SEQUENCE LISTING

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<120> ANTI PD-1 ANTIBODIES

<130> CRBI-006/01WO

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<170> PatentIn version 3.5

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<213> Homo sapiens

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gccttccccg aggaccgcag ccagcccggc caggactgcc gcttccgtgt cacacaactg 240

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

Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu
50 55 60

Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg Val Thr Gln Leu
65 70 75 80

Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg Ala Arg Arg Asn
85 90 95

Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala
100 105 110

Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg
115 120 125

Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly
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Gln Phe Gln Thr Leu Val
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gccttccccg aggaccgcag ccagcccggc caggactgcc gcttccgtgt cacacaactg 240

cccaacgggc gtgacttcca catgagcgtg gtcagggccc ggcgcaatga cagcggcacc 300

tacctctgtg gggccatctc cctggccccc aaggcgcaga tcaaagagag cctgcgggca 360

gagctcaggg tgacagagag aagggcagaa gtgcccacag cccaccccag cccctcaccc 420

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gacttctttc ccgaggacat caccgtcgaa tggcagtgga acggccagcc cgccgagaac 960

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<213> Homo sapiens

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            20                  25                  30

Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr
        35                  40                  45

Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu
    50                  55                  60

Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg Val Thr Gln Leu
65                  70                  75                  80

Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg Ala Arg Arg Asn
                85                  90                  95

Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala
            100                 105                 110

Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg
        115                 120                 125

Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly
    130                 135                 140

Gln Phe Gln Thr Leu Val Gly Thr Arg Ser Arg Gly Cys Lys Pro Cys
145                 150                 155                 160

Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys
                165                 170                 175

Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val
            180                 185                 190

Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe
        195                 200                 205

Val Asp Asp Val Glu Val His Thr Ala Gln Thr Gln Pro Arg Glu Glu
    210                 215                 220

Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro Ile Met His
225                 230                 235                 240

Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala
                245                 250                 255
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Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg
260 265 270

Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met
275 280 285

Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asp Phe Phe Pro
290 295 300

Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn
305 310 315 320

Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Val
325 330 335

Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr
340 345 350

Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His His Thr Glu
355 360 365

Lys Ser Leu Ser His Ser Pro Gly Lys
370 375

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<212> DNA
<213> Homo sapiens

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gagagcttcg tgctaaactg gtaccgcatg agccccagca accagacgga caagctggcc 180

gccttccccg aggaccgcag ccagcccggc caggactgcc gcttccgtgt cacacaactg 240

cccaacgggc gtgacttcca catgagcgtg gtcagggccc ggcgcaatga cagcggcacc 300

tacctctgtg gggccatctc cctggccccc aaggcgcaga tcaaagagag cctgcgggca 360

gagctcaggg tgacagagag aagggcagaa gtgcccacag cccaccccag cccctcaccc 420

aggccagccg gccagttcca aaccctggtg ggtaccagat ctagagagcc caaatcttct 480

gacaaaactc acacatgccc accgtgccca gcacctgaat tcgagggtgc accgtcagtc 540

ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggactcc tgaggtcaca 600

tgcgtggtgg tggacgtaag ccacgaagac cctgaggtca agttcaactg gtacgtggac 660

ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac 720

cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 780

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<210> 6
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<213> Homo sapiens

<400> 6

Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr
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Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly Asp Asn Ala Thr Phe
20 25 30

Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr
35 40 45

Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu
50 55 60

Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg Val Thr Gln Leu
65 70 75 80

Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg Ala Arg Arg Asn
85 90 95

Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala
100 105 110

Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg
115 120 125

Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly
130 135 140

Gln Phe Gln Thr Leu Val Gly Thr Arg Ser Arg Glu Pro Lys Ser Ser
145 150 155 160

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly
165 170 175

Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
180 185 190

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
195 200 205

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
210 215 220

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
225 230 235 240

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
245 250 255

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Thr Pro Ile
260 265 270

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
275 280 285

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

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
325 330 335

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
340 345 350

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
355 360 365

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
370 375 380

Pro Gly Lys
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<212> DNA
<213> Cynomolgous sp.

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gccttccccg aggaccgcag ccagcccggc caggactgcc gcttccgtgt cacacaactg 240

cccaacgggc gtgacttcca catgagcgtg gtcagggccc ggcgcaatga cagcggcacc 300

tacctctgtg gggccatctc cctggccccc aaggcgcaga tcaaagagag cctgcgggca 360

gagctcaggg tgacagagag aagggcagaa gtgcccacag cccaccccag cccctcaccc 420

aggccagctg gccagttcca agccggtacc agatctagag gctgcaaacc ctgtatctgc 480

acagtgcccg aggtgagctc cgtgttcatc tttcccccca agcccaagga cgtgctgacc 540

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gtccagttca gctggttcgt ggacgacgtg gaggtgcaca ccgctcagac ccaacccaga 660

gaggagcagt ttaactccac cttcaggtcc gtgtccgagc tccccatcat gcaccaggac 720

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gagaagacca tctccaagac caagggaagg cccaaggccc cccaggtgta caccattccc 840

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<211> 375
<212> PRT
<213> Cynomolgous sp.

<400> 8

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Phe Ser Pro Ala Leu Leu Leu Val Thr Glu Gly Asp Asn Ala Thr Phe
20 25 30

Thr Cys Ser Phe Ser Asn Ala Ser Glu Ser Phe Val Leu Asn Trp Tyr
35 40 45

Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu
50 55 60

Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg Val Thr Gln Leu
65 70 75 80

Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg Ala Arg Arg Asn
85 90 95

Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala
100 105 110

Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg
115 120 125

Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly
130 135 140

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Gln Phe Gln Ala Gly Thr Arg Ser Arg Gly Cys Lys Pro Cys Ile Cys
145                 150                 155                 160

Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys
                165                 170                 175

Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val
            180                 185                 190

Asp Ile Ser Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp
        195                 200                 205

Asp Val Glu Val His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe
    210                 215                 220

Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp
225                 230                 235                 240

Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe
                245                 250                 255

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys
            260                 265                 270

Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys
        275                 280                 285

Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp
    290                 295                 300

Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys
305                 310                 315                 320

Asn Thr Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser
                325                 330                 335

Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr
            340                 345                 350

Cys Ser Val Leu His Glu Gly Leu His Asn His His Thr Glu Lys Ser
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Leu Ser His Ser Pro Gly Lys
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<211> 660
<212> DNA
<213> Homo sapiens

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atggaggata agaacattat tcaatttgtg catggagagg aagacctgaa ggttcagcat 180

agtagctaca gacagagggc ccggctgttg aaggaccagc tctccctggg aaatgctgca 240

cttcagatca cagatgtgaa attgcaggat gcaggggtgt accgctgcat gatcagctat 300

ggtggtgccg actacaagcg aattactgtg aaagtcaatg ccccatacaa caaaatcaac 360

caaagaattt tggttgtgga tccagtcacc tctgaacatg aactgacatg tcaggctgag 420

ggctacccca aggccgaagt catctggaca agcagtgacc atcaagtcct gagtggtaag 480

accaccacca ccaattccaa gagagaggag aagcttttca atgtgaccag cacactgaga 540

atcaacacaa caactaatga gattttctac tgcacttta ggagattaga tcctgaggaa 600

aaccatacag ctgaattggt catcccagaa ctacctctgg cacatcctcc aaatgaaagg 660

<210> 10
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<212> PRT
<213> Homo sapiens

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Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

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Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg
    210                 215                 220
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<210> 11
<211> 681
<212> DNA
<213> Homo sapiens

<400> 11

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atggaggata agaacattat tcaatttgtg catggagagg aagacctgaa ggttcagcat      180

agtagctaca gacagagggc ccggctgttg aaggaccagc tctccctggg aaatgctgca      240

cttcagatca cagatgtgaa attgcaggat gcaggggtgt accgctgcat gatcagctat      300

ggtggtgccg actacaagcg aattactgtg aaagtcaatg ccccatacaa caaaatcaac      360

caaagaattt tggttgtgga tccagtcacc tctgaacatg aactgacatg tcaggctgag      420

ggctacccca aggccgaagt catctggaca agcagtgacc atcaagtcct gagtggtaag      480

accaccacca ccaattccaa gagagaggag aagcttttca atgtgaccag cacactgaga      540

atcaacacaa caactaatga gattttctac tgcactttta ggagattaga tcctgaggaa      600

aaccatacag ctgaattggt catcccagaa ctacctctgg cacatcctcc aaatgaaagg      660

catcatcacc accatcacta a                                                681
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<210> 12
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<212> PRT
<213> Homo sapiens

<400> 12

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            20                  25                  30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
        35                  40                  45
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Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg His His His His
210 215 220

His His
225

<210> 13
<211> 1344
<212> DNA
<213> Homo sapiens

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atggaggata agaacattat tcaatttgtg catggagagg aagacctgaa ggttcagcat 180

agtagctaca gacagagggc ccggctgttg aaggaccagc tctccctggg aaatgctgca 240

cttcagatca cagatgtgaa attgcaggat gcaggggtgt accgctgcat gatcagctat 300

ggtggtgccg actacaagcg aattactgtg aaagtcaatg ccccatacaa caaaatcaac 360

caaagaattt tggttgtgga tccagtcacc tctgaacatg aactgacatg tcaggctgag 420

ggctacccca aggccgaagt catctggaca agcagtgacc atcaagtcct gagtggtaag 480

accaccacca ccaattccaa gagagaggag aagcttttca atgtgaccag cacactgaga 540

atcaacacaa caactaatga gattttctac tgcactttta ggagattaga tcctgaggaa 600

aaccatacag ctgaattggt catcccagaa ctacctctgg cacatcctcc aaatgaaagg 660

ggtaccagat ctagaggctg caaaccctgt atctgcacag tgcccgaggt gagctccgtg 720

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aggtccgtgt ccgagctccc catcatgcac caggactggc tgaatggcaa ggagttcaag 960

tgcagggtga actccgctgc tttccccgcc cccattgaga agaccatctc caagaccaag 1020

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gacaaggtgt ccctgacctg tatgatcacc gacttctttc ccgaggacat caccgtcgaa 1140

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gacggcagct acttcgtgta tagcaagctc aacgtgcaga agagcaactg ggaagccgga 1260

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<210> 14
<211> 447
<212> PRT
<213> Homo sapiens

<400> 14

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Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

