SEQUENCE LISTING

<110> CENTOCOR ORTHO BIOTECH INC.

<120> TOLL-LIKE RECEPTOR 3 ANTAGONISTS

<130> CEN5242PCT

<140> TO BE ASSIGNED
<141> 2009-10-30

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<151> 2008-10-31

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<170> FastSEQ for Windows Version 4.0

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Glu Val Ala Asp Cys Ser His Leu Lys Leu Thr Gln Val Pro Asp Asp
        35   40   45
Leu Pro Thr Asn Ile Thr Val Leu Asn Leu Thr His Asn Gln Leu Arg
    50   55   60
Arg Leu Pro Ala Ala Asn Phe Thr Arg Tyr Ser Gln Leu Thr Ser Leu
65   70   75   80
Asp Val Gly Phe Asn Thr Ile Ser Lys Leu Glu Pro Glu Leu Cys Gln
                85   90   95
Lys Leu Pro Met Leu Lys Val Leu Asn Leu Gln His Asn Glu Leu Ser
            100   105   110
Gln Leu Ser Asp Lys Thr Phe Ala Phe Cys Thr Asn Leu Thr Glu Leu
        115   120   125
His Leu Met Ser Asn Ser Ile Gln Lys Ile Lys Asn Asn Pro Phe Val
    130   135   140
Lys Gln Lys Asn Leu Ile Thr Leu Asp Leu Ser His Asn Gly Leu Ser
145   150   155   160
Ser Thr Lys Leu Gly Thr Gln Val Gln Leu Glu Asn Leu Gln Glu Leu
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Leu Leu Ser Asn Asn Lys Ile Gln Ala Leu Lys Ser Glu Glu Leu Asp
            180   185   190
Ile Phe Ala Asn Ser Ser Leu Lys Lys Leu Glu Leu Ser Ser Asn Gln
        195   200   205
Ile Lys Glu Phe Ser Pro Gly Cys Phe His Ala Ile Gly Arg Leu Phe
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Gly Leu Phe Leu Asn Asn Val Gln Leu Gly Pro Ser Leu Thr Glu Lys
225   230   235   240
Leu Cys Leu Glu Leu Ala Asn Thr Ser Ile Arg Asn Leu Ser Leu Ser
                245   250   255
Asn Ser Gln Leu Ser Thr Thr Ser Asn Thr Thr Phe Leu Gly Leu Lys
            260   265   270
Trp Thr Asn Leu Thr Met Leu Asp Leu Ser Tyr Asn Asn Leu Asn Val
        275   280   285
Val Gly Asn Asp Ser Phe Ala Trp Leu Pro Gln Leu Glu Tyr Phe Phe
    290   295   300
Leu Glu Tyr Asn Asn Ile Gln His Leu Phe Ser His Ser Leu His Gly
305   310   315   320
Leu Phe Asn Val Arg Tyr Leu Asn Leu Lys Arg Ser Phe Thr Lys Gln
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Ser Ile Ser Leu Ala Ser Leu Pro Lys Ile Asp Asp Phe Ser Phe Gln
            340   345   350
Trp Leu Lys Cys Leu Glu His Leu Asn Met Glu Asp Asn Asp Ile Pro
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Gly Ile Lys Ser Asn Met Phe Thr Gly Leu Ile Asn Leu Lys Tyr Leu
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Leu Glu Val Leu Asp Leu Gly Leu Asn Glu Ile Gly Gln Glu Leu Thr
435 440 445
Gly Gln Glu Trp Arg Gly Leu Glu Asn Ile Phe Glu Ile Tyr Leu Ser
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Ile Pro Val Glu Val Phe Lys Asp Leu Phe Glu Leu Lys Ile Ile Asp
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595 600 605
Gln Val Ser Leu Lys Ser Leu Asn Leu Gln Lys Asn Leu Ile Thr Ser
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Val Glu Lys Lys Val Phe Gly Pro Ala Phe Arg Asn Leu Thr Glu Leu
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Asp Met Arg Phe Asn Pro Phe Asp Cys Thr Cys Glu Ser Ile Ala Trp
645 650 655
Phe Val Asn Trp Ile Asn Glu Thr His Thr Asn Ile Pro Glu Leu Ser
660 665 670
Ser His Tyr Leu Cys Asn Thr Pro Pro His Tyr His Gly Phe Pro Val
675 680 685
Arg Leu Phe Asp Thr Ser Ser Cys Lys Asp Ser Ala Pro Phe Glu Leu
690 695 700
Phe Phe Met Ile Asn Thr Ser Ile Leu Leu Ile Phe Ile Phe Ile Val
705 710 715 720
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725 730 735
Ser Val His Arg Val Leu Gly Phe Lys Glu Ile Asp Arg Gln Thr Glu
740 745 750
Gln Phe Glu Tyr Ala Ala Tyr Ile Ile His Ala Tyr Lys Asp Lys Asp
755 760 765
Trp Val Trp Glu His Phe Ser Ser Met Glu Lys Glu Asp Gln Ser Leu
770 775 780
Lys Phe Cys Leu Glu Glu Arg Asp Phe Glu Ala Gly Val Phe Glu Leu
785 790 795 800
Glu Ala Ile Val Asn Ser Ile Lys Arg Ser Arg Lys Ile Ile Phe Val
805 810 815
Ile Thr His His Leu Leu Lys Asp Pro Leu Cys Lys Arg Phe Lys Val
820 825 830
His His Ala Val Gln Gln Ala Ile Glu Gln Asn Leu Asp Ser Ile Ile
835 840 845
Leu Val Phe Leu Glu Glu Ile Pro Asp Tyr Lys Leu Asn His Ala Leu
850 855 860
Cys Leu Arg Arg Gly Met Phe Lys Ser His Cys Ile Leu Asn Trp Pro
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Val Gln Lys Glu Arg Ile Gly Ala Phe Arg His Lys Leu Gln Val Ala
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<211> 2109
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<213> Homo sapiens

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

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

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            180                 185                 190
Ile Phe Ala Asn Ser Ser Leu Lys Lys Leu Glu Leu Ser Ser Asn Gln
        195                 200                 205
Ile Lys Glu Phe Ser Pro Gly Cys Phe His Ala Ile Gly Arg Leu Phe
    210                 215                 220
Gly Leu Phe Leu Asn Asn Val Gln Leu Gly Pro Ser Leu Thr Glu Lys
225                 230                 235                 240
Leu Cys Leu Glu Leu Ala Asn Thr Ser Ile Arg Asn Leu Ser Leu Ser
                245                 250                 255
Asn Ser Gln Leu Ser Thr Thr Ser Asn Thr Thr Phe Leu Gly Leu Lys
            260                 265                 270
Trp Thr Asn Leu Thr Met Leu Asp Leu Ser Tyr Asn Asn Leu Asn Val
        275                 280                 285
Val Gly Asn Asp Ser Phe Ala Trp Leu Pro Gln Leu Glu Tyr Phe Phe
    290                 295                 300
Leu Glu Tyr Asn Asn Ile Gln His Leu Phe Ser His Ser Leu His Gly
305                 310                 315                 320
Leu Phe Asn Val Arg Tyr Leu Asn Leu Lys Arg Ser Phe Thr Lys Gln
                325                 330                 335
Ser Ile Ser Leu Ala Ser Leu Pro Lys Ile Asp Asp Phe Ser Phe Gln
            340                 345                 350
Trp Leu Lys Cys Leu Glu His Leu Asn Met Glu Asp Asn Asp Ile Pro
        355                 360                 365
Gly Ile Lys Ser Asn Met Phe Thr Gly Leu Ile Asn Leu Lys Tyr Leu
    370                 375                 380
Ser Leu Ser Asn Ser Phe Thr Ser Leu Arg Thr Leu Thr Asn Glu Thr
385                 390                 395                 400
Phe Val Ser Leu Ala His Ser Pro Leu His Ile Leu Asn Leu Thr Lys
                405                 410                 415
Asn Lys Ile Ser Lys Ile Glu Ser Asp Ala Phe Ser Trp Leu Gly His
            420                 425                 430
Leu Glu Val Leu Asp Leu Gly Leu Asn Glu Ile Gly Gln Glu Leu Thr
        435                 440                 445
Gly Gln Glu Trp Arg Gly Leu Glu Asn Ile Phe Glu Ile Tyr Leu Ser
    450                 455                 460
Tyr Asn Lys Tyr Leu Gln Leu Thr Arg Asn Ser Phe Ala Leu Val Pro
465                 470                 475                 480
Ser Leu Gln Arg Leu Met Leu Arg Arg Val Ala Leu Lys Asn Val Asp
                485                 490                 495
Ser Ser Pro Ser Pro Phe Gln Pro Leu Arg Asn Leu Thr Ile Leu Asp
            500                 505                 510
Leu Ser Asn Asn Asn Ile Ala Asn Ile Asn Asp Asp Met Leu Glu Gly
        515                 520                 525
Leu Glu Lys Leu Glu Ile Leu Asp Leu Gln His Asn Asn Leu Ala Arg
    530                 535                 540
Leu Trp Lys His Ala Asn Pro Gly Gly Pro Ile Tyr Phe Leu Lys Gly
545                 550                 555                 560
Leu Ser His Leu His Ile Leu Asn Leu Glu Ser Asn Gly Phe Asp Glu
                565                 570                 575
Ile Pro Val Glu Val Phe Lys Asp Leu Phe Glu Leu Lys Ile Ile Asp
            580                 585                 590
Leu Gly Leu Asn Asn Leu Asn Thr Leu Pro Ala Ser Val Phe Asn Asn
        595                 600                 605
Gln Val Ser Leu Lys Ser Leu Asn Leu Gln Lys Asn Leu Ile Thr Ser
    610                 615                 620
Val Glu Lys Lys Val Phe Gly Pro Ala Phe Arg Asn Leu Thr Glu Leu
625                 630                 635                 640
Asp Met Arg Phe Asn Pro Phe Asp Cys Thr Cys Glu Ser Ile Ala Trp
                645                 650                 655
Phe Val Asn Trp Ile Asn Glu Thr His Thr Asn Ile Pro Glu Leu Ser
            660                 665                 670
Ser His Tyr Leu Cys Asn Thr Pro Pro His Tyr His Gly Phe Pro Val
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Arg Leu Phe Asp Thr Ser Ser Cys Lys Asp Ser Ala Pro Phe Glu
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<213> Artificial Sequence

<220>
<223> candidate 16 VL

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

<210> 6
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> candidate 16 VH

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Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Asn Asn Tyr
            20   25   30
Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
        35   40   45
Gly Ile Ile Asp Pro Gly Asp Ser Tyr Thr Asn Tyr Ala Pro Ser Phe
    50   55   60
Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65   70   75   80
Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
                85   90   95
Ala Arg Asn Ile Tyr Glu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100   105   110
Thr Val Ser Ser
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<210> 7
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> candidate 17 VL

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Thr Ala Arg Ile Ser Cys Ser Gly Asp Ala Leu Gly Gly Tyr Phe Val
            20   25   30
Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr

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


<210> 8
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> candidate 17 VH

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


<210> 9
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> candidate 18 VL


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


<210> 10
<211> 122
<212> PRT
<213> Artificial Sequence
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<220>
<223> candidate 18 VH

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Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Asn
            20   25   30
Ser Ala Ala Trp Gly Trp Ile Arg Gln Ser Pro Gly Arg Gly Leu Glu
        35   40   45
Trp Leu Gly Ile Ile Gln Lys Arg Ser Lys Trp Tyr Asn Asn Tyr Ala
    50   55   60
Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65   70   75   80
Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
                85   90   95
Tyr Tyr Cys Ala Arg Tyr Ser Tyr Pro Phe Tyr Ser Ile Asp Tyr Trp
            100   105   110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

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

<220>
<223> candidate 19 VL

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

<210> 12
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> candidate 19 VH

<400> 12
Gln Val Glu Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1   5   10   15
Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Asn Tyr
            20   25   30
Trp Val Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
        35   40   45
Gly Phe Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Ala Pro Ser Phe
    50   55   60
Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr

65 70 75 80
Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95
Ala Arg Glu Leu Tyr Gln Gly Tyr Met Asp Thr Phe Asp Ser Trp Gly
100 105 110
Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 13
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> candidate 1 VL

<400> 13
Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Tyr Ile Asp Ile Ser
20 25 30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
Ile Tyr Asp Ala Ser Ser Arg Ala Thr Gly Val Pro Ala 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 Tyr Ser Leu Ser
85 90 95
Ile Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 14
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> candidate 1 VH

<400> 14
Gly Val Glu Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15
Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Asp Asn
20 25 30
Trp Ile Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
35 40 45
Gly Val Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Ala Pro Ser Phe
50 55 60
Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80
Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95
Ala Arg Glu Trp Gly Ile Gly Gly Met Val Asp Ile Trp Gly Gln Gly
100 105 110
Thr Leu Val Thr Val Ser Ser
115

<210> 15
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> candidate 2 VL

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

<210> 16
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> candidate 2 VH

<400> 16
Gln Val Glu Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1   5   10   15
Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Asn Asn Tyr
            20   25   30
Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
        35   40   45
Gly Ile Ile Asp Pro Gln Asp Ser Trp Thr Asn Tyr Ala Pro Ser Phe
    50   55   60
Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65   70   75   80
Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
                85   90   95
Ala Arg Asn Ile Tyr Glu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100   105   110
Thr Val Ser Ser
        115

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

<220>
<223> candidate 3 VL

<400> 17
Asp Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
 1   5   10   15
Thr Ala Arg Ile Ser Cys Ser Gly Asp Ala Leu Gly Gly Tyr Phe Val
            20   25   30
Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
        35   40   45
Asp Asp Asp Asn Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50   55   60
Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu
65   70   75   80
Asp Glu Ala Asp Tyr Tyr Cys Ala Ser Tyr Asp Gly Asp Glu Phe Thr
                85   90   95
Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu

100 105

<210> 18
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> candidate 3 VH

<400> 18
Gln Val Glu Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15
Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Thr Arg
20 25 30
Ser Ala Ala Trp Gly Trp Ile Arg Gln Ser Pro Gly Arg Gly Leu Glu
35 40 45
Trp Leu Gly Arg Ile His Arg Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
50 55 60
Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65 70 75 80
Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
85 90 95
Tyr Tyr Cys Ala Arg His Thr Tyr Pro Tyr Leu Ser Phe Asp Val Trp
100 105 110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 19
<211> 107
<213> Artificial Sequence

<220>
<223> candidate 4 VL

<400> 19
Asp Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1 5 10 15
Thr Ala Arg Ile Ser Cys Ser Gly Asp Ala Leu Gly Gly Tyr Phe Val
20 25 30
Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
35 40 45
Asp Asp Asp Asn Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60
Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu
65 70 75 80
Asp Glu Ala Asp Tyr Tyr Cys Ala Ser Tyr Asp Gly Asp Glu Phe Thr
85 90 95
Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 20
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> candidate 4 VH

<400> 20
Gln Val Glu Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15
Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Thr Arg
20 25 30
Ser Ala Ala Trp Gly Trp Ile Arg Gln Ser Pro Gly Arg Gly Leu Glu

35 40 45
Trp Leu Gly Lys Ile Ser Tyr Arg Ser Arg Trp Tyr Asn Asp Tyr Ala
50 55 60
Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65 70 75 80
Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
85 90 95
Tyr Tyr Cys Ala Arg His Thr Tyr Pro Tyr Leu Ser Phe Asp Val Trp
100 105 110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 21
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> candidate 5 VL

<400> 21
Asp Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1 5 10 15
Thr Ala Arg Ile Ser Cys Ser Gly Asp Ala Leu Gly Gly Tyr Phe Val
20 25 30
Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
35 40 45
Asp Asp Asp Asn Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60
Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu
65 70 75 80
Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Glu Asp Ser Ala Thr
85 90 95
Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 22
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> candidate 5 VH

<400> 22
Gln Val Glu Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15
Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Thr Arg
20 25 30
Ser Ala Ala Trp Gly Trp Ile Arg Gln Ser Pro Gly Arg Gly Leu Glu
35 40 45
Trp Leu Gly Arg Ile Tyr Met Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
50 55 60
Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65 70 75 80
Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
85 90 95
Tyr Tyr Cys Ala Arg His Thr Tyr Pro Tyr Leu Ser Phe Asp Val Trp
100 105 110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 23
<211> 107

<212> PRT
<213> Artificial Sequence

<220>
<223> candidate 6 VL

<400> 23
Asp Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
 1   5   10   15
Thr Ala Arg Ile Ser Cys Ser Gly Asp Ala Leu Gly Gly Tyr Phe Val
            20   25   30
Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
        35   40   45
Asp Asp Asp Asn Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50   55   60
Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu
65   70   75   80
Asp Glu Ala Asp Tyr Tyr Cys Gly Ser Tyr Asp Ser Asn Ser Leu Thr
                85   90   95
Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100   105

<210> 24
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> candidate 6 VH

<400> 24
Gln Val Glu Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1   5   10   15
Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Thr Arg
            20   25   30
Ser Ala Ala Trp Gly Trp Ile Arg Gln Ser Pro Gly Arg Gly Leu Glu
        35   40   45
Trp Leu Gly Arg Ile Tyr Met Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
    50   55   60
Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65   70   75   80
Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
                85   90   95
Tyr Tyr Cys Ala Arg His Thr Tyr Pro Tyr Leu Ser Phe Asp Val Trp
            100   105   110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 25
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> candidate 7 VL

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

65 70 75 80
Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Asp Ser Asp Ser Leu Thr
85 90 95
Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 26
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> candidate 7 VH

<400> 26
Gln Val Glu Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15
Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Thr Arg
20 25 30
Ser Ala Ala Trp Gly Trp Ile Arg Gln Ser Pro Gly Arg Gly Leu Glu
35 40 45
Trp Leu Gly Arg Ile Tyr Met Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
50 55 60
Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65 70 75 80
Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
85 90 95
Tyr Tyr Cys Ala Arg His Thr Tyr Pro Tyr Leu Ser Phe Asp Val Trp
100 105 110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

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

<220>
<223> candidate 8 VL

<400> 27
Asp Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1 5 10 15
Thr Ala Arg Ile Ser Cys Ser Gly Asp Asn Ile Gly Ser Tyr Tyr Val
20 25 30
His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
35 40 45
Glu Asp Ser Glu Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60
Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu
65 70 75 80
Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Gln Phe Ser Phe
85 90 95
Gly Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 28
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> candidate 8 VH

<400> 28

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

<210> 29
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> candidate 9 VL

<400> 29

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

<210> 30
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> candidate 9 VH

<400> 30

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

<210> 31
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> candidate 10 VL

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

<210> 32
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> candidate 10 VH

<400> 32
Gln Val Glu Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1   5   10   15
Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Asn
            20   25   30
Ser Ala Ala Trp Gly Trp Ile Arg Gln Ser Pro Gly Arg Gly Leu Glu
        35   40   45
Trp Leu Gly Ile Ile Gln Lys Arg Ser Lys Trp Tyr Asn Asn Tyr Ala
    50   55   60
Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65   70   75   80
Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
                85   90   95
Tyr Tyr Cys Ala Arg Tyr Ser Tyr Pro Phe Tyr Ser Ile Asp Tyr Trp
            100   105   110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

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

<220>
<223> candidate 11 VL

<400> 33
Asp Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
 1   5   10   15
Thr Ala Arg Ile Ser Cys Ser Gly Asp Asn Ile Gly Ser Tyr Tyr Val
            20   25   30

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


<210> 34
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> candidate 11 VH

<400> 34
Gln Val Glu Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1               5                  10                  15
Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Asn
            20                  25                  30
Ser Ala Ala Trp Gly Trp Ile Arg Gln Ser Pro Gly Arg Gly Leu Glu
        35                  40                  45
Trp Leu Gly Ile Ile Gln Lys Arg Ser Lys Trp Tyr Asn Asn Tyr Ala
    50                  55                  60
Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65                  70                  75                  80
Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
                85                  90                  95
Tyr Tyr Cys Ala Arg Tyr Ser Tyr Pro Phe Tyr Ser Ile Asp Tyr Trp
            100                 105                 110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 35
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> candidate 12 VL

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


<210> 36
<211> 122
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<212> PRT
<213> Artificial Sequence

<220>
<223> candidate 12 VH

<400> 36
Gln Val Glu Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1   5   10   15
Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Asn
            20   25   30
Ser Ala Ala Trp Gly Trp Ile Arg Gln Ser Pro Gly Arg Gly Leu Glu
        35   40   45
Trp Leu Gly Ile Ile Gln Lys Arg Ser Lys Trp Tyr Asn Asn Tyr Ala
    50   55   60
Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65   70   75   80
Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
                85   90   95
Tyr Tyr Cys Ala Arg Tyr Ser Tyr Pro Phe Tyr Ser Ile Asp Tyr Trp
            100   105   110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

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

<220>
<223> candidate 13 VL

<400> 37
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Leu Tyr
            20   25   30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Glu Ser Ile Leu Ser
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 38
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> candidate 13 VH

<400> 38
Gln Val Glu Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1   5   10   15
Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Asn Tyr
            20   25   30
Trp Val Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
        35   40   45
Gly Phe Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Ala Pro Ser Phe
    50   55   60
Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr

65 70 75 80
Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95
Ala Arg Glu Leu Tyr Gln Gly Tyr Met Asp Thr Phe Asp Ser Trp Gly
100 105 110
Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

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

<220>
<223> candidate 14 VL

<400> 39
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Leu Tyr
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Glu Thr Val Ser Pro
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 40
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> candidate 14 VH

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

<210> 41
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> candidate 15 VL

<400> 41
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 Gly Leu Tyr
            20   25   30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Ser Tyr
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 42
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> candidate 15 VH

<400> 42
Gln Val Glu Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1   5   10   15
Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Asn Tyr
            20   25   30
Trp Val Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
        35   40   45
Gly Phe Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Ala Pro Ser Phe
    50   55   60
Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65   70   75   80
Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
                85   90   95
Ala Arg Glu Leu Tyr Gln Gly Tyr Met Asp Thr Phe Asp Ser Trp Gly
            100   105   110
Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 43
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> candidate 1 LCDR1

<400> 43
Gln Tyr Ile Asp Ile Ser Tyr
 1   5

<210> 44
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> candidate 1 LCDR2

<400> 44
Asp Ala Ser

1

<210> 45
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> candidate 1 LCDR3

<400> 45
Gln Gln Tyr Tyr Ser Leu Ser Ile Thr
1 5

<210> 46
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> candidate 1 HCDR1

<400> 46
Gly Tyr Ser Phe Thr Asp Asn Trp
1 5

<210> 47
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> candidate 1 HCDR2

<400> 47
Ile Asp Pro Ser Asp Ser Gln Thr
1 5

<210> 48
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> candidate 1 HCDR3

<400> 48
Ala Arg Glu Trp Gly Ile Gly Gly Met Val Asp Ile
1 5 10

<210> 49
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> candidate 2 LCDR1

<400> 49
Gln Gly Ile Ser Ser Trp
1 5

<210> 50
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> candidate 2 LCDR2

<400> 50
Gly Ala Ser
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<210> 51
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> candidate 2 LCDR3

<400> 51
Gln Gln Tyr Asp Asp Phe Ser Ile Thr
 1   5

<210> 52
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> candidate 2 HCDR1

<400> 52
Gly Tyr Ser Phe Asn Asn Tyr Trp
 1   5

<210> 53
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> candidate 2 HCDR2

<400> 53
Ile Asp Pro Gln Asp Ser Trp Thr
 1   5

<210> 54
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> candidate 2 HCDR3

<400> 54
Ala Arg Asn Ile Tyr Glu Phe Asp Tyr
 1   5

<210> 55
<211> 6
<212> PRT

<213> Artificial Sequence

<220>
<223> Candidates 3,4,5,6, 7 LCDR1

<400> 55
Ala Leu Gly Gly Tyr Phe
 1   5

<210> 56
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidates 3,4,5,6, 7 LCDR2

<400> 56
Asp Asp Asp
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<210> 57
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidates 3,4 LCDR3

<400> 57
Ala Ser Tyr Asp Gly Asp Glu Phe Thr Val
 1   5   10

<210> 58
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidates 3 HCDR1

<400> 58
Gly Asp Ser Val Ser Thr Arg Ser Ala Ala
 1   5   10

<210> 59
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidates 3 HCDR2

<400> 59
Ile His Arg Arg Ser Lys Tyr Trp Asn Asp
 1   5   10

<210> 60

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

<220>
<223> Candidates 3,4,5,6,7 HCDR3

<400> 60
Ala Arg His Thr Tyr Pro Tyr Leu Ser Phe Asp Val
 1   5   10

<210> 61
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidates 4,5,6,7 HCDR1

<400> 61
Gly Asp Ser Val Ser Thr Arg Ser Ala Ala
 1   5   10

<210> 62
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 4 HCDR2

<400> 62
Ile Ser Tyr Arg Ser Arg Trp Tyr Asn Asp
 1   5   10

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

<220>
<223> Candidate 5 LCDR3

<400> 63
Gln Ser Tyr Asp Glu Asp Ser Ala Thr Val
 1   5   10

<210> 64
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidates 5,6,7 HCDR2

<400> 64
Ile Tyr Met Arg Ser Lys Trp Tyr Asn
 1   5

<210> 65
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 6 LCDR3

<400> 65
Gly Ser Tyr Asp Ser Asn Ser Leu Thr Val
 1   5   10

<210> 66
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 7 LCDR3

<400> 66
Ser Ser Tyr Asp Ser Asp Ser Leu Thr Val
 1   5   10

<210> 67
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 8,9,10,11,12 LCDR1

<400> 67
Asn Ile Gly Ser Tyr Tyr
 1   5

<210> 68
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 8,9,10,11,12 LCDR2

<400> 68
Glu Asp Ser
 1

<210> 69
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 8,9 LCDR3

<400> 69

Gln Ser Tyr Asp Ser Gln Phe Ser Phe Gly Val
 1   5   10

<210> 70
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 78,9,10,11,12 HCDR1

<400> 70
Gly Asp Ser Val Ser Ser Asn Ser Ala Ala
 1   5   10

<210> 71
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 8 HCDR2

<400> 71
Ile Gln Thr Arg Ser Lys Tyr Trp Asn
 1   5

<210> 72
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 8,9,10,11,12 HCDR3

<400> 72
Ala Arg Tyr Ser Tyr Pro Phe Tyr Ser Ile Asp Tyr
 1   5   10

<210> 73
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 9 HCDR2

<400> 73
Ile Gln Ile Arg Ser Lys Tyr Trp Asn
 1   5

<210> 74
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 10 LCDR3

<400> 74
Gln Ser Tyr Asp Thr Pro Val Tyr Ser Val
 1   5   10

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

<220>
<223> Candidate 10 HCDR2

<400> 75
Ile Gln Lys Arg Ser Lys Tyr Trp Asn
 1   5

<210> 76
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 11 LCDR3

<400> 76
Ser Ser Tyr Asp Glu Pro Asn Phe Asn Val
 1   5   10

<210> 77
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 11,12 HCDR2

<400> 77
Ile Gln Lys Arg Ser Lys Trp Tyr Asn
 1   5

<210> 78
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 12 LCDR3

<400> 78
Ser Ser Tyr Asp Asp Pro Asn Phe Gln Val
 1   5   10

<210> 79
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 13, 14, 15 LCDR1

<400> 79
Gln Ser Ile Gly Leu Tyr
 1   5

<210> 80
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 13, 14, 15 LCDR2

<400> 80
Ala Ala Ser
 1

<210> 81
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 13 LCDR3

<400> 81
Gln Gln Gly Glu Ser Ile Leu Ser Thr
 1   5

<210> 82
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 13, 14, 15 HCDR1

<400> 82
Gly Tyr Ser Phe Thr Asn Tyr Trp
 1   5

<210> 83
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 13 HCDR2

<400> 83
Ile Asp Pro Ser Asp Ser Tyr Thr
 1   5

<210> 84
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidates 13, 14, 15, 15-1, 15-2, 15-3, 15-4, 15-5, 15-7,15-8 HCDR3

<400> 84
Ala Arg Glu Leu Tyr Gln Gly Tyr Met Asp Thr Phe Asp Ser
 1   5   10

<210> 85
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 14 LCDR3

<400> 85
Gln Gln Ala Glu Thr Val Ser Pro Thr
 1   5

<210> 86
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 14, 15 HCDR2

<400> 86
Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr
 1   5   10

<210> 87
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 15 LCDR3

<400> 87
Gln Gln Gly Asn Thr Leu Ser Tyr Thr
 1   5

<210> 88
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 16 HCDR3

<400> 88
Ile Asp Pro Gly Asp Ser Tyr Thr
 1   5

<210> 89
<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 10 LCDR3

<400> 89
Gln Gln Tyr Gly Ser Val Ser Ile Thr
 1   5

<210> 90
<211> 443
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 16 Full length heavy chain

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

```
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
    370                 375                 380
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
385                 390                 395                 400
Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly
                405                 410                 415
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
            420                 425                 430
Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440


<210> 91
<211> 449
<212> PRT
<213> Artificial Sequence


<220>
<223> Candidate 17 Full length heavy chain

<400> 91
Gln Val Glu Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1               5                  10                  15
Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Thr Arg
            20                  25                  30
Ser Ala Ala Trp Gly Trp Ile Arg Gln Ser Pro Gly Arg Gly Leu Glu
        35                  40                  45
Trp Leu Gly Arg Ile Tyr Met Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
    50                  55                  60
Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65                  70                  75                  80
Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
                85                  90                  95
Tyr Tyr Cys Ala Arg His Thr Tyr Pro Tyr Leu Ser Phe Asp Val Trp
            100                 105                 110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
        115                 120                 125
Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr
    130                 135                 140
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145                 150                 155                 160
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
                165                 170                 175
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
            180                 185                 190
Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp
        195                 200                 205
His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr
    210                 215                 220
Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro
225                 230                 235                 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp
            260                 265                 270
Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val
    290                 295                 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys
                325                 330                 335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350
Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365
```

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385 390 395 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys
405 410 415
Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
435 440 445
Lys

<210> 92
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 18 Full length heavy chain

<400> 92
Gln Val Glu Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15
Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Asn
20 25 30
Ser Ala Ala Trp Gly Trp Ile Arg Gln Ser Pro Gly Arg Gly Leu Glu
35 40 45
Trp Leu Gly Ile Ile Gln Lys Arg Ser Lys Trp Tyr Asn Asn Tyr Ala
50 55 60
Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65 70 75 80
Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
85 90 95
Tyr Tyr Cys Ala Arg Tyr Ser Tyr Pro Phe Tyr Ser Ile Asp Tyr Trp
100 105 110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
115 120 125
Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr
130 135 140
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145 150 155 160
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
165 170 175
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
180 185 190
Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp
195 200 205
His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr
210 215 220
Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro
225 230 235 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
245 250 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp
260 265 270
Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
275 280 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val
290 295 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305 310 315 320
Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys
325 330 335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
340 345 350

```
Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys
                405                 410                 415
Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
        435                 440                 445
Lys
```

<210> 93
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 19 Full length heavy chain

<400> 93

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

```
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
            340                 345                 350
Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
        355                 360                 365
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
    370                 375                 380
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385                 390                 395                 400
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser
                405                 410                 415
Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            420                 425                 430
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440                 445


<210> 94
<211> 446
<212> PRT
<213> Artificial Sequence


<220>
<223> Candidate 1 Full length heavy chain

<400> 94
Gln Val Glu Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1               5                  10                  15
Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Asp Asn
            20                  25                  30
Trp Ile Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
        35                  40                  45
Gly Val Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Ala Pro Ser Phe
    50                  55                  60
Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80
Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
                85                  90                  95
Ala Arg Glu Trp Gly Ile Gly Gly Met Val Asp Ile Trp Gly Gln Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125
Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
    130                 135                 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190
Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
        195                 200                 205
Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
    210                 215                 220
Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
225                 230                 235                 240
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                245                 250                 255
Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
            260                 265                 270
Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285
Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
    290                 295                 300
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305                 310                 315                 320
Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
                325                 330                 335
```

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            340   345   350
Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
        355   360   365
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    370   375   380
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385   390   395   400
Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
                405   410   415
Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            420   425   430
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435   440   445

<210> 95
<211> 443
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 2 Full length heavy chain

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

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu
340 345 350
Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
355 360 365
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
370 375 380
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
385 390 395 400
Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly
405 410 415
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
420 425 430
Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440

<210> 96
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 3 Full length heavy chain

<400> 96
Gln Val Glu Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15
Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Thr Arg
20 25 30
Ser Ala Ala Trp Gly Trp Ile Arg Gln Ser Pro Gly Arg Gly Leu Glu
35 40 45
Trp Leu Gly Arg Ile His Arg Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
50 55 60
Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65 70 75 80
Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
85 90 95
Tyr Tyr Cys Ala Arg His Thr Tyr Pro Tyr Leu Ser Phe Asp Val Trp
100 105 110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
115 120 125
Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr
130 135 140
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145 150 155 160
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
165 170 175
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
180 185 190
Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp
195 200 205
His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr
210 215 220
Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro
225 230 235 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
245 250 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp
260 265 270
Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
275 280 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val
290 295 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305 310 315 320
Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys
325 330 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340   345   350
Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
        355   360   365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370   375   380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385   390   395   400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys
                405   410   415
Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420   425   430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
        435   440   445
Lys

<210> 97
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 4 Full length heavy chain

<400> 97
Gln Val Glu Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1   5   10   15
Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Thr Arg
            20   25   30
Ser Ala Ala Trp Gly Trp Ile Arg Gln Ser Pro Gly Arg Gly Leu Glu
        35   40   45
Trp Leu Gly Lys Ile Ser Tyr Arg Ser Arg Trp Tyr Asn Asp Tyr Ala
    50   55   60
Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65   70   75   80
Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
                85   90   95
Tyr Tyr Cys Ala Arg His Thr Tyr Pro Tyr Leu Ser Phe Asp Val Trp
            100   105   110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
        115   120   125
Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr
    130   135   140
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145   150   155   160
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
                165   170   175
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
            180   185   190
Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp
        195   200   205
His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr
    210   215   220
Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro
225   230   235   240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245   250   255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp
            260   265   270
Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275   280   285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val
    290   295   300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305   310   315   320

Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys
325 330 335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
340 345 350
Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
355 360 365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385 390 395 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys
405 410 415
Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
435 440 445
Lys

<210> 98
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 5,6,7 Full length heavy chain

<400> 98
Gln Val Glu Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15
Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Thr Arg
20 25 30
Ser Ala Ala Trp Gly Trp Ile Arg Gln Ser Pro Gly Arg Gly Leu Glu
35 40 45
Trp Leu Gly Arg Ile Tyr Met Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
50 55 60
Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65 70 75 80
Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
85 90 95
Tyr Tyr Cys Ala Arg His Thr Tyr Pro Tyr Leu Ser Phe Asp Val Trp
100 105 110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
115 120 125
Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr
130 135 140
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145 150 155 160
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
165 170 175
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
180 185 190
Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp
195 200 205
His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr
210 215 220
Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro
225 230 235 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
245 250 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp
260 265 270
Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
275 280 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val
290 295 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305 310 315 320
Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys
325 330 335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
340 345 350
Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
355 360 365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385 390 395 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys
405 410 415
Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
435 440 445
Lys

<210> 99
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 8 Full length heavy chain

<400> 99
Gln Val Glu Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15
Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Asn
20 25 30
Ser Ala Ala Trp Gly Trp Ile Arg Gln Ser Pro Gly Arg Gly Leu Glu
35 40 45
Trp Leu Gly Ile Ile Gln Thr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
50 55 60
Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65 70 75 80
Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
85 90 95
Tyr Tyr Cys Ala Arg Tyr Ser Tyr Pro Phe Tyr Ser Ile Asp Tyr Trp
100 105 110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
115 120 125
Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr
130 135 140
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145 150 155 160
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
165 170 175
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
180 185 190
Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp
195 200 205
His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr
210 215 220
Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro
225 230 235 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
245 250 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp
260 265 270
Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val
290 295 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305 310 315 320
Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys
325 330 335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
340 345 350
Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
355 360 365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385 390 395 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys
405 410 415
Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
435 440 445
Lys

<210> 100
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 9 Full length heavy chain

<400> 100
Gln Val Glu Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15
Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Asn
20 25 30
Ser Ala Ala Trp Gly Trp Ile Arg Gln Ser Pro Gly Arg Gly Leu Glu
35 40 45
Trp Leu Gly Ile Ile Gln Ile Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
50 55 60
Leu Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65 70 75 80
Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
85 90 95
Tyr Tyr Cys Ala Arg Tyr Ser Tyr Pro Phe Tyr Ser Ile Asp Tyr Trp
100 105 110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
115 120 125
Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr
130 135 140
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145 150 155 160
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
165 170 175
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
180 185 190
Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp
195 200 205
His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr
210 215 220
Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro
225 230 235 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
245 250 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp
260 265 270

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

<210> 101
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 10,11, 12 Full length heavy chain

<400> 101
Gln Val Glu Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1   5   10   15
Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Asn
            20   25   30
Ser Ala Ala Trp Gly Trp Ile Arg Gln Ser Pro Gly Arg Gly Leu Glu
        35   40   45
Trp Leu Gly Ile Ile Gln Lys Arg Ser Lys Trp Tyr Asn Asn Tyr Ala
    50   55   60
Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65   70   75   80
Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
                85   90   95
Tyr Tyr Cys Ala Arg Tyr Ser Tyr Pro Phe Tyr Ser Ile Asp Tyr Trp
            100   105   110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
        115   120   125
Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr
    130   135   140
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145   150   155   160
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
                165   170   175
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
            180   185   190
Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp
        195   200   205
His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr
    210   215   220
Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro
225   230   235   240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245   250   255

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Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp
            260                 265                 270
Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val
    290                 295                 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys
                325                 330                 335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350
Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys
                405                 410                 415
Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
        435                 440                 445
Lys
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<210> 102
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 13,14,15,15-7,15-8 Full length heavy chain

<400> 102

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

<210> 103
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal leader sequence for expressing heavy chains

<400> 103
Met Ala Trp Val Trp Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser
1 5 10 15
Ile Gln Ala

<210> 104
<211> 1401
<212> DNA
<213> Artificial Sequence

<220>
<223> Full length IgG4 Heavy chains of Candidate 15EVQ
with leader sequence

<400> 104
atggcttggg tgtggacctt gctattcctg atggcagctg cccaaagtat ccaagcagag 60
gtgcagctgg tgcagagcgg cgccgaggtg aagaagcccg gcgagagcct gaagatcagc 120
tgcaagggca gcggctacag cttcaccaac tactgggtgg gctgggtgcg ccagatgccc 180
ggcaagggcc tggagtggat gggcttcatc gaccccagcg acagctacac caactacgcg 240
cctagcttcc agggccaggt gaccatcagc gccgacaaga gcatcagcac cgcctacctg 300
cagtggagca gcctgaaggc cagcgacacc gccatgtact actgcgcccg cgagctgtac 360
cagggctaca tggacacgtt cgacagctgg ggccagggca ccctggtgac cgtgagcagc 420
gcttccacca agggcccatc cgtcttcccc ctggcgccct gctccaggag cacctccgag 480
agcacagccg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 540
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 600
ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacgaaaacc 660
tacacctgca acgtagatca caagcccagc aacaccaagg tggacaagag agttgagtcc 720
aaatatggtc ccccatgccc accatgccca gcacctgagg ccgccggggg accatcagtc 780
ttcctgttcc ccccaaaacc caaggacact ctcatgatct cccggacccc tgaggtcacg 840

tgcgtggtgg tggacgtgag ccaggaagac cccgaggtcc agttcaactg gtacgtggat 900
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagttcaa cagcacgtac 960
cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaacggcaa ggagtacaag 1020
tgcaaggtct ccaacaaagg cctcccgtcc tccatcgaga aaaccatctc caaagccaaa 1080
gggcagcccc gagagccaca ggtgtacacc ctgcccccat cccaggagga gatgaccaag 1140
aaccaggtca gcctgacctg cctggtcaaa ggcttctacc ccagcgacat cgccgtggag 1200
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 1260
gacggctcct tcttcctcta cagcaggcta accgtggaca agagcaggtg gcaggagggg 1320
aatgtcttct catgctccgt gatgcatgag gctctgcaca accactacac acagaagagc 1380
ctctccctgt ctctgggtaa a 1401

<210> 105
<211> 1344
<212> DNA
<213> Artificial Sequence

<220>
<223> IgG4 Heavy chains of Candidate 15EVQ without
leader sequence

<400> 105
gaggtgcagc tggtgcagag cggcgccgag gtgaagaagc ccggcgagag cctgaagatc 60
agctgcaagg gcagcggcta cagcttcacc aactactggg tgggctgggt gcgccagatg 120
cccggcaagg gcctggagtg gatgggcttc atcgacccca gcgacagcta caccaactac 180
gcgcctagct tccagggcca ggtgaccatc agcgccgaca agagcatcag caccgcctac 240
ctgcagtgga gcagcctgaa ggccagcgac accgccatgt actactgcgc ccgcgagctg 300
taccagggct acatggacac gttcgacagc tggggccagg gcaccctggt gaccgtgagc 360
agcgcttcca ccaagggccc atccgtcttc cccctggcgc cctgctccag gagcacctcc 420
gagagcacag ccgccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540
tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacgaaa 600
acctacacct gcaacgtaga tcacaagccc agcaacacca aggtggacaa gagagttgag 660
tccaaatatg gtcccccatg cccaccatgc ccagcacctg aggccgccgg gggaccatca 720
gtcttcctgt tcccccccaaa acccaaggac actctcatga tctcccggac ccctgaggtc 780
acgtgcgtgg tggtggacgt gagccaggaa gaccccgagg tccagttcaa ctggtacgtg 840
gatggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagtt caacagcacg 900
taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaacgg caaggagtac 960
aagtgcaagg tctccaacaa aggcctcccg tcctccatcg agaaaaccat ctccaaagcc 1020
aaagggcagc cccgagagcc acaggtgtac accctgcccc catcccagga ggagatgacc 1080
aagaaccagg tcagcctgac ctgcctggtc aaaggcttct accccagcga catcgccgtg 1140
gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200
tccgacggct ccttcttcct ctacagcagg ctaaccgtgg acaagagcag gtggcaggag 1260
gggaatgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacacagaag 1320
agcctctccc tgtctctggg taaa 1344

<210> 106
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> N-termina leader sequence for expressing light chains

<400> 106
Met Gly Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr
 1   5   10   15
Asp Ala Arg Cys
            20

<210> 107
<211> 702
<212> DNA
<213> Artificial Sequence

<220>
<223> Full length light chain of Candidate 15 with
leader sequence

<400> 107
atgggtgtgc caactcaggt attaggatta ctgctgctgt ggcttacaga tgcaagatgt 60
gacatccaga tgacccagag ccccagcagc ctgagcgcca gcgtgggcga ccgcgtgacc 120
atcacctgcc gcgccagcca gagcatcggc ctgtacctgg cctggtacca gcagaagccc 180
ggcaaggccc ccaagctgct gatctacgcc gccagcagcc tgcagagcgg cgtgcccagc 240
cgcttcagcg gcagcggcag cggcaccgac ttcaccctga ccatcagcag cctgcagccc 300
gaggacttcg ccacctacta ctgccagcag ggcaacaccc tgagctacac cttcggccag 360
ggcaccaagg tggagatcaa gcgtacggtg 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 gt 702

<210> 108
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> Light chain of Candidate 15 without leader
sequence (starts DIQ)

<400> 108
gacatccaga tgacccagag ccccagcagc ctgagcgcca gcgtgggcga ccgcgtgacc 60
atcacctgcc gcgccagcca gagcatcggc ctgtacctgg cctggtacca gcagaagccc 120
ggcaaggccc ccaagctgct gatctacgcc gccagcagcc tgcagagcgg cgtgcccagc 180
cgcttcagcg gcagcggcag cggcaccgac ttcaccctga ccatcagcag cctgcagccc 240
gaggacttcg ccacctacta ctgccagcag ggcaacaccc tgagctacac cttcggccag 300
ggcaccaagg tggagatcaa gcgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 109
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidates 15, 15-1, 15-2, 15-3, 15-4, 15-5, 15-6, 15-9 LCDR1 composite
sequence

<400> 109
Arg Ala Ser Gln Ser Ile Gly Leu Tyr Leu Ala
1 5 10

<210> 110
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidates 15, 15-1 ┬ 15-9 LCDR2

<400> 110
Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 111
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidates 15, 15-1, 15-4, 15-7, 15-8 HCDR1 composite sequence

<400> 111
Gly Tyr Ser Phe Thr Asn Tyr Trp Val Gly
 1   5   10

<210> 112
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidates 15, 15-2, 15-3, 15-6, 15-7, 15-8 HCDR2 composite sequence

<400> 112
Phe Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Ala Pro Ser Phe Gln
 1   5   10   15
Gly

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

<220>
<223> Candidates 15, 15-1 ┬ 15-9 LCDR3 conmposite sequence

<400> 113
Gln Gln Gly Asn Thr Leu Ser Tyr Thr
 1   5

<210> 114
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidates 15-1 HCDR2

<400> 114
Arg Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Ala Pro Ser Phe Gln
 1   5   10   15
Gly

<210> 115
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidates 15-2 HCDR1

<400> 115
Gly Tyr Ser Phe Thr Asn Tyr Trp Ile Gly
 1   5   10

<210> 116
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidates 15-3, 15-5, 15-6, 15-9 HCDR1

<400> 116
Gly Tyr Ser Phe Thr Asn Tyr Trp Ile Ser
 1   5   10

<210> 117
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidates 15-4 HCDR2

<400> 117
Phe Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Ser Pro Ser Phe Gln
 1   5   10   15
Gly

<210> 118
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidates 15-5, 15-9 HCDR2

<400> 118
Arg Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Ser Pro Ser Phe Gln
 1   5   10   15
Gly

<210> 119
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidates 15-6, 15-9 HCDR3

<400> 119
Ala Arg Gln Leu Tyr Gln Gly Tyr Met Asp Thr Phe Asp Ser
 1   5   10

<210> 120
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidates 15-7 LCDR1

<400> 120
Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Ala

1 5 10

<210> 121
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidates 15-8 LCDR1

<400> 121
Arg Ala Ser Gln Ser Ile Gly Leu Tyr Leu Asn
1 5 10

<210> 122
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidates 15-7 VL

<400> 122
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 Ser Tyr
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Ser Tyr
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 123
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidates 15-8 VL

<400> 123
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 Gly Leu Tyr
20 25 30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Ser Tyr
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 124
<211> 121

<212> PRT
<213> Artificial Sequence

<220>
<223> Candidates 15-1 VH

<400> 124
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1   5   10   15
Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Asn Tyr
            20   25   30
Trp Val Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
        35   40   45
Gly Arg Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Ala Pro Ser Phe
    50   55   60
Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65   70   75   80
Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
                85   90   95
Ala Arg Glu Leu Tyr Gln Gly Tyr Met Asp Thr Phe Asp Ser Trp Gly
            100   105   110
Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 125
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 15-2 VH

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

<210> 126
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 15-3 VH

<400> 126
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1   5   10   15
Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Asn Tyr
            20   25   30
Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
        35   40   45

Gly Phe Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Ala Pro Ser Phe
50 55 60
Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80
Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95
Ala Arg Glu Leu Tyr Gln Gly Tyr Met Asp Thr Phe Asp Ser Trp Gly
100 105 110
Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 127
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 15-4 VH

<400> 127
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15
Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Asn Tyr
20 25 30
Trp Val Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45
Gly Phe Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Ser Pro Ser Phe
50 55 60
Gln Gly His Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80
Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95
Ala Arg Glu Leu Tyr Gln Gly Tyr Met Asp Thr Phe Asp Ser Trp Gly
100 105 110
Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 128
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 15-5 VH

<400> 128
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15
Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Asn Tyr
20 25 30
Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45
Gly Arg Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Ser Pro Ser Phe
50 55 60
Gln Gly His Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80
Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95
Ala Arg Glu Leu Tyr Gln Gly Tyr Met Asp Thr Phe Asp Ser Trp Gly
100 105 110
Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 129
<211> 121

<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 15-6 VH

<400> 129
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1   5   10   15
Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Asn Tyr
            20   25   30
Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
        35   40   45
Gly Phe Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Ala Pro Ser Phe
    50   55   60
Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65   70   75   80
Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
                85   90   95
Ala Arg Gln Leu Tyr Gln Gly Tyr Met Asp Thr Phe Asp Ser Trp Gly
            100   105   110
Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 130
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 15-1 full length heavy chain

<400> 130
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1   5   10   15
Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Asn Tyr
            20   25   30
Trp Val Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
        35   40   45
Gly Arg Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Ala Pro Ser Phe
    50   55   60
Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65   70   75   80
Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
                85   90   95
Ala Arg Glu Leu Tyr Gln Gly Tyr Met Asp Thr Phe Asp Ser Trp Gly
            100   105   110
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
        115   120   125
Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
    130   135   140
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145   150   155   160
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165   170   175
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180   185   190
Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His
        195   200   205
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly
    210   215   220
Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser
225   230   235   240
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245   250   255
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro
            260   265   270

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

<210> 131
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 15-2 full length heavy chain

<400> 131
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1   5   10   15
Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Asn Tyr
            20   25   30
Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
        35   40   45
Gly Phe Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Ala Pro Ser Phe
    50   55   60
Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65   70   75   80
Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
                85   90   95
Ala Arg Glu Leu Tyr Gln Gly Tyr Met Asp Thr Phe Asp Ser Trp Gly
            100   105   110
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
        115   120   125
Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
    130   135   140
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145   150   155   160
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165   170   175
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180   185   190
Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His
        195   200   205
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly
    210   215   220
Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser
225   230   235   240
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245   250   255
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro
            260   265   270
Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala

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

<210> 132
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 15-3 full length heavy chain

<400> 132
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15
Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Asn Tyr
20 25 30
Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45
Gly Phe Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Ala Pro Ser Phe
50 55 60
Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80
Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95
Ala Arg Glu Leu Tyr Gln Gly Tyr Met Asp Thr Phe Asp Ser Trp Gly
100 105 110
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125
Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
130 135 140
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190
Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His
195 200 205
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly
210 215 220
Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser
225 230 235 240
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro
260 265 270
Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val
290 295 300
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320
Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr
325 330 335
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
340 345 350
Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser
405 410 415
Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 133
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 15-4 full length heavy chain

<400> 133
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15
Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Asn Tyr
20 25 30
Trp Val Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45
Gly Phe Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Ser Pro Ser Phe
50 55 60
Gln Gly His Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80
Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95
Ala Arg Glu Leu Tyr Gln Gly Tyr Met Asp Thr Phe Asp Ser Trp Gly
100 105 110
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125
Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
130 135 140
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190
Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His
195 200 205
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly
210 215 220
Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser
225 230 235 240
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro
260 265 270
Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285
Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val

290 295 300
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320
Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr
325 330 335
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
340 345 350
Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser
405 410 415
Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 134
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 15-5 full length heavy chain

<400> 134
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15
Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Asn Tyr
20 25 30
Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45
Gly Arg Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Ser Pro Ser Phe
50 55 60
Gln Gly His Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80
Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95
Ala Arg Glu Leu Tyr Gln Gly Tyr Met Asp Thr Phe Asp Ser Trp Gly
100 105 110
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125
Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
130 135 140
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190
Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His
195 200 205
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly
210 215 220
Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser
225 230 235 240
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro
260 265 270
Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285
Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val
290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320
Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr
325 330 335
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
340 345 350
Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser
405 410 415
Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 135
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 15-6 full length heavy chain

<400> 135
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15
Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Asn Tyr
20 25 30
Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45
Gly Phe Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Ala Pro Ser Phe
50 55 60
Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80
Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95
Ala Arg Gln Leu Tyr Gln Gly Tyr Met Asp Thr Phe Asp Ser Trp Gly
100 105 110
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125
Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
130 135 140
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190
Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His
195 200 205
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly
210 215 220
Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser
225 230 235 240
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro
260 265 270
Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285
Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val
290 295 300
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr

305 310 315 320
Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr
325 330 335
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
340 345 350
Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser
405 410 415
Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 136
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 136
ccttacccat aatcaactcg agagattacc agccgccaac 40

<210> 137
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 137
caagagcttc tattatcaaa caatgagatt caagcgctaa aaagtgaag 49

<210> 138
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 138
ccttacacat actcaaccta accgagaata aaatctcaaa aatag 45

<210> 139
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 139
gaaatctatc tttcctacaa cgaggccctg cagctgacta ggaactc 47

<210> 140
<211> 58
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 140
gccttcaacg actgatgctc gaggaggtgg cccttgagaa tgtggatagc tctccttc 58

<210> 141
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 141
gtacctgcag ctgtctacga gctcctttgc cttggtccc 39

<210> 142
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 142
gcctggagtg gatgggccgg atcgacccca gcg 33

<210> 143
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 143
cgctggggtc gatccggccc atccactcca ggc 33

<210> 144
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 144
agaggtaact cccgttgcgg 20

<210> 145
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 145
gcatctggcg cacccagccg atccagtagt tggtgaag 38

<210> 146
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 146
agaggtaact cccgttgcgg 20

<210> 147
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 147
gcatctggcg cacccagctg atccagtagt tggtgaag 38

<210> 148
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 148
cgctgatggt cacgtggccc tggaagctag ggctgtagtt ggtgtag 47

<210> 149
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 149
cttcaccaac tactggatca gctgggtgcg ccagatgc 38

<210> 150
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 150
cgccatgtac tactgcgccc gccagctgta ccagggctac 40

<210> 151
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 151
gtagccctgg tacagctggc gggcgcagta gtacatggcg 40

<210> 152
<211> 40
<212> DNA
<213> Homo sapiens

<400> 152
gccagccaga gcatcagcag ctacctggcc tggtaccagc 40

<210> 153

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

<220>
<223> Primer

<400> 153
gctggtacca ggccaggtag ctgctgatgc tctggctggc 40

<210> 154
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 154
cgggcttctg ctggtaccag ttcaggtagc tgctgatgct ctg 43

<210> 155
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 14 full length light chain

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

<210> 156
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 15, 15-1, 15-2, 15-3, 15-4, 15-5, 15-6, 15-9 full length light chain

<400> 156
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 Gly Leu Tyr
            20   25   30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Ser Tyr
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100   105   110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115   120   125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130   135   140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145   150   155   160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165   170   175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180   185   190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195   200   205
Phe Asn Arg Gly Glu Cys
    210

<210> 157
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 15-7 full length light cahin

<400> 157
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 Ser Tyr
            20   25   30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Ser Tyr
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100   105   110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115   120   125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130   135   140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145   150   155   160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165   170   175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180   185   190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195   200   205
Phe Asn Arg Gly Glu Cys

210

<210> 158
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 15-8 full length light chain

<400> 158
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 Gly Leu Tyr
20 25 30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Ser Tyr
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205
Phe Asn Arg Gly Glu Cys
210

<210> 159
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 15-9 VH

<400> 159
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15
Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Asn Tyr
20 25 30
Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45
Gly Arg Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Ser Pro Ser Phe
50 55 60
Gln Gly His Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80
Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95
Ala Arg Gln Leu Tyr Gln Gly Tyr Met Asp Thr Phe Asp Ser Trp Gly
100 105 110
Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 160
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 15-9 full length heavy chain

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

<210> 161
<211> 2718
<212> DNA
<213> Mus musculus

<400> 161
atgaaagggt gttcctctta tctaatgtac tcctttgggg gacttttgtc cctatggatt 60
cttctggtgt cttccacaaa ccaatgcact gtgagataca acgtagctga ctgcagccat 120
ttgaagctaa cacacatacc tgatgatctt ccctctaaca taacagtgtt gaatcttact 180
cacaaccaac tcagaagatt accacctacc aactttacaa gatacagcca acttgctatc 240
ttggatgcag gatttaactc catttcaaaa ctggagccag aactgtgcca aatactccct 300
ttgttgaaag tattgaacct gcaacataat gagctctctc agatttctga tcaaaccttt 360
gtcttctgca cgaacctgac agaactcgat ctaatgtcta actcaataca caaaattaaa 420
agcaaccctt tcaaaaacca gaagaatcta atcaaattag atttgtctca taatggttta 480
tcatctacaa agttgggaac gggggtccaa ctggagaacc tccaagaact gctcttagca 540
aaaaataaaa tccttgcgtt gcgaagtgaa gaacttgagt ttcttggcaa ttcttcttta 600
cgaaagttgg acttgtcatc aaatccactt aaagagttct ccccggggtg tttccagaca 660
attggcaagt tattcgccct cctcttgaac aacgcccaac tgaaccccca cctcacagag 720
aagctttgct gggaactttc aaacacaagc atccagaatc tctctctggc taacaaccag 780
ctgctggcca ccagcgagag cactttctct gggctgaagt ggacaaatct cacccagctc 840
gatctttcct acaacaacct ccatgatgtc ggcaacggtt ccttctccta tctcccaagc 900
ctgaggtatc tgtctctgga gtacaacaat atacagcgtc tgtcccctcg ctctttttat 960
ggactctcca acctgaggta cctgagtttg aagcgagcat ttactaagca aagtgtttca 1020
cttgcttcac atcccaacat tgacgatttt tcctttcaat ggttaaaata tttggaatat 1080
ctcaacatgg atgacaataa tattccaagt accaaaagca ataccttcac gggattggtg 1140
agtctgaagt acctaagtct ttccaaaact ttcacaagtt tgcaaacttt aacaaatgaa 1200
acatttgtgt cacttgctca ttctcccttg ctcactctca acttaacgaa aaatcacatc 1260
tcaaaaatag caaatggtac tttctcttgg ttaggccaac tcaggatact tgatctcggc 1320
cttaatgaaa ttgaacaaaa actcagcggc caggaatgga gaggtctgag aaatatattt 1380
gagatctacc tatcctataa caaatacctc caactgtcta ccagttcctt tgcattggtc 1440
cccagccttc aaagactgat gctcaggagg gtggccctta aaaatgtgga tatctcccct 1500
tcacctttcc gccctcttcg taacttgacc attctggact taagcaacaa caacatagcc 1560
aacataaatg aggacttgct ggagggtctt gagaatctag aaatcctgga ttttcagcac 1620
aataacttag ccaggctctg gaaacgcgca aaccccggtg gtcccgttaa tttcctgaag 1680
gggctgtctc acctccacat cttgaattta gagtccaacg gcttagatga aatcccagtc 1740
ggggttttca agaacttatt cgaactaaag agcatcaatc taggactgaa taacttaaac 1800
aaacttgaac cattcatttt tgatgaccag acatctctaa ggtcactgaa cctccagaag 1860
aacctcataa catctgttga gaaggatgtt ttcgggccgc cttttcaaaa cctgaacagt 1920
ttagatatgc gcttcaatcc gttcgactgc acgtgtgaaa gtatttcctg gtttgttaac 1980
tggatcaacc agacccacac taatatctct gagctgtcca ctcactacct ctgtaacact 2040
ccacatcatt attatggctt ccccctgaag cttttcgata catcatcctg taaagacagc 2100
gccccctttg aactcctctt cataatcagc accagtatgc tcctggtttt tatacttgtg 2160
gtactgctca ttcacatcga gggctggagg atctcttttt actggaatgt ttcagtgcat 2220
cggattcttg gtttcaagga aatagacaca caggctgagc agtttgaata tacagcctac 2280
ataattcatg cccataaaga cagagactgg gtctgggaac atttctcccc aatggaagaa 2340
caagaccaat ctctcaaatt ttgcctagaa gaaagggact ttgaagcagg cgtccttgga 2400
cttgaagcaa ttgttaatag catcaaaaga agccgaaaaa tcattttcgt tatcacacac 2460
catttattaa aagaccctct gtgcagaaga ttcaaggtac atcacgcagt tcagcaagct 2520
attgagcaaa atctggattc aattatactg atttttctcc agaatattcc agattataaa 2580
ctaaaccatg cactctgttt gcgaagagga atgtttaaat ctcattgcat cttgaactgg 2640
ccagttcaga aagaacggat aaatgccttt catcataaat tgcaagtagc acttggatct 2700
cggaattcag cacattaa 2718

<210> 162
<211> 905
<212> PRT
<213> Mus musculus

<400> 162
Met Lys Gly Cys Ser Ser Tyr Leu Met Tyr Ser Phe Gly Gly Leu Leu
 1   5   10   15
Ser Leu Trp Ile Leu Leu Val Ser Ser Thr Asn Gln Cys Thr Val Arg
            20   25   30
Tyr Asn Val Ala Asp Cys Ser His Leu Lys Leu Thr His Ile Pro Asp
        35   40   45
Asp Leu Pro Ser Asn Ile Thr Val Leu Asn Leu Thr His Asn Gln Leu
    50   55   60
Arg Arg Leu Pro Pro Thr Asn Phe Thr Arg Tyr Ser Gln Leu Ala Ile

65 70 75 80
Leu Asp Ala Gly Phe Asn Ser Ile Ser Lys Leu Glu Pro Glu Leu Cys
85 90 95
Gln Ile Leu Pro Leu Leu Lys Val Leu Asn Leu Gln His Asn Glu Leu
100 105 110
Ser Gln Ile Ser Asp Gln Thr Phe Val Phe Cys Thr Asn Leu Thr Glu
115 120 125
Leu Asp Leu Met Ser Asn Ser Ile His Lys Ile Lys Ser Asn Pro Phe
130 135 140
Lys Asn Gln Lys Asn Leu Ile Lys Leu Asp Leu Ser His Asn Gly Leu
145 150 155 160
Ser Ser Thr Lys Leu Gly Thr Gly Val Gln Leu Glu Asn Leu Gln Glu
165 170 175
Leu Leu Leu Ala Lys Asn Lys Ile Leu Ala Leu Arg Ser Glu Glu Leu
180 185 190
Glu Phe Leu Gly Asn Ser Ser Leu Arg Lys Leu Asp Leu Ser Ser Asn
195 200 205
Pro Leu Lys Glu Phe Ser Pro Gly Cys Phe Gln Thr Ile Gly Lys Leu
210 215 220
Phe Ala Leu Leu Leu Asn Asn Ala Gln Leu Asn Pro His Leu Thr Glu
225 230 235 240
Lys Leu Cys Trp Glu Leu Ser Asn Thr Ser Ile Gln Asn Leu Ser Leu
245 250 255
Ala Asn Asn Gln Leu Leu Ala Thr Ser Glu Ser Thr Phe Ser Gly Leu
260 265 270
Lys Trp Thr Asn Leu Thr Gln Leu Asp Leu Ser Tyr Asn Asn Leu His
275 280 285
Asp Val Gly Asn Gly Ser Phe Ser Tyr Leu Pro Ser Leu Arg Tyr Leu
290 295 300
Ser Leu Glu Tyr Asn Asn Ile Gln Arg Leu Ser Pro Arg Ser Phe Tyr
305 310 315 320
Gly Leu Ser Asn Leu Arg Tyr Leu Ser Leu Lys Arg Ala Phe Thr Lys
325 330 335
Gln Ser Val Ser Leu Ala Ser His Pro Asn Ile Asp Asp Phe Ser Phe
340 345 350
Gln Trp Leu Lys Tyr Leu Glu Tyr Leu Asn Met Asp Asp Asn Asn Ile
355 360 365
Pro Ser Thr Lys Ser Asn Thr Phe Thr Gly Leu Val Ser Leu Lys Tyr
370 375 380
Leu Ser Leu Ser Lys Thr Phe Thr Ser Leu Gln Thr Leu Thr Asn Glu
385 390 395 400
Thr Phe Val Ser Leu Ala His Ser Pro Leu Leu Thr Leu Asn Leu Thr
405 410 415
Lys Asn His Ile Ser Lys Ile Ala Asn Gly Thr Phe Ser Trp Leu Gly
420 425 430
Gln Leu Arg Ile Leu Asp Leu Gly Leu Asn Glu Ile Glu Gln Lys Leu
435 440 445
Ser Gly Gln Glu Trp Arg Gly Leu Arg Asn Ile Phe Glu Ile Tyr Leu
450 455 460
Ser Tyr Asn Lys Tyr Leu Gln Leu Ser Thr Ser Ser Phe Ala Leu Val
465 470 475 480
Pro Ser Leu Gln Arg Leu Met Leu Arg Arg Val Ala Leu Lys Asn Val
485 490 495
Asp Ile Ser Pro Ser Pro Phe Arg Pro Leu Arg Asn Leu Thr Ile Leu
500 505 510
Asp Leu Ser Asn Asn Asn Ile Ala Asn Ile Asn Glu Asp Leu Leu Glu
515 520 525
Gly Leu Glu Asn Leu Glu Ile Leu Asp Phe Gln His Asn Asn Leu Ala
530 535 540
Arg Leu Trp Lys Arg Ala Asn Pro Gly Gly Pro Val Asn Phe Leu Lys
545 550 555 560
Gly Leu Ser His Leu His Ile Leu Asn Leu Glu Ser Asn Gly Leu Asp
565 570 575
Glu Ile Pro Val Gly Val Phe Lys Asn Leu Phe Glu Leu Lys Ser Ile
580 585 590
Asn Leu Gly Leu Asn Asn Leu Asn Lys Leu Glu Pro Phe Ile Phe Asp
595 600 605
Asp Gln Thr Ser Leu Arg Ser Leu Asn Leu Gln Lys Asn Leu Ile Thr

610 615 620
Ser Val Glu Lys Asp Val Phe Gly Pro Pro Phe Gln Asn Leu Asn Ser
625 630 635 640
Leu Asp Met Arg Phe Asn Pro Phe Asp Cys Thr Cys Glu Ser Ile Ser
645 650 655
Trp Phe Val Asn Trp Ile Asn Gln Thr His Thr Asn Ile Ser Glu Leu
660 665 670
Ser Thr His Tyr Leu Cys Asn Thr Pro His His Tyr Tyr Gly Phe Pro
675 680 685
Leu Lys Leu Phe Asp Thr Ser Ser Cys Lys Asp Ser Ala Pro Phe Glu
690 695 700
Leu Leu Phe Ile Ile Ser Thr Ser Met Leu Leu Val Phe Ile Leu Val
705 710 715 720
Val Leu Leu Ile His Ile Glu Gly Trp Arg Ile Ser Phe Tyr Trp Asn
725 730 735
Val Ser Val His Arg Ile Leu Gly Phe Lys Glu Ile Asp Thr Gln Ala
740 745 750
Glu Gln Phe Glu Tyr Thr Ala Tyr Ile Ile His Ala His Lys Asp Arg
755 760 765
Asp Trp Val Trp Glu His Phe Ser Pro Met Glu Glu Gln Asp Gln Ser
770 775 780
Leu Lys Phe Cys Leu Glu Glu Arg Asp Phe Glu Ala Gly Val Leu Gly
785 790 795 800
Leu Glu Ala Ile Val Asn Ser Ile Lys Arg Ser Arg Lys Ile Ile Phe
805 810 815
Val Ile Thr His His Leu Leu Lys Asp Pro Leu Cys Arg Arg Phe Lys
820 825 830
Val His His Ala Val Gln Gln Ala Ile Glu Gln Asn Leu Asp Ser Ile
835 840 845
Ile Leu Ile Phe Leu Gln Asn Ile Pro Asp Tyr Lys Leu Asn His Ala
850 855 860
Leu Cys Leu Arg Arg Gly Met Phe Lys Ser His Cys Ile Leu Asn Trp
865 870 875 880
Pro Val Gln Lys Glu Arg Ile Asn Ala Phe His His Lys Leu Gln Val
885 890 895
Ala Leu Gly Ser Arg Asn Ser Ala His
900 905

<210> 163
<211> 107
<212> PRT
<213> Rattus rattus

<400> 163
Asp Ile Gln Met Thr Gln Ser Pro Thr Ser Leu Ser Ala Ser Leu Gly
1 5 10 15
Glu Thr Val Thr Ile Glu Cys Arg Ala Ser Glu Asp Ile Tyr Asn Gly
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Gln Leu Leu Ile
35 40 45
Tyr Asp Ser Asn Ser Leu His Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Arg Gly Ser Gly Thr Gln Tyr Ser Leu Arg Ile Asn Ser Leu Gln Ser
65 70 75 80
Glu Asp Val Ala Ser Tyr Phe Cys Gln Gln Tyr Tyr Asp Tyr Pro Leu
85 90 95
Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 164
<211> 119
<212> PRT
<213> Rattus rattus

<400> 164
Glu Val Gln Leu Val Ala Ser Gly Gly Gly Leu Val Lys Pro Gly Ala

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

<210> 165
<211> 234
<212> PRT
<213> Artificial Sequence

<220>
<223> Hybrid of rat variable region and mouse constant region

<400> 165

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Met Gly Val Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp Ile Thr
 1               5                  10                  15
Asp Ala Ile Cys Asp Ile Gln Met Thr Gln Ser Pro Thr Ser Leu Ser
            20                  25                  30
Ala Ser Leu Gly Glu Thr Val Thr Ile Glu Cys Arg Ala Ser Glu Asp
        35                  40                  45
Ile Tyr Asn Gly Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro
    50                  55                  60
Gln Leu Leu Ile Tyr Asp Ser Asn Ser Leu His Thr Gly Val Pro Ser
65                  70                  75                  80
Arg Phe Ser Gly Arg Gly Ser Gly Thr Gln Tyr Ser Leu Arg Ile Asn
                85                  90                  95
Ser Leu Gln Ser Glu Asp Val Ala Ser Tyr Phe Cys Gln Gln Tyr Tyr
            100                 105                 110
Asp Tyr Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile 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
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<210> 166
<211> 462
<212> PRT
<213> Artificial Sequence

<220>
<223> Hybrid of rat variable region and mouse constant region

<400> 166
Met Lys Leu Arg Leu Ser Leu Ile Phe Ile Cys Ala Leu Leu Lys Asp
 1   5   10   15
Val Gln Cys Glu Val Gln Leu Val Ala Ser Gly Gly Gly Leu Val Lys
            20   25   30
Pro Gly Ala Ser Leu Lys Leu Ser Cys Val Ala Ser Gly Phe Thr Phe
        35   40   45
Ser Asp Tyr Trp Met Ala Trp Val Arg Gln Thr Pro Gly Lys Pro Met
    50   55   60
Glu Tyr Ile Gly Asp Ile Lys Ser Asp Gly Ser Lys Val Asn Tyr Ala
65   70   75   80
Pro Ser Leu Lys Asn Arg Phe Thr Ile Ser Arg Asp Asn Ala Arg Thr
                85   90   95
Thr Leu Tyr Leu Gln Met Ser Asn Val Arg Ser Glu Asp Thr Ala Thr
            100   105   110
Tyr Tyr Cys Asn Arg Asp Ile Gly Pro Asp Trp Tyr Phe Asp Phe Trp
        115   120   125
Gly Pro Gly Thr Met Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro
    130   135   140
Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met
145   150   155   160
Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr
                165   170   175
Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro
            180   185   190
Ala Val Leu Glu Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val
        195   200   205
Pro Ser Ser Pro Arg Pro Ser Glu Thr Val Thr Cys Asn Val Ala His
    210   215   220
Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys
225   230   235   240
Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe
                245   250   255
Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro
            260   265   270
Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val
        275   280   285
Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr
    290   295   300
Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu
305   310   315   320
Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys
                325   330   335
Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser
            340   345   350
Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro
        355   360   365
Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile
    370   375   380
Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly
385   390   395   400
Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asn Thr Asn
                405   410   415
Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp
            420   425   430
Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His
        435   440   445
Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
    450   455   460

<210> 167
<211> 234
<212> PRT
<213> Rattus rattus

<400> 167
Met Gly Val Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp Ile Thr

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 1               5                  10                  15
Asp Ala Ile Cys Asp Ile Gln Met Thr Gln Ser Pro Thr Ser Leu Ser
            20                  25                  30
Ala Ser Leu Gly Glu Thr Val Thr Ile Glu Cys Arg Ala Ser Glu Asp
        35                  40                  45
Ile Tyr Asn Gly Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro
    50                  55                  60
Gln Leu Leu Ile Tyr Asp Ser Asn Ser Leu His Thr Gly Val Pro Ser
65                  70                  75                  80
Arg Phe Ser Gly Arg Gly Ser Gly Thr Gln Tyr Ser Leu Arg Ile Asn
                85                  90                  95
Ser Leu Gln Ser Glu Asp Val Ala Ser Tyr Phe Cys Gln Gln Tyr Tyr
            100                 105                 110
Asp Tyr Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile 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
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<210> 168
<211> 462
<212> PRT
<213> Rattus rattus

<400> 168

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

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

<210> 169
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide for mutagenesis for TLR3

<400> 169
gaagaactgg atatctttgc cgcttcatct ttaaaaaaat tagagttg 48

<210> 170
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide for mutagenesis for TLR3 variant

<400> 170
gtcatctaca aaattaggaa ctgcggttca gctggaaaat ctcc 44

<210> 171
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide for mutagenesis for TLR3 variant

<400> 171
ctcataatgg cttgtcatct acagaattag gaactcaggt tcagc 45

<210> 172
<211> 57
<212> DNA
<213> Artificial Sequence

<220>

<223> Oligonucleotide for mutagenesis for TLR3 variant

<400> 172
gaaaattaaa aataatccct ttgtcaagca ggagaattta atcacattag atctgtc 57

<210> 173
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide for mutagenesis for TLR3 variant

<400> 173
gaaaattaaa aataatccct ttgtcgagca gaagaattta atcacattag 50

<210> 174
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide for mutagenesis for TLR3 variant

<400> 174
cagaaaatta aaaataatcc ctttgcaaag cagaagaatt taatcacatt ag 52

<210> 175
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide for mutagenesis for TLR3 variant

<400> 175
ccaactcaat ccagaaaatt aaagctaatc cctttgtcaa gcagaag 47

<210> 176
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide for mutagenesis for TLR3 variant

<400> 176
caatgagcta tctcaacttt ctcgtaaaac ctttgccttc tgcac 45

<210> 177
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide for mutagenesis for TLR3 variant

<400> 177
gtcttgagaa actagaaatt ctcaagttgc agcataacaa cttagcac 48

<210> 178
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide for mutagenesis for TLR3 variant

<400> 178
cttgagaaac tagaaattct cgcattgcag cataacaact tagcac 46

<210> 179
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide for mutagenesis for TLR3 variant

<400> 179
ctaaagtcat tgaaccttca ggagaatctc ataacatccg ttg 43

<210> 180
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide for mutagenesis for TLR3 variant

<400> 180
ctctaaagtc attgaacctt caggcgaatc tcataacatc cgttgag 47

<210> 181
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide for mutagenesis for TLR3 variant

<400> 181
ccacatcctt aacttgaggt ccaacggctt tgacgag 37

<210> 182
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide for mutagenesis for TLR3 variant

<400> 182
gaaattctcg atttgcagca taacgcctta gcacggctct ggaaac 46

<210> 183
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide for mutagenesis for TLR3 variant

<400> 183
gagaaactag aaattctcga tttggcgcat aacaacttag cacggc 46

<210> 184
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide for mutagenesis for TLR3 variant

<400> 184
ctagaaattc tcgatttgca ggaaaacaac ttagcacggc tctg 44

<210> 185
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide for mutagenesis for TLR3 variant

<400> 185
ctagaaattc tcgatttgca ggctaacaac ttagcacggc tctg 44

<210> 186
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide for mutagenesis for TLR3 variant

<400> 186
cattctggat ctaagcaaca acgccatagc caacataaat gatgac 46

<210> 187
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide for mutagenesis for TLR3 variant

<400> 187
gaaaatattt tcgaaatcta tctttccgcc aacaagtacc tgcagctgac 50

<210> 188
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide for mutagenesis for TLR3 variant

<400> 188
gccttcaacg actgatgctg aaagggtggc ccttaaaaat g 41

<210> 189
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide for mutagenesis for TLR3 variant

<400> 189
cttcaacgac tgatgctccg agaggtggcc cttaaaaatg tgg 43

<210> 190
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide for mutagenesis for TLR3 variant

<400> 190
cgaaatctat ctttcctaca acgagtacct gcagctgact ag 42

<210> 191

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

<220>
<223> Consensus sequence for family 17 LCDR3

<220>
<221> misc_feature
<222> (1)
<223> Wherein Xaa can be Ala, Gln, Gly or Ser

<220>
<221> misc_feature
<222> (5)
<223> Wherein Xaa can be Gly, Glu or Ser

<220>
<221> misc_feature
<222> (6)
<223> Wherein Xaa can be Asp or Asn

<220>
<221> misc_feature
<222> (7)
<223> Wherein Xaa and be Glu or Ser

<220>
<221> misc_feature
<222> (8)
<223> Wherein Xaa can be Phe, Ala or Leu

<400> 191
Xaa Ser Tyr Asp Xaa Xaa Xaa Xaa Thr Val
 1   5   10

<210> 192
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence for family 17 HCDR2

<220>
<221> misc_feature
<222> (1)
<223> Wherein Xaa can be Arg or Lys

<220>
<221> misc_feature
<222> (3)
<223> Wherein Xaa can be Tyr, His or Ser

<220>
<221> misc_feature
<222> (4)
<223> Wherein Xaa can be Met, Arg or Tyr

<220>
<221> misc_feature
<222> (7)
<223> Wherein Xaa can be Lys or Arg

<400> 192
Xaa Ile Xaa Xaa Arg Ser Xaa Trp Tyr Asn Asp Tyr Ala Val Ser Val

 1   5   10   15
Lys Ser

<210> 193
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence for family 18B LCDR3

<220>
<221> misc_feature
<222> (1)
<223> Wherein Xaa can be Gln or Ser

<220>
<221> misc_feature
<222> (5)
<223> Wherein Xaa can be Thr, Glu or Asp

<220>
<221> misc_feature
<222> (7)
<223> Wherein Xaa can be Val or Asn

<220>
<221> misc_feature
<222> (8)
<223> Wherein Xaa can be Tyr or Phe

<220>
<221> misc_feature
<222> (9)
<223> Wherein Xaa can be Ser, Asn or Gln

<400> 193
Xaa Ser Tyr Asp Xaa Pro Xaa Xaa Xaa Val
 1   5   10

<210> 194
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence for family 18B HCDR3

<220>
<221> misc_feature
<222> (4)
<223> Wherein Xaa can be Lys, Thr or Ile

<220>
<221> misc_feature
<222> (11)
<223> Wherein Xaa can be Asn or Asp

<220>
<221> misc_feature
<222> (14)
<223> Wherein Xaa can be Val or Leu

<400> 194

Ile Ile Gln Xaa Arg Ser Lys Trp Tyr Asn Xaa Tyr Ala Xaa Ser Val
 1   5   10   15
Lys Ser

<210> 195
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence for family 19 LCDR3

<220>
<221> misc_feature
<222> (3)
<223> Wherein Xaa can be Tyr, Gly or Ala

<220>
<221> misc_feature
<222> (4)
<223> Wherein Xaa can be Gly, Glu or Asn

<220>
<221> misc_feature
<222> (5)
<223> Wherein Xaa can be Ser or Thr

<220>
<221> misc_feature
<222> (6)
<223> Wherein Xaa can be Val, Ile or Leu

<220>
<221> misc_feature
<222> (7)
<223> Wherein Xaa can be Ser or Leu

<220>
<221> misc_feature
<222> (8)
<223> Wherein Xaa can be Ile, Ser, Pro or Tyr

<400> 195
Gln Gln Xaa Xaa Xaa Xaa Xaa Xaa Thr
 1   5

<210> 196
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence for family 19 HCDR2

<220>
<221> misc_feature
<222> (1)
<223> Wherein Xaa can be Phe or Arg

<220>
<221> misc_feature
<222> (12)
<223> Wherein Xaa can be Ala or Ser

<400> 196
Xaa Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Xaa Pro Ser Phe Gln
 1   5   10   15
Gly

<210> 197
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus variable light chain family 17

<220>
<221> misc_feature
<222> (88)
<223> Wherein Xaa can be Ala, Gln, Gly or Ser

<220>
<221> misc_feature
<222> (92)
<223> Wherein Xaa can be Gly, Glu or Ser

<220>
<221> misc_feature
<222> (93)
<223> Wherein Xaa can be Asp or Asn

<220>
<221> misc_feature
<222> (94)
<223> Wherein Xaa can be Glu or Ser

<220>
<221> misc_feature
<222> (95)
<223> Wherein Xaa can be Phe, Ala or Leu

<400> 197
Asp Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
 1   5   10   15
Thr Ala Arg Ile Ser Cys Ser Gly Asp Ala Leu Gly Gly Tyr Phe Val
            20   25   30
Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
        35   40   45
Asp Asp Asp Asn Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50   55   60
Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu
65   70   75   80
Asp Glu Ala Asp Tyr Tyr Cys Xaa Ser Tyr Asp Xaa Xaa Xaa Xaa Thr
                85   90   95
Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100   105

<210> 198
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus variable heavy chain family 17

<220>
<221> misc_feature
<222> (52)
<223> Wherein Xaa can be Arg or Lys

<220>
<221> misc_feature
<222> (54)
<223> Wherein Xaa can be Tyr, His or Ser

<220>
<221> misc_feature
<222> (55)
<223> Wherein Xaa can be Met, Arg or Tyr

<220>
<221> misc_feature
<222> (58)
<223> Wherein Xaa can be Lys or Arg

<400> 198
Gln Val Glu Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1   5   10   15
Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Thr Arg
            20   25   30
Ser Ala Ala Trp Gly Trp Ile Arg Gln Ser Pro Gly Arg Gly Leu Glu
        35   40   45
Trp Leu Gly Xaa Ile Xaa Xaa Arg Ser Xaa Trp Tyr Asn Asp Tyr Ala
    50   55   60
Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65   70   75   80
Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
                85   90   95
Tyr Tyr Cys Ala Arg His Thr Tyr Pro Tyr Leu Ser Phe Asp Val Trp
            100   105   110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 199
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus variable light chain family 18B

<220>
<221> misc_feature
<222> (88)
<223> Wherein Xaa can be Gln or Ser

<220>
<221> misc_feature
<222> (92)
<223> Wherein Xaa can be Thr, Glu or Asp

<220>
<221> misc_feature
<222> (94)
<223> Wherein Xaa can be Val or Asn

<220>
<221> misc_feature
<222> (95)
<223> Wherein Xaa can be Tyr or Phe

<220>
<221> misc_feature
<222> (96)
<223> Wherein Xaa can be Ser, Asn or Gln

<400> 199
Asp Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
 1   5   10   15
Thr Ala Arg Ile Ser Cys Ser Gly Asp Asn Ile Gly Ser Tyr Tyr Val
            20   25   30
His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
        35   40   45
Glu Asp Ser Glu Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50   55   60
Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu
65   70   75   80
Asp Glu Ala Asp Tyr Tyr Cys Xaa Ser Tyr Asp Xaa Pro Xaa Xaa Xaa
                85   90   95
Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100   105

<210> 200
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus variable heavy chain family 18A and 18B
<220>
<221> misc_feature
<222> (55)
<223> Wherein Xaa can be Lys, Thr or Ile

<220>
<221> misc_feature
<222> (62)
<223> Wherein Xaa can be Asn or Asp

<220>
<221> misc_feature
<222> (65)
<223> Wherein Xaa can be Val or Leu

<400> 200
Gln Val Glu Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1   5   10   15
Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Asn
            20   25   30
Ser Ala Ala Trp Gly Trp Ile Arg Gln Ser Pro Gly Arg Gly Leu Glu
        35   40   45
Trp Leu Gly Ile Ile Gln Xaa Arg Ser Lys Trp Tyr Asn Xaa Tyr Ala
    50   55   60
Xaa Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65   70   75   80
Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
                85   90   95
Tyr Tyr Cys Ala Arg Tyr Ser Tyr Pro Phe Tyr Ser Ile Asp Tyr Trp
            100   105   110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 201
<211> 107
<212> PRT

<213> Artificial Sequence

<220>
<223> Consensus variable light chain family 19

<220>
<221> misc_feature
<222> (91)
<223> Wherein Xaa can be Tyr, Gly or Ala

<220>
<221> misc_feature
<222> (92)
<223> Wherein Xaa can be Gly, Glu or Asn

<220>
<221> misc_feature
<222> (93)
<223> Wherein Xaa can be Ser or Thr

<220>
<221> misc_feature
<222> (94)
<223> Wherein Xaa can be Val, Ile or Leu

<220>
<221> misc_feature
<222> (95)
<223> Wherein Xaa can be Ser or Leu

<220>
<221> misc_feature
<222> (96)
<223> Wherein Xaa can be Ile, Ser, Pro or Tyr

