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

```
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Lys
450

<210> 38
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> 1638 gH33 IgG4 heavy chain (V + human gamma-4P constant)

<400> 38
gaggttcagc tggtcgagtc tggaggcggg cttgtccagc ctggagggag cctgcgtctc 60

tcttgtgcag cgtccggctt ctctctgtct acctacggcg ttggtgttgg ttgggtacgt 120

caggctccag gtaaaggtct ggaatggctc gcaaacatct ggtgggacga cgataaacgc 180

tacaacccgt ccctggagaa ccgcttcacc attagccgtg ataacgcgaa aaactccgcg 240

tatctccaga tgaactccct gcgtgccgaa gacacggctg tgtactattg cgcgcgcact 300

ccggcgtact atggctctca cccaccgttt gattactggg gtcagggtac aatggttacc 360

gtctcgtctg cctccaccaa gggcccctcc gtgttccctc tggcccctg ctcccggtcc 420

acctccgagt ctaccgccgc tctgggctgc ctggtcaagg actacttccc cgagcccgtg 480

acagtgtcct ggaactctgg cgccctgacc tccggcgtgc acaccttccc tgccgtgctg 540

cagtcctccg gcctgtactc cctgtcctcc gtcgtgaccg tgccctcctc cagcctgggc 600

accaagacct acacctgtaa cgtggaccac aagccctcca acaccaaggt ggacaagcgg 660

gtggaatcta agtacggccc tccctgcccc ccctgccctg cccctgaatt tctgggcgga 720

ccttccgtgt tcctgttccc cccaaagccc aaggacaccc tgatgatctc ccggacccct 780

gaagtgacct gcgtggtggt ggacgtgtcc caggaagatc ccgaggtcca gttcaattgg 840

tacgtggacg gcgtggaagt gcacaatgcc aagaccaagc ccagagagga acagttcaac 900

tccacctacc gggtggtgtc cgtgctgacc gtgctgcacc aggactggct gaacggcaaa 960

gagtacaagt gcaaggtgtc caacaagggc ctgccctcca gcatcgaaaa gaccatctcc 1020

aaggccaagg gccagccccg cgagccccag gtgtacaccc tgcccctag ccaggaagag 1080

atgaccaaga accaggtgtc cctgacctgt ctggtcaagg gcttctaccc ctccgacatt 1140

gccgtggaat gggagtccaa cggccagccc gagaacaact acaagaccac ccccctgtg 1200

ctggacagcg acggctcctt cttcctgtac tctcggctga ccgtggacaa gtcccggtgg 1260

caggaaggca acgtcttctc ctgctccgtg atgcacgagg ccctgcacaa ccactacacc 1320

cagaagtccc tgtccctgag cctgggcaag 1350

<210> 39
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> 1638 gH33 IgG4 heavy chain (V + human gamma-4P constant

eolf-seql
mammalian, no c-terminal lys)

<400> 39

```
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 Ser Leu Ser Thr Tyr
            20                  25                  30

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

Trp Leu Ala Asn Ile Trp Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ser
    50                  55                  60

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

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

Cys Ala Arg Thr Pro Ala Tyr Tyr Gly Ser His Pro Pro Phe Asp Tyr
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

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

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

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

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly
```

<210> 40
<211> 341
<212> PRT
<213> Artificial Sequence

<220>
<223> 1638 gL7 FabFv light chain

<400> 40

```
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 Thr Ser Glu Asp Ile Tyr Thr Asn
            20                  25                  30
```

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

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

Ser Gly Ser Gly Thr His Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gln Gly Phe Lys Phe Pro Trp
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

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

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

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

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

Phe Asn Arg Gly Glu Cys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    210                 215                 220

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

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

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

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

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
    290                 295                 300
```

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

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

Glu Ile Lys Arg Thr
340

<210> 41
<211> 1023
<212> DNA
<213> Artificial Sequence

<220>
<223> 1638 gL7 FabFv light chain

<400> 41
gatatccaga tgacccagag tccaagcagt ctctccgcca gcgtaggcga tcgtgtgact 60

attacctgtc gcactagcga ggacatctac accaacctgg cgtggtatca gcagaaacca 120

ggcaaagtgc cgaaactgct gatctacgtc gcgaaaaccc tccaggaagg tgtaccgtct 180

cgcttttccg gctctggtag cggtactcac tacaccctga ccatctcttc cctccagccg 240

gaagatgttg ctacctacta ttgcctccag ggcttcaaat tcccgtggac tttcggtggc 300

ggcacgaaag tggaaatcaa acgtacggta gcggccccat ctgtcttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gtggtggagg tggctctggc 660

ggtggtggct ccggaggcgg aggaagcgac atccagatga cccagagccc ttcctctgta 720

agcgccagtg tcggagacag agtgactatt acctgccaaa gctccccttc agtctggtcc 780

aattttctat cctggtatca gcaaaagccc ggaaaggctc ctaaattgct gatctacgaa 840

gcaagcaaac tcaccagcgg cgtgcccagc aggttcagcg gcagtgggtc tggaactgac 900

tttaccctga caatctcctc actccagccc gaggacttcg ccacctatta ctgcggtgga 960

ggttacagta gcataagtga tacgacattt ggatgcggca ctaaagtgga aatcaagcgt 1020

acc 1023

<210> 42
<211> 363
<212> PRT
<213> Artificial Sequence

<220>
<223> 1638 gH33 FabFv heavy chain

<400> 42

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 Ser Leu Ser Thr Tyr
20 25 30

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

Trp Leu Ala Asn Ile Trp Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ser
50 55 60

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

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

Cys Ala Arg Thr Pro Ala Tyr Tyr Gly Ser His Pro Pro Phe Asp Tyr
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125

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

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

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

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
180 185 190

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

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
210 215 220

Ser Cys Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Thr Gly Gly Gly
225 230 235 240

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

Gly Gly Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Ile Asp Leu Ser
260 265 270

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

Trp Ile Gly Ile Ile Trp Ala Ser Gly Thr Thr Phe Tyr Ala Thr Trp
290 295 300

Ala Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val
305 310 315 320

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
325 330 335

Cys Ala Arg Thr Val Pro Gly Tyr Ser Thr Ala Pro Tyr Phe Asp Leu
340 345 350

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
355 360

<210> 43
<211> 1089
<212> DNA
<213> Artificial Sequence

<220>
<223> 1638 gH33 FabFv heavy chain

<400> 43
gaggttcagc tggtcgagtc tggaggcggg cttgtccagc ctggagggag cctgcgtctc 60

tcttgtgcag cgtccggctt ctctctgtct acctacggcg ttggtgttgg ttgggtacgt 120

caggctccag gtaaaggtct ggaatggctc gcaaacatct ggtgggacga cgataaacgc 180

tacaacccgt ccctggagaa ccgcttcacc attagccgtg ataacgcgaa aaactccgcg 240

tatctccaga tgaactccct gcgtgccgaa gacacggctg tgtactattg cgcgcgcact 300

ccggcgtact atggctctca cccaccgttt gattactggg gtcagggtac aatggttacc 360

gtctcgtccg cttctacaaa gggcccatcg gtcttccccc tggcaccctc ctccaagagc 420

acctctgggg gcacagcggc cctgggctgc ctggtcaagg actacttccc cgaaccggtg 480

acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta 540

cagtcctctg gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc 600

acccagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa 660

gttgagccca aatcttgttc cggaggtggc ggttccggag gtggcggtac aggtggcggt 720

gggtccgaag tccagctgct tgaatccgga ggcggactcg tgcagcccgg aggcagtctt 780

cgcttgtcct gcgctgtatc tggaatcgac ctgagcaatt acgccatcaa ctgggtgaga 840

caggcacctg ggaaatgcct cgaatggatc ggcattatat gggctagtgg gacgaccttt 900

tatgctacat gggcgaaggg tagattcaca atctcacggg ataatagtaa gaacacagtg 960

tacctgcaga tgaactccct gcgagcagag gataccgccg tttactattg tgctcgcact 1020

gtcccaggtt atagcactgc accctacttt gatctgtggg ggcagggcac tctggtcacc 1080

gtctcgtcc 1089

<210> 44
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Human IGKV1-27 JK4 acceptor framework

<400> 44

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 Ser Asn Tyr
20 25 30

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

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

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

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

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

<210> 45
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Human IGKV1-27 JK4 acceptor framework

