SEQUENCE LISTING

<110> Amgen Inc.

<120> High Concentration Antibody Formulations

<130> SG3530A

<140> US-61/334,986
<141> 2010-05-14

<160> 248

<170> PatentIn version 3.5

<210> 1
<211> 13
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<220>
<223> Ab-A & Ab-1 LCDR1

<400> 1

Gln Ser Ser Gln Ser Val Tyr Asp Asn Asn Trp Leu Ala
1 5 10

<210> 2
<211> 7
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<220>
<223> Ab-A and Ab-1 LCDR2

<400> 2

Asp Ala Ser Asp Leu Ala Ser
1 5

<210> 3
<211> 10
<212> PRT
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<220>
<223> Ab-A and Ab-1 LCDR3

<400> 3

Gln Gly Ala Tyr Asn Asp Val Ile Tyr Ala
1 5 10

<210> 4
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-A and Ab-1 HCDR1

<400> 4

Ser Tyr Trp Met Asn
1 5

<210> 5
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-1 and Ab-2 HCDR2

<400> 5

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

<210> 6
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-A and Ab-1 HCDR3

<400> 6

Asn Trp Asn Leu
1

<210> 7
<211> 654
<212> DNA
<213> Artificial Sequence

<220>
<223> Rabbit-Mouse Chimera

<220>
<221> misc_feature
<223> Ab-A light chain (no signal)

<400> 7
gcgcaagtgc tgacccagac tccagcctcc gtgtctgcag ctgtgggagg cacagtcacc 60

atcaattgcc agtccagtca gagtgtttat gataacaact ggttagcctg gtttcagcag 120

aaaccagggc agcctcccaa gctcctgatt tatgatgcat ccgatctggc atctggggtc 180

ccatcgcggt tcagtggcag tggatctggg acacagttca ctctcaccat cagcggcgtg 240

cagtgtgccg atgctgccac ttactactgt caaggcgctt ataatgatgt tatttatgct 300

ttcggcggag ggaccgaggt ggtggtcaaa cgtacggatg ctgcaccaac tgtatccatc 360

ttcccaccat ccagtgagca gttaacatct ggaggtgcct cagtcgtgtg cttcttgaac 420

aacttctacc ccaaagacat caatgtcaag tggaagattg atggcagtga acgacaaaat 480

ggcgtcctga acagttggac tgatcaggac agcaaagaca gcacctacag catgagcagc 540

accctcacgt tgaccaagga cgagtatgaa cgacataaca gctatacctg tgaggccact 600

cacaagacat caacttcacc cattgtcaag agcttcaaca ggaatgagtg ttag 654

<210> 8
<211> 217

<212> PRT
<213> Artificial Sequence

<220>
<223> Rabbit-Mouse Chimera

<220>
<221> MISC_FEATURE
<223> Ab-A light chain (no signal)

<400> 8

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

Gly Thr Val Thr Ile Asn Cys Gln Ser Ser Gln Ser Val Tyr Asp Asn
            20                  25                  30

Asn Trp Leu Ala Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu
        35                  40                  45

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

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

Gln Cys Ala Asp Ala Ala Thr Tyr Tyr Cys Gln Gly Ala Tyr Asn Asp
                85                  90                  95

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

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

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

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

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

Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His
            180                 185                 190

Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile
        195                 200                 205

Val Lys Ser Phe Asn Arg Asn Glu Cys
    210                 215
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<210> 9
<211> 1302
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized Antibody

<220>
<221> misc_feature
<223> Ab-A heavy chain (no signal)

<400> 9
cagtcgctgg aggagtccgg gggtcgcctg gtcacgcctg ggacacccct gacactcacc 60

tgcacagcct ctggattctc cctcagtagt tattggatga actgggtccg ccaggctcca 120

ggggaggggc tggaatggat cggaaccatt gattctggtg gtaggacgga ctacgcgagc 180

tgggcaaaag gccgattcac catctccaga acctcgacta cgatggatct gaaaatgacc 240

agtctgacga ccggggacac ggcccgttat ttctgtgcca gaaattggaa cttgtggggc 300

caaggcaccc tcgtcaccgt ctcgagcgct tctacaaagg gcccatctgt ctatccactg 360

gcccctggat ctgctgccca aactaactcc atggtgaccc tgggatgcct ggtcaagggc 420

tatttccctg agccagtgac agtgacctgg aactctggat ccctgtccag cggtgtgcac 480

accttcccag ctgtcctgca gtctgacctc tacactctga gcagctcagt gactgtcccc 540

tccagcacct ggcccagcga gaccgtcacc tgcaacgttg cccacccggc cagcagcacc 600

aaggtggaca agaaaattgt gcccagggat tgtggttgta agccttgcat atgtacagtc 660

ccagaagtat catctgtctt catcttcccc ccaaagccca aggatgtgct caccattact 720

ctgactccta aggtcacgtg tgttgtggta gacatcagca aggatgatcc cgaggtccag 780

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aatggcaagg agttcaaatg cagggtcaac agtgcagctt tccctgcccc catcgagaaa 960

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aaggagcaga tggccaagga taaagtcagt ctgacctgca tgataacaga cttcttccct 1080

gaagacatta ctgtggagtg gcagtggaat gggcagccag cggagaacta caagaacact 1140

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agcaactggg aggcaggaaa tactttcacc tgctctgtgt tacatgaggg cctgcacaac 1260

caccatactg agaagagcct ctcccactct cctggtaaat ga 1302

<210> 10
<211> 433
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized antibody

<220>

<221> MISC_FEATURE
<223> Ab-A heavy chain (no signal)

<400> 10

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

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

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

Thr Ile Asp Ser Gly Gly Arg Thr Asp Tyr Ala Ser Trp Ala Lys Gly
    50                  55                  60

Arg Phe Thr Ile Ser Arg Thr Ser Thr Thr Met Asp Leu Lys Met Thr
65                  70                  75                  80

Ser Leu Thr Thr Gly Asp Thr Ala Arg Tyr Phe Cys Ala Arg Asn Trp
                85                  90                  95

Asn Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
            100                 105                 110

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

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

Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His
145                 150                 155                 160

Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser
                165                 170                 175

Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn
            180                 185                 190

Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro
        195                 200                 205

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

Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr
225                 230                 235                 240

Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp
                245                 250                 255
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Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr
            260                 265                 270

Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser
        275                 280                 285

Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu
    290                 295                 300

Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys
305                 310                 315                 320

Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr
                325                 330                 335

Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr
            340                 345                 350

Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln
        355                 360                 365

Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met
    370                 375                 380

Asn Thr Asn Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys
385                 390                 395                 400

Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu
                405                 410                 415

Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly
            420                 425                 430

Lys
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<210> 11
<211> 390
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized antibody

<220>
<221> misc_feature
<223> Ab-1 light variable (with signal)

<400> 11
atggacacga gggccccac tcagctgctg gggctcctgc tgctctggct cccaggtgcc 60

acatttgctc aagttctgac ccagagtcca agcagtctct ccgccagcgt aggcgatcgt 120

gtgactatta cctgtcaatc tagtcagagc gtgtatgata acaattggct ggcgtggtac 180

cagcaaaaac cgggcaaagc cccgaagctg ctcatctatg acgcgtccga tctggctagc 240

ggtgtgccaa gccgtttcag tggcagtggc agcggtactg actttaccct cacaatttcg 300

tctctccagc cggaagattt cgccacttac tattgtcaag gtgcttacaa cgatgtgatt 360

tatgccttcg gtcagggcac taaagtagaa 390

<210> 12
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized antibody

<220>
<221> MISC_FEATURE
<223> Ab-1 light variable (with signal)

<400> 12

Met Asp Thr Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

Leu Pro Gly Ala Thr Phe Ala Gln Val Leu Thr Gln Ser Pro Ser Ser
20 25 30

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

Gln Ser Val Tyr Asp Asn Asn Trp Leu Ala Trp Tyr Gln Gln Lys Pro
50 55 60

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

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
85 90 95

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
100 105 110

Gln Gly Ala Tyr Asn Asp Val Ile Tyr Ala Phe Gly Gln Gly Thr Lys
115 120 125

Val Glu Ile Lys Arg
130

<210> 13
<211> 393
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized antibody

<220>

<221> misc_feature
<223> Ab-1 heavy variable (with signal)

<400> 13
atggagactg ggctgcgctg gcttctcctg gtcgctgtgc tcaaaggtgt ccactgtgag 60

gtgcagctgt tggagtctgg aggcgggctt gtccagcctg gagggagcct gcgtctctct 120

tgtgcagcaa gcggcttcag cttatcctct tactggatga attgggtgcg gcaggcacct 180

gggaagggcc tggagtgggt gggcaccatt gattccggag gccgtacaga ctacgcgtct 240

tgggcaaagg gccgtttcac catttcccgc gacaactcca aaaataccat gtacctccag 300

atgaactctc tccgcgcaga ggacacagca cgttattact gtgcacgcaa ctggaatctg 360

tggggtcaag gtactcttgt aacagtctcg agc 393

<210> 14
<211> 131
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized antibody

<400> 14

Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
1 5 10 15

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

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

Ser Ser Tyr Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

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

Trp Ala Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
85 90 95

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

Tyr Cys Ala Arg Asn Trp Asn Leu Trp Gly Gln Gly Thr Leu Val Thr
115 120 125

Val Ser Ser
130

<210> 15
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-B LCDR1

<400> 15

Ser Ala Ser Ser Ser Val Ser Phe Val Asp
1 5 10

<210> 16
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-B LCDR2

<400> 16

Arg Thr Ser Asn Leu Gly Phe
1 5

<210> 17
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> LCDR3

<400> 17

Gln Gln Arg Ser Thr Tyr Pro Pro Thr
1 5

<210> 18
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-B HCDR1

<400> 18

Thr Ser Gly Met Gly Val Gly
1 5

<210> 19
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-B HCDR2

<400> 19

His Ile Trp Trp Asp Asp Val Lys Arg Tyr Asn Pro Val Leu Lys Ser
1 5 10 15

<210> 20
<211> 14
<212> PRT

<213> Artificial Sequence

<220>
<223> Ab-B HCDR3

<400> 20

Glu Asp Phe Asp Tyr Asp Glu Glu Tyr Tyr Ala Met Asp Tyr
1 5 10

<210> 21
<211> 642
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<223> Ab-B light chain (no signal)

<400> 21
caaattgttc tcacccagtc tccaacaatc gtgtctgcat ctccagggga gaaggtcacc 60

ctaatctgca gtgccagttc aagtgtaagt ttcgtggact ggttccagca gaagccaggc 120

acttctccca aacgctggat ttacagaaca tccaacctgg gttttggagt ccctgctcgc 180

ttcagtggcg gtggatctgg gacctctcac tctctcacaa tcagccgaat ggaggctgaa 240

gatgctgcca cttattactg ccagcaaagg agtacttacc cacccacgtt cggtgctggg 300

accaagctgg aactgaaacg ggctgatgct gcaccaactg tatccatctt cccaccatcc 360

agtgagcagt taacatctgg aggtgcctca gtcgtgtgct tcttgaacaa cttctacccc 420

aaagacatca atgtcaagtg gaagattgat ggcagtgaac gacaaaatgg cgtcctgaac 480

agttggactg atcaggacag caaagacagc acctacagca tgagcagcac cctcacgttg 540

accaaggacg agtatgaacg acataacagc tatacctgtg aggccactca caagacatca 600

acttcaccca ttgtcaagag cttcaacagg aatgagtgtt ag 642

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

<220>
<221> MISC_FEATURE
<223> Ab-B light chain (no signal)

<400> 22

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

Glu Lys Val Thr Leu Ile Cys Ser Ala Ser Ser Ser Val Ser Phe Val
20 25 30

Asp Trp Phe Gln Gln Lys Pro Gly Thr Ser Pro Lys Arg Trp Ile Tyr
35 40 45

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

Gly Ser Gly Thr Ser His Ser Leu Thr Ile Ser Arg Met Glu Ala Glu
65                  70                  75                  80

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

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

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

Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn
    130                 135                 140

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

Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser
                165                 170                 175

Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr
            180                 185                 190

Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser Phe
        195                 200                 205

Asn Arg Asn Glu Cys
    210
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<210> 23
<211> 1350
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<223> Ab-B heavy chain (no signal)

<400> 23
caggttactc tgaaagagtc tggccctggg atattgcagc cctcccagac cctcagtctg 60

acttgttctt tctctgggtt ttcactgagc acttctggta tgggtgtagg ctggattcgt 120

cacccatcag ggaagaatct ggagtggctg gcacacattt ggtgggatga tgtcaagcgc 180

tataacccag tcctgaagag ccgactgact atctccaagg atacctccaa cagccaggta 240

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gaggactttg attacgacga ggagtattat gctatggact actggggtca aggaacctca 360

gtcatcgtct cctcagccaa aacgacaccc ccatctgtct atccactggc ccctggatct 420

gctgcccaaa ctaactccat ggtgaccctg ggatgcctgg tcaagggcta tttccctgag 480

ccagtgacag tgacctggaa ctctggatcc ctgtccagcg gtgtgcacac cttcccagct 540

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accaaaggca gaccgaaggc tccacaggtg tacaccattc cacctcccaa ggagcagatg 1080

gccaaggata aagtcagtct gacctgcatg ataacagact tcttccctga agacattact 1140

gtggagtggc agtggaatgg gcagccagcg gagaactaca agaacactca gcccatcatg 1200

gacacagatg gctcttactt cgtctacagc aagctcaatg tgcagaagag caactgggag 1260

gcaggaaata ctttcacctg ctctgtgtta catgagggcc tgcacaacca ccatactgag 1320

aagagcctct cccactctcc tggtaaatga 1350

<210> 24
<211> 449
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<223> Ab-B heavy chain (no signal)

