SEQUENCE LISTING

<110> CENTOCOR, INC.

<120> TOLL LIKE RECEPTOR 3 ANTAGONISTS,
METHODS AND USES

<130> CEN5083 PCT

<140> TO BE ASSIGNED
<141> 2005-11-30

<150> 60/631,815
<151> 2004-11-30

<150> 60/636,399
<151> 2004-12-15

<150> 60/641,877
<151> 2005-01-06

<150> 60/713,195
<151> 2005-08-31

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<160> 63

<170> FastSEQ for Windows Version 4.0

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aagttgactc aggtacccga tgatctaccc acaaacataa cagtgttgaa ccttacccat 180
aatcaactca gaagattacc agccgccaac ttcacaaggt atagccagct aactagcttg 240
gatgtaggat ttaacaccat ctcaaaactg gagccagaat tgtgccagaa acttcccatg 300
ttaaaagttt tgaacctcca gcacaatgag ctatctcaac tttctgataa aacctttgcc 360
ttctgcacga atttgactga actccatctc atgtccaact caatccagaa aattaaaaat 420
aatccctttg tcaagcagaa gaatttaatc acattagatc tgtctcataa tggcttgtca 480
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ggaagattat ttggcctctt tctgaacaat gtccagctgg gtcccagcct tacagagaag 720
ctatgtttgg aattagcaaa cacaagcatt cggaatctgt ctctgagtaa cagccagctg 780
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gaatatttct tcctagagta taataatata cagcatttgt tttctcactc tttgcacggg 960
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gcctcactcc ccaagattga tgatttttct tttcagtggc taaaatgttt ggagcacctt 1080
aacatggaag ataatgatat tccaggcata aaaagcaata tgttcacagg attgataaac 1140
ctgaaatact taagtctatc caactccttt acaagtttgc gaactttgac aaatgaaaca 1200

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<212> PRT
<213> Homo sapiens

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            20                  25                  30

Glu Val Ala Asp Cys Ser His Leu Lys Leu Thr Gln Val Pro Asp Asp
        35                  40                  45
Leu Pro Thr Asn Ile Thr Val Leu Asn Leu Thr His Asn Gln Leu Arg
    50                  55                  60
Arg Leu Pro Ala Ala Asn Phe Thr Arg Tyr Ser Gln Leu Thr Ser Leu
65                  70                  75                  80
Asp Val Gly Phe Asn Thr Ile Ser Lys Leu Glu Pro Glu Leu Cys Gln
                85                  90                  95
Lys Leu Pro Met Leu Lys Val Leu Asn Leu Gln His Asn Glu Leu Ser
            100                 105                 110
Gln Leu Ser Asp Lys Thr Phe Ala Phe Cys Thr Asn Leu Thr Glu Leu
        115                 120                 125
His Leu Met Ser Asn Ser Ile Gln Lys Ile Lys Asn Asn Pro Phe Val
    130                 135                 140
Lys Gln Lys Asn Leu Ile Thr Leu Asp Leu Ser His Asn Gly Leu Ser
145                 150                 155                 160

Ser Thr Lys Leu Gly Thr Gln Val Gln Leu Glu Asn Leu Gln Glu Leu
                165                 170                 175
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Leu Leu Ser Asn Asn Lys Ile Gln Ala Leu Lys Ser Glu Glu Leu Asp
180 185 190
Ile Phe Ala Asn Ser Ser Leu Lys Lys Leu Glu Leu Ser Ser Asn Gln
195 200 205
Ile Lys Glu Phe Ser Pro Gly Cys Phe His Ala Ile Gly Arg Leu Phe
210 215 220
Gly Leu Phe Leu Asn Asn Val Gln Leu Gly Pro Ser Leu Thr Glu Lys
225 230 235 240
Leu Cys Leu Glu Leu Ala Asn Thr Ser Ile Arg Asn Leu Ser Leu Ser
245 250 255
Asn Ser Gln Leu Ser Thr Thr Ser Asn Thr Thr Phe Leu Gly Leu Lys
260 265 270
Trp Thr Asn Leu Thr Met Leu Asp Leu Ser Tyr Asn Asn Leu Asn Val
275 280 285
Val Gly Asn Asp Ser Phe Ala Trp Leu Pro Gln Leu Glu Tyr Phe Phe
290 295 300
Leu Glu Tyr Asn Asn Ile Gln His Leu Phe Ser His Ser Leu His Gly
305 310 315 320
Leu Phe Asn Val Arg Tyr Leu Asn Leu Lys Arg Ser Phe Thr Lys Gln
325 330 335
Ser Ile Ser Leu Ala Ser Leu Pro Lys Ile Asp Asp Phe Ser Phe Gln
340 345 350
Trp Leu Lys Cys Leu Glu His Leu Asn Met Glu Asp Asn Asp Ile Pro
355 360 365
Gly Ile Lys Ser Asn Met Phe Thr Gly Leu Ile Asn Leu Lys Tyr Leu
370 375 380
Ser Leu Ser Asn Ser Phe Thr Ser Leu Arg Thr Leu Thr Asn Glu Thr
385 390 395 400
Phe Val Ser Leu Ala His Ser Pro Leu His Ile Leu Asn Leu Thr Lys
405 410 415
Asn Lys Ile Ser Lys Ile Glu Ser Asp Ala Phe Ser Trp Leu Gly His
420 425 430
Leu Glu Val Leu Asp Leu Gly Leu Asn Glu Ile Gly Gln Glu Leu Thr
435 440 445
Gly Gln Glu Trp Arg Gly Leu Glu Asn Ile Phe Glu Ile Tyr Leu Ser
450 455 460
Tyr Asn Lys Tyr Leu Gln Leu Thr Arg Asn Ser Phe Ala Leu Val Pro
465 470 475 480
Ser Leu Gln Arg Leu Met Leu Arg Arg Val Ala Leu Lys Asn Val Asp
485 490 495
Ser Ser Pro Ser Pro Phe Gln Pro Leu Arg Asn Leu Thr Ile Leu Asp
500 505 510
Leu Ser Asn Asn Asn Ile Ala Asn Ile Asn Asp Asp Met Leu Glu Gly
515 520 525
Leu Glu Lys Leu Glu Ile Leu Asp Leu Gln His Asn Asn Leu Ala Arg
530 535 540
Leu Trp Lys His Ala Asn Pro Gly Gly Pro Ile Tyr Phe Leu Lys Gly
545 550 555 560
Leu Ser His Leu His Ile Leu Asn Leu Glu Ser Asn Gly Phe Asp Glu
565 570 575
Ile Pro Val Glu Val Phe Lys Asp Leu Phe Glu Leu Lys Ile Ile Asp
580 585 590
Leu Gly Leu Asn Asn Leu Asn Thr Leu Pro Ala Ser Val Phe Asn Asn
595 600 605