<400> 45
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcgagtca gggcattagc aattatttag cctggtatca gcagaaacca 120

gggaaagttc ctaagctcct gatctatgct gcatccactt tgcaatcagg ggtcccatct 180

cggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240

gaagatgttg caacttatta ctgtcaaaag tataacagtg cccctctcac tttcggcgga 300

gggaccaagg tggagatcaa a 321

<210> 46
<211> 114

<212> PRT
<213> Artificial Sequence

<220>
<223> Human IGHV3-7 JH3 acceptor framework

<400> 46

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 Asp Ala Phe Asp Val Trp Gly Gln Gly Thr Met Val Thr Val
100 105 110

Ser Ser

<210> 47
<211> 342
<212> DNA
<213> Artificial Sequence

<220>
<223> Human IGHV3-7 JH3 acceptor framework

<400> 47
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagt agctattgga tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtggccaac ataaagcaag atggaagtga gaaatactat 180

gtggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctcactgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagatgct 300

tttgatgtct ggggccaagg gacaatggtc accgtctctt ca 342

<210> 48
<211> 274
<212> PRT
<213> Artificial Sequence

<220>

<223> Human FcRn alpha chain extracellular sequence

<400> 48

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

Ser Ser

<210> 49
<211> 99
<212> PRT
<213> Artificial Sequence

<220>
<223> Rat ?2M

<400> 49

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

<210> 50
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Human ?2M including signal sequence

<400> 50

Met Ser Arg Ser Val Ala Leu Ala Val Leu Ala Leu Leu Ser Leu Ser
1 5 10 15

Gly Leu Glu Ala Ile Gln Arg Thr Pro Lys Ile Gln Val Tyr Ser Arg
20 25 30

His Pro Ala Glu Asn Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser
35 40 45

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

Arg Ile Glu Lys Val Glu His Ser Asp Leu Ser Phe Ser Lys Asp Trp
65 70 75 80

Ser Phe Tyr Leu Leu Tyr Tyr Thr Glu Phe Thr Pro Thr Glu Lys Asp
85 90 95

Glu Tyr Ala Cys Arg Val Asn His Val Thr Leu Ser Gln Pro Lys Ile
100 105 110

Val Lys Trp Asp Arg Asp Met
115

<210> 51
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> 1638gL2 V-region

<400> 51

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 Thr Ser Glu Asp Ile Tyr Thr Asn
20 25 30

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

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

Ser Gly Ser Gly Thr His Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gln Gly Phe Lys Phe Pro Trp
85 90 95

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

<210> 52
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> 1638gL2 V-region

<400> 52
gatatccaga tgacccagag tccaagcagt ctctccgcca gcgtaggcga tcgtgtgact 60

attacctgtc gcactagcga ggacatctac accaacctgg cgtggtatca gcagaaacca 120

ggcaaagtgc cgaaactgct gatctacgtc gcgaaaaccc tccaggacgg tgtaccgtct 180

cgcttttccg gctctggtag cggtactcac tacaccctga ccatctcttc cctccagccg 240

gaagatgttg ctacctacta ttgcctccag ggcttcaaat tcccgtggac tttcggtggc 300

ggcacgaaag tggaaatcaa a 321

<210> 53
<211> 128
<212> PRT
<213> Artificial Sequence

<220>
<223> 1638 gL2 V-region (E. coli expression)

<400> 53

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 Arg Thr Ser Glu
35 40 45

Asp Ile Tyr Thr Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val
50 55 60

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

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr His Tyr Thr Leu Thr Ile
85 90 95

Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gln Gly
100 105 110

Phe Lys Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
115 120 125

<210> 54
<211> 384
<212> DNA
<213> Artificial Sequence

<220>
<223> 1638 gL2 V-region (E. coli expression)

<400> 54
atgaaaaaga cagctatcgc aattgcagtg gccttggctg gtttcgctac cgtagcgcaa 60

gctgatatcc agatgaccca gagtccaagc agtctctccg ccagcgtagg cgatcgtgtg 120

actattacct gtcgcactag cgaggacatc tacaccaacc tggcgtggta tcagcagaaa 180

ccaggcaaag tgccgaaact gctgatctac gtcgcgaaaa ccctccagga cggtgtaccg 240

tctcgctttt ccggctctgg tagcggtact cactacaccc tgaccatctc ttccctccag 300

ccggaagatg ttgctaccta ctattgcctc cagggcttca aattcccgtg gactttcggt 360

ggcggcacga aagtggaaat caaa 384

<210> 55
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> 1638 gL2 light chain (V + constant)

