SEQUENCE LISTING

<110> Alexion Pharmaceuticals, Inc.
Bowdish, Katherine
Kretz-Rommel, Anke
Faas McKnight, Susan J.
Springhorn, Jeremy P.
Wu, Dayang

<120> ANTIBODIES TO OX-2/CD200 AND USES THEREOF

<130> ALEX-PW3-060

<140> PCT/US2007/000711
<141> 2007-01-11

<150> US 60/758,426
<151> 2006-01-12

<150> US 60/759,085
<151> 2006-01-12

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<151> 2006-05-18

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<223> Primer C2aB7 rev

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<220>
<223> Primer lacpri

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<212> DNA
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<220>
<223> Primer LeadVHpAX

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<211> 2010
<212> DNA
<213> Artificial Sequence

<220>
<223> heavy chain chC2aB7-hG1, genomic sequence hG1

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tcctgcaagg cttctggtta ttcattcact gactacatca tactctgggt gaagcagaac 180
catggaaaga gccttgagtg gattggacat attgatcctt actatggtag ttctaactac 240
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atgcagctca acagtctgac atctgaggac tctgcagtct attactgtgg aagatctaag 360
agggactact ttgactactg gggccaaggc accactctca cagtttcctc agcctccacc 420
aagggcccat cggtcttccc cctggcaccc tcctccaaga gcacctctgg cggcacagcg 480
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cagggaggga gggtgtctgc tggaagccag gctcagcgct cctgcctgga cgcatcccgg 780
ctatgcagtc ccagtccagg gcagcaaggc aggccccgtc tgcctcttca cccggaggcc 840
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gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1860
gactccgacg gctccttctt cctctatagc aagctcaccg tggacaagag caggtggcag 1920
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aagagcctct ccctgtcccc gggtaaatga 2010

<210> 7
<211> 467
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain chC2aB7-hG1

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20 25 30
Lys Pro Gly Ala Ser Leu Lys Met Ser Cys Lys Ala Ser Gly Tyr Ser
35 40 45
Phe Thr Asp Tyr Ile Ile Leu Trp Val Lys Gln Asn His Gly Lys Ser
50 55 60
Leu Glu Trp Ile Gly His Ile Asp Pro Tyr Tyr Gly Ser Ser Asn Tyr
65 70 75 80
Asn Leu Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser
85 90 95
Ser Thr Ala Tyr Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala
100 105 110
Val Tyr Tyr Cys Gly Arg Ser Lys Arg Asp Tyr Phe Asp Tyr Trp Gly
115 120 125
Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
130 135 140
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
165 170 175
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210 215 220
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225 230 235 240
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
245 250 255
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260 265 270
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305 310 315 320
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
325 330 335
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
340 345 350
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
355 360 365
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
370 375 380
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385 390 395 400
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val

```
            420                 425                 430
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460
Pro Gly Lys
465
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<210> 8
<211> 1401
<212> DNA
<213> Artificial Sequence

<220>
<223> hB7V4V1-hG1 Heavy chain (cDNA hG1)

<400> 8

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tgcaaggctt ctggttattc attcactgac tacatcatac tctggatcag gcagcatagc 180
ggaaagggcc ttgagtggat tggacatatt gatccttact atggtagttc taactacaat 240
ctgaaattca agggcagggt cacaatcact gcagacaaat ctaccaggac aacctacatg 300
gagctcacca gtctgacatc tgaggacact gcagtctatt actgtggaag atctaagagg 360
gactactttg actactgggg ccaaggcacc actctcacag tttcctcagc ctccaccaag 420
ggcccatcgg tcttcccgct agcaccctcc tccaagagca cctctggggg cacagcggcc 480
ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 540
gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc 600
ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 660
gtgaatcaca agcccagcaa caccaaggtg gacaagagag ttgagcccaa atcttgtgac 720
aaaactcaca catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc 780
ctcttccccc caaaacccaa ggacaccctc atgatctccc ggaccccctga ggtcacatgc 840
gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 900
gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt 960
gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 1020
aaggtctcca acaaagccct cccagccccc atcgagaaaa ccatctccaa agccaaaggg 1080
cagccccgag aaccacaggt gtacaccctg cccccatccc gggaggagat gaccaagaac 1140
caggtcagcc tgacctgcct ggtcaaaggc ttctatcccca gcgacatcgc cgtggagtgg 1200
gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1260
ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1320
gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1380
tccctgtctc cgggtaaatg a                                          1401
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<210> 9
<211> 466
<212> PRT
<213> Artificial Sequence

<220>
<223> hB7V4V1-hG1 Heavy chain

<400> 9

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Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Val Thr Ala Gly
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Val Phe Ser Glu Val Gln Leu Val Glu Ser Gly Pro Glu Val Lys Lys
            20                  25                  30
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe
        35                  40                  45
Thr Asp Tyr Ile Ile Leu Trp Ile Arg Gln His Ser Gly Lys Gly Leu
    50                  55                  60
Glu Trp Ile Gly His Ile Asp Pro Tyr Tyr Gly Ser Ser Asn Tyr Asn
65                  70                  75                  80
Leu Lys Phe Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Arg
                85                  90                  95
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Thr Thr Tyr Met Glu Leu Thr Ser Leu Thr Ser Glu Asp Thr Ala Val
            100                 105                 110
Tyr Tyr Cys Gly Arg Ser Lys Arg Asp Tyr Phe Asp Tyr Trp Gly Gln
        115                 120                 125
Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
    130                 135                 140
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
145                 150                 155                 160
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
                165                 170                 175
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
            180                 185                 190
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
        195                 200                 205
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
    210                 215                 220
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
225                 230                 235                 240
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
                245                 250                 255
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
            260                 265                 270
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
        275                 280                 285
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
    290                 295                 300
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
305                 310                 315                 320
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
                325                 330                 335
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
            340                 345                 350
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
        355                 360                 365
Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
    370                 375                 380
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
385                 390                 395                 400
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
                405                 410                 415
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
            420                 425                 430
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
        435                 440                 445
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
    450                 455                 460
Gly Lys
465
```

<210> 10
<211> 1401
<212> DNA
<213> Artificial Sequence

<220>
<223> hB7V3V1-hG1 Heavy chain (cDNA hG1)

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tgcaaggctt ctggttattc attcactgac tacatcatac tctgggtgag gcagaaccct 180
ggaaagggcc ttgagtggat tggacatatt gatccttact atggtagttc taactacaat 240
ctgaaattca agggcagagt gacaatcacc gccgaccagt ctaccaccac agcctacatg 300

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gagctctcca gtctgagatc tgaggacact gcagtctatt actgtggaag atctaagagg 360
gactactttg actactgggg ccaaggcacc actctcacag tttcctcagc ctccaccaag 420
ggcccatcgg tcttcccgct agcaccctcc tccaagagca cctctggggg cacagcggcc 480
ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 540
gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc 600
ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 660
gtgaatcaca agcccagcaa caccaaggtg gacaagagag ttgagcccaa atcttgtgac 720
aaaactcaca catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc 780
ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 840
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gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt 960
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caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1200
gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1260
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gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1380
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<210> 11
<211> 466
<212> PRT
<213> Artificial Sequence

