SEQUENCE LISTING

<110> KIRCHNER, Jacqueline A
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BARONE, Dauphine

<120> Human GM-CSF Antigen Binding Proteins

<130> A-1292-WO-PCT

<140> to be assigned
<141> 2008-09-18

<150> 60/994,343
<151> 2007-09-18

<150> 61/087,551
<151> 2008-08-08

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<170> PatentIn version 3.2

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Gly Ala Tyr Gly Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala
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Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser
35 40 45

Ile Leu Tyr Ser Ser Ser Asn Glu Asn Phe Leu Thr Trp Tyr Gln Gln
50 55 60

Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
65 70 75 80

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

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

Tyr Cys Gln Gln Tyr Phe Ser Val Phe Arg Thr Phe Gly Gln Gly Thr
115 120 125

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

130 135 140

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

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

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln
180 185 190

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

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His
210 215 220

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235 240

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atcaactgca agtccagcca gagtatttta tacagctcca gcaatgagaa cttcttaact 180

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 240

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 300

atcagcagcc tgcagcctga agatgtggca gtttattact gtcagcaata ttttagtgtt 360

tttcggacgt tcggccaagg gaccagggtg gaaatcaaac gtacggtggc tgcaccatct 420

gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc 480

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caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 600

ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 660

gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 720

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<213> Artificial Sequence

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<400> 3

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Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Ile Leu Tyr Ser
20 25 30

Ser Ser Asn Glu Asn Phe Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

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

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

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

Tyr Phe Ser Val Phe Arg Thr Phe Gly Gln Gly Thr Arg Val Glu Ile
100 105 110

Lys

<210> 4
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<400> 4

Lys Ser Ser Gln Ser Ile Leu Tyr Ser Ser Ser Asn Glu Asn Phe Leu
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Thr

<210> 5
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<400> 5

Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 6

<211> 9
<212> PRT
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<220>
<223> CDR3

<400> 6

Gln Gln Tyr Phe Ser Val Phe Arg Thr
1 5

<210> 7
<211> 465
<212> PRT
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<220>
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<400> 7

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Ala His Ser Gln 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 Tyr Thr Phe
35 40 45

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

Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Ser Ala
65 70 75 80

Gln Lys Phe Arg Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser
85 90 95

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

Tyr Tyr Cys Ala Arg Glu Gly Gly Tyr Ser Tyr Gly Tyr Phe Asp Tyr
115 120 125

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
130 135 140

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser
145 150 155 160

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
165 170 175

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe

180 185 190

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
195 200 205

Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val
210 215 220

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

Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro
245 250 255

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
260 265 270

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
275 280 285

Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
290 295 300

Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val
305 310 315 320

Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu
325 330 335

Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys
340 345 350

Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
355 360 365

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
370 375 380

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
385 390 395 400

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu
405 410 415

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
420 425 430

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
435 440 445

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly

450 455 460

Lys
465

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<211> 1395
<212> DNA
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<220>
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tgcaaggctt ctggatacac cttcaccggc tactatatac actgggtgcg acaggcccct 180

ggacaagggc ttgagtggat gggatggatc aaccctaaca gtggtggcac aaactctgca 240

cagaagtttc ggggcagggt caccatgacc agggacacgt ccatcagcac agcctacatg 300

gagctgagca ggctgagatc tgacgacacg gccgtgtatt actgtgcgcg agagggtgga 360

tacagctatg gttactttga ctactggggc cagggaaccc tggtcaccgt ctcctcagct 420

agcaccaagg gcccatcggt cttccccctg gcgccctgct ccaggagcac ctccgagagc 480

acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 540

aactcaggcg ctctgaccag cggcgtgcac accttcccag ctgtcctaca gtcctcagga 600

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca acttcggcac ccagacctac 660

acctgcaacg tagatcacaa gcccagcaac accaaggtgg acaagacagt tgagcgcaaa 720

tgttgtgtcg agtgcccacc gtgcccagca ccacctgtgg caggaccgtc agtcttcctc 780

ttccccccaa aacccaagga caccctcatg atctcccgga ccctgaggt cacgtgcgtg 840

gtggtggacg tgagccacga agaccccgag gtccagttca actggtacgt ggacggcgtg 900

gaggtgcata atgccaagac aaagccacgg gaggagcagt tcaacagcac gttccgtgtg 960

gtcagcgtcc tcaccgttgt gcaccaggac tggctgaacg gcaaggagta caagtgcaag 1020

gtctccaaca aaggcctccc agccccccatc gagaaaacca tctccaaaac caaagggcag 1080

ccccgagaac cacaggtgta caccctgccc ccatcccggg aggagatgac caagaaccag 1140

gtcagcctga cctgcctggt caaaggcttc taccccagcg acatcgccgt ggagtgggag 1200

agcaatgggc agccggagaa caactacaag accacacctc ccatgctgga ctccgacggc 1260

tccttcttcc tctacagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc 1320

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ctgtctccgg gtaaa 1395

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<211> 120
<212> PRT

<213> Artificial Sequence

<220>
<223> variable domain

<400> 9

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

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

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

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

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

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 10
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1

<400> 10

Gly Tyr Tyr Ile His
1 5

<210> 11
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2

<400> 11

Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Ser Ala Gln Lys Phe Arg
1 5 10 15

Gly

<210> 12
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
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<400> 12

Glu Gly Gly Tyr Ser Tyr Gly Tyr Phe Asp Tyr
1 5 10

<210> 13
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> light chain

<400> 13

Met Glu Thr Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

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

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

Val Ser Ser Ser Tyr Phe Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
50 55 60

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

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
85 90 95

Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr
100 105 110

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

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

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

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

165 170 175

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

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

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

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

<210> 14
<211> 705
<212> DNA
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<400> 14
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gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga cagagccacc 120

ctctcctgca gggccagtca gagtgttagt agcagctact ttgcctggta ccagcagaaa 180

cctggccagg ctcccaggct cctcatttat ggtgcatcca gtagggccac tggcatccca 240

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 300

cctgaagatt ttgcagtgta ttactgtcag cagtatgata ggtcacctcg gacgttcggc 360

caagggacca aggtggaaat caaacgtacg gtggctgcac catctgtctt catcttcccg 420

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 480

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 540

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 600

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 660

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgt 705

<210> 15
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> variable domain

<400> 15

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

Asp Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser

20 25 30

Tyr Phe Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

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

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

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

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

<210> 16
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1

<400> 16

Arg Ala Ser Gln Ser Val Ser Ser Ser Tyr Phe Ala
1 5 10

<210> 17
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2

<400> 17

Gly Ala Ser Ser Arg Ala Thr
1 5

<210> 18
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3

<400> 18

Gln Gln Tyr Asp Arg Ser Pro Arg Thr
1 5

<210> 19
<211> 463
<212> PRT

<213> Artificial Sequence

<220>
<223> heavy chain

<400> 19

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Ala His Ser Gln 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 Ser Ser Gly Tyr Thr Phe
        35                  40                  45

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

Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala
65                  70                  75                  80

Gln Lys Phe Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser
                85                  90                  95

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

Tyr Tyr Cys Ala Arg Asp Lys Trp Leu Asp Gly Phe Asp Tyr Trp Gly
        115                 120                 125

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

Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
145                 150                 155                 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

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

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His
    210                 215                 220

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

Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val
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245 250 255

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
260 265 270

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
275 280 285

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
290 295 300

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser
305 310 315 320

Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
325 330 335

Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile
340 345 350

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

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
370 375 380

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
385 390 395 400

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser
405 410 415

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
420 425 430

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
435 440 445

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455 460

<210> 20
<211> 1389
<212> DNA
<213> Artificial Sequence

<220>
<223> heavy chain

<400> 20
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tgtaagtctt ctggatacac cttcaccggc tactatatgc actgggtgcg acaggcccct 180

ggacaagggc ttgagtggat gggatggatc aaccctaaca gtggtggcac aaactatgca 240

cagaagttta agggcagggt caccatgacc agggacacgt ccatcagcac agcctacatg 300

gagctgagca ggctgagatc tgacgacacg gccgtgtatt actgtgcgag agataagtgg 360

ctggacggct ttgactactg gggccaggga accctggtca ccgtctcctc agctagcacc 420

aagggcccat cggtcttccc cctggcgccc tgctccagga gcacctccga gagcacagcg 480

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 540

ggcgctctga ccagcggcgt gcacaccttc ccagctgtcc tacagtcctc aggactctac 600

tccctcagca gcgtggtgac cgtgccctcc agcaacttcg gcacccagac ctacacctgc 660

aacgtagatc acaagcccag caacaccaag gtggacaaga cagttgagcg caaatgttgt 720

gtcgagtgcc caccgtgccc agcaccacct gtggcaggac cgtcagtctt cctcttcccc 780

ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacgtg cgtggtggtg 840

gacgtgagcc acgaagaccc cgaggtccag ttcaactggt acgtggacgg cgtggaggtg 900

cataatgcca agacaaagcc acgggaggag cagttcaaca gcacgttccg tgtggtcagc 960

gtcctcaccg ttgtgcacca ggactggctg aacggcaagg agtacaagtg caaggtctcc 1020

aacaaaggcc tcccagcccc catcgagaaa accatctcca aaaccaaagg gcagccccga 1080

gaaccacagg tgtacaccct gcccccatcc cgggaggaga tgaccaagaa ccaggtcagc 1140

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ccgggtaaa 1389

<210> 21
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> variable domain

<400> 21

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
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Ser Val Lys Val Ser Cys Lys Ser Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

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

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe

50 55 60

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

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

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

Leu Val Thr Val Ser Ser
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<210> 22
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1

<400> 22

Gly Tyr Tyr Met His
1 5

<210> 23
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2

<400> 23

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

Gly

<210> 24
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3

<400> 24

Asp Lys Trp Leu Asp Gly Phe Asp Tyr
1 5

<210> 25
<211> 235
<212> PRT

<213> Artificial Sequence

<220>
<223> light chain

<400> 25

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

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
        35                  40                  45

Val Ser Ser Ser Tyr Phe Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
    50                  55                  60

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

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

Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr
            100                 105                 110

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

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

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

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

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

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

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

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235
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<210> 26

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

<220>
<223> light chain

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ctctcctgca gggccagtca gagtgttagc agcagctact tcgcctggta ccaacagaaa 180

cctggccagg ctcccaggct cctcatctat ggtacatcca gcagggccac tggcatccca 240

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccgtcag cagactggag 300

cctgaggatt ttgcagtgta ttactgtcag cagtatgata ggtcacctcg gacgttcggc 360

caagggacca aggtggaaat caaacgtacg gtggctgcac catctgtctt catcttcccg 420

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 480

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 540

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 600

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 660

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgt 705

<210> 27
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> variable domain

<400> 27

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30

Tyr Phe Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

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

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

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

Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

100 105

<210> 28
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<220>
<221> MISC_FEATURE
<222> (11)..(11)
<223> Xaa is Tyr or Ser

<220>
<221> MISC_FEATURE
<222> (13)..(13)
<223> Xaa is Gln or Arg

<220>
<221> MISC_FEATURE
<222> (14)..(14)
<223> Xaa is Lys or Arg

<220>
<221> MISC_FEATURE
<222> (16)..(16)
<223> Xaa is Lys, Arg or Gln

<400> 28

Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Xaa Ala Xaa Xaa Phe Xaa
1 5 10 15

Gly

<210> 29
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2

<400> 29

Gly Thr Ser Ser Arg Ala Thr
1 5

<210> 30
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<220>
<221> MISC_FEATURE
<222> (5)..(5)

<223> Xaa is Ser or Tyr

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa is Val, Ile or Leu

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa is Ser or Asn

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> Xaa is Ser or Cys

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> Xaa is Ser, Thr or Ile

<220>
<221> MISC_FEATURE
<222> (11)..(11)
<223> Xaa is Phe or Leu

<400> 30

Arg Ala Ser Gln Xaa Xaa Xaa Xaa Xaa Tyr Xaa Ala
1 5 10

<210> 31
<211> 463
<212> PRT
<213> Artificial Sequence sequence

<220>
<223> heavy chain

<400> 31

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Ala Val Lys Lys
20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

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

Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala
65 70 75 80

Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser
85 90 95

Thr Ala Ser Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val

100 105 110

Tyr Phe Cys Ala Arg Asp Arg Trp Leu Asp Ala Phe Asp Ile Trp Gly
115 120 125

Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
130 135 140

Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
165 170 175

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

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His
210 215 220

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

Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val
245 250 255

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
260 265 270

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
275 280 285

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
290 295 300

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser
305 310 315 320

Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
325 330 335

Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile
340 345 350

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

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu

370 375 380

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
385 390 395 400

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser
405 410 415

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
420 425 430

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
435 440 445

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455 460

<210> 32
<211> 1389
<212> DNA
<213> Artificial Sequence

<220>
<223> heavy chain

<400> 32
atggattgga cctggcgtat tctgtttctg gtggcggcgg cgaccggcgc gcatagccag 60

gtgcagttgg tgcagtctgg ggctgcggtg aagaagcctg gggcctcagt gaaggtctcc 120

tgcaaggctt ctggatacac cttcaccggc tactatatac actgggtgcg acaggcccct 180

ggacaagggc ttgagtggat gggatggatc aaccctaaca gtggtggcac aaactatgca 240

caaaagtttc agggcagggt caccatgacc agggacacgt ccatcagcac agcctccatg 300

gaactgagca ggctgagatc tgacgacacg gccgtttatt tctgtgcgag agatcggtgg 360

ctggatgctt ttgatatctg gggccaaggg acaatggtca ccgtctcttc tgctagcacc 420

aagggcccat cggtcttccc cctggcgccc tgctccagga gcacctccga gagcacagcg 480

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 540

ggcgctctga ccagcggcgt gcacaccttc ccagctgtcc tacagtcctc aggactctac 600

tccctcagca gcgtggtgac cgtgccctcc agcaacttcg gcacccagac ctacacctgc 660

aacgtagatc acaagcccag caacaccaag gtggacaaga cagttgagcg caaatgttgt 720

gtcgagtgcc caccgtgccc agcaccacct gtggcaggac cgtcagtctt cctcttcccc 780

ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacgtg cgtggtggtg 840

gacgtgagcc acgaagaccc cgaggtccag ttcaactggt acgtggacgg cgtggaggtg 900

cataatgcca agacaaagcc acgggaggag cagttcaaca gcacgttccg tgtggtcagc 960

gtcctcaccg ttgtgcacca ggactggctg aacggcaagg agtacaagtg caaggtctcc 1020

aacaaaggcc tcccagcccc catcgagaaa accatctcca aaaccaaagg gcagccccga 1080

gaaccacagg tgtacaccct gcccccatcc cgggaggaga tgaccaagaa ccaggtcagc 1140

ctgacctgcc tggtcaaagg cttctacccc agcgacatcg ccgtggagtg ggagagcaat 1200

gggcagccgg agaacaacta caagaccaca cctcccatgc tggactccga cggctccttc 1260

ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1320

tgctccgtga tgcatgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1380

ccgggtaaa 1389

<210> 33
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> variable domain

<400> 33

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

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

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

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

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Ser
65 70 75 80

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

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

Met Val Thr Val Ser Ser
115

<210> 34
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> Xaa is Ala or Thr

<400> 34

Gly Xaa Ser Ser Arg Ala Thr
1 5

<210> 35
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2

<400> 35

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

Gly

<210> 36
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3

<400> 36

Asp Arg Trp Leu Asp Ala Phe Asp Ile
1 5

<210> 37
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> light chain

<400> 37

Met Glu Thr Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

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

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Tyr
35 40 45

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

Pro Arg Leu Leu Ile Tyr Gly Ala Ala Thr Arg Ala Thr Gly Ile Pro
65 70 75 80

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile
85 90 95

Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr
100 105 110

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

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

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

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

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

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

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

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

<210> 38
<211> 705
<212> DNA
<213> Artificial Sequence

<220>
<223> light chain

<400> 38
atggaaaccc cggcgcagct gctgtttctg ctgctgctgt ggctgccgga taccaccggc 60

gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 120

ctctcctgca gggccagtca gtatattagc aacacctatt tagcctggtt ccagcagaaa 180

cctggccagg ctcccaggct cctcatctat ggtgcagcca ccagggccac tggcatccca 240

gacaggttca gtggcagtgg gtctgggaca gacttcactt tcaccatcag cagactggag 300

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccgtg gacgttcggc 360

caagggacca cggtggaaat caaacgtacg gtggctgcac catctgtctt catcttcccg 420

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 480

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 540

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 600

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 660

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgt 705

<210> 39
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> variable domain

<400> 39

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

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

Tyr Leu Ala Trp Phe Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

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

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

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

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

<210> 40
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1

<400> 40

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

<210> 41
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2

<400> 41

Gly Ala Ala Thr Arg Ala Thr
1 5

<210> 42
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3

<400> 42

Gln Gln Tyr Gly Ser Ser Pro Trp Thr
1 5

<210> 43
<211> 463
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain

<400> 43

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Ala His Ser Gln 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 Tyr Thr Phe
35 40 45

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

Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala
65 70 75 80

Gln Arg Phe Arg Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser
85 90 95

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

Tyr Tyr Cys Ala Arg Ala Pro Tyr Asp Trp Thr Phe Asp Tyr Trp Gly
115 120 125

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

Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
165 170 175

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

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His
210 215 220

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

Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val
245 250 255

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
260 265 270

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
275 280 285

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
290 295 300

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser
305 310 315 320

Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
325 330 335

Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile
340 345 350

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

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
370 375 380

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
385 390 395 400

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser
405 410 415

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
420 425 430

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
435 440 445

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455 460

<210> 44
<211> 1389
<212> DNA
<213> Artificial Sequence

<220>
<223> heavy chain

<400> 44
atggattgga cctggcgtat tctgtttctg gtggcggcgg cgaccggcgc gcatagccag 60

gtgcagttgg tgcagtctgg ggctgaggtg aagaagcctg gggcctcagt gaaggtctcc 120

tgcaaggctt ctggatacac cttcaccggc tactatatgc actgggtgcg acaggcccct 180

ggacaagggc ttgagtggat gggatggatc aaccctaaca gtggtggcac aaactatgca 240

cagaggtttc ggggcagggt caccatgacc agggacacgt ccatcagcac agcctacatg 300

gaactgagca ggctgagatc tgacgacacg gccgtgtatt actgtgcgag agccccgtat 360

gactggacct ttgactactg gggccaggga accctggtca ccgtctcctc agctagcacc 420

aagggcccat cggtcttccc cctggcgccc tgctccagga gcacctccga gagcacagcg 480

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 540

ggcgctctga ccagcggcgt gcacaccttc ccagctgtcc tacagtcctc aggactctac 600

tccctcagca gcgtggtgac cgtgccctcc agcaacttcg gcacccagac ctacacctgc 660

aacgtagatc acaagcccag caacaccaag gtggacaaga cagttgagcg caaatgttgt 720

gtcgagtgcc caccgtgccc agcaccacct gtggcaggac cgtcagtctt cctcttcccc 780

ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacgtg cgtggtggtg 840

gacgtgagcc acgaagaccc cgaggtccag ttcaactggt acgtggacgg cgtggaggtg 900

cataatgcca agacaaagcc acgggaggag cagttcaaca gcacgttccg tgtggtcagc 960

gtcctcaccg ttgtgcacca ggactggctg aacggcaagg agtacaagtg caaggtctcc 1020

aacaaaggcc tcccagcccc catcgagaaa accatctcca aaaccaaagg gcagccccga 1080

gaaccacagg tgtacaccct gccccatcc cgggaggaga tgaccaagaa ccaggtcagc 1140

ctgacctgcc tggtcaaagg cttctacccc agcgacatcg ccgtggagtg ggagagcaat 1200

gggcagccgg agaacaacta caagaccaca cctcccatgc tggactccga cggctccttc 1260

ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1320

tgctccgtga tgcatgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1380

ccgggtaaa 1389

<210> 45

<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> variable domain

<400> 45

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

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

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

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Arg Phe
50 55 60

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

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

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

Leu Val Thr Val Ser Ser
115

<210> 46
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa is Tyr or Ser

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa is Phe, Gly or Ala

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa is Ser, Thr or Trp

<220>
<221> MISC_FEATURE
<222> (6)..(6)

<223> Xaa is Val, Ser or Phe

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa is Phe or Pro

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> Xaa is Arg, Trp, or Ile

<400> 46

Gln Gln Xaa Xaa Xaa Xaa Xaa Xaa Thr
1 5

<210> 47
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2

<400> 47

Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Arg Phe Arg
1 5 10 15

Gly

<210> 48
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3

<400> 48

Ala Pro Tyr Asp Trp Thr Phe Asp Tyr
1 5

<210> 49
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> light chain

<400> 49

Met Glu Thr Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Val Val Leu Thr Gln Ser Pro Gly Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
35 40 45

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

Pro Arg Leu Leu Ile Ser Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro
65 70 75 80

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
85 90 95

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

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

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

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

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

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

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

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

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

<210> 50
<211> 705
<212> DNA
<213> Artificial Sequence

<220>
<223> light chain

<400> 50
atggaaaccc cggcgcagct gctgtttctg ctgctgctgt ggctgccgga taccaccggc 60

gaagttgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 120

ctctcctgca gggccagtca gagcgtttgc agcagctact tagcctggta ccagcagaaa 180

cctgaccagg ctcccaggct cctcatctct ggtgcgtcca gcagggccac tggcatccca 240

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagcctggag 300

cctgaagatt ttgcagtgta ttactgtcag cagtatgata ggtcacctcg gacgttcggc 360

caagggacca aggtggagat caaacgtacg gtggctgcac catctgtctt catcttcccg 420

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 480

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 540

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 600

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 660

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgt 705

<210> 51
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> variable domain

<400> 51

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Cys Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Asp Gln Ala Pro Arg Leu Leu
35 40 45

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

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

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

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

<210> 52
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1

<400> 52

Arg Ala Ser Gln Ser Val Cys Ser Ser Tyr Leu Ala
1 5 10

<210> 53
<211> 144
<212> PRT
<213> Macaca fascicularis

<400> 53

Met Trp Leu Gln Gly Leu Leu Leu Leu Gly Thr Val Ala Cys Ser Ile
1 5 10 15

Ser Ala Pro Ala Arg Ser Pro Ser Pro Gly Thr Gln Pro Trp Glu His
20 25 30

Val Asn Ala Ile Gln Glu Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp
35 40 45

Thr Ala Ala Glu Met Asn Lys Thr Val Glu Val Val Ser Glu Met Phe
50 55 60

Asp Leu Gln Glu Pro Ser Cys Leu Gln Thr Arg Leu Glu Leu Tyr Lys
65 70 75 80

Gln Gly Leu Gln Gly Ser Leu Thr Lys Leu Lys Gly Pro Leu Thr Met
85 90 95

Met Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser
100 105 110

Cys Ala Thr Gln Ile Ile Thr Phe Gln Ser Phe Lys Glu Asn Leu Lys
115 120 125

Asp Phe Leu Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val Gln Glu
130 135 140

<210> 54
<211> 144
<212> PRT
<213> Canis familiaris

<400> 54

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

Ser Ala Pro Thr Arg Ser Pro Thr Leu Val Thr Arg Pro Ser Gln His
20 25 30

Val Asp Ala Ile Gln Glu Ala Leu Ser Leu Leu Asn Asn Ser Asn Asp
35 40 45

Val Thr Ala Val Met Asn Lys Ala Val Lys Val Val Ser Glu Val Phe
50 55 60

```
Asp Pro Glu Gly Pro Thr Cys Leu Glu Thr Arg Leu Gln Leu Tyr Lys
65                  70                  75                  80

Glu Gly Leu Gln Gly Ser Leu Thr Ser Leu Lys Asn Pro Leu Thr Met
                85                  90                  95

Met Ala Asn His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Ser Pro
            100                 105                 110

Cys Ala Thr Gln Asn Ile Asn Phe Lys Ser Phe Lys Glu Asn Leu Lys
        115                 120                 125

Asp Phe Leu Phe Asn Ile Pro Phe Asp Cys Trp Lys Pro Val Lys Lys
    130                 135                 140
```

<210> 55
<211> 463
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain

<400> 55

```
Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1               5                   10                  15

Ala His Ser Gln 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 Tyr Thr Phe
        35                  40                  45

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

Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Gly Arg Asn Tyr Ala
65                  70                  75                  80

Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser
                85                  90                  95

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

Tyr Tyr Cys Ala Arg Asp Arg Trp Leu Asp Ala Phe Glu Ile Trp Gly
        115                 120                 125

Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
145                 150                 155                 160
```

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
165 170 175

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

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His
210 215 220

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

Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val
245 250 255

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
260 265 270

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
275 280 285

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
290 295 300

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser
305 310 315 320

Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
325 330 335

Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile
340 345 350

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

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
370 375 380

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
385 390 395 400

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser
405 410 415

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
420 425 430

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
435 440 445

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455 460

<210> 56
<211> 1389
<212> DNA
<213> Artificial Sequence

<220>
<223> heavy chain

<400> 56
atggattgga cctggcgtat tctgtttctg gtggcggcgg cgaccggcgc gcatagccag 60

gtgcagctgg tgcagtctgg ggctgaggtg aagaagcctg gggcctcagt gaaggtctcc 120

tgcaaggctt ctggatacac cttcaccggc tactatatac actgggtgcg acaggcccct 180

ggacaagggc ttgagtggat gggatggatc aaccctaaca gtggtggcag aaactatgca 240

cagaagtttc agggcagggt caccatgacc agggacacgt ccatcagcac agcctacatg 300

gagctgagca ggctgagatc tgacgacacg gccgtgtatt actgtgcgag agaccggtgg 360

ctggatgctt ttgagatctg gggccaaggg acaatggtca ccgtctcttc agctagcacc 420

aagggcccat cggtcttccc cctggcgccc tgctccagga gcacctccga gagcacagcg 480

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 540

ggcgctctga ccagcggcgt gcacaccttc ccagctgtcc tacagtcctc aggactctac 600

tccctcagca gcgtggtgac cgtgccctcc agcaacttcg gcacccagac ctacacctgc 660

aacgtagatc acaagcccag caacaccaag gtggacaaga cagttgagcg caaatgttgt 720

gtcgagtgcc caccgtgccc agcaccacct gtggcaggac cgtcagtctt cctcttcccc 780

ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacgtg cgtggtggtg 840

gacgtgagcc acgaagaccc cgaggtccag ttcaactggt acgtggacgg cgtggaggtg 900

cataatgcca agacaaagcc acgggaggag cagttcaaca gcacgttccg tgtggtcagc 960

gtcctcaccg ttgtgcacca ggactggctg aacggcaagg agtacaagtg caaggtctcc 1020

aacaaaggcc tcccagcccc catcgagaaa accatctcca aaaccaaagg gcagccccga 1080

gaaccacagg tgtacaccct gccccatcc cgggaggaga tgaccaagaa ccaggtcagc 1140

ctgacctgcc tggtcaaagg cttctacccc agcgacatcg ccgtggagtg ggagagcaat 1200

gggcagccgg agaacaacta caagaccaca cctcccatgc tggactccga cggctccttc 1260

ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1320

tgctccgtga tgcatgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1380

ccgggtaaa 1389

<210> 57
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> variable domain

<400> 57

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

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

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

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

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

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

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

Met Val Thr Val Ser Ser
115

<210> 58
<211> 81
<212> PRT
<213> Mus musculus

<400> 58

Met Trp Leu Gln Asn Leu Leu Phe Leu Gly Ile Val Val Tyr Ser Leu
1 5 10 15

Ser Ala Pro Thr Arg Ser Pro Ile Thr Val Thr Arg Pro Trp Lys His
20 25 30

Val Glu Ala Ile Lys Glu Ala Leu Asn Leu Leu Asp Asp Met Pro Val
35 40 45

Thr Leu Asn Glu Glu Val Glu Val Val Ser Asn Glu Ile Asp Ser Leu
50 55 60

Lys Thr Phe Leu Thr Asp Ile Pro Phe Glu Cys Lys Lys Pro Val Gln
65 70 75 80

Lys

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

<220>
<223> CDR2

<400> 59

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

Gly

<210> 60
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3

<400> 60

Asp Arg Trp Leu Asp Ala Phe Glu Ile
1 5

<210> 61
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> light chain

<400> 61

Met Ala Trp Ala Pro Leu Leu Leu Thr Leu Leu Ala His Cys Thr Gly
1 5 10 15

Ser Trp Ala Asn Phe Met Leu Ala Gln Pro His Ser Val Ser Glu Ser
20 25 30

Pro Gly Lys Thr Val Thr Ile Ser Cys Ile Arg Thr Ser Gly Ser Ile
35 40 45

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

Thr Thr Val Ile Tyr Glu Asp Asp Gln Arg Pro Ser Gly Val Pro Asp
65 70 75 80

Arg Phe Ser Gly Ser Ile Asp Ser Ser Ser Asn Ser Ala Ser Leu Thr

85 90 95

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

Cys Asp Ile Ser Asn Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val
115 120 125

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

Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser
145 150 155 160

Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser
165 170 175

Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn
180 185 190

Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp
195 200 205

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

Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
225 230 235

<210> 62
<211> 705
<212> DNA
<213> Artificial Sequence

<220>
<223> light chain

<400> 62
atggcgtggg cgccgctgct gctgaccctg ctggcgcatt gcaccggcag ctgggcgaat 60

tttatgctgg ctcagcccca ctctgtgtcg gagtctccgg ggaagacggt aaccatctcc 120

tgtattcgca ccagtggcag cattgccagc aactatgtac agtggtatca gcagcgcccg 180

ggcagttccc ccaccactgt gatctatgag gatgaccaaa gaccctctgg ggtccctgat 240

cgattctctg gctccatcga cagctcctcc aattctgcct ccctcaccat ctctggactg 300

aagactgagg acgaggctga ctactactgt cagtcttgtg atatcagcaa tgtggtattc 360

ggcggaggga ccaagctgac cgtcctaggc caaccgaaag cggcgccctc ggtcactctg 420

ttcccgccct cctctgagga gcttcaagcc aacaaggcca cactggtgtg tctcataagt 480

gacttctacc cgggagccgt gacagtggcc tggaaggcag atagcagccc cgtcaaggcg 540

ggagtggaga ccaccacacc ctccaaacaa agcaacaaca agtacgcggc cagcagctat 600

ctgagcctga cgcctgagca gtggaagtcc cacagaagct acagctgcca ggtcacgcat 660

gaagggagca ccgtggagaa gacagtggcc cctacagaat gttca 705

<210> 63
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> variable domain

<400> 63

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

Thr Val Thr Ile Ser Cys Ile Arg Thr Ser Gly Ser Ile Ala Ser Asn
20 25 30

Tyr Val Gln Trp Tyr Gln Gln Arg Pro Gly Ser Ser Pro Thr Thr Val
35 40 45

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

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

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

Ser Asn Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 64
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1

<400> 64

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

<210> 65
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2

<400> 65

Glu Asp Asp Gln Arg Pro Ser

1 5

<210> 66
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3

<400> 66

Gln Ser Cys Asp Ile Ser Asn Val Val
1 5

<210> 67
<211> 463
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain

<400> 67

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

Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Gln
20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Glu Ala Ser Gly Tyr Thr Phe
35 40 45

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

Glu Trp Met Gly Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asp Tyr Ala
65 70 75 80

Gln Lys Leu Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser
85 90 95

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

Tyr Tyr Cys Ala Arg Gln Arg Tyr Tyr Tyr Ser Met Asp Val Trp Gly
115 120 125

Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
130 135 140

Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val

165 170 175

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

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His
210 215 220

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

Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val
245 250 255

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
260 265 270

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
275 280 285

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
290 295 300

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser
305 310 315 320

Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
325 330 335

Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile
340 345 350

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

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
370 375 380

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
385 390 395 400

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser
405 410 415

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
420 425 430

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

435 440 445

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455 460

<210> 68
<211> 1389
<212> DNA
<213> Artificial Sequence

<220>
<223> heavy chain

<400> 68
atggattgga cctggagcat tctgtttctg gtggcggcgc cgaccggcgc gcatagccag 60

gttcagctgg tgcagtctgg agctgaggtg aagcagcctg gggcctcagt gaaggtctcc 120

tgcgaggctt ctggttacac cttcaccagc tatggtatca gctgggtgcg acaggcccct 180

ggacaagggc ttgagtggat gggatggatc agcgcttaca atggtaacac agactatgca 240

cagaagctcc agggcagagt caccatgacc acagacacat ccacgagcgc agcctacatg 300

gagctgagga gcctgagatc tgacgacacg gccgtgtatt actgtgcgag acaacggtat 360

tactacagta tggacgtctg gggccaaggg accacggtca ccgtctcctc agctagcacc 420

aagggcccat cggtcttccc cctggcgccc tgctccagga gcacctccga gagcacagcg 480

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 540

ggcgctctga ccagcggcgt gcacaccttc ccagctgtcc tacagtcctc aggactctac 600

tccctcagca gcgtggtgac cgtgccctcc agcaacttcg gcacccagac ctacacctgc 660

aacgtagatc acaagcccag caacaccaag gtggacaaga cagttgagcg caaatgttgt 720

gtcgagtgcc caccgtgccc agcaccacct gtggcaggac cgtcagtctt cctcttcccc 780

ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacgtg cgtggtggtg 840

gacgtgagcc acgaagaccc cgaggtccag ttcaactggt acgtggacgg cgtggaggtg 900

cataatgcca agacaaagcc acgggaggag cagttcaaca gcacgttccg tgtggtcagc 960

gtcctcaccg ttgtgcacca ggactggctg aacggcaagg agtacaagtg caaggtctcc 1020

aacaaaggcc tcccagcccc catcgagaaa accatctcca aaaccaaagg gcagccccga 1080

gaaccacagg tgtacaccct gccccatcc cgggaggaga tgaccaagaa ccaggtcagc 1140

ctgacctgcc tggtcaaagg cttctacccc agcgacatcg ccgtggagtg ggagagcaat 1200

gggcagccgg agaacaacta caagaccaca cctcccatgc tggactccga cggctccttc 1260

ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1320

tgctccgtga tgcatgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1380

ccgggtaaa 1389

<210> 69
<211> 118
<212> PRT

<213> Artificial Sequence

<220>
<223> variable domain

<400> 69

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

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

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

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

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

Thr Val Thr Val Ser Ser
        115
```

<210> 70
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1

<400> 70

```
Ser Tyr Gly Ile Ser
1               5
```

<210> 71
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2

<400> 71

```
Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asp Tyr Ala Gln Lys Leu Gln
1               5                   10                  15

Gly
```

<210> 72
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3

<400> 72

Gln Arg Tyr Tyr Tyr Ser Met Asp Val
1 5

<210> 73
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> light chain

<400> 73

Met Glu Thr Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

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

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
35 40 45

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

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

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

Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Leu Gln Tyr
100 105 110

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

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

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

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

165 170 175

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

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

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

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

<210> 74
<211> 705
<212> DNA
<213> Artificial Sequence

<220>
<223> light chain

<400> 74
atggaaaccc cggcgcagct gctgtttctg ctgctgctgt ggctgccgga taccaccggc 60

gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 120

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 180

cctggccagg ttcccaggct cctcatctat ggtacatcca gcagggccac tggcatccca 240

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccgtcag cagactggag 300

cctgaagatt ttgcagtgta ttactgtctc cagtatgata ggtcacctcg gacgttcggc 360

caagggacca aggtggaaat caaacgtacg gtggctgcac catctgtctt catcttcccg 420

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 480

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 540

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 600

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 660

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgt 705

<210> 75
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> variable domain

<400> 75

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser

20 25 30

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

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

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

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

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

<210> 76
<211> 127
<212> PRT
<213> Rattus rattus

<400> 76

Ala Pro Thr Arg Ser Pro Asn Pro Val Thr Arg Pro Trp Lys His Val
1 5 10 15

Asp Ala Ile Lys Glu Ala Leu Ser Leu Leu Asn Asp Met Arg Ala Leu
20 25 30

Glu Asn Glu Lys Asn Glu Asp Val Asp Ile Ile Ser Asn Glu Phe Ser
35 40 45

Ile Gln Arg Pro Thr Cys Val Gln Thr Arg Leu Lys Leu Tyr Lys Gln
50 55 60

Gly Leu Arg Gly Asn Leu Thr Lys Leu Asn Gly Ala Leu Thr Met Ile
65 70 75 80

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

Glu Ile Glu Val Thr Thr Phe Glu Asp Phe Ile Lys Asn Leu Lys Gly
100 105 110

Phe Leu Phe Asp Ile Pro Phe Asp Cys Trp Lys Pro Val Gln Lys
115 120 125

<210> 77
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> CDR2

<400> 77

Gly Thr Ser Ser Arg Ala Thr
1 5

<210> 78
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3

<400> 78

Leu Gln Tyr Asp Arg Ser Pro Arg Thr
1 5

<210> 79
<211> 462
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain

<400> 79

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

Ala His Ser Gln 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 Tyr Thr Phe
35 40 45

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

Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala
65 70 75 80

Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser
85 90 95

Thr Ala Tyr Met Glu Leu Ser Trp Leu Arg Ser Asp Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Asp Arg Trp Leu Asp Ala Phe Asp Ile Trp Gly
115 120 125

Gln Gly Thr Met Val Thr Val Ser Ala Ser Thr Lys Gly Pro Ser Val
130 135 140

```
Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
145                 150                 155                 160

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
                165                 170                 175

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

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
        195                 200                 205

Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys
    210                 215                 220

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

Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe
                245                 250                 255

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
            260                 265                 270

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
        275                 280                 285

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
    290                 295                 300

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val
305                 310                 315                 320

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

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

Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
        355                 360                 365

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
    370                 375                 380

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
385                 390                 395                 400

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp
                405                 410                 415
```

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

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

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455 460

<210> 80
<211> 1386
<212> DNA
<213> Artificial Sequence

<220>
<223> heavy chain

<400> 80
atggattgga cctggagcat tctgtttctg gtggcggcgc cgaccggcgc gcatagccag 60

gtgcagctgg tgcagtctgg ggctgaggtg aagaagcctg gggcctcagt gaaggtctcc 120

tgcaaggctt ctggatacac cttcaccggc tactatatgc actgggtgcg acaggcccct 180

ggacaagggc ttgagtggat gggatggatc aaccctaaca gtggtggcac aaactatgca 240

cagaagtttc agggcagggt caccatgacc agggacacgt ccatcagcac agcctacatg 300

gagctgagct ggctgagatc tgacgacacg gccgtatatt actgtgcgag agaccggtgg 360

ctggatgctt ttgatatctg gggccaaggg acaatggtca ccgtctctgc tagcaccaag 420

ggcccatcgg tcttcccccct ggcgccctgc tccaggagca cctccgagag cacagcggcc 480

ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 540

gctctgacca gcggcgtgca caccttccca gctgtcctac agtcctcagg actctactcc 600

ctcagcagcg tggtgaccgt gccctccagc aacttcggca cccagaccta cacctgcaac 660

gtagatcaca agcccagcaa caccaaggtg gacaagacag ttgagcgcaa atgttgtgtc 720

gagtgcccac cgtgcccagc accacctgtg gcaggaccgt cagtcttcct cttccccca 780

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacgtgcgt ggtggtggac 840

gtgagccacg aagaccccga ggtccagttc aactggtacg tggacggcgt ggaggtgcat 900

aatgccaaga caaagccacg ggaggagcag ttcaacagca cgttccgtgt ggtcagcgtc 960

ctcaccgttg tgcaccagga ctggctgaac ggcaaggagt acaagtgcaa ggtctccaac 1020

aaaggcctcc cagccccat cgagaaaacc atctccaaaa ccaaagggca gccccgagaa 1080

ccacaggtgt acaccctgcc cccatcccgg gaggagatga ccaagaacca ggtcagcctg 1140

acctgcctgg tcaaaggctt ctaccccagc gacatcgccg tggagtggga gagcaatggg 1200

cagccggaga acaactacaa gaccacacct cccatgctgg actccgacgg ctccttcttc 1260

ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc 1320

tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg 1380

ggtaaa 1386

<210> 81
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> variable domain

<400> 81

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

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

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

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

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

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

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

Met Val Thr Val Ser
115

<210> 82
<211> 144
<212> PRT
<213> Oryctolagus cuniculus

<400> 82

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

Ser Ala Pro Thr His Gln Pro Asn Thr Val Ser Gln Pro Leu Lys His
20 25 30

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

Ser Ala Ala Val Pro Gly Glu Met Val Glu Val Val Ser Glu Met Phe
50 55 60

Asp Pro Gln Lys Pro Thr Cys Leu Gln Thr Arg Leu Glu Leu Tyr Lys

65 70 75 80

Gln Gly Leu Arg Gly Ser Leu Glu Arg Leu Ser Ser Thr Leu Thr Leu
85 90 95

Met Ala Ser His Tyr Lys Gln Asn Cys Pro Pro Thr Pro Glu Thr Ser
100 105 110

Cys Glu Thr Glu Phe Ile Thr Phe Lys Ser Phe Lys Glu Asn Leu Lys
115 120 125

Cys Phe Leu Phe Val Ile Pro Phe Asn Cys Trp Glu Pro Val Gln Lys
130 135 140

<210> 83
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa is Glu or no amino acid residue

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> Xaa is Gly or no amino acid residue

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa is Pro, Asp or Gly

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa is Tyr, Trp, Arg or Lys

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa is Ser, Trp, Phe or Thr

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa is Thr or Leu

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa is Asp or Gly

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> Xaa is Tyr or no amino acid residue

<220>
<221> MISC_FEATURE
<222> (11)..(11)
<223> Xaa iis Met, Thr or Val

<400> 83

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Asp Xaa
1 5 10

<210> 84
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa is Gln or Leu

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa is Gln or Leu

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa is Thr or Ser

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa is Asp, Gly or Phe

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa is Arg, Thr or Ser

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa is Ser or Val

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa is Phe or Pro

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> Xaa is Arg or Trp

<400> 84

Xaa Gln Xaa Xaa Xaa Xaa Xaa Xaa Thr
1 5

<210> 85
<211> 235

<212> PRT
<213> Artificial Sequence

<220>
<223> light chain

<400> 85

```
Met Glu Thr Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1               5                  10                  15

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

Leu Ser Leu Gly Glu Arg Ala Ile Leu Ser Cys Arg Ala Ser Gln Ser
        35                  40                  45

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

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

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
                85                  90                  95

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

Ala Thr Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys
        115                 120                 125

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

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

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

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

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

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

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

<210> 86
<211> 704
<212> DNA
<213> Artificial Sequence

<220>
<223> light chain

<400> 86
atggaaaccc cggcgcagct gctgtttctg ctgctgctgt ggctgccgga taccaccggc 60

gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctctagggga aagagccatc 120

ctctcctgca gggccagtca gagtcttagc agcatctact tagcctggta ccagcagaaa 180

cctggccagg ctcccggtct cctcatctat ggtgcttcca gcagggccac tggcatccca 240

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag tagtctggag 300

cctgaagatt ttgcagtgta ttactgtcag cagtatgcta cctcaccgtg gacgttcggc 360

caagggacca aggtggaagt caaacgtacg gtggctgcac catctgtctt catcttcccg 420

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 480

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 540

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 600

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 660

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtg 704

<210> 87
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> variable domain

<400> 87

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

Glu Arg Ala Ile Leu Ser Cys Arg Ala Ser Gln Ser Leu Ser Ser Ile
20 25 30

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

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

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

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

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys
100 105

<210> 88
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1

<400> 88

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

<210> 89
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa is Ser or Ala

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> Xaa is Ser or Ala

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa is Trp or Phe

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa is Asp or Thr

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> Xaa is Gly, Trp or no amino acid residue

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa is Val, Leu or Pro

<220>
<221> MISC_FEATURE
<222> (11)..(11)
<223> Xaa is Val or no amino acid residue

<400> 89

Xaa Xaa Xaa Xaa Asp Ser Ser Asn Xaa Xaa Xaa
1 5 10

<210> 90
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3

<400> 90

Gln Gln Tyr Ala Thr Ser Pro Trp Thr
1 5

<210> 91
<211> 463
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain

<400> 91

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

Ala His Ser Gln 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 Thr Phe
35 40 45

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

Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala
65 70 75 80

Arg Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser
85 90 95

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

Tyr Tyr Cys Ala Arg Arg Pro Trp Glu Leu Pro Phe Asp Tyr Trp Gly
115 120 125

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

Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
165 170 175

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

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His
210 215 220

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

Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val
245 250 255

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
260 265 270

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
275 280 285

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
290 295 300

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser
305 310 315 320

Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
325 330 335

Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile
340 345 350

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

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
370 375 380

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
385 390 395 400

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser
405 410 415

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
420 425 430

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
435 440 445

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455 460

<210> 92
<211> 1389
<212> DNA
<213> Artificial Sequence

<220>
<223> heavy chain

<400> 92
atggattgga cctggagcat tctgtttctg gtggcggcgc cgaccggcgc gcatagccag 60

gtgcagctgg tgcagtctgg ggctgaggtg aagaagcctg gggcctcagt gaaggtctcc 120

tgcaaggctt ctggattcac cttcagcggc tactatatgt actgggtgcg acaggcccct 180

ggacaagggc ttgagtggat gggatggatc aaccctaaca gtggtggcac aaactatgca 240

cggaagtttc agggcagggt caccatgacc agggacacgt ccatcagcac agcctacatg 300

gagctgagca ggctgagatc tgacgacacg gccgtatatt actgtgcgag gagaccgtgg 360

gagcttccct ttgactactg gggccaggga accctggtca ccgtctcctc agctagcacc 420

aagggcccat cggtcttccc cctggcgccc tgctccagga gcacctccga gagcacagcg 480

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 540

ggcgctctga ccagcggcgt gcacaccttc ccagctgtcc tacagtcctc aggactctac 600

tccctcagca gcgtggtgac cgtgccctcc agcaacttcg gcacccagac ctacacctgc 660

aacgtagatc acaagcccag caacaccaag gtggacaaga cagttgagcg caaatgttgt 720

gtcgagtgcc caccgtgccc agcaccacct gtggcaggac cgtcagtctt cctcttcccc 780

ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacgtg cgtggtggtg 840

gacgtgagcc acgaagaccc cgaggtccag ttcaactggt acgtggacgg cgtggaggtg 900

cataatgcca agacaaagcc acgggaggag cagttcaaca gcacgttccg tgtggtcagc 960

gtcctcaccg ttgtgcacca ggactggctg aacggcaagg agtacaagtg caaggtctcc 1020

aacaaaggcc tcccagcccc catcgagaaa accatctcca aaaccaaagg gcagccccga 1080

gaaccacagg tgtacaccct gccccatcc cgggaggaga tgaccaagaa ccaggtcagc 1140

ctgacctgcc tggtcaaagg cttctacccc agcgacatcg ccgtggagtg ggagagcaat 1200

gggcagccgg agaacaacta caagaccaca cctcccatgc tggactccga cggctccttc 1260

ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1320

tgctccgtga tgcatgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1380

ccgggtaaa 1389

<210> 93
<211> 118
<212> PRT
<213> Artificial Sequence

<220>

<223> variable domain

<400> 93

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

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

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

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Arg Lys Phe
50 55 60

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

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

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

Leu Val Thr Val Ser Ser
115

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

<220>
<223> CDR1

<400> 94

Gly Tyr Tyr Met Tyr
1 5

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

<220>
<223> CDR2

<400> 95

Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Arg Lys Phe Gln
1 5 10 15

Gly

<210> 96
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3

<400> 96

Arg Pro Trp Glu Leu Pro Phe Asp Tyr
1 5

<210> 97
<211> 234
<212> PRT
<213> Artificial Sequence

<220>
<223> light chain

<400> 97

Met Glu Thr Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly 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 Ser
35 40 45

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

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

Arg Phe Ser Gly Arg 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 Ser Phe
100 105 110

Ser Phe Pro Ile Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg
115 120 125

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

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

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

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

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

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

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

<210> 98
<211> 701
<212> DNA
<213> Artificial Sequence

<220>
<223> light chain

<400> 98
atggaaaccc cggcgcagct gctgtttctg ctgctgctgt ggctgccgga taccaccggc 60

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 120

atcacttgcc gggcaagtca gagcattagc aactatttaa attggtatca gcagaaacca 180

gggaaagccc ctaagctcct gatctatact gcatccagtt tgcaaagtgg ggtcccatca 240

aggttcagtg gcagaggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 300

gaagattttg caacttacta ctgtcaacag agtttcagtt tcccaatcac tttcggccct 360

gggaccaaag tggatatcaa acgtacggtg gctgcaccat ctgtcttcat cttcccgcca 420

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 480

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 540

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 600

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 660

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt g 701

<210> 99
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> variable domain

<400> 99

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

Arg 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 Ser Phe Ser Phe Pro Ile
                85                  90                  95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
            100                 105
```

<210> 100
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1

<400> 100

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

<210> 101
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2

<400> 101

```
Thr Ala Ser Ser Leu Gln Ser
1               5
```

<210> 102
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3

<400> 102

```
Gln Gln Ser Phe Ser Phe Pro Ile Thr
1               5
```

<210> 103
<211> 465
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain

<400> 103

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

Ala His Ser Gln 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 Tyr Thr Phe
        35                  40                  45

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

Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala
65                  70                  75                  80

Gln Lys Phe Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser
                85                  90                  95

Thr Ala His Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val
            100                 105                 110

Tyr Tyr Cys Val Arg Asn Gly Asp Tyr Val Phe Thr Tyr Phe Asp Tyr
        115                 120                 125

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
    130                 135                 140

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser
145                 150                 155                 160

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
                165                 170                 175

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

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
        195                 200                 205

Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val
    210                 215                 220

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

Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro
                245                 250                 255
```

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
260 265 270

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
275 280 285

Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
290 295 300

Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val
305 310 315 320

Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu
325 330 335

Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys
340 345 350

Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
355 360 365

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
370 375 380

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
385 390 395 400

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu
405 410 415

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
420 425 430

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
435 440 445

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
450 455 460

Lys
465

<210> 104
<211> 1395
<212> DNA
<213> Artificial Sequence

<220>
<223> heavy chain

<400> 104
atggattgga cctggagcat tctgtttctg gtggcggcgc cgaccggcgc gcatagccag 60

gtgcagctgg tgcagtctgg ggctgaggtg aagaagcctg gggcctcagt gaaggtctcc 120

tgcaaggctt ctggatacac cttcaccggc tactatatgc actgggtgcg acaggcccct 180

ggacaagggc ttgagtggat gggatggatc aaccctaaca gtggtggcac aaactatgca 240

cagaagttta agggcagggt caccatgacc agggacacgt ccatcagcac agcccacatg 300

gagctgagca ggctgagatc tgacgacacg gccgtgtatt actgtgtgag aaacggtgac 360

tatgttttta cctactttga ctactggggc cagggaaccc tggtcaccgt ctcctcagct 420

agcaccaagg gcccatcggt cttccccctg gcgccctgct ccaggagcac ctccgagagc 480

acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 540

aactcaggcg ctctgaccag cggcgtgcac accttcccag ctgtcctaca gtcctcagga 600

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca acttcggcac ccagacctac 660

acctgcaacg tagatcacaa gcccagcaac accaaggtgg acaagacagt tgagcgcaaa 720

tgttgtgtcg agtgcccacc gtgcccagca ccacctgtgg caggaccgtc agtcttcctc 780

ttccccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacgtgcgtg 840

gtggtggacg tgagccacga agaccccgag gtccagttca actggtacgt ggacggcgtg 900

gaggtgcata atgccaagac aaagccacgg gaggagcagt tcaacagcac gttccgtgtg 960

gtcagcgtcc tcaccgttgt gcaccaggac tggctgaacg gcaaggagta caagtgcaag 1020

gtctccaaca aaggcctccc agccccccatc gagaaaacca tctccaaaac caaagggcag 1080

ccccgagaac cacaggtgta caccctgccc ccatcccggg aggagatgac caagaaccag 1140

gtcagcctga cctgcctggt caaaggcttc taccccagcg acatcgccgt ggagtgggag 1200

agcaatgggc agccggagaa caactacaag accacacctc ccatgctgga ctccgacggc 1260

tccttcttcc tctacagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc 1320

ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc 1380

ctgtctccgg gtaaa 1395

<210> 105
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> variable domain

<400> 105

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

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

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

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

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

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

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 106
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa is Trp or no amino acid residue

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> Xaa is Ile or Tyr

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa is Asn, Ser or Ile

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa is Pro, Ala, Tyr

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa is Asn or Tyr

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa is Ser or Asn

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> Xaa is Gly or Asn

<220>
<221> MISC_FEATURE
<222> (9)..(9)

<223> Xaa is Thr or Arg

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa is Asn or Asp

<220>
<221> MISC_FEATURE
<222> (11)..(11)
<223> Xaa is Tyr or Ser

<220>
<221> MISC_FEATURE
<222> (12)..(12)
<223> Xaa is Ala or Asn

<220>
<221> MISC_FEATURE
<222> (13)..(13)
<223> Xaa is Gln or Arg

<220>
<221> MISC_FEATURE
<222> (14)..(14)
<223> Xaa is Lys or Arg

<220>
<221> MISC_FEATURE
<222> (15)..(15)
<223> Xaa is Phe or Lys

<220>
<221> MISC_FEATURE
<222> (16)..(16)
<223> Xaa is Gln, Lys or Arg

<400> 106

Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Gly

<210> 107
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa is Val or Ile

<220>
<221> MISC_FEATURE
<222> (11)..(11)
<223> Xaa is Ser or Asn

<220>
<221> MISC_FEATURE

<222> (13)..(13)
<223> Xaa is Glu or Lys

<220>
<221> MISC_FEATURE
<222> (15)..(15)
<223> Xaa is Try or Phe

<220>
<221> MISC_FEATURE
<222> (17)..(17)
<223> Xaa is Thr or Ala

<400> 107

Lys Ser Ser Gln Ser Xaa Leu Tyr Ser Ser Xaa Asn Xaa Asn Xaa Leu
1 5 10 15

Xaa

<210> 108
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3

<400> 108

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

<210> 109
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> light chain

<400> 109

Met Ala Trp Ala Pro Leu Leu Leu Thr Leu Leu Ala His Cys Thr Gly
1 5 10 15

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

Pro Gly Gln Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val
35 40 45

Gly Gly Tyr Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala
50 55 60

Pro Lys Leu Met Ile Tyr Glu Val Ser Gly Arg Pro Ser Gly Val Ser
65 70 75 80

Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile

85 90 95

Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Phe
100 105 110

Thr Gly Ser Ser Thr Trp Leu Phe Gly Gly Gly Thr Lys Leu Thr Val
115 120 125

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

Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser
145 150 155 160

Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser
165 170 175

Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn
180 185 190

Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp
195 200 205

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

Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
225 230 235

<210> 110
<211> 705
<212> DNA
<213> Artificial Sequence

<220>
<223> light chain

<400> 110
atggcgtggg cgccgctgct gctgaccctg ctggcgcatt gcaccggcag ctgggcgcag 60

tctgccctga ctcagcctgc ctccgtgtct gggtctcctg gacagtcgat caccatctcc 120

tgcactggaa ccagcagtga cgttggtggt tataactatg tctcctggta ccagcagcac 180

ccaggcaaag cccccaaact catgatttat gaggtcagtg gtcggccctc aggggtttct 240

aatcgcttct ctggctccaa gtctggcaac acggcctccc tgaccatctc tggactccag 300

gctgaggacg aggctgatta ttactgcagc tcttttacag gcagcagcac ttggttattc 360

ggcggaggga ccaaactgac cgtcctaggc caaccgaaag cggcgccctc ggtcactctg 420

ttcccgccct cctctgagga gcttcaagcc aacaaggcca cactggtgtg tctcataagt 480

gacttctacc cgggagccgt gacagtggcc tggaaggcag atagcagccc cgtcaaggcg 540

ggagtggaga ccaccacacc ctccaaacaa agcaacaaca agtacgcggc cagcagctat 600

ctgagcctga cgcctgagca gtggaagtcc cacagaagct acagctgcca ggtcacgcat 660

gaagggagca ccgtggagaa gacagtggcc cctacagaat gttca 705

<210> 111
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> variable domain

<400> 111

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

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

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

Met Ile Tyr Glu Val Ser Gly Arg Pro Ser Gly Val Ser Asn Arg Phe
50 55 60

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

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

Ser Thr Trp Leu Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 112
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1

<400> 112

Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr Asn Tyr Val Ser
1 5 10

<210> 113
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2

<400> 113

Glu Val Ser Gly Arg Pro Ser

1 5

<210> 114
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3

<400> 114

Ser Ser Phe Thr Gly Ser Ser Thr Trp Leu
1 5 10

<210> 115
<211> 464
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain

<400> 115

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

Ala His Ser Gln 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 Tyr Thr Phe
35 40 45

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

Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala
65 70 75 80

Gln Lys Phe Arg Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser
85 90 95

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

Tyr Tyr Cys Ala Arg Phe Gly Tyr Phe Gly Tyr Tyr Phe Asp Tyr Trp
115 120 125

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

Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr
145 150 155 160

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr

165 170 175

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

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
195 200 205

Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp
210 215 220

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

Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser
245 250 255

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

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
275 280 285

Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
290 295 300

Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val
305 310 315 320

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

Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr
340 345 350

Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
355 360 365

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
370 375 380

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
385 390 395 400

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp
405 410 415

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
420 425 430

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala

435 440 445

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455 460

<210> 116
<211> 1392
<212> DNA
<213> Artificial Sequence

<220>
<223> heavy chain

<400> 116
atggattgga cctggagcat tctgtttctg gtggcggcgc cgaccggcgc gcatagccag 60

gtgcaactgg tgcagtctgg ggctgaggtg aagaagcctg gggcctcagt gaaggtctcc 120

tgcaaggctt ctggatacac cttcaccggc tactatatgc actgggtgcg acaggcccct 180

ggacaagggc ttgagtggat gggatggatc aatcctaaca gtggtggcac aaactatgca 240

cagaagtttc ggggcagggt caccatgacc agggacacgt ccatcagcac agcctacatg 300

gagctgagca ggctgagatc tgacgacacg gccgtgtatt actgtgcgag atttggatat 360

tttggctact actttgacta ctggggccag ggaaccctgg tcaccgtctc ctcagctagc 420

accaagggcc catcggtctt ccccctggcg ccctgctcca ggagcacctc cgagagcaca 480

gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 540

tcaggcgctc tgaccagcgg cgtgcacacc ttcccagctg tcctacagtc ctcaggactc 600

tactccctca gcagcgtggt gaccgtgccc tccagcaact tcggcaccca gacctacacc 660

tgcaacgtag atcacaagcc cagcaacacc aaggtggaca agacagttga gcgcaaatgt 720

tgtgtcgagt gcccaccgtg cccagcacca cctgtggcag gaccgtcagt cttcctcttc 780

cccccaaaac ccaaggacac cctcatgatc tcccggaccc ctgaggtcac gtgcgtggtg 840

gtggacgtga gccacgaaga ccccgaggtc cagttcaact ggtacgtgga cggcgtggag 900

gtgcataatg ccaagacaaa gccacgggag gagcagttca acagcacgtt ccgtgtggtc 960

agcgtcctca ccgttgtgca ccaggactgg ctgaacggca aggagtacaa gtgcaaggtc 1020

tccaacaaag gcctcccagc ccccatcgag aaaaccatct ccaaaaccaa agggcagccc 1080

cgagaaccac aggtgtacac cctgccccca tcccgggagg agatgaccaa gaaccaggtc 1140

agcctgacct gcctggtcaa aggcttctac cccagcgaca tcgccgtgga gtgggagagc 1200

aatgggcagc cggagaacaa ctacaagacc acacctccca tgctggactc cgacggctcc 1260

ttcttcctct acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc 1320

tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg 1380

tctccgggta aa 1392

<210> 117
<211> 119
<212> PRT

<213> Artificial Sequence

<220>
<223> variable domain

<400> 117

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

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

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

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

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

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

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

Thr Leu Val Thr Val Ser Ser
        115
```

<210> 118
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa is Gln or Pro

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa is Ser or Tyr

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa is Val, Leu or Ile

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa is Ser or Cys

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> Xaa is Ser or Asn

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> Xaa is Ser, Ile, Thr or no amino acid residue

<220>
<221> MISC_FEATURE
<222> (11)..(11)
<223> Xaa is Phe or Leu

<220>
<221> MISC_FEATURE
<222> (12)..(12)
<223> Xaa is Ala or Asn

<400> 118

Arg Ala Ser Xaa Xaa Xaa Xaa Xaa Xaa Tyr Xaa Xaa
1 5 10

<210> 119
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2

<400> 119

Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe Arg
1 5 10 15

Gly

<210> 120
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3

<400> 120

Phe Gly Tyr Phe Gly Tyr Tyr Phe Asp Tyr
1 5 10

<210> 121
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> light chain

<400> 121

Met Glu Thr Pro Ala Gln Leu Leu Phe Leu Leu Leu Trp Leu Pro
1 5 10 15

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

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Pro Ser
35 40 45

Val Ser Ser Ser Tyr Phe Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
50 55 60

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

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
85 90 95

Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr
100 105 110

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

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

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

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

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

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

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

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

<210> 122
<211> 704
<212> DNA
<213> Artificial Sequence

<220>
<223> light chain

<400> 122
atggaaaccc cggcgcagct gctgtttctg ctgctgctgt ggctgccgga taccaccggc 60

gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 120

ctctcctgca gggccagtcc gagtgttagc agcagctact ttgcctggta ccagcaaaaa 180

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 240

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 300

cctgaagatt ttgcagtgta ttactgtcag cagtatggtt ggtcacctcg gacgttcggc 360

caagggacca aggtggaaat caaacgtacg gtggctgcac catctgtctt catcttcccg 420

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 480

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 540

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 600

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 660

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtg 704

<210> 123
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> variable domain

<400> 123

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Pro Ser Val Ser Ser Ser
20 25 30

Tyr Phe Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

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

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

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

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

<210> 124
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1

<400> 124

Arg Ala Ser Pro Ser Val Ser Ser Ser Tyr Phe Ala
1 5 10

<210> 125
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa is Ile, Ser or Thr

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> Xaa is Arg or Gly

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa is Thr or Ser

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa is Arg or Ser

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa is Gly or Ser

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa is Ser, His or Asp

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> Xaa is Ile or Val

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> Xaa is Ala or Gly

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa is Gly or no amino acid residue

<220>
<221> MISC_FEATURE
<222> (11)..(11)
<223> Xaa is Ser or Tyr

<220>
<221> MISC_FEATURE
<222> (13)..(13)
<223> Xaa is Tyr or Thr

<220>
<221> MISC_FEATURE
<222> (15)..(15)
<223> Xaa is Gln, Asn or Ser

<400> 125

Xaa Xaa Xaa Xaa Xaa Xaa Tyr Xaa Xaa Xaa Xaa Asn Xaa Val Xaa
1 5 10 15

<210> 126
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3

<400> 126

Gln Gln Tyr Gly Trp Ser Pro Arg Thr
1 5

<210> 127
<211> 463
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain

<400> 127

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

Ala His Ser Gln 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 Tyr Thr Phe
35 40 45

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

Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala
65 70 75 80

Gln Lys Phe Arg Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser
85 90 95

Thr Ala Tyr Val Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val
100 105 110

```
Tyr Tyr Cys Ala Arg Asp Pro Tyr Thr Ser Gly Phe Asp Tyr Trp Gly
        115                 120                 125

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

Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
145                 150                 155                 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

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

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His
    210                 215                 220

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

Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val
                245                 250                 255

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
            260                 265                 270

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
        275                 280                 285

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
    290                 295                 300

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser
305                 310                 315                 320

Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
                325                 330                 335

Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile
            340                 345                 350

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

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
    370                 375                 380
```

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
385 390 395 400

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser
405 410 415

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
420 425 430

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
435 440 445

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455 460

<210> 128
<211> 1389
<212> DNA
<213> Artificial Sequence

<220>
<223> heavy chain

<400> 128
atggattgga cctggagcat tctgtttctg gtggcggcgc cgaccggcgc gcatagccag 60

gtacaactgg tgcagtctgg ggctgaggtg aagaagcctg gggcctcagt gaaggtctcc 120

tgcaaggctt ctggatacac cttcaccggc tactatatgc actgggtgcg acaggcccct 180

ggacaagggc ttgagtggat gggatggatc aaccctaaca gtggtggcac aaattatgca 240

cagaagtttc ggggcagggt caccatgacc agggacacgt ccatcagcac agcctacgtg 300

gagctgagca ggctgagatc tgacgacacg gccgtatatt actgtgcgag agacccgtat 360

accagtggct ttgactactg gggccaggga accctggtca ccgtctcctc agctagcacc 420

aagggcccat cggtcttccc cctggcgccc tgctccagga gcacctccga gagcacagcg 480

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 540

ggcgctctga ccagcggcgt gcacaccttc ccagctgtcc tacagtcctc aggactctac 600

tccctcagca gcgtggtgac cgtgccctcc agcaacttcg gcacccagac ctacacctgc 660

aacgtagatc acaagcccag caacaccaag gtggacaaga cagttgagcg caaatgttgt 720

gtcgagtgcc caccgtgccc agcaccacct gtggcaggac cgtcagtctt cctcttcccc 780

ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacgtg cgtggtggtg 840

gacgtgagcc acgaagaccc cgaggtccag ttcaactggt acgtggacgg cgtggaggtg 900

cataatgcca agacaaagcc acgggaggag cagttcaaca gcacgttccg tgtggtcagc 960

gtcctcaccg ttgtgcacca ggactggctg aacggcaagg agtacaagtg caaggtctcc 1020

aacaaaggcc tcccagcccc catcgagaaa accatctcca aaaccaaagg gcagccccga 1080

gaaccacagg tgtacaccct gcccccatcc cgggaggaga tgaccaagaa ccaggtcagc 1140

ctgacctgcc tggtcaaagg cttctacccc agcgacatcg ccgtggagtg ggagagcaat 1200

gggcagccgg agaacaacta caagaccaca cctcccatgc tggactccga cggctccttc 1260

ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1320

tgctccgtga tgcatgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1380

ccgggtaaa 1389

<210> 129
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> variable

<400> 129

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

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

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

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

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

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

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

Leu Val Thr Val Ser Ser
115

<210> 130
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa is Gly, Thr or Trp

<220>

<221> MISC_FEATURE
<222> (2)..(2)
<223> Xaa is Thr or Ala

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa is Ser or Ala

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa is Ser or Thr

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa is Arg or Leu

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa is Ala, Glu or Gln

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa is Thr or Ser

<400> 130

Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 131
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa is Glu or Ser

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> Xaa is Asp, Val or Asn

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa is Asp, Ser or Asn

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa is Gln, Gly or His

<400> 131

Xaa Xaa Xaa Xaa Arg Pro Ser
1 5

<210> 132
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3

<400> 132

Asp Pro Tyr Thr Ser Gly Phe Asp Tyr
1 5

<210> 133
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> light chain

<400> 133

Met Ala Trp Ala Pro Leu Leu Leu Thr Leu Leu Ala His Cys Thr Gly
1 5 10 15

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

Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly Ser Arg Ser His Ile
35 40 45

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

Lys Leu Leu Ile Tyr Ser Asn Asn His Arg Pro Ser Gly Val Pro Asp
65 70 75 80

Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser
85 90 95

Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp
100 105 110

Asp Ser Leu Asn Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val
115 120 125

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

Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser
145 150 155 160

Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser
165 170 175

Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn
180 185 190

Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp
195 200 205

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

Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
225 230 235

<210> 134
<211> 705
<212> DNA
<213> Artificial Sequence

<220>
<223> light chain

<400> 134
atggcgtggg cgccgctgct gctgaccctg ctggcgcatt gcaccggcag ctgggcgcag 60

tctgtgctga ctcagccacc ctcagcgtct gggaccccg ggcagagggt caccatctct 120

tgttctggaa gccgctccca catcggaagt aatactgtaa actggtacca gcacctccca 180

ggaacggccc ccaaactcct catctatagt aataatcatc ggccctcagg ggtccctgac 240

cgattctctg gctccaagtc tggcacctca gcctccctgg ccatcagtgg gctccagtct 300

gaggatgagg ctgattatta ctgtgcagca tgggatgaca gcctgaatgg tccggtattc 360

ggcggaggga ccaagctgac cgtcctaggc caaccgaaag cggcgccctc ggtcactctg 420

ttcccgccct cctctgagga gcttcaagcc aacaaggcca cactggtgtg tctcataagt 480

gacttctacc cgggagccgt gacagtggcc tggaaggcag atagcagccc cgtcaaggcg 540

ggagtggaga ccaccacacc ctccaaacaa agcaacaaca agtacgcggc cagcagctat 600

ctgagcctga cgcctgagca gtggaagtcc cacagaagct acagctgcca ggtcacgcat 660

gaagggagca ccgtggagaa gacagtggcc cctacagaat gttca 705

<210> 135
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<400> 135

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Arg Ser His Ile Gly Ser Asn
20 25 30

Thr Val Asn Trp Tyr Gln His Leu Pro Gly Thr Ala Pro Lys Leu Leu
35 40 45

Ile Tyr Ser Asn Asn His Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
85 90 95

Asn Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 136
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1

<400> 136

Ser Gly Ser Arg Ser His Ile Gly Ser Asn Thr Val Asn
1 5 10

<210> 137
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2

<400> 137

Ser Asn Asn His Arg Pro Ser
1 5

<210> 138
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3

<400> 138

Ala Ala Trp Asp Asp Ser Leu Asn Gly Pro Val
1 5 10

<210> 139
<211> 465
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain

<400> 139

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

Ala His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys
            20                  25                  30

Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile
        35                  40                  45

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

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

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

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

Val Tyr Tyr Cys Ala Arg Glu Asp Thr Ala Met Asp Tyr Phe Asp Tyr
        115                 120                 125

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
    130                 135                 140

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser
145                 150                 155                 160

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
                165                 170                 175

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

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
        195                 200                 205

Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val
    210                 215                 220

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

Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro
                245                 250                 255
```

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
260 265 270

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
275 280 285

Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
290 295 300

Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val
305 310 315 320

Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu
325 330 335

Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys
340 345 350

Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
355 360 365

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
370 375 380

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
385 390 395 400

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu
405 410 415

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
420 425 430

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
435 440 445

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
450 455 460

Lys
465

<210> 140
<211> 1395
<212> DNA
<213> Artificial Sequence

<220>
<223> heavy chain

<400> 140
atggattgga cctggagcat tctgtttctg gtggcggcgc cgaccggcgc gcatagccag 60

gtgcagctgc aggagtcggg cccaggactg gtgaagcctt cacagaccct gtccctcacc 120

tgcactgtct ctggtggctc catcagaagt ggtggttact actggagctg gatccgccag 180

cacccaggga agggcctgga gtggattggg tatatctatt acagtgggag cacctactac 240

aacccgtccc tcaagagtcg agttaccata tcagtagaca cgtctaagaa ccagttctcc 300

ctgaagctga actctgtgac tgccgcggac acggccgtgt attactgtgc gagagaggat 360

acagctatgg actactttga ctactggggc cagggaaccc tggtcaccgt ctcctcagct 420

agcaccaagg gcccatcggt cttccccctg gcgccctgct ccaggagcac ctccgagagc 480

acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 540

aactcaggcg ctctgaccag cggcgtgcac accttcccag ctgtcctaca gtcctcagga 600

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca acttcggcac ccagacctac 660

acctgcaacg tagatcacaa gcccagcaac accaaggtgg acaagacagt tgagcgcaaa 720

tgttgtgtcg agtgcccacc gtgcccagca ccacctgtgg caggaccgtc agtcttcctc 780

ttccccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacgtgcgtg 840

gtggtggacg tgagccacga agaccccgag gtccagttca actggtacgt ggacggcgtg 900

gaggtgcata atgccaagac aaagccacgg gaggagcagt tcaacagcac gttccgtgtg 960

gtcagcgtcc tcaccgttgt gcaccaggac tggctgaacg gcaaggagta caagtgcaag 1020

gtctccaaca aaggcctccc agcccccatc gagaaaacca tctccaaaac caaagggcag 1080

ccccgagaac cacaggtgta caccctgccc ccatcccggg aggagatgac caagaaccag 1140

gtcagcctga cctgcctggt caaaggcttc taccccagcg acatcgccgt ggagtgggag 1200

agcaatgggc agccggagaa caactacaag accacacctc ccatgctgga ctccgacggc 1260

tccttcttcc tctacagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc 1320

ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc 1380

ctgtctccgg gtaaa 1395

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

<220>
<223> consensus sequence

<400> 141

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Arg Ser Gly
20 25 30

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

```
Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60

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

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

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

Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 142
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1

<400> 142

```
Ser Gly Gly Tyr Tyr Trp Ser
1               5
```

<210> 143
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2

<400> 143

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

<210> 144
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3

<400> 144

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

<210> 145
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> GM-CSF-Ile

<400> 145

Ala Pro Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro Trp Glu His Val
1 5 10 15

Asn Ala Ile Gln Glu Ala Leu Arg Leu Leu Asp Leu Ser Arg Asp Thr
20 25 30

Ala Ala Glu Met Asn Glu Glu Val Glu Val Ile Ser Glu Met Phe Asp
35 40 45

Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg Leu Glu Leu Tyr Lys Gln
50 55 60

Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro Leu Thr Met Met
65 70 75 80

Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser Cys
85 90 95

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

Phe Leu Leu Val Ile Pro Phe Asp Cys Trp Lys Pro Val Gln Glu
115 120 125

<210> 146
<211> 127
<212> PRT
<213> Homo sapiens

<400> 146

Ala Pro Ser Arg Ser Pro Ser Pro Ser Arg Gln Pro Trp Glu His Val
1 5 10 15

Asn Ala Ile Gln Glu Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp Thr
20 25 30

Ala Ala Glu Ile Asn Glu Thr Val Glu Val Val Ser Glu Met Phe Asp
35 40 45

Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg Leu Glu Leu Tyr Lys Gln
50 55 60

Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro Leu Thr Met Met
65 70 75 80

Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser Cys
85 90 95

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

Phe Leu Leu Val Thr Pro Phe Asp Cys Trp Glu Pro Val Gln Gly
115 120 125

<210> 147
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa is Gly or no amino acid residue

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> Xaa is Gly or no amino acid residue

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa is Tyr or Phe

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa is Thr or Ser

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa is Thr, Ser or Gly

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> Xaa is Gly or Ser

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa is Tyr or Gly

<220>
<221> MISC_FEATURE
<222> (11)..(11)
<223> Xaa is Ile or Met

<220>
<221> MISC_FEATURE
<222> (12)..(12)
<223> Xaa is His or Ser

<400> 147

Xaa Xaa Gly Xaa Xaa Phe Xaa Xaa Tyr Xaa Xaa Xaa
1 5 10