SEQUENCE LISTING

<110> GlaxoSmithKline Intellectual Property Development Limited

<120> Antigen Binding Proteins

<130> PB65397P

<160> 112

<170> PatentIn version 3.5

<210> 1
<211> 17
<212> PRT
<213> Artificial

<220>
<223> H5L7, CDRL1 (Kabat defined)

<400> 1

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

Ala

<210> 2
<211> 7
<212> PRT
<213> Murine

<400> 2

Phe Ala Ser Thr Arg Asp Ser
1 5

<210> 3
<211> 9
<212> PRT
<213> Murine

<400> 3

Leu Gln His Phe Gly Thr Pro Pro Thr
1 5

<210> 4
<211> 114
<212> PRT
<213> Artificial

<220>
<223> H5L7, VL

<400> 4

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

Asp Arg Val Thr Ile Thr Cys Lys Ser Ser Gln Ser Leu Leu Asn Pro
20 25 30

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

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

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

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

His Phe Gly Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
            100                 105                 110

Lys Arg
```

<210> 5
<211> 220
<212> PRT
<213> Artificial

<220>
<223> H5L7, light chain humanised construct

<400> 5

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

Asp Arg Val Thr Ile Thr Cys Lys Ser Ser Gln Ser Leu Leu Asn Pro
            20                  25                  30

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

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

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

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

His Phe Gly Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
            100                 105                 110

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

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180 185 190

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

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> 6
<211> 5
<212> PRT
<213> Murine

<400> 6

Ala Tyr Gly Val Asn
1 5

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

<220>
<223> H5L7, CDRH2 (Kabat defined)

<400> 7

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

<210> 8
<211> 8
<212> PRT
<213> Murine

<400> 8

Glu Gly Asp Val Ala Phe Asp Tyr
1 5

<210> 9
<211> 116
<212> PRT
<213> Artificial

<220>
<223> H5L7, VH

<400> 9

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

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

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

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

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

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

Thr Val Ser Ser
115

<210> 10
<211> 446
<212> PRT
<213> Artificial

<220>
<223> H5L7, heavy chain humanised construct

<400> 10

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

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

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

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

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

```
Arg Glu Gly Asp Val Ala 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 Ser Ser Lys Ser Thr Ser Gly Gly 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 Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        195                 200                 205

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

Cys Pro Pro Cys Pro Ala Pro Glu Leu 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 His Glu Asp Pro Glu Val
            260                 265                 270

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285

Lys Pro Arg Glu Glu Gln Tyr 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 Ala Leu Pro Ala Pro 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 Arg Asp Glu Leu 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 Lys Leu Thr Val Asp Lys Ser Arg Trp
                405                 410                 415

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

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

<210> 11
<211> 220
<212> PRT
<213> Artificial

<220>
<223> H1L7, light chain humanised construct

<400> 11

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

Asp Arg Val Thr Ile Thr Cys Lys Ser Ser Gln Ser Leu Leu Asn Pro
            20                  25                  30

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

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

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

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

His Phe Gly Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
            100                 105                 110

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

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
    130                 135                 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145                 150                 155                 160
```

```
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
                165                 170                 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
            180                 185                 190

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

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215                 220
```

<210> 12
<211> 446
<212> PRT
<213> Artificial

<220>
<223> H1L7, heavy chain humanised construct

<400> 12

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

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

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

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

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Glu Gly Asp Val Ala 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 Ser Ser Lys Ser Thr Ser Gly Gly 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 Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        195                 200                 205

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

Cys Pro Pro Cys Pro Ala Pro Glu Leu 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 His Glu Asp Pro Glu Val
            260                 265                 270

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285

Lys Pro Arg Glu Glu Gln Tyr 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 Ala Leu Pro Ala Pro 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 Arg Asp Glu Leu 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 Lys Leu Thr Val Asp Lys Ser Arg Trp
                405                 410                 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            420                 425                 430
```

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

<210> 13
<211> 220
<212> PRT
<213> Artificial

<220>
<223> J7L7, light chain humanised construct

<400> 13

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

Asp Arg Val Thr Ile Thr Cys Lys Ser Ser Gln Ser Leu Leu Asn Pro
20 25 30

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

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

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

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

His Phe Gly Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
100 105 110

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

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180 185 190

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

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> 14
<211> 446
<212> PRT
<213> Artificial

<220>
<223> J7L7, heavy chain humanised construct

<400> 14

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

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

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

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

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

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

Arg Glu Gly Asp Val Ala 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 Ser Ser Lys Ser Thr Ser Gly Gly 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 Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        195                 200                 205

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    210                 215                 220
```

```
Cys Pro Pro Cys Pro Ala Pro Glu Leu 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 His Glu Asp Pro Glu Val
            260                 265                 270

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285

Lys Pro Arg Glu Glu Gln Tyr 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 Ala Leu Pro Ala Pro 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 Arg Asp Glu Leu 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 Lys Leu Thr Val Asp Lys Ser Arg Trp
                405                 410                 415