<220>
<223> hB7V3V1-hG1 Heavy chain

<400> 11

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Val His Cys Gln Val Gln Leu Gln Gln Ser Gly Ser Glu Leu Lys Lys
            20                  25                  30
Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe
        35                  40                  45
Thr Asp Tyr Ile Ile Leu Trp Val Arg Gln Asn Pro Gly Lys Gly Leu
    50                  55                  60
Glu Trp Ile Gly His Ile Asp Pro Tyr Tyr Gly Ser Ser Asn Tyr Asn
65                  70                  75                  80
Leu Lys Phe Lys Gly Arg Val Thr Ile Thr Ala Asp Gln Ser Thr Thr
                85                  90                  95
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110
Tyr Tyr Cys Gly Arg Ser Lys Arg Asp Tyr Phe Asp Tyr Trp Gly Gln
        115                 120                 125
Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
    130                 135                 140
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
145                 150                 155                 160
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
                165                 170                 175
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
            180                 185                 190
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
        195                 200                 205
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
    210                 215                 220
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
225                 230                 235                 240
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
                245                 250                 255
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
            260                 265                 270
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
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        275                 280                 285
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
    290                 295                 300
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
305                 310                 315                 320
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
                325                 330                 335
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
            340                 345                 350
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
        355                 360                 365
Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
    370                 375                 380
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
385                 390                 395                 400
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
                405                 410                 415
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
            420                 425                 430
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
        435                 440                 445
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
    450                 455                 460
Gly Lys
465
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<210> 12
<211> 2002
<212> DNA
<213> Artificial Sequence

<220>
<223> hB7V3V2-hG2G4 Heavy chain (genomic sequence hG2G4)

<400> 12

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agggactact ttgactactg gggccaaggc accactctca cagtttcctc agcctccacc 420
aagggcccat ccgtcttccc cctggcgccc tgctccagga gcacctccga gagcacagcc 480
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gctcggccca ccctctgccc tgggagtgac cgctgtgcca acctctgtcc ctacagggca 1680
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ctccttcttc ctctacagca ggctaaccgt ggacaagagc aggtggcagg aggggaatgt 1920
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<210> 13
<211> 462
<212> PRT
<213> Artificial Sequence

<220>
<223> hB7V3V2-hG2G4 Heavy chain

<400> 13

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            20                  25                  30
Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe
        35                  40                  45
Thr Asp Tyr Ile Ile Leu Trp Val Arg Gln Asn Pro Gly Lys Gly Leu
    50                  55                  60
Glu Trp Ile Gly His Ile Asp Pro Tyr Tyr Gly Ser Ser Asn Tyr Asn
65                  70                  75                  80
Leu Lys Phe Lys Gly Arg Val Thr Ile Thr Ala Asp Gln Ser Thr Thr
                85                  90                  95
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110
Tyr Tyr Cys Gly Arg Ser Lys Arg Asp Tyr Phe Asp Tyr Trp Gly Gln
        115                 120                 125
Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
    130                 135                 140
Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
145                 150                 155                 160
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
                165                 170                 175
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
            180                 185                 190
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
        195                 200                 205
Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys
    210                 215                 220
Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val
225                 230                 235                 240
Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe
                245                 250                 255
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
            260                 265                 270
Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
        275                 280                 285
Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
    290                 295                 300
Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
305                 310                 315                 320
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
                325                 330                 335
Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
            340                 345                 350
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
        355                 360                 365
Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
    370                 375                 380
```

```
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
385                 390                 395                 400
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
                405                 410                 415
Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
            420                 425                 430
Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
        435                 440                 445
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
    450                 455                 460
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<210> 14
<211> 1999
<212> DNA
<213> Artificial Sequence

<220>
<223> chC2aB7-hG2G4 Heavy chain (genomic sequence hG2G4)