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Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
        115                 120                 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
    130                 135                 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145                 150                 155                 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
                165                 170                 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
            180                 185                 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
        195                 200                 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Gly Thr Arg Ser
    210                 215                 220

Arg Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val
225                 230                 235                 240

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

Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu
            260                 265                 270

Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln
        275                 280                 285

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

Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys
305                 310                 315                 320

Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile
                325                 330                 335

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

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

Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn
    370                 375                 380
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Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr
385                 390                 395                 400

Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn
                405                 410                 415

Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu
            420                 425                 430

His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
        435                 440                 445
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<210> 15
<211> 1374
<212> DNA
<213> Homo sapiens

<400> 15

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gaatgcaaat tcccagtaga aaaacaatta gacctggctg cactaattgt ctattgggaa      120
atggaggata agaacattat tcaatttgtg catggagagg aagacctgaa ggttcagcat      180
agtagctaca gacagagggc ccggctgttg aaggaccagc tctccctggg aaatgctgca      240
cttcagatca cagatgtgaa attgcaggat gcaggggtgt accgctgcat gatcagctat      300
ggtggtgccg actacaagcg aattactgtg aaagtcaatg ccccatacaa caaaatcaac      360
caaagaattt tggttgtgga tccagtcacc tctgaacatg aactgacatg tcaggctgag      420
ggctacccca aggccgaagt catctggaca agcagtgacc atcaagtcct gagtggtaag      480
accaccacca ccaattccaa gagagaggag aagcttttca atgtgaccag cacactgaga      540
atcaacacaa caactaatga gattttctac tgcactttta ggagattaga tcctgaggaa      600
aaccatacag ctgaattggt catcccagaa ctacctctgg cacatcctcc aaatgaaagg      660
ggtaccagat ctagagagcc caaatcttct gacaaaactc acacatgccc accgtgccca      720
gcacctgaat tcgagggtgc accgtcagtc ttcctcttcc ccccaaaacc caaggacacc      780
ctcatgatct cccggactcc tgaggtcaca tgcgtggtgg tggacgtaag ccacgaagac      840
cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag      900
ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac      960
caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccaacc     1020
cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc     1080
ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa     1140
ggcttctatc caagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac     1200
tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc     1260
accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag     1320
gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa atga           1374
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<210> 16
<211> 457
<212> PRT
<213> Homo sapiens

<400> 16

Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
1 5 10 15

Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
20 25 30

Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
35 40 45

Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
50 55 60

Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
65 70 75 80

Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
85 90 95

Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val
100 105 110

Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
115 120 125

Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
130 135 140

Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
145 150 155 160

Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
165 170 175

Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
180 185 190

Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
195 200 205

Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Gly Thr Arg Ser
210 215 220

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

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Ala Pro Glu Phe Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys
                245                 250                 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            260                 265                 270

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

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    290                 295                 300

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

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                325                 330                 335

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

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

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    370                 375                 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385                 390                 395                 400

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

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            420                 425                 430

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        435                 440                 445

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455
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<210> 17
<211> 354
<212> DNA
<213> Mus sp.

<400> 17

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tcctgtgcag cctctggatt cactttcagt agttatggca tgtcttggct tcgccagact      120

ccggagaaga ggctggagtg ggtcgcaacc atgagtggtg ggggtcgtga catctactat      180
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ccagacagta tgaaggggcg attcaccatc tccagagaca atgccaagaa caacctgtac 240

ctgcaaatga gcagtctgag gtctgaggac acggccttat attactgtgc aagacaatat 300

tacgacgact ggtttgctta ctggggccaa gggactctgg tcactgtctc tgca 354

<210> 18
<211> 118
<212> PRT
<213> Mus sp.

<400> 18

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

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

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

Ala Thr Met Ser Gly Gly Gly Arg Asp Ile Tyr Tyr Pro Asp Ser Met
50 55 60

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

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

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

Leu Val Thr Val Ser Ala
115

<210> 19
<211> 5
<212> PRT
<213> Mus sp.

<400> 19

Ser Tyr Gly Met Ser
1 5

<210> 20
<211> 17
<212> PRT
<213> Mus sp.

<400> 20

Thr Met Ser Gly Gly Gly Arg Asp Ile Tyr Tyr Pro Asp Ser Met Lys
1 5 10 15

Gly

<210> 21
<211> 9
<212> PRT
<213> Mus sp.

<400> 21

Gln Tyr Tyr Asp Asp Trp Phe Ala Tyr
1 5

<210> 22
<211> 324
<212> DNA
<213> Mus sp.

<400> 22
gatattgtgc tcacacagac tccagccacc ctgtctgtga ctccaggaga tagcgtcagt 60

ctctcctgca gggccagcca aagtattagc aacaacctac actggtatca acaaaaatca 120

catgagtctc caaggcttct catcaagtat gcttcccagt ccatctctgg gatcccctcc 180

aggttcagtg gcagtggatc agggacagac ttcactctca atatcaacag tgtggagacc 240

gaagattttg gaatgtattt ctgtcaacag agtaacagct ggccgctcac gttcggtgct 300

gggaccaagc tggagctgaa acgg 324

<210> 23
<211> 108
<212> PRT
<213> Mus sp.

<400> 23

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

Asp Ser Val Ser Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser Asn Asn
20 25 30

Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu Leu Ile
35 40 45

Lys Tyr Ala Ser Gln Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile Asn Ser Val Glu Thr
65 70 75 80

Glu Asp Phe Gly Met Tyr Phe Cys Gln Gln Ser Asn Ser Trp Pro Leu
85 90 95

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

<210> 24
<211> 11
<212> PRT
<213> Mus sp.

<400> 24

Arg Ala Ser Gln Ser Ile Ser Asn Asn Leu His
1 5 10

<210> 25
<211> 7
<212> PRT
<213> Mus sp.

<400> 25

Tyr Ala Ser Gln Ser Ile Ser
1 5

<210> 26
<211> 9
<212> PRT
<213> Mus sp.

<400> 26

Gln Gln Ser Asn Ser Trp Pro Leu Thr
1 5

<210> 27
<211> 366
<212> DNA
<213> Mus sp.

<400> 27
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acctgcacag tctctggttt ctcattaact acctatggtg tacactgggt tcgccagtct 120

ccaggaaagg gtctggagtg gctgggggtg atatggagtg gtggaagcac agactataat 180

gcggctttca tatccagact gaccatcagc aaggacaatg ccaggagcca agttttcttt 240

aaaatgaaca gtctgcaagt taatgacaca gccatgtatt actgtgccag agagaaaagc 300

gtctatggta attacgtggg ggctatggac tactggggtc aaggaacctc agtcaccgtc 360

tcctca 366

<210> 28
<211> 122
<212> PRT
<213> Mus sp.

<400> 28

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

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

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

Gly Val Ile Trp Ser Gly Gly Ser Thr Asp Tyr Asn Ala Ala Phe Ile
50 55 60

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

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

Arg Glu Lys Ser Val Tyr Gly Asn Tyr Val Gly Ala Met Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Ser Val Thr Val Ser Ser
115 120

<210> 29
<211> 5
<212> PRT
<213> Mus sp.

<400> 29

Thr Tyr Gly Val His
1 5

<210> 30
<211> 16
<212> PRT
<213> Mus sp.

<400> 30

Val Ile Trp Ser Gly Gly Ser Thr Asp Tyr Asn Ala Ala Phe Ile Ser
1 5 10 15

<210> 31
<211> 14
<212> PRT
<213> Mus sp.

<400> 31

Glu Lys Ser Val Tyr Gly Asn Tyr Val Gly Ala Met Asp Tyr
1 5 10

<210> 32
<211> 324
<212> DNA
<213> Mus sp.

<400> 32
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ataacctgca aggccagtca gagtgtgagt gatgatgtag cttggtacca acagaagcca 120

gggcagtctc ctaaactgct gatatactat gcattcaatc gctacactgg agtccctgat 180

cgcttcactg gcagtggata tgggacggat ttcactttca ccatcagcac tgtgcagtct 240

gaagacctgg cagtttattt ctgtcagcag gattatcgct ctccgtggac gttcggtgga 300

ggcaccaagc tggaaatcaa acgg 324

<210> 33
<211> 108
<212> PRT
<213> Mus sp.

<400> 33

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

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Ser Asp Asp
20 25 30

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

Tyr Tyr Ala Phe Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ser
65 70 75 80

Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Arg Ser Pro Trp
85 90 95

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

<210> 34
<211> 11
<212> PRT
<213> Mus sp.

<400> 34

Lys Ala Ser Gln Ser Val Ser Asp Asp Val Ala
1 5 10

<210> 35
<211> 7
<212> PRT
<213> Mus sp.

<400> 35

Tyr Ala Phe Asn Arg Tyr Thr
1 5

<210> 36

<211> 9
<212> PRT
<213> Mus sp.

<400> 36

Gln Gln Asp Tyr Arg Ser Pro Trp Thr
1 5

<210> 37
<211> 9
<212> PRT
<213> Mus sp.

<400> 37

Gln Gln Asp Tyr Arg Ser Pro Trp Thr
1 5

<210> 38
<211> 354
<212> DNA
<213> Mus sp.

<400> 38
gaagtgaagt tggtggagtc gggggggaggc ttagtgaagc ctggagggtc cctgaaactc 60

tcctgtggag cctctggatt cactttcagt agttatggca tgtcttgggt tcgccagact 120

ccggagaaga ggctggagtg ggtcgcaacc attagtggtg gtggtagaga tatttattat 180

ccagacagtg tgaaggggcg actcaccatc tccagagaca atgccaagaa caacctgtac 240

ctgcaaatga gcagtctgag gtctgaggac acggccttgt attactgtgt aagacaatat 300

tacgacgact ggttcgctta ttggggccaa gggactctgg tcactgtctc tgca 354

<210> 39
<211> 118
<212> PRT
<213> Mus sp.

<400> 39

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

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

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

Ala Thr Ile Ser Gly Gly Gly Arg Asp Ile Tyr Tyr Pro Asp Ser Val
50 55 60

Lys Gly Arg Leu Thr Ile Ser Arg Asp Asn Ala Lys Asn Asn Leu Tyr
65 70 75 80

Leu Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Leu Tyr Tyr Cys

85 90 95

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

Leu Val Thr Val Ser Ala
115

<210> 40
<211> 5
<212> PRT
<213> Mus sp.

<400> 40

Ser Tyr Gly Met Ser
1 5

<210> 41
<211> 17
<212> PRT
<213> Mus sp.

<400> 41

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

Gly

<210> 42
<211> 9
<212> PRT
<213> Mus sp.

<400> 42

Gln Tyr Tyr Asp Asp Trp Phe Ala Tyr
1 5

<210> 43
<211> 324
<212> DNA
<213> Mus sp.

<400> 43
gacattgtgc tgacacagtc tccagccacc ctgtctgtga ctccaggaga tagcgtcagt 60

ctttcctgca gggccagcca aagtattagc aacgaccttc actggtatca acaaaaatca 120

catgagtctc caaggcttct catcaagtat gtttcccagt ccatctctgg gatcccctcc 180

aggttcagtg gcagtggatc agggacggat ttcactctca gtatcaacag tgtggagact 240

gaggattttg gaatgtattt ctgtcaacag agtgacagct ggccgctcac gttcggtgct 300

gggaccaagc tggagctgaa acgg 324

<210> 44

<211> 108
<212> PRT
<213> Mus sp.

<400> 44

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

Asp Ser Val Ser Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser Asn Asp
20 25 30

Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu Leu Ile
35 40 45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Ser Val Glu Thr
65 70 75 80

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

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

<210> 45
<211> 11
<212> PRT
<213> Mus sp.

<400> 45

Arg Ala Ser Gln Ser Ile Ser Asn Asp Leu His
1 5 10

<210> 46
<211> 7
<212> PRT
<213> Mus sp.

<400> 46

Tyr Val Ser Gln Ser Ile Ser
1 5

<210> 47
<211> 9
<212> PRT
<213> Mus sp.

<400> 47

Gln Gln Ser Asp Ser Trp Pro Leu Thr
1 5

<210> 48

<211> 360
<212> DNA
<213> Mus sp.

<400> 48
gatgtgcagc ttcaggagtc gggacctggc ctggtgaaac cttctcagtc tctgtccctc 60

acctgcactg tcactggcta ctcaatcacc agtgattatg cctggaactg gatccggcag 120

tttccaggaa accaactgga gtggatggcc tacattagtt acagtggtta cactagctac 180

aacccatctc tcaaaagtcg aatctctatc actcgagaca catccaagaa ccagttcttc 240

ctgcagttga attctgtgac tactgaggac acagccacat attactgtgc aagatctctt 300

gactatgatt acggaactat ggactactgg ggtcaaggaa cctcagtcac cgtctcctca 360

<210> 49
<211> 120
<212> PRT
<213> Mus sp.

<400> 49

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

Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Asp
20 25 30

Tyr Ala Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Gln Leu Glu Trp
35 40 45

Met Ala Tyr Ile Ser Tyr Ser Gly Tyr Thr Ser Tyr Asn Pro Ser Leu
50 55 60

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

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

Ala Arg Ser Leu Asp Tyr Asp Tyr Gly Thr Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Ser Val Thr Val Ser Ser
115 120

<210> 50
<211> 6
<212> PRT
<213> Mus sp.

<400> 50

Ser Asp Tyr Ala Trp Asn
1 5

<210> 51
<211> 16
<212> PRT
<213> Mus sp.

<400> 51

Tyr Ile Ser Tyr Ser Gly Tyr Thr Ser Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

<210> 52
<211> 11
<212> PRT
<213> Mus sp.

<400> 52

Ser Leu Asp Tyr Asp Tyr Gly Thr Met Asp Tyr
1 5 10

<210> 53
<211> 321
<212> DNA
<213> Mus sp.

<400> 53
caaattgttc tctcccagtc tccagcaatc ctgtctgcat ctccagggga gaaggtcaca 60

atgacctgca gggccaactc aagtgtaagt tccatgcact ggtaccagca gaagccagga 120

tcctcccccg aaccctggat ttatgccatt tccaacctgg cttttggagt ccctactcgc 180

ttcagtggca gtgggtctgg gacctcttac tctctcacaa tcagcagagt ggaggctgaa 240

gatgctgcca cttatttctg ccagcagtgg agtagtagac cacccacgtt cggaggggg 300

accaagctgg aaataaaacg g 321

<210> 54
<211> 107
<212> PRT
<213> Mus sp.

<400> 54

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

Glu Lys Val Thr Met Thr Cys Arg Ala Asn Ser Ser Val Ser Ser Met
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Glu Pro Trp Ile Tyr
35 40 45

Ala Ile Ser Asn Leu Ala Phe Gly Val Pro Thr Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Phe Cys Gln Gln Trp Ser Ser Arg Pro Pro Thr
85 90 95

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

<210> 55
<211> 10
<212> PRT
<213> Mus sp.

<400> 55

Arg Ala Asn Ser Ser Val Ser Ser Met His
1 5 10

<210> 56
<211> 7
<212> PRT
<213> Mus sp.

<400> 56

Ala Ile Ser Asn Leu Ala Phe
1 5

<210> 57
<211> 9
<212> PRT
<213> Mus sp.

<400> 57

Gln Gln Trp Ser Ser Arg Pro Pro Thr
1 5

<210> 58
<211> 351
<212> DNA
<213> Mus sp.

<400> 58
gaagtgaagc tggtggagtc tgggggaggc ttagtgaagc ctggagggtc cctgaaactc 60

tcctgtgcag cctctggatt cgctttccgt agctatgaca tgtcttgggt tcgccagact 120

ccggagaaga tcctggagtg ggtcgcaacc attagtggtg gtggtagtta cacctactat 180

caagacagtg tgaagggccg attcaccatc tccagagaca atgccaggaa caccctgtac 240

ctgcaaatga gcagtctgag gtctgaggac acggccttgt attactgtgc aagcccctat 300

ggcccctact ttgactactg gggccaaggc accactctca cagtctcctc a 351

<210> 59
<211> 117
<212> PRT
<213> Mus sp.

<400> 59

Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly

1 5 10 15

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

Asp Met Ser Trp Val Arg Gln Thr Pro Glu Lys Ile Leu Glu Trp Val
35 40 45

Ala Thr Ile Ser Gly Gly Gly Ser Tyr Thr Tyr Tyr Gln Asp Ser Val
50 55 60

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

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

Ala Ser Pro Tyr Gly Pro Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Leu Thr Val Ser Ser
115

<210> 60
<211> 5
<212> PRT
<213> Mus sp.

<400> 60

Ser Tyr Asp Met Ser
1 5

<210> 61
<211> 17
<212> PRT
<213> Mus sp.

<400> 61

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

Gly

<210> 62
<211> 8
<212> PRT
<213> Mus sp.

<400> 62

Pro Tyr Gly Pro Tyr Phe Asp Tyr
1 5

<210> 63
<211> 324
<212> DNA
<213> Mus sp.

<400> 63
gacatccaga tgaaccagtc tccatccagt ctgtctgcat cccttggaga cacgattacc 60

atcacttgcc atgccagtca gagcattaat gtttggttaa gctggtacca gcagaaacca 120

ggaaatattc ctaaactatt gatctatagg gcttccaact tgcacacagg cgtcccatca 180

aggtttagtg gcagtggatc tggaacaggt ttcacattaa ccatcagcag cctgcagcct 240

gacgacattg ccacttacta ctgtcaacag ggtcaaagtt atccgtggac gttcggtgga 300

ggcaccaagc tggaaatcaa acgg 324

<210> 64
<211> 108
<212> PRT
<213> Mus sp.

<400> 64

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

Asp Thr Ile Thr Ile Thr Cys His Ala Ser Gln Ser Ile Asn Val Trp
20 25 30

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

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

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

Asp Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Gly Gln Ser Tyr Pro Trp
85 90 95

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

<210> 65
<211> 11
<212> PRT
<213> Mus sp.

<400> 65

His Ala Ser Gln Ser Ile Asn Val Trp Leu Ser
1 5 10

<210> 66
<211> 6
<212> PRT

<213> Mus sp.

<400> 66

Ala Ser Asn Leu His Thr
1 5

<210> 67
<211> 9
<212> PRT
<213> Mus sp.

<400> 67

Gln Gln Gly Gln Ser Tyr Pro Trp Thr
1 5

<210> 68
<211> 360
<212> DNA
<213> Mus sp.

<400> 68
gatgtgcagc ttcaggagtc gggacctggc ctggtgaaac cttctcagtc tctgtccctc 60

acctgcactg tcactggcta ctcaatcacc agtgattatg cctggaactg gatccggcag 120

tttccaggaa accaactgga gtggatggcc tacattagct acagtggtta cactagctac 180

aacccatctc tcaaaagtcg aatctctatc actcgagaca catccaggaa ccagttcttc 240

ctgcagttga attctgtgac tactgaggac acagccacat attactgtgc aagatctctt 300

gactatgatt acggaactat ggactactgg ggtcaaggaa cctcagtcac cgtctcctca 360

<210> 69
<211> 120
<212> PRT
<213> Mus sp.

<400> 69

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

Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Asp
20 25 30

Tyr Ala Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Gln Leu Glu Trp
35 40 45

Met Ala Tyr Ile Ser Tyr Ser Gly Tyr Thr Ser Tyr Asn Pro Ser Leu
50 55 60

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

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

Ala Arg Ser Leu Asp Tyr Asp Tyr Gly Thr Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Ser Val Thr Val Ser Ser
115 120

<210> 70
<211> 6
<212> PRT
<213> Mus sp.

<400> 70

Ser Asp Tyr Ala Trp Asn
1 5

<210> 71
<211> 16
<212> PRT
<213> Mus sp.

<400> 71

Tyr Ile Ser Tyr Ser Gly Tyr Thr Ser Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

<210> 72
<211> 11
<212> PRT
<213> Mus sp.

<400> 72

Ser Leu Asp Tyr Asp Tyr Gly Thr Met Asp Tyr
1 5 10

<210> 73
<211> 321
<212> DNA
<213> Mus sp.

<400> 73
caaattgttc tctcccagtc tccagcaatc ctgtctgcat ctccagggga gaaggtcaca 60

atgacctgca gggccaactc aagtgtaagt tccatgcact ggtaccaaca gaagccagga 120

tcctcccccg aaccctggat ttatgccatt tccaacctgg cttttggagt ccctgctcgc 180

ttcagtggca gtgggtctgg gacctcttac tctctcacaa tcagcagagt ggaggctgaa 240

gatgctgcca cttatttctg ccagcaatgg aatagtagac cacccacgtt cggaggggg 300

accaagctgg aaataaaacg g 321

<210> 74
<211> 107
<212> PRT
<213> Mus sp.

