SEQUENCE LISTING

<110> Glaxo Group Limited
Alexander H. TAYLOR
Yu XUE

<120> CD127 Binding Proteins

<130> PB64061 WO

<150> 61/299010
<151> 2010-01-28

<160> 138

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<220>
<223> human CD127

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            20                  25                  30
Ala Glu Leu Asp Asp Tyr Ser Phe Ser Cys Gln Leu Glu Val Asn Gly
        35                  40                  45
Ser Gln His Ser Leu Thr Cys Ala Phe Glu Asp Pro Asp Val Asn Thr
    50                  55                  60
Thr Asn Leu Glu Phe Glu Ile Cys Gly Ala Leu Val Glu Val Lys Cys
65                  70                  75                  80
Leu Asn Phe Arg Lys Leu Gln Glu Ile Tyr Phe Ile Glu Thr Lys Lys
                85                  90                  95
Phe Leu Leu Ile Gly Lys Ser Asn Ile Cys Val Lys Val Gly Glu Lys
            100                 105                 110
Ser Leu Thr Cys Lys Lys Ile Asp Leu Thr Thr Ile Val Lys Pro Glu
        115                 120                 125
Ala Pro Phe Asp Leu Ser Val Ile Tyr Arg Glu Gly Ala Asn Asp Phe
    130                 135                 140
Val Val Thr Phe Asn Thr Ser His Leu Gln Lys Lys Tyr Val Lys Val
145                 150                 155                 160
Leu Met His Asp Val Ala Tyr Arg Gln Glu Lys Asp Glu Asn Lys Trp
                165                 170                 175
Thr His Val Asn Leu Ser Ser Thr Lys Leu Thr Leu Leu Gln Arg Lys
            180                 185                 190
Leu Gln Pro Ala Ala Met Tyr Glu Ile Lys Val Arg Ser Ile Pro Asp
        195                 200                 205
His Tyr Phe Lys Gly Phe Trp Ser Glu Trp Ser Pro Ser Tyr Tyr Phe
    210                 215                 220
Arg Thr Pro Glu Ile Asn Asn Ser Ser Gly Glu Met Asp Pro Ile Leu
225                 230                 235                 240
Leu Thr Ile Ser Ile Leu Ser Phe Phe Ser Val Leu Val Ile Leu Ala
                245                 250                 255
Cys Val Leu Trp Lys Lys Arg Ile Lys Pro Ile Val Trp Pro Ser Leu
            260                 265                 270
Pro Asp His Lys Lys Thr Leu Glu His Leu Cys Lys Lys Pro Arg Lys
        275                 280                 285
Asn Leu Asn Val Ser Phe Asn Pro Glu Ser Phe Leu Asp Cys Gln Ile
    290                 295                 300
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His Arg Val Asp Asp Ile Gln Ala Arg Asp Glu Val Glu Gly Phe Leu
305                 310                 315                 320
Gln Asp Thr Phe Pro Gln Gln Leu Glu Glu Ser Glu Lys Gln Arg Leu
                325                 330                 335
Gly Gly Asp Val Gln Ser Pro Asn Cys Pro Ser Glu Asp Val Val Val
            340                 345                 350
Thr Pro Glu Ser Phe Gly Arg Asp Ser Ser Leu Thr Cys Leu Ala Gly
        355                 360                 365
Asn Val Ser Ala Cys Asp Ala Pro Ile Leu Ser Ser Ser Arg Ser Leu
    370                 375                 380
Asp Cys Arg Glu Ser Gly Lys Asn Gly Pro His Val Tyr Gln Asp Leu
385                 390                 395                 400
Leu Leu Ser Leu Gly Thr Thr Asn Ser Thr Leu Pro Pro Pro Phe Ser
                405                 410                 415
Leu Gln Ser Gly Ile Leu Thr Leu Asn Pro Val Ala Gln Gly Gln Pro
            420                 425                 430
Ile Leu Thr Ser Leu Gly Ser Asn Gln Glu Glu Ala Tyr Val Thr Met
        435                 440                 445
Ser Ser Phe Tyr Gln Asn Gln
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<210> 2
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<213> Mus musculus

<220>
<223> 1A11 CDR H1

<400> 2
Gly Tyr Thr Met Asn
 1   5

<210> 3
<211> 17
<212> PRT
<213> Mus musculus

<220>
<223> 1A11 CDR H2

<400> 3
Leu Ile Asn Pro Tyr Asn Gly Val Thr Ser Tyr Asn Gln Lys Phe Lys
 1   5   10   15
Gly

<210> 4
<211> 10
<212> PRT
<213> Mus musculus

<220>
<223> 1A11 CDR H3

<400> 4
Gly Asp Gly Asn Tyr Trp Tyr Phe Asp Val
 1   5   10

<210> 5
<211> 10
<212> PRT
<213> Mus musculus

<220>
<223> 1A11 CDR L1

<400> 5
Ser Ala Ser Ser Ser Val Thr Tyr Met His
 1   5   10

<210> 6
<211> 7
<212> PRT
<213> Mus musculus

<220>
<223> 1A11 CDR L2

<400> 6
Glu Ile Ser Lys Leu Ala Ser
 1   5

<210> 7
<211> 8
<212> PRT
<213> Mus musculus

<220>
<223> 1A11 CDR L3

<400> 7
Gln Glu Trp Asn Tyr Pro Tyr Thr
 1   5

<210> 8
<211> 119
<212> PRT
<213> Mus musculus

<220>
<223> 1A11 VH

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

115

<210> 9
<211> 105
<212> PRT
<213> Mus musculus

<220>
<223> 1A11 Vk

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

<210> 10
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> 1A11.H0 VH

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

<210> 11
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> 1A11.H1 VH

<400> 11
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala

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 1               5                  10                  15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
            20                  25                  30
Thr Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45
Gly Leu Ile Asn Pro Tyr Asn Gly Val Thr Ser Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Gly Arg Val Thr Met Thr Val Asp Thr Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80
Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Gly Asp Gly Asn Tyr Trp Tyr Phe Asp Val Trp Gly Gln Gly
            100                 105                 110
Thr Thr Val Thr Val Ser Ser
        115
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<210> 12
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> 1A11.H2 VH

<400> 12

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1               5                  10                  15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
            20                  25                  30
Thr Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45
Gly Leu Ile Asn Pro Tyr Asn Gly Val Thr Ser Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Gly Lys Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80
Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Gly Asp Gly Asn Tyr Trp Tyr Phe Asp Val Trp Gly Gln Gly
            100                 105                 110
Thr Thr Val Thr Val Ser Ser
        115
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<210> 13
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> 1A11.H3 VH

<400> 13

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1               5                  10                  15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
            20                  25                  30
Thr Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45
Gly Leu Ile Asn Pro Tyr Asn Gly Val Thr Ser Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Gly Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80
Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Gly Asp Gly Asn Tyr Trp Tyr Phe Asp Val Trp Gly Gln Gly
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100 105 110
Thr Thr Val Thr Val Ser Ser
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<210> 14
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> 1A11.H4 VH

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

<210> 15
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> 1A11.H5 VH

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

<210> 16
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> 1A11.H6 VH

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

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

<220>
<223> 1A11.H7 VH

<400> 17
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30
Thr Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Leu Ile Asn Pro Tyr Asn Gly Val Thr Ser Tyr Asn Gln Lys Phe
50 55 60
Lys Gly Lys Val Thr Leu Thr Val Ala Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Gly Asp Gly Asn Tyr Trp Tyr Phe Asp Val Trp Gly Gln Gly
100 105 110
Thr Thr Val Thr Val Ser Ser
115

<210> 18
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> 1A11.L0 Vk

<400> 18
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Ser Ala Ser Ser Ser Val Thr Tyr Met
20 25 30
His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
35 40 45
Glu Ile Ser Lys Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60
Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu

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

<210> 19
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> 1A11.L1 Vk

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

<210> 20
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> 1A11.L2 Vk

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

<210> 21
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> 1A11.L3 Vk

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

<210> 22
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> 1A11.L4 Vk

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

<210> 23
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> 1A11.L5 Vk

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

<210> 24
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> 1A11.L6 Vk

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

<210> 25
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> 1A11.L7 Vk

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

<210> 26
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> 1A11.L8 Vk

<400> 26
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1   5   10   15
Glu Arg Ala Thr Leu Ser Cys Ser Ala Ser Ser Ser Val Thr Tyr Met
            20   25   30