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

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


<210>  15
<211>  220
<212>  PRT
<213>  Artificial

<220>
<223>  H4L7, light chain humanised construct

<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 Lys Ser Ser Gln Ser Leu Leu Asn Pro
            20                  25                  30

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

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

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

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

His Phe Gly Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
            100                 105                 110

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

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
    130                 135                 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145                 150                 155                 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
                165                 170                 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
            180                 185                 190

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

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215                 220


<210>  16
<211>  446
<212>  PRT
<213>  Artificial

<220>
<223>  H4L7, heavy chain humanised construct

<400>  16

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

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

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

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

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Glu Gly Asp Val Ala 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 Ser Ser Lys Ser Thr Ser Gly Gly 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 Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        195                 200                 205

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

Cys Pro Pro Cys Pro Ala Pro Glu Leu 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 His Glu Asp Pro Glu Val
            260                 265                 270

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285
```

Lys Pro Arg Glu Glu Gln Tyr 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 Ala Leu Pro Ala Pro 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 Arg Asp Glu Leu 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 Lys Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

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

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

<210> 17
<211> 220
<212> PRT
<213> Artificial

<220>
<223> J11L7, light chain humanised construct

<400> 17

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

Asp Arg Val Thr Ile Thr Cys Lys Ser Ser Gln Ser Leu Leu Asn Pro
20 25 30

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

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

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

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

His Phe Gly Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
            100                 105                 110

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

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
    130                 135                 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145                 150                 155                 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
                165                 170                 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
            180                 185                 190

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

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215                 220
```

<210> 18
<211> 446
<212> PRT
<213> Artificial

<220>
<223> J11L7, heavy chain humanised construct

<400> 18

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

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

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

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

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

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

Arg Glu Gly Asp Val Ala 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 Ser Ser Lys Ser Thr Ser Gly Gly 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 Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        195                 200                 205

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

Cys Pro Pro Cys Pro Ala Pro Glu Leu 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 His Glu Asp Pro Glu Val
            260                 265                 270

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285

Lys Pro Arg Glu Glu Gln Tyr 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 Ala Leu Pro Ala Pro 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 Arg Asp Glu Leu 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 Lys Leu Thr Val Asp Lys Ser Arg Trp
                405                 410                 415

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

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


<210>  19
<211>  220
<212>  PRT
<213>  Artificial

<220>
<223>  H2L7, light chain humanised construct

<400>  19

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

Asp Arg Val Thr Ile Thr Cys Lys Ser Ser Gln Ser Leu Leu Asn Pro
            20                  25                  30

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

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

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

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

His Phe Gly Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
            100                 105                 110

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

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
    130                 135                 140
```

```
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145                 150                 155                 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
                165                 170                 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
            180                 185                 190

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

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215                 220
```

<210> 20
<211> 446
<212> PRT
<213> Artificial

<220>
<223> H2L7, heavy chain humanised construct

<400> 20

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

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

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

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

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Glu Gly Asp Val Ala 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 Ser Ser Lys Ser Thr Ser Gly Gly 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 Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        195                 200                 205

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

Cys Pro Pro Cys Pro Ala Pro Glu Leu 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 His Glu Asp Pro Glu Val
            260                 265                 270

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285

Lys Pro Arg Glu Glu Gln Tyr 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 Ala Leu Pro Ala Pro 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 Arg Asp Glu Leu 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 Lys Leu Thr Val Asp Lys Ser Arg Trp
                405                 410                 415
```

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

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

<210> 21
<211> 220
<212> PRT
<213> Artificial

<220>
<223> J13L7, light chain humanised construct

<400> 21

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

Asp Arg Val Thr Ile Thr Cys Lys Ser Ser Gln Ser Leu Leu Asn Pro
20 25 30

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

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

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

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

His Phe Gly Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
100 105 110

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

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180 185 190

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

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> 22
<211> 446
<212> PRT
<213> Artificial

<220>
<223> J13L7, heavy chain humanised construct

<400> 22

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

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

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

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

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

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

Arg Glu Gly Asp Val Ala 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 Ser Ser Lys Ser Thr Ser Gly Gly 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 Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
195 200 205

```
Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    210                 215                 220

Cys Pro Pro Cys Pro Ala Pro Glu Leu 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 His Glu Asp Pro Glu Val
            260                 265                 270

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285

Lys Pro Arg Glu Glu Gln Tyr 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 Ala Leu Pro Ala Pro 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 Arg Asp Glu Leu 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 Lys Leu Thr Val Asp Lys Ser Arg Trp
                405                 410                 415

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

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

<210> 23
<211> 220
<212> PRT
<213> Artificial

<220>
<223> H7L7, light chain humanised construct

<400> 23

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

Asp Arg Val Thr Ile Thr Cys Lys Ser Ser Gln Ser Leