<110> GILEAD BIOLOGICS, INC.
SMITH, Victoria
MCCAULEY, Scott

<120> ANTIBODIES TO MATRIX METALLOPROTEINASE 9

<130> 246102008540

<140> Not Yet Assigned
<141> Concurrently Herewith

<160> 50

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 470
<212> PRT
<213> Mus musculus

<220>
<221> CHAIN
<222> (1)...(470)
<223> AB0041 heavy chain

<220>
<221> PEPTIDE
<222> (1)...(19)
<223> signal peptide

<220>
<221> misc_feature
<222> (135)...(470)
<223> IgG2b constant region

<400> 1
Met Ala Val Leu Val Leu Phe Leu Cys Leu Val Ala Phe Pro Ser Cys
1 5 10 15
Val Leu Ser Gln Val Gln Leu Lys Glu Ser Gly Pro Gly Leu Val Ala
20 25 30
Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu
35 40 45
Leu Ser Tyr Gly Val His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu
50 55 60
Glu Trp Leu Gly Val Ile Trp Thr Gly Gly Thr Thr Asn Tyr Asn Ser
65 70 75 80
Ala Leu Met Ser Arg Leu Ser Ile Ser Lys Asp Asp Ser Lys Ser Gln
85 90 95
Val Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr
100 105 110
Tyr Cys Ala Arg Tyr Tyr Tyr Gly Met Asp Tyr Trp Gly Gln Gly Thr
115 120 125
Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro
130 135 140
Leu Ala Pro Gly Cys Gly Asp Thr Thr Gly Ser Ser Val Thr Leu Gly
145 150 155 160
Cys Leu Val Lys Gly Tyr Phe Pro Glu Ser Val Thr Val Thr Trp Asn
165 170 175
Ser Gly Ser Leu Ser Ser Ser Val His Thr Phe Pro Ala Leu Leu Gln
180 185 190
Ser Gly Leu Tyr Thr Met Ser Ser Ser Val Thr Val Pro Ser Ser Thr
195 200 205
Trp Pro Ser Gln Thr Val Thr Cys Ser Val Ala His Pro Ala Ser Ser
210 215 220
Thr Thr Val Asp Lys Lys Leu Glu Pro Ser Gly Pro Ile Ser Thr Ile
225 230 235 240
Asn Pro Cys Pro Pro Cys Lys Glu Cys His Lys Cys Pro Ala Pro Asn

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                245                 250                 255
Leu Glu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Asn Ile Lys Asp
            260                 265                 270
Val Leu Met Ile Ser Leu Thr Pro Lys Val Thr Cys Val Val Val Asp
        275                 280                 285
Val Ser Glu Asp Asp Pro Asp Val Arg Ile Ser Trp Phe Val Asn Asn
    290                 295                 300
Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn
305                 310                 315                 320
Ser Thr Ile Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp
                325                 330                 335
Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro
            340                 345                 350
Ser Pro Ile Glu Arg Thr Ile Ser Lys Ile Lys Gly Leu Val Arg Ala
        355                 360                 365
Pro Gln Val Tyr Ile Leu Pro Pro Pro Ala Glu Gln Leu Ser Arg Lys
    370                 375                 380
Asp Val Ser Leu Thr Cys Leu Val Val Gly Phe Asn Pro Gly Asp Ile
385                 390                 395                 400
Ser Val Glu Trp Thr Ser Asn Gly His Thr Glu Glu Asn Tyr Lys Asp
                405                 410                 415
Thr Ala Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Ile Tyr Ser Lys
            420                 425                 430
Leu Asp Ile Lys Thr Ser Lys Trp Glu Lys Thr Asp Ser Phe Ser Cys
        435                 440                 445
Asn Val Arg His Glu Gly Leu Lys Asn Tyr Tyr Leu Lys Lys Thr Ile
    450                 455                 460
Ser Arg Ser Pro Gly Lys
465                 470


<210> 2
<211> 234
<212> PRT
<213> Mus musculus

<220>
<221> CHAIN
<222> (1)...(234)
<223> AB0041 light chain

<220>
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<222> (1)...(20)
<223> signal peptide

<220>
<221> misc_feature
<222> (128)...(234)
<223> kappa constant region

<400> 2
Met Glu Ser Gln Ile Gln Val Phe Val Phe Val Phe Leu Trp Leu Ser
 1               5                  10                  15
Gly Val Asp Gly Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser
            20                  25                  30
Thr Ser Val Gly Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp
        35                  40                  45
Val Arg Asn Thr Val Ala Trp Tyr Gln Gln Lys Thr Gly Gln Ser Pro
    50                  55                  60
Lys Leu Leu Ile Tyr Ser Ser Ser Tyr Arg Asn Thr Gly Val Pro Asp
65                  70                  75                  80
Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser
                85                  90                  95
Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln His Tyr
            100                 105                 110
Ile Thr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
        115                 120                 125
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Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln
    130                 135                 140
Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr
145                 150                 155                 160
Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln
                165                 170                 175
Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr
            180                 185                 190
Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg
        195                 200                 205
His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro
    210                 215                 220
Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
225                 230
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<210> 3
<211> 115
<212> PRT
<213> Mus musculus

<220>
<221> CHAIN
<222> (1)...(115)
<223> variable region of the IgG2b heavy chain of AB0041

<220>
<221> misc_feature
<222> (26)...(35)
<223> complementarity-determining region (CDR)

<220>
<221> misc_feature
<222> (50)...(65)
<223> complementarity-determining region (CDR)