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His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Lys Pro Trp Ile Tyr
        35                  40                  45
Glu Ile Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
    50                  55                  60
Gly Ser Gly Thr Ser Tyr Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
65                  70                  75                  80
Asp Phe Ala Val Tyr Tyr Cys Gln Glu Trp Asn Tyr Pro Tyr Thr Phe
                85                  90                  95
Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105
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<210> 27
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> 1A11.L9 Vk

<400> 27

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Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1               5                  10                  15
Glu Arg Ala Thr Leu Ser Cys Ser Ala Ser Ser Ser Val Thr Tyr Met
            20                  25                  30
His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Lys Pro Trp Ile Tyr
        35                  40                  45
Glu Ile Ser Lys Leu Ala Ser Gly Val Pro Val Arg Phe Ser Gly Ser
    50                  55                  60
Gly Ser Gly Thr Ser Tyr Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
65                  70                  75                  80
Asp Phe Ala Val Tyr Tyr Cys Gln Glu Trp Asn Tyr Pro Tyr Thr Phe
                85                  90                  95
Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105
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<210> 28
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> 1A11c VH

<400> 28

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Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Leu Lys Pro Gly Ala
 1               5                  10                  15
Ser Met Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
            20                  25                  30
Thr Met Asn Trp Val Lys Gln Ser His Gly Lys Asn Leu Glu Trp Ile
        35                  40                  45
Gly Leu Ile Asn Pro Tyr Asn Gly Val Thr Ser Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Gly Lys Ala Thr Leu Thr Val Ala Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80
Met Glu Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Gly Asp Gly Asn Tyr Trp Tyr Phe Asp Val Trp Gly Ala Gly
            100                 105                 110
Thr Thr Val Thr Val Ser Ser
        115
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<210> 29
<211> 105

<212> PRT
<213> Artificial Sequence

<220>
<223> 1A11c Vk

<400> 29
Glu Ile Val Leu Thr Gln Ser Pro Ala Ile Thr Ala Ala Ser Leu Gly
 1   5   10   15
Gln Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Thr Tyr Met
            20   25   30
His Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Pro Trp Ile Tyr
        35   40   45
Glu Ile Ser Lys Leu Ala Ser Gly Val Pro Val Arg Phe Ser Gly Ser
    50   55   60
Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
65   70   75   80
Asp Ala Ala Ile Tyr Tyr Cys Gln Glu Trp Asn Tyr Pro Tyr Thr Phe
                85   90   95
Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100   105

<210> 30
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence encoding 1A11.H1 VH

<400> 30
caggtgcagc tggtgcagag cggagccgag gtgaagaaac ccggagccag cgtgaaggtg 60
agctgcaagg ccagcggcta caccttcacc ggctacacca tgaactgggt gaggcaggcc 120
cccggccagg gactcgagtg gatgggcctg atcaacccct acaacggcgt gaccagctac 180
aaccagaagt tcaagggcag ggtgaccatg accgtggata ccagcatcag caccgcttac 240
atggaactga gcaggctgag gtccgacgac accgccgtgt attactgcgc caggggcgac 300
ggcaactact ggtacttcga tgtgtggggc cagggcacca ccgtcacagt gagcagc   357

<210> 31
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence encoding 1A11.H2 VH

<400> 31
caggtgcagc tggtgcagag cggagccgag gtgaagaaac ccggagccag cgtgaaggtg 60
agctgcaagg ccagcggcta caccttcacc ggctacacca tgaactgggt gaggcaggcc 120
cccggccagg gactcgagtg gatgggcctg atcaacccct acaacggcgt gaccagctac 180
aaccagaagt tcaagggcaa ggtgaccatg accagggata ccagcatcag caccgcttac 240
atggaactga gcaggctgag gtccgacgac accgccgtgt attactgcgc caggggcgac 300
ggcaactact ggtacttcga tgtgtggggc cagggcacca ccgtcacagt gagcagc   357

<210> 32
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence encoding 1A11.H3 VH

<400> 32

caggtgcagc tggtgcagag cggagccgag gtgaagaaac ccggagccag cgtgaaggtg 60
agctgcaagg ccagcggcta caccttcacc ggctacacca tgaactgggt gaggcaggcc 120
cccggccagg gactcgagtg gatgggcctg atcaacccct acaacggcgt gaccagctac 180
aaccagaagt tcaagggcag ggtgaccctg accagggata ccagcatcag caccgcttac 240
atggaactga gcaggctgag gtccgacgac accgccgtgt attactgcgc caggggcgac 300
ggcaactact ggtacttcga tgtgtggggc cagggcacca ccgtcacagt gagcagc 357

<210> 33
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence encoding 1A11.H4 VH

<400> 33
caggtgcagc tggtgcagag cggagccgag gtgaagaaac ccggagccag cgtgaaggtg 60
agctgcaagg ccagcggcta caccttcacc ggctacacca tgaactgggt gaggcaggcc 120
cccggccagg gactcgagtg gatgggcctg atcaacccct acaacggcgt gaccagctac 180
aaccagaagt tcaagggcaa ggtgaccatg accgtggata ccagcatcag caccgcttac 240
atggaactga gcaggctgag gtccgacgac accgccgtgt attactgcgc caggggcgac 300
ggcaactact ggtacttcga tgtgtggggc cagggcacca ccgtcacagt gagcagc 357

<210> 34
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence encoding 1A11.H5 VH

<400> 34
caggtgcagc tggtgcagag cggagccgag gtgaagaaac ccggagccag cgtgaaggtg 60
agctgcaagg ccagcggcta caccttcacc ggctacacca tgaactgggt gaggcaggcc 120
cccggccagg gactcgagtg gatgggcctg atcaacccct acaacggcgt gaccagctac 180
aaccagaagt tcaagggcaa ggtgaccctg accgtggata ccagcatcag caccgcttac 240
atggaactga gcaggctgag gtccgacgac accgccgtgt attactgcgc caggggcgac 300
ggcaactact ggtacttcga tgtgtggggc cagggcacca ccgtcacagt gagcagc 357

<210> 35
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence encoding 1A11.H6 VH

<400> 35
caggtgcagc tggtgcagag cggagccgag gtgaagaaac ccggagccag cgtgaaggtg 60
agctgcaagg ccagcggcta caccttcacc ggctacacca tgaactgggt gaggcaggcc 120
cccggccagg gactcgagtg gatgggcctg atcaacccct acaacggcgt gaccagctac 180
aaccagaagt tcaagggcaa ggtgaccctg accgtggata agagcatcag caccgcttac 240
atggaactga gcaggctgag gtccgacgac accgccgtgt attactgcgc caggggcgac 300
ggcaactact ggtacttcga tgtgtggggc cagggcacca ccgtcacagt gagcagc 357

<210> 36
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence encoding 1A11.H7 VH

<400> 36

caggtgcagc tggtgcagag cggagccgag gtgaagaaac ccggagccag cgtgaaggtg 60
agctgcaagg ccagcggcta caccttcacc ggctacacca tgaactgggt gaggcaggcc 120
cccggccagg gactcgagtg gatgggcctg atcaacccct acaacggcgt gaccagctac 180
aaccagaagt tcaagggcaa ggtgaccctg accgtggcca agagcatcag caccgcttac 240
atggaactga gcaggctgag gtccgacgac accgccgtgt attactgcgc caggggcgac 300
ggcaactact ggtacttcga tgtgtggggc cagggcacca ccgtcacagt gagcagc 357

<210> 37
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide encoding 1A11c VH

<400> 37
gaggtgcagc tgcagcagag cggccccgaa ctgctgaagc ccggcgctag catgaagatc 60
agctgcaagg ccagcggcta cagcttcacc ggctacacca tgaactgggt caagcagtcc 120
cacggcaaga acctggagtg gatcggcctg atcaacccct acaacggcgt gacctcctac 180
aaccagaagt tcaagggcaa ggccaccctc acagtggcca aaagcagcag caccgcctac 240
atggaactgc tgagcctgac cagcgaggac agcgccgtgt actattgcgc caggggcgac 300
ggcaattact ggtacttcga cgtgtggggc gccggaacca ccgtgaccgt gtctagc 357

<210> 38
<211> 315
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide encoding 1A11c Vk