Gln Val Ser Leu Lys Ser Leu Asn Leu Gln Lys Asn Leu Ile Thr Ser
610 615 620

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Val Glu Lys Lys Val Phe Gly Pro Ala Phe Arg Asn Leu Thr Glu Leu
625                 630                 635                 640
Asp Met Arg Phe Asn Pro Phe Asp Cys Thr Cys Glu Ser Ile Ala Trp
                645                 650                 655
Phe Val Asn Trp Ile Asn Glu Thr His Thr Asn Ile Pro Glu Leu Ser
            660                 665                 670
Ser His Tyr Leu Cys Asn Thr Pro Pro His Tyr His Gly Phe Pro Val
        675                 680                 685
Arg Leu Phe Asp Thr Ser Ser Cys Lys Asp Ser Ala Pro Phe Glu Leu
    690                 695                 700
Phe Phe Met Ile Asn Thr Ser Ile Leu Leu Ile Phe Ile Phe Ile Val
705                 710                 715                 720
Leu Leu Ile His Phe Glu Gly Trp Arg Ile Ser Phe Tyr Trp Asn Val
                725                 730                 735
Ser Val His Arg Val Leu Gly Phe Lys Glu Ile Asp Arg Gln Thr Glu
            740                 745                 750
Gln Phe Glu Tyr Ala Ala Tyr Ile Ile His Ala Tyr Lys Asp Lys Asp
        755                 760                 765
Trp Val Trp Glu His Phe Ser Ser Met Glu Lys Glu Asp Gln Ser Leu
    770                 775                 780
Lys Phe Cys Leu Glu Glu Arg Asp Phe Glu Ala Gly Val Phe Glu Leu
785                 790                 795                 800
Glu Ala Ile Val Asn Ser Ile Lys Arg Ser Arg Lys Ile Ile Phe Val
                805                 810                 815
Ile Thr His His Leu Leu Lys Asp Pro Leu Cys Lys Arg Phe Lys Val
            820                 825                 830
His His Ala Val Gln Gln Ala Ile Glu Gln Asn Leu Asp Ser Ile Ile
        835                 840                 845
Leu Val Phe Leu Glu Glu Ile Pro Asp Tyr Lys Leu Asn His Ala Leu
    850                 855                 860
Cys Leu Arg Arg Gly Met Phe Lys Ser His Cys Ile Leu Asn Trp Pro
865                 870                 875                 880
Val Gln Lys Glu Arg Ile Gly Ala Phe Arg His Lys Leu Gln Val Ala
                885                 890                 895
Leu Gly Ser Lys Asn Ser Val His
            900
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<210> 3
<211> 2109
<212> DNA
<213> Homo sapiens

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aagttgactc aggtacccga tgatctaccc acaaacataa cagtgttgaa ccttacccat 180
aatcaactca gaagattacc agccgccaac ttcacaaggt atagccagct aactagcttg 240
gatgtaggat ttaacaccat ctcaaaactg gagccagaat tgtgccagaa acttcccatg 300
ttaaaagttt tgaacctcca gcacaatgag ctatctcaac tttctgataa aacctttgcc 360
ttctgcacga atttgactga actccatctc atgtccaact caatccagaa aattaaaaat 420
aatccctttg tcaagcagaa gaatttaatc acattagatc tgtctcataa tggcttgtca 480
tctacaaaat taggaactca ggttcagctg gaaaatctcc aagagcttct attatcaaac 540
aataaaattc aagcgctaaa aagtgaagaa ctggatatct ttgccaattc atctttaaaa 600
aaattagagt tgtcatcgaa tcaaattaaa gagttttctc cagggtgttt tcacgcaatt 660
ggaagattat ttggcctctt tctgaacaat gtccagctgg gtcccagcct tacagagaag 720
ctatgtttgg aattagcaaa cacaagcatt cggaatctgt ctctgagtaa cagccagctg 780

tccaccacca gcaatacaac tttcttggga ctaaagtgga caaatctcac tatgctcgat 840
ctttcctaca acaacttaaa tgtggttggt aacgattcct ttgcttggct tccacaacta 900
gaatatttct tcctagagta taataatata cagcatttgt tttctcactc tttgcacggg 960
cttttcaatg tgaggtacct gaatttgaaa cggtctttta ctaaacaaag tatttccctt 1020
gcctcactcc ccaagattga tgatttttct tttcagtggc taaaatgttt ggagcacctt 1080
aacatggaag ataatgatat tccaggcata aaaagcaata tgttcacagg attgataaac 1140
ctgaaatact taagtctatc caactccttt acaagtttgc gaactttgac aaatgaaaca 1200
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aaaatagaga gtgatgcttt ctcttggttg ggccacctag aagtacttga cctgggcctt 1320
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attaacgaga cccataccaa catccctgag ctgtcaagcc actacctttg caacactcca 2040
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ccctttgaa 2109