<400> 14

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gaggtccagc tgcaacagtc tggacctgag ctggtgaagc ctggggcttc actgaagatg 120
tcctgcaagg cttctggtta ttcattcact gactacatca tactctgggt gaagcagaac 180
catggaaaga gccttgagtg gattggacat attgatcctt actatggtag ttctaactac 240
aatctgaaat tcaagggcaa ggccacattg actgtagaca aatcttccag cacagcctac 300
atgcagctca acagtctgac atctgaggac tctgcagtct attactgtgg aagatctaag 360
agggactact ttgactactg gggccaaggc accactctca cagtttcctc agcctccacc 420
aagggcccat ccgtcttccc cctggcgccc tgctccagga gcacctccga gagcacagcc 480
gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 540
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 600
tccctcagca gcgtggtgac cgtgccctcc agcaacttcg gcacccagac ctacacctgc 660
aacgtagatc acaagcccag caacaccaag gtggacaaga cagttggtga gaggccagct 720
cagggaggga gggtgtctgc tggaagccag gctcagccct cctgcctgga cgcaccccgg 780
ctgtgcagcc ccagcccagg gcagcaaggc aggccccatc tgtctcctca cccggaggcc 840
tctgcccgcc ccactcatgc tcagggagag ggtcttctgg cttttttccac caggctccag 900
gcaggcacag gctgggtgcc cctaccccag gcccttcaca cacaggggca ggtgcttggc 960
tcagacctgc caaaagccat atccgggagg accctgcccc tgacctaagc cgaccccaaa 1020
ggccaaactg tccactccct cagctcggac accttctctc ctcccagatc cgagtaactc 1080
ccaatcttct ctctgcagag cgcaaatgtt gtgtcgagtg cccaccgtgc ccaggtaagc 1140
cagcccaggc ctcgccctcc agctcaaggc gggacaggtg ccctagagta gcctgcatcc 1200
agggacaggc cccagctggg tgctgacacg tccacctcca tctcttcctc agcaccacct 1260
gtggcaggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 1320
cggaccctg aggtcacgtg cgtggtggtg gacgtgagcc aggaagaccc cgaggtccag 1380
ttcaactggt acgtggatgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 1440
cagttcaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 1500
aacggcaagg agtacaagtg caaggtctcc aacaaaggcc tcccgtcctc catcgagaaa 1560
accatctcca aagccaaagg tgggacccac ggggtgcgag ggccacatgg acagaggtca 1620
gctcggccca ccctctgccc tgggagtgac cgctgtgcca acctctgtcc ctacagggca 1680
gccccgagag ccacaggtgt acaccctgcc cccatcccag gaggagatga ccaagaacca 1740
ggtcagcctg acctgcctgg tcaaaggctt ctaccccagc gacatcgccg tggagtggga 1800
gagcaatggg cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg 1860
ctccttcttc ctctacagca ggctaaccgt ggacaagagc aggtggcagg aggggaatgt 1920
cttctcatgc tccgtgatgc atgaggctct gcacaaccac tacacacaga agagcctctc 1980
cctgtctctg ggtaaatga                                              1999
```

<210> 15
<211> 463
<212> PRT
<213> Artificial Sequence

<220>
<223> chC2aB7-hG2G4 Heavy chain

<400> 15
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15
Val His Ser Leu Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val
20 25 30
Lys Pro Gly Ala Ser Leu Lys Met Ser Cys Lys Ala Ser Gly Tyr Ser
35 40 45
Phe Thr Asp Tyr Ile Ile Leu Trp Val Lys Gln Asn His Gly Lys Ser
50 55 60
Leu Glu Trp Ile Gly His Ile Asp Pro Tyr Tyr Gly Ser Ser Asn Tyr
65 70 75 80
Asn Leu Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser
85 90 95
Ser Thr Ala Tyr Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala
100 105 110
Val Tyr Tyr Cys Gly Arg Ser Lys Arg Asp Tyr Phe Asp Tyr Trp Gly
115 120 125
Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
130 135 140
Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
145 150 155 160
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
165 170 175
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205
Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His
210 215 220
Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys
225 230 235 240
Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val
245 250 255
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
260 265 270
Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
275 280 285
Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
290 295 300
Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
305 310 315 320
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
325 330 335
Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
340 345 350
Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
355 360 365
Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
370 375 380
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
385 390 395 400
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
405 410 415
Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
420 425 430
Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
435 440 445
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
450 455 460

<210> 16
<211> 1391
<212> DNA

<213> Artificial Sequence

<220>
<223> hB7V3V2-cG2G4 Heavy chain (cDNA G2G4)

<400> 16
atgggatgga gccggatctt tctcttcctc ctgtcaataa ttgcaggtgt ccattgccag 60
gtccagctgc aacagtctgg atctgagctg aagaagcctg gggcttcagt gaagatctcc 120
tgcaaggctt ctggttattc attcactgac tacatcatac tctgggtgag gcagaaccct 180
ggaaagggcc ttgagtggat tggacatatt gatccttact atggtagttc taactacaat 240
ctgaaattca agggcagagt gacaatcacc gccgaccagt ctaccaccac agcctacatg 300
gagctctcca gtctgagatc tgaggacact gcagtctatt actgtggaag atctaagagg 360
gactactttg actactgggg ccaaggcacc actctcacag tttcctcagc ctccaccaag 420
ggcccatccg tcttcccccc ggcgccctgc tccaggagca cctccgagag cacagccgcc 480
ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 540
gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc 600
ctcagcagcg tggtgaccgt gccctccagc aacttcggca cccagaccta cacctgcaac 660
gtagatcaca agcccagcaa caccaaggtg gacaagacag ttgagcgcaa atgttgtgtc 720
gagtgcccac cgtgcccagc accacctgtg gcaggaccgt cagtcttcct cttcccccca 780
aaacccaagg acaccctcat gatctcccgg acccctgagg tcacgtgcgt ggtggtggac 840
gtgagccagg aagaccccga ggtccagttc aactggtacg tggatggcgt ggaggtgcat 900
aatgccaaga caaagccgcg ggaggagcag ttcaacagca cgtaccgtgt ggtcagcgtc 960
ctcaccgtcc tgcaccagga ctggctgaac ggcaaggagt acaagtgcaa ggtctccaac 1020
aaaggcctcc cgtcctccat cgagaaaacc atctccaaag ccaaagggca gccccgagag 1080
ccacaggtgt acaccctgcc cccatcccag gaggagatga ccaagaacca ggtcagcctg 1140
acctgcctgg tcaaaggctt ctaccccagc gacatcgccg tggagtggga gagcaatggg 1200
cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc 1260
ctctacagca ggctaaccgt ggacaagagc aggtggcagg aggggaatgt cttctcatgc 1320
tccgtgatgc atgaggctct gcacaaccac tacacacaga agagcctctc cctgtctctg 1380
ggtaaatgat g 1391

<210> 17
<211> 2005
<212> DNA
<213> Artificial Sequence

<220>
<223> ChC7-hG2G4 Heavy chain (genomic sequence hG2G4)

<400> 17
atgggatgga gctgtatcat cctcttcttg gtagcaacag ctacaggtgt ccactccctc 60
gaggtccaac tgcagcagtc tggacctgag ctggagaagc ctggcgcttc agtgaagata 120
tcctgcaagg cttctggtta ctcattcact ggctacaaca tgaactgggt gaagcagagc 180
agtggaaaga gccttgagtg gattggaaat tttgatcctt actatggtgt tattacctac 240
aaccagaagt tcaagggcaa ggccacattg actgtagaca aatcctccag cacagcctac 300
atgcagctca agagcctgac atctgaggac tctgcagtct attactgtgc aagaacggct 360
acggctctct atactatgga ctactggggt caaggaacct cagtcaccgt ctcctcagcc 420
tccaccaagg gcccatccgt cttccccctg gcgccctgct ccaggagcac ctccgagagc 480
acagccgccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 540
aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 600
ctctactccc tcagcagcgt ggtgaccgtg ccctccagca acttcggcac ccagacctac 660
acctgcaacg tagatcacaa gcccagcaac accaaggtgg acaagacagt tggtgagagg 720
ccagctcagg gagggagggt gtctgctgga agccaggctc agccctcctg cctggacgca 780
ccccggctgt gcagccccag cccagggcag caaggcaggc cccatctgtc tcctcacccg 840
gaggcctctg cccgccccac tcatgctcag ggagagggtc ttctggcttt ttccaccagg 900
ctccaggcag gcacaggctg ggtgccccta ccccaggccc ttcacacaca ggggcaggtg 960
cttggctcag acctgccaaa agccatatcc gggaggaccc tgcccctgac ctaagccgac 1020
cccaaaggcc aaactgtcca ctccctcagc tcggacacct tctctcctcc cagatccgag 1080
taactcccaa tcttctctct gcagagcgca aatgttgtgt cgagtgccca ccgtgcccag 1140
gtaagccagc ccaggcctcg ccctccagct caaggcggga caggtgccct agagtagcct 1200
gcatccaggg acaggcccca gctgggtgct gacacgtcca cctccatctc ttcctcagca 1260
ccacctgtgg caggaccgtc agtcttcctc ttccccccaa aacccaagga caccctcatg 1320
atctcccgga cccctgaggt cacgtgcgtg gtggtggacg tgagccagga agaccccgag 1380
gtccagttca actggtacgt ggatggcgtg gaggtgcata atgccaagac aaagccgcgg 1440

gaggagcagt tcaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 1500
tggctgaacg gcaaggagta caagtgcaag gtctccaaca aaggcctccc gtcctccatc 1560
gagaaaacca tctccaaagc caaaggtggg acccacgggg tgcgagggcc acatggacag 1620
aggtcagctc ggcccaccct ctgccctggg agtgaccgct gtgccaacct ctgtccctac 1680
agggcagccc cgagagccac aggtgtacac cctgccccca tcccaggagg agatgaccaa 1740
gaaccaggtc agcctgacct gcctggtcaa aggcttctac cccagcgaca tcgccgtgga 1800
gtgggagagc aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc 1860
cgacggctcc ttcttcctct acagcaggct aaccgtggac aagagcaggt ggcaggaggg 1920
gaatgtcttc tcatgctccg tgatgcatga ggctctgcac aaccactaca cacagaagag 1980
cctctccctg tctctgggta aatga 2005

<210> 18
<211> 468
<212> PRT
<213> Artificial Sequence

<220>
<223> ChC7-hG2G4 Heavy chain (genomic sequence hG2G4)

<400> 18
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1   5   10   15
Val His Ser Leu Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Glu
            20   25   30
Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser
        35   40   45
Phe Thr Gly Tyr Asn Met Asn Trp Val Lys Gln Ser Ser Gly Lys Ser
    50   55   60
Leu Glu Trp Ile Gly Asn Phe Asp Pro Tyr Tyr Gly Val Ile Thr Tyr
65   70   75   80
Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser
                85   90   95
Ser Thr Ala Tyr Met Gln Leu Lys Ser Leu Thr Ser Glu Asp Ser Ala
            100   105   110
Val Tyr Tyr Cys Ala Arg Thr Ala Thr Ala Leu Tyr Thr Met Asp Tyr
        115   120   125
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly
    130   135   140
Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser
145   150   155   160
Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
                165   170   175
Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
            180   185   190
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
        195   200   205
Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val
    210   215   220
Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys
225   230   235   240
Cys Cys Val Glu Cys Pro Pro Cys Pro Gly Lys Pro Ala Pro Pro Val
                245   250   255
Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            260   265   270
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        275   280   285
Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu
    290   295   300
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr
305   310   315   320
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                325   330   335
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser
            340   345   350

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
355 360 365
Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val
370 375 380
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
385 390 395 400
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
405 410 415
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr
420 425 430
Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val
435 440 445
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
450 455 460
Ser Leu Gly Lys
465

<210> 19
<211> 2025
<212> DNA
<213> Artificial Sequence

<220>
<223> D1B5-hG1 Heavy chain (genomic sequence hG1 constant region)

<400> 19
atgggatgga gctgtatcat cctcttcttg gtagcaacag ctacaggtgt ccactccctc 60
gaggtccaac tgcagcagcc tggggcagag cttgtgaggt caggggcctc agtcaagttg 120
tcctgcaaag cttctggctt caacattaaa gactactata tacactgggt gaagcagagg 180
cctgaacagg gcctggagtg gattggatgg attgatcctg agattggtgc tactaaatat 240
gtcccgaagt tccagggcaa ggccactatg actacagaca catcctccaa cacagcctac 300
ctgcagctca gcagcctgac atctgaggac actgccgtct attactgtaa tgccctctat 360
ggtaactacg accgttacta tgctatggac tactggggtc aaggaacctc agtcaccgtc 420
tcctcagcct ccaccaaggg cccatcggtc ttcccctgg caccctcctc caagagcacc 480
tctggcggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 540
gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag 600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagagagtt 720
ggtgagaggc cagcacaggg agggagggtg tctgctggaa gccaggctca gcgctcctgc 780
ctggacgcat cccggctatg cagtcccagt ccagggcagc aaggcaggcc ccgtctgcct 840
cttcacccgg aggcctctgc ccgccccact catgctcagg gagagggtct tctggctttt 900
tccccaggct ctgggcaggc acaggctagg tgcccctaac ccaggccctg cacacaaagg 960
ggcaggtgct gggctcagac ctgccaagag ccatatccgg gaggaccctg ccctgacct 1020
aagcccaccc caaaggccaa actctccact ccctcagctc ggacaccttc tctcctccca 1080
gattccagta actcccaatc ttctctctgc agagcccaaa tcttgtgaca aaactcacac 1140
atgcccaccg tgcccaggta agccagccca ggcctcgccc tccagctcaa ggcgggacag 1200
gtgccctaga gtagcctgca tccagggaca ggccccagcc gggtgctgac acgtccacct 1260
ccatctcttc ctcagcacct gaactcctgg ggggaccgtc agtcttcctc ttcccccaa 1320
aacccaagga caccctcatg atctcccgga ccctgaggt cacatgcgtg gtggtggacg 1380
tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg gaggtgcata 1440
atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc 1500
tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcaag gtctccaaca 1560
aagccctccc agccccatc gagaaaacca tctccaaagc caaaggtggg acccgtgggg 1620
tgcgagggcc acatggacag aggccggctc ggcccaccct ctgccctgag agtgaccgct 1680
gtaccaacct ctgtccctac agggcagccc cgagaaccac aggtgtacac cctgccccca 1740
tcccgggagg agatgaccaa gaaccaggtc agcctgacct gcctggtcaa aggcttctat 1800
cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1860
acgcctcccg tgctggactc cgacggctcc ttcttcctct atagcaagct caccgtggac 1920
aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 1980
aaccactaca cgcagaagag cctctccctg tccccgggta aatga 2025

<210> 20

<211> 472
<212> PRT
<213> Artificial Sequence

<220>
<223> D1B5-hG1 Heavy chain

<400> 20

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Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
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Val His Ser Leu Glu Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val
            20                  25                  30
Arg Ser Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Phe Asn
        35                  40                  45
Ile Lys Asp Tyr Tyr Ile His Trp Val Lys Gln Arg Pro Glu Gln Gly
    50                  55                  60
Leu Glu Trp Ile Gly Trp Ile Asp Pro Glu Ile Gly Ala Thr Lys Tyr
65                  70                  75                  80
Val Pro Lys Phe Gln Gly Lys Ala Thr Met Thr Thr Asp Thr Ser Ser
                85                  90                  95
Asn Thr Ala Tyr Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala
            100                 105                 110
Val Tyr Tyr Cys Asn Ala Leu Tyr Gly Asn Tyr Asp Arg Tyr Tyr Ala
        115                 120                 125
Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser
    130                 135                 140
Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr
145                 150                 155                 160
Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
                165                 170                 175
Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
            180                 185                 190
His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
        195                 200                 205
Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile
    210                 215                 220
Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val
225                 230                 235                 240
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
                245                 250                 255
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            260                 265                 270
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        275                 280                 285
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    290                 295                 300
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
305                 310                 315                 320
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                325                 330                 335
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            340                 345                 350
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        355                 360                 365
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
    370                 375                 380
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
385                 390                 395                 400
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                405                 410                 415
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            420                 425                 430
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        435                 440                 445
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Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    450                 455                 460
Ser Leu Ser Leu Ser Pro Gly Lys
465                 470
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<210> 21
<211> 2026
<212> DNA
<213> Artificial Sequence

<220>
<223> G2G4 63L1D Heavy chain (genomic sequence hG2G4)

<400> 21

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tgcaaggcct ctggaggcac cttcagcaac tatgctacca gttgggtgcg acaggcccct 180
ggacaaggtc ttgagtggct gggagggatc atccccgtct tcggtactgc aaactacgca 240
cagaagtttc agggcagagt caccattacc gcggacgagt ccacgagcac agcctacatg 300
gagttgaata gtctgacatt tgacgacacg gccgtctatt actgtgcgag agggggtggg 360
ggatggggag gccggaacta ctactactac tactacatgg acgtctgggg caaagggacc 420
actgtcaccg tctcctcagc ctccaccaag ggcccatccg tcttccccct ggcgccctgc 480
tccaggagca cctccgagag cacagccgcc ctgggctgcc tggtcaagga ctacttcccc 540
gaaccggtga cggtgtcgtg gaactcaggc gccctgacca gcggcgtgca caccttcccg 600
gctgtcctac agtcctcagg actctactcc ctcagcagcg tggtgaccgt gccctccagc 660
aacttcggca cccagaccta cacctgcaac gtagatcaca agcccagcaa caccaaggtg 720
gacaagacag ttggtgagag gccagctcag ggagggaggg tgtctgctgg aagccaggct 780
cagccctcct gcctggacgc accccggctg tgcagcccca gcccagggca gcaaggcagg 840
ccccatctgt ctcctcaccc ggaggcctct gcccgcccca ctcatgctca gggagagggt 900
cttctggctt tttccaccag gctccaggca ggcacaggct gggtgccct accccaggcc 960
cttcacacac aggggcaggt gcttggctca gacctgccaa aagccatatc cgggaggacc 1020
ctgcccctga cctaagccga ccccaaaggc caaactgtcc actccctcag ctcggacacc 1080
ttctctcctc ccagatccga gtaactccca atcttctctc tgcagagcgc aaatgttgtg 1140
tcgagtgccc accgtgccca ggtaagccag cccaggcctc gccctccagc tcaaggcggg 1200
acaggtgccc tagagtagcc tgcatccagg gacaggcccc agctgggtgc tgacacgtcc 1260
acctccatct cttcctcagc accacctgtg gcaggaccgt cagtcttcct cttccccca 1320
aaacccaagg acaccctcat gatctcccgg acccctgagg tcacgtgcgt ggtggtggac 1380
gtgagccagg aagaccccga ggtccagttc aactggtacg tggatggcgt ggaggtgcat 1440
aatgccaaga caaagccgcg ggaggagcag ttcaacagca cgtaccgtgt ggtcagcgtc 1500
ctcaccgtcc tgcaccagga ctggctgaac ggcaaggagt acaagtgcaa ggtctccaac 1560
aaaggcctcc cgtcctccat cgagaaaacc atctccaaag ccaaaggtgg gacccacggg 1620
gtgcgagggc cacatggaca gaggtcagct cggcccaccc tctgccctgg gagtgaccgc 1680
tgtgccaacc tctgtcccta cagggcagcc ccgagagcca caggtgtaca ccctgccccc 1740
atcccaggag gagatgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta 1800
ccccagcgac atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac 1860
cacgcctccc gtgctggact ccgacggctc cttcttcctc tacagcaggc taaccgtgga 1920
caagagcagg tggcaggagg ggaatgtctt ctcatgctcc gtgatgcatg aggctctgca 1980
caaccactac acacagaaga gcctctccct gtctctgggt aaatga                 2026
```