<400> 38
gagatcgtgc tgacccagag ccccgcaatt accgccgcca gcctgggcca gaaggtgacc 60
atcacctgca gcgcaagcag cagcgtgacc tacatgcact ggtaccagca gaagagcggc 120
accagcccca agccctggat ctacgagatc tccaagctcg cctctggagt ccctgtgagg 180
ttcagcggca gcggcagcgg cactagctac tcactgacca tcagcagcat ggaggccgaa 240
gacgccgcca tctattactg ccaggagtgg aactaccct acaccttcgg cggcggcacc 300
aaactggaga tcaag 315

<210> 39
<211> 6
<212> PRT
<213> Mus musculus

<220>
<223> 6A3 CDR H1

<400> 39
Thr Asp Tyr Ala Trp Asn
1 5

<210> 40
<211> 16
<212> PRT
<213> Mus musculus

<220>
<223> 6A3 CDR H2

<400> 40
Tyr Ile Phe Tyr Ser Gly Ser Thr Thr Tyr Thr Pro Ser Leu Lys Ser
1 5 10 15

<210> 41
<211> 11
<212> PRT
<213> Mus musculus

<220>
<223> 6A3 CDR H3

<400> 41
Gly Gly Tyr Asp Val Asn Tyr Phe Asp Tyr Trp
 1   5   10

<210> 42
<211> 7
<212> PRT
<213> Mus musculus

<220>
<223> 6A3 CDR L1

<400> 42
Leu Ala Ser Gln Thr Ile Gly
 1   5

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

<220>
<223> 6A3 CDR L2

<400> 43
Ala Ala Thr Arg Leu Ala Asp
 1   5

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

<220>
<223> 6A3 CDR L3

<400> 44
Gln Gln Phe Phe Ser Thr Pro Trp Thr
 1   5

<210> 45
<211> 119
<212> PRT
<213> Mus musculus

<220>
<223> 6A3 VH

<400> 45

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

<210> 46
<211> 107
<212> PRT
<213> Mus musculus

<220>
<223> 6A3 Vk

<400> 46

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

<210> 47
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> 6A3.IGHV4_61.H0 VH

<400> 47

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

Thr Thr Val Thr Val Ser Ser
115

<210> 48
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> 6A3.IGHV4_61.H1 VH

<400> 48
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Val Ser Thr Asp
20 25 30
Tyr Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
35 40 45
Ile Gly Tyr Ile Phe Tyr Ser Gly Ser Thr Thr Tyr Thr Pro Ser Leu
50 55 60
Lys Ser Arg Val Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80
Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Gly Gly Tyr Asp Val Asn Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110
Thr Thr Val Thr Val Ser Ser
115

<210> 49
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> 6A3.IGHV4_61.H2 VH

<400> 49
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Val Ser Thr Asp
20 25 30
Tyr Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
35 40 45
Ile Gly Tyr Ile Phe Tyr Ser Gly Ser Thr Thr Tyr Thr Pro Ser Leu
50 55 60
Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80
Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Gly Gly Tyr Asp Val Asn Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110
Thr Thr Val Thr Val Ser Ser
115

<210> 50
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> 6A3.IGHV4_61.H3 VH

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

<210> 51
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> 6A3.IGHV4_61.H4 VH

<400> 51
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1   5   10   15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Val Ser Thr Asp
            20   25   30
Tyr Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
        35   40   45
Ile Gly Tyr Ile Phe Tyr Ser Gly Ser Thr Thr Tyr Thr Pro Ser Leu
    50   55   60
Lys Ser Arg Ile Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser
65   70   75   80
Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Gly Gly Tyr Asp Val Asn Tyr Phe Asp Tyr Trp Gly Gln Gly
            100   105   110
Thr Thr Val Thr Val Ser Ser
        115

<210> 52
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> 6A3.IGHV4_61.H5 VH

<400> 52
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1   5   10   15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Val Ser Thr Asp
            20   25   30
Tyr Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
        35   40   45
Met Gly Tyr Ile Phe Tyr Ser Gly Ser Thr Thr Tyr Thr Pro Ser Leu
    50   55   60
Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser
65   70   75   80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Gly Gly Tyr Asp Val Asn Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110
Thr Thr Val Thr Val Ser Ser
115

<210> 53
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> 6A3.IGHV4_61.H6 VH

<400> 53
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Val Ser Thr Asp
20 25 30
Tyr Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
35 40 45
Ile Gly Tyr Ile Phe Tyr Ser Gly Ser Thr Thr Tyr Thr Pro Ser Leu
50 55 60
Lys Ser Arg Val Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80
Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Gly Gly Tyr Asp Val Asn Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110
Thr Thr Val Thr Val Ser Ser
115

<210> 54
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> 6A3.IGHV4_61.H7 VH

<400> 54
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Val Thr Thr Asp
20 25 30
Tyr Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
35 40 45
Ile Gly Tyr Ile Phe Tyr Ser Gly Ser Thr Thr Tyr Thr Pro Ser Leu
50 55 60
Lys Ser Arg Val Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80
Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Gly Gly Tyr Asp Val Asn Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110
Thr Thr Val Thr Val Ser Ser
115

<210> 55
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> 6A3.IGHV4_61.H8 VH

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

<210> 56
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> 6A3.IGHV4_61.H9 VH

<400> 56
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Val Thr Thr Asp
20 25 30
Tyr Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
35 40 45
Met Gly Tyr Ile Phe Tyr Ser Gly Ser Thr Thr Tyr Thr Pro Ser Leu
50 55 60
Lys Ser Arg Ile Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80
Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Gly Gly Tyr Asp Val Asn Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110
Thr Thr Val Thr Val Ser Ser
115

<210> 57
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> 6A3.IGHV3-33.H0 VH

<400> 57
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Asp
20 25 30
Tyr Ala Trp Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
35 40 45

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

<210> 58
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> 6A3.IGHV3-33.H1 VH

<400> 58
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Phe Ser Thr Asp
20 25 30
Tyr Ala Trp Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
35 40 45
Val Ala Tyr Ile Phe Tyr Ser Gly Ser Thr Thr Tyr Thr Pro Ser Leu
50 55 60
Lys Ser Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Gly Gly Tyr Asp Val Asn Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110
Thr Thr Val Thr Val Ser Ser
115

<210> 59
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> 6A3.IGHV3-33.H2 VH

<400> 59
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Thr Asp
20 25 30
Tyr Ala Trp Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
35 40 45
Val Ala Tyr Ile Phe Tyr Ser Gly Ser Thr Thr Tyr Thr Pro Ser Leu
50 55 60
Lys Ser Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Gly Gly Tyr Asp Val Asn Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110
Thr Thr Val Thr Val Ser Ser
115

<210> 60
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> 6A3.IGHV3-33.H3 VH

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

<210> 61
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> 6A3.IGHV3-33.H4 VH

<400> 61
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Ile Ser Thr Asp
20 25 30
Tyr Ala Trp Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
35 40 45
Val Ala Tyr Ile Phe Tyr Ser Gly Ser Thr Thr Tyr Thr Pro Ser Leu
50 55 60
Lys Ser Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Gly Gly Tyr Asp Val Asn Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110
Thr Thr Val Thr Val Ser Ser
115

<210> 62
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> 6A3.IGHV3-33.H5 VH

<400> 62
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

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

<210> 63
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> 6A3.IGHV3-33.H6 VH

<400> 63

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

<210> 64
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> 6A3.IGHV3-33.H7 VH

<400> 64

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

Thr Thr Val Thr Val Ser Ser
115

<210> 65
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> 6A3.IGHV3-33.H8 VH

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

<210> 66
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> 6A3.IGHV3-33.H9 VH

<400> 66
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Asp
20 25 30
Tyr Ala Trp Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
35 40 45
Val Ala Tyr Ile Phe Tyr Ser Gly Ser Thr Thr Tyr Thr Pro Ser Leu
50 55 60
Lys Ser Arg Phe Ser Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Gly Gly Tyr Asp Val Asn Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110
Thr Thr Val Thr Val Ser Ser
115

<210> 67
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> 6A3.IGHV3-33.H10 VH

<400> 67
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Thr Phe Ser Thr Asp
            20   25   30
Tyr Ala Trp Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
        35   40   45
Val Ala Tyr Ile Phe Tyr Ser Gly Ser Thr Thr Tyr Thr Pro Ser Leu
    50   55   60
Lys Ser Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Gly Gly Tyr Asp Val Asn Tyr Phe Asp Tyr Trp Gly Gln Gly
            100   105   110
Thr Thr Val Thr Val Ser Ser
        115

<210> 68
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> 6A3.IGHV3-33.H11 VH