<220>
<221> misc_feature
<222> (98)...(104)
<223> complementarity-determining region (CDR)

<400> 3

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Gln Val Gln Leu Lys Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln
 1                5                  10                  15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Leu Ser Tyr
            20                  25                  30
Gly Val His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45
Gly Val Ile Trp Thr Gly Gly Thr Thr Asn Tyr Asn Ser Ala Leu Met
    50                  55                  60
Ser Arg Leu Ser Ile Ser Lys Asp Asp Ser Lys Ser Gln Val Phe Leu
65                  70                  75                  80
Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala
                85                  90                  95
Arg Tyr Tyr Tyr Gly Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr
            100                 105                 110
Val Ser Ser
        115
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<210> 4
<211> 107
<212> PRT
<213> Mus musculus

<220>
<221> CHAIN
<222> (1)...(107)

<223> variable region of the kappa light chain of AB0041

<220>
<221> misc_feature
<222> (24)...(34)
<223> complementarity-determining region (CDR)

<220>
<221> misc_feature
<222> (50)...(56)
<223> complementarity-determining region (CDR)

<220>
<221> misc_feature
<222> (89)...(97)
<223> complementarity-determining region (CDR)

<400> 4
Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser Thr Ser Val Gly
 1   5   10   15
Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val Arg Asn Thr
            20   25   30
Val Ala Trp Tyr Gln Gln Lys Thr Gly Gln Ser Pro Lys Leu Leu Ile
        35   40   45
Tyr Ser Ser Ser Tyr Arg Asn Thr Gly Val Pro Asp Arg Phe Thr Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Val Gln Ala
65   70   75   80
Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln His Tyr Ile Thr Pro Tyr
                85   90   95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100   105

<210> 5
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct

<220>
<221> VARIANT
<222> (1)...(115)
<223> VH1 heavy chain variant

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

<210> 6
<211> 115

<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct

<220>
<221> VARIANT
<222> (1)...(115)
<223> VH2 heavy chain variant

<400> 6
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1   5   10   15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Leu Ser Tyr
            20   25   30
Gly Val His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
        35   40   45
Gly Val Ile Trp Thr Gly Gly Thr Thr Asn Tyr Asn Ser Ala Leu Met
    50   55   60
Ser Arg Leu Thr Ile Ser Lys Asp Asp Ser Lys Asn Thr Val Tyr Leu
65   70   75   80
Lys Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Ile Tyr Tyr Cys Ala
                85   90   95
Arg Tyr Tyr Tyr Gly Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
            100   105   110
Val Ser Ser
        115

<210> 7
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct

<220>
<221> VARIANT
<222> (1)...(115)
<223> VH3 heavy chain variant

<400> 7
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1   5   10   15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Leu Ser Tyr
            20   25   30
Gly Val His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
        35   40   45
Gly Val Ile Trp Thr Gly Gly Thr Thr Asn Tyr Asn Ser Ala Leu Met
    50   55   60
Ser Arg Phe Thr Ile Ser Lys Asp Asp Ser Lys Asn Thr Val Tyr Leu
65   70   75   80
Lys Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Ile Tyr Tyr Cys Ala
                85   90   95
Arg Tyr Tyr Tyr Gly Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
            100   105   110
Val Ser Ser
        115

<210> 8
<211> 115
<212> PRT
<213> Artificial Sequence

<220>

<223> synthetic construct

<220>
<221> VARIANT
<222> (1)...(115)
<223> VH4 heavy chain variant

<400> 8
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1   5   10   15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Leu Ser Tyr
            20   25   30
Gly Val His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
        35   40   45
Gly Val Ile Trp Thr Gly Gly Thr Thr Asn Tyr Asn Ser Ala Leu Met
    50   55   60
Ser Arg Phe Thr Ile Ser Lys Asp Asp Ser Lys Asn Thr Leu Tyr Leu
65   70   75   80
Lys Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Ile Tyr Tyr Cys Ala
                85   90   95
Arg Tyr Tyr Tyr Gly Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
            100   105   110
Val Ser Ser
        115

<210> 9
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct

<220>
<221> VARIANT
<222> (1)...(107)
<223> Vk1 light chain variant

<400> 9
Asp Ile Val Met Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val Arg Asn Thr
            20   25   30
Val Ala Trp Tyr Gln Gln Lys Thr Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45
Tyr Ser Ser Ser Tyr Arg Asn Thr Gly Val Pro Asp Arg Phe Thr Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala
65   70   75   80
Glu Asp Val Ala Val Tyr Phe Cys Gln Gln His Tyr Ile Thr Pro Tyr
                85   90   95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 10
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct

<220>
<221> VARIANT
<222> (1)...(107)
<223> Vk2 light chain variant

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

<210> 11
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct

<220>
<221> VARIANT
<222> (1)...(107)
<223> Vk3 light chain variant

<400> 11
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val Arg Asn Thr
            20   25   30
Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45
Tyr Ser Ser Ser Tyr Arg Asn Thr Gly Val Pro Asp Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala
65   70   75   80
Glu Asp Val Ala Val Tyr Phe Cys Gln Gln His Tyr Ile Thr Pro Tyr
                85   90   95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 12
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct

<220>
<221> VARIANT
<222> (1)...(107)
<223> Vk4 light chain variant

<400> 12
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val Arg Asn Thr
            20   25   30
Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45