<400> 55

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 Thr Ser Glu Asp Ile Tyr Thr Asn
20 25 30

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

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

Ser Gly Ser Gly Thr His Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gln Gly Phe Lys Phe Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

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

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

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

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

Phe Asn Arg Gly Glu Cys
210

<210> 56
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> 1638 gL2 light chain (V + constant, codon optimized for E. coli expression)

<400> 56
gatatccaga tgacccagag tccaagcagt ctctccgcca gcgtaggcga tcgtgtgact 60

attacctgtc gcactagcga ggacatctac accaacctgg cgtggtatca gcagaaacca 120

ggcaaagtgc cgaaactgct gatctacgtc gcgaaaaccc tccaggacgg tgtaccgtct 180

cgcttttccg gctctggtag cggtactcac tacaccctga ccatctcttc cctccagccg 240

gaagatgttg ctacctacta ttgcctccag ggcttcaaat tcccgtggac tttcggtggc 300

ggcacgaaag tggaaatcaa acgtacggta gcggccccat ctgtcttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcac cagtaacaaa aagttttaat agaggggagt gt 642

<210> 57
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> 1638 gL2 light chain (E. coli expression)

<400> 57

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 Arg Thr Ser Glu
35 40 45

Asp Ile Tyr Thr Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val
50 55 60

Pro Lys Leu Leu Ile Tyr Val Ala Lys Thr Leu Gln Asp Gly Val Pro

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65 70 75 80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr His Tyr Thr Leu Thr Ile
85 90 95

Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gln Gly
100 105 110

Phe Lys Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
115 120 125

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

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

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

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

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

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

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

<210> 58
<211> 705
<212> DNA
<213> Artificial Sequence

<220>
<223> 1638 gL2 light chain (E. coli expression)

<400> 58
atgaaaaaga cagctatcgc aattgcagtg gccttggctg gtttcgctac cgtagcgcaa 60

gctgatatcc agatgaccca gagtccaagc agtctctccg ccagcgtagg cgatcgtgtg 120

actattacct gtcgcactag cgaggacatc tacaccaacc tggcgtggta tcagcagaaa 180

ccaggcaaag tgccgaaact gctgatctac gtcgcgaaaa ccctccagga cggtgtaccg 240

tctcgctttt ccggctctgg tagcggtact cactacaccc tgaccatctc ttccctccag 300

ccggaagatg ttgctaccta ctattgcctc cagggcttca aattcccgtg gactttcggt 360

ggcggcacga aagtggaaat caaacgtacg gtagcggccc catctgtctt catcttcccg 420

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 480

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 540

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 600

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 660

ggcctgagct caccagtaac aaaaagtttt aatagagggg agtgt 705

<210> 59
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> 1638gH2 V-region

<400> 59

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 Phe Ser Gly Phe Ser Leu Ser Thr Tyr
20 25 30

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

Trp Leu Ala Asn Ile Trp Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ser
50 55 60

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

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

Cys Val Arg Thr Pro Ala Tyr Tyr Gly Ser His Pro Pro Phe Asp Tyr
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser
115 120

<210> 60
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> 1638gH2 V-region

<400> 60
gaggttcagc tggtcgagtc tggaggcggg cttgtccagc ctggagggag cctgcgtctc 60

tcttgtgcat tctccggctt ctctctgtct acctacggcg ttggtgttgg ttgggtacgt 120

caggctccag gtaaaggtct ggaatggctc gcaaacatct ggtgggacga cgataaacgc 180

tacaacccgt ccctggagaa ccgcttcacc attagcaaag ataccgcgaa aaactccgcg 240

tatctccaga tgaactccct gcgtgccgaa gacacggctg tgtactattg cgttcgcact 300

ccggcgtact atggctctca cccaccgttt gattactggg gtcagggtac catggttacc 360

gtctcg 366

<210> 61
<211> 143
<212> PRT
<213> Artificial Sequence

<220>
<223> 1638 gH2 V-region with signal sequence underlined and italicized (E. coli expression)