<400> 68
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Asp
            20   25   30
Tyr Ala Trp Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
        35   40   45
Met Ala Tyr Ile Phe Tyr Ser Gly Ser Thr Thr Tyr Thr Pro Ser Leu
    50   55   60
Lys Ser Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Gly Gly Tyr Asp Val Asn Tyr Phe Asp Tyr Trp Gly Gln Gly
            100   105   110
Thr Thr Val Thr Val Ser Ser
        115

<210> 69
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> 6A3.L0 Vk

<400> 69
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 Leu Ala Ser Gln Thr Ile Gly Ala Trp
            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 Thr Arg Leu Ala Asp 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 Phe Phe Ser Thr Pro Trp
85 90 95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 70
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> 6A3.L1 Vk

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

<210> 71
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> 6A3.L2 Vk

<400> 71
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 Leu Ala Ser Gln Thr Ile Gly Ala Trp
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 Thr Arg Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Lys Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Phe Phe Ser Thr Pro Trp
85 90 95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 72
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> 6A3.L3 Vk

<400> 72

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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 Leu Ala Ser Gln Thr Ile Gly Ala Trp
            20                  25                  30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Gln Leu Leu Ile
        35                  40                  45
Tyr Ala Ala Thr Arg Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Lys Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Phe Phe Ser Thr Pro Trp
                85                  90                  95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105
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<210> 73
<211> 119
<212> PRT
<213> Mus musculus

<220>
<223> 6A3c VH

<400> 73

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Asp Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1               5                  10                  15
Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Thr Asp
            20                  25                  30
Tyr Ala Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
        35                  40                  45
Met Gly Tyr Ile Phe Tyr Ser Gly Ser Thr Thr Tyr Thr Pro Ser Leu
    50                  55                  60
Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
65                  70                  75                  80
Leu Gln Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys
                85                  90                  95
Ala Arg Gly Gly Tyr Asp Val Asn Tyr Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110
Thr Thr Leu Thr Val Ser Ser
        115
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<210> 74
<211> 107
<212> PRT
<213> Mus musculus

<220>
<223> 6A3c Vk

<400> 74

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Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Gln Ser Ala Ser Leu Gly
 1               5                  10                  15
Glu Ser Val Thr Ile Thr Cys Leu Ala Ser Gln Thr Ile Gly Ala Trp
            20                  25                  30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Gln Leu Leu Ile
        35                  40                  45
Tyr Ala Ala Thr Arg Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Lys Phe Ser Phe Lys Ile Ser Ser Leu Gln Ala
65                  70                  75                  80
Glu Asp Phe Val Ser Tyr Tyr Cys Gln Gln Phe Phe Ser Thr Pro Trp
                85                  90                  95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105
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<210> 75
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence encoding 6A3.IGHV4_61.H0
VH

<400> 75
caggtgcagc tgcaggagag cggacccggc ctggtgaaac ccagcgagac cctgagcctg 60
acctgcacag tgagcggcgg ctccgtgagc accgactacg cttggaactg gatcaggcag 120
cctcccggca agggcctgga gtggatcggc tacatcttct acagcggcag caccacctac 180
acccccagcc tcaagtccag ggtgaccatc agcgtcgaca ccagcaagaa ccagttcagc 240
ctgaagctga gcagcgtgac cgccgccgat accgccgtgt actactgcgc caggggaggc 300
tacgacgtga actacttcga ctactggggc cagggcacca cctatactgt gagcagc 357

<210> 76
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence encoding 6A3.IGHV4_61.H1
VH

<400> 76
caggtgcagc tgcaggagag cggacccggc ctggtgaaac ccagcgagac cctgagcctg 60
acctgcacag tgagcggcgg ctccgtgagc accgactacg cttggaactg gatcaggcag 120
cctcccggca agggcctgga gtggatcggc tacatcttct acagcggcag caccacctac 180
acccccagcc tcaagtccag ggtgaccatc agcagggaca ccagcaagaa ccagttcagc 240
ctgaagctga gcagcgtgac cgccgccgat accgccgtgt actactgcgc caggggaggc 300
tacgacgtga actacttcga ctactggggc cagggcacca cctatactgt gagcagc 357

<210> 77
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence encoding 6A3.IGHV4_61.H2
VH

<400> 77
caggtgcagc tgcaggagag cggacccggc ctggtgaaac ccagcgagac cctgagcctg 60
acctgcacag tgagcggcta ctccgtgagc accgactacg cttggaactg gatcaggcag 120
cctcccggca agggcctgga gtggatcggc tacatcttct acagcggcag caccacctac 180
acccccagcc tcaagtccag ggtgaccatc agcgtcgaca ccagcaagaa ccagttcagc 240
ctgaagctga gcagcgtgac cgccgccgat accgccgtgt actactgcgc caggggaggc 300
tacgacgtga actacttcga ctactggggc cagggcacca cctatactgt gagcagc 357

<210> 78
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence encoding 6A3.IGHV4_61.H3
VH

<400> 78

caggtgcagc tgcaggagag cggacccggc ctggtgaaac ccagcgagac cctgagcctg 60
acctgcacag tgagcggcgg ctccgtgacc accgactacg cttggaactg gatcaggcag 120
cctcccggca agggcctgga gtggatcggc tacatcttct acagcggcag caccacctac 180
acccccagcc tcaagtccag ggtgaccatc agcgtcgaca ccagcaagaa ccagttcagc 240
ctgaagctga gcagcgtgac cgccgccgat accgccgtgt actactgcgc caggggaggc 300
tacgacgtga actacttcga ctactggggc cagggcacca cctatactgt gagcagc 357

<210> 79
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence encoding 6A3.IGHV4_61.H4
VH

<400> 79
caggtgcagc tgcaggagag cggacccggc ctggtgaaac ccagcgagac cctgagcctg 60
acctgcacag tgagcggcgg ctccgtgagc accgactacg cttggaactg gatcaggcag 120
cctcccggca agggcctgga gtggatcggc tacatcttct acagcggcag caccacctac 180
acccccagcc tcaagtccag gatcaccatc agcgtcgaca ccagcaagaa ccagttcagc 240
ctgaagctga gcagcgtgac cgccgccgat accgccgtgt actactgcgc caggggaggc 300
tacgacgtga actacttcga ctactggggc cagggcacca cctatactgt gagcagc 357

<210> 80
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence encoding 6A3.IGHV4_61.H5
VH

<400> 80
caggtgcagc tgcaggagag cggacccggc ctggtgaaac ccagcgagac cctgagcctg 60
acctgcacag tgagcggcgg ctccgtgagc accgactacg cttggaactg gatcaggcag 120
cctcccggca agggcctgga gtggatgggc tacatcttct acagcggcag caccacctac 180
acccccagcc tcaagtccag ggtgaccatc agcgtcgaca ccagcaagaa ccagttcagc 240
ctgaagctga gcagcgtgac cgccgccgat accgccgtgt actactgcgc caggggaggc 300
tacgacgtga actacttcga ctactggggc cagggcacca cctatactgt gagcagc 357

<210> 81
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence encoding 6A3.IGHV4_61.H6
VH

<400> 81
caggtgcagc tgcaggagag cggacccggc ctggtgaaac ccagcgagac cctgagcctg 60
acctgcacag tgagcggcta ctccgtgagc accgactacg cttggaactg gatcaggcag 120
cctcccggca agggcctgga gtggatcggc tacatcttct acagcggcag caccacctac 180
acccccagcc tcaagtccag ggtgaccatc agcagggaca ccagcaagaa ccagttcagc 240
ctgaagctga gcagcgtgac cgccgccgat accgccgtgt actactgcgc caggggaggc 300
tacgacgtga actacttcga ctactggggc cagggcacca cctatactgt gagcagc 357

<210> 82
<211> 357
<212> DNA
<213> Artificial Sequence

<220>

<223> polynucleotide sequence encoding 6A3.IGHV4_61.H7
VH

<400> 82
caggtgcagc tgcaggagag cggacccggc ctggtgaaac ccagcgagac cctgagcctg 60
acctgcacag tgagcggcta ctccgtgacc accgactacg cttggaactg gatcaggcag 120
cctcccggca agggcctgga gtggatcggc tacatcttct acagcggcag caccacctac 180
acccccagcc tcaagtccag ggtgaccatc agcagggaca ccagcaagaa ccagttcagc 240
ctgaagctga gcagcgtgac cgccgccgat accgccgtgt actactgcgc caggggaggc 300
tacgacgtga actacttcga ctactggggc cagggcacca cctatactgt gagcagc 357