<400> 74

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

Glu Lys Val Thr Met Thr Cys Arg Ala Asn Ser Ser Val Ser Ser Met
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Glu Pro Trp Ile Tyr
35 40 45

Ala Ile Ser Asn Leu Ala Phe Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Phe Cys Gln Gln Trp Asn Ser Arg Pro Pro Thr
85 90 95

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

<210> 75
<211> 10
<212> PRT
<213> Mus sp.

<400> 75

Arg Ala Asn Ser Ser Val Ser Ser Met His
1 5 10

<210> 76
<211> 7
<212> PRT
<213> Mus sp.

<400> 76

Ala Ile Ser Asn Leu Ala Phe
1 5

<210> 77
<211> 9
<212> PRT
<213> Mus sp.

<400> 77

Gln Gln Trp Asn Ser Arg Pro Pro Thr
1 5

<210> 78
<211> 351
<212> DNA
<213> Mus sp.

<400> 78
gaagtgaaac tggtggagtc tgggggaggc ttagtgaagc ctggagggtc cctgaaactc 60

tcctgttcag cctctggatt cagtttcagt tactatgaca tgtcttgggt tcggcagact 120

ccggagaagg gactggagtg ggtcgcaacc attagtggtg gtggtagaaa tacctatttt 180

atagacagtg tgaaggggcg attcaccatc tccagagaca atgtcaagaa caacctgtat 240

ctgctaatga gcagtctgag gtctgaggat acggccttgt attactgtgc aagcccctat 300

gaggggggctg tggacttctg gggtcaagga acctcagtca ccgtctcctc a 351

<210> 79
<211> 117
<212> PRT
<213> Mus sp.

<400> 79

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

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

Asp Met Ser Trp Val Arg Gln Thr Pro Glu Lys Gly Leu Glu Trp Val
35 40 45

Ala Thr Ile Ser Gly Gly Gly Arg Asn Thr Tyr Phe Ile Asp Ser Val
50 55 60

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

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

Ala Ser Pro Tyr Glu Gly Ala Val Asp Phe Trp Gly Gln Gly Thr Ser
100 105 110

Val Thr Val Ser Ser
115

<210> 80
<211> 5
<212> PRT
<213> Mus sp.

<400> 80

Tyr Tyr Asp Met Ser
1 5

<210> 81
<211> 17
<212> PRT
<213> Mus sp.

<400> 81

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

Gly

<210> 82
<211> 8
<212> PRT
<213> Mus sp.

<400> 82

Pro Tyr Glu Gly Ala Val Asp Phe
1 5

<210> 83
<211> 324
<212> DNA
<213> Mus sp.

<400> 83
gacattgtga tgacccagtc tcacaaagtc atgtccacat cagtaggaga cagggtcagc 60

atcacctgca aggccagtca ggatgtggat aatgctgtag cctggtatca acagaatccc 120

ggacaatctc ctaaactact gattaagtgg gcatccaccc gacaccatgg agtccctgat 180

cgcttcacag gcagtggatc tgggacagat ttcactctca ccattagcac tgtgcaatct 240

gaagacttgg cagatttttt ctgtcagcaa tatagcacct ttccgtacac gttcggaggg 300

gggaccaagc tggaaataaa acgg 324

<210> 84
<211> 108
<212> PRT
<213> Mus sp.

<400> 84

Asp Ile Val Met Thr Gln Ser His Lys Val Met Ser Thr Ser Val Gly
1 5 10 15

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

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

Lys Trp Ala Ser Thr Arg His His Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

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

Glu Asp Leu Ala Asp Phe Phe Cys Gln Gln Tyr Ser Thr Phe Pro Tyr
85 90 95

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

<210> 85
<211> 11
<212> PRT
<213> Mus sp.

<400> 85

Lys Ala Ser Gln Asp Val Asp Asn Ala Val Ala
1 5 10

<210> 86
<211> 7
<212> PRT
<213> Mus sp.

<400> 86

Trp Ala Ser Thr Arg His His
1 5

<210> 87
<211> 9
<212> PRT
<213> Mus sp.

<400> 87

Gln Gln Tyr Ser Thr Phe Pro Tyr Thr
1 5

<210> 88
<211> 354
<212> DNA
<213> Mus sp.

<400> 88
gaagtgaagt tggtggagtc tgggggaggc ttagtgaagc ctggagggtc cctgaaactc 60

tcctgtgcag cctctggatt cactttcagt agctatggca tgtcttgggt tcgccagact 120

ccggagaaga ggctggagtg ggtcgcaacc attagtggtg gtggtcgtga cacctactat 180

ctagacagtg tgaaggggcg attcaccatc tccagagaca atgccaagaa caacctgtat 240

ttgcaaatga gcagtctgag gtctgaggac acggccttgt attactgtgt gagacagtat 300

tacgacgact ggtttgctta ctggggccaa gggactctgg tctctaactc tgca 354

<210> 89
<211> 118
<212> PRT
<213> Mus sp.

<400> 89

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

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


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


Ala Thr Ile Ser Gly Gly Gly Arg Asp Thr Tyr Tyr Leu Asp Ser Val
    50                  55                  60


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


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


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


Leu Val Ser Asn Ser Ala
        115


<210>  90
<211>  5
<212>  PRT
<213>  Mus sp.

<400>  90

Ser Tyr Gly Met Ser
1               5


<210>  91
<211>  17
<212>  PRT
<213>  Mus sp.

<400>  91

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


Gly



<210>  92
<211>  9
<212>  PRT
<213>  Mus sp.

<400>  92

Gln Tyr Tyr Asp Asp Trp Phe Ala Tyr
1               5


<210>  93
<211>  321
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<212> DNA
<213> Mus sp.

<400> 93
gatattgtgc tcacccagac tccagccacc ctttctgtga ctccaggaga tagtgtcagt 60

ctttcctgca gggccagcca aagtcttagc aacaacctac actggtatca acaaaaatca 120

catgagtctc caaggcttct catcaagtat gcttcccagt ccatctctgg gatcccctcc 180

aggttcagtg gcagtggatc agggacagat ttcactctca gtatcaacag tgtggagact 240

gaagattttg gaatgtattt ctgtcaacag agtaacagct ggccgctcac gttcggtgct 300

gggaccaagc tggagatgaa a 321

<210> 94
<211> 108
<212> PRT
<213> Mus sp.

<400> 94

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

Asp Ser Val Ser Leu Ser Cys Arg Ala Ser Gln Ser Leu Ser Asn Asn
20 25 30

Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu Leu Ile
35 40 45

Lys Tyr Ala Ser Gln Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Ser Val Glu Thr
65 70 75 80

Glu Asp Phe Gly Met Tyr Phe Cys Gln Gln Ser Asn Ser Trp Pro Leu
85 90 95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Met Lys Arg
100 105

<210> 95
<211> 11
<212> PRT
<213> Mus sp.

<400> 95

Arg Ala Ser Gln Ser Leu Ser Asn Asn Leu His
1 5 10

<210> 96
<211> 7
<212> PRT
<213> Mus sp.

<400> 96

Tyr Ala Ser Gln Ser Ile Ser
1 5

<210> 97
<211> 9
<212> PRT
<213> Mus sp.

<400> 97

Gln Gln Ser Asn Ser Trp Pro Leu Thr
1 5

<210> 98
<211> 360
<212> DNA
<213> Mus sp.

<400> 98
caggtccagc tgcagcagtc tggagatgag ctggtaaggc ctgggacttc agtgaagatg 60

tcctgcaagg ctgctggata caccttcact aacaactgga taggttgggt aaagcagagg 120

cctggacatg gccttgagtg gattggagat ttctaccctg gaggtggtta tactaactac 180

aatgagaagt tcaagggcaa ggccacactg actgcagaca catcctccag cacagcctac 240

atgcagctca gcagcctgac atctgaggac tctgccatct attactgtgc aagaggctac 300

ggtactaact actggtactt cgatgtctgg ggcgcaggga ccacggtcac cgtctcctca 360

<210> 99
<211> 120
<212> PRT
<213> Mus sp.

<400> 99

Gln Val Gln Leu Gln Gln Ser Gly Asp Glu Leu Val Arg Pro Gly Thr
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ala Gly Tyr Thr Phe Thr Asn Asn
20 25 30

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

Gly Asp Phe Tyr Pro Gly Gly Gly Tyr Thr Asn Tyr Asn Glu Lys Phe
50 55 60

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

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr Cys
85 90 95

Ala Arg Gly Tyr Gly Thr Asn Tyr Trp Tyr Phe Asp Val Trp Gly Ala

100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 100
<211> 5
<212> PRT
<213> Mus sp.

<400> 100

Asn Asn Trp Ile Gly
1 5

<210> 101
<211> 17
<212> PRT
<213> Mus sp.

<400> 101

Asp Phe Tyr Pro Gly Gly Gly Tyr Thr Asn Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 102
<211> 11
<212> PRT
<213> Mus sp.

<400> 102

Gly Tyr Gly Thr Asn Tyr Trp Tyr Phe Asp Val
1 5 10

<210> 103
<211> 324
<212> DNA
<213> Mus sp.

<400> 103
aatattgtga tgacccagac tcccaaaatc ctgtttatat cagcaggaga cagggttacc 60

ataacctgca aggccagtca gagtgtgagt aatgatgtag cttggtacca acagaagcca 120

gggcagtctc ctaaactgct gatatactat gcattcactc gctacattgg agtccctgat 180

cgcttcactg gcagtggata tgggacggat ttcactttca ccatcagcac tgtgcaggct 240

gaagacctgg cagtttattt ctgtcagcag gattatagct ctccttacac gttcggaggg 300

gggaccaagc tggaaataaa acgg 324

<210> 104
<211> 108
<212> PRT
<213> Mus sp.

<400> 104

Asn Ile Val Met Thr Gln Thr Pro Lys Ile Leu Phe Ile Ser Ala Gly
1 5 10 15

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

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

Tyr Tyr Ala Phe Thr Arg Tyr Ile Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala
65 70 75 80

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

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

<210> 105
<211> 11
<212> PRT
<213> Mus sp.

<400> 105

Lys Ala Ser Gln Ser Val Ser Asn Asp Val Ala
1 5 10

<210> 106
<211> 7
<212> PRT
<213> Mus sp.

<400> 106

Tyr Ala Phe Thr Arg Tyr Ile
1 5

<210> 107
<211> 9
<212> PRT
<213> Mus sp.

<400> 107

Gln Gln Asp Tyr Ser Ser Pro Tyr Thr
1 5

<210> 108
<211> 342
<212> DNA
<213> Mus sp.

<400> 108
cagatccact tggtgcagtc tggacctgaa ctgaagaagc ctggagagac agtcaagatc 60

tcctgcaagg cttctggata taccttcaca aactttggaa tgaactgggt gaagcaggct 120

ccaggaaagg gtttaaagtg gatgggctgg ataagtggct acactaggga gccaacatat 180

gctgctgact tcaagggacg atttgccatc tctttggaaa cctctgccag cactgcctat 240

ttgcagatca acgacctcaa aaatgaagac atggctacat atttctgtgc aagagacgtt 300

tttgactact ggggccaagg caccactctc acagtctcct ca 342

<210> 109
<211> 114
<212> PRT
<213> Mus sp.

<400> 109

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

Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Phe
20 25 30

Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
35 40 45

Gly Trp Ile Ser Gly Tyr Thr Arg Glu Pro Thr Tyr Ala Ala Asp Phe
50 55 60

Lys Gly Arg Phe Ala Ile Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Leu Gln Ile Asn Asp Leu Lys Asn Glu Asp Met Ala Thr Tyr Phe Cys
85 90 95

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

Ser Ser

<210> 110
<211> 5
<212> PRT
<213> Mus sp.

<400> 110

Asn Phe Gly Met Asn
1 5

<210> 111
<211> 17
<212> PRT
<213> Mus sp.

<400> 111

Trp Ile Ser Gly Tyr Thr Arg Glu Pro Thr Tyr Ala Ala Asp Phe Lys
1 5 10 15

Gly

<210> 112
<211> 5
<212> PRT
<213> Mus sp.

<400> 112

Asp Val Phe Asp Tyr
1 5

<210> 113
<211> 333
<212> DNA
<213> Mus sp.

<400> 113
gacattgtgc tgacccaatc tccagcttct ttggctgtgt ctctagggca gagggccacc 60

atttcctgca gagccagtga aagtgttgat aattatggct atagttttat gaactggttc 120

cagcagaaac caggacagcc acccaaactc ctcatctatc gtgcatccaa cctagaatct 180

gggatccctg ccaggttcag tggcagtggg tctaggacaa acttcaccct caccattaat 240

cctgtggagg ctgatgatgt tgcaacctat ttctgtcagc aaagtaatgc ggatccgacg 300

ttcggtggag gcaccaacct ggaaatcaaa cgg 333

<210> 114
<211> 111
<212> PRT
<213> Mus sp.

<400> 114

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

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

Gly Tyr Ser Phe Met Asn Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

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

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

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

Ala Asp Pro Thr Phe Gly Gly Gly Thr Asn Leu Glu Ile Lys Arg
100 105 110

<210> 115
<211> 15
<212> PRT
<213> Mus sp.

<400> 115

Arg Ala Ser Glu Ser Val Asp Asn Tyr Gly Tyr Ser Phe Met Asn
1 5 10 15

<210> 116
<211> 7
<212> PRT
<213> Mus sp.

<400> 116

Arg Ala Ser Asn Leu Glu Ser
1 5

<210> 117
<211> 8
<212> PRT
<213> Mus sp.

<400> 117

Gln Gln Ser Asn Ala Asp Pro Thr
1 5

<210> 118
<211> 1335
<212> DNA
<213> Artificial Sequence

<220>
<223> 7A4-IgG1 D265A chimeric antibody heavy chain full length DNA sequence

<400> 118
cagatccact tggtgcagtc tggacctgaa ctgaagaagc ctggagagac agtcaagatc 60

tcctgcaagg cttctggata taccttcaca aactttggaa tgaactgggt gaagcaggct 120

ccaggaaagg gtttaaagtg gatgggctgg ataagtggct acactaggga gccaacatat 180

gctgctgact tcaagggacg atttgccatc tctttggaaa cctctgccag cactgcctat 240

ttgcagatca acgacctcaa aaatgaagac atggctacat atttctgtgc aagagacgtt 300

tttgactact ggggccaagg caccactctc acagtctcga gcgcctccac taagggccca 360

tccgtgttcc ctctggcacc ctccagcaag agcacaagcg gaggcaccgc cgcactgggc 420

tgcctcgtga aggactactt cccagaaccc gtgaccgtca gctggaatag cggcgctctg 480

accagcggag tccacacttt ccccgcagtg ctgcagtcca gcggcctgta cagcctgagc 540

agcgtggtca ctgtgccaag cagcagcctg ggcactcaga cctacatctg caacgtcaac 600

cacaagccca gcaacacaaa ggtggacaag aaggtcgagc ccaagtcctg cgataagacc 660

cacacctgcc ctccatgtcc cgcccccgag ctgctgggag gacccagcgt cttcctgttt 720

cccccccaagc caaaggacac cctgatgatc agcaggaccc ccgaagtgac ctgcgtcgtg 780

gtggccgtga gccacgaaga tcccgaggtg aagttcaact ggtacgtgga cggcgtggaa 840

gtgcacaacg ccaagacaaa acccagggag gagcagtatg ccagcaccta cagggtcgtg 900

agcgtcctga ccgtgctgca ccaagactgg ctgaacggca aggagtataa gtgcaaggtg 960

agcaacaagg cactgcccgc ccccatcgag aagaccattt ccaaggccaa ggggcaacct 1020

agggagccac aggtctacac tctgcccccct agcagggacg agctgaccaa gaaccaggtc 1080

tccctgactt gcctggtgaa ggggttttat cccagcgaca tcgccgtcga gtgggagagc 1140

aatggccagc ccgaaaacaa ctacaagacc acacccccctg tgctggacag cgacggcagc 1200

ttctttctgt atagcaaact gacagtggat aagagcagat ggcagcaggg caacgtgttc 1260

tcctgctccg tgatgcacga ggccctgcac aatcactaca cccagaagtc cctgagcctg 1320

tcccccggaa aatga 1335

<210> 119
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> 7A4-IgG1 D265A chimeric antibody heavy chain full length protein sequence

<400> 119

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

Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Phe
20 25 30

Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
35 40 45

Gly Trp Ile Ser Gly Tyr Thr Arg Glu Pro Thr Tyr Ala Ala Asp Phe
50 55 60

Lys Gly Arg Phe Ala Ile Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Leu Gln Ile Asn Asp Leu Lys Asn Glu Asp Met Ala Thr Tyr Phe Cys
85 90 95

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

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

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
    130                 135                 140

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
145                 150                 155                 160

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

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

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

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

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

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

Thr Cys Val Val Val Ala Val Ser His Glu Asp Pro Glu Val Lys Phe
            260                 265                 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
        275                 280                 285

Arg Glu Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr
    290                 295                 300

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

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
                325                 330                 335

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
        355                 360                 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
    370                 375                 380
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Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
385                 390                 395                 400


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


Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
            420                 425                 430


Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440


<210>  120
<211>  1323
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  7A4-IgG4 F234A L235A chimeric antibody heavy chain full length
       DNA sequence

<400>  120
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tcctgcaagg cttctggata taccttcaca aactttggaa tgaactgggt gaagcaggct      120

ccaggaaagg gtttaaagtg gatgggctgg ataagtggct acactaggga gccaacatat      180

gctgctgact tcaagggacg atttgccatc tctttggaaa cctctgccag cactgcctat      240

ttgcagatca acgacctcaa aaatgaagac atggctacat atttctgtgc aagagacgtt      300

tttgactact ggggccaagg caccactctc acagtctcga gcgcctccac caagggaccc      360

agcgtgtttc ccctggcccc ctgttccaga tccacctccg aaagcacagc cgctctcggc      420

tgcctggtca aggattactt ccctgagccc gtgacagtct cctggaatag cggcgctctg      480

acctccggcg tgcatacctt ccctgctgtg ctgcaatcct ccggactgta cagcctgagc      540

agcgtggtca ccgtgccttc ctccagcctg ggaaccaaaa cctacacatg caacgtggac      600

cacaagccca gcaacaccaa agtggacaag agggtggagt ccaagtacgg acccccttgt      660

cctccctgcc ctgctcctga agccgctgga ggacctagcg tgttcctgtt tccccccaag      720

cccaaggaca ccctcatgat ctccaggacc cccgaggtga cctgtgtcgt ggtggacgtg      780

agccaagagg accccgaggt gcagttcaac tggtacgtgg atggcgtcga ggtccataac      840

gccaagacca agcctaggga ggagcagttc aacagcacct acagagtggt gagcgtcctg      900

accgtgctcc accaagactg gctgaacggc aaggaataca agtgcaaggt ctccaacaag      960

ggactccctt cctccatcga gaagaccatc agcaaggcca agggccagcc cagagaaccc     1020

caagtctaca cactgccccc cagccaagag gaaatgacca agaaccaggt gagcctgacc     1080

tgcctggtga aaggcttcta ccccagcgac attgctgtcg aatgggagag caacggccaa     1140

cccgagaaca actacaagac cacccccccct gtgctcgaca gcgacggctc cttcttcctc     1200

tacagcaggc tgacagtgga caagtccagg tggcaagagg gcaatgtctt cagctgtagc     1260
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gtcatgcacg aggccctcca caaccactac acccagaaga gcctgtccct ctccctgggc 1320

tga 1323

<210> 121
<211> 440
<212> PRT
<213> Artificial Sequence

<220>
<223> 7A4-IgG4 F234A L235A chimeric antibody heavy chain full length protein sequence

<400> 121

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

Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Phe
20 25 30

Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
35 40 45

Gly Trp Ile Ser Gly Tyr Thr Arg Glu Pro Thr Tyr Ala Ala Asp Phe
50 55 60

Lys Gly Arg Phe Ala Ile Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Leu Gln Ile Asn Asp Leu Lys Asn Glu Asp Met Ala Thr Tyr Phe Cys
85 90 95