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

<210> 13
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct

<220>
<221> misc_feature
<222> (1)...(10)
<223> complementarity-determining region (CDR1) of heavy chain of anti-MMP9 antibody

<400> 13
Gly Phe Ser Leu Leu Ser Tyr Gly Val His
1 5 10

<210> 14
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct

<220>
<221> misc_feature
<222> (1)...(16)
<223> complementarity-determining region (CDR2) of heavy chain of anti-MMP9 antibody

<400> 14
Val Ile Trp Thr Gly Gly Thr Thr Asn Tyr Asn Ser Ala Leu Met Ser
1 5 10 15

<210> 15
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct

<220>
<221> misc_feature
<222> (1)...(7)
<223> complementarity-determining region (CDR3) of heavy chain of anti-MMP9 antibody

<400> 15
Tyr Tyr Tyr Gly Met Asp Tyr
1 5

<210> 16

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

<220>
<223> synthetic construct

<220>
<221> misc_feature
<222> (1)...(11)
<223> complementarity-determining region (CDR1) of light chain of anti-MMP9 antibody

<400> 16
Lys Ala Ser Gln Asp Val Arg Asn Thr Val Ala
 1   5   10

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

<220>
<223> synthetic construct

<220>
<221> misc_feature
<222> (1)...(7)
<223> complementarity-determining region (CDR2) of light chain of anti-MMP9 antibody

<400> 17
Ser Ser Ser Tyr Arg Asn Thr
 1   5

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

<220>
<223> synthetic construct

<220>
<221> misc_feature
<222> (1)...(9)
<223> complementarity-determining region (CDR3) of light chain of anti-MMP9 antibody

<400> 18
Gln Gln His Tyr Ile Thr Pro Tyr Thr
 1   5

<210> 19
<211> 345
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic construct

<220>
<221> misc_feature
<222> (1)...(345)
<223> nucleotide sequence encoding VH1 heavy chain amino

acid sequence

<400> 19
caggtgcagc tgcaggaatc cggccctggc ctggtcaagc cctccgagac actgtccctg 60
acctgcaccg tgtccggctt ctccctgctg tcctacggcg tgcactgggt ccgacagcct 120
ccagggaagg gcctggaatg gctgggcgtg atctggaccg gcggcaccac caactacaac 180
tccgccctga tgtcccggct gaccatctcc aaggacgact ccaagtccac cgtgtacctg 240
aagatgaact ccctgaaaac cgaggacacc gccatctact actgcgcccg gtactactac 300
ggcatggact actggggcca gggcacctcc gtgaccgtgt cctca 345

<210> 20
<211> 345
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic construct

<220>
<221> misc_feature
<222> (1)...(345)
<223> nucleotide sequence encoding VH2 heavy chain amino
acid sequence

<400> 20
caggtgcagc tgcaggaatc cggccctggc ctggtcaagc cctccgagac actgtccctg 60
acctgcaccg tgtccggctt ctccctgctg tcctacggcg tgcactgggt ccgacagcct 120
ccaggcaaag gcctggaatg gctgggcgtg atctggaccg gcggcaccac caactacaac 180
tccgccctga tgtcccggct gaccatctcc aaggacgact ccaagaacac cgtgtacctg 240
aagatgaact ccctgaaaac cgaggacacc gccatctact actgcgcccg gtactactac 300
ggcatggact actggggcca gggcaccctg gtcaccgtgt cctca 345

<210> 21
<211> 345
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic construct

<220>
<221> misc_feature
<222> (1)...(345)
<223> nucleotide sequence encoding VH3 heavy chain amino
acid sequence

<400> 21
caggtgcagc tgcaggaatc cggccctggc ctggtcaagc cctccgagac actgtccctg 60
acctgcaccg tgtccggctt ctccctgctg tcctacggcg tgcactgggt ccgacagcct 120
ccaggcaaag gcctggaatg gctgggcgtg atctggaccg gcggcaccac caactacaac 180
tccgccctga tgtcccggtt caccatctcc aaggacgact ccaagaacac cgtgtacctg 240
aagatgaact ccctgaaaac cgaggacacc gccatctact actgcgcccg gtactactac 300
ggcatggact actggggcca gggcaccctg gtcaccgtgt cctca 345

<210> 22
<211> 345
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic construct

<220>
<221> misc_feature
<222> (1)...(345)
<223> nucleotide sequence encoding VH4 heavy chain amino
acid sequence

<400> 22
caggtgcagc tgcaggaatc cggccctggc ctggtcaagc cctccgagac actgtccctg 60
acctgcaccg tgtccggctt ctccctgctg tcctacggcg tgcactgggt ccgacagcct 120
ccaggcaaag gcctggaatg gctgggcgtg atctggaccg gcggcaccac caactacaac 180
tccgccctga tgtcccggtt caccatctcc aaggacgact ccaagaacac cctgtacctg 240
aagatgaact ccctgaaaac cgaggacacc gccatctact actgcgcccg gtactactac 300
ggcatggact actggggcca gggcaccctg gtcaccgtgt cctca 345

<210> 23
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic construct

<220>
<221> misc_feature
<222> (1)...(321)
<223> nucleotide sequence encoding Vk1 light chain amino
acid sequence

<400> 23
gacatcgtga tgacccagtc ccccagcttc ctgtccgcct ccgtgggcga cagagtgacc 60
atcacatgca aggcctctca ggacgtgcgg aacaccgtgg cctggtatca gcagaaaacc 120
ggcaaggccc ccaagctgct gatctactcc tcctcctacc ggaacaccgg cgtgcccgac 180
cggtttaccg gctctggctc cggcaccgac tttaccctga ccatcagctc cctgcaggcc 240
gaggacgtgg ccgtgtactt ctgccagcag cactacatca ccccctacac cttcggcgga 300
ggcaccaagg tggaaataaa a 321

<210> 24
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic construct

<220>
<221> misc_feature
<222> (1)...(321)
<223> nucleotide sequence encoding Vk2 light chain amino
acid sequence

<400> 24
gacatcgtga tgacccagtc cccctccagc ctgtccgcct ctgtgggcga cagagtgacc 60
atcacatgca aggcctctca ggacgtgcgg aacaccgtgg cctggtatca gcagaagccc 120
ggcaaggccc ccaagctgct gatctactcc tcctcctacc ggaacaccgg cgtgcccgac 180
cggtttaccg gctctggctc cggcaccgac tttaccctga ccatcagctc cctgcaggcc 240
gaggacgtgg ccgtgtactt ctgccagcag cactacatca ccccctacac cttcggcgga 300
ggcaccaagg tggaaataaa a 321

<210> 25
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic construct

<220>
<221> misc_feature
<222> (1)...(321)
<223> nucleotide sequence encoding Vk3 light chain amino
acid sequence

<400> 25
gacatccaga tgacccagtc cccctccagc ctgtccgcct ctgtgggcga cagagtgacc 60

atcacatgca aggcctccca ggacgtgcgg aacaccgtgg cctggtatca gcagaagccc 120
ggcaaggccc ccaagctgct gatctactcc tcctcctacc ggaacaccgg cgtgcccgac 180
cggttctctg gctctggaag cggcaccgac tttaccctga ccatcagctc cctgcaggcc 240
gaggacgtgg ccgtgtactt ctgccagcag cactacatca ccccctacac cttcggcgga 300
ggcaccaagg tggaaataaa a 321

<210> 26
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic construct

<220>
<221> misc_feature
<222> (1)...(321)
<223> nucleotide sequence encoding Vk4 light chain amino
acid sequence

<400> 26
gacatccaga tgacccagtc cccctccagc ctgtccgcct ctgtgggcga cagagtgacc 60
atcacatgca aggcctctca ggacgtgcgg aacaccgtgg cctggtatca gcagaagccc 120
ggcaaggccc ccaagctgct gatctactcc tcctcctacc ggaacaccgg cgtgcccgac 180
cggttctctg gctctggaag cggcaccgac tttaccctga ccatcagctc cctgcaggcc 240
gaggacgtgg ccgtgtacta ctgccagcag cactacatca ccccctacac cttcggcgga 300
ggcaccaagg tggaaataaa a 321

<210> 27
<211> 707
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(707)
<223> matrix metalloproteinase 9 (MMP9)

<220>
<221> PEPTIDE
<222> (1)...(19)
<223> signal peptide

<220>
<221> DOMAIN
<222> (38)...(98)
<223> peptidoglycan binding domain

<220>
<221> SITE
<222> (98)...(99)
<223> propeptide cleavage site

<220>
<221> DOMAIN
<222> (112)...(445)
<223> Zn dependent metalloproteinase domain

<220>
<221> DOMAIN
<222> (223)...(271)
<223> fibronectin type II domain (gelatin binding
domain)

<220>
<221> DOMAIN
<222> (281)...(329)
<223> fibronectin type II domain (gelatin binding

domain)

<220>
<221> DOMAIN
<222> (340)...(388)
<223> fibronectin type II domain (gelatin binding domain)

<220>
<221> misc_feature
<222> (400)...(411)
<223> Zn binding region

<220>
<221> DOMAIN
<222> (521)...(565)
<223> hemopexin-like domain

<220>
<221> DOMAIN
<222> (567)...(608)
<223> hemopexin-like domain

<220>
<221> DOMAIN
<222> (613)...(659)
<223> hemopexin-like domain

<220>
<221> DOMAIN
<222> (661)...(704)
<223> hemopexin-like domain

<400> 27

```
Met Ser Leu Trp Gln Pro Leu Val Leu Val Leu Leu Val Leu Gly Cys
 1               5                  10                  15
Cys Phe Ala Ala Pro Arg Gln Arg Gln Ser Thr Leu Val Leu Phe Pro
            20                  25                  30
Gly Asp Leu Arg Thr Asn Leu Thr Asp Arg Gln Leu Ala Glu Glu Tyr
        35                  40                  45
Leu Tyr Arg Tyr Gly Tyr Thr Arg Val Ala Glu Met Arg Gly Glu Ser
    50                  55                  60
Lys Ser Leu Gly Pro Ala Leu Leu Leu Leu Gln Lys Gln Leu Ser Leu
65                  70                  75                  80
Pro Glu Thr Gly Glu Leu Asp Ser Ala Thr Leu Lys Ala Met Arg Thr
                85                  90                  95
Pro Arg Cys Gly Val Pro Asp Leu Gly Arg Phe Gln Thr Phe Glu Gly
            100                 105                 110
Asp Leu Lys Trp His His His Asn Ile Thr Tyr Trp Ile Gln Asn Tyr
        115                 120                 125
Ser Glu Asp Leu Pro Arg Ala Val Ile Asp Asp Ala Phe Ala Arg Ala
    130                 135                 140
Phe Ala Leu Trp Ser Ala Val Thr Pro Leu Thr Phe Thr Arg Val Tyr
145                 150                 155                 160
Ser Arg Asp Ala Asp Ile Val Ile Gln Phe Gly Val Ala Glu His Gly
                165                 170                 175
Asp Gly Tyr Pro Phe Asp Gly Lys Asp Gly Leu Leu Ala His Ala Phe
            180                 185                 190
Pro Pro Gly Pro Gly Ile Gln Gly Asp Ala His Phe Asp Asp Asp Glu
        195                 200                 205
Leu Trp Ser Leu Gly Lys Gly Val Val Val Pro Thr Arg Phe Gly Asn
    210                 215                 220
Ala Asp Gly Ala Ala Cys His Phe Pro Phe Ile Phe Glu Gly Arg Ser
225                 230                 235                 240
Tyr Ser Ala Cys Thr Thr Asp Gly Arg Ser Asp Gly Leu Pro Trp Cys
                245                 250                 255
Ser Thr Thr Ala Asn Tyr Asp Thr Asp Asp Arg Phe Gly Phe Cys Pro
```

260 265 270
Ser Glu Arg Leu Tyr Thr Arg Asp Gly Asn Ala Asp Gly Lys Pro Cys
275 280 285
Gln Phe Pro Phe Ile Phe Gln Gly Gln Ser Tyr Ser Ala Cys Thr Thr
290 295 300
Asp Gly Arg Ser Asp Gly Tyr Arg Trp Cys Ala Thr Thr Ala Asn Tyr
305 310 315 320
Asp Arg Asp Lys Leu Phe Gly Phe Cys Pro Thr Arg Ala Asp Ser Thr
325 330 335
Val Met Gly Gly Asn Ser Ala Gly Glu Leu Cys Val Phe Pro Phe Thr
340 345 350
Phe Leu Gly Lys Glu Tyr Ser Thr Cys Thr Ser Glu Gly Arg Gly Asp
355 360 365
Gly Arg Leu Trp Cys Ala Thr Thr Ser Asn Phe Asp Ser Asp Lys Lys
370 375 380
Trp Gly Phe Cys Pro Asp Gln Gly Tyr Ser Leu Phe Leu Val Ala Ala
385 390 395 400
His Glu Phe Gly His Ala Leu Gly Leu Asp His Ser Ser Val Pro Glu
405 410 415
Ala Leu Met Tyr Pro Met Tyr Arg Phe Thr Glu Gly Pro Pro Leu His
420 425 430
Lys Asp Asp Val Asn Gly Ile Arg His Leu Tyr Gly Pro Arg Pro Glu
435 440 445
Pro Glu Pro Arg Pro Pro Thr Thr Thr Thr Pro Gln Pro Thr Ala Pro
450 455 460
Pro Thr Val Cys Pro Thr Gly Pro Pro Thr Val His Pro Ser Glu Arg
465 470 475 480
Pro Thr Ala Gly Pro Thr Gly Pro Pro Ser Ala Gly Pro Thr Gly Pro
485 490 495
Pro Thr Ala Gly Pro Ser Thr Ala Thr Thr Val Pro Leu Ser Pro Val
500 505 510
Asp Asp Ala Cys Asn Val Asn Ile Phe Asp Ala Ile Ala Glu Ile Gly
515 520 525
Asn Gln Leu Tyr Leu Phe Lys Asp Gly Lys Tyr Trp Arg Phe Ser Glu
530 535 540
Gly Arg Gly Ser Arg Pro Gln Gly Pro Phe Leu Ile Ala Asp Lys Trp
545 550 555 560
Pro Ala Leu Pro Arg Lys Leu Asp Ser Val Phe Glu Glu Pro Leu Ser
565 570 575
Lys Lys Leu Phe Phe Phe Ser Gly Arg Gln Val Trp Val Tyr Thr Gly
580 585 590
Ala Ser Val Leu Gly Pro Arg Arg Leu Asp Lys Leu Gly Leu Gly Ala
595 600 605
Asp Val Ala Gln Val Thr Gly Ala Leu Arg Ser Gly Arg Gly Lys Met
610 615 620
Leu Leu Phe Ser Gly Arg Arg Leu Trp Arg Phe Asp Val Lys Ala Gln
625 630 635 640
Met Val Asp Pro Arg Ser Ala Ser Glu Val Asp Arg Met Phe Pro Gly
645 650 655
Val Pro Leu Asp Thr His Asp Val Phe Gln Tyr Arg Glu Lys Ala Tyr
660 665 670
Phe Cys Gln Asp Arg Phe Tyr Trp Arg Val Ser Ser Arg Ser Glu Leu
675 680 685
Asn Gln Val Asp Gln Val Gly Tyr Val Thr Tyr Asp Ile Leu Gln Cys
690 695 700
Pro Glu Asp
705

<210> 28
<211> 688
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(688)
<223> mature full-length matrix metalloproteinase 9

(MMP9)

<400> 28

```
Ala Pro Arg Gln Arg Gln Ser Thr Leu Val Leu Phe Pro Gly Asp Leu
 1               5                  10                  15
Arg Thr Asn Leu Thr Asp Arg Gln Leu Ala Glu Glu Tyr Leu Tyr Arg
            20                  25                  30
Tyr Gly Tyr Thr Arg Val Ala Glu Met Arg Gly Glu Ser Lys Ser Leu
        35                  40                  45
Gly Pro Ala Leu Leu Leu Leu Gln Lys Gln Leu Ser Leu Pro Glu Thr
    50                  55                  60
Gly Glu Leu Asp Ser Ala Thr Leu Lys Ala Met Arg Thr Pro Arg Cys
65                  70                  75                  80
Gly Val Pro Asp Leu Gly Arg Phe Gln Thr Phe Glu Gly Asp Leu Lys
                85                  90                  95
Trp His His His Asn Ile Thr Tyr Trp Ile Gln Asn Tyr Ser Glu Asp
            100                 105                 110
Leu Pro Arg Ala Val Ile Asp Asp Ala Phe Ala Arg Ala Phe Ala Leu
        115                 120                 125
Trp Ser Ala Val Thr Pro Leu Thr Phe Thr Arg Val Tyr Ser Arg Asp
    130                 135                 140
Ala Asp Ile Val Ile Gln Phe Gly Val Ala Glu His Gly Asp Gly Tyr
145                 150                 155                 160
Pro Phe Asp Gly Lys Asp Gly Leu Leu Ala His Ala Phe Pro Pro Gly
                165                 170                 175
Pro Gly Ile Gln Gly Asp Ala His Phe Asp Asp Asp Glu Leu Trp Ser
            180                 185                 190
Leu Gly Lys Gly Val Val Val Pro Thr Arg Phe Gly Asn Ala Asp Gly
        195                 200                 205
Ala Ala Cys His Phe Pro Phe Ile Phe Glu Gly Arg Ser Tyr Ser Ala
    210                 215                 220
Cys Thr Thr Asp Gly Arg Ser Asp Gly Leu Pro Trp Cys Ser Thr Thr
225                 230                 235                 240
Ala Asn Tyr Asp Thr Asp Asp Arg Phe Gly Phe Cys Pro Ser Glu Arg
                245                 250                 255
Leu Tyr Thr Arg Asp Gly Asn Ala Asp Gly Lys Pro Cys Gln Phe Pro
            260                 265                 270
Phe Ile Phe Gln Gly Gln Ser Tyr Ser Ala Cys Thr Thr Asp Gly Arg
        275                 280                 285
Ser Asp Gly Tyr Arg Trp Cys Ala Thr Thr Ala Asn Tyr Asp Arg Asp
    290                 295                 300
Lys Leu Phe Gly Phe Cys Pro Thr Arg Ala Asp Ser Thr Val Met Gly
305                 310                 315                 320
Gly Asn Ser Ala Gly Glu Leu Cys Val Phe Pro Phe Thr Phe Leu Gly
                325                 330                 335
Lys Glu Tyr Ser Thr Cys Thr Ser Glu Gly Arg Gly Asp Gly Arg Leu
            340                 345                 350
Trp Cys Ala Thr Thr Ser Asn Phe Asp Ser Asp Lys Lys Trp Gly Phe
        355                 360                 365
Cys Pro Asp Gln Gly Tyr Ser Leu Phe Leu Val Ala Ala His Glu Phe
    370                 375                 380
Gly His Ala Leu Gly Leu Asp His Ser Ser Val Pro Glu Ala Leu Met
385                 390                 395                 400
Tyr Pro Met Tyr Arg Phe Thr Glu Gly Pro Pro Leu His Lys Asp Asp
                405                 410                 415
Val Asn Gly Ile Arg His Leu Tyr Gly Pro Arg Pro Glu Pro Glu Pro
            420                 425                 430
Arg Pro Pro Thr Thr Thr Thr Pro Gln Pro Thr Ala Pro Pro Thr Val
        435                 440                 445
Cys Pro Thr Gly Pro Pro Thr Val His Pro Ser Glu Arg Pro Thr Ala
    450                 455                 460
Gly Pro Thr Gly Pro Pro Ser Ala Gly Pro Thr Gly Pro Pro Thr Ala
465                 470                 475                 480
Gly Pro Ser Thr Ala Thr Thr Val Pro Leu Ser Pro Val Asp Asp Ala
                485                 490                 495
Cys Asn Val Asn Ile Phe Asp Ala Ile Ala Glu Ile Gly Asn Gln Leu
            500                 505                 510
Tyr Leu Phe Lys Asp Gly Lys Tyr Trp Arg Phe Ser Glu Gly Arg Gly
```

```
        515                 520                 525
Ser Arg Pro Gln Gly Pro Phe Leu Ile Ala Asp Lys Trp Pro Ala Leu
    530                 535                 540
Pro Arg Lys Leu Asp Ser Val Phe Glu Glu Pro Leu Ser Lys Lys Leu
545                 550                 555                 560
Phe Phe Phe Ser Gly Arg Gln Val Trp Val Tyr Thr Gly Ala Ser Val
                565                 570                 575
Leu Gly Pro Arg Arg Leu Asp Lys Leu Gly Leu Gly Ala Asp Val Ala
            580                 585                 590
Gln Val Thr Gly Ala Leu Arg Ser Gly Arg Gly Lys Met Leu Leu Phe
        595                 600                 605
Ser Gly Arg Arg Leu Trp Arg Phe Asp Val Lys Ala Gln Met Val Asp
    610                 615                 620
Pro Arg Ser Ala Ser Glu Val Asp Arg Met Phe Pro Gly Val Pro Leu
625                 630                 635                 640
Asp Thr His Asp Val Phe Gln Tyr Arg Glu Lys Ala Tyr Phe Cys Gln
                645                 650                 655
Asp Arg Phe Tyr Trp Arg Val Ser Ser Arg Ser Glu Leu Asn Gln Val
            660                 665                 670
Asp Gln Val Gly Tyr Val Thr Tyr Asp Ile Leu Gln Cys Pro Glu Asp
        675                 680                 685


<210> 29
<211> 19
<212> PRT
<213> Homo sapiens

<400> 29
Met Ser Leu Trp Gln Pro Leu Val Leu Val Leu Leu Val Leu Gly Cys
 1               5                  10                  15
Cys Phe Ala



<210> 30
<211> 470
<212> PRT
<213> Mus musculus

<220>
<221> CHAIN
<222> (1)...(470)
<223> M4 heavy chain (IgG2b)

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

```
Ser Gly Ser Leu Ser Ser Ser Val His Thr Phe Pro Ala Leu Leu Gln
            180                 185                 190
Ser Gly Leu Tyr Thr Met Ser Ser Ser Val Thr Val Pro Ser Ser Thr
        195                 200                 205
Trp Pro Ser Gln Thr Val Thr Cys Ser Val Ala His Pro Ala Ser Ser
    210                 215                 220
Thr Thr Val Asp Lys Lys Leu Glu Pro Ser Gly Pro Ile Ser Thr Ile
225                 230                 235                 240
Asn Pro Cys Pro Pro Cys Lys Glu Cys His Lys Cys Pro Ala Pro Asn
                245                 250                 255
Leu Glu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Asn Ile Lys Asp
            260                 265                 270
Val Leu Met Ile Ser Leu Thr Pro Lys Val Thr Cys Val Val Val Asp
        275                 280                 285
Val Ser Glu Asp Asp Pro Asp Val Arg Ile Ser Trp Phe Val Asn Asn
    290                 295                 300
Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn
305                 310                 315                 320
Ser Thr Ile Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp
                325                 330                 335
Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro
            340                 345                 350
Ser Pro Ile Glu Arg Thr Ile Ser Lys Ile Lys Gly Leu Val Arg Ala
        355                 360                 365
Pro Gln Val Tyr Ile Leu Pro Pro Pro Ala Glu Gln Leu Ser Arg Lys
    370                 375                 380
Asp Val Ser Leu Thr Cys Leu Val Val Gly Phe Asn Pro Gly Asp Ile
385                 390                 395                 400
Ser Val Glu Trp Thr Ser Asn Gly His Thr Glu Glu Asn Tyr Lys Asp
                405                 410                 415
Thr Ala Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Ile Tyr Ser Lys
            420                 425                 430
Leu Asp Ile Lys Thr Ser Lys Trp Glu Lys Thr Asp Ser Phe Ser Cys
        435                 440                 445
Asn Val Arg His Glu Gly Leu Lys Asn Tyr Tyr Leu Lys Lys Thr Ile
    450                 455                 460
Ser Arg Ser Pro Gly Lys
465                 470


<210> 31
<211> 234
<212> PRT
<213> Mus musculus

<220>
<221> CHAIN
<222> (1)...(234)
<223> M4 light chain (kappa)

<400> 31
Met Glu Ser Gln Ile Gln Val Phe Val Phe Val Phe Leu Trp Leu Ser
 1               5                  10                  15
Gly Val Asp Gly Asp Ile Val Met Thr Gln Ser His Lys Phe Met Phe
            20                  25                  30
Thr Ser Val Gly Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp
        35                  40                  45
Val Arg Asn Thr Val Ala Trp Tyr Gln Gln Lys Thr Gly Gln Ser Pro
    50                  55                  60
Lys Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Asn Thr Gly Val Pro Asp
65                  70                  75                  80
Arg Phe Thr Gly Ser Ile Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser
                85                  90                  95
Ser Val Gln Ala Glu Asp Leu Ala Leu Tyr Tyr Cys Gln Gln His Tyr
            100                 105                 110
Ser Thr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Val Lys Arg
        115                 120                 125
Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln
```

130 135 140
Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr
145 150 155 160
Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln
165 170 175
Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr
180 185 190
Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg
195 200 205
His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro
210 215 220
Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
225 230

<210> 32
<211> 115
<212> PRT
<213> Mus musculus

<400> 32
Gln Val Gln Leu Lys Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln
1 5 10 15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Leu Ser Tyr
20 25 30
Gly Val His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45
Gly Val Ile Trp Thr Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
50 55 60
Ser Arg Leu Ser Ile Ser Lys Asp Asp Ser Lys Ser Gln Val Phe Leu
65 70 75 80
Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys Ala
85 90 95
Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr
100 105 110
Val Ser Ser
115

<210> 33
<211> 107
<212> PRT
<213> Mus musculus

<400> 33
Asp Ile Val Met Thr Gln Ser His Lys Phe Met Phe Thr Ser Val Gly
1 5 10 15
Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val Arg Asn Thr
20 25 30
Val Ala Trp Tyr Gln Gln Lys Thr Gly Gln Ser Pro Lys Leu Leu Ile
35 40 45
Tyr Ser Ala Ser Tyr Arg Asn Thr Gly Val Pro Asp Arg Phe Thr Gly
50 55 60
Ser Ile Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Val Gln Ala
65 70 75 80
Glu Asp Leu Ala Leu Tyr Tyr Cys Gln Gln His Tyr Ser Thr Pro Tyr
85 90 95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Val Lys
100 105

<210> 34
<211> 10
<212> PRT
<213> Mus musculus

<400> 34

Gly Phe Ser Leu Leu Ser Tyr Gly Val His
 1   5   10

<210> 35
<211> 10
<212> PRT
<213> Mus musculus

<400> 35
Val Ile Trp Thr Gly Gly Ser Thr Asn Tyr
 1   5   10

<210> 36
<211> 7
<212> PRT
<213> Mus musculus

<400> 36
Tyr Tyr Tyr Ala Met Asp Tyr
 1   5

<210> 37
<211> 11
<212> PRT
<213> Mus musculus

<400> 37
Lys Ala Ser Gln Asp Val Arg Asn Thr Val Ala
 1   5   10

<210> 38
<211> 7
<212> PRT
<213> Mus musculus

<400> 38
Ser Ala Ser Tyr Arg Asn Thr
 1   5

<210> 39
<211> 9
<212> PRT
<213> Mus musculus

<400> 39
Gln Gln His Tyr Ser Thr Pro Tyr Thr
 1   5

<210> 40
<211> 229
<212> PRT
<213> Mus musculus

<220>
<221> CHAIN
<222> (1)...(229)
<223> M12 kappa chain

<400> 40
Gln Val Phe Val Tyr Met Leu Leu Trp Leu Ser Gly Val Asp Gly Asp
 1   5   10   15
Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val Gly Asp

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

<210> 41
<211> 107
<212> PRT
<213> Mus musculus

<400> 41

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

<210> 42
<211> 11
<212> PRT
<213> Mus musculus

<400> 42

```
Lys Ala Ser Gln Asn Val Gly Thr Asn Val Ala
 1               5                  10
```

<210> 43
<211> 7
<212> PRT
<213> Mus musculus

<400> 43

```
Ser Ala Ser Tyr Arg Phe Ser
```

1 5

<210> 44
<211> 9
<212> PRT
<213> Mus musculus

<400> 44
Gln Gln Tyr Asn Ser Tyr Pro Tyr Thr
1 5

<210> 45
<211> 233
<212> PRT
<213> Mus musculus

<220>
<221> CHAIN
<222> (1)...(233)
<223> AB0046 kappa light chain

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

<210> 46
<211> 460
<212> PRT
<213> Mus musculus

<220>
<221> CHAIN
<222> (1)...(460)
<223> AB0046 IgG1 heavy chain

<400> 46
Met Gly Trp Ser Ser Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly

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

<210> 47
<211> 117
<212> PRT
<213> Mus musculus

<400> 47

```
Gln Val Gln Leu Gln Gln Pro Gly Ser Val Leu Val Arg Pro Gly Ala
 1               5                  10                  15
Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
```

```
            20                  25                  30
Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45
Gly Glu Ile Tyr Pro Ile Ser Gly Arg Thr Asn Tyr Asn Glu Lys Phe
    50                  55                  60
Lys Val Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80
Met Asp Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Ser Arg Ala Asn Trp Asp Asp Tyr Trp Gly Gln Gly Thr Thr
            100                 105                 110
Leu Thr Val Ser Ser
        115


<210> 48
<211> 107
<212> PRT
<213> Mus musculus

<400> 48
Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
 1               5                  10                  15
Asp Arg Val Thr Ile Ser Cys Ser Ala Ser Gln Gly Ile Ser Asn Tyr
            20                  25                  30
Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Phe Lys Leu Leu Ile
        35                  40                  45
Tyr Tyr Thr Ser Ile Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Pro
65                  70                  75                  80
Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Gly Trp Leu Pro Arg
                85                  90                  95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105


<210> 49
<211> 461
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct

<220>
<221> CHAIN
<222> (1)...(461)
<223> AB0045 heavy chain

<400> 49
Met Gly Trp Ser Leu Ile Leu Leu Phe Leu Val Ala Val Ala Thr Arg
 1               5                  10                  15
Val His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys
            20                  25                  30
Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu
        35                  40                  45
Leu Ser Tyr Gly Val His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu
    50                  55                  60
Glu Trp Leu Gly Val Ile Trp Thr Gly Gly Thr Thr Asn Tyr Asn Ser
65                  70                  75                  80
Ala Leu Met Ser Arg Phe Thr Ile Ser Lys Asp Asp Ser Lys Asn Thr
                85                  90                  95
Val Tyr Leu Lys Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Ile Tyr
            100                 105                 110
Tyr Cys Ala Arg Tyr Tyr Tyr Gly Met Asp Tyr Trp Gly Gln Gly Thr
        115                 120                 125
Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
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    130                 135                 140
Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
145                 150                 155                 160
Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
                165                 170                 175
Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
            180                 185                 190
Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
        195                 200                 205
Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
    210                 215                 220
Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
225                 230                 235                 240
Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
                245                 250                 255
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
            260                 265                 270
Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
        275                 280                 285
Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
    290                 295                 300
Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
305                 310                 315                 320
Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
                325                 330                 335
Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
            340                 345                 350
Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
        355                 360                 365
Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
    370                 375                 380
Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
385                 390                 395                 400
Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
                405                 410                 415
Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
            420                 425                 430
Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
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His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
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Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
            20                  25                  30
Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp
        35                  40                  45
Val Arg Asn Thr Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
    50                  55                  60
Lys Leu Leu Ile Tyr Ser Ser Ser Tyr Arg Asn Thr Gly Val Pro Asp
65                  70                  75                  80
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
```

```
                85                  90                  95
Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln His Tyr
            100                 105                 110
Ile Thr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
        115                 120                 125
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
    130                 135                 140
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145                 150                 155                 160
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
                165                 170                 175
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
            180                 185                 190
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
        195                 200                 205
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
    210                 215                 220
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230
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