<400> 61

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

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

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

Gly Lys Gly Leu Glu Trp Leu Ala Asn Ile Trp Trp Asp Asp Asp Lys
65 70 75 80

Arg Tyr Asn Pro Ser Leu Glu Asn Arg Phe Thr Ile Ser Lys Asp Thr
85 90 95

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

Thr Ala Val Tyr Tyr Cys Val Arg Thr Pro Ala Tyr Tyr Gly Ser His
115 120 125

Pro Pro Phe Asp Tyr Trp Gly Gln Gly Thr Met Val Thr Val Ser
130 135 140

<210> 62
<211> 429
<212> DNA
<213> Artificial Sequence

<220>
<223> 1638 gH2 V-region with signal sequence underlined and italicized (E. coli expression)

<400> 62
atgaagaaga ctgctatagc aattgcagtg gcgctagctg gtttcgccac cgtggcgcaa 60

gctgaggttc agctggtcga gtctggaggc gggcttgtcc agcctggagg gagcctgcgt 120

ctctcttgtg cattctccgg cttctctctg tctacctacg gcgttggtgt tggttgggta 180

cgtcaggctc caggtaaagg tctggaatgg ctcgcaaaca tctggtggga cgacgataaa 240

cgctacaacc cgtccctgga gaaccgcttc accattagca aagataccgc gaaaaactcc 300

gcgtatctcc agatgaactc cctgcgtgcc gaagacacgg ctgtgtacta ttgcgttcgc 360

actccggcgt actatggctc tcacccaccg tttgattact ggggtcaggg taccatggtt 420

accgtctcg 429

<210> 63
<211> 234
<212> PRT
<213> Artificial Sequence

<220>
<223> 1638 gH2 Fab' heavy chain (V + human gamma-1 CH1 + hinge)

<400> 63

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 Phe Ser Gly Phe Ser Leu Ser Thr Tyr
20 25 30

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

Trp Leu Ala Asn Ile Trp Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ser
50 55 60

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

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

Cys Val Arg Thr Pro Ala Tyr Tyr Gly Ser His Pro Pro Phe Asp Tyr
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125

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

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

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

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val

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180 185 190

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

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
210 215 220

Ser Cys Asp Lys Thr His Thr Cys Ala Ala
225 230

<210> 64
<211> 702
<212> DNA
<213> Artificial Sequence

<220>
<223> 1638 gH2 Fab' heavy chain (V + human gamma-1 CH1 + hinge)

<400> 64
gaggttcagc tggtcgagtc tggaggcggg cttgtccagc ctggagggag cctgcgtctc 60

tcttgtgcat tctccggctt ctctctgtct acctacggcg ttggtgttgg ttgggtacgt 120

caggctccag gtaaaggtct ggaatggctc gcaaacatct ggtgggacga cgataaacgc 180

tacaacccgt ccctggagaa ccgcttcacc attagcaaag ataccgcgaa aaactccgcg 240

tatctccaga tgaactccct gcgtgccgaa gacacggctg tgtactattg cgttcgcact 300

ccggcgtact atggctctca cccaccgttt gattactggg gtcagggtac catggttacc 360

gtctcgagcg cttctacaaa gggcccatcg gtcttccccc tggcaccctc ctccaagagc 420

acctctgggg gcacagcggc cctgggctgc ctggtcaagg actacttccc cgaaccggtg 480

acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta 540

cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc 600

acccagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt cgacaagaaa 660

gttgagccca aatcttgtga caaaactcac acatgcgccg cg 702

<210> 65
<211> 255
<212> PRT
<213> Artificial Sequence

<220>
<223> 1638 gH2 Fab' heavy chain (E. coli expression)

<400> 65

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

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Phe Ser Gly Phe

35 40 45

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

Gly Lys Gly Leu Glu Trp Leu Ala Asn Ile Trp Trp Asp Asp Asp Lys
65 70 75 80

Arg Tyr Asn Pro Ser Leu Glu Asn Arg Phe Thr Ile Ser Lys Asp Thr
85 90 95

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

Thr Ala Val Tyr Tyr Cys Val Arg Thr Pro Ala Tyr Tyr Gly Ser His
115 120 125

Pro Pro Phe Asp Tyr Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
130 135 140