<210> 22
<211> 472
<212> PRT
<213> Artificial Sequence

<220>
<223> G2G4 63L1D Heavy chain

<400> 22

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Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1               5                  10                  15
Val His Ser Gln Met Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30
Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe
```

```
        35                  40                  45
Ser Asn Tyr Ala Thr Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
    50                  55                  60
Glu Trp Leu Gly Gly Ile Ile Pro Val Phe Gly Thr Ala Asn Tyr Ala
65                  70                  75                  80
Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser
                85                  90                  95
Thr Ala Tyr Met Glu Leu Asn Ser Leu Thr Phe Asp Asp Thr Ala Val
            100                 105                 110
Tyr Tyr Cys Ala Arg Gly Gly Gly Gly Trp Gly Gly Arg Asn Tyr Tyr
        115                 120                 125
Tyr Tyr Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val
    130                 135                 140
Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys
145                 150                 155                 160
Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys
                165                 170                 175
Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
            180                 185                 190
Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
        195                 200                 205
Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr
    210                 215                 220
Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val
225                 230                 235                 240
Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro
                245                 250                 255
Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            260                 265                 270
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        275                 280                 285
Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val
    290                 295                 300
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
305                 310                 315                 320
Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                325                 330                 335
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly
            340                 345                 350
Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        355                 360                 365
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr
    370                 375                 380
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
385                 390                 395                 400
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                405                 410                 415
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            420                 425                 430
Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe
        435                 440                 445
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    450                 455                 460
Ser Leu Ser Leu Ser Leu Gly Lys
465                 470
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<210> 23
<211> 705
<212> DNA
<213> Artificial Sequence

<220>
<223> Light Chain chC2aB7-hG1, human Ck

<400> 23
atgggatgga gctgtatcat cctcttcttg gtagcaacag ctacaggtgt ccactctaga 60
gacatccaga tgacacagtc tccatcttcc atgtatgcat ctctaggaga gagagtcact 120
atcacttgca aggcgagtca ggacattaat agctatttaa gctggttcca gcagaaacca 180
gggaaatctc ctaagaccct gatctatcgt gcaaacagat tggtagatgg ggttccatca 240
aggttcagtg gcagtggatc tgggcaagat tattctctca ccatcagcag cctggagtat 300
gaagatatgg gaatttatta ttgtctacag tatgatgagt ttccgtacac gttcggaggg 360
gggaccaagc tggaaataaa acggactgtg gctgcaccat ctgtcttcat cttcccgcca 420
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 480
cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 540
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 600
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 660
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gttaa 705

<210> 24
<211> 234
<212> PRT
<213> Artificial Sequence

<220>
<223> Light Chain chC2aB7-hG1, human Ck

<400> 24
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1   5   10   15
Val His Ser Arg Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Met Tyr
            20   25   30
Ala Ser Leu Gly Glu Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp
        35   40   45
Ile Asn Ser Tyr Leu Ser Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro
    50   55   60
Lys Thr Leu Ile Tyr Arg Ala Asn Arg Leu Val Asp Gly Val Pro Ser
65   70   75   80
Arg Phe Ser Gly Ser Gly Ser Gly Gln Asp Tyr Ser Leu Thr Ile Ser
                85   90   95
Ser Leu Glu Tyr Glu Asp Met Gly Ile Tyr Tyr Cys Leu Gln Tyr Asp
            100   105   110
Glu Phe Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
        115   120   125
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
    130   135   140
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145   150   155   160
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
                165   170   175
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
            180   185   190
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
        195   200   205
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
    210   215   220
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225   230

<210> 25
<211> 711
<212> DNA
<213> Artificial Sequence

<220>
<223> hB7V4V1-hG1 light chain

<400> 25
atggacatga gggtctctgc tcagctcctg gggctcctgc tgctctggct ctcaggagcc 60
agatgtgaca tccagatgac acagtctcca tcttccctgt ctgcatctat aggagacaga 120
gtcactatca cttgcaaggc gagtcaggac attaatagct atttaagctg gtaccagcag 180
aaaccaggga aagctcctaa gtccctgatc tatcgtgcaa acagattggt agatggggtt 240
ccatcaaggt tcagtggcag tggatctggg acagattata ctctcaccat cagcagcctg 300
cagcctgaag atttcgcagt ttattattgt ctacagtatg atgagtttcc gtacacgttc 360
ggaggggga ccaagctgga aataaaacgt acggtggctg caccatctgt cttcatcttc 420
ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 480
ttctatccca gagaggccaa agtacagtgg aaggtggata acgccctcca atcgggtaac 540
tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 600
ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 660
cagggcctga gctcgcccgt cacaaagagc ttcaacaggg gagagtgtta g 711

<210> 26
<211> 236
<212> PRT
<213> Artificial Sequence

<220>
<223> hB7V4V1-hG1 Light chain (human Ck)

<400> 26
Met Asp Met Arg Val Ser Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
 1   5   10   15
Leu Ser Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
            20   25   30
Leu Ser Ala Ser Ile Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser
        35   40   45
Gln Asp Ile Asn Ser Tyr Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys
    50   55   60
Ala Pro Lys Ser Leu Ile Tyr Arg Ala Asn Arg Leu Val Asp Gly Val
65   70   75   80
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr
                85   90   95
Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Val Tyr Tyr Cys Leu Gln
            100   105   110
Tyr Asp Glu Phe Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
        115   120   125
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
    130   135   140
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
145   150   155   160
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
                165   170   175
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
            180   185   190
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
        195   200   205
Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
    210   215   220
Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225   230   235

<210> 27
<211> 711
<212> DNA
<213> Artificial Sequence

<220>
<223> hB7V3V2-hG1 Light Chain

<400> 27

atggacatga gggtctctgc tcagctcctg gggctcctgc tgctctggct ctcaggggcc 60
aggtgtgaca tccagatgac acagtctcca tcttccctgt ctgcatctat aggagacaga 120
gtcactatca cttgcaaggc gagtcaggac attaatagct atttaagctg gttccagcag 180
aaaccaggga aagctcctaa gctgctgatc tatcgtgcaa acagattggt agatggggtt 240
ccatcaaggt tcagtggcag tggatctggg acagattata ctctcaccat cagcagcctg 300
cagcctgaag atttcgcagt ttattattgt ctacagtatg atgagtttcc gtacacgttc 360
ggaggggggа ccaagctgga aataaaacgt acggtggctg caccatctgt cttcatcttc 420
ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 480
ttctatccca gagaggccaa agtacagtgg aaggtggata acgccctcca atcgggtaac 540
tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 600
ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 660
cagggcctga gctcgcccgt cacaaagagc ttcaacaggg gagagtgtta g 711

<210> 28
<211> 236
<212> PRT
<213> Artificial Sequence

<220>
<223> hB7V3V2-hG1 Light Chain (human Ck)

<400> 28
Met Asp Met Arg Val Ser Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
 1   5   10   15
Leu Ser Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
            20   25   30
Leu Ser Ala Ser Ile Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser
        35   40   45
Gln Asp Ile Asn Ser Tyr Leu Ser Trp Phe Gln Gln Lys Pro Gly Lys
    50   55   60
Ala Pro Lys Leu Leu Ile Tyr Arg Ala Asn Arg Leu Val Asp Gly Val
65   70   75   80
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr
                85   90   95
Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Val Tyr Tyr Cys Leu Gln
            100   105   110
Tyr Asp Glu Phe Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
        115   120   125
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
    130   135   140
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
145   150   155   160
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
                165   170   175
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
            180   185   190
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
        195   200   205
Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
    210   215   220
Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225   230   235

<210> 29
<211> 708
<212> DNA
<213> Artificial Sequence

<220>
<223> ChC7-hG2G4 Light chain

<400> 29
atgggatgga gctgtatcat cctcttcttg gtagcaacag ctacaggtgt ccactctaga 60

gaaattgtgc tcacccagtc tccagcaatc atgtctgcat ctccagggga aaaggtcacc 120
atgacctgca gggccagctc aagtgtaagt tccagttact tgcactggta ccagcagaag 180
tcaggtgcct cccccaaact ctggatttat agcacatcca acttggcttc tggagtccct 240
gctcgcttca gtggcagtgg gtctgggacc tcttactctc tcacaatcag cagtgtggag 300
gctgaagatg ctgccactta ttactgccag cagtacagtg gttacccact cacgttcggc 360
tcggggacaa agttggaaat aaaacggact gtggctgcac catctgtctt catcttcccg 420
ccatccgatg 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 cgcccgtcac aaagagcttc aacaggggag agtgttaa 708

<210> 30
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> ChC7-hG2G4 Light chain (human Ck)

<400> 30
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15
Val His Ser Arg Glu Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser
20 25 30
Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser
35 40 45
Val Ser Ser Ser Tyr Leu His Trp Tyr Gln Gln Lys Ser Gly Ala Ser
50 55 60
Pro Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85 90 95
Ser Ser Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Tyr
100 105 110
Ser Gly Tyr Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu 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> 31
<211> 705
<212> DNA
<213> Artificial Sequence

<220>
<223> D1B5-hG1 Light chain

<400> 31
atgggatgga gctgtatcat cctcttcttg gtagcaacag ctacaggtgt ccactctaga 60
gacattgtga tgacccagtc tcaaaaattc atgtccacat cagtaggaga cagggtcagc 120

atcacctgca aggccagtca gaatgttcgt actgctgtag cctggtatca acagaaacca 180
gggcagtctc ctaaagcact gatttacttg gcatccaacc ggcacactgg agtccctgat 240
cgcttcacag gcagtggatc tgggacagat ttcactctca ccattagcaa tgtgcaatct 300
gaagacctgg cagattattt ctgtctgcaa cattggaatt atcctctcac gttcggtgct 360
gggaccaagc tggagctgaa acggactgtg gctgcaccat ctgtcttcat cttcccgcca 420
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 480
cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 540
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcaa caccctgacg 600
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 660
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gttaa 705

<210> 32
<211> 234
<212> PRT
<213> Artificial Sequence

<220>
<223> D1B5-hG1 Light chain (human Ck)

<400> 32
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15
Val His Ser Arg Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser
20 25 30
Thr Ser Val Gly Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asn
35 40 45
Val Arg Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro
50 55 60
Lys Ala Leu Ile Tyr Leu Ala Ser Asn Arg His Thr Gly Val Pro Asp
65 70 75 80
Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
85 90 95
Asn Val Gln Ser Glu Asp Leu Ala Asp Tyr Phe Cys Leu Gln His Trp
100 105 110
Asn Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
115 120 125
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
130 135 140
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145 150 155 160
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
165 170 175
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
180 185 190
Tyr Ser Leu Ser Asn Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
195 200 205
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
210 215 220
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230

<210> 33
<211> 696
<212> DNA
<213> Artificial Sequence

<220>
<223> G2G4 63L1D Light chain

<400> 33
atgggatgga gctgtatcat cctcttcttg gtagcaacag ctacaggtgt ccactcttcc 60
tatgtgctga ctcagccacc ctcggagtca gtggccccag gacagacggc caggatttcc 120
tgtgggggga gcaacattgg aagttacggt gtgcactggt accagcagaa ggcaggacag 180

gcccctgtgc tggtcgtcca tgatgattcc gaccggccct cagggattcc tgagcgattc 240
tctggctcca attctgggaa cacggccacc ctgaccatca gcagtgtcga agccggcgat 300
gaggccgact attactgtca ggtgtgggat aatagtgctg tgatattcgg cggagggacc 360
aaactaaccg tcctaagtca gcccaaggct gccccctcgg tcactctgtt cccgccctcc 420
tctgaggagc ttcaagccaa caaggccaca ctggtgtgtc tcataagtga cttctacccg 480
ggagctgtga cagtggcttg gaaagcagat agcagccccg tcaaggcggg agtggagacc 540
accacaccct ccaaacaaag caacaacaag tacgcggcca gcagctatct gagcctgacg 600
cctgagcagt ggaagtccca cagaagctac agctgccagg tcacgcatga agggagcacc 660
gtggagaaga cagtggcccc tacagaatgt tcataa 696

<210> 34
<211> 231
<212> PRT
<213> Artificial Sequence

<220>
<223> G2G4 63L1D Light chain (human CL)

<400> 34
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15
Val His Ser Ser Tyr Val Leu Thr Gln Pro Pro Ser Glu Ser Val Ala
20 25 30
Pro Gly Gln Thr Ala Arg Ile Ser Cys Gly Gly Ser Asn Ile Gly Ser
35 40 45
Tyr Gly Val His Trp Tyr Gln Gln Lys Ala Gly Gln Ala Pro Val Leu
50 55 60
Val Val His Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe
65 70 75 80
Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Ser Val
85 90 95
Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Asn Ser
100 105 110
Ala Val Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Gln Pro
115 120 125
Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu
130 135 140
Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro
145 150 155 160
Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala
165 170 175
Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala
180 185 190
Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg
195 200 205
Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr
210 215 220
Val Ala Pro Thr Glu Cys Ser
225 230

<210> 35
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> forward primer

<400> 35
gacaagcttg caaggatgga gaggctggtg a 31

<210> 36
<211> 33

<212> DNA
<213> Artificial Sequence

<220>
<223> reverse primer

<400> 36
gacggatccg ccccttttcc tcctgctttt ctc 33

<210> 37
<211> 2160
<212> DNA
<213> Artificial Sequence

<220>
<223> chC2aB7-hG1 Heavy chain

<400> 37
gcgcgccacc agacataata gctgacagac taacagactg ttcctttcca tgggtctttt 60
ctgcagtcac cgtccttgac acgaggcgcg ccgccaccat gggatggagc tgtatcatcc 120
tcttcttggt agcaacagct acaggtgtcc actccctcga ggtccagctg caacagtctg 180
gacctgagct ggtgaagcct ggggcttcac tgaagatgtc ctgcaaggct tctggttatt 240
cattcactga ctacatcata ctctgggtga agcagaacca tggaaagagc cttgagtgga 300
ttggacatat tgatccttac tatggtagtt ctaactacaa tctgaaattc aagggcaagg 360
ccacattgac tgtagacaaa tcttccagca cagcctacat gcagctcaac agtctgacat 420
ctgaggactc tgcagtctat tactgtggaa gatctaagag ggactacttt gactactggg 480
gccaaggcac cactctcaca gtttcctcag cctccaccaa gggcccatcg gtcttccccc 540
tggcaccctc ctccaagagc acctctggcg gcacagcggc cctgggctgc ctggtcaagg 600
actacttccc cgaaccggtg acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc 660
acaccttccc ggctgtccta cagtcctcag gactctactc cctcagcagc gtggtgaccg 720
tgccctccag cagcttgggc acccagacct acatctgcaa cgtgaatcac aagcccagca 780
acaccaaggt ggacaagaga gttggtgaga ggccagcaca gggagggagg gtgtctgctg 840
gaagccaggc tcagcgctcc tgcctggacg catcccggct atgcagtccc agtccagggc 900
agcaaggcag gccccgtctg cctcttcacc cggaggcctc tgcccgcccc actcatgctc 960
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cgggaggacc ctgcccctga cctaagccca ccccaaaggc caaactctcc actccctcag 1140
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cacaggtgta caccctgccc ccatcccggg aggagatgac caagaaccag gtcagcctga 1860
cctgcctggt caaaggcttc tatcccagcg acatcgccgt ggagtgggag agcaatgggc 1920
agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc tccttcttcc 1980
tctatagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc ttctcatgct 2040
ccgtgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc ctgtccccgg 2100
gtaaatgagt gcgacggcca gaattcattg atcataatca gccataccac atttgtagag 2160

<210> 38
<211> 720
<212> DNA
<213> Artificial Sequence

<220>
<223> chC2aB7-hG1 Light chain

<400> 38
aagcttgccg ccaccatggg atggagctgt atcatcctct tcttggtagc aacagctaca 60
ggtgtccact ctagagacat ccagatgaca cagtctccat cttccatgta tgcatctcta 120
ggagagagag tcactatcac ttgcaaggcg agtcaggaca ttaatagcta tttaagctgg 180
ttccagcaga aaccagggaa atctcctaag accctgatct atcgtgcaaa cagattggta 240
gatggggttc catcaaggtt cagtggcagt ggatctgggc aagattattc tctcaccatc 300
agcagcctgg agtatgaaga tatgggaatt tattattgtc tacagtatga tgagtttccg 360
tacacgttcg gaggggggac caagctggaa ataaaacgga ctgtggctgc accatctgtc 420
ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg 480
ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa 540
tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc 600
agcagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 660
gtcacccatc agggcctgag ctcgcccgtc acaaagagct tcaacagggg agagtgttaa 720

<210> 39
<211> 1402
<212> DNA
<213> Artificial Sequence

<220>
<223> hB7V4V1-hG1 Heavy chain

<400> 39
catgggatgg agctggatct ttctctttct cctgtcagta actgcaggtg tgttctctga 60
ggtccagctg gtggagtccg gacctgaggt gaagaagcct ggggcttcag tgaaggtgtc 120
ctgcaaggct tctggttatt cattcactga ctacatcata ctctggatca ggcagcatag 180
cggaaagggc cttgagtgga ttggacatat tgatccttac tatggtagtt ctaactacaa 240
tctgaaattc aagggcaggg tcacaatcac tgcagacaaa tctaccagga caacctacat 300
ggagctcacc agtctgacat ctgaggacac tgcagtctat tactgtggaa gatctaagag 360
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gggcccatcg gtcttcccgc tagcaccctc ctccaagagc acctctgggg gcacagcggc 480
cctgggctgc ctggtcaagg actacttccc cgaaccggtg acggtgtcgt ggaactcagg 540
cgccctgacc agcggcgtgc acaccttccc ggctgtccta cagtcctcag gactctactc 600
cctcagcagc gtggtgaccg tgccctccag cagcttgggc acccagacct acatctgcaa 660
cgtgaatcac aagcccagca acaccaaggt ggacaagaga gttgagccca aatcttgtga 720
caaaactcac acatgcccac cgtgcccagc acctgaactc ctgggggggac cgtcagtctt 780
cctcttcccc ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg 840
cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg 900
cgtggaggtg cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg 960
tgtggtcagc gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg 1020
caaggtctcc aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg 1080
gcagccccga gaaccacagg tgtacaccct gccccatcc cgggaggaga tgaccaagaa 1140
ccaggtcagc ctgacctgcc tggtcaaagg cttctatccc agcgacatcg ccgtggagtg 1200
ggagagcaat gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga 1260
cggctccttc ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa 1320
cgtcttctca tgctccgtga tgcatgaggc tctgcacaac cactacacgc agaagagcct 1380
ctccctgtct ccgggtaaat ga 1402

<210> 40
<211> 765
<212> DNA
<213> Artificial Sequence

<220>
<223> hB7V4V1-hG1 and hB7V3V1-hG1 Light chains

<400> 40
tttccatggg tcttttctgc agtcaccgtc cttgacacga agcttgccgc caccatggac 60
atgagggtct ctgctcagct cctggggctc ctgctgctct ggctctcagg agccagatgt 120
gacatccaga tgacacagtc tccatcttcc ctgtctgcat ctataggaga cagagtcact 180
atcacttgca aggcgagtca ggacattaat agctatttaa gctggtacca gcagaaacca 240
gggaaagctc ctaagtccct gatctatcgt gcaaacagat tggtagatgg ggttccatca 300
aggttcagtg gcagtggatc tgggacagat tatactctca ccatcagcag cctgcagcct 360

gaagatttcg cagtttatta ttgtctacag tatgatgagt ttccgtacac gttcggaggg 420
gggaccaagc tggaaataaa acgtacggtg gctgcaccat ctgtcttcat cttcccgcca 480
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 540
cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 600
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 660
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 720
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gttag 765

<210> 41
<211> 1402
<212> DNA
<213> Artificial Sequence

<220>
<223> hB7V3V1-hG1 and hB7V3V2-hG1 Heavy chains

<400> 41
catgggatgg agccggatct ttctcttcct cctgtcaata attgcaggtg tccattgcca 60
ggtccagctg caacagtctg gatctgagct gaagaagcct ggggcttcag tgaagatctc 120
ctgcaaggct tctggttatt cattcactga ctacatcata ctctgggtga ggcagaaccc 180
tggaaagggc cttgagtgga ttggacatat tgatccttac tatggtagtt ctaactacaa 240
tctgaaattc aagggcagag tgacaatcac cgccgaccag tctaccacca cagcctacat 300
ggagctctcc agtctgagat ctgaggacac tgcagtctat tactgtggaa gatctaagag 360
ggactacttt gactactggg gccaaggcac cactctcaca gtttcctcag cctccaccaa 420
gggcccatcg gtcttcccgc tagcaccctc ctccaagagc acctctgggg gcacagcggc 480
cctgggctgc ctggtcaagg actacttccc cgaaccggtg acggtgtcgt ggaactcagg 540
cgccctgacc agcggcgtgc acaccttccc ggctgtccta cagtcctcag gactctactc 600
cctcagcagc gtggtgaccg tgccctccag cagcttgggc acccagacct acatctgcaa 660
cgtgaatcac aagcccagca acaccaaggt ggacaagaga gttgagccca aatcttgtga 720
caaaactcac acatgcccac cgtgcccagc acctgaactc ctgggggggac cgtcagtctt 780
cctcttcccc ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg 840
cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg 900
cgtggaggtg cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg 960
tgtggtcagc gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg 1020
caaggtctcc aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg 1080
gcagccccga gaaccacagg tgtacaccct gccccatcc cgggaggaga tgaccaagaa 1140
ccaggtcagc ctgacctgcc tggtcaaagg cttctatccc agcgacatcg ccgtggagtg 1200
ggagagcaat gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga 1260
cggctccttc ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa 1320
cgtcttctca tgctccgtga tgcatgaggc tctgcacaac cactacacgc agaagagcct 1380
ctccctgtct ccgggtaaat ga 1402

<210> 42
<211> 765
<212> DNA
<213> Artificial Sequence

<220>
<223> hB7V3V2-hG1 and hB7V3V2-hG2G4 Light chains

<400> 42
tttccatggg tcttttctgc agtcaccgtc cttgacacga agcttgccgc caccatggac 60
atgagggtct ctgctcagct cctggggctc ctgctgctct ggctctcagg ggccaggtgt 120
gacatccaga tgacacagtc tccatcttcc ctgtctgcat ctataggaga cagagtcact 180
atcacttgca aggcgagtca ggacattaat agctatttaa gctggttcca gcagaaacca 240
gggaaagctc ctaagctgct gatctatcgt gcaaacagat tggtagatgg ggttccatca 300
aggttcagtg gcagtggatc tgggacagat tatactctca ccatcagcag cctgcagcct 360
gaagatttcg cagtttatta ttgtctacag tatgatgagt ttccgtacac gttcggaggg 420
gggaccaagc tggaaataaa acgtacggtg gctgcaccat ctgtcttcat cttcccgcca 480
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 540
cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 600
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 660
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 720
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gttag 765

<210> 43
<211> 2159
<212> DNA
<213> Artificial Sequence

<220>
<223> hB7V3V2-hG2G4 Heavy chain

<400> 43
ccaccagaca taatagctga cagactaaca gactgttcct ttccatgggt cttttctgca 60
gtcaccgtcc ttgacacgaa gcttgccgcc accatgggat ggagccggat ctttctcttc 120
ctcctgtcaa taattgcagg tgtccattgc caggtccagc tgcaacagtc tggatctgag 180
ctgaagaagc ctggggcttc agtgaagatc tcctgcaagg cttctggtta ttcattcact 240
gactacatca tactctgggt gaggcagaac cctggaaagg gccttgagtg gattggacat 300
attgatcctt actatggtag ttctaactac aatctgaaat tcaagggcag agtgacaatc 360
accgccgacc agtctaccac cacagcctac atggagctct ccagtctgag atctgaggac 420
actgcagtct attactgtgg aagatctaag agggactact ttgactactg gggccaaggc 480
accactctca cagtttcctc agcctccacc aagggcccat ccgtcttccc cctggcgccc 540
tgctccagga gcacctccga gagcacagcc gccctgggct gcctggtcaa ggactacttc 600
cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 660
ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc 720
agcaacttcg gcacccagac ctacacctgc aacgtagatc acaagcccag caacaccaag 780
gtggacaaga cagttggtga gaggccagct cagggaggga gggtgtctgc tggaagccag 840
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accctgcccc tgacctaagc cgaccccaaa ggccaaactg tccactccct cagctcggac 1140
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gtgtcgagtg cccaccgtgc ccaggtaagc cagcccaggc ctcgccctcc agctcaaggc 1260
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ccaaaaccca aggacaccct catgatctcc cggaccctg aggtcacgtg cgtggtggtg 1440
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cataatgcca agacaaagcc gcgggaggag cagttcaaca gcacgtaccg tgtggtcagc 1560
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aacaaaggcc tcccgtcctc catcgagaaa accatctcca aagccaaagg tgggacccac 1680
ggggtgcgag ggccacatgg acagaggtca gctcggccca ccctctgccc tgggagtgac 1740
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gaccacgcct cccgtgctgg actccgacgg ctccttcttc ctctacagca ggctaaccgt 1980
ggacaagagc aggtggcagg aggggaatgt cttctcatgc tccgtgatgc atgaggctct 2040
gcacaaccac tacacacaga agagcctctc cctgtctctg ggtaaatgat gagaattcat 2100
tgatcataat cagccatacc acatttgtag aggttttact tgctttaaaa aacctcccac 2160

<210> 44
<211> 1600
<212> DNA
<213> Artificial Sequence

<220>
<223> chC2aB7-hG2G4 Heavy chain

<400> 44
gctgacagac taacagactg ttcctttcca tgggtctttt ctgcagtcac cgtccttgac 60
acgaggcgcg ccgccaccat gggatggagc tgtatcatcc tcttcttggt agcaacagct 120
acaggtgtcc actccctcga ggtccagctg caacagtctg gacctgagct ggtgaagcct 180
ggggcttcac tgaagatgtc ctgcaaggct tctggttatt cattcactga ctacatcata 240
ctctgggtga agcagaacca tggaaagagc cttgagtgga ttggacatat tgatccttac 300
tatggtagtt ctaactacaa tctgaaattc aagggcaagg ccacattgac tgtagacaaa 360
tcttccagca cagcctacat gcagctcaac agtctgacat ctgaggactc tgcagtctat 420
tactgtggaa gatctaagag ggactacttt gactactggg gccaaggcac cactctcaca 480

gtttcctcag cctccaccaa gggcccatcc gtcttccccc tggcgccctg ctccaggagc 540
acctccgaga gcacagccgc cctgggctgc ctggtcaagg actacttccc cgaaccggtg 600
acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta 660
cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag caacttcggc 720
acccagacct acacctgcaa cgtagatcac aagcccagca acaccaaggt ggacaagaca 780
gttggtgaga ggccagctca gggagggagg gtgtctgctg gaagccaggc tcagccctcc 840
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caggggcagg tgcttggctc agacctgcca aaagccatat ccgggaggac cctgcccctg 1080
acctaagccg accccaaagg ccaaactgtc cactccctca gctcggacac cttctctcct 1140
cccagatccg agtaactccc aatcttctct ctgcagagcg caaatgttgt gtcgagtgcc 1200
caccgtgccc aggtaagcca gcccaggcct cgccctccag ctcaaggcgg gacaggtgcc 1260
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gacaccctca tgatctcccg gaccctgag gtcacgtgcg tggtggtgga cgtgagccag 1440
gaagaccccg aggtccagtt caactggtac gtggatggcg tggaggtgca taatgccaag 1500
acaaagccgc gggaggagca gttcaacagc acgtaccgtg tggtcagcgt cctcaccgtc 1560
ctgcaccagg actggctgaa cggcaaggag tacaagtgca 1600

<210> 45
<211> 337
<212> PRT
<213> Artificial Sequence

<220>
<223> chC2aB7-hG2G4 Heavy chain

<400> 45
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
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Val His Ser Leu Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val
            20   25   30
Lys Pro Gly Ala Ser Leu Lys Met Ser Cys Lys Ala Ser Gly Tyr Ser
        35   40   45
Phe Thr Asp Tyr Ile Ile Leu Trp Val Lys Gln Asn His Gly Lys Ser
    50   55   60
Leu Glu Trp Ile Gly His Ile Asp Pro Tyr Tyr Gly Ser Ser Asn Tyr
65   70   75   80
Asn Leu Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser
                85   90   95
Ser Thr Ala Tyr Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala
            100   105   110
Val Tyr Tyr Cys Gly Arg Ser Lys Arg Asp Tyr Phe Asp Tyr Trp Gly
        115   120   125
Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130   135   140
Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
145   150   155   160
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165   170   175
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180   185   190
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195   200   205
Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His
    210   215   220
Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys
225   230   235   240
Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val
                245   250   255
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
            260   265   270
Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu

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        275                 280                 285
Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
    290                 295                 300
Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
305                 310                 315                 320
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
                325                 330                 335
Cys
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<210> 46
<211> 735
<212> DNA
<213> Artificial Sequence

<220>
<223> chC2aB7-hG2G4 Light chain

<400> 46
aagcttgccg ccaccatggg atggagctgt atcatcctct tcttggtagc aacagctaca 60
ggtgtccact ctagagacat ccagatgaca cagtctccat cttccatgta tgcatctcta 120
ggagagagag tcactatcac ttgcaaggcg agtcaggaca ttaatagcta tttaagctgg 180
ttccagcaga aaccagggaa atctcctaag accctgatct atcgtgcaaa cagattggta 240
gatggggttc catcaaggtt cagtggcagt ggatctgggc aagattattc tctcaccatc 300
agcagcctgg agtatgaaga tatgggaatt tattattgtc tacagtatga tgagtttccg 360
tacacgttcg gaggggggac caagctggaa ataaaacgga ctgtggctgc accatctgtc 420
ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg 480
ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa 540
tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc 600
agcagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 660
gtcacccatc agggcctgag ctcgcccgtc acaaagagct tcaacagggg agagtgttca 720
gcggccgcaa ttcattga 738

<210> 47
<211> 240
<212> PRT
<213> Artificial Sequence

<220>
<223> chC2aB7-hG2G4 Light chain

<400> 47
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Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1               5                  10                  15
Val His Ser Arg Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Met Tyr
            20                  25                  30
Ala Ser Leu Gly Glu Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp
        35                  40                  45
Ile Asn Ser Tyr Leu Ser Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro
    50                  55                  60
Lys Thr Leu Ile Tyr Arg Ala Asn Arg Leu Val Asp Gly Val Pro Ser
65                  70                  75                  80
Arg Phe Ser Gly Ser Gly Ser Gly Gln Asp Tyr Ser Leu Thr Ile Ser
                85                  90                  95
Ser Leu Glu Tyr Glu Asp Met Gly Ile Tyr Tyr Cys Leu Gln Tyr Asp
            100                 105                 110
Glu Phe Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
        115                 120                 125
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
    130                 135                 140
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145                 150                 155                 160
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
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                165                 170                 175
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
            180                 185                 190
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
        195                 200                 205
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
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225                 230                 235                 240
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<210> 48
<211> 1560
<212> DNA
<213> Artificial Sequence

<220>
<223> hB7V3V2-cG2G4 Heavy chain

<400> 48

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<210> 49
<211> 772
<212> DNA
<213> Artificial Sequence

<220>
<223> hB7V3V2-cG2G4 Light chain

<400> 49

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<210> 50
<211> 2158
<212> DNA
<213> Artificial Sequence

<220>
<223> DIB5-hG1 Heavy chain

<400> 50
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<210> 51
<211> 720
<212> DNA
<213> Artificial Sequence

<220>
<223> DIB5-hG1 Light chain

<400> 51
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