<400> 24

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

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

Gly Met Gly Val Gly Trp Ile Arg His Pro Ser Gly Lys Asn Leu Glu
35 40 45

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

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

Phe Leu Lys Ile Ala Asn Val Asp Thr Ala Asp Thr Ala Thr Tyr Tyr
85 90 95

```
Cys Ala Arg Ile Glu Asp Phe Asp Tyr Asp Glu Glu Tyr Tyr Ala Met
            100                 105                 110

Asp Tyr Trp Gly Gln Gly Thr Ser Val Ile Val Ser Ser Ala Lys Thr
        115                 120                 125

Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr
    130                 135                 140

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

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

Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser
            180                 185                 190

Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn
        195                 200                 205

Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro
    210                 215                 220

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

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

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

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

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

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

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

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

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

Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln
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370 375 380

Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met
385 390 395 400

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

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

Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly
435 440 445

Lys

<210> 25
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-C LCDR1

<400> 25

Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn
1 5 10 15

<210> 26
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-C LCDR2

<400> 26

Ala Ala Ser Asn Leu Glu Ser
1 5

<210> 27
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-C LCDR3

<400> 27

Gln Gln Ser Asn Glu Asp Pro Trp Thr
1 5

<210> 28
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-C HCDR1

<400> 28

Asp Cys Tyr Met Asn
1 5

<210> 29
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-C HCDR2

<400> 29

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

Gly

<210> 30
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-C HCDR3

<400> 30

Ser His Tyr Tyr Phe Asp Gly Arg Val Pro Trp Asp Ala Met Asp Tyr
1 5 10 15

<210> 31
<211> 657
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<223> Ab-C light chain (no signal)

<400> 31
gacattgtgc tgacccaatc tccagcttct ttgactgtgt ctctaggcct gagggccacc 60

atctcctgca aggccagcca aagtgttgat tatgatggtg atagttatat gaactggtac 120

cagcagaaac caggacagcc acccaaactc ctcatctatg ctgcatccaa tctagaatct 180

gggatcccag ccaggtttag tggcaatggg tctgggacag acttcaccct caacatccat 240

cctgtggagg aggaggatgc tgtaacctat tactgtcaac aaagtaatga ggatccgtgg 300

acgttcggtg gaggcaccaa gctggaaatc aaacgggctg atgctgcacc aactgtatcc 360

atcttcccac catccagtga gcagttaaca tctggaggtg cctcagtcgt gtgcttcttg 420

aacaacttct accccaaaga catcaatgtc aagtggaaga ttgatggcag tgaacgacaa 480

aatggcgtcc tgaacagttg gactgatcag gacagcaaag acagcaccta cagcatgagc 540

agcaccctca cgttgaccaa ggacgagtat gaacgacata acagctatac ctgtgaggcc 600

actcacaaga catcaacttc acccattgtc aagagcttca acaggaatga gtgttag 657

<210> 32
<211> 218
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<223> Ab-C light chain (no signal)

<400> 32

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

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

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

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

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

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

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

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

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

Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln
145 150 155 160

Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr
165 170 175

Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg
180 185 190

His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro
195 200 205

Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
210 215

<210> 33
<211> 1350
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<223> Ab-C heavy chain (no signal)

<400> 33
gaggtccagc tgcaacaatc tggacctgag ctggtgaagc ctgggacttc agtgaagatg 60

tcctgtaagg cttctggata cacattcact gactgctaca tgaactgggt gaagcagagc 120

catgggaaga gccttgaatg gattggagat attaatcctt tcaacggtgg tactacctac 180

aaccagaagt tcaagggcaa ggccacattg actgtagaca aatcctccag cacagcctac 240

atgcagctca acagcctgac atctgacgac tctgcagtct attactgtgc aagatcccat 300

tattacttcg atggtagagt cccttgggat gctatggact actggggtca aggaacctca 360

gtcaccgtct cctcagccaa aacgacaccc ccatctgtct atccactggc ccctggatct 420

gctgcccaaa ctaactccat ggtgaccctg ggatgcctgg tcaagggcta tttccctgag 480

ccagtgacag tgacctggaa ctctggatcc ctgtccagcg gtgtgcacac cttcccagct 540

gtcctgcagt ctgacctcta cactctgagc agctcagtga ctgtcccctc cagcacctgg 600

cccagcgaga ccgtcacctg caacgttgcc cacccggcca gcagcaccaa ggtggacaag 660

aaaattgtgc ccagggattg tggttgtaag ccttgcatat gtacagtccc agaagtatca 720

tctgtcttca tcttcccccc aaagcccaag gatgtgctca ccattactct gactcctaag 780

gtcacgtgtg ttgtggtaga catcagcaag gatgatcccg aggtccagtt cagctggttt 840

gtagatgatg tggaggtgca cacagctcag acgcaacccc gggaggagca gttcaacagc 900

actttccgct cagtcagtga acttcccatc atgcaccagg actggctcaa tggcaaggag 960

ttcaaatgca gggtcaacag tgcagctttc cctgccccca tcgagaaaac catctccaaa 1020

accaaaggca gaccgaaggc tccacaggtg tacaccattc cacctcccaa ggagcagatg 1080

gccaaggata aagtcagtct gacctgcatg ataacagact tcttccctga agacattact 1140

gtggagtggc agtggaatgg gcagccagcg gagaactaca agaacactca gcccatcatg 1200

gacacagatg gctcttactt catctacagc aagctcaatg tgcagaagag caactgggag 1260

gcaggaaata ctttcacctg ctctgtgtta catgagggcc tgcacaacca ccatactgag 1320

aagagcctct cccactctcc tggtaaatga 1350

<210> 34
<211> 449
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<223> Ab-C heavy chain (no signal)

<400> 34

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

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

Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
        35                  40                  45

Gly Asp Ile Asn Pro Phe Asn Gly Gly Thr Thr Tyr Asn Gln Lys Phe
    50                  55                  60

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

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

Ala Arg Ser His Tyr Tyr Phe Asp Gly Arg Val Pro Trp Asp Ala Met
            100                 105                 110

Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr
        115                 120                 125

Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr
    130                 135                 140

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

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

Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser
            180                 185                 190

Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn
        195                 200                 205

Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro
    210                 215                 220

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

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

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

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

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

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

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

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

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

Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln
370 375 380

Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met
385 390 395 400

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

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

Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly
435 440 445

Lys

<210> 35
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-D LCDR1

<400> 35

Gln Ala Ser Gln Gly Thr Ser Ile Asn Leu Asn
1 5 10

<210> 36

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

<220>
<223> Ab-D LCDR2

<400> 36

Gly Ser Ser Asn Leu Glu Asp
1 5

<210> 37
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-D LCDR3

<400> 37

Leu Gln His Ser Tyr Leu Pro Tyr Thr
1 5

<210> 38
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-D HCDR1

<400> 38

Asp His Tyr Met Ser
1 5

<210> 39
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-D HCDR2

<400> 39

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

Gly

<210> 40
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-D HCDR3

<400> 40

```
Asp Asp Tyr Asp Ala Ser Pro Phe Ala Tyr
1               5                  10
```

<210> 41
<211> 645
<212> DNA
<213> Mus musculus

<400> 41

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gatgtccaga tgattcagtc tccatcctcc ctgtctgcat ctttgggaga catagtcacc       60

atgacttgcc aggcaagtca gggcactagc attaatttaa actggtttca gcaaaaacca      120

gggaaggctc ctaagctcct gatctatggt tcaagcaact tggaagatgg ggtcccatca      180

aggttcagtg gcagtagata tgggacagat ttcactctca ccatcagcag cctggaggat      240

gaagatctgg caacttattt ctgtctacaa catagttatc tcccgtacac gttcggaggg      300

gggaccaagc tggaaataaa acgggctgat gctgcaccaa ctgtatccat cttcccacca      360

tccagtgagc agttaacatc tggaggtgcc tcagtcgtgt gcttcttgaa caacttctac      420

cccaaagaca tcaatgtcaa gtggaagatt gatggcagtg aacgacaaaa tggcgtcctg      480

aacagttgga ctgatcagga cagcaaagac agcacctaca gcatgagcag caccctcacg      540

ttgaccaagg acgagtatga acgacataac agctatacct gtgaggccac tcacaagaca      600

tcaacttcac ccattgtcaa gagcttcaac aggaatgagt gttag                      645
```

<210> 42
<211> 214
<212> PRT
<213> Mus musculus

<400> 42

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

Asp Ile Val Thr Met Thr Cys Gln Ala Ser Gln Gly Thr Ser Ile Asn
            20                  25                  30

Leu Asn Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Gly Ser Ser Asn Leu Glu Asp Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

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

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

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

Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly
```

115 120 125

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

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

Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser
165 170 175

Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr
180 185 190

Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser
195 200 205

Phe Asn Arg Asn Glu Cys
210

<210> 43
<211> 1332
<212> DNA
<213> Mus musculus

<400> 43
gaggtccagc tgcaacagtc tggacctgaa ctggtgacgc ctggggcttc agtgaagata 60

tcttgtaagg cttctggata cacattcact gaccactaca tgagctgggt gaagcagagt 120

catggaaaaa gccttgagtg gattggagat attaatccct attctggtga aactacctac 180

aaccagaagt tcaagggcac ggccacattg actgtagaca agtcttccag tatagcctac 240

atggagatcc gcggcctgac atctgaggac tctgcagtct attactgtgc aagagatgat 300

tacgacgcct ctccgtttgc ttactggggc caagggactc tggtcactgt ctctgcagcc 360

aaaacgacac ccccatctgt ctatccactg gcccctggat ctgctgccca aactaactcc 420

atggtgaccc tgggatgcct ggtcaagggc tatttccctg agccagtgac agtgacctgg 480

aactctggat ccctgtccag cggtgtgcac accttcccag ctgtcctgca gtctgacctc 540

tacactctga gcagctcagt gactgtcccc tccagcacct ggcccagcga gaccgtcacc 600

tgcaacgttg cccacccggc cagcagcacc aaggtggaca agaaaattgt gcccagggat 660

tgtggttgta agccttgcat atgtacagtc ccagaagtat catctgtctt catcttcccc 720

ccaaagccca aggatgtgct caccattact ctgactccta aggtcacgtg tgttgtggta 780

gacatcagca aggatgatcc cgaggtccag ttcagctggt ttgtagatga tgtggaggtg 840

cacacagctc agacgcaacc ccgggaggag cagttcaaca gcactttccg ctcagtcagt 900

gaacttccca tcatgcacca ggactggctc aatggcaagg agttcaaatg cagggtcaac 960

agtccagctt tccctgcccc catcgagaaa accatctcca aaaccaaagg cagaccgaag 1020

gctccacagg tgtacaccat tccacctccc aaggagcaga tggccaagga taaagtcagt 1080

ctgacctgca tgataacaga cttcttccct gaagacatta ctgtggagtg gcagtggaat 1140

gggcagccag cggagaacta caagaacact cagcccatca tggacacaga tggctcttac 1200

ttcatctaca gcaagctcaa tgtgcagaag agcaactggg aggcaggaaa tactttcacc 1260

tgctctgtgt tacatgaggg cctgcacaac caccatactg agaagagcct ctcccactct 1320

cctggtaaat ga 1332

<210> 44
<211> 443
<212> PRT
<213> Mus musculus

<400> 44

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

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

Tyr Met Ser Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

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

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

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

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

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

Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu
130 135 140

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

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

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

Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala Ser
195 200 205

```
Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Cys Lys
    210                 215                 220

Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe Pro
225                 230                 235                 240

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

Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln Phe Ser
            260                 265                 270

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

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

Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val Asn
305                 310                 315                 320

Ser Pro Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys
                325                 330                 335

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

Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asp Phe
        355                 360                 365

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

Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr
385                 390                 395                 400

Phe Ile Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala Gly
                405                 410                 415

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

Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
        435                 440
```

<210> 45
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-2 LCDR1

<400> 45

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

<210> 46
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-2 LCDR2

<400> 46

Ala Thr Ser Asn Leu Ala Ser
1 5

<210> 47
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-3 LCDR3

<400> 47

Gln Gln Trp Ser Ser Asp Pro Leu Thr
1 5

<210> 48
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-2 HCDR1

<400> 48

Asp Tyr Phe Ile His
1 5

<210> 49
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-2 HCDR2

<400> 49

Arg Leu Asp Pro Glu Asp Gly Glu Ser Asp Tyr Ala Pro Lys Phe Gln
1 5 10 15

Asp

<210> 50
<211> 12
<212> PRT

<213> Artificial Sequence

<220>
<223> Ab-2 HCDR3

<400> 50

Glu Asp Tyr Asp Gly Thr Tyr Thr Phe Phe Pro Tyr
1 5 10

<210> 51
<211> 642
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<223> Ab-2 light chain (no signal)

<400> 51
caaattgttc tctcccagtc tccagcaatc ctgtctacat ctccagggga gaaggtcaca 60

atgacttgca gggccagctc aagtgtatat tacatgcact ggtaccagca gaagccagga 120

tcctcccccа aaccctggat ttatgccaca tccaacctgg cttctggagt ccctgttcgc 180

ttcagtggca gtgggtctgg gacctcttac tctctcacaa tcaccagagt ggaggctgaa 240

gatgctgcca cttattactg ccagcagtgg agtagtgacc cactcacgtt cggtgctggg 300

accaagctgg agctgaaacg ggctgatgct gcaccaactg tatccatctt cccaccatcc 360

agtgagcagt taacatctgg aggtgcctca gtcgtgtgct tcttgaacaa cttctacccc 420

aaagacatca atgtcaagtg gaagattgat ggcagtgaac gacaaaatgg cgtcctgaac 480

agttggactg atcaggacag caaagacagc acctacagca tgagcagcac cctcacgttg 540

accaaggacg agtatgaacg acataacagc tatacctgtg aggccactca caagacatca 600

acttcaccca ttgtcaagag cttcaacagg aatgagtgtt ag 642

<210> 52
<211> 213
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<223> Ab-2 light chain (no signal)

<400> 52

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

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

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

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

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

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

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

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

Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn
    130                 135                 140

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

Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser
                165                 170                 175

Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr
            180                 185                 190

Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser Phe
        195                 200                 205

Asn Arg Asn Glu Cys
    210
```

<210> 53
<211> 1338
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<223> Ab-2 heavy chain (no signal)

<400> 53

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gaggttcagg tgcagcagtc tgggccagaa cttgtgaagc caggggcctc agtcaagttg       60

tcctgcacag cttctggctt caacattaaa gactacttta tacactgggt gaagcagagg      120

cctgaacagg gcctggagtg gattggaagg cttgatcctg aggatggtga aagtgattat      180

gccccgaagt tccaggacaa ggccattatg acagcagaca catcatccaa cacagcctat      240

cttcagctca gaagcctgac atctgaggac actgccatct attattgtga gagagaggac      300

tacgatggta cctacacctt ttttccttac tggggccaag ggactctggt cactgtctct      360

gcagccaaaa cgacacccca atctgtctat ccactggccc ctggatctgc tgcccaaact      420
```

aactccatgg tgaccctggg atgcctggtc aagggctatt tccctgagcc agtgacagtg 480

acctggaact ctggatccct gtccagcggt gtgcacacct tcccagctgt cctgcagtct 540

gacctctaca ctctgagcag ctcagtgact gtcccctcca gcacctggcc cagcgagacc 600

gtcacctgca acgttgccca cccggccagc agcaccaagg tggacaagaa aattgtgccc 660

agggattgtg gttgtaagcc ttgcatatgt acagtcccag aagtatcatc tgtcttcatc 720

ttcccccaa agcccaagga tgtgctcacc attactctga ctcctaaggt cacgtgtgtt 780

gtggtagaca tcagcaagga tgatcccgag gtccagttca gctggtttgt agatgatgtg 840

gaggtgcaca cagctcagac gcaaccccgg gaggagcagt tcaacagcac tttccgctca 900

gtcagtgaac ttcccatcat gcaccaggac tggctcaatg gcaaggagtt caaatgcagg 960

gtcaacagtg cagctttccc tgcccccatc gagaaaacca tctccaaaac caaaggcaga 1020

ccgaaggctc cacaggtgta caccattcca cctcccaagg agcagatggc caaggataaa 1080

gtcagtctga cctgcatgat aacagacttc ttccctgaag acattactgt ggagtggcag 1140

tggaatgggc agccagcgga gaactacaag aacactcagc ccatcatgga cacagatggc 1200

tcttacttca tctacagcaa gctcaatgtg cagaagagca actgggaggc aggaaatact 1260

ttcacctgct ctgtgttaca tgagggcctg cacaaccacc atactgagaa gagcctctcc 1320

cactctcctg gtaaatga 1338

<210> 54
<211> 445
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<223> Ab-2 heavy chain (no signal)

<400> 54

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

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

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

Gly Arg Leu Asp Pro Glu Asp Gly Glu Ser Asp Tyr Ala Pro Lys Phe
50 55 60

Gln Asp Lys Ala Ile Met Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
65 70 75 80

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

```
Glu Arg Glu Asp Tyr Asp Gly Thr Tyr Thr Phe Phe Pro Tyr Trp Gly
            100                 105                 110

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

Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val
    130                 135                 140

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

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

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

Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro
        195                 200                 205

Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly
    210                 215                 220