<400> 201
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 Gly Leu Tyr
            20   25   30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Xaa Xaa Xaa Xaa Xaa Xaa
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 202
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus variable heavy chain family 19

<220>
<221> misc_feature
<222> (50)
<223> Wherein Xaa can be Phe or Arg

<220>
<221> misc_feature

<222> (61)
<223> Wherein Xaa can be Ala or Ser

<400> 202
Gln Val Glu Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1   5   10   15
Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Asn Tyr
            20   25   30
Trp Val Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
        35   40   45
Gly Xaa Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Xaa Pro Ser Phe
    50   55   60
Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65   70   75   80
Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
                85   90   95
Ala Arg Glu Leu Tyr Gln Gly Tyr Met Asp Thr Phe Asp Ser Trp Gly
            100   105   110
Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 203
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Full length consensus light chain, family 17

<220>
<221> misc_feature
<222> (88)
<223> Wherein Xaa can be Ala, Gln, Gly or Ser

<220>
<221> misc_feature
<222> (92)
<223> Wherein Xaa can be Gly, Glu or Ser

<220>
<221> misc_feature
<222> (93)
<223> Wherein Xaa can be Asp or Asn

<220>
<221> misc_feature
<222> (94)
<223> Wherein Xaa can be Glu or Ser

<220>
<221> misc_feature
<222> (95)
<223> Wherein Xaa can be Phe, Ala or Leu

<400> 203
Asp Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
 1   5   10   15
Thr Ala Arg Ile Ser Cys Ser Gly Asp Ala Leu Gly Gly Tyr Phe Val
            20   25   30
Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
        35   40   45
Asp Asp Asp Asn Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50   55   60
Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu
65   70   75   80

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

<210> 204
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Full length consensus heavy chain, family 17

<220>
<221> misc_feature
<222> (52)
<223> Wherein Xaa can be Arg or Lys

<220>
<221> misc_feature
<222> (54)
<223> Wherein Xaa can be Tyr, His or Ser

<220>
<221> misc_feature
<222> (55)
<223> Wherein Xaa can be Met, Arg or Tyr

<220>
<221> misc_feature
<222> (58)
<223> Wherein Xaa can be Lys or Arg

<400> 204
Gln Val Glu Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1   5   10   15
Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Thr Arg
            20   25   30
Ser Ala Ala Trp Gly Trp Ile Arg Gln Ser Pro Gly Arg Gly Leu Glu
        35   40   45
Trp Leu Gly Xaa Ile Xaa Xaa Arg Ser Xaa Trp Tyr Asn Asp Tyr Ala
    50   55   60
Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65   70   75   80
Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
                85   90   95
Tyr Tyr Cys Ala Arg His Thr Tyr Pro Tyr Leu Ser Phe Asp Val Trp
            100   105   110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
        115   120   125
Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr
    130   135   140

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Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145                 150                 155                 160
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
                165                 170                 175
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
            180                 185                 190
Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp
        195                 200                 205
His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr
    210                 215                 220
Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro
225                 230                 235                 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp
            260                 265                 270
Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val
    290                 295                 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys
                325                 330                 335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350
Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys
                405                 410                 415
Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
        435                 440                 445
Lys
```

<210> 205
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Full length consensus light chain family 18B

<220>
<221> misc_feature
<222> (88)
<223> Wherein Xaa can be Gln or Ser

<220>
<221> misc_feature
<222> (92)
<223> Wherein Xaa can be Thr, Glu or Asp

<220>
<221> misc_feature
<222> (94)
<223> Wherein Xaa can be Val or Asn

<220>
<221> misc_feature
<222> (95)

<223> Wherein Xaa can be Tyr or Phe

<220>
<221> misc_feature
<222> (96)
<223> Wherein Xaa can be Ser, Asn or Gln

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

<210> 206
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Full length consensus heavy chain family 18A and 18B

<220>
<221> misc_feature
<222> (55)
<223> Wherein Xaa can be Lys, Thr or Ile

<220>
<221> misc_feature
<222> (62)
<223> Wherein Xaa can be Asn or Asp

<220>
<221> misc_feature
<222> (65)
<223> Wherein Xaa can be Val or Leu

<400> 206
Gln Val Glu Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1   5   10   15
Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Asn

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

<210> 207
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Full length consensus light chain family 19

<220>
<221> misc_feature
<222> (91)

<223> Wherein Xaa can be Tyr, Gly or Ala

<220>
<221> misc_feature
<222> (92)
<223> Wherien Xaa can be Gly, Glu or Asn

<220>
<221> misc_feature
<222> (93)
<223> Wherein Xaa can be Ser or Thr

<220>
<221> misc_feature
<222> (94)
<223> Wherein Xaa can be Val, Ile or Leu

<220>
<221> misc_feature
<222> (95)
<223> Wherein Xaa can be Ser or Leu

<220>
<221> misc_feature
<222> (96)
<223> Wherein Xaa can be Ile, Ser, Pro or Tyr

<400> 207
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 Gly Leu Tyr
            20   25   30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Xaa Xaa Xaa Xaa Xaa Xaa
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100   105   110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115   120   125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130   135   140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145   150   155   160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165   170   175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180   185   190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195   200   205
Phe Asn Arg Gly Glu Cys
    210

<210> 208
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> Full length consensus heavy chain family 19

<220>

<221> misc_feature
<222> (50)
<223> Wherein Xaa can be Phe or Arg

<220>
<221> misc_feature
<222> (61)
<223>

<400> 208

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

<210> 209
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> QSV Variant of candidate 9 variable light chain

<400> 209
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
 1   5   10   15
Thr Ala Arg Ile Ser Cys Ser Gly Asp Asn Ile Gly Ser Tyr Tyr Val
            20   25   30
His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
        35   40   45
Glu Asp Ser Glu Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50   55   60
Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu
65   70   75   80
Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Gln Phe Ser Phe
                85   90   95
Gly Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100   105

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

<220>
<223> QSV variant of candidate 10 variable light chain

<400> 210
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
 1   5   10   15
Thr Ala Arg Ile Ser Cys Ser Gly Asp Asn Ile Gly Ser Tyr Tyr Val
            20   25   30
His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
        35   40   45
Glu Asp Ser Glu Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50   55   60
Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu
65   70   75   80
Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Thr Pro Val Tyr Ser
                85   90   95
Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100   105

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

<220>
<223> QSV variant of candidate 12 variable light chain

<400> 211
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
 1   5   10   15
Thr Ala Arg Ile Ser Cys Ser Gly Asp Asn Ile Gly Ser Tyr Tyr Val
            20   25   30
His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
        35   40   45
Glu Asp Ser Glu Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50   55   60

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

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

<220>
<223> QVQ variant of candidate 9 variable heavy chain

<400> 212
Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15
Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Asn
20 25 30
Ser Ala Ala Trp Gly Trp Ile Arg Gln Ser Pro Gly Arg Gly Leu Glu
35 40 45
Trp Leu Gly Ile Ile Gln Ile Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
50 55 60
Leu Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65 70 75 80
Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
85 90 95
Tyr Tyr Cys Ala Arg Tyr Ser Tyr Pro Phe Tyr Ser Ile Asp Tyr Trp
100 105 110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

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

<220>
<223> QVQ variant of candidate 10 variable heavy chain

<400> 213
Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15
Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Asn
20 25 30
Ser Ala Ala Trp Gly Trp Ile Arg Gln Ser Pro Gly Arg Gly Leu Glu
35 40 45
Trp Leu Gly Ile Ile Gln Lys Arg Ser Lys Trp Tyr Asn Asn Tyr Ala
50 55 60
Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65 70 75 80
Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
85 90 95
Tyr Tyr Cys Ala Arg Tyr Ser Tyr Pro Phe Tyr Ser Ile Asp Tyr Trp
100 105 110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 214
<211> 122
<212> PRT
<213> Artificial Sequence

<220>

<223> QVQ variant of candidate 12 variable heavy chain

<400> 214
Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1   5   10   15
Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Asn
            20   25   30
Ser Ala Ala Trp Gly Trp Ile Arg Gln Ser Pro Gly Arg Gly Leu Glu
        35   40   45
Trp Leu Gly Ile Ile Gln Lys Arg Ser Lys Trp Tyr Asn Asn Tyr Ala
    50   55   60
Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65   70   75   80
Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
                85   90   95
Tyr Tyr Cys Ala Arg Tyr Ser Tyr Pro Phe Tyr Ser Ile Asp Tyr Trp
            100   105   110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 215
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> EVQ variant of candidate 14

<400> 215
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1   5   10   15
Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Asn Tyr
            20   25   30
Trp Val Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
        35   40   45
Gly Phe Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Ala Pro Ser Phe
    50   55   60
Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65   70   75   80
Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
                85   90   95
Ala Arg Glu Leu Tyr Gln Gly Tyr Met Asp Thr Phe Asp Ser Trp Gly
            100   105   110
Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 216
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> EVQ variant of candidate 15

<400> 216
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1   5   10   15
Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Asn Tyr
            20   25   30
Trp Val Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
        35   40   45
Gly Phe Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Ala Pro Ser Phe
    50   55   60
Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65   70   75   80
Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys

85 90 95
Ala Arg Glu Leu Tyr Gln Gly Tyr Met Asp Thr Phe Asp Ser Trp Gly
100 105 110
Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 217
<211> 2712
<212> DNA
<213> Macaca fascicularis

<400> 217
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tgtgcatcct ccaccaacaa atgcactgtt agccaagaag ttgctgactg cagccacctg 120
aagttaactc aggtacccga tgatctcccc acaaacataa cagtgttgaa tcttacccat 180
aatcaactca gaagattacc agctgccaat tttacaagat atagccaact aactatcttg 240
gatgtaggat ttaactccat ctcaaaactg gagccagaat tgtgccaaaa acttcccatg 300
ttaaaagttt tgaacctcca gcacaatgag ctatctcaac tttctgataa aacttttgcc 360
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aatccctttg taaagcagaa gaatttaatc acattagatc tgtctcataa tggcttgtca 480
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gaacaaaatc tggattccat tatattgatt ttccttgagg agattccaga ttataaactg 2580
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<210> 218
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Candidate 9EVQ full length heavy chain with S229P,
F235A/L236A

<400> 218
Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1   5   10   15
Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Asn
            20   25   30
Ser Ala Ala Trp Gly Trp Ile Arg Gln Ser Pro Gly Arg Gly Leu Glu
        35   40   45
Trp Leu Gly Ile Ile Gln Ile Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
    50   55   60
Leu Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65   70   75   80
Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
                85   90   95
Tyr Tyr Cys Ala Arg Tyr Ser Tyr Pro Phe Tyr Ser Ile Asp Tyr Trp
            100   105   110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
        115   120   125
Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr
    130   135   140
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145   150   155   160
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
                165   170   175
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
            180   185   190
Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp
        195   200   205
His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr
    210   215   220
Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro
225   230   235   240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245   250   255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp
            260   265   270
Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275   280   285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val
    290   295   300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305   310   315   320
Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys
                325   330   335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340   345   350
Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
        355   360   365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370   375   380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385   390   395   400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys
                405   410   415
Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420   425   430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
        435   440   445
Lys

<210> 219
<211> 449
<212> PRT
<213> Artificial Sequence

<220>

<223> Candidates 10EVQ, 12EVQ heavy chain with S229P, F235A/L236A

<400> 219
Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1   5   10   15
Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Asn
            20   25   30
Ser Ala Ala Trp Gly Trp Ile Arg Gln Ser Pro Gly Arg Gly Leu Glu
        35   40   45
Trp Leu Gly Ile Ile Gln Lys Arg Ser Lys Trp Tyr Asn Asn Tyr Ala
    50   55   60
Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65   70   75   80
Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
                85   90   95
Tyr Tyr Cys Ala Arg Tyr Ser Tyr Pro Phe Tyr Ser Ile Asp Tyr Trp
            100   105   110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
        115   120   125
Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr
    130   135   140
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145   150   155   160
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
                165   170   175
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
            180   185   190
Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp
        195   200   205
His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr
    210   215   220
Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro
225   230   235   240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245   250   255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp
            260   265   270
Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275   280   285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val
    290   295   300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305   310   315   320
Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys
                325   330   335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340   345   350
Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
        355   360   365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370   375   380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385   390   395   400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys
                405   410   415
Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420   425   430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
        435   440   445
Lys

<210> 220
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> EVQ variant mAb14 and mAb15 full length heavy
Chain S229P, F235A/L236A

<400> 220

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