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

Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys
115 120 125

Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys
130 135 140

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
145 150 155 160

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

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

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

```
Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro
    210                 215                 220

Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
225                 230                 235                 240

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

Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
            260                 265                 270

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
        275                 280                 285

Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
    290                 295                 300

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

Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
                325                 330                 335

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met
            340                 345                 350

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
        355                 360                 365

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
    370                 375                 380

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
385                 390                 395                 400

Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val
                405                 410                 415

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
            420                 425                 430

Lys Ser Leu Ser Leu Ser Leu Gly
        435                 440
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<210> 122
<211> 654
<212> DNA
<213> Artificial Sequence

<220>
<223> 7A4 chimeric antibody light chain full length DNA sequence

<400> 122
gacattgtgc tgacccaatc tccagcttct ttggctgtgt ctctagggca gagggccacc 60

atttcctgca gagccagtga aagtgttgat aattatggct atagttttat gaactggttc 120

cagcagaaac caggacagcc acccaaactc ctcatctatc gtgcatccaa cctagaatct 180

gggatccctg ccaggttcag tggcagtggg tctaggacaa acttcaccct caccattaat 240

cctgtggagg ctgatgatgt tgcaacctat ttctgtcagc aaagtaatgc ggatccgacg 300

ttcggtggag gcaccaacct ggaaatcaaa cgtacggtgg ccgcaccaag cgtcttcatc 360

ttcccgccat ctgatgagca gttgaaatct ggaactgcct ctgttgtgtg cctgctgaat 420

aacttctatc ccagagaggc caaagtacag tggaaggtgg ataacgccct ccaatcgggt 480

aactcccagg agagtgtcac agagcaggac agcaaggaca gcacctacag cctcagcagc 540

accctgacgc tgagcaaagc agactacgag aaacacaaag tctacgcctg cgaagtcacc 600

catcagggcc tgagctcgcc cgtcacaaag agctttaaca gaggcgagtg ctga 654

<210> 123
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> 7A4 chimeric antibody light chain full length protein sequence

<400> 123

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

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

Gly Tyr Ser Phe Met Asn Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

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

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

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

Ala Asp Pro Thr Phe Gly Gly Gly Thr Asn Leu Glu Ile Lys Arg Thr
100 105 110

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

Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro

130 135 140

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

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

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

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

Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 124
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> 13F1-IgG1 D265A chimeric antibody heavy chain full length DNA sequence

<400> 124
gatgtgcagc ttcaggagtc gggacctggc ctggtgaaac cttctcagtc tctgtccctc 60

acctgcactg tcactggcta ctcaatcacc agtgattatg cctggaactg gatccggcag 120

tttccaggaa accaactgga gtggatggcc tacattagtt acagtggtta cactagctac 180

aacccatctc tcaaaagtcg aatctctatc actcgagaca catccaagaa ccagttcttc 240

ctgcagttga attctgtgac tactgaggac acagccacat attactgtgc aagatctctt 300

gactatgatt acggaactat ggactactgg ggtcaaggaa cctcagtcac cgtctcgagc 360

gcctccacta agggcccatc cgtgttccct ctggcaccct ccagcaagag cacaagcgga 420

ggcaccgccg cactgggctg cctcgtgaag gactacttcc cagaacccgt gaccgtcagc 480

tggaatagcg gcgctctgac cagcggagtc cacactttcc ccgcagtgct gcagtccagc 540

ggcctgtaca gcctgagcag cgtggtcact gtgccaagca gcagcctggg cactcagacc 600

tacatctgca acgtcaacca caagcccagc aacacaaagg tggacaagaa ggtcgagccc 660

aagtcctgcg ataagaccca cacctgccct ccatgtcccg cccccgagct gctgggagga 720

cccagcgtct tcctgtttcc ccccaagcca aaggacaccc tgatgatcag caggaccccc 780

gaagtgacct gcgtcgtggt ggccgtgagc cacgaagatc ccgaggtgaa gttcaactgg 840

tacgtggacg gcgtggaagt gcacaacgcc aagacaaaac ccagggagga gcagtatgcc 900

agcacctaca gggtcgtgag cgtcctgacc gtgctgcacc aagactggct gaacggcaag 960

gagtataagt gcaaggtgag caacaaggca ctgcccgccc ccatcgagaa gaccatttcc 1020

aaggccaagg ggcaacctag ggagccacag gtctacactc tgccccctag cagggacgag 1080

ctgaccaaga accaggtctc cctgacttgc ctggtgaagg ggttttatcc cagcgacatc 1140

gccgtcgagt gggagagcaa tggccagccc gaaaacaact acaagaccac acccccctgtg 1200

ctggacagcg acggcagctt ctttctgtat agcaaactga cagtggataa gagcagatgg 1260

cagcagggca acgtgttctc ctgctccgtg atgcacgagg ccctgcacaa tcactacacc 1320

cagaagtccc tgagcctgtc ccccggaaaa tga 1353

<210> 125
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> 13F1-IgG1 D265A chimeric antibody heavy chain full length protein sequence

<400> 125

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

Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Asp
20 25 30

Tyr Ala Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Gln Leu Glu Trp
35 40 45

Met Ala Tyr Ile Ser Tyr Ser Gly Tyr Thr Ser Tyr Asn Pro Ser Leu
50 55 60

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

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

Ala Arg Ser Leu Asp Tyr Asp Tyr Gly Thr Met Asp Tyr Trp Gly Gln
100 105 110

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

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

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

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

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

180 185 190

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

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

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

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Ala Val Ser His Glu
260 265 270

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

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

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

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

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

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

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

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

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

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

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

Gly Lys

450

<210> 126
<211> 1341
<212> DNA
<213> Artificial Sequence

<220>
<223> 13F1-IgG4 F234A L235A chimeric antibody heavy chain full length DNA sequence

<400> 126
gatgtgcagc ttcaggagtc gggacctggc ctggtgaaac cttctcagtc tctgtccctc 60

acctgcactg tcactggcta ctcaatcacc agtgattatg cctggaactg gatccggcag 120

tttccaggaa accaactgga gtggatggcc tacattagtt acagtggtta cactagctac 180

aacccatctc tcaaaagtcg aatctctatc actcgagaca catccaagaa ccagttcttc 240

ctgcagttga attctgtgac tactgaggac acagccacat attactgtgc aagatctctt 300

gactatgatt acggaactat ggactactgg ggtcaaggaa cctcagtcac cgtctcgagc 360

gcctccacca agggacccag cgtgtttccc ctggcccccc gttccagatc cacctccgaa 420

agcacagccg ctctcggctg cctggtcaag gattacttcc ctgagcccgt gacagtctcc 480

tggaatagcg gcgctctgac ctccggcgtg cataccttcc ctgctgtgct gcaatcctcc 540

ggactgtaca gcctgagcag cgtggtcacc gtgccttcct ccagcctggg aaccaaaacc 600

tacacatgca acgtggacca caagcccagc aacaccaaag tggacaagag ggtggagtcc 660

aagtacggac ccccttgtcc tccctgccct gctcctgaag ccgctggagg acctagcgtg 720

ttcctgtttc cccccaagcc caaggacacc ctcatgatct ccaggacccc cgaggtgacc 780

tgtgtcgtgg tggacgtgag ccaagaggac cccgaggtgc agttcaactg gtacgtggat 840

ggcgtcgagg tccataacgc caagaccaag cctagggagg agcagttcaa cagcacctac 900

agagtggtga gcgtcctgac cgtgctccac caagactggc tgaacggcaa ggaatacaag 960

tgcaaggtct ccaacaaggg actcccttcc tccatcgaga agaccatcag caaggccaag 1020

ggccagccca gagaacccca agtctacaca ctgccccccа gccaagagga aatgaccaag 1080

aaccaggtga gcctgacctg cctggtgaaa ggcttctacc ccagcgacat tgctgtcgaa 1140

tgggagagca acggccaacc cgagaacaac tacaagacca ccccccctgt gctcgacagc 1200

gacggctcct tcttcctcta cagcaggctg acagtggaca agtccaggtg gcaagagggc 1260

aatgtcttca gctgtagcgt catgcacgag gccctccaca accactacac ccagaagagc 1320

ctgtccctct ccctgggctg a 1341

<210> 127
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> 13F1-IgG4 F234A L235A chimeric antibody heavy chain full length protein sequence

<400> 127

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

Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Asp
            20                  25                  30

Tyr Ala Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Gln Leu Glu Trp
        35                  40                  45

Met Ala Tyr Ile Ser Tyr Ser Gly Tyr Thr Ser Tyr Asn Pro Ser Leu
    50                  55                  60

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

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

Ala Arg Ser Leu Asp Tyr Asp Tyr Gly Thr Met Asp Tyr Trp Gly Gln
            100                 105                 110

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

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

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

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

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

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

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

Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225                 230                 235                 240

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

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

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

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

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

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

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

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

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

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

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

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

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
435 440 445

<210> 128
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> 13F1 chimeric antibody light chain full length DNA sequence

<400> 128
caaattgttc tctcccagtc tccagcaatc ctgtctgcat ctccagggga gaaggtcaca 60

atgacctgca gggccaactc aagtgtaagt tccatgcact ggtaccagca gaagccagga 120

tcctcccccg aaccctggat ttatgccatt tccaacctgg cttttggagt ccctactcgc 180

ttcagtggca gtgggtctgg gacctcttac tctctcacaa tcagcagagt ggaggctgaa 240

gatgctgcca cttatttctg ccagcagtgg agtagtagac cacccacgtt cggaggggg 300

accaagctgg aaataaaacg tacggtggcc gcaccaagcg tcttcatctt cccgccatct 360

gatgagcagt tgaaatctgg aactgcctct gttgtgtgcc tgctgaataa cttctatccc 420

agagaggcca aagtacagtg gaaggtggat aacgccctcc aatcgggtaa ctcccaggag 480

agtgtcacag agcaggacag caaggacagc acctacagcc tcagcagcac cctgacgctg 540

agcaaagcag actacgagaa acacaaagtc tacgcctgcg aagtcaccca tcagggcctg 600

agctcgcccg tcacaaagag ctttaacaga ggcgagtgct ga 642

<210> 129
<211> 213
<212> PRT
<213> Artificial Sequence

<220>
<223> 13F1 chimeric antibody light chain full length protein sequence

<400> 129

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

Glu Lys Val Thr Met Thr Cys Arg Ala Asn Ser Ser Val Ser Ser Met
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Glu Pro Trp Ile Tyr
35 40 45

Ala Ile Ser Asn Leu Ala Phe Gly Val Pro Thr Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Phe Cys Gln Gln Trp Ser Ser Arg Pro Pro Thr
85 90 95

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

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

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

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

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

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

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

Asn Arg Gly Glu Cys
210

<210> 130
<211> 342
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized 7A4 antibody heavy chain variable region DNA sequence

<400> 130
cagatccagc tggtgcagag cgggagcgaa ctgaaaaaac ctggggcaag cgtgaaagtc 60

tcatgtaaag caagcggcta cacatttacc aacttcggca tgaattgggt caggcaggca 120

ccaggacagg gactgaagtg gatggggtgg atctccggat acactcggga gcctacctat 180

gccgctgact tcaaagggag atttgtgatc agtctggata catcagtcag cactgcttac 240

ctgcagatta gctccctgaa ggcagaagac acagccgtgt actattgcgc acgggacgtc 300

tttgattatt ggggacaggg caccctggtg acagtctcga gc 342

<210> 131
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized 7A4 antibody heavy chain variable region protein sequence

<400> 131

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

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

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

Gly Trp Ile Ser Gly Tyr Thr Arg Glu Pro Thr Tyr Ala Ala Asp Phe
50 55 60

Lys Gly Arg Phe Val Ile Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr
65 70 75 80

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

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

Ser Ser

<210> 132
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized 7A4 antibody light chain variable region DNA sequence

<400> 132
gacatcgtcc tgacacagtc tcccgcatcc ctggccgtct ctcccggaca gcgagcaaca 60

atcacctgcc gagcatctga aagcgtggat aactacgggt atagcttcat gaattggttt 120

cagcagaagc ccggacagcc ccctaaactg ctgatctaca gggcaagtaa cctggagtca 180

ggagtgccag cacgattcag cggatccggg tctagaacag actttaccct gacaattaac 240

cccgtcgaag ccaacgatac cgctaattac tattgccagc agtctaatgc tgaccctact 300

ttcggacagg gcaccaagct ggagatcaaa 330

<210> 133
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized 7A4 antibody light chain variable region protein sequence

<400> 133

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

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

Gly Tyr Ser Phe Met Asn Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

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

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

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

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

<210> 134

<211> 1335
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized 7A4-IgG1 D265A antibody heavy chain full length DNA sequence

<400> 134
cagatccagc tggtgcagag cgggagcgaa ctgaaaaaac ctggggcaag cgtgaaagtc 60

tcatgtaaag caagcggcta cacatttacc aacttcggca tgaattgggt caggcaggca 120

ccaggacagg gactgaagtg gatggggtgg atctccggat acactcggga gcctacctat 180

gccgctgact tcaaagggag atttgtgatc agtctggata catcagtcag cactgcttac 240

ctgcagatta gctccctgaa ggcagaagac acagccgtgt actattgcgc acgggacgtc 300

tttgattatt ggggacaggg caccctggtg acagtctcga gcgcctccac taagggccca 360

tccgtgttcc ctctggcacc ctccagcaag agcacaagcg gaggcaccgc cgcactgggc 420

tgcctcgtga aggactactt cccagaaccc gtgaccgtca gctggaatag cggcgctctg 480

accagcggag tccacacttt ccccgcagtg ctgcagtcca gcggcctgta cagcctgagc 540

agcgtggtca ctgtgccaag cagcagcctg ggcactcaga cctacatctg caacgtcaac 600

cacaagccca gcaacacaaa ggtggacaag aaggtcgagc ccaagtcctg cgataagacc 660

cacacctgcc ctccatgtcc cgcccccgag ctgctgggag gacccagcgt cttcctgttt 720

cccccaagc caaaggacac cctgatgatc agcaggaccc ccgaagtgac ctgcgtcgtg 780

gtggccgtga gccacgaaga tcccgaggtg aagttcaact ggtacgtgga cggcgtggaa 840

gtgcacaacg ccaagacaaa acccagggag gagcagtata acagcaccta cagggtcgtg 900

agcgtcctga ccgtgctgca ccaagactgg ctgaacggca aggagtataa gtgcaaggtg 960

agcaacaagg cactgcccgc ccccatcgag aagaccattt ccaaggccaa ggggcaacct 1020

agggagccac aggtctacac tctgcccccc agcagggacg agctgaccaa gaaccaggtc 1080

tccctgactt gcctggtgaa ggggttttat cccagcgaca tcgccgtcga gtgggagagc 1140

aatggccagc ccgaaaacaa ctacaagacc acacccccctg tgctggacag cgacggcagc 1200

ttctttctgt atagcaaact gacagtggat aagagcagat ggcagcaggg caacgtgttc 1260

tcctgctccg tgatgcacga ggccctgcac aatcactaca cccagaagtc cctgagcctg 1320

tcccccggaa aatga 1335

<210> 135
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized 7A4-IgG1 D265A antibody heavy chain full length protein sequence

<400> 135

Gln Ile Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala

```
1               5                   10                  15

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

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

Gly Trp Ile Ser Gly Tyr Thr Arg Glu Pro Thr Tyr Ala Ala Asp Phe
    50                  55                  60

Lys Gly Arg Phe Val Ile Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr
65                  70                  75                  80

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

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

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

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
    130                 135                 140

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
145                 150                 155                 160

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

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

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

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

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

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

Thr Cys Val Val Val Ala Val Ser His Glu Asp Pro Glu Val Lys Phe
            260                 265                 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
```

275 280 285

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
290 295 300

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

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
325 330 335

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
355 360 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
370 375 380

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

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

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
420 425 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 136
<211> 1323
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized 7A4-IgG4 F234A L235A antibody heavy chain full length DNA sequence

<400> 136
cagatccagc tggtgcagag cgggagcgaa ctgaaaaaac ctggggcaag cgtgaaagtc 60

tcatgtaaag caagcggcta cacatttacc aacttcggca tgaattgggt caggcaggca 120

ccaggacagg gactgaagtg gatggggtgg atctccggat acactcggga gcctacctat 180

gccgctgact tcaaagggag atttgtgatc agtctggata catcagtcag cactgcttac 240

ctgcagatta gctccctgaa ggcagaagac acagccgtgt actattgcgc acgggacgtc 300

tttgattatt ggggacaggg caccctggtg acagtctcga gcgcctccac caagggaccc 360

agcgtgtttc ccctggcccc ctgttccaga tccacctccg aaagcacagc cgctctcggc 420

tgcctggtca aggattactt ccctgagccc gtgacagtct cctggaatag cggcgctctg 480

acctccggcg tgcatacctt ccctgctgtg ctgcaatcct ccggactgta cagcctgagc 540

agcgtggtca ccgtgccttc ctccagcctg ggaaccaaaa cctacacatg caacgtggac 600

cacaagccca gcaacaccaa agtggacaag agggtggagt ccaagtacgg acccccttgt 660

cctccctgcc ctgctcctga agccgctgga ggacctagcg tgttcctgtt tcccccaag 720

cccaaggaca ccctcatgat ctccaggacc cccgaggtga cctgtgtcgt ggtggacgtg 780

agccaagagg accccgaggt gcagttcaac tggtacgtgg atggcgtcga ggtccataac 840

gccaagacca agcctaggga ggagcagttc aacagcacct acagagtggt gagcgtcctg 900

accgtgctcc accaagactg gctgaacggc aaggaataca agtgcaaggt ctccaacaag 960

ggactccctt cctccatcga gaagaccatc agcaaggcca agggccagcc cagagaaccc 1020

caagtctaca cactgccccc cagccaagag gaaatgacca agaaccaggt gagcctgacc 1080

tgcctggtga aaggcttcta ccccagcgac attgctgtcg aatgggagag caacggccaa 1140

cccgagaaca actacaagac cacccccccct gtgctcgaca gcgacggctc cttcttcctc 1200

tacagcaggc tgacagtgga caagtccagg tggcaagagg gcaatgtctt cagctgtagc 1260

gtcatgcacg aggccctcca caaccactac acccagaaga gcctgtccct ctccctgggc 1320

tga 1323

<210> 137
<211> 440
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized 7A4-IgG4 F234A L235A antibody heavy chain full length protein sequence

<400> 137

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

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

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

Gly Trp Ile Ser Gly Tyr Thr Arg Glu Pro Thr Tyr Ala Ala Asp Phe
50 55 60

Lys Gly Arg Phe Val Ile Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Asp Val Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val

100 105 110

Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys
115 120 125

Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys
130 135 140

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
145 150 155 160

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

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

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

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

Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
225 230 235 240

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

Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
260 265 270

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
275 280 285

Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
290 295 300

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

Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
325 330 335

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met
340 345 350

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
355 360 365

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

370 375 380

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
385 390 395 400

Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val
405 410 415

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
420 425 430

Lys Ser Leu Ser Leu Ser Leu Gly
435 440

<210> 138
<211> 654
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized 7A4 antibody light chain full length DNA sequence

<400> 138
gacatcgtcc tgacacagtc tcccgcatcc ctggccgtct ctcccggaca gcgagcaaca 60

atcacctgcc gagcatctga aagcgtggat aactacgggt atagcttcat gaattggttt 120

cagcagaagc ccggacagcc ccctaaactg ctgatctaca gggcaagtaa cctggagtca 180

ggagtgccag cacgattcag cggatccggg tctagaacag actttaccct gacaattaac 240

cccgtcgaag ccaacgatac cgctaattac tattgccagc agtctaatgc tgaccctact 300

ttcggacagg gcaccaagct ggagatcaaa cgtacggtgg ccgcaccaag cgtcttcatc 360

ttcccgccat ctgatgagca gttgaaatct ggaactgcct ctgttgtgtg cctgctgaat 420

aacttctatc ccagagaggc caaagtacag tggaaggtgg ataacgccct ccaatcgggt 480

aactcccagg agagtgtcac agagcaggac agcaaggaca gcacctacag cctcagcagc 540

accctgacgc tgagcaaagc agactacgag aaacacaaag tctacgcctg cgaagtcacc 600

catcagggcc tgagctcgcc cgtcacaaag agctttaaca gaggcgagtg ctga 654

<210> 139
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized 7A4 antibody light chain full length protein sequence

<400> 139

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

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

```
Gly Tyr Ser Phe Met Asn Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45

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

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

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

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

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

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

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

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

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

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

Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215
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<210> 140
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized 13F1 antibody heavy chain variable region DNA sequence