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

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

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

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

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

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

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

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

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

Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln
```

370 375 380

Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly
385 390 395 400

Ser Tyr Phe Ile Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu
405 410 415

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

His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
435 440 445

<210> 55
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-3 and Ab-15 LCDR1

<400> 55

Ser Val Ser Ser Thr Ile Ser Ser Asn His Leu His
1 5 10

<210> 56
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-3 and Ab-15 LCDR2

<400> 56

Gly Thr Ser Asn Leu Ala Ser
1 5

<210> 57
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-3 and Ab-15 LCDR3

<400> 57

Gln Gln Trp Ser Ser Tyr Pro Leu Thr
1 5

<210> 58
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-3 and Ab-15 HCDR1

<400> 58

Asp Phe Tyr Leu His
1 5

<210> 59
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-3 and Ab-15 HCDR2

<400> 59

Arg Ile Asp Pro Glu Asn Gly Asp Thr Leu Tyr Asp Pro Lys Phe Gln
1 5 10 15

Asp

<210> 60
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-3 and Ab-15 HCDR3

<400> 60

Glu Ala Asp Tyr Phe His Asp Gly Thr Ser Tyr Trp Tyr Phe Asp Val
1 5 10 15

<210> 61
<211> 648
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<223> Ab-3 light chain

<400> 61
gaaattgtgc tcacccagtc tccagcactc atggctgcat ctccggggga gaaggtcacc 60

atcacctgca gtgtcagttc aactataagt tccaaccact tgcactggtt ccagcagaag 120

tcagacacct cccccaaacc ctggatttat ggcacatcca acctggcttc tggagtccct 180

gttcgcttca gtggcagtgg atctgggacc tcttattctc tcacaatcag cagcatggag 240

gctgaggatg ctgccactta ttactgtcaa cagtggagta gttacccact cacgttcggc 300

gctgggacca agctggagct gagacgggct gatgctgcac caactgtatc catcttccca 360

ccatccagtg agcagttaac atctggaggt gcctcagtcg tgtgcttctt gaacaacttc 420

taccccaaag acatcaatgt caagtggaag attgatggca gtgaacgaca aaatggcgtc 480

ctgaacagtt ggactgatca ggacagcaaa gacagcacct acagcatgag cagcaccctc 540

acgttgacca aggacgagta tgaacgacat aacagctata cctgtgaggc cactcacaag 600

acatcaactt cacccattgt caagagcttc aacaggaatg agtgttag 648

<210> 62
<211> 215
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<223> Ab-3 light chain (no signal)

<400> 62

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

Glu Lys Val Thr Ile Thr Cys Ser Val Ser Ser Thr Ile Ser Ser Asn
20 25 30

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

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

Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu
65 70 75 80

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

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

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

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

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

Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met
165 170 175

Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser
180 185 190

Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys
195 200 205

Ser Phe Asn Arg Asn Glu Cys
210 215

<210> 63
<211> 1350
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<223> Ab-3 heavy chain

<400> 63
gaggttcagc tgcagcagtc tggggctgaa cttgtgaggc caggggcctt agtcaagttg 60

tcctgcacag cttctgactt caacattaaa gacttctatc tacactggat gaggcagcgg 120

cctgaacagg gcctggactg gattggaagg attgatcctg agaatggtga tactttatat 180

gacccgaagt tccaggacaa ggccactctt acaacagaca catcctccaa cacagcctac 240

ctgcagctca gcggcctgac atctgagacc actgccgtct attactgttc tagagaggcg 300

gattatttcc acgatggtac ctcctactgg tacttcgatg tctggggcgc agggaccaca 360

atcaccgtct cctcagccaa aacgacaccc ccatctgtct atccactggc ccctggatct 420

gctgcccaaa ctaactccat ggtgaccctg ggatgcctgg tcaagggcta tttccctgag 480

ccagtgacag tgacctggaa ctctggatcc ctgtccagcg gtgtgcacac cttcccagct 540

gtcctgcagt ctgacctcta cactctgagc agctcagtga ctgtccctc cagcacctgg 600

cccagcgaga ccgtcacctg caacgttgcc cacccggcca gcagcaccaa ggtggacaag 660

aaaattgtgc ccagggattg tggttgtaag ccttgcatat gtacagtccc agaagtatca 720

tctgtcttca tcttcccccc aaagcccaag gatgtgctca ccattactct gactcctaag 780

gtcacgtgtg ttgtggtaga catcagcaag gatgatcccg aggtccagtt cagctggttt 840

gtagatgatg tggaggtgca cacagctcag acgcaacccc gggaggagca gttcaacagc 900

actttccgct cagtcagtga acttcccatc atgcaccagg actggctcaa tggcaaggag 960

ttcaaatgca gggtcaacag tgcagctttc cctgccccca tcgagaaaac catctccaaa 1020

accaaaggca gaccgaaggc tccacaggtg tacaccattc cacctcccaa ggagcagatg 1080

gccaaggata aagtcagtct gacctgcatg ataacagact tcttccctga agacattact 1140

gtggagtggc agtggaatgg gcagccagcg gagaactaca agaacactca gcccatcatg 1200

gacacagatg gctcttactt catctacagc aagctcaatg tgcagaagag caactgggag 1260

gcaggaaata ctttcacctg ctctgtgtta catgagggcc tgcacaacca ccatactgag 1320

aagagcctct cccactctcc tggtaaatga 1350

<210> 64
<211> 449
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<223> Ab-3 heavy chain (no signal)

<400> 64

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

Leu Val Lys Leu Ser Cys Thr Ala Ser Asp Phe Asn Ile Lys Asp Phe
            20                  25                  30

Tyr Leu His Trp Met Arg Gln Arg Pro Glu Gln Gly Leu Asp Trp Ile
        35                  40                  45

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

Gln Asp Lys Ala Thr Leu Thr Thr Asp Thr Ser Ser Asn Thr Ala Tyr
65                  70                  75                  80

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

Ser Arg Glu Ala Asp Tyr Phe His Asp Gly Thr Ser Tyr Trp Tyr Phe
            100                 105                 110

Asp Val Trp Gly Ala Gly Thr Thr Ile Thr Val Ser Ser Ala Lys Thr
        115                 120                 125

Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr
    130                 135                 140

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

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

Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser
            180                 185                 190

Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn
        195                 200                 205

Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro
    210                 215                 220

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

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

Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp
            260                 265                 270
```

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

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

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

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

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

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

Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln
    370                 375                 380

Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met
385                 390                 395                 400

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

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

Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly
        435                 440                 445

Lys
```

<210> 65
<211> 324
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<223> Ab-15 light variable

<400> 65
gacatccaga tgacccagtc tccatcctcc ctctcagcat ccgtaggcga tagagttaca 60

ataacatgca gcgtatcatc aactatatca tcaaatcatc ttcattggtt ccaacagaaa 120

cccggcaaag cacctaaatc acttatatac ggcacatcaa atctcgcatc aggcgttcct 180

tcaagatttt caggctctgg ctcaggcacc gactttactc ttacaatatc ctccctccaa 240

cccgaagact tcgcaaccta ttactgtcaa caatggtcct catatccact cacatttggc 300

ggcggcacaa aagtagaaat taaa 324

<210> 66
<211> 108
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<223> Ab-15 light variable

<400> 66

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

Asp Arg Val Thr Ile Thr Cys Ser Val Ser Ser Thr Ile Ser Ser Asn
20 25 30

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

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

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

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

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

<210> 67
<211> 375
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<223> Ab-15 heavy variable

<400> 67
gaggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctgactt caacattaaa gacttctatc tacactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gattggaagg attgatcctg agaatggtga tactttatat 180

gacccgaagt tccaggacaa ggtcaccatg accacagaca cgtccaccag cacagcctac 240

atggagctga ggagcctgag atctgacgac acggccgtgt attactgtgc gagagaggcg 300

gattatttcc acgatggtac ctcctactgg tacttcgatg tctggggccg tggcaccctg 360

gtcaccgtct ctagt 375

<210> 68
<211> 125
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<223> Ab-15 heavy variable

<400> 68

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

Ser Val Lys Val Ser Cys Lys Ala Ser Asp Phe Asn Ile Lys Asp Phe
20 25 30

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

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

Gln Asp Lys Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Glu Ala Asp Tyr Phe His Asp Gly Thr Ser Tyr Trp Tyr Phe
100 105 110

Asp Val Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 69
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized antibody

<220>
<221> misc_feature
<223> Ab-15 light chain

<400> 69
gacatccaga tgacccagtc tccatcctcc ctctcagcat ccgtaggcga tagagttaca 60

ataacatgca gcgtatcatc aactatatca tcaaatcatc ttcattggtt ccaacagaaa 120

cccggcaaag cacctaaatc acttatatac ggcacatcaa atctcgcatc aggcgttcct 180

tcaagatttt caggctctgg ctcaggcacc gactttactc ttacaatatc ctccctccaa 240

cccgaagact tcgcaaccta ttactgtcaa caatggtcct catatccact cacatttggc 300

ggcggcacaa aagtagaaat taaacgtacg gtggctgcac catctgtctt catcttcccg 360

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 480

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 600

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgt 645

<210> 70
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized antibody sequence

<220>
<221> MISC_FEATURE
<223> Ab-15 light chain

<400> 70

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

Asp Arg Val Thr Ile Thr Cys Ser Val Ser Ser Thr Ile Ser Ser Asn
20 25 30

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

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

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

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

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

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

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

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

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

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

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

Ser Phe Asn Arg Gly Glu Cys
    210                 215
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<210> 71
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized antibody

<220>
<221> misc_feature
<223> Ab-15 heavy chain

<400> 71

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gaggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc      60

tcctgcaagg cttctgactt caacattaaa gacttctatc tacactgggt gcgacaggcc     120

cctggacaag ggcttgagtg gattggaagg attgatcctg agaatggtga tactttatat     180

gacccgaagt tccaggacaa ggtcaccatg accacagaca cgtccaccag cacagcctac     240

atggagctga ggagcctgag atctgacgac acggccgtgt attactgtgc gagagaggcg     300

gattatttcc acgatggtac ctcctactgg tacttcgatg tctggggccg tggcaccctg     360

gtcaccgtct ctagtgcctc caccaagggc ccatcggtct tcccctggc gccctgctcc      420

aggagcacct ccgagagcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa     480

ccggtgacgg tgtcgtggaa ctcaggcgct ctgaccagcg gcgtgcacac cttcccagct     540

gtcctacagt cctcaggact ctactccctc agcagcgtgg tgaccgtgcc ctccagcaac     600

ttcggcaccc agacctacac ctgcaacgta gatcacaagc ccagcaacac caaggtggac     660

aagacagttg agcgcaaatg ttgtgtcgag tgcccaccgt gcccagcacc acctgtggca     720

ggaccgtcag tcttcctctt ccccccaaaa cccaaggaca ccctcatgat ctcccggacc     780

cctgaggtca cgtgcgtggt ggtggacgtg agccacgaag accccgaggt ccagttcaac     840

tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccacggga ggagcagttc     900

aacagcacgt tccgtgtggt cagcgtcctc accgttgtgc accaggactg gctgaacggc     960

aaggagtaca agtgcaaggt ctccaacaaa ggcctcccag ccccatcga gaaaaccatc     1020

tccaaaacca aagggcagcc ccgagaacca caggtgtaca ccctgccccc atcccgggag     1080

gagatgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta ccccagcgac     1140

atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacacctccc     1200
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atgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg 1260

tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1320

acgcagaaga gcctctccct gtctccgggt aaa 1353

<210> 72
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized antibody sequence

<220>
<221> MISC_FEATURE
<223> Ab-15 heavy chain

<400> 72

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

Ser Val Lys Val Ser Cys Lys Ala Ser Asp Phe Asn Ile Lys Asp Phe
20 25 30

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

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

Gln Asp Lys Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Glu Ala Asp Tyr Phe His Asp Gly Thr Ser Tyr Trp Tyr Phe
100 105 110

Asp Val Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
115 120 125

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

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

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

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

```
Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys
        195                 200                 205

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

Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala
225                 230                 235                 240

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

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

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

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

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

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

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

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

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

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

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

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

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

Pro Gly Lys
    450
```

<210> 73
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-4 and Ab-5 LCDR1

<400> 73

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

<210> 74
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-4 and Ab-5 LCDR2

<400> 74

Tyr Thr Ser Arg Leu Leu Ser
1 5

<210> 75
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-4 and Ab-5 LCDR3

<400> 75

Gln Gln Gly Asp Thr Leu Pro Tyr Thr
1 5

<210> 76
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-4 and Ab-5 HCDR1

<400> 76

Asp Tyr Asn Met His
1 5

<210> 77
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-4 and Ab-5 HCDR2

<400> 77

Glu Ile Asn Pro Asn Ser Gly Gly Ala Gly Tyr Asn Gln Lys Phe Lys
1 5 10 15

Gly

<210> 78
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> HCDR3

<400> 78

Leu Gly Tyr Asp Asp Ile Tyr Asp Asp Trp Tyr Phe Asp Val
1 5 10

<210> 79
<211> 645
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<223> Ab-4 light chain

<400> 79
gatatccaga tgacacagat tacatcctcc ctgtctgcct ctctgggaga cagggtctcc 60

atcagttgca gggcaagtca agacattagc aattatttaa actggtatca gcagaaacca 120

gatggaactt ttaaactcct tatcttctac acatcaagat tactctcagg agtcccatca 180

aggttcagtg gcagtgggtc tggaacagat tattctctca ccatttacaa cctggagcaa 240

gaagattttg ccacttactt ttgccaacag ggagatacgc ttccgtacac tttcggaggg 300

gggaccaagc tggaaataaa acgggctgat gctgcaccaa ctgtatccat cttcccacca 360

tccagtgagc agttaacatc tggaggtgcc tcagtcgtgt gcttcttgaa caacttctac 420

cccaaagaca tcaatgtcaa gtggaagatt gatggcagtg aacgacaaaa tggcgtcctg 480

aacagttgga ctgatcagga cagcaaagac agcacctaca gcatgagcag caccctcacg 540

ttgaccaagg acgagtatga acgacataac agctatacct gtgaggccac tcacaagaca 600

tcaacttcac ccattgtcaa gagcttcaac aggaatgagt gttag 645

<210> 80
<211> 214
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<223> Ab-4 light chain

<400> 80

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Phe Lys Leu Leu Ile
        35                  40                  45

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

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

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

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

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

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

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

Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser
                165                 170                 175

Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr
            180                 185                 190

Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser
        195                 200                 205

Phe Asn Arg Asn Glu Cys
    210
```

<210> 81
<211> 1344
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<223> Ab-4 heavy chain

<400> 81
gaggtccaac tgcaacagtc tggacctgaa ctaatgaagc ctggggcttc agtgaagatg 60

tcctgcaagg cttctggata tacattcact gactacaaca tgcactgggt gaagcagaac 120

caaggaaaga ccctagagtg gataggagaa attaatccta acagtggtgg tgctggctac 180

```
aaccagaagt tcaagggcaa ggccacattg actgtagaca agtcctccac cacagcctac      240
atggagctcc gcagcctgac atctgaggac tctgcagtct attactgtgc aagattgggc      300
tacgatgata tctacgacga ctggtacttc gatgtctggg gcgcagggac cacggtcacc      360
gtctcctcag ccaaaacgac acccccatct gtctatccac tggccctgg atctgctgcc       420
caaactaact ccatggtgac cctgggatgc ctggtcaagg gctatttccc tgagccagtg      480
acagtgacct ggaactctgg atccctgtcc agcggtgtgc acaccttccc agctgtcctg      540
cagtctgacc tctacactct gagcagctca gtgactgtcc cctccagcac ctggcccagc      600
gagaccgtca cctgcaacgt tgcccacccg gccagcagca ccaaggtgga caagaaaatt      660
gtgcccaggg attgtggttg taagccttgc atatgtacag tcccagaagt atcatctgtc      720
ttcatcttcc ccccaaagcc caaggatgtg ctcaccatta ctctgactcc taaggtcacg      780
tgtgttgtgg tagacatcag caaggatgat cccgaggtcc agttcagctg gtttgtagat      840
gatgtggagg tgcacacagc tcagacgcaa ccccgggagg agcagttcaa cagcactttc      900
cgctcagtca gtgaacttcc catcatgcac caggactggc tcaatggcaa ggagttcaaa      960
tgcagggtca acagtgcagc tttccctgcc cccatcgaga aaaccatctc caaaaccaaa     1020
ggcagaccga aggctccaca ggtgtacacc attccacctc ccaaggagca gatggccaag     1080
gataaagtca gtctgacctg catgataaca gacttcttcc ctgaagacat tactgtggag     1140
tggcagtgga atgggcagcc agcggagaac tacaagaaca ctcagcccat catggacaca     1200
gatggctctt acttcatcta cagcaagctc aatgtgcaga agagcaactg ggaggcagga     1260
aatactttca cctgctctgt gttacatgag ggcctgcaca accaccatac tgagaagagc     1320
ctctcccact ctcctggtaa atga                                            1344
```

<210> 82
<211> 447
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<223> Ab-4 heavy chain

<400> 82

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

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

Asn Met His Trp Val Lys Gln Asn Gln Gly Lys Thr Leu Glu Trp Ile
        35                  40                  45

Gly Glu Ile Asn Pro Asn Ser Gly Gly Ala Gly Tyr Asn Gln Lys Phe
    50                  55                  60
```

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

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

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

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

Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser
    130                 135                 140

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

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

Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr
            180                 185                 190

Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala
        195                 200                 205

His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp
    210                 215                 220

Cys 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

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 Ile 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
```

<210> 83
<211> 321
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<223> Ab-5 light variable

<400> 83

```
gacatccaga tgacccagtc tccatcctcc ctctccgcat ccgtaggcga ccgcgtaacc       60

ataacatgta gagcatctca agatatttcc aactatttga attggtacca acaaaaaccc      120

ggcaaagcac ctaaactcct catttactat acatcaagac tcctctccgg cgttccatca      180

cgattctcag gctccggctc cggcacagat ttcacactca ctatttcctc cctccaacca      240

gaagattttg caacctatta ctgtcaacaa ggcgatacac tcccatacac attcggcggc      300

ggcacaaaag ttgaaattaa a                                                321
```

<210> 84
<211> 107
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<223> Ab-5 light variable

<400> 84

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr
```

```
            20                  25                  30

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

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

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

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

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

<210> 85
<211> 369
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<223> Ab-5 heavy variable

<400> 85

```
gaggtgcagc tggtgcagag cggcgccgag gtaaaaaaac caggagcaag cgttaaagtt       60

tcttgtaaag caagcggata tacatttaca gattacaaca tgcattgggt aagacaagcg      120

ccaggacaag gattggaatg gatgggcgaa attaacccta atagtggagg agcaggctac      180

aatcaaaaat tcaaagggag agttacaatg acaacagaca caagcacttc aacagcatat      240

atggaactgc gatcacttag aagcgacgat acagctgtat actattgcgc acgacttggg      300

tatgatgata tatatgatga ctggtatttc gatgtttggg gccagggaac aacagttacc      360

gtctctagt                                                              369
```

<210> 86
<211> 123
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<223> Ab-5 heavy variable

<400> 86

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

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

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

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

Lys Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

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

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

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

<210> 87
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized antibody

<220>
<221> misc_feature
<223> Ab-5 light chain

<400> 87

```
gacatccaga tgacccagtc tccatcctcc ctctccgcat ccgtaggcga ccgcgtaacc       60

ataacatgta gagcatctca agatatttcc aactatttga attggtacca acaaaaaccc      120

ggcaaagcac ctaaactcct catttactat acatcaagac tcctctccgg cgttccatca      180

cgattctcag gctccggctc cggcacagat ttcacactca ctatttcctc cctccaacca      240

gaagattttg caacctatta ctgtcaacaa ggcgatacac tcccatacac attcggcggc      300

ggcacaaaag ttgaaattaa acgtacggtg gctgcaccat ctgtcttcat cttcccgcca      360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat      420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag      480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg      540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc      600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt                         642
```

<210> 88
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized antibody

<220>
<221> MISC_FEATURE
<223> Ab-5 light chain

<400> 88

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

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

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

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

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

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

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

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys
    210
```

<210> 89
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>

<223> Humanized antibody

<220>
<221> misc_feature
<223> Ab-5 heavy chain

<400> 89
gaggtgcagc tggtgcagag cggcgccgag gtaaaaaaac caggagcaag cgttaaagtt 60

tcttgtaaag caagcggata tacatttaca gattacaaca tgcattgggt aagacaagcg 120

ccaggacaag gattggaatg gatgggcgaa attaacccta atagtggagg agcaggctac 180

aatcaaaaat tcaaagggag agttacaatg acaacagaca caagcacttc aacagcatat 240

atggaactgc gatcacttag aagcgacgat acagctgtat actattgcgc acgacttggg 300

tatgatgata tatatgatga ctggtatttc gatgtttggg gccagggaac aacagttacc 360

gtctctagtg cctccaccaa gggcccatcg gtcttccccc tggcgccctg ctccaggagc 420

acctccgaga gcacagcggc cctgggctgc ctggtcaagg actacttccc cgaaccggtg 480

acggtgtcgt ggaactcagg cgctctgacc agcggcgtgc acaccttccc agctgtccta 540

cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag caacttcggc 600

acccagacct acacctgcaa cgtagatcac aagcccagca acaccaaggt ggacaagaca 660

gttgagcgca aatgttgtgt cgagtgccca ccgtgcccag caccacctgt ggcaggaccg 720

tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gaccccctgag 780

gtcacgtgcg tggtggtgga cgtgagccac gaagaccccg aggtccagtt caactggtac 840

gtggacggcg tggaggtgca taatgccaag acaaagccac gggaggagca gttcaacagc 900

acgttccgtg tggtcagcgt cctcaccgtt gtgcaccagg actggctgaa cggcaaggag 960

tacaagtgca aggtctccaa caaaggcctc ccagccccca tcgagaaaac catctccaaa 1020

accaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggaggagatg 1080

accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctaccccag cgacatcgcc 1140

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacacc tcccatgctg 1200

gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320

aagagcctct ccctgtctcc gggtaaa 1347

<210> 90
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized antibody

<220>
<221> MISC_FEATURE
<223> Ab-5 heavy chain

<400> 90

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

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

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

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

Lys Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys
```

<210> 91
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-6 LCDR1

<400> 91

```
Arg Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn
1               5                   10
```

<210> 92
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-6 LCDR2

<400> 92

Tyr Thr Ser Arg Leu His Ser
1 5

<210> 93
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-6 LCDR3

<400> 93

Gln Gln Gly Asp Thr Leu Pro Tyr Thr
1 5

<210> 94
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-6 HCDR1

<400> 94

Asp Tyr Asn Met His
1 5

<210> 95
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-6 HCDR2

<400> 95

Glu Ile Asn Pro Asn Ser Gly Gly Ser Gly Tyr Asn Gln Lys Phe Lys
1 5 10 15

Gly

<210> 96
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-6 HCDR3

<400> 96

Leu Val Tyr Asp Gly Ser Tyr Glu Asp Trp Tyr Phe Asp Val
1 5 10

<210> 97
<211> 645

<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<223> Ab-6 light chain

<400> 97
gatatccaga tgacacagac tacatcctcc ctgtctgcct ctctgggaga cagagtcacc 60

atcagttgca gggcaagtca ggacattagc aattatttaa actggtttca gcagaaacca 120

gatggaactc ttaaactcct gatcttctac acatcaagat tacactcagg agttccatca 180

aggttcagtg gcagtgggtc tggaacagat tattctctca ccattagcaa cctggagcaa 240

gaagatattg ccacttactt ttgccaacag ggtgatacgc ttccgtacac gttcgggggg 300

gggaccaagc tggaaataag acgggctgat gctgcaccaa ctgtatccat cttcccacca 360

tccagtgagc agttaacatc tggaggtgcc tcagtcgtgt gcttcttgaa caacttctac 420

cccaaagaca tcaatgtcaa gtggaagatt gatggcagtg aacgacaaaa tggcgtcctg 480

aacagttgga ctgatcagga cagcaaagac agcacctaca gcatgagcag caccctcacg 540

ttgaccaagg acgagtatga acgacataac agctatacct gtgaggccac tcacaagaca 600

tcaacttcac ccattgtcaa gagcttcaac aggaatgagt gttag 645

<210> 98
<211> 214
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<223> Ab-6 light chain

<400> 98

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

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

Leu Asn Trp Phe Gln Gln Lys Pro Asp Gly Thr Leu Lys Leu Leu Ile
35 40 45

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

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

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

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Arg Arg Ala Asp Ala Ala

```
            100                 105                 110

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

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

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

Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser
                165                 170                 175

Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr
            180                 185                 190

Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser
        195                 200                 205

Phe Asn Arg Asn Glu Cys
    210
```

<210> 99
<211> 1344
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<223> Ab-6 heavy chain

<400> 99

```
gaggtccagc tgcaacagtc tggacctgaa ctaatgaagc ctggggcttc agtgaagatg       60

tcctgcaagg cttctggata cacattcact gactacaaca tgcactgggt gaaacagaac      120

caaggaaaga gcctagagtg gataggagaa attaatccta acagtggtgg tagtggctac      180

aaccaaaagt tcaaaggcaa ggccacattg actgtagaca agtcttccag cacagcctac      240

atggagctcc gcagcctgac atctgaggac tctgcagtct attactgtgc aagattggtc      300

tacgatggca gctacgagga ctggtacttc gatgtctggg gcgcagggac cacggtcacc      360

gtctcctcag ccaaaacgac acccccatct gtctatccac tggcccctgg atctgctgcc      420

caaactaact ccatggtgac cctgggatgc ctggtcaagg gctatttccc tgagccagtg      480

acagtgacct ggaactctgg atccctgtcc agcggtgtgc acaccttccc agctgtcctg      540

cagtctgacc tctacactct gagcagctca gtgactgtcc cctccagcac ctggcccagc      600

gagaccgtca cctgcaacgt tgcccacccg gccagcagca ccaaggtgga caagaaaatt      660

gtgcccaggg attgtggttg taagccttgc atatgtacag tcccagaagt atcatctgtc      720

ttcatcttcc ccccaaagcc caaggatgtg ctcaccatta ctctgactcc taaggtcacg      780

tgtgttgtgg tagacatcag caaggatgat cccgaggtcc agttcagctg gtttgtagat      840
```

gatgtggagg tgcacacagc tcagacgcaa ccccgggagg agcagttcaa cagcactttc 900

cgctcagtca gtgaacttcc catcatgcac caggactggc tcaatggcaa ggagttcaaa 960

tgcagggtca acagtgcagc tttccctgcc cccatcgaga aaaccatctc caaaaccaaa 1020

ggcagaccga aggctccaca ggtgtacacc attccacctc ccaaggagca gatggccaag 1080

gataaagtca gtctgacctg catgataaca gacttcttcc ctgaagacat tactgtggag 1140

tggcagtgga atgggcagcc agcggagaac tacaagaaca ctcagcccat catggacaca 1200

gatggctctt acttcatcta cagcaagctc aatgtgcaga agagcaactg ggaggcagga 1260

aatactttca cctgctctgt gttacatgag ggcctgcaca accaccatac tgagaagagc 1320

ctctcccact ctcctggtaa atga 1344

<210> 100
<211> 447
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<223> Ab-6 heavy chain

<400> 100

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

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

Asn Met His Trp Val Lys Gln Asn Gln Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Glu Ile Asn Pro Asn Ser Gly Gly Ser Gly Tyr Asn Gln Lys Phe
50 55 60

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

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

Ala Arg Leu Val Tyr Asp Gly Ser Tyr Glu Asp Trp Tyr Phe Asp Val
100 105 110

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

Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser
130 135 140

Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val

```
145                 150                 155                 160

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

Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr
            180                 185                 190

Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala
        195                 200                 205

His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp
    210                 215                 220

Cys 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

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 Ile 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
```

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His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
        435                 440                 445


<210>  101
<211>  11
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Ab-7 LCDR1

<400>  101

Arg Ala Ser Gln Val Ile Thr Asn Tyr Leu Tyr
1               5                   10


<210>  102
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Ab-7 LCDR2

<400>  102

Tyr Thr Ser Arg Leu His Ser
1               5


<210>  103
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Ab-7 LCDR3

<400>  103

Gln Gln Gly Asp Thr Leu Pro Tyr Thr
1               5


<210>  104
<211>  5
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Ab-7 HCDR1

<400>  104

Asp Tyr Asn Met His
1               5


<210>  105
<211>  17
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Ab-7 HCDR2
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<400> 105

Glu Ile Asn Pro Asn Ser Gly Gly Ala Gly Tyr Asn Gln Gln Phe Lys
1 5 10 15

Gly

<210> 106
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-7 HCDR3

<400> 106

Leu Gly Tyr Val Gly Asn Tyr Glu Asp Trp Tyr Phe Asp Val
1 5 10

<210> 107
<211> 642
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<223> Ab-7 light chain

<400> 107
gatatccaga tgacacagac tacatcctcc ctgtctgcct ctctgggaga cagagtcacc 60

atctgttgca gggcaagtca ggtcattacc aattatttat actggtatca gcagaaacca 120

gatggaactt ttaaactcct gatctactac acatcaagat tacactcagg agtcccatca 180

aggttcagtg gcagtgggtc tggaacagat tattctctca ccattagcaa cctggaacag 240

gaagatattg ccacttactt ttgccaacag ggtgatacgc ttccgtacac gttcggaggg 300

gggaccaagc tggaaataaa acgggctgat gctgcaccaa ctgtatccat cttcccacca 360

tccagtgagc agttaacatc tggaggtgcc tcagtcgtgt gcttcttgaa caacttctac 420

cccaaagaca tcaatgtcaa gtggaagatt gatggcagtg aacgacaaaa tggcgtcctg 480

aacagttgga ctgatcagga cagcaaagac agcacctaca gcatgagcag caccctcacg 540

ttgaccaagg acgagtatga acgacataac agctatacct gtgaggccac tcacaagaca 600

tcaacttcac ccattgtcaa gagcttcaac aggaatgagt gt 642

<210> 108
<211> 214
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<223> Ab-7 light chain

<400> 108

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

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

Leu Tyr Trp Tyr Gln Gln Lys Pro Asp Gly Thr Phe Lys Leu Leu Ile
35 40 45

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

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

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

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

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

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

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

Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser
165 170 175

Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr
180 185 190

Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser
195 200 205

Phe Asn Arg Asn Glu Cys
210

<210> 109
<211> 1341
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<223> Ab-7 heavy chain

<400> 109

gaggtccagc tgcaacagtc tggacctgaa ctaatgaagc ctggggcttc agtgaagatg 60

tcctgcaagg cttctggata cacattcact gactacaaca tgcactggat gaagcagaac 120

caaggaaaga gcctagaatg gataggagaa attaatccta acagtggtgg tgctggctac 180

aaccagcagt tcaaaggcaa ggccacattg actgtagaca agtcctccag gacagcctac 240

atggagctcc gcagcctgac atctgaggac tctgcagtct attactgtgc aagattgggc 300

tacgttggta attacgagga ctggtacttc gatgtctggg gcgcagggac cacggtcacc 360

gtctcctcag ccaaaacgac acccccatct gtctatccac tggcccctgg atctgctgcc 420

caaactaact ccatggtgac cctgggatgc ctggtcaagg gctatttccc tgagccagtg 480

acagtgacct ggaactctgg atccctgtcc agcggtgtgc acaccttccc agctgtcctg 540

cagtctgacc tctacactct gagcagctca gtgactgtcc cctccagcac ctggcccagc 600

gagaccgtca cctgcaacgt tgcccacccg gccagcagca ccaaggtgga caagaaaatt 660

gtgcccaggg attgtggttg taagccttgc atatgtacag tcccagaagt atcatctgtc 720

ttcatcttcc ccccaaagcc caaggatgtg ctcaccatta ctctgactcc taaggtcacg 780

tgtgttgtgg tagacatcag caaggatgat cccgaggtcc agttcagctg gtttgtagat 840

gatgtggagg tgcacacagc tcagacgcaa ccccgggagg agcagttcaa cagcactttc 900

cgctcagtca gtgaacttcc catcatgcac caggactggc tcaatggcaa ggagttcaaa 960

tgcagggtca acagtgcagc tttccctgcc cccatcgaga aaaccatctc caaaaccaaa 1020

ggcagaccga aggctccaca ggtgtacacc attccacctc ccaaggagca gatggccaag 1080

gataaagtca gtctgacctg catgataaca gacttcttcc ctgaagacat tactgtggag 1140

tggcagtgga atgggcagcc agcggagaac tacaagaaca ctcagcccat catggacaca 1200

gatggctctt acttcatcta cagcaagctc aatgtgcaga agagcaactg ggaggcagga 1260

aatactttca cctgctctgt gttacatgag ggcctgcaca accaccatac tgagaagagc 1320

ctctcccact ctcctggtaa a 1341

<210> 110
<211> 447
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<223> Ab-7 heavy chain

<400> 110

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

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

Asn Met His Trp Met Lys Gln Asn Gln Gly Lys Ser Leu Glu Trp Ile
35 40 45

```
Gly Glu Ile Asn Pro Asn Ser Gly Gly Ala Gly Tyr Asn Gln Gln Phe
    50                  55                  60

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

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

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

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

Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser
    130                 135                 140

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

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

Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr
            180                 185                 190

Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala
        195                 200                 205

His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp
    210                 215                 220

Cys 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
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```
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

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 Ile 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
```

<210> 111
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-8 LCDR1

<400> 111

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Arg Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn
1               5                   10
```

<210> 112
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-8 LCDR2

<400> 112