<210> 4
<211> 703
<212> PRT
<213> Homo sapiens

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            20   25   30
Glu Val Ala Asp Cys Ser His Leu Lys Leu Thr Gln Val Pro Asp Asp
        35   40   45
Leu Pro Thr Asn Ile Thr Val Leu Asn Leu Thr His Asn Gln Leu Arg
    50   55   60
Arg Leu Pro Ala Ala Asn Phe Thr Arg Tyr Ser Gln Leu Thr Ser Leu
65   70   75   80
Asp Val Gly Phe Asn Thr Ile Ser Lys Leu Glu Pro Glu Leu Cys Gln
                85   90   95
Lys Leu Pro Met Leu Lys Val Leu Asn Leu Gln His Asn Glu Leu Ser
            100   105   110
Gln Leu Ser Asp Lys Thr Phe Ala Phe Cys Thr Asn Leu Thr Glu Leu
        115   120   125
His Leu Met Ser Asn Ser Ile Gln Lys Ile Lys Asn Asn Pro Phe Val
    130   135   140
Lys Gln Lys Asn Leu Ile Thr Leu Asp Leu Ser His Asn Gly Leu Ser
145   150   155   160
Ser Thr Lys Leu Gly Thr Gln Val Gln Leu Glu Asn Leu Gln Glu Leu
                165   170   175
Leu Leu Ser Asn Asn Lys Ile Gln Ala Leu Lys Ser Glu Glu Leu Asp
            180   185   190

Ile Phe Ala Asn Ser Ser Leu Lys Lys Leu Glu Leu Ser Ser Asn Gln
        195   200   205

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Ile Lys Glu Phe Ser Pro Gly Cys Phe His Ala Ile Gly Arg Leu Phe
    210                 215                 220
Gly Leu Phe Leu Asn Asn Val Gln Leu Gly Pro Ser Leu Thr Glu Lys
225                 230                 235                 240
Leu Cys Leu Glu Leu Ala Asn Thr Ser Ile Arg Asn Leu Ser Leu Ser
                245                 250                 255
Asn Ser Gln Leu Ser Thr Thr Ser Asn Thr Thr Phe Leu Gly Leu Lys
            260                 265                 270
Trp Thr Asn Leu Thr Met Leu Asp Leu Ser Tyr Asn Asn Leu Asn Val
        275                 280                 285
Val Gly Asn Asp Ser Phe Ala Trp Leu Pro Gln Leu Glu Tyr Phe Phe
    290                 295                 300
Leu Glu Tyr Asn Asn Ile Gln His Leu Phe Ser His Ser Leu His Gly
305                 310                 315                 320
Leu Phe Asn Val Arg Tyr Leu Asn Leu Lys Arg Ser Phe Thr Lys Gln
                325                 330                 335
Ser Ile Ser Leu Ala Ser Leu Pro Lys Ile Asp Asp Phe Ser Phe Gln
            340                 345                 350
Trp Leu Lys Cys Leu Glu His Leu Asn Met Glu Asp Asn Asp Ile Pro
        355                 360                 365
Gly Ile Lys Ser Asn Met Phe Thr Gly Leu Ile Asn Leu Lys Tyr Leu
    370                 375                 380
Ser Leu Ser Asn Ser Phe Thr Ser Leu Arg Thr Leu Thr Asn Glu Thr
385                 390                 395                 400
Phe Val Ser Leu Ala His Ser Pro Leu His Ile Leu Asn Leu Thr Lys
                405                 410                 415
Asn Lys Ile Ser Lys Ile Glu Ser Asp Ala Phe Ser Trp Leu Gly His
            420                 425                 430
Leu Glu Val Leu Asp Leu Gly Leu Asn Glu Ile Gly Gln Glu Leu Thr
        435                 440                 445
Gly Gln Glu Trp Arg Gly Leu Glu Asn Ile Phe Glu Ile Tyr Leu Ser
    450                 455                 460
Tyr Asn Lys Tyr Leu Gln Leu Thr Arg Asn Ser Phe Ala Leu Val Pro
465                 470                 475                 480
Ser Leu Gln Arg Leu Met Leu Arg Arg Val Ala Leu Lys Asn Val Asp
                485                 490                 495
Ser Ser Pro Ser Pro Phe Gln Pro Leu Arg Asn Leu Thr Ile Leu Asp
            500                 505                 510
Leu Ser Asn Asn Asn Ile Ala Asn Ile Asn Asp Asp Met Leu Glu Gly
        515                 520                 525
Leu Glu Lys Leu Glu Ile Leu Asp Leu Gln His Asn Asn Leu Ala Arg
    530                 535                 540
Leu Trp Lys His Ala Asn Pro Gly Gly Pro Ile Tyr Phe Leu Lys Gly
545                 550                 555                 560
Leu Ser His Leu His Ile Leu Asn Leu Glu Ser Asn Gly Phe Asp Glu
                565                 570                 575
Ile Pro Val Glu Val Phe Lys Asp Leu Phe Glu Leu Lys Ile Ile Asp
            580                 585                 590
Leu Gly Leu Asn Asn Leu Asn Thr Leu Pro Ala Ser Val Phe Asn Asn
        595                 600                 605
Gln Val Ser Leu Lys Ser Leu Asn Leu Gln Lys Asn Leu Ile Thr Ser
    610                 615                 620
Val Glu Lys Lys Val Phe Gly Pro Ala Phe Arg Asn Leu Thr Glu Leu
625                 630                 635                 640

Asp Met Arg Phe Asn Pro Phe Asp Cys Thr Cys Glu Ser Ile Ala Trp
                645                 650                 655
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Phe Val Asn Trp Ile Asn Glu Thr His Thr Asn Ile Pro Glu Leu Ser
            660                 665                 670
Ser His Tyr Leu Cys Asn Thr Pro Pro His Tyr His Gly Phe Pro Val
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Arg Leu Phe Asp Thr Ser Ser Cys Lys Asp Ser Ala Pro Phe Glu
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<210> 5
<211> 381
<212> DNA
<213> Mus musculus

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atcacatgtc gagcaagtgg gaatattcac aattatttag catggtatca gcagaaacag 180
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agattcagtg gcagtgaatc aggaacacaa tattctctca agatcaacag cctgcagcct 300
gaagattttg ggagttatta ctgtcaacat ttttggagta ctccatttac gttcggctcg 360
gggacaaagt tggaactaaa a 381

<210> 6
<211> 138
<212> PRT
<213> Mus musculus

<400> 6
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Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Gln
            20                  25                  30
Pro Gly Thr Ser Val Arg Leu Ser Cys Lys Ala Ser Gly Tyr Ile Phe
        35                  40                  45
Thr Thr Tyr Trp Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
    50                  55                  60
Glu Trp Ile Gly Glu Ile Asn Pro Asn Asn Gly Arg Ile Asn Tyr Asn
65                  70                  75                  80

Glu Lys Phe Lys Thr Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser
                85                  90                  95
Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
            100                 105                 110
Tyr Tyr Cys Thr Arg Val Gly Val Met Ile Thr Thr Phe Pro Tyr Trp
        115                 120                 125
Gly Gln Gly Thr Leu Val Thr Val Ser Ala
    130                 135
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<210> 7
<211> 19
<212> PRT
<213> Mus musculus

<400> 7
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Met Gly Trp Ser Tyr Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Asp
 1               5                  10                  15
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Val His Ser

<210> 8
<211> 29
<212> PRT
<213> Mus musculus

<400> 8
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Gln Pro Gly Thr
 1   5   10   15
Ser Val Arg Leu Ser Cys Lys Ala Ser Gly Tyr Ile Phe
            20   25

<210> 9
<211> 6
<212> PRT
<213> Mus musculus

<400> 9
Thr Thr Tyr Trp Ile His
 1   5

<210> 10
<211> 14
<212> PRT
<213> Mus musculus

<400> 10
Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly
 1   5   10

<210> 11
<211> 17
<212> PRT
<213> Mus musculus

<400> 11
Glu Ile Asn Pro Asn Asn Gly Arg Ile Asn Tyr Asn Glu Lys Phe Lys
 1   5   10   15
Thr

<210> 12
<211> 32
<212> PRT
<213> Mus musculus

<400> 12

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

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            20                  25                  30


<210> 13
<211> 10
<212> PRT
<213> Mus musculus

<400> 13
Val Gly Val Met Ile Thr Thr Phe Pro Tyr
 1               5                  10


<210> 14
<211> 11
<212> PRT
<213> Mus musculus

<400> 14
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
 1               5                  10


<210> 15
<211> 381
<212> DNA
<213> Mus musculus

<400> 15
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atcacatgtc gagcaagtgg gaatattcac aattatttag catggtatca gcagaaacag 180
ggaaaatctc ctcagctcct ggtctataat gcaaaaacct tagcagatgg tgtgccatca 240
agattcagtg gcagtgaatc aggaacacaa tattctctca agatcaacag cctgcagcct 300
gaagattttg ggagttatta ctgtcaacat ttttggagta ctccatttac gttcggctcg 360
gggacaaagt tggaactaaa a                                           381

<210> 16
<211> 127
<212> PRT
<213> Mus musculus

<400> 16
Met Ser Val Leu Thr Gln Val Leu Ala Leu Leu Leu Leu Trp Leu Thr
 1               5                  10                  15
Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser
            20                  25                  30
Ala Ser Val Gly Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Gly Asn
        35                  40                  45
Ile His Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro
    50                  55                  60
Gln Leu Leu Val Tyr Asn Ala Lys Thr Leu Ala Asp Gly Val Pro Ser
65                  70                  75                  80

Arg Phe Ser Gly Ser Glu Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn
                85                  90                  95
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Ser Leu Gln Pro Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His Phe Trp
100 105 110
Ser Thr Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Leu Lys
115 120 125

<210> 17
<211> 20
<212> PRT
<213> Mus musculus

<400> 17
Met Ser Val Leu Thr Gln Val Leu Ala Leu Leu Leu Leu Trp Leu Thr
1 5 10 15
Gly Ala Arg Cys
20

<210> 18
<211> 23
<212> PRT
<213> Mus musculus

<400> 18
Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Glu Thr Val Thr Ile Thr Cys
20

<210> 19
<211> 11
<212> PRT
<213> Mus musculus

<400> 19
Arg Ala Ser Gly Asn Ile His Asn Tyr Leu Ala
1 5 10

<210> 20
<211> 15
<212> PRT
<213> Mus musculus

<400> 20
Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val Tyr
1 5 10 15

<210> 21
<211> 7
<212> PRT
<213> Mus musculus

<400> 21
Asn Ala Lys Thr Leu Ala Asp

1 5

<210> 22
<211> 32
<212> PRT
<213> Mus musculus

<400> 22
Gly Val Pro Ser Arg Phe Ser Gly Ser Glu Ser Gly Thr Gln Tyr Ser
1 5 10 15
Leu Lys Ile Asn Ser Leu Gln Pro Glu Asp Phe Gly Ser Tyr Tyr Cys
20 25 30

<210> 23
<211> 7
<212> PRT
<213> Mus musculus

<400> 23
Gln His Phe Trp Ser Thr Pro
1 5

<210> 24
<211> 12
<212> PRT
<213> Mus musculus

<400> 24
Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Leu Lys
1 5 10

<210> 25
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Human-adapted heavy chain HV1

<400> 25
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Thr Tyr
20 25 30
Trp Ile His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45
Gly Glu Ile Asn Pro Asn Asn Gly Arg Ile Asn Tyr Asn Glu Lys Phe
50 55 60
Lys Thr Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

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

```
Ala Arg Val Gly Val Met Ile Thr Thr Phe Pro Tyr Trp Gly Gln Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ser
        115
```

<210> 26
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Human-adapted heavy chain HV1

<400> 26
caggtgcagc tggtgcagag cggcgcggaa gtgaaaaaac cgggcgcgag cgtgaaagtg 60
agctgcaaag cgagcggcta tacctttacc acctattgga ttcattgggt gcgccaggcg 120
ccgggccagc gcctggaatg gatgggcgaa attaacccga acaacggccg cattaactat 180
aacgaaaaat ttaaaacccg cgtgaccatt acccgcgata ccagcgcgag caccgcgtat 240
atggaactga gcagcctgcg cagcgaagat accgcggtgt attattgcgc gcgcgtgggc 300
gtgatgatta ccacctttcc gtattggggc cagggcaccc tggtgaccgt gagcagc 357

<210> 27
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Human-adapted heavy chain HV4

<400> 27
```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1               5                  10                  15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Thr Tyr
            20                  25                  30
Trp Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45
Gly Glu Ile Asn Pro Asn Asn Gly Arg Ile Asn Tyr Asn Glu Lys Phe
    50                  55                  60
Lys Thr Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Val Gly Val Met Ile Thr Thr Phe Pro Tyr Trp Gly Gln Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ser
        115
```

<210> 28
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Human-adapted heavy chain HV4

<400> 28
caggtgcagc tggtgcagag cggcgcggaa gtgaaaaaac cgggcgcgag cgtgaaagtg 60
agctgcaaag cgagcggcta tacctttacc acctattgga ttcattgggt gcgccaggcg 120
ccgggccagg gcctggaatg gatgggcgaa attaacccga acaacggccg cattaactat 180
aacgaaaaat ttaaaacccg cgtgaccatg acccgcgata ccagcattag caccgcgtat 240
atggaactga gccgcctgcg cagcgatgat accgcggtgt attattgcgc gcgcgtgggc 300
gtgatgatta ccacctttcc gtattggggc cagggcaccc tggtgaccgt gagcagc 357

<210> 29
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Human-adapted heavy chain HV5

<400> 29
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1   5   10   15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Thr Tyr
            20   25   30
Trp Ile His Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Glu Trp Met
        35   40   45
Gly Glu Ile Asn Pro Asn Asn Gly Arg Ile Asn Tyr Asn Glu Lys Phe
    50   55   60
Lys Thr Arg Val Thr Met Thr Arg Asn Thr Ser Ile Ser Thr Ala Tyr
65   70   75   80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Val Gly Val Met Ile Thr Thr Phe Pro Tyr Trp Gly Gln Gly
            100   105   110
Thr Leu Val Thr Val Ser Ser
        115

<210> 30
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Human-adapted heavy chain HV5

<400> 30
caggtgcagc tggtgcagag cggcgcggaa gtgaaaaaac cgggcgcgag cgtgaaagtg 60
agctgcaaag cgagcggcta tacctttacc acctattgga ttcattgggt gcgccaggcg 120
accggccagg gcctggaatg gatgggcgaa attaacccga acaacggccg cattaactat 180
aacgaaaaat ttaaaacccg cgtgaccatg acccgcaaca ccagcattag caccgcgtat 240
atggaactga gcagcctgcg cagcgaagat accgcggtgt attattgcgc gcgcgtgggc 300
gtgatgatta ccacctttcc gtattggggc cagggcaccc tggtgaccgt gagcagc 357

<210> 31
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Human-adapted heavy chain HV7

<400> 31
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1   5   10   15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Thr Tyr
            20   25   30
Trp Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45
Gly Glu Ile Asn Pro Asn Asn Gly Arg Ile Asn Tyr Asn Glu Lys Phe
    50   55   60
Lys Thr Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65   70   75   80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Val Gly Val Met Ile Thr Thr Phe Pro Tyr Trp Gly Arg Gly
            100   105   110
Thr Leu Val Thr Val Ser Ser
        115

<210> 32
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Human-adapted heavy chain HV7

<400> 32
caggtgcagc tggtgcagag cggcgcggaa gtgaaaaaac cgggcagcag cgtgaaagtg 60
agctgcaaag cgagcggcgg cacctttagc acctattgga ttcattgggt gcgccaggcg 120
ccgggccagg gcctggaatg gatgggcgaa attaacccga acaacggccg cattaactat 180
aacgaaaaat ttaaaacccg cgtgaccatt accgcggatg aaagcaccag caccgcgtat 240
atggaactga gcagcctgcg cagcgaagat accgcggtgt attattgcgc gcgcgtgggc 300
gtgatgatta ccacctttcc gtattggggc cgcggcaccc tggtgaccgt gagcagc   357

<210> 33
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Human-adapted light chain LV1