<400> 140
caggtgcagc tgcaggagag cggacccgga ctggtgaagc ctagccagac actgagcctg 60

acttgtactg tgagcggata ttccattagc tccgactacg cttggaactg gatcaggcag 120

ccacctggca agggactgga gtggatggcc tacatttcct attctgggta caccagctat 180

aaccccagtc tgaaatcacg gatcacaatt agcagagaca cttccaagaa tcagttctct 240

ctgaaactgt ctagtgtgac tgccgctgat accgcagtct actattgcgc ccggtccctg 300

gactacgatt atggcacaat ggattattgg ggacagggca ccctggtgac agtctcgagc 360

<210> 141
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized 13F1 antibody heavy chain variable region protein sequence

<400> 141

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Ser Ser Asp
20 25 30

Tyr Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
35 40 45

Met Ala Tyr Ile Ser Tyr Ser Gly Tyr Thr Ser Tyr Asn Pro Ser Leu
50 55 60

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

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Leu Asp Tyr Asp Tyr Gly Thr Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 142
<211> 318
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized 13F1 antibody light chain variable region DNA sequence

<400> 142
gaaatcgtcc tgacccagag tcccgccacc ctgtcactga gccccggaga aagagccaca 60

ctgagttgta gagcaaatag cagcgtgagc tccatgcact ggtaccagca gaagcctgga 120

cagtccccag agccctggat ctatgccatt agcaacctgg ctttcggcgt gccagcaagg 180

ttttccggct ctgggagtgg aacagactac accctgacaa tctctagtct ggagcccgaa 240

gatttcgccg tctactattg ccagcagtgg tcaagccggc cccctacttt tggccagggg 300

accaagctgg agatcaag 318

<210> 143
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized 13F1 antibody light chain variable region protein sequence

<400> 143

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Asn Ser Ser Val Ser Ser Met
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Glu Pro Trp Ile Tyr
35 40 45

Ala Ile Ser Asn Leu Ala Phe Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
65 70 75 80

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ser Arg Pro Pro Thr
85 90 95

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

<210> 144
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized 13F1-IgG1 D265A antibody heavy chain full length DNA sequence

<400> 144
caggtgcagc tgcaggagag cggacccgga ctggtgaagc ctagccagac actgagcctg 60

acttgtactg tgagcggata ttccattagc tccgactacg cttggaactg gatcaggcag 120

ccacctggca agggactgga gtggatggcc tacatttcct attctgggta caccagctat 180

aaccccagtc tgaaatcacg gatcacaatt agcagagaca cttccaagaa tcagttctct 240

ctgaaactgt ctagtgtgac tgccgctgat accgcagtct actattgcgc ccggtccctg 300

gactacgatt atggcacaat ggattattgg ggacagggca ccctggtgac agtctcgagc 360

gcctccacta agggcccatc cgtgttccct ctggcaccct ccagcaagag cacaagcgga 420

ggcaccgccg cactgggctg cctcgtgaag gactacttcc cagaacccgt gaccgtcagc 480

tggaatagcg gcgctctgac cagcggagtc cacactttcc ccgcagtgct gcagtccagc 540

ggcctgtaca gcctgagcag cgtggtcact gtgccaagca gcagcctggg cactcagacc 600

tacatctgca acgtcaacca caagcccagc aacacaaagg tggacaagaa ggtcgagccc 660

aagtcctgcg ataagaccca cacctgccct ccatgtcccg cccccgagct gctgggagga 720

cccagcgtct tcctgtttcc ccccaagcca aaggacaccc tgatgatcag caggaccccc 780

gaagtgacct gcgtcgtggt ggccgtgagc cacgaagatc ccgaggtgaa gttcaactgg 840

tacgtggacg gcgtggaagt gcacaacgcc aagacaaaac ccagggagga gcagtataac 900

agcacctaca gggtcgtgag cgtcctgacc gtgctgcacc aagactggct gaacggcaag 960

gagtataagt gcaaggtgag caacaaggca ctgcccgccc ccatcgagaa gaccatttcc 1020

aaggccaagg ggcaacctag ggagccacag gtctacactc tgcccctag cagggacgag 1080

ctgaccaaga accaggtctc cctgacttgc ctggtgaagg ggttttatcc cagcgacatc 1140

gccgtcgagt gggagagcaa tggccagccc gaaaacaact acaagaccac acccctgtg 1200

ctggacagcg acggcagctt ctttctgtat agcaaactga cagtggataa gagcagatgg 1260

cagcagggca acgtgttctc ctgctccgtg atgcacgagg ccctgcacaa tcactacacc 1320

cagaagtccc tgagcctgtc ccccggaaaa tga 1353

<210> 145
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized 13F1-IgG1 D265A antibody heavy chain full length protein sequence

<400> 145

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Ser Ser Asp
20 25 30

Tyr Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
35 40 45

Met Ala Tyr Ile Ser Tyr Ser Gly Tyr Thr Ser Tyr Asn Pro Ser Leu
50 55 60

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

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Leu Asp Tyr Asp Tyr Gly Thr Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val

115 120 125

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

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

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

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

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

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

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

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Ala Val Ser His Glu
260 265 270

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

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

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

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

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

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

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

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val

385 390 395 400

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

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

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

Gly Lys
450

<210> 146
<211> 1341
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized 13F1-IgG4 F234A L235A antibody heavy chain full length DNA sequence

<400> 146
caggtgcagc tgcaggagag cggacccgga ctggtgaagc ctagccagac actgagcctg 60

acttgtactg tgagcggata ttccattagc tccgactacg cttggaactg gatcaggcag 120

ccacctggca agggactgga gtggatggcc tacatttcct attctgggta caccagctat 180

aaccccagtc tgaaatcacg gatcacaatt agcagagaca cttccaagaa tcagttctct 240

ctgaaactgt ctagtgtgac tgccgctgat accgcagtct actattgcgc ccggtccctg 300

gactacgatt atggcacaat ggattattgg ggacagggca ccctggtgac agtctcgagc 360

gcctccacca agggacccag cgtgtttccc ctggcccct gttccagatc cacctccgaa 420

agcacagccg ctctcggctg cctggtcaag gattacttcc ctgagcccgt gacagtctcc 480

tggaatagcg gcgctctgac ctccggcgtg cataccttcc ctgctgtgct gcaatcctcc 540

ggactgtaca gcctgagcag cgtggtcacc gtgccttcct ccagcctggg aaccaaaacc 600

tacacatgca acgtggacca caagcccagc aacaccaaag tggacaagag ggtggagtcc 660

aagtacggac ccccttgtcc tccctgccct gctcctgaag ccgctggagg acctagcgtg 720

ttcctgtttc cccccaagcc caaggacacc ctcatgatct ccaggacccc cgaggtgacc 780

tgtgtcgtgg tggacgtgag ccaagaggac cccgaggtgc agttcaactg gtacgtggat 840

ggcgtcgagg tccataacgc caagaccaag cctagggagg agcagttcaa cagcacctac 900

agagtggtga gcgtcctgac cgtgctccac caagactggc tgaacggcaa ggaatacaag 960

tgcaaggtct ccaacaaggg actcccttcc tccatcgaga agaccatcag caaggccaag 1020

ggccagccca gagaacccca agtctacaca ctgccccca gccaagagga aatgaccaag 1080

aaccaggtga gcctgacctg cctggtgaaa ggcttctacc ccagcgacat tgctgtcgaa 1140

tgggagagca acggccaacc cgagaacaac tacaagacca ccccccctgt gctcgacagc 1200

gacggctcct tcttcctcta cagcaggctg acagtggaca agtccaggtg gcaagagggc 1260

aatgtcttca gctgtagcgt catgcacgag gccctccaca accactacac ccagaagagc 1320

ctgtccctct ccctgggctg a 1341

<210> 147
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized 13F1-IgG4 F234A L235A antibody heavy chain full length protein sequence

<400> 147

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Ser Ser Asp
20 25 30

Tyr Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
35 40 45

Met Ala Tyr Ile Ser Tyr Ser Gly Tyr Thr Ser Tyr Asn Pro Ser Leu
50 55 60

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

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Leu Asp Tyr Asp Tyr Gly Thr Met Asp Tyr Trp Gly Gln
100 105 110

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

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

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

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

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

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys

195 200 205

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

Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
435 440 445

<210> 148
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized 13F1 antibody light chain full length DNA sequence

<400> 148
gaaatcgtcc tgacccagag tcccgccacc ctgtcactga gccccggaga aagagccaca 60

ctgagttgta gagcaaatag cagcgtgagc tccatgcact ggtaccagca gaagcctgga 120

cagtccccag agccctggat ctatgccatt agcaacctgg ctttcggcgt gccagcaagg 180

ttttccggct ctgggagtgg aacagactac accctgacaa tctctagtct ggagcccgaa 240

gatttcgccg tctactattg ccagcagtgg tcaagccggc cccctacttt tggccagggg 300

accaagctgg agatcaagcg tacggtggcc gcaccaagcg tcttcatctt cccgccatct 360

gatgagcagt tgaaatctgg aactgcctct gttgtgtgcc tgctgaataa cttctatccc 420

agagaggcca aagtacagtg gaaggtggat aacgccctcc aatcgggtaa ctcccaggag 480

agtgtcacag agcaggacag caaggacagc acctacagcc tcagcagcac cctgacgctg 540

agcaaagcag actacgagaa acacaaagtc tacgcctgcg aagtcaccca tcagggcctg 600

agctcgcccg tcacaaagag ctttaacaga ggcgagtgct ga 642

<210> 149
<211> 213
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized 13F1 antibody light chain full length protein sequence

<400> 149

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Asn Ser Ser Val Ser Ser Met
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Glu Pro Trp Ile Tyr
35 40 45

Ala Ile Ser Asn Leu Ala Phe Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
65 70 75 80

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ser Arg Pro Pro Thr
85 90 95

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

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

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

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

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

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

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

Asn Arg Gly Glu Cys
    210
```

<210> 150
<211> 330
<212> PRT
<213> Homo sapiens

<400> 150

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 151
<211> 326
<212> PRT
<213> Homo sapiens

<400> 151

```
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

325

<210> 152
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> 7A4D Humanized Light chain variable

<400> 152

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

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

Gly Tyr Ser Phe Met Asn Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

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

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

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

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

<210> 153
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> 7A4D Humanized Full light chain

<400> 153

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

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

Gly Tyr Ser Phe Met Asn Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

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

Arg Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Asn

```
65                  70                  75                  80

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

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

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

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

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

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

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

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

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