<210> 83
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence encoding 6A3.IGHV4_61.H8
VH

<400> 83
caggtgcagc tgcaggagag cggacccggc ctggtgaaac ccagcgagac cctgagcctg 60
acctgcacag tgagcggcgg ctccgtgagc accgactacg cttggaactg gatcaggcag 120
cctcccggca agggcctgga gtggatcggc tacatcttct acagcggcag caccacctac 180
acccccagcc tcaagtccag ggtgaccatc agcgtcgaca ccagcaagaa ccagttcagc 240
ctgaagctga gcagcgtgac cgccgccgat accgccgtgt actactgcgc caggggaggc 300
tacgacgtga actacttcga ctactggggc cagggcacca cctatactgt gagcagc 357

<210> 84
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence encoding 6A3.IGHV4_61.H9
VH

<400> 84
caggtgcagc tgcaggagag cggacccggc ctggtgaaac ccagcgagac cctgagcctg 60
acctgcacag tgagcggcta ctccgtgacc accgactacg cttggaactg gatcaggcag 120
cctcccggca agggcctgga gtggatcggc tacatcttct acagcggcag caccacctac 180
acccccagcc tcaagtccag gatcaccatc agcagggaca ccagcaagaa ccagttcagc 240
ctgaagctga gcagcgtgac cgccgccgat accgccgtgt actactgcgc caggggaggc 300
tacgacgtga actacttcga ctactggggc cagggcacca cctatactgt gagcagc 357

<210> 85
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence encoding 6A3.IGHV3_33.H0
VH

<400> 85
caggtgcagc tggtggagag cggcggcggc gtggtgcagc ccggcaggag cctgaggctc 60
tcttgcgccg ccagcggatt caccttcagc accgactacg cctggaattg ggtgaggcag 120
gcccccggga agggcctgga gtgggtcgcc tacatcttct acagcggcag caccacctac 180
acccccagcc tgaagagcag gttcaccatc agcagggaca acagcaagaa caccctgtac 240
ctgcagatga acagcctgag ggccgaggac accgccgtgt attactgcgc taggggggac 300
tacgacgtga actacttcga ctactggggc cagggcacaa ccgtgaccgt gagcagc 357

<210> 86
<211> 357

<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence encoding 6A3.IGHV3_33.H1
VH

<400> 86
caggtgcagc tggtggagag cggcggcggc gtggtgcagc ccggcaggag cctgaggctc 60
tcttgcgccg ccagcggata caccttcagc accgactacg cctggaattg ggtgaggcag 120
gcccccggga agggcctgga gtgggtcgcc tacatcttct acagcggcag caccacctac 180
acccccagcc tgaagagcag gttcaccatc agcagggaca acagcaagaa caccctgtac 240
ctgcagatga acagcctgag ggccgaggac accgccgtgt attactgcgc taggggggc 300
tacgacgtga actacttcga ctactggggc cagggcacaa ccgtgaccgt gagcagc 357

<210> 87
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence encoding 6A3.IGHV3_33.H2
VH

<400> 87
caggtgcagc tggtggagag cggcggcggc gtggtgcagc ccggcaggag cctgaggctc 60
tcttgcgccg ccagcggatt caccttcacc accgactacg cctggaattg ggtgaggcag 120
gcccccggga agggcctgga gtgggtcgcc tacatcttct acagcggcag caccacctac 180
acccccagcc tgaagagcag gttcaccatc agcagggaca acagcaagaa caccctgtac 240
ctgcagatga acagcctgag ggccgaggac accgccgtgt attactgcgc taggggggc 300
tacgacgtga actacttcga ctactggggc cagggcacaa ccgtgaccgt gagcagc 357

<210> 88
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence encoding 6A3.IGHV3_33.H3
VH

<400> 88
caggtgcagc tggtggagag cggcggcggc gtggtgcagc ccggcaggag cctgaggctc 60
tcttgcgccg ccagcggatt cagcttcagc accgactacg cctggaattg ggtgaggcag 120
gcccccggga agggcctgga gtgggtcgcc tacatcttct acagcggcag caccacctac 180
acccccagcc tgaagagcag gttcaccatc agcagggaca acagcaagaa caccctgtac 240
ctgcagatga acagcctgag ggccgaggac accgccgtgt attactgcgc taggggggc 300
tacgacgtga actacttcga ctactggggc cagggcacaa ccgtgaccgt gagcagc 357

<210> 89
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence encoding 6A3.IGHV3_33.H4
VH

<400> 89
caggtgcagc tggtggagag cggcggcggc gtggtgcagc ccggcaggag cctgaggctc 60
tcttgcgccg ccagcggatt caccatcagc accgactacg cctggaattg ggtgaggcag 120
gcccccggga agggcctgga gtgggtcgcc tacatcttct acagcggcag caccacctac 180
acccccagcc tgaagagcag gttcaccatc agcagggaca acagcaagaa caccctgtac 240
ctgcagatga acagcctgag ggccgaggac accgccgtgt attactgcgc taggggggc 300

tacgacgtga actacttcga ctactggggc cagggcacaa ccgtgaccgt gagcagc 357

<210> 90
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence encoding 6A3.IGHV3_33.H5
VH

<400> 90
caggtgcagc tggtggagag cggcggcggc gtggtgcagc ccggcaggag cctgaggctc 60
tcttgcgccg ccagcggatt caccttcagc accgactacg cctggaattg ggtgaggcag 120
gccccccggga agggcctgga gtgggtcgcc tacatcttct acagcggcag caccacctac 180
acccccagcc tgaagagcag gatcaccatc agcagggaca acagcaagaa caccctgtac 240
ctgcagatga acagcctgag ggccgaggac accgccgtgt attactgcgc taggggggc 300
tacgacgtga actacttcga ctactggggc cagggcacaa ccgtgaccgt gagcagc 357

<210> 91
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence encoding 6A3.IGHV3_33.H6
VH

<400> 91
caggtgcagc tggtggagag cggcggcggc gtggtgcagc ccggcaggag cctgaggctc 60
tcttgcgccg ccagcggatt caccttcagc accgactacg cctggaattg ggtgaggcag 120
gccccccggga agggcctgga gtgggtcgcc tacatcttct acagcggcag caccacctac 180
acccccagcc tgaagagcag gttcaccatc agcagggaca ccagcaagaa caccctgtac 240
ctgcagatga acagcctgag ggccgaggac accgccgtgt attactgcgc taggggggc 300
tacgacgtga actacttcga ctactggggc cagggcacaa ccgtgaccgt gagcagc 357

<210> 92
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence encoding 6A3.IGHV3_33.H7
VH

<400> 92
caggtgcagc tggtggagag cggcggcggc gtggtgcagc ccggcaggag cctgaggctc 60
tcttgcgccg ccagcggatt caccttcagc accgactacg cctggaattg ggtgaggcag 120
gccccccggga agggcctgga gtgggtcgcc tacatcttct acagcggcag caccacctac 180
acccccagcc tgaagagcag gttcaccatc agcagggaca acagcaagaa caccttctac 240
ctgcagatga acagcctgag ggccgaggac accgccgtgt attactgcgc taggggggc 300
tacgacgtga actacttcga ctactggggc cagggcacaa ccgtgaccgt gagcagc 357

<210> 93
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence encoding 6A3.IGHV3_33.H8
VH

<400> 93
caggtgcagc tggtggagag cggcggcggc gtggtgcagc ccggcaggag cctgaggctc 60

tcttgcgccg ccagcggatt caccttcagc accgactacg cctggaattg ggtgaggcag 120
gcccccggga agggcctgga gtgggtcggc tacatcttct acagcggcag caccacctac 180
acccccagcc tgaagagcag gttcaccatc agcagggaca acagcaagaa caccctgtac 240
ctgcagatga acagcctgag ggccgaggac accgccgtgt attactgcgc taggggggc 300
tacgacgtga actacttcga ctactggggc cagggcacaa ccgtgaccgt gagcagc 357

<210> 94
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence encoding 6A3.IGHV3_33.H9
VH

<400> 94
caggtgcagc tggtggagag cggcggcggc gtggtgcagc ccggcaggag cctgaggctc 60
tcttgcgccg ccagcggatt caccttcagc accgactacg cctggaattg ggtgaggcag 120
gcccccggga agggcctgga gtgggtcgcc tacatcttct acagcggcag caccacctac 180
acccccagcc tgaagagcag gttcagcatc agcagggaca acagcaagaa caccctgtac 240
ctgcagatga acagcctgag ggccgaggac accgccgtgt attactgcgc taggggggc 300
tacgacgtga actacttcga ctactggggc cagggcacaa ccgtgaccgt gagcagc 357