<400> 33
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 Gly Asn Ile His Asn Tyr
            20   25   30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45
Tyr Asn Ala Lys Thr Leu Ala Asp 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 Phe Ala Thr Tyr Tyr Cys Gln His Phe Trp Ser Thr Pro Phe
                85                  90                  95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105
```

<210> 34
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Human-adapted light chain LV1

<400> 34
gatattcaga tgacccagag cccgagcagc ctgagcgcga gcgtgggcga tcgcgtgacc 60
attacctgcc gcgcgagcgg caacattcat aactatctgg cgtggtatca gcagaaaccg 120
ggcaaagcgc cgaaactgct gatttataac gcgaaaaccc tggcggatgg cgtgccgagc 180
cgctttagcg gcagcggcag cggcaccgat tttaccctga ccattagcag cctgcagccg 240
gaagattttg cgacctatta ttgccagcat ttttggagca ccccgtttac ctttggccag 300
ggcaccaaac tggaaattaa a 321

<210> 35
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Human-adapted light chain LV3

<400> 35
```
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 Gly Asn Ile His Asn Tyr
            20                  25                  30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
        35                  40                  45
Tyr Asn Ala Lys Thr Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Phe Trp Ser Thr Pro Phe
                85                  90                  95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105
```

<210> 36
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Human-adapted light chain LV3

<400> 36

gatattcaga tgacccagag cccgagcagc ctgagcgcga gcgtgggcga tcgcgtgacc 60
attacctgcc gcgcgagcgg caacattcat aactatctgg cgtggtatca gcagaaaccg 120
ggcaaagcgc cgaaacgcct gatttataac gcgaaaaccc tggcggatgg cgtgccgagc 180
cgctttagcg gcagcggcag cggcaccgaa tttaccctga ccattagcag cctgcagccg 240
gaagattttg cgacctatta ttgccagcat ttttggagca ccccgtttac ctttggccag 300
ggcaccaaac tggaaattaa a 321

<210> 37
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Human-adapted light chain LV5

<400> 37
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 Gly Asn Ile His 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 Asn Ala Lys Thr Leu Ala Asp 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 His Phe Trp Ser Thr Pro Phe
85 90 95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 38
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Human-adapted light chain LV5

<400> 38
gatattcaga tgacccagag cccgagcagc ctgagcgcga gcgtgggcga tcgcgtgacc 60
attacctgcc gcgcgagcgg caacattcat aactatctgg cgtggtatca gcagaaaccg 120
ggcaaagtgc cgaaactgct gatttataac gcgaaaaccc tggcggatgg cgtgccgagc 180
cgctttagcg gcagcggcag cggcaccgat tttaccctga ccattagcag cctgcagccg 240
gaagatgtgg cgacctatta ttgccagcat ttttggagca ccccgtttac ctttggcggc 300
ggcaccaaag tggaaattaa a 321

<210> 39
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Human-adapted light chain LV7

<400> 39

```
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 Gly Asn Ile His Asn Tyr
            20                  25                  30
Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile
        35                  40                  45
Tyr Asn Ala Lys Thr Leu Ala Asp 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 Phe Ala Thr Tyr Tyr Cys Gln His Phe Trp Ser Thr Pro Phe
                85                  90                  95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105
```

<210> 40
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Human-adapted light chain LV7

<400> 40

```
gatattcaga tgacccagag cccgagcagc ctgagcgcga gcgtgggcga tcgcgtgacc 60
attacctgcc gcgcgagcgg caacattcat aactatctgg cgtggtttca gcagaaaccg 120
ggcaaagcgc cgaaaagcct gatttataac gcgaaaaccc tggcggatgg cgtgccgagc 180
cgctttagcg gcagcggcag cggcaccgat tttaccctga ccattagcag cctgcagccg 240
gaagattttg cgacctatta ttgccagcat ttttggagca ccccgtttac ctttggccag 300
ggcaccaaac tggaaattaa a                                          321
```

<210> 41
<211> 327
<212> PRT
<213> Artificial Sequence

<220>
<223> Human IgG4 heavy chain constant region variant

<400> 41

```
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
 1               5                  10                  15
Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20                  25                  30
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35                  40                  45
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50                  55                  60
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
65                  70                  75                  80
Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95

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

```
Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
        115                 120                 125
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
    130                 135                 140
Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145                 150                 155                 160
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
                165                 170                 175
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
            180                 185                 190
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
        195                 200                 205
Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
    210                 215                 220
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
225                 230                 235                 240
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
                245                 250                 255
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
            260                 265                 270
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
        275                 280                 285
Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
    290                 295                 300
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
305                 310                 315                 320
Leu Ser Leu Ser Leu Gly Lys
                325
```

<210> 42
<211> 981
<212> DNA
<213> Artificial Sequence

<220>
<223> Human IgG4 heavy chain constant region variant

<400> 42
```
gcgagcacca aaggcccgag cgtgtttccg ctggcgccgt gcagccgcag caccagcgaa 60
agcaccgcgg cgctgggctg cctggtgaaa gattattttc cggaaccggt gaccgtgagc 120
tggaacagcg gcgcgctgac cagcggcgtg cataccttтc cggcggtgct gcagagcagc 180
ggcctgtata gcctgagcag cgtggtgacc gtgccgagca gcagcctggg caccaaaacc 240
tatacctgca acgtggatca taaaccgagc aacaccaaag tggataaacg cgtggaaagc 300
aaatatggcc cgccgtgccc gccgtgcccg gcgccggaag cggcgggcgg cccgagcgtg 360
tttctgtttc cgccgaaacc gaaagatacc ctgatgatta gccgcacccc ggaagtgacc 420
tgcgtggtgg tggatgtgag ccaggaagat ccggaagtgc agtttaactg gtatgtggat 480
ggcgtggaag tgcataacgc gaaaaccaaa ccgcgcgaag aacagtttaa cagcacctat 540
cgcgtggtga gcgtgctgac cgtgctgcat caggattggc tgaacggcaa agaatataaa 600
tgcaaagtga gcaacaaagg cctgccgagc agcattgaaa aaaccattag caaagcgaaa 660
ggccagccgc gcgaaccgca ggtgtatacc ctgccgccga gccaggaaga aatgaccaaa 720
aaccaggtga gcctgacctg cctggtgaaa ggcttttatc cgagcgatat tgcggtggaa 780
tgggaaagca acggccagcc ggaaaacaac tataaaacca ccccgccggt gctggatagc 840
gatggcagct tttttctgta tagccgcctg accgtggata aaagccgctg gcaggaaggc 900
aacgtgttta gctgcagcgt gatgcatgaa gcgctgcata accattatac ccagaaaagc 960
ctgagcctga gcctgggcaa a                                          981
```