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

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
165 170 175

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

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
195 200 205

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
210 215 220

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
225 230 235 240

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Ala Ala
245 250 255

<210> 66
<211> 765
<212> DNA
<213> Artificial Sequence

<220>
<223> 1638 gH2 Fab' heavy chain d (E. coli expression)

<400> 66
atgaagaaga ctgctatagc aattgcagtg gcgctagctg gtttcgccac cgtggcgcaa 60

gctgaggttc agctggtcga gtctggaggc gggcttgtcc agcctggagg gagcctgcgt 120

ctctcttgtg cattctccgg cttctctctg tctacctacg gcgttggtgt tggttgggta 180

cgtcaggctc caggtaaagg tctggaatgg ctcgcaaaca tctggtggga cgacgataaa 240

cgctacaacc cgtccctgga gaaccgcttc accattagca aagataccgc gaaaaactcc 300

gcgtatctcc agatgaactc cctgcgtgcc gaagacacgg ctgtgtacta ttgcgttcgc 360

actccggcgt actatggctc tcacccaccg tttgattact ggggtcaggg taccatggtt 420

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gtgacggtgt cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc 600

ctacagtcct caggactcta ctccctcagc agcgtggtga ccgtgccctc cagcagcttg 660

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<212> PRT
<213> Artificial Sequence

<220>
<223> N-termial sequence Heavy chain

<400> 67

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

<210> 68
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal sequence Light chain

<400> 68

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

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

<220>
<223> human JH3

<400> 69

Asp Ala Phe Asp Val Trp Gly Gln Gly Thr Met Val Thr Val Ser
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<210> 70
<211> 5
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<213> Artificial Sequence

<220>
<223> part of CDR-H3

<400> 70

Asp Ala Phe Asp Val
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<210> 71
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<400> 71

Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
1 5 10

<210> 72
<211> 99
<212> PRT
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<220>
<223> Human ?2-microglobulin

<400> 72

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

Ser Asp Ile Glu Val Asp Leu Leu Lys Asn Gly Glu Arg Ile Glu Lys
35 40 45

Val Glu His Ser Asp Leu Ser Phe Ser Lys Asp Trp Ser Phe Tyr Leu
50 55 60

Leu Tyr Tyr Thr Glu Phe Thr Pro Thr Glu Lys Asp Glu Tyr Ala Cys
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Arg Val Asn His Val Thr Leu Ser Gln Pro Lys Ile Val Lys Trp Asp
85 90 95

Arg Asp Met

<210> 73
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> 1638gH33 IgG1 heavy chain (V + human gamma-1 constant)

<400> 73

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Leu Ser Thr Tyr
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Gly Val Gly Val Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
        35                  40                  45

Trp Leu Ala Asn Ile Trp Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ser
    50                  55                  60

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

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

Cys Ala Arg Thr Pro Ala Tyr Tyr Gly Ser His Pro Pro Phe Asp Tyr
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

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

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

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

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

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

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
    210                 215                 220

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

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255
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Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

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

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

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

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

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

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

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

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

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

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

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
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Leu Ser Pro Gly Lys
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<210> 74
<211> 1965
<212> DNA
<213> Artificial Sequence

<220>
<223> 1638gH33 IgG1 heavy chain (V + human gamma-1 constant, exons underlined)

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tacaacccgt ccctggagaa ccgcttcacc attagccgtg ataacgcgaa aaactccgcg 240

tatctccaga tgaactccct gcgtgccgaa gacacggctg tgtactattg cgcgcgcact 300

ccggcgtact atggctctca cccaccgttt gattactggg gtcagggtac aatggttacc 360

gtctcgagcg cttctacaaa gggcccatcg gtcttccccc tggcaccctc ctccaagagc 420

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acccagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt cgacaagaaa 660

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tgcctggacg catcccggct atgcagcccc agtccagggc agcaaggcag gccccgtctg 780

cctcttcacc cggaggcctc tgcccgcccc actcatgctc agggagaggg tcttctggct 840

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ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt gtggtcagcg 1440

tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc aaggtctcca 1500

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gggtgcgagg gccacatgga cagaggccgg ctcggcccac cctctgccct gagagtgacc 1620

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