<210> 95
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence encoding 6A3.IGHV3_33.H10
VH

<400> 95
caggtgcagc tggtggagag cggcggcggc gtggtgcagc ccggcaggag cctgaggctc 60
tcttgcgccg tgagcggatt caccttcagc accgactacg cctggaattg ggtgaggcag 120
gcccccggga agggcctgga gtgggtcgcc tacatcttct acagcggcag caccacctac 180
acccccagcc tgaagagcag gttcaccatc agcagggaca acagcaagaa caccctgtac 240
ctgcagatga acagcctgag ggccgaggac accgccgtgt attactgcgc taggggggc 300
tacgacgtga actacttcga ctactggggc cagggcacaa ccgtgaccgt gagcagc 357

<210> 96
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence encoding 6A3.IGHV3_33.H11
VH

<400> 96
caggtgcagc tggtggagag cggcggcggc gtggtgcagc ccggcaggag cctgaggctc 60
tcttgcgccg ccagcggatt caccttcagc accgactacg cctggaattg ggtgaggcag 120
gcccccggga agggcctgga gtggatggcc tacatcttct acagcggcag caccacctac 180
acccccagcc tgaagagcag gttcaccatc agcagggaca acagcaagaa caccctgtac 240
ctgcagatga acagcctgag ggccgaggac accgccgtgt attactgcgc taggggggc 300
tacgacgtga actacttcga ctactggggc cagggcacaa ccgtgaccgt gagcagc 357

<210> 97
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence encoding 6A3.L0 Vk

<400> 97
gacatccaga tgacccagag ccccagctcc ctgagcgcca gcgtgggcga tagggtgacc 60
atcacctgcc tggccagcca gaccattggc gcctggctgg cctggtacca gcagaagccc 120
ggcaaggccc ccaaactgct gatctacgcc gcaactaggc tcgccgacgg cgtgccctct 180
aggtttagcg gcagcggaag cggcaccgac ttcaccctga ccatcagcag cctgcagccc 240
gaggacttcg ccacctacta ctgccagcag ttcttcagca ccccctggac cttcggcggg 300
ggcacaaagg tggagatcaa g 321

<210> 98
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence encoding 6A3.L1 Vk

<400> 98
gacatccaga tgacccagag ccccagctcc ctgagcgcca gcgtgggcga tagggtgacc 60
atcacctgcc tggccagcca gaccattggc gcctggctgg cctggtacca gcagaagccc 120
ggcaaggccc cccagctgct gatctacgcc gcaactaggc tcgccgacgg cgtgccctct 180
aggtttagcg gcagcggaag cggcaccgac ttcaccctga ccatcagcag cctgcagccc 240
gaggacttcg ccacctacta ctgccagcag ttcttcagca ccccctggac cttcggcggg 300
ggcacaaagg tggagatcaa g 321

<210> 99
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence encoding 6A3.L2 Vk

<400> 99
gacatccaga tgacccagag ccccagctcc ctgagcgcca gcgtgggcga tagggtgacc 60
atcacctgcc tggccagcca gaccattggc gcctggctgg cctggtacca gcagaagccc 120
ggcaaggccc ccaaactgct gatctacgcc gcaactaggc tcgccgacgg cgtgccctct 180
aggtttagcg gcagcggaag cggcaccaag ttcaccctga ccatcagcag cctgcagccc 240
gaggacttcg ccacctacta ctgccagcag ttcttcagca ccccctggac cttcggcggg 300
ggcacaaagg tggagatcaa g 321

<210> 100
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence encoding 6A3.L3 Vk

<400> 100
gacatccaga tgacccagag ccccagctcc ctgagcgcca gcgtgggcga tagggtgacc 60
atcacctgcc tggccagcca gaccattggc gcctggctgg cctggtacca gcagaagccc 120
ggcaaggccc cccagctgct gatctacgcc gcaactaggc tcgccgacgg cgtgccctct 180
aggtttagcg gcagcggaag cggcaccaag ttcaccctga ccatcagcag cctgcagccc 240
gaggacttcg ccacctacta ctgccagcag ttcttcagca ccccctggac cttcggcggg 300
ggcacaaagg tggagatcaa g 321

<210> 101
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence encoding 6A3c VH

<400> 101
gacgtccagc tgcaggagag cggccccggg ctggtgaagc cctctcagag cctgagcctg 60
acctgcaccg tgaccggcta cagcatcacc accgactacg cctggaactg gatcaggcag 120
ttccccggca acaagctgga gtggatgggc tacatcttct acagcggcag caccacctat 180
acccccagcc tcaagagcag gatcagcatc accagggaca cctccaagaa ccagttcttc 240
ctgcagctga acagcgtgac cacagaggac accgccacct actactgcgc caggggcgga 300
tacgacgtga actacttcga ctactggggc cagggcacca ctctgaccgt gagcagc 357

<210> 102
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence encoding 6A3c Vk

<400> 102
gacatccaga tgacccagag ccccgccagc cagagcgcct ctctgggcga gagcgtgaca 60
atcacctgcc tggccagcca gaccattggc gcttggctgg cctggtacca gcagaagccc 120
ggcaagagcc cccagctgct gatctacgcc gccactaggc tggccgacgg cgtgcccagc 180
aggtttagcg gcagcggcag cggcaccaag ttcagcttca agatcagcag cctgcaggcc 240
gaggacttcg tgtcctacta ctgccagcag ttcttcagca ccccctggac cttcggcggc 300
ggaaccaaac tcgagatcaa g 321

<210> 103
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleic acid sequence encoding 1A11.H0

<400> 103
caggtgcagc tggtgcagag cggagccgag gtgaagaagc ccggagccag cgtgaaggtg 60
agctgcaaag cctccggcta caccttcacc ggctacacca tgaactgggt caggcaggct 120
cccggccagg gcctggagtg gatgggcctg atcaacccct acaacggcgt gaccagctac 180
aaccagaagt tcaagggcag ggtgaccatg accagggaca ccagcatcag caccgcctac 240
atggaactga gcaggctgag gagcgacgac accgccgtgt attactgcgc caggggcgac 300
gggaactact ggtacttcga cgtatggggc cagggaacaa ccgtgaccgt gagcagc 357

<210> 104
<211> 315
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleic acid sequence encoding 1A11.L0

<400> 104
gagatcgtgc tgacacagag ccccgccacc ctgtctctga gccctggcga gagggccacc 60
ctgagctgca gcgccagcag cagcgtgacc tacatgcact ggtaccagca gaaacccggc 120
caggcccctc gcctgctgat ctacgagatc tctaagctgg ccagcggcat tcccgctagg 180
ttcagcggca gcggctcagg caccgacttc accctcacca tcagcagcct ggagcccgaa 240
gacttcgccg tctactactg ccaggagtgg aactaccccc ataccttcgg cggcgggacc 300
aaggtggaga tcaag 315

<210> 105
<211> 315
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleic acid sequence encoding 1A11.L1

<400> 105
gagatcgtgc tgactcagag ccccgccacc ctgagcctga gccccggcga aagggccaca 60
ctgagctgca gcgctagcag cagcgtgacc tacatgcact ggtaccagca gaagcccggc 120
caggccccta ggctgtggat ctacgagatc agcaagctgg ccagcggcat tcccgccagg 180
ttctcaggca gcggaagcgg caccgacttc accctcacca tcagctctct ggagcccgag 240
gacttcgccg tctactactg ccaggagtgg aactaccccc ataccttcgg cggcggcacc 300
aaggtggaga tcaag 315

<210> 106
<211> 315
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleic acid sequence encoding 1A11.L2

<400> 106
gagatcgtgc tgacccagag ccccgcaacc ctgagcctca gccctggcga gagggccact 60
ctgagctgct ctgccagcag cagcgtgacc tacatgcact ggtaccagca gaagcccgga 120
caggccccca ggctgctgat ctacgagatc agcaagctgg cctctggcat tcccgccagg 180
ttcagcggct caggcagcgg caccgactac accctgacca tcagcagcct ggaacccgag 240
gacttcgccg tctactactg ccaggagtgg aactatccct acaccttcgg cggcggcacc 300
aaggtggaga tcaag 315