```
Tyr Thr Ser Arg Leu Leu Ser
1               5
```

<210> 113
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-8 LCDR3

<400> 113

Gln Gln Gly Asp Thr Leu Pro Tyr Thr
1 5

<210> 114
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-8 HCDR1

<400> 114

Asp Tyr Asn Met His
1 5

<210> 115
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-8 HCDR2

<400> 115

Glu Ile Asn Pro Asn Ser Gly Gly Ala Gly Tyr Asn Gln Lys Phe Lys
1 5 10 15

Gly

<210> 116
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-8 HCDR3

<400> 116

Leu Gly Tyr Asp Asp Ile Tyr Asp Asp Trp Tyr Phe Asp Val
1 5 10

<210> 117
<211> 645
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<223> Ab-8 light chain

<400> 117
gatatccaga tgacacagac tacatcctcc ctgtctgcct ctctgggaga cagggtctcc 60

atcagttgca gggcaagtca agacattagc aattatttaa actggtatca gcagaaacca 120

gatggaactt ttaaactcct tatcttctac acatcaagat tactctcagg agtcccatca 180

aggttcagtg gcagtgggtc tggaacagat tattctctca ccatttacaa cctggagcaa 240

gaagattttg ccacttactt ttgccaacag ggagatacgc ttccgtacac tttcggaggg 300

gggaccaaac tggaaataaa acgggctgat gctgcaccaa ctgtatccat cttcccacca 360

tccagtgagc agttaacatc tggaggtgcc tcagtcgtgt gcttcttgaa caacttctac 420

cccaaagaca tcaatgtcaa gtggaagatt gatggcagtg aacgacaaaa tggcgtcctg 480

aacagttgga ctgatcagga cagcaaagac agcacctaca gcatgagcag caccctcacg 540

ttgaccaagg acgagtatga acgacataac agctatacct gtgaggccac tcacaagaca 600

tcaacttcac ccattgtcaa gagcttcaac aggaatgagt gttag 645

<210> 118
<211> 214
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<223> Ab-8 light chain

<400> 118

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Phe Lys Leu Leu Ile
35 40 45

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

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

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

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

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

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

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

Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser
165 170 175

Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr
180 185 190

Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser
195 200 205

Phe Asn Arg Asn Glu Cys
210

<210> 119
<211> 1344
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<223> Ab-8 heavy chain

<400> 119
gaggtccaac tgcaacagtc tggacctgaa ctaatgaagc ctggggcttc agtgaagatg 60

tcctgcaagg cttctggata tacattcact gactacaaca tgcactgggt gaagcagaac 120

caaggaaaga ccctagactg gataggagaa attaatccta acagtggtgg tgctggctac 180

aaccagaagt tcaagggcaa ggccacattg actgtagaca agtcctccac cacagcctac 240

atggagctcc gcagcctgac atctgaggac tctgcagtct attactgtgc aagattgggc 300

tacgatgata tctacgacga ctggtacttc gatgtctggg gcgcagggac cacggtcacc 360

gtctcctcag ccaaaacgac acccccatct gtctatccac tggccctgg atctgctgcc 420

caaactaact ccatggtgac cctgggatgc ctggtcaagg gctatttccc tgagccagtg 480

acagtgacct ggaactctgg atccctgtcc agcggtgtgc acaccttccc agctgtcctg 540

cagtctgacc tctacactct gagcagctca gtgactgtcc cctccagcac ctggcccagc 600

gagaccgtca cctgcaacgt tgcccacccg gccagcagca ccaaggtgga caagaaaatt 660

gtgcccaggg attgtggttg taagccttgc atatgtacag tcccagaagt atcatctgtc 720

ttcatcttcc ccccaaagcc caaggatgtg ctcaccatta ctctgactcc taaggtcacg 780

tgtgttgtgg tagacatcag caaggatgat cccgaggtcc agttcagctg gtttgtagat 840

gatgtggagg tgcacacagc tcagacgcaa ccccgggagg agcagttcaa cagcactttc 900

cgctcagtca gtgaacttcc catcatgcac caggactggc tcaatggcaa ggagttcaaa 960

tgcagggtca acagtgcagc tttccctgcc cccatcgaga aaaccatctc caaaaccaaa 1020

ggcagaccga aggctccaca ggtgtacacc attccacctc ccaaggagca gatggccaag 1080

gataaagtca gtctgacctg catgataaca gacttcttcc ctgaagacat tactgtggag 1140

tggcagtgga atgggcagcc agcggagaac tacaagaaca ctcagcccat catggacaca 1200

gatggctctt acttcatcta cagcaagctc aatgtgcaga agagcaactg ggaggcagga 1260

aatactttca cctgctctgt gttacatgag ggcctgcaca accaccatac tgagaagagc 1320

ctctcccact ctcctggtaa atga 1344

<210> 120
<211> 447
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<223> Ab-8 heavy chain

<400> 120

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

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

Asn Met His Trp Val Lys Gln Asn Gln Gly Lys Thr Leu Asp Trp Ile
35 40 45

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

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

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

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

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

Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser
130 135 140

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

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

Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr
180 185 190

Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala
195 200 205

```
His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp
    210                 215                 220

Cys 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

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 Ile 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> 121
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-9 LCDR1

<400> 121

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

<210> 122
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-9 LCDR2

<400> 122

Tyr Thr Ser Arg Leu Phe Ser
1 5

<210> 123
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-9 LCDR3

<400> 123

Gln Gln Gly Asp Thr Leu Pro Tyr Thr
1 5

<210> 124
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-9 HCDR1

<400> 124

Asp Tyr Asn Met His
1 5

<210> 125
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-9 HCDR2

<400> 125

Glu Ile Asn Pro Asn Ser Gly Gly Ala Gly Tyr Asn Gln Lys Phe Lys
1 5 10 15

Gly

<210> 126
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-9 HCDR3

<400> 126

Leu Gly Tyr Asp Asp Ile Tyr Asp Asp Trp Tyr Phe Asp Val
1 5 10

<210> 127
<211> 642
<212> DNA
<213> Mus musculus

<400> 127
gatatccaga tgacacagat tacatcctcc ctgtctgcct ctctgggaga cagggtctcc 60

atcagttgca gggcaagtca agacattagc aattatttaa attggtatca gcagaaacca 120

gatggaactt ttaaactcct tatcttctac acatcaagat tattttcagg agtcccatca 180

aggttcagtg gcagtgggtc tggaacagat tattctctca ccatttacaa cctggagcaa 240

gaagattttg ccacttactt ttgccaacag ggagatacgc ttccgtacac tttcggaggg 300

gggaccaagg tggaaataaa acgggctgat gctgcaccaa ctgtatccat cttcccacca 360

tccagtgagc agttaacatc tggaggtgcc tcagtcgtgt gcttcttgaa caacttctac 420

cccaaagaca tcaatgtcaa gtggaagatt gatggcagtg aacgacaaaa tggcgtcctg 480

aacagttgga ctgatcagga cagcaaagac agcacctaca gcatgagcag caccctcacg 540

ttgaccaagg acgagtatga acgacataac agctatacct gtgaggccac tcacaagaca 600

tcaacttcac ccattgtcaa gagcttcaac aggaatgagt gt 642

<210> 128
<211> 214
<212> PRT
<213> Mus musculus

<400> 128

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Phe Lys Leu Leu Ile
35 40 45

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

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

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

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

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

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

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

Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser
                165                 170                 175

Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr
            180                 185                 190

Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser
        195                 200                 205

Phe Asn Arg Asn Glu Cys
    210
```

<210> 129
<211> 1350
<212> DNA
<213> Mus musculus

<400> 129

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gaggtccaac tgcaacagtc tggacctgaa ctaatgaagc ctgggacttc agtgaagatg       60
tcctgcaagg cttctggata tacattcact gactacaaca tgcactgggt gaagcagacc      120
caaggaaaga ccctagagtg gataggagaa attaatccta acagtggtgg tgctggctac      180
aaccagaagt tcaagggcaa ggccacattg actgtagaca agtcctccac cacagcctac      240
atggagctcc gcagcctgac atctgaggac tctgcagtct attactgtgc aaaattgggc      300
tacgatgata tctacgacga ctggtatttc gatgtctggg gcgcagggac cacggtcacc      360
gtctcctcag ccaaaacaac agccccatcg gtctatccac tggccctgt gtgtggagat       420
acaactggct cctcggtgac tctaggatgc ctggtcaagg gttatttccc tgagccagtg      480
accttgacct ggaactctgg atccctgtcc agtgatgtgc acaccttccc agctctcctg      540
cagtctggcc tctacaccct cagcagctca gtgactgtaa ccacctggcc cagccagacc      600
atcacctgca atgtggccca cccggcaagc agcaccaaag tggacaagaa aattgagccc      660
agagggtccc caacacataa accctgtcct ccatgcccag ctcctaacct cttgggtgga      720
ccatccgtct tcatcttccc tccaaagatc aaggatgtac tcatgatctc cctgagcccc      780
atggtcacgt gtgtggtggt ggatgtgagc gaggatgacc cagatgtcca tgtcagctgg      840
ttcgtgaaca acgtggaagt acacacagct cagacacaaa cccatagaga ggattacaac      900
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agtactatcc gggtggtcag tgccctcccc atccagcacc aggactggat gagtggcaag 960

gagttcaaat gcaaggtcaa caacaaagcc ctcccagcgc ccatcgagag aaccatctca 1020

aaacccaaag ggccagtaag agctccacag gtatatgtct tgcctccacc agaagaagag 1080

atgactaaga aacaggtcac tctgacctgc atgatcacag acttcatgcc tgaagacatt 1140

tacgtggagt ggaccaacaa cgggcaaaca gagctaaact acaagaacac tgaaccagtc 1200

ctggactctg atggttctta cttcatgtac agcaagctga gagtggaaaa gaagaactgg 1260

gtggaaagaa atagctactc ctgttcagtg gtccacgagg gtctgcacaa tcaccacacg 1320

actaagagct tctcccggac tccgggtaaa 1350

<210> 130
<211> 450
<212> PRT
<213> Mus musculus

<400> 130

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

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

Asn Met His Trp Val Lys Gln Thr Gln Gly Lys Thr Leu Glu Trp Ile
35 40 45

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

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

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

Ala Lys Leu Gly Tyr Asp Asp Ile Tyr Asp Asp Trp Tyr Phe Asp Val
100 105 110

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

Pro Ser Val Tyr Pro Leu Ala Pro Val Cys Gly Asp Thr Thr Gly Ser
130 135 140

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

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

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

```
            180                 185                 190

Val Thr Thr Trp Pro Ser Gln Thr Ile Thr Cys Asn Val Ala His Pro
        195                 200                 205

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

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

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

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

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

Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Ile Arg
    290                 295                 300

Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys
305                 310                 315                 320

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

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

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

Thr Cys Met Ile Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp
    370                 375                 380

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

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

Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His
            420                 425                 430

Glu Gly Leu His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro
        435                 440                 445

Gly Lys
    450
```

<210> 131
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-10 LCDR1

<400> 131

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

<210> 132
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-10 LCDR2

<400> 132

Tyr Thr Ser Arg Leu Leu Ser
1 5

<210> 133
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-10 LCDR3

<400> 133

Gln Gln Gly Asp Thr Leu Pro Tyr Thr
1 5

<210> 134
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-10 HCDR1

<400> 134

Asp Tyr Asn Met His
1 5

<210> 135
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-10 HCDR2

<400> 135

Glu Ile Asn Pro Asn Ser Gly Gly Ala Gly Tyr Asn Gln Lys Phe Lys

1 5 10 15

Gly

<210> 136
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-10 HCDR3

<400> 136

Leu Gly Tyr Asp Asp Ile Tyr Asp Asp Trp Tyr Phe Asp Val
1 5 10

<210> 137
<211> 645
<212> DNA
<213> Mus musculus

<400> 137
gatatccaga tgacacagac tacatcctcc ctgtctgcct ctctgggaga cagggtctcc 60

atcagttgca gggcaagtca agacattagc aattatttaa actggtatca gcagaaacca 120

gatggaactt ttaaactcct tatcttctac acatcaagat tactctcagg agtcccatca 180

aggttcagtg gcagtgggtc tggaacagat tattctctca ccatttacaa cctggagcaa 240

gaagattttg ccacttactt ttgccaacag ggagatacgc ttccgtacac tttcggaggg 300

gggaccaaac tggaaataaa acgggctgat gctgcaccaa ctgtatccat cttcccacta 360

tccagtgagc agttaacatc tggaggtgcc tcagtcgtgt gcttcttgaa caacttctac 420

cccaaagaca tcaatgtcaa gtggaagatt gatggcagtg aacgacaaaa tggcgtcctg 480

aacagttgga ctgatcagga cagcaaagac agcacctaca gcatgagcag caccctcacg 540

ttgaccaagg acgagtatga acgacataac agctatacct gtgaggccac tcacaagaca 600

tcaacttcac ccattgtcaa gagcttcaac aggaatgagt gttag 645

<210> 138
<211> 214
<212> PRT
<213> Mus musculus

<400> 138

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Phe Lys Leu Leu Ile
35 40 45

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

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

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

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

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

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

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

Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser
                165                 170                 175

Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr
            180                 185                 190

Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser
        195                 200                 205

Phe Asn Arg Asn Glu Cys
    210
```

<210> 139
<211> 1344
<212> DNA
<213> Mus musculus

<400> 139
gaggtccaac tgcaacagtc tggacctgaa ctaatgaagc ctggggcttc agtgaagatg 60

tcctgcaagg cttctggata tacattcact gactacaaca tgcactgggt gaagcagaac 120

caaggaaaga ccctagaatg gataggagaa attaatccta acagtggtgg tgctggctac 180

aaccagaagt tcaagggcaa ggccacattg actgtagaca agtcctccac cacagcctac 240

atggagctcc gcagcctgac atctgaggac tctgcagtct attactgtgc aagattgggc 300

tacgatgata tctacgacga ctggtacttc gatgtctggg gcgcagggac cacggtcacc 360

gtctcctcag ccaaaacgac acccccatct gtctatccac tggcccctgg atctgctgcc 420

caaactaact ccatggtgac cctgggatgc ctggtcaagg gctatttccc tgagccagtg 480

acagtgacct ggaactctgg atccctgtcc agcggtgtgc acaccttccc agctgtcctg 540

cagtctgacc tctacactct gagcagctca gtgactgtcc cctccagcac ctggcccagc 600

gagaccgtca cctgcaacgt tgcccacccg gccagcagca ccaaggtgga caagaaaatt 660

gtgcccaggg attgtggttg taagccttgc atatgtacag tcccagaagt atcatctgtc 720

ttcatcttcc ccccaaagcc caaggatgtg ctcaccatta ctctgactcc taaggtcacg 780

tgtgttgtgg tagacatcag caaggatgat cccgaggtcc agttcagctg gtttgtagat 840

gatgtggagg tgcacacagc tcagacgcaa ccccgggagg agcagttcaa cagcactttc 900

cgctcagtca gtgaacttcc catcatgcac caggactggc tcaatggcaa ggagttcaaa 960

tgcagggtca acagtgcagc tttccctgcc cccatcgaga aaaccatctc caaaaccaaa 1020

ggcagaccga aggctccaca ggtgtacacc attccacctc ccaaggagca gatggccaag 1080

gataaagtca gtctgacctg catgataaca gacttcttcc ctgaagacat tactgtggag 1140

tggcagtgga atgggcagcc agcggagaac tacaagaaca ctcagcccat catggacaca 1200

gatggctctt acttcatcta cagcaagctc aatgtgcaga agagcaactg ggaggcagga 1260

aatactttca cctgctctgt gttacatgag ggcctgcaca accaccatac tgagaagagc 1320

ctctcccact ctcctggtaa atga 1344

<210> 140
<211> 447
<212> PRT
<213> Mus musculus

<400> 140

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

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

Asn Met His Trp Val Lys Gln Asn Gln Gly Lys Thr Leu Glu Trp Ile
35 40 45

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

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

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

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

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

Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser
130 135 140

```
Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

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

Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr
            180                 185                 190

Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala
        195                 200                 205

His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp
    210                 215                 220

Cys 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

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 Ile 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

<210> 141
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-11 and Ab-16 LCDR1

<400> 141

Arg Ala Ser Ser Ser Ile Ser Tyr Ile His
1 5 10

<210> 142
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-11 and Ab-16 LCDR2

<400> 142

Ala Thr Ser Asn Leu Ala Ser
1 5

<210> 143
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-11 and Ab-16 LCDR3

<400> 143

Gln Gln Trp Ser Ser Asp Pro Leu Thr
1 5

<210> 144
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-11 and Ab-16 HCDR1

<400> 144

Asp Tyr Tyr Ile His
1 5

<210> 145
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-11 and Ab-16 HCDR2

<400> 145

Arg Val Asp Pro Asp Asn Gly Glu Thr Glu Phe Ala Pro Lys Phe Pro
1 5 10 15

Gly

<210> 146
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-11 and Ab-16 HCDR3

<400> 146

Glu Asp Tyr Asp Gly Thr Tyr Thr Trp Phe Pro Tyr
1 5 10

<210> 147
<211> 642
<212> DNA
<213> Mus musculus

<400> 147
caaattgttc tctcccagtc tccagcattc ctgtctgtat ctccagggga taaggtcaca 60

atgacttgca gggccagctc aagtataagt tacatacact ggtttcagca gaagccagga 120

tcctcccccа gatcctggat ttatgccaca tccaacctgg cttctggagt ccctggtcgc 180

ttcagtggca gtgggtctgg gacctcttac tctctcacaa tcagcagagt ggaggctgag 240

gatgctgcca cttattactg ccagcagtgg agtagtgacc cactcacgtt cggtgctggg 300

accaagctgg agctgaaacg ggctgatgct gcaccaactg tatccatctt cccaccatcc 360

agtgagcagt taacatctgg aggtgcctca gtcgtgtgct tcttgaacaa cttctacccc 420

aaagacatca atgtcaagtg gaagattgat ggcagtgaac gacaaaatgg cgtcctgaac 480

agttggactg atcaggacag caaagacagc acctacagca tgagcagcac cctcacgttg 540

accaaggacg agtatgaacg acataacagc tatacctgtg aggccactca caagacatca 600

acttcaccca ttgtcaagag cttcaacagg aatgagtgtt ag 642

<210> 148
<211> 213
<212> PRT
<213> Mus musculus

<400> 148

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

Asp Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Ile Ser Tyr Ile

```
            20                  25                  30

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

Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Gly 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 Tyr Cys Gln Gln Trp Ser Ser Asp Pro Leu Thr
                85                  90                  95

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

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

Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn
    130                 135                 140

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

Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser
                165                 170                 175

Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr
            180                 185                 190

Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser Phe
        195                 200                 205

Asn Arg Asn Glu Cys
    210
```

<210> 149
<211> 1338
<212> DNA
<213> Mus musculus

<400> 149
gaagttcagc tgcaacagtc tggggcagac cttgtgcagc caggggcctc agtcaaggtg 60

tcctgcacag cttctggctt cgacattaag gactactata tacactggat gaaacagagg 120

cctgaccagg gcctggagtg gattggaagg gttgatcctg acaatggtga gactgaattt 180

gccccgaagt tcccgggcaa ggccactttt acaacagaca catcctccaa cacagcctac 240

ctacaactca gaggcctgac atctgaggac actgccatct attactgtgg gagagaagac 300

tacgatggta cctacacctg gtttccttat tggggccaag ggactctggt cactgtctct 360

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gcagccaaaa cgacaccccc atctgtctat ccactggccc ctggatctgc tgcccaaact      420
aactccatgg tgaccctggg atgcctggtc aagggctatt tccctgagcc agtgacagtg      480
acctggaact ctggatccct gtccagcggt gtgcacacct tcccagctgt cctgcagtct      540
gacctctaca ctctgagcag ctcagtgact gtcccctcca gcacctggcc cagcgagacc      600
gtcacctgca acgttgccca cccggccagc agcaccaagg tggacaagaa aattgtgccc      660
agggattgtg gttgtaagcc ttgcatatgt acagtcccag aagtatcatc tgtcttcatc      720
ttcccccaa agcccaagga tgtgctcacc attactctga ctcctaaggt cacgtgtgtt      780
gtggtagaca tcagcaagga tgatcccgag gtccagttca gctggtttgt agatgatgtg      840
gaggtgcaca cagctcagac gcaaccccgg gaggagcagt tcaacagcac tttccgctca      900
gtcagtgaac ttcccatcat gcaccaggac tggctcaatg gcaaggagtt caaatgcagg      960
gtcaacagtg cagctttccc tgcccccatc gagaaaacca tctccaaaac caaaggcaga     1020
ccgaaggctc cacaggtgta caccattcca cctcccaagg agcagatggc caaggataaa     1080
gtcagtctga cctgcatgat aacagacttc ttccctgaag acattactgt ggagtggcag     1140
tggaatgggc agccagcgga gaactacaag aacactcagc ccatcatgga cacagatggc     1200
tcttacttca tctacagcaa gctcaatgtg cagaagagca actgggaggc aggaaatact     1260
ttcacctgct ctgtgttaca tgagggcctg cacaaccacc atactgagaa gagcctctcc     1320
cactctcctg gtaaatga                                                   1338
```

<210> 150
<211> 445
<212> PRT
<213> Mus musculus

<400> 150

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

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

Tyr Ile His Trp Met Lys Gln Arg Pro Asp Gln Gly Leu Glu Trp Ile
        35                  40                  45

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

Pro Gly Lys Ala Thr Phe Thr Thr Asp Thr Ser Ser Asn Thr Ala Tyr
65                  70                  75                  80

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

Gly Arg Glu Asp Tyr Asp Gly Thr Tyr Thr Trp Phe Pro Tyr Trp Gly
            100                 105                 110
```

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

Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val
    130                 135                 140

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

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

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

Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro
        195                 200                 205

Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly
    210                 215                 220

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

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

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

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

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

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

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

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

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

Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln
    370                 375                 380
```

```
Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly
385                 390                 395                 400

Ser Tyr Phe Ile Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu
                405                 410                 415

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

His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
        435                 440                 445
```

<210> 151
<211> 318
<212> DNA
<213> Mus musculus

<400> 151

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gacatccagt tgacccagtc tccatccttc ctgtctgcat ctgtaggaga cagagtcacc       60

atcacttgca gggccagctc aagtataagt tacatacact ggtatcagca aaaaccaggg      120

aaagccccta agctcctgat ctatgccaca tccaacctgg cttctggggt cccatcaagg      180

ttcagcggca gtggatctgg gacagaattc actctcacaa tcagcagcct gcagcctgaa      240

gattttgcaa cttattactg tcagcagtgg agtagtgacc cactcacgtt cggcggaggg      300

accaaggtgg agatcaaa                                                    318
```

<210> 152
<211> 106
<212> PRT
<213> Mus musculus

<400> 152

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

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

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

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

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

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

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

<210> 153
<211> 363
<212> DNA
<213> Mus musculus

<400> 153
gaggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt cgacattaag gactactata tacactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatcggaagg gttgatcctg acaatggtga gactgaattt 180

gccccgaagt tcccgggcaa ggtcaccatg accacagaca cgtccatcag cacagcctac 240

atggagctga gcaggctgag atctgacgac acggccgtgt attactgtgc gagagaagac 300

tacgatggta cctacacctg gtttccttat tggggccaag ggactctggt caccgtctct 360

agt 363

<210> 154
<211> 121
<212> PRT
<213> Mus musculus

<400> 154

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

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

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

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

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

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

Ala Arg Glu Asp Tyr Asp Gly Thr Tyr Thr Trp Phe Pro Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 155
<211> 639
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized antibody sequence

<400> 155
gacatccagt tgacccagtc tccatccttc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgca gggccagctc aagtataagt tacatacact ggtatcagca aaaaccaggg 120

aaagccccta agctcctgat ctatgccaca tccaacctgg cttctggggt cccatcaagg 180

ttcagcggca gtggatctgg gacagaattc actctcacaa tcagcagcct gcagcctgaa 240

gattttgcaa cttattactg tcagcagtgg agtagtgacc cactcacgtt cggcggaggg 300

accaaggtgg agatcaaacg tacggtggct gcaccatctg 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 cttcaacagg ggagagtgt 639

<210> 156
<211> 213
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized antibody sequence

<400> 156

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

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

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

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

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

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

Phe Gly Gly Gly Thr Lys Val 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> 157
<211> 1341
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized antibody sequence

<400> 157

```
gaggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc       60

tcctgcaagg cttctggatt cgacattaag gactactata tacactgggt gcgacaggcc      120

cctggacaag ggcttgagtg gatcggaagg gttgatcctg acaatggtga gactgaattt      180

gccccgaagt tcccgggcaa ggtcaccatg accacagaca cgtccatcag cacagcctac      240

atggagctga gcaggctgag atctgacgac acggccgtgt attactgtgc gagagaagac      300

tacgatggta cctacacctg gtttccttat tggggccaag ggactctggt caccgtctct      360

agtgcctcca ccaagggccc atcggtcttc cccctggcgc cctgctccag gagcacctcc      420

gagagcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg      480

tcgtggaact caggcgctct gaccagcggc gtgcacacct tcccagctgt cctacagtcc      540

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcaactt cggcacccag      600

acctacacct gcaacgtaga tcacaagccc agcaacacca aggtggacaa gacagttgag      660

cgcaaatgtt gtgtcgagtg cccaccgtgc ccagcaccac ctgtggcagg accgtcagtc      720

ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcacg      780

tgcgtggtgg tggacgtgag ccacgaagac cccgaggtcc agttcaactg gtacgtggac      840

ggcgtggagg tgcataatgc caagacaaag ccacgggagg agcagttcaa cagcacgttc      900

cgtgtggtca gcgtcctcac cgttgtgcac caggactggc tgaacggcaa ggagtacaag      960

tgcaaggtct ccaacaaagg cctcccagcc cccatcgaga aaaccatctc caaaaccaaa     1020

gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggagga gatgaccaag     1080

aaccaggtca gcctgacctg cctggtcaaa ggcttctacc ccagcgacat cgccgtggag     1140

tgggagagca atgggcagcc ggagaacaac tacaagacca cacctcccat gctggactcc     1200
```

gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg 1260

aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 1320

ctctccctgt ctccgggtaa a 1341

<210> 158
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized antibody sequence

<400> 158

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

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

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

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

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

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

Ala Arg Glu Asp Tyr Asp Gly Thr Tyr Thr Trp Phe Pro Tyr Trp Gly
100 105 110

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

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

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

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

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

Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His
195 200 205

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

Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala 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 His 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 Phe Arg Val Val Ser
    290                 295                 300

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

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

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

Pro Ser Arg 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 Met Leu Asp Ser
385                 390                 395                 400

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

Trp Gln Gln 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 Pro Gly Lys
        435                 440                 445
```

<210> 159
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-12 LCDR1

<400> 159

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

<210> 160
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-12 LCDR2

<400> 160

Tyr Thr Ser Thr Leu Gln Ser
1 5

<210> 161
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-12 LCDR3

<400> 161

Gln Gln Gly Asp Thr Leu Pro Tyr Thr
1 5

<210> 162
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-12 HCDR1

<400> 162

Asp Tyr Asn Met His
1 5

<210> 163
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-12 HCDR2

<400> 163

Glu Ile Asn Pro Asn Ser Gly Gly Ser Gly Tyr Asn Gln Lys Phe Lys
1 5 10 15

Gly

<210> 164
<211> 14
<212> PRT

<213> Artificial Sequence

<220>
<223> Ab-12 HCDR3

<400> 164

Leu Gly Tyr Tyr Gly Asn Tyr Glu Asp Trp Tyr Phe Asp Val
1 5 10

<210> 165
<211> 645
<212> DNA
<213> Mus musculus

<400> 165
gatctccaga tgacacagac tacttcctcc ctgtctgcct ctctgggaga cagagtcacc 60

atcagttgca gggcaagtca ggacattagc aattatttaa actggtatca gcagaaacca 120

gatggaactg ttaagctcct gatcttctac acatcaacat tacagtcagg agtcccatcg 180

aggttcagtg gcagtgggtc tggaacaaat tattctctca ccattaccaa cctggagcaa 240

gatgatgctg ccacttactt ttgccaacag ggtgatacgc ttccgtacac gttcggaggg 300

gggaccaagc tggaaataaa acgggctgat gctgcaccaa ctgtatccat cttcccacca 360

tccagtgagc agttaacatc tggaggtgcc tcagtcgtgt gcttcttgaa caacttctac 420

cccaaagaca tcaatgtcaa gtggaagatt gatggcagtg aacgacaaaa tggcgtcctg 480

aacagttgga ctgatcagga cagcaaagac agcacctaca gcatgagcag caccctcacg 540

ttgaccaagg acgagtatga acgacataac agctatacct gtgaggccac tcacaagaca 600

tcaacttcac ccattgtcaa gagcttcaac aggaatgagt gttag 645

<210> 166
<211> 214
<212> PRT
<213> Mus musculus

<400> 166

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

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

Ser Gly Ser Gly Thr Asn Tyr Ser Leu Thr Ile Thr Asn Leu Glu Gln
65 70 75 80

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

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

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

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

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

Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser
                165                 170                 175

Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr
            180                 185                 190

Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser
        195                 200                 205

Phe Asn Arg Asn Glu Cys
    210
```

<210> 167
<211> 1344
<212> DNA
<213> Mus musculus

<400> 167
gaggtccagt tgcaacagtc tggacctgaa ctaatgaagc ctggggcttc agtgaagatg 60

tcctgcaagg cttctggata cacattcact gactacaaca tgcactggat gaagcagaac 120

caaggaaaga gcctagagtg gataggagag attaatccta acagtggtgg ttctggttac 180

aaccagaagt tcaaaggcaa ggccacattg actgtagaca agtcctccag cacagcctac 240

atggagctcc gcagcctgac atctgaggac tctgcagtct attactgtgc aagattgggc 300

tactatggta actacgagga ctggtatttc gatgtctggg gcgcagggac cacggtcacc 360

gtctcctctg ccaaaacgac acccccatct gtctatccac tggcccctgg atctgctgcc 420

caaactaact ccatggtgac cctgggatgc ctggtcaagg gctatttccc tgagccagtg 480

acagtgacct ggaactctgg atccctgtcc agcggtgtgc acaccttccc agctgtcctg 540

cagtctgacc tctacactct gagcagctca gtgactgtcc cctccagcac ctggcccagc 600

gagaccgtca cctgcaacgt tgcccacccg gccagcagca ccaaggtgga caagaaaatt 660

gtgcccaggg attgtggttg taagccttgc atatgtacag tcccagaagt atcatctgtc 720

ttcatcttcc ccccaaagcc caaggatgtg ctcaccatta ctctgactcc taaggtcacg 780

tgtgttgtgg tagacatcag caaggatgat cccgaggtcc agttcagctg gtttgtagat 840

gatgtggagg tgcacacagc tcagacgcaa ccccgggagg agcagttcaa cagcactttc 900

cgctcagtca gtgaacttcc catcatgcac caggactggc tcaatggcaa ggagttcaaa 960

tgcagggtca acagtgcagc tttccctgcc cccatcgaga aaaccatctc caaaaccaaa 1020

ggcagaccga aggctccaca ggtgtacacc attccacctc ccaaggagca gatggccaag 1080

gataaagtca gtctgacctg catgataaca gacttcttcc ctgaagacat tactgtggag 1140

tggcagtgga atgggcagcc agcggagaac tacaagaaca ctcagcccat catggacaca 1200

gatggctctt acttcatcta cagcaagctc aatgtgcaga agagcaactg ggaggcagga 1260

aatactttca cctgctctgt gttacatgag ggcctgcaca accaccatac tgagaagagc 1320

ctctcccact ctcctggtaa atga 1344

<210> 168
<211> 447
<212> PRT
<213> Mus musculus

<400> 168

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

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

Asn Met His Trp Met Lys Gln Asn Gln Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Glu Ile Asn Pro Asn Ser Gly Gly Ser Gly Tyr Asn Gln Lys Phe
50 55 60

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

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

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

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

Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser
130 135 140

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

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

```
Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr
            180                 185                 190

Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala
        195                 200                 205

His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp
    210                 215                 220

Cys 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

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 Ile 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
```

<210> 169

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

<220>
<223> Ab-13 and Ab-14 LCDR1

<400> 169

Arg Ala Ser Ser Ser Val Thr Ser Ser Tyr Leu Asn
1 5 10

<210> 170
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-13 and Ab-14 LCDR2

<400> 170

Ser Thr Ser Asn Leu Ala Ser
1 5

<210> 171
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-13 and Ab-14 LCDR3

<400> 171

Gln Gln Tyr Asp Phe Phe Pro Ser Thr
1 5

<210> 172
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-13 and Ab-14 HCDR1

<400> 172

Asp Tyr Tyr Met Asn
1 5

<210> 173
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-13 and Ab-14 HCDR2

<400> 173

Asp Ile Asn Pro Tyr Asn Asp Asp Thr Thr Tyr Asn His Lys Phe Lys
1 5 10 15

Gly

<210> 174
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-13 and Ab-14 HCDR3

<400> 174

Glu Thr Ala Val Ile Thr Thr Asn Ala Met Asp
1 5 10

<210> 175
<211> 645
<212> DNA
<213> Mus musculus

<400> 175
cagattgttc tcacccagtc tccagcaatc atgtctgcat ctccagggga gaaggtcacc 60

atgacctgca gggccagctc aagtgtaact tccagttact tgaactggta ccagcagaag 120

ccaggatctt cccccaaact ctggatttat agcacatcca acctggcttc aggagtccca 180

gctcgcttca gtggcagtgg gtctgggacc tcttactctc tcacaatcag cagtgtggag 240

gctgaggatg ctgccactta ttactgccag cagtatgatt ttttcccatc gacgttcggt 300

ggaggcacca agctggaaat caagcgggct gatgctgcac caactgtatc catcttccca 360

ccatccagtg agcagttaac atctggaggt gcctcagtcg tgtgcttctt gaacaacttc 420

taccccaaag acatcaatgt caagtggaag attgatggca gtgaacgaca aaatggcgtc 480

ctgaacagtt ggactgatca ggacagcaaa gacagcacct acagcatgag cagcaccctc 540

acgttgacca aggacgagta tgaacgacat aacagctata cctgtgaggc cactcacaag 600

acatcaactt cacccatcgt caagagcttc aacaggaatg agtgt 645

<210> 176
<211> 215
<212> PRT
<213> Mus musculus

<400> 176

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

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

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

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

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

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

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

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

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

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

Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met
                165                 170                 175

Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser
            180                 185                 190

Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys
        195                 200                 205

Ser Phe Asn Arg Asn Glu Cys
    210                 215
```

<210> 177
<211> 1335
<212> DNA
<213> Mus musculus

<400> 177

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gaggtccagc tgcaacaatc tggacctgag ctggtgaagc ctggggcttc agtgaagatg       60

tcctgtaagg cttctggata cacattcact gactactaca tgaactgggt gaagcagagc      120

catggagaga gccttgagtg gattggagat attaatcctt acaacgatga tactacctac      180

aaccacaagt tcaagggcaa ggccacattg actgtagaca aatcctccaa cacagcctac      240

atgcagctca acagcctgac atctgaggac tctgcagtct attactgtgc aagagagacg      300

gccgttatta ctacgaatgc tatggactac tggggtcaag gaacctcagt caccgtctcc      360

tcagccaaaa cgacaccccc atctgtctat ccactggccc ctggatctgc tgcccaaact      420

aactccatgg tgaccctggg atgcctggtc aagggctatt tccctgagcc agtgacagtg      480

acctggaact ctggatccct gtccagcggt gtgcacacct tcccagctgt cctgcagtct      540

gacctctaca ctctgagcag ctcagtgact gtcccctcca gcacctggcc cagcgagacc      600

gtcacctgca acgttgccca cccggccagc agcaccaagg tggacaagaa aattgtgccc      660
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agggattgtg gttgtaagcc ttgcatatgt acagtcccag aagtatcatc tgtcttcatc 720

ttccccccaa agcccaagga tgtgctcacc attactctga ctcctaaggt cacgtgtgtt 780

gtggtagaca tcagcaagga tgatcccgag gtccagttca gctggtttgt agatgatgtg 840

gaggtgcaca cagctcagac gcaaccccgg gaggagcagt tcaacagcac tttccgctca 900

gtcagtgaac ttcccatcat gcaccaggac tggctcaatg gcaaggagtt caaatgcagg 960

gtcaacagtg cagctttccc tgcccccatc gagaaaacca tctccaaaac caaaggcaga 1020

ccgaaggctc cacaggtgta caccattcca cctcccaagg agcagatggc caaggataaa 1080

gtcagtctga cctgcatgat aacagacttc ttccctgaag acattactgt ggagtggcag 1140

tggaatgggc agccagcgga gaactacaag aacactcagc ccatcatgga cacagatggc 1200

tcttacttca tctacagcaa gctcaatgtg cagaagagca actgggaggc aggaaatact 1260

ttcacctgct ctgtgttaca tgagggcctg cacaaccacc atactgagaa gagcctctcc 1320

cactctcctg gtaaa 1335

<210> 178
<211> 445
<212> PRT
<213> Mus musculus

<400> 178

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

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

Tyr Met Asn Trp Val Lys Gln Ser His Gly Glu Ser Leu Glu Trp Ile
35 40 45

Gly Asp Ile Asn Pro Tyr Asn Asp Asp Thr Thr Tyr Asn His Lys Phe
50 55 60

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

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

Ala Arg Glu Thr Ala Val Ile Thr Thr Asn Ala Met Asp Tyr Trp Gly
100 105 110

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

Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val
130 135 140

Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val

145 150 155 160

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

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

Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro
195 200 205

Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly
210 215 220

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

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

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

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

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

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

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

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

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

Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln
370 375 380

Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly
385 390 395 400

Ser Tyr Phe Ile Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu
405 410 415

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

```
His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
        435                 440                 445


<210>  179
<211>  324
<212>  DNA
<213>  Mus musculus

<400>  179
gacatccagc tgacccagag ccccagcttc ctttccgcat ccgttggtga ccgagtaaca       60

atcacatgcc gcgcctcatc ttcagttaca tcttcttatc ttaattggta tcaacaaaaa      120

ccaggaaaag cacctaaact tcttatatac tctacatcta atctcgcatc aggagttccc      180

tctcgatttt caggatctgg atcaggcaca gaatttacac ttactatatc atcactccaa      240

ccagaagact tcgccactta ttactgccaa caatacgatt tttttccaag cacattcgga      300

ggaggtacaa aagtagaaat caag                                             324


<210>  180
<211>  108
<212>  PRT
<213>  Mus musculus

<400>  180

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


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


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


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


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


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


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


<210>  181
<211>  363
<212>  DNA
<213>  Mus musculus

<400>  181
gaggtgcagc tggtgcagag cggcgccgag gtcaagaaac ctggagcaag cgtaaaggtt       60

agttgcaaag catctggata cacatttacc gactactaca tgaattgggt acgacaagcc      120
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cctggacaaa gacttgaatg gatgggagac attaaccctt ataacgacga cactacatac 180

aatcataaat ttaaaggaag agttacaatt acaagagata catccgcatc aaccgcctat 240

atggaacttt cctcattgag atctgaagac actgctgttt attactgtgc aagagaaact 300

gccgttatta ctactaacgc tatggattac tggggtcaag gaaccactgt taccgtctct 360

agt 363

<210> 182
<211> 121
<212> PRT
<213> Mus musculus

<400> 182

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

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

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

Gly Asp Ile Asn Pro Tyr Asn Asp Asp Thr Thr Tyr Asn His Lys Phe
50 55 60

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

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

Ala Arg Glu Thr Ala Val Ile Thr Thr Asn Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 183
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized antibody sequence

<400> 183
gaggtgcagc tggtgcagag cggcgccgag gtcaagaaac ctggagcaag cgtaaaggtt 60

agttgcaaag catctggata cacatttacc gactactaca tgaattgggt acgacaagcc 120

cctggacaaa gacttgaatg gatgggagac attaaccctt ataacgacga cactacatac 180

aatcataaat ttaaaggaag agttacaatt acaagagata catccgcatc aaccgcctat 240

atggaacttt cctcattgag atctgaagac actgctgttt attactgtgc aagagaaact 300

gccgttatta ctactaacgc tatggattac tggggtcaag gaaccactgt taccgtctct 360

agt 363

<210> 184
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized antibody sequence

<400> 184

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Phe Asn Arg Gly Glu Cys

210 215

<210> 185
<211> 1341
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized antibody sequence

<400> 185
gaggtgcagc tggtgcagag cggcgccgag gtcaagaaac ctggagcaag cgtaaaggtt 60

agttgcaaag catctggata cacatttacc gactactaca tgaattgggt acgacaagcc 120

cctggacaaa gacttgaatg gatgggagac attaaccctt ataacgacga cactacatac 180

aatcataaat ttaaaggaag agttacaatt acaagagata catccgcatc aaccgcctat 240

atggaacttt cctcattgag atctgaagac actgctgttt attactgtgc aagagaaact 300

gccgttatta ctactaacgc tatggattac tggggtcaag gaaccactgt taccgtctct 360

agtgcctcca ccaagggccc atcggtcttc cccctggcgc cctgctccag gagcacctcc 420

gagagcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480

tcgtggaact caggcgctct gaccagcggc gtgcacacct tcccagctgt cctacagtcc 540

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcaactt cggcacccag 600

acctacacct gcaacgtaga tcacaagccc agcaacacca aggtggacaa gacagttgag 660

cgcaaatgtt gtgtcgagtg cccaccgtgc ccagcaccac ctgtggcagg accgtcagtc 720

ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcacg 780

tgcgtggtgg tggacgtgag ccacgaagac cccgaggtcc agttcaactg gtacgtggac 840

ggcgtggagg tgcataatgc caagacaaag ccacgggagg agcagttcaa cagcacgttc 900

cgtgtggtca gcgtcctcac cgttgtgcac caggactggc tgaacggcaa ggagtacaag 960

tgcaaggtct ccaacaaagg cctcccagcc cccatcgaga aaaccatctc caaaaccaaa 1020

gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggagga gatgaccaag 1080

aaccaggtca gcctgacctg cctggtcaaa ggcttctacc ccagcgacat cgccgtggag 1140

tgggagagca atgggcagcc ggagaacaac tacaagacca cacctcccat gctggactcc 1200

gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg 1260

aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 1320

ctctccctgt ctccgggtaa a 1341

<210> 186
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized antibody sequence

<400> 186

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

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

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

Gly Asp Ile Asn Pro Tyr Asn Asp Asp Thr Thr Tyr Asn His Lys Phe
    50                  55                  60

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

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

Ala Arg Glu Thr Ala Val Ile Thr Thr Asn Ala Met Asp Tyr Trp Gly
            100                 105                 110

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

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

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

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

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

Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His
        195                 200                 205

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

Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala 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 His 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 Phe Arg Val Val Ser
290 295 300

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

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

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

Pro Ser Arg 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 Met Leu Asp Ser
385 390 395 400

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

Trp Gln Gln 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 Pro Gly Lys
435 440 445

<210> 187
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-17 and Ab-18 LCDR1

<400> 187

Ser Val Ser Ser Ser Ile Ser Ser Ser Asn Leu His
1 5 10

<210> 188
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-17 and Ab-18 LCDR2

<400> 188

Gly Thr Ser Asn Leu Ala Ser
1 5

<210> 189
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> LCDR3

<400> 189

Gln Gln Trp Thr Thr Thr Tyr Thr
1 5

<210> 190
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-17 and Ab-18 HCDR1

<400> 190

Asp Tyr Tyr Ile His
1 5

<210> 191
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-17 and Ab-18 HCDR2

<400> 191

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

Gly

<210> 192
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 192

Glu Gly Leu Asp Tyr Gly Asp Tyr Tyr Ala Val Asp Tyr
1 5 10

<210> 193
<211> 390
<212> DNA
<213> Mus musculus

<400> 193
atggattttc aggtgcagat tttcagcttc atgctaatca gtgtcacagt catattgtcc 60

agtggagaaa ttgtgctcac ccagtctcca gcactcatgg ctgcatctcc aggggagaag 120

gtcaccatca cctgcagtgt cagctcgagt ataagttcca gcaacttaca ctggtcccag 180

cagaagtcag gaacctcccc caaactctgg atttatggca catccaacct tgcttctgga 240

gtccctgttc gcttcagtgg cagtggatct gggacctctt attctctcac aatcagcagc 300

atggaggctg aagatgctgc cacttattac tgtcaacagt ggactactac gtatacgttc 360

ggatcgggga ccaagctgga gctgaaacgt 390

<210> 194
<211> 130
<212> PRT
<213> Mus musculus

<400> 194

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

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

Met Ala Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Val Ser
35 40 45

Ser Ser Ile Ser Ser Ser Asn Leu His Trp Ser Gln Gln Lys Ser Gly
50 55 60

Thr Ser Pro Lys Leu Trp Ile Tyr Gly Thr Ser Asn Leu Ala Ser Gly
65 70 75 80

Val Pro Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu
85 90 95

Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
100 105 110

Gln Trp Thr Thr Thr Tyr Thr Phe Gly Ser Gly Thr Lys Leu Glu Leu
115 120 125

Lys Arg
130

<210> 195
<211> 423
<212> DNA
<213> Mus musculus

<400> 195
atgggatgga actggatcat cttcttcctg atggcagtgg ttacaggggt caattcagag 60

gtgcagttgc ggcagtctgg ggcagacctt gtgaagccag gggcctcagt caagttgtcc 120

tgcacagctt ctggcttcaa cattaaagac tactatatac actgggtgaa gcagaggcct 180

gaacagggcc tggagtggat tggaaggatt gatcctgata atggtgaaag tacatatgtc 240

ccgaagttcc agggcaaggc cactataaca gcagacacat catccaacac agcctaccta 300

caactcagaa gcctgacatc tgaggacact gccatctatt attgtgggag agaggggctc 360

gactatggtg actactatgc tgtggactac tggggtcaag gaacctcggt cacagtctcg 420

agc 423

<210> 196
<211> 141
<212> PRT
<213> Mus musculus

<400> 196

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

Val Asn Ser Glu Val Gln Leu Arg Gln Ser Gly Ala Asp Leu Val Lys
20 25 30

Pro Gly Ala Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile
35 40 45

Lys Asp Tyr Tyr Ile His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu
50 55 60

Glu Trp Ile Gly Arg Ile Asp Pro Asp Asn Gly Glu Ser Thr Tyr Val
65 70 75 80

Pro Lys Phe Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn
85 90 95

Thr Ala Tyr Leu Gln Leu Arg Ser Leu Thr Ser Glu Asp Thr Ala Ile
100 105 110

Tyr Tyr Cys Gly Arg Glu Gly Leu Asp Tyr Gly Asp Tyr Tyr Ala Val
115 120 125

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

<210> 197
<211> 390
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized antibody sequence

<400> 197
atggatatgc gcgtgccggc gcagctgctg ggcctgctgc tgctgtggct gccgggcgcg 60

cgctgcgata ttcagctgac ccagagcccg agctttctga gcgcgagcgt gggcgatcgc 120

gtgaccatta cctgcagcgt gagcagcagc attagcagca gcaacctgca ttggtatcag 180

cagaaaccgg gcaaagcgcc gaaactgctg atttatggca ccagcaacct ggcgagcggc 240

gtgccgagcc gctttagcgg cagcggcagc ggcaccgaat ttaccctgac cattagcagc 300

ctgcagccgg aagattttgc gacctattat tgccagcagt ggaccaccac ctatacctttt 360

ggccagggca ccaaactgga aattaaacgt 390

<210> 198
<211> 130
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized antibody sequence

<400> 198

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

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

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

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

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

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu
85 90 95

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
100 105 110

Gln Trp Thr Thr Thr Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
115 120 125

Lys Arg
130

<210> 199
<211> 423
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized antibody sequence

<400> 199
atggattgga cctggagcat tctgtttctg gtggcggcgc cgaccggcgc gcatagcgaa 60

gtgcagctgg tgcagagcgg cgcggaagtg aaaaaaccgg gcgcgagcgt gaaagtgagc 120

tgcaaagcga gcggctttaa cattaaagat tattatattc attgggtgcg ccaggcgccg 180

ggccagggcc tggaatggat gggccgcatt gatccggata acggcgaaag cacctatgtg 240

ccgaaatttc agggccgcgt gaccatgacc accgatacca gcaccagcac cgcgtatatg 300

gaactgcgca gcctgcgcag cgatgatacc gcggtgtatt attgcgcgcg cgaaggcctg 360

gattatggcg attattatgc ggtggattat tggggccagg gcaccctggt gaccgtctcg 420

agc 423

<210> 200
<211> 141
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized antibody sequence

<400> 200

Met Asp Trp Thr Trp Ser Ile Leu Phe Leu Val Ala Ala Pro Thr Gly
1 5 10 15

Ala His Ser Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile
35 40 45

Lys Asp Tyr Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

Glu Trp Met Gly Arg Ile Asp Pro Asp Asn Gly Glu Ser Thr Tyr Val
65 70 75 80

Pro Lys Phe Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser
85 90 95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Glu Gly Leu Asp Tyr Gly Asp Tyr Tyr Ala Val
115 120 125

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
130 135 140

<210> 201
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-19, Ab-20 and Ab-23 LCDR1

<400> 201

Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn

1 5 10

<210> 202
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-19, Ab-20 and Ab-23 LCDR2

<400> 202

Ser Thr Ser Arg Leu Asn Ser
1 5

<210> 203
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-19, Ab-20 and Ab-23 LCDR3

<400> 203

Gln Gln Asp Ile Lys His Pro Thr
1 5

<210> 204
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-19, Ab-20 and Ab-23 HCDR1

<400> 204

Asp Tyr Ile Met His
1 5

<210> 205
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-19, Ab-20 and Ab-23 HCDR2

<400> 205

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

Gly

<210> 206
<211> 11
<212> PRT
<213> Artificial Sequence

<220>

<223> Ab-19, Ab-20 and Ab-23 HCDR3

<400> 206

Ser Ile Tyr Tyr Tyr Asp Ala Pro Phe Ala Tyr
1 5 10

<210> 207
<211> 107
<212> PRT
<213> Mus musculus

<400> 207

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

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

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

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Asp Ile Lys His Pro Thr
85 90 95

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

<210> 208
<211> 120
<212> PRT
<213> Mus musculus

<400> 208

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

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

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

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

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

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

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

Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 209
<211> 381
<212> DNA
<213> Mus musculus

<400> 209

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atgatgtcct ctgctcagtt ccttggtctc ctgttgctct gttttcaagg taccagatgt       60

gatatccaga tgacacagac tacatcctcc ctgtctgcct ctctgggaga cagagtcaac      120

atcagctgca gggcaagtca ggacattagc agttatttaa actggtatca gcagaaacca      180

gatggaactg ttaaactcct gatctactcc acatcaagat taaactcagg agtcccatca      240

aggttcagtg gcagtgggtc tgggacagat tattctctca ctattagcaa cctggcacaa      300

gaagatattg ccacttactt ttgccaacag gatattaagc atccgacgtt cggtggaggc      360

accaagttgg agctgaaacg t                                                381
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<210> 210
<211> 127
<212> PRT
<213> Mus musculus

<400> 210

```
Met Met Ser Ser Ala Gln Phe Leu Gly Leu Leu Leu Leu Cys Phe Gln
1               5                   10                  15

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

Ala Ser Leu Gly Asp Arg Val Asn Ile Ser Cys Arg Ala Ser Gln Asp
        35                  40                  45

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

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

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

Asn Leu Ala Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Asp Ile
            100                 105                 110
```

Lys His Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys Arg
115 120 125

<210> 211
<211> 417
<212> DNA
<213> Mus musculus

<400> 211
atggaatgga tctggatatt tctcttcctc ctgtcaggaa ctgcaggtgt ccactctgag 60

gtccagctgc agcagtctgg acctgagctg gtaaagcctg gggcttcagt gaagatgtcc 120

tgcaaggctt ctgggttcac attcactgac tacattatgc actgggtgaa gcagaagcct 180

gggcagggcc ttgagtggat tggatatatt aatccttaca atgatgatac tgaatacaat 240

gagaagttca aaggcaaggc cacactgact tcagacaaat cctccagcac agcctacatg 300

gatctcagca gtctgacctc tgagggctct gcggtctatt actgtgcaag atcgatttat 360

tactacgatg ccccgtttgc ttactggggc caagggactc tggtcacagt ctcgagc 417

<210> 212
<211> 139
<212> PRT
<213> Mus musculus

<400> 212

Met Glu Trp Ile Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
1 5 10 15

Val His Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
20 25 30

Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Phe Thr Phe
35 40 45

Thr Asp Tyr Ile Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu
50 55 60

Glu Trp Ile Gly Tyr Ile Asn Pro Tyr Asn Asp Asp Thr Glu Tyr Asn
65 70 75 80

Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Ser
85 90 95

Thr Ala Tyr Met Asp Leu Ser Ser Leu Thr Ser Glu Gly Ser Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Ser Ile Tyr Tyr Tyr Asp Ala Pro Phe Ala Tyr
115 120 125

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
130 135

<210> 213

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

<220>
<223> Humanized antibody sequence

<400> 213
atgatgtcct ctgctcagtt ccttggtctc ctgttgctct gttttcaagg taccagatgt 60

gatatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggtga ccgtgtcacc 120

atcacttgcc gcgcaagtca ggatattagc agctatttaa attggtatca gcagaaacca 180

gggaaagccc ctaagctcct gatctattct acttcccgtt tgaatagtgg ggtcccatca 240

cgcttcagtg gcagtggctc tgggacagat ttcactctca ccatcagcag tctgcaacct 300

gaagattttg caacttacta ctgtcaacag gatattaaac accctacgtt cggtcaaggc 360

accaaggtgg agatcaaacg t 381

<210> 214
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized antibody sequence

<400> 214

Met Met Ser Ser Ala Gln Phe Leu Gly Leu Leu Leu Leu Cys Phe Gln
1 5 10 15

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

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp
35 40 45

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

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

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
85 90 95

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asp Ile
100 105 110

Lys His Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
115 120 125

<210> 215
<211> 417
<212> DNA
<213> Mus musculus

<400> 215
atggaatgga tctggatatt tctcttcctc ctgtcaggaa ctgcaggtgt ccactctgag 60

gtgcagctgg tgcagtctgg ggctgaggtg aagaagcctg ggtcctcggt gaaggtctcc 120

tgcaaggctt ctggttttac cttcaccgac tatattatgc actgggtgcg tcaggcccct 180

ggtcaagggc ttgagtggat gggctatatc aacccttata atgatgacac cgaatacaac 240

gagaagttca agggccgtgt cacgattacc gcggacaaat ccacgagcac agcctacatg 300

gagctgagca gcctgcgctc tgaggacacg gccgtgtatt actgtgcgcg ttcgatttat 360

tactacgatg ccccgtttgc ttactggggc caagggactc tggtcacagt ctcgagc 417

<210> 216
<211> 139
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized antibody sequence

<400> 216

Met Glu Trp Ile Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
1 5 10 15

Val His Ser Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
35 40 45

Thr Asp Tyr Ile Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

Glu Trp Met Gly Tyr Ile Asn Pro Tyr Asn Asp Asp Thr Glu Tyr Asn
65 70 75 80

Glu Lys Phe Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser
85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Ser Ile Tyr Tyr Tyr Asp Ala Pro Phe Ala Tyr
115 120 125

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
130 135

<210> 217
<211> 318
<212> DNA
<213> Mus musculus

<400> 217

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggtga ccgtgtcacc 60

atcacttgcc gcgcaagtca ggatattagc agctatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctattct acttcccgtt tgaatagtgg ggtcccatca 180

cgcttcagtg gcagtggctc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag gatattaaac accctacgtt cggtcaaggc 300

accaaggtgg agatcaaa 318

<210> 218
<211> 106
<212> PRT
<213> Mus musculus

<400> 218

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

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

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asp Ile Lys His Pro Thr
85 90 95

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

<210> 219
<211> 360
<212> DNA
<213> Mus musculus

<400> 219
gaggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cttctggttt taccttcacc gactatatta tgcactgggt gcgtcaggcc 120

cctggtcaag ggcttgagtg gatgggctat atcaaccctt ataatgatga caccgaatac 180

aacgagaagt tcaagggccg tgtcacgatt accgcggaca aatccacgag cacagcctac 240

atggagctga gcagcctgcg ctctgaggac acggccgtgt attactgtgc gcgttcgatt 300

tattactacg atgccccgtt tgcttactgg ggccaaggga ctctggtcac cgtctctagt 360

<210> 220
<211> 120

<212> PRT
<213> Mus musculus

<400> 220

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

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

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

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

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

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

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 221
<211> 639
<212> DNA
<213> Mus musculus

<400> 221
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggtga ccgtgtcacc 60

atcacttgcc gcgcaagtca ggatattagc agctatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctattct acttcccgtt tgaatagtgg ggtcccatca 180

cgcttcagtg gcagtggctc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag gatattaaac accctacgtt cggtcaaggc 300

accaaggtgg agatcaaacg tacggtggct gcaccatctg 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 cttcaacagg ggagagtgt 639

<210> 222
<211> 213
<212> PRT

<213> Mus musculus

<400> 222

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

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

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asp Ile Lys His Pro Thr
                85                  90                  95

Phe Gly Gln Gly Thr Lys Val 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> 223
<211> 1338
<212> DNA
<213> Mus musculus

<400> 223

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gaggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc       60

tcctgcaagg cttctggttt taccttcacc gactatatta tgcactgggt gcgtcaggcc      120
```

cctggtcaag ggcttgagtg gatgggctat atcaaccctt ataatgatga caccgaatac 180

aacgagaagt tcaagggccg tgtcacgatt accgcggaca aatccacgag cacagcctac 240

atggagctga gcagcctgcg ctctgaggac acggccgtgt attactgtgc gcgttcgatt 300

tattactacg atgccccgtt tgcttactgg ggccaaggga ctctggtcac cgtctctagt 360

gcctccacca agggcccatc ggtcttcccc ctggcgccct gctccaggag cacctccgag 420

agcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480

tggaactcag gcgctctgac cagcggcgtg cacaccttcc cagctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcaacttcgg cacccagacc 600

tacacctgca acgtagatca caagcccagc aacaccaagg tggacaagac agttgagcgc 660

aaatgttgtg tcgagtgccc accgtgccca gcaccacctg tggcaggacc gtcagtcttc 720

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacgtgc 780

gtggtggtgg acgtgagcca cgaagacccc gaggtccagt tcaactggta cgtggacggc 840

gtggaggtgc ataatgccaa gacaaagcca cgggaggagc agttcaacag cacgttccgt 900

gtggtcagcg tcctcaccgt tgtgcaccag gactggctga acggcaagga gtacaagtgc 960

aaggtctcca acaaaggcct cccagccccc atcgagaaaa ccatctccaa aaccaaaggg 1020

cagccccgag aaccacaggt gtacaccctg cccccatccc gggaggagat gaccaagaac 1080

caggtcagcc tgacctgcct ggtcaaaggc ttctacccca gcgacatcgc cgtggagtgg 1140

gagagcaatg ggcagccgga gaacaactac aagaccacac ctcccatgct ggactccgac 1200

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1260

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1320

tccctgtctc cgggtaaa 1338

<210> 224
<211> 446
<212> PRT
<213> Mus musculus

<400> 224

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

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

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

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

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

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

Ala Arg Ser Ile Tyr Tyr Tyr Asp Ala Pro Phe Ala 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 Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys
        195                 200                 205

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 225
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-21 and Ab-22 LCDR1

<400> 225

```
Lys Ala Ser Gln Asp Val Phe Thr Ala Val Ala
1               5                   10
```

<210> 226
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-21 and Ab-22 LCDR2

<400> 226

```
Trp Ala Ser Thr Arg His Thr
1               5
```

<210> 227
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-21 and Ab-22 LCDR3

<400> 227

```
Gln Gln Tyr Ser Ser Tyr Pro Leu Thr
1               5
```

<210> 228
<211> 5

<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-21 and Ab-22 HCDR1

<400> 228

Asp Tyr Tyr Met His
1 5

<210> 229
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-21 and Ab-22 HCDR2

<400> 229

Arg Ile Asp Pro Glu Asn Gly Asp Ile Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 230
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab-21 and Ab-22 HCDR3

<400> 230

Asp Ala Gly Asp Pro Ala Trp Phe Thr Tyr
1 5 10

<210> 231
<211> 381
<212> DNA
<213> Mus musculus

<400> 231
atgaagtcac agacccaggt ctttgtatac atgttgctgt ggttgtctgg tgttgaagga 60

gacattgtga tgacccagtc tcacaaattc atgtccacgt cagtaggaga cagggtcacc 120

atcacctgca aggccagtca ggatgtcttt actgctgtag cctggtatca acagaaacca 180

ggacaatctc ctaaactact gatttactgg gcatccaccc ggcacactgg agtccctgat 240

cgcttcacag gcagtggatc tgggacagat ttcactctca ccattagcaa tgtgcagtct 300

gaagacttgg cagattattt ctgtcaacaa tatagcagct atcctctcac gttcggtgct 360

gggaccaagt tggagctgaa a 381

<210> 232
<211> 128
<212> PRT
<213> Mus musculus

<400> 232

Met Lys Ser Gln Thr Gln Val Phe Val Tyr Met Leu Leu Trp Leu Ser
1 5 10 15

Gly Val Glu Gly Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser
20 25 30

Thr Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp
35 40 45

Val Phe Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro
50 55 60

Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp
65 70 75 80

Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
85 90 95

Asn Val Gln Ser Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser
100 105 110

Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
115 120 125

<210> 233
<211> 411
<212> DNA
<213> Mus musculus

<400> 233
atgggatgga actggatcat cttcttcctg atggcagtgg ttacaggggt caattcagag 60

gttcagctgc agcagtctgg ggctgagctt gtgaggccag gggccttagt caagttgtcc 120

tgcaaagctt ctggcttcaa tattaaagac tactatatgc actgggtgaa gcagaggcct 180

gaacagggcc tggagtggat tggaaggatt gatcctgaga atggtgatat tatatatgac 240

ccgaagttcc agggcaaggc cagtataaca acagacacat cctccaacac agcctacctg 300

cagctcagca gcctgacgtc tgaggacact gccgtctatt actgtgctta cgatgctggt 360

gaccccgcct ggtttactta ctggggccaa gggactctgg tcaccgtctc g 411

<210> 234
<211> 138
<212> PRT
<213> Mus musculus

<400> 234

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

Val Asn Ser Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
20 25 30

```
Pro Gly Ala Leu Val Lys Leu Ser Cys Lys Ala Ser Gly Phe Asn Ile
        35                  40                  45

Lys Asp Tyr Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu
    50                  55                  60

Glu Trp Ile Gly Arg Ile Asp Pro Glu Asn Gly Asp Ile Ile Tyr Asp
65                  70                  75                  80

Pro Lys Phe Gln Gly Lys Ala Ser Ile Thr Thr Asp Thr Ser Ser Asn
                85                  90                  95

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

Tyr Tyr Cys Ala Tyr Asp Ala Gly Asp Pro Ala Trp Phe Thr Tyr Trp
        115                 120                 125

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
    130                 135
```

<210> 235
<211> 324
<212> DNA
<213> Mus musculus

<400> 235

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gatatccaga tgacccagag cccgagcagc ctgagcgcga gcgtgggcga tcgcgtgacc        60

attacctgca aagcgagcca ggatgtgttt accgcggtgg cgtggtatca gcagaaaccg       120

ggcaaagcgc cgaaactgct gatttattgg gcgagcaccc gccataccgg cgtgccgagt       180

cgctttagcg gcagcggcag cggcaccgat tttaccctga ccattagcag cctgcagccg       240

gaagattttg cgacctatta ttgccagcag tatagcagct atccgctgac ctttggcggc       300

ggcaccaaag tggaaattaa acgt                                              324
```

<210> 236
<211> 108
<212> PRT
<213> Mus musculus

<400> 236

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

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

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

Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Ser Arg Phe Ser Gly
```

50 55 60

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

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

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

<210> 237
<211> 357
<212> DNA
<213> Mus musculus

<400> 237
gaagtgcagc tggtgcagag cggcgcggaa gtgaaaaaac cgggcgcgag cgtgaaagtg 60

agctgcaaag cgagcggctt taacattaaa gattattata tgcattgggt gcgccaggcg 120

ccgggccagg gcctggaatg gatcggccgc attgatccgg aaaacggcga tattatttat 180

gatccgaaat ttcagggccg cgtgaccatg accaccgata ccagcaccag caccgcgtat 240

atggaactgc gcagcctgcg cagcgatgat accgcggtgt attattgcgc gtatgatgcg 300

ggcgatccgg cgtggtttac ctattggggc cagggcaccc tggtgaccgt ctcgagc 357

<210> 238
<211> 119
<212> PRT
<213> Mus musculus

<400> 238

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

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

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

Gly Arg Ile Asp Pro Glu Asn Gly Asp Ile Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

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

Thr Leu Val Thr Val Ser Ser
115

<210> 239
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 239

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

<210> 240
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 240

Ala Ala Ser Asn Leu Glu Ser
1 5

<210> 241
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 241

Gln Gln Ser Asn Glu Asp Pro Phe Thr
1 5

<210> 242
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 242

Thr Tyr Trp Met Asn
1 5

<210> 243
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 243

Met Ile His Pro Ser Ala Ser Glu Ile Arg Leu Asp Gln Lys Phe Lys
1 5 10 15

Asp

<210> 244
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 244

Ser Gly Glu Trp Gly Ser Met Asp Tyr
1 5

<210> 245
<211> 657
<212> DNA
<213> Mus musculus

<400> 245
gacattgtgt tgacccagtc tccagcttct ttggctgtgt ctctagggca gagggccacc 60

atcgcctgca aggccagcca aagtgttgat tatgatggta ctagttatat gaattggtac 120

caacagaaac caggacagcc acccaaactc ctcatctatg ctgcatccaa tctagaatct 180

gagatcccag ccaggtttag tggcactggg tctgggacag acttcaccct caacatccat 240

cctgtggagg aggaggatat cacaacctat tactgtcagc aaagtaatga ggatccgttc 300

acgttcggag gggggaccaa gttggaaata aaacgggctg atgctgcacc aactgtatcc 360

atcttcccac catccagtga gcagttaaca tctggaggtg cctcagtcgt gtgcttcttg 420

aacaacttct accccaaaga catcaatgtc aagtggaaga ttgatggcag tgaacgacaa 480

aatggcgtcc tgaacagttg gactgatcag gacagcaaag acagcaccta cagcatgagc 540

agcaccctca cgttgaccaa ggacgagtat gaacgacata acagctatac ctgtgaggcc 600

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<213> Mus musculus

<400> 246

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

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

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

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

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

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

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

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

Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln
145                 150                 155                 160

Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr
                165                 170                 175

Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg
            180                 185                 190

His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro
        195                 200                 205

Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
    210                 215

<210>  247
<211>  442
<212>  PRT
<213>  Mus musculus

<400>  247

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

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

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

Gly Met Ile His Pro Ser Ala Ser Glu Ile Arg Leu Asp Gln Lys Phe
    50                  55                  60
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Lys Asp Lys Ala Thr Leu Thr Leu Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80

Met His Leu Ser Gly Pro Thr Ser Val Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95

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

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

Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu Gly
    130                 135                 140

Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr Trp Asn
145                 150                 155                 160

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

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

Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala Ser Ser
        195                 200                 205

Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Cys Lys Pro
    210                 215                 220

Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe Pro Pro
225                 230                 235                 240

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

Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln Phe Ser Trp
            260                 265                 270

Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Gln Pro Arg Glu
        275                 280                 285

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

His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val Asn Ser
305                 310                 315                 320

Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly
                325                 330                 335

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

Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asp Phe Phe
355 360 365

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

Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe
385 390 395 400

Ile Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala Gly Asn
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Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His His Thr
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Glu Lys Ser Leu Ser His Ser Pro Gly Lys
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cctggacaag gccttgagtg gattggcatg attcatcctt ccgcaagtga aattaggttg 180

gatcagaaat tcaaggacaa ggccacattg actcttgaca aatcctccag cacagcctat 240

atgcacctca gcggcccgac atctgtggat tctgcggtct attactgtgc aagatcaggg 300

gaatgggggt ctatggacta ctggggtcaa ggaacctcag tcaccgtctc ctcagccaaa 360

acgacacccc catctgtcta tccactggcc cctggatctg ctgcccaaac taactccatg 420

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acctgcatga taacagactt cttccctgaa gacattactg tggagtggca gtggaatggg 1140

cagccagcgg agaactacaa gaacactcag cccatcatgg acacagatgg ctcttacttc 1200

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tctgtgttac atgagggcct gcacaaccac catactgaga agagcctctc ccactctcct 1320

ggtaaatga 1329