<210> 43
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Human k constant region

<400> 43
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
 1   5   10   15
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
            20   25   30
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
        35   40   45
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
    50   55   60
Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65   70   75   80
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
                85   90   95
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
            100   105

<210> 44
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Human k constant region

<400> 44
gcgcgcaccg tggcggcgcc gagcgtgttt atttttccgc cgagcgatga acagctgaaa 60
agcggcaccg cgagcgtggt gtgcctgctg aacaactttt atccgcgcga agcgaaagtg 120
cagtggaaag tggataacgc gctgcagagc ggcaacagcc aggaaagcgt gaccgaacag 180
gatagcaaag atagcaccta tagcctgagc agcaccctga ccctgagcaa agcggattat 240
gaaaaacata aagtgtatgc gtgcgaagtg acccatcagg gcctgagcag cccggtgacc 300
aaaagcttta accgcggcga atgc   324

<210> 45
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Human-adapted heavy chain variant HBV1

<400> 45
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1   5   10   15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Thr Tyr
            20   25   30

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

```
Gly Glu Ile Asn Pro Asn Asn Gly Arg Ile Asn Tyr Asn Glu Lys Phe
    50                  55                  60
Lys Thr Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65                  70                  75                  80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Val Gly Val Met Ile Thr Thr Phe Pro Tyr Trp Gly Gln Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ser
        115
```

<210> 46
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Human-adapted heavy chain variant HBV1

<400> 46
caggtgcagc tggtgcagag cggcgcggaa gtgaaaaaac cgggcgcgag cgtgaaagtg 60
agctgcaaag cgagcggcta taccttacc acctattgga tgcattgggt gcgccaggcg 120
ccgggccagc gcctggaatg gatgggcgaa attaacccga acaacggccg cattaactat 180
aacgaaaaat ttaaaacccg cgtgaccatt acccgcgata ccagcgcgag caccgcgtat 240
atggaactga gcagcctgcg cagcgaagat accgcggtgt attattgcgc gcgcgtgggc 300
gtgatgatta ccacctttcc gtattggggc cagggcaccc tggtgaccgt gagcagc 357

<210> 47
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Human-adapted heavy chain variant HBV2

<400> 47
```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1               5                  10                  15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Thr Tyr
            20                  25                  30
Trp Ile His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
        35                  40                  45

Gly Glu Ile Asn Pro Asn Asn Gly Arg Ile Asn Gly Asn Glu Lys Phe
    50                  55                  60
Lys Thr Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65                  70                  75                  80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Val Gly Val Met Ile Thr Thr Phe Pro Tyr Trp Gly Gln Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ser
        115
```

<210> 48

<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Human-adapted heavy chain variant HBV2

<400> 48
caggtgcagc tggtgcagag cggcgcggaa gtgaaaaaac cgggcgcgag cgtgaaagtg 60
agctgcaaag cgagcggcta tacctttacc acctattgga ttcattgggt gcgccaggcg 120
ccgggccagc gcctggaatg gatgggcgaa attaacccga acaacggccg cattaacggc 180
aacgaaaaat ttaaaacccg cgtgaccatt acccgcgata ccagcgcgag caccgcgtat 240
atggaactga gcagcctgcg cagcgaagat accgcggtgt attattgcgc gcgcgtgggc 300
gtgatgatta ccacctttcc gtattggggc cagggcaccc tggtgaccgt gagcagc 357

<210> 49
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Human-adapted heavy chain variant HBV3

<400> 49
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1   5   10   15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Thr Tyr
            20   25   30
Trp Ile His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
        35   40   45
Gly Glu Ile Asn Pro Asn Asn Gly Arg Ile Asn Tyr Ala Glu Lys Phe
    50   55   60
Lys Thr Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65   70   75   80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Val Gly Val Met Ile Thr Thr Phe Pro Tyr Trp Gly Gln Gly
            100   105   110
Thr Leu Val Thr Val Ser Ser
        115

<210> 50
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Human-adapted heavy chain variant HBV3

<400> 50
caggtgcagc tggtgcagag cggcgcggaa gtgaaaaaac cgggcgcgag cgtgaaagtg 60
agctgcaaag cgagcggcta tacctttacc acctattgga ttcattgggt gcgccaggcg 120
ccgggccagc gcctggaatg gatgggcgaa attaacccga acaacggccg cattaactat 180
gcggaaaaat ttaaaacccg cgtgaccatt acccgcgata ccagcgcgag caccgcgtat 240
atggaactga gcagcctgcg cagcgaagat accgcggtgt attattgcgc gcgcgtgggc 300
gtgatgatta ccacctttcc gtattggggc cagggcaccc tggtgaccgt gagcagc 357

<210> 51
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Human-adapted heavy chain variant HBV4

<400> 51
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1   5   10   15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Thr Tyr
            20   25   30
Trp Ile His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
        35   40   45
Gly Glu Ile Asn Pro Asn Asn Gly Arg Ile Asn Tyr Asn Glu Lys Gly
    50   55   60
Lys Thr Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65   70   75   80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Val Gly Val Met Ile Thr Thr Phe Pro Tyr Trp Gly Gln Gly
            100   105   110
Thr Leu Val Thr Val Ser Ser
        115

<210> 52
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Human-adapted heavy chain variant HBV4

<400> 52
caggtgcagc tggtgcagag cggcgcggaa gtgaaaaaac cgggcgcgag cgtgaaagtg 60
agctgcaaag cgagcggcta tacctttacc acctattgga ttcattgggt gcgccaggcg 120
ccgggccagc gcctggaatg gatgggcgaa attaacccga acaacggccg cattaactat 180
aacgaaaaag gcaaaacccg cgtgaccatt acccgcgata ccagcgcgag caccgcgtat 240
atggaactga gcagcctgcg cagcgaagat accgcggtgt attattgcgc gcgcgtgggc 300
gtgatgatta ccacctttcc gtattggggc cagggcaccc tggtgaccgt gagcagc   357

<210> 53
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Human-adapted heavy chain variant HBV5

<400> 53
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1   5   10   15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Thr Tyr
            20   25   30

```
Trp Ile His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
        35                  40                  45
Gly Glu Ile Asn Pro Asn Asn Gly Arg Ile Asn Tyr Asn Glu Lys Phe
    50                  55                  60
Lys Thr Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65                  70                  75                  80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Val Gly Val Ile Ile Thr Thr Phe Pro Tyr Trp Gly Gln Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ser
        115
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<210> 54
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Human-adapted heavy chain variant HBV5

<400> 54
caggtgcagc tggtgcagag cggcgcggaa gtgaaaaaac cgggcgcgag cgtgaaagtg 60
agctgcaaag cgagcggcta tacctttacc acctattgga ttcattgggt gcgccaggcg 120
ccgggccagc gcctggaatg gatgggcgaa attaacccga acaacggccg cattaactat 180
aacgaaaaat ttaaaacccg cgtgaccatt acccgcgata ccagcgcgag caccgcgtat 240
atggaactga gcagcctgcg cagcgaagat accgcggtgt attattgcgc gcgcgtgggc 300
gtgattatta ccacctttcc gtattggggc cagggcaccc tggtgaccgt gagcagc 357

<210> 55
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Human-adapted light chain variant HBV6

<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 Ala Ser Gly Asn Ile Ser Asn Tyr
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45
Tyr Asn Ala Lys Thr Leu Ala Asp 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 Phe Ala Thr Tyr Tyr Cys Gln His Phe Trp Ser Thr Pro Phe
                85                  90                  95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105
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<210> 56

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

<220>
<223> Human-adapted light chain variant HBV6

<400> 56
gatattcaga tgacccagag cccgagcagc ctgagcgcga gcgtgggcga tcgcgtgacc 60
attacctgcc gcgcgagcgg caacattagc aactatctgg cgtggtatca gcagaaaccg 120
ggcaaagcgc cgaaactgct gatttataac gcgaaaaccc tggcggatgg cgtgccgagc 180
cgctttagcg gcagcggcag cggcaccgat tttaccctga ccattagcag cctgcagccg 240
gaagattttg cgacctatta ttgccagcat ttttggagca ccccgtttac ctttggccag 300
ggcaccaaac tggaaattaa a 321

<210> 57
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Human-adapted light chain variant HBV7

<400> 57
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 Gly Asn Ile Ser Ser Tyr
            20   25   30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45
Tyr Asn Ala Lys Thr Leu Ala Asp 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 Phe Ala Thr Tyr Tyr Cys Gln His Phe Trp Ser Thr Pro Phe
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100   105

<210> 58
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Human-adapted light chain variant HBV7

<400> 58
gatattcaga tgacccagag cccgagcagc ctgagcgcga gcgtgggcga tcgcgtgacc 60
attacctgcc gcgcgagcgg caacattagc agctatctgg cgtggtatca gcagaaaccg 120
ggcaaagcgc cgaaactgct gatttataac gcgaaaaccc tggcggatgg cgtgccgagc 180
cgctttagcg gcagcggcag cggcaccgat tttaccctga ccattagcag cctgcagccg 240
gaagattttg cgacctatta ttgccagcat ttttggagca ccccgtttac ctttggccag 300
ggcaccaaac tggaaattaa a 321

<210> 59

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

<220>
<223> Human-adapted light chain variant HBV8

<400> 59
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 Gly Gly Ile Ser Ser Tyr
            20   25   30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45
Tyr Asn Ala Lys Thr Leu Ala Asp 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 Phe Ala Thr Tyr Tyr Cys Gln His Phe Trp Ser Thr Pro Phe
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100   105

<210> 60
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Human-adapted light chain variant HBV8

<400> 60
gatattcaga tgacccagag cccgagcagc ctgagcgcga gcgtgggcga tcgcgtgacc 60
attacctgcc gcgcgagcgg cggcattagc agctatctgg cgtggtatca gcagaaaccg 120
ggcaaagcgc cgaaactgct gatttataac gcgaaaaccc tggcggatgg cgtgccgagc 180
cgctttagcg gcagcggcag cggcaccgat tttaccctga ccattagcag cctgcagccg 240
gaagattttg cgacctatta ttgccagcat ttttggagca ccccgtttac ctttggccag 300
ggcaccaaac tggaaattaa a   321

<210> 61
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> unsure
<222> (5)
<223> Heavy chain CDR1 wherein Xaa at position 5 can be Isoleucine or
<223> Methionine

<400> 61
Thr Thr Tyr Trp Xaa His
 1   5

<210> 62
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> unsure
<222> (11)
<223> Heavy chain CDR2 wherein Xaa at position 11 can be Tyrosine or
<223> Glycine

<220>
<221> unsure
<222> (12)
<223> Heavy chain CDR2 wherein Xaa at position 12 can be Asparagine or
<223> Alanine

<220>
<221> unsure
<222> (15)
<223> Heavy chain CDR2 wherein Xaa at position 15 can be Phenylalanine or
<223> Glycine

<400> 62
Glu Ile Asn Pro Asn Asn Gly Arg Ile Asn Xaa Xaa Glu Lys Xaa Lys
 1   5   10   15
Thr

<210> 63
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> unsure
<222> (4)
<223> Heavy chain CDR3 wherein Xaa at position 4 can be Methionine or
<223> Isoleucine

<400> 63
Val Gly Val Xaa Ile Thr Thr Phe Pro Tyr
 1   5   10