<210> 107
<211> 315
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleic acid sequence encoding 1A11.L3

<400> 107
gagatcgtgc tgacccagag ccccgccaca ctgtcactgt ctcccggcga aagggccacc 60
ctgagctgca gcgcctctag cagcgtgacc tacatgcact ggtaccagca gaagcccggc 120
caggctccca ggctgtggat ctacgagatc agcaagctgg ccagcggcat ccctgccagg 180
ttcagcggca gcggcagcgg caccgactat accctgacca tcagcagcct cgagcccgag 240
gacttcgccg tctactactg ccaggagtgg aactaccccc acaccttcgg cggcgggacc 300
aaagtggaga tcaag 315

<210> 108
<211> 315
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleic acid sequence encoding 1A11.L4

<400> 108
gaaattgtgc tgacccagag ccccgccacc ctgagcctgt caccaggcga gagggcaact 60
ctgagctgca gcgccagctc tagcgtgacc tacatgcact ggtaccagca gaaacccgga 120
caggcccccc ggcccctgat ctacgagatc tccaagctgg ccagcggcat ccccgccagg 180
tttagcggca gcggcagcgg caccgacttc accctgacca tcagcagcct cgagcccgag 240
gacttcgccg tgtattactg ccaggagtgg aactaccccc acaccttcgg cggcggcacc 300
aaggtggaga tcaag 315

<210> 109
<211> 315
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleic acid sequence encoding 1A11.L5

<400> 109
gaaatcgtgc tgacccagag ccccgcaacc ctgagcctga gccccggaga gagggccact 60
ctgagctgca gcgccagcag cagcgtgacc tacatgcact ggtaccagca gaagcccggc 120
caggccccaa ggccctggat ctacgagatt agcaagctgg cctccggcat ccctgccagg 180
ttcagcggct caggcagcgg caccgactat accctcacca tcagcagcct ggagcccgag 240
gacttcgccg tctactactg ccaggagtgg aactaccccc acaccttcgg cggcggcacc 300
aaggtggaga tcaag 315

<210> 110
<211> 315
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleic acid sequence encoding 1A11.L6

<400> 110
gagatcgtgc tgacccagtc acccgcaaca ctgagcctga gcccaggaga gagggccacc 60
ctgagctgca gcgcctctag ctccgtgacc tacatgcact ggtaccagca gaagcccggc 120
caggccccca gaccctggat ctacgagatc agcaagctcg ccagcggcgt ccccgccagg 180
ttcagcggaa gcggcagcgg gaccgactac accctgacca tcagcagcct ggaacccgag 240
gacttcgccg tgtattactg ccaggagtgg aactaccccc acaccttcgg cggcggcacc 300
aaggtggaga tcaag 315

<210> 111
<211> 315
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleic acid sequence encoding 1A11.L7

<400> 111
gaaattgtgc tgacccagag ccccgccacc ctgagcctgt caccaggcga gagggcaact 60
ctgagctgca gcgccagctc tagcgtgacc tacatgcact ggtaccagca gaaacccgga 120
caggccccca agccctggat ctacgagatc tccaagctgg ccagcggcgt gcccgccagg 180
tttagcggca gcggcagcgg caccgactac accctgacca tcagcagcct cgagcccgag 240
gacttcgccg tgtattactg ccaggagtgg aactaccccc acaccttcgg cggcggcacc 300
aaggtggaga tcaag 315

<210> 112
<211> 315
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleic acid sequence encoding 1A11.L8

<400> 112
gaaatcgtgc tgacccagag ccccgcaacc ctgagcctga gccccggaga gagggccact 60
ctgagctgca gcgccagcag cagcgtgacc tacatgcact ggtaccagca gaagcccggc 120
caggccccaa agccctggat ctacgagatt agcaagctgg cctccggcgt ccctgccagg 180
ttcagcggct caggcagcgg cacctcctat accctcacca tcagcagcct ggagcccgag 240
gacttcgccg tctactactg ccaggagtgg aactaccccc acaccttcgg cggcggcacc 300
aaggtggaga tcaag 315

<210> 113
<211> 315
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleic acid sequence encoding 1A11.L9

<400> 113
gagatcgtgc tgacccagtc acccgcaaca ctgagcctga gcccaggaga gagggccacc 60
ctgagctgca gcgcctctag ctccgtgacc tacatgcact ggtaccagca gaagcccggc 120
caggccccca agccctggat ctacgagatc agcaagctcg ccagcggcgt ccccgtcagg 180
ttcagcggaa gcggcagcgg gaccagctac accctgacca tcagcagcct ggaacccgag 240
gacttcgccg tgtattactg ccaggagtgg aactaccct acaccttcgg cggcggcacc 300
aaggtggaga tcaag 315

<210> 114
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> 1A11.H3FL (Full length)

<400> 114
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30
Thr Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Leu Ile Asn Pro Tyr Asn Gly Val Thr Ser Tyr Asn Gln Lys Phe
50 55 60
Lys Gly Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Gly Asp Gly Asn Tyr Trp Tyr Phe Asp Val Trp Gly Gln Gly
100 105 110
Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly 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 Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
195 200 205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
210 215 220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu 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 His Glu Asp
260 265 270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
275 280 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr 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 Ala Leu Pro Ala Pro 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 Arg Asp Glu Leu 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 Lys Leu Thr Val Asp Lys
405 410 415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445
Lys

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

<220>
<223> 1A11.L4FL (Full length)

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

<210> 116
<211> 117
<212> PRT
<213> Homo Sapiens

<220>
<223> Human immunoglobulin heavy chain IGHV1-2 V gene
(leader plus V region) sequence

<400> 116
Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15
Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe

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

<210> 117
<211> 113
<212> PRT
<213> Homo Sapiens

<220>
<223> Human immunoglobulin kappa light chain IGKV3-11 V gene (leader plus V region)sequence

<400> 117

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

<210> 118
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> 1A11_H3-Fc (FULL LENGTH)

<400> 118

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

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly 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 Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
195 200 205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
210 215 220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Ala Gly Ala Pro
225 230 235 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
245 250 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
260 265 270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
275 280 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr 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 Ala Leu Pro Ala Pro 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 Arg Asp Glu Leu 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 Lys Leu Thr Val Asp Lys
405 410 415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445
Lys

<210> 119
<211> 1407
<212> DNA
<213> Artificial Sequence

<220>
<223> 1A11_VH3-Fc DNA (FULL LENGTH, WITH SIGNAL SEQUENCE)

<400> 119
atgggctggt cctgcatcat cctgtttctg gtggccaccg ccaccggtgt gcacagccag 60
gtgcagctgg tgcagagcgg agccgaggtg aagaaacccg gagccagcgt gaaggtgagc 120
tgcaaggcca gcggctacac cttcaccggc tacaccatga actgggtgag gcaggccccc 180
ggccagggac tcgagtggat gggcctgatc aacccctaca acggcgtgac cagctacaac 240
cagaagttca agggcagggt gaccctgacc agggatacca gcatcagcac cgcttacatg 300
gaactgagca ggctgaggtc cgacgacacc gccgtgtatt actgcgccag gggcgacggc 360
aactactggt acttcgatgt gtggggccag ggcaccaccg tcacagtgag cagcgccagc 420
accaagggcc ccagcgtgtt ccccctggcg cccagcagca agagcaccag cggcggcaca 480
gccgccctgg gctgcctggt gaaggactac ttccccgagc cagtgaccgt gtcctggaac 540
agcggagccc tgaccagcgg cgtgcacacc ttcccagctg tcctgcagag cagcggcctg 600
tacagcctga gcagcgtggt gaccgtgccc agcagcagcc tgggcaccca gacctacatc 660
tgtaacgtga accacaagcc cagcaacacc aaggtggaca agaaggtgga gcccaagagc 720
tgtgacaaga cccacacctg ccccccctgc cctgcccccg agctggccgg agcccccagc 780

gtgttcctgt tccccccaa gcctaaggac accctgatga tcagcagaac ccccgaggtg 840
acctgtgtgg tggtggatgt gagccacgag gaccctgagg tgaagttcaa ctggtacgtg 900
gacggcgtgg aggtgcacaa tgccaagacc aagcccaggg aggagcagta caacagcacc 960
taccgggtgg tgtccgtgct gaccgtgctg caccaggatt ggctgaacgg caaggagtac 1020
aagtgtaagg tgtccaacaa ggccctgcct gcccctatcg agaaaaccat cagcaaggcc 1080
aagggccagc ccagagagcc ccaggtgtac accctgcccc ctagcagaga tgagctgacc 1140
aagaaccagg tgtccctgac ctgcctggtg aagggcttct accccagcga catcgccgtg 1200
gagtgggaga gcaacggcca gcccgagaac aactacaaga ccacccccc tgtgctggac 1260
agcgatggca gcttcttcct gtacagcaag ctgaccgtgg acaagagcag atggcagcag 1320
ggcaacgtgt tcagctgctc cgtgatgcac gaggccctgc acaatcacta cacccagaag 1380
agcctgagcc tgtcccctgg caagtga 1407

<210> 120
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleic acid encoding 1A11 VH3 N98D

<400> 120
caggtgcagc tggtgcagag cggagccgag gtgaagaaac ccggagccag cgtgaaggtg 60
agctgcaagg ccagcggcta caccttcacc ggctacacca tgaactgggt gaggcaggcc 120
cccggccagg gactcgagtg gatgggcctg atcaacccct acaacggcgt gaccagctac 180
aaccagaagt tcaagggcag ggtgaccctg accagggata ccagcatcag caccgcttac 240
atggaactga gcaggctgag gtccgacgac accgccgtgt attactgcgc caggggcgac 300
ggcgactact ggtacttcga tgtgtggggc cagggcacca ccgtcacagt gagcagc 357

<210> 121
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> 1A11 VH3 N98D

<400> 121
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1   5   10   15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
            20   25   30
Thr Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45
Gly Leu Ile Asn Pro Tyr Asn Gly Val Thr Ser Tyr Asn Gln Lys Phe
    50   55   60
Lys Gly Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65   70   75   80
Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Gly Asp Gly Asp Tyr Trp Tyr Phe Asp Val Trp Gly Gln Gly
            100   105   110
Thr Thr Val Thr Val Ser Ser
        115

<210> 122
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleic acid encoding 1A11 VH3 N98E

<400> 122
caggtgcagc tggtgcagag cggagccgag gtgaagaaac ccggagccag cgtgaaggtg 60

agctgcaagg ccagcggcta caccttcacc ggctacacca tgaactgggt gaggcaggcc 120
cccggccagg gactcgagtg gatgggcctg atcaacccct acaacggcgt gaccagctac 180
aaccagaagt tcaagggcag ggtgaccctg accagggata ccagcatcag caccgcttac 240
atggaactga gcaggctgag gtccgacgac accgccgtgt attactgcgc caggggcgac 300
ggcgagtact ggtacttcga tgtgtggggc cagggcacca ccgtcacagt gagcagc 357

<210> 123
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> 1A11 VH3 N98E

<400> 123
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30
Thr Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Leu Ile Asn Pro Tyr Asn Gly Val Thr Ser Tyr Asn Gln Lys Phe
50 55 60
Lys Gly Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Gly Asp Gly Glu Tyr Trp Tyr Phe Asp Val Trp Gly Gln Gly
100 105 110
Thr Thr Val Thr Val Ser Ser
115

<210> 124
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleic acid encoding 1A11 VH3 F100bE

<400> 124
caggtgcagc tggtgcagag cggagccgag gtgaagaaac ccggagccag cgtgaaggtg 60
agctgcaagg ccagcggcta caccttcacc ggctacacca tgaactgggt gaggcaggcc 120
cccggccagg gactcgagtg gatgggcctg atcaacccct acaacggcgt gaccagctac 180
aaccagaagt tcaagggcag ggtgaccctg accagggata ccagcatcag caccgcttac 240
atggaactga gcaggctgag gtccgacgac accgccgtgt attactgcgc caggggcgac 300
ggcaactact ggtacgagga tgtgtggggc cagggcacca ccgtcacagt gagcagc 357

<210> 125
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> 1A11 VH3 F100bE

<400> 125
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30
Thr Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Leu Ile Asn Pro Tyr Asn Gly Val Thr Ser Tyr Asn Gln Lys Phe

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    50                  55                  60
Lys Gly Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80
Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Gly Asp Gly Asn Tyr Trp Tyr Glu Asp Val Trp Gly Gln Gly
            100                 105                 110
Thr Thr Val Thr Val Ser Ser
        115
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<210> 126
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleic acid encoding VH3 F100bH

<400> 126
caggtgcagc tggtgcagag cggagccgag gtgaagaaac ccggagccag cgtgaaggtg 60
agctgcaagg ccagcggcta caccttcacc ggctacacca tgaactgggt gaggcaggcc 120
cccggccagg gactcgagtg gatgggcctg atcaacccct acaacggcgt gaccagctac 180
aaccagaagt tcaagggcag ggtgaccctg accagggata ccagcatcag caccgcttac 240
atggaactga gcaggctgag gtccgacgac accgccgtgt attactgcgc caggggcgac 300
ggcaactact ggtaccacga tgtgtggggc cagggcacca ccgtcacagt gagcagc   357

<210> 127
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> 1A11 VH3 F100bH

<400> 127
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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1               5                  10                  15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
            20                  25                  30
Thr Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45
Gly Leu Ile Asn Pro Tyr Asn Gly Val Thr Ser Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Gly Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80
Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Gly Asp Gly Asn Tyr Trp Tyr His Asp Val Trp Gly Gln Gly
            100                 105                 110
Thr Thr Val Thr Val Ser Ser
        115
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<210> 128
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleic acid encoding VH3 F100bI

<400> 128
caggtgcagc tggtgcagag cggagccgag gtgaagaaac ccggagccag cgtgaaggtg 60
agctgcaagg ccagcggcta caccttcacc ggctacacca tgaactgggt gaggcaggcc 120

cccggccagg gactcgagtg gatgggcctg atcaacccct acaacggcgt gaccagctac 180
aaccagaagt tcaagggcag ggtgaccctg accagggata ccagcatcag caccgcttac 240
atggaactga gcaggctgag gtccgacgac accgccgtgt attactgcgc caggggcgac 300
ggcaactact ggtacatcga tgtgtggggc cagggcacca ccgtcacagt gagcagc 357

<210> 129
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> VH3 F100bI

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

<210> 130
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleic acid encoding VH3 F100bV

<400> 130
caggtgcagc tggtgcagag cggagccgag gtgaagaaac ccggagccag cgtgaaggtg 60
agctgcaagg ccagcggcta caccttcacc ggctacacca tgaactgggt gaggcaggcc 120
cccggccagg gactcgagtg gatgggcctg atcaacccct acaacggcgt gaccagctac 180
aaccagaagt tcaagggcag ggtgaccctg accagggata ccagcatcag caccgcttac 240
atggaactga gcaggctgag gtccgacgac accgccgtgt attactgcgc caggggcgac 300
ggcaactact ggtacgtgga tgtgtggggc cagggcacca ccgtcacagt gagcagc 357

<210> 131
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> VH3 F100bV

<400> 131
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30
Thr Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Leu Ile Asn Pro Tyr Asn Gly Val Thr Ser Tyr Asn Gln Lys Phe
50 55 60

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

<210> 132
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> VH3 N98D CDRH3

<400> 132
Gly Asp Gly Asp Tyr Trp Tyr Phe Asp Val
1 5 10

<210> 133
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> VH3 N98E CDRH3

<400> 133
Gly Asp Gly Glu Tyr Trp Tyr Phe Asp Val
1 5 10

<210> 134
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> VH3 F100bE CDRH3

<400> 134
Gly Asp Gly Asn Tyr Trp Tyr Glu Asp Val
1 5 10

<210> 135
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> VH3 F100bH CDRH3

<400> 135
Gly Asp Gly Asn Tyr Trp Tyr His Asp Val
1 5 10

<210> 136
<211> 10

<212> PRT
<213> Artificial Sequence

<220>
<223> VH3 F100bI CDRH3

<400> 136
Gly Asp Gly Asn Tyr Trp Tyr Ile Asp Val
 1   5   10

<210> 137
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> VH3 F100bV CDRH3

<400> 137
Gly Asp Gly Asn Tyr Trp Tyr Val Asp Val
 1   5   10

<210> 138
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> 6A3.L27 Vk

<400> 138
Asp Ile Gln Met Leu Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Leu Ala Ser Gln Thr Ile Gly Tyr Trp
            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 Thr Arg Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Met Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Phe Phe Ser Tyr Pro Trp
                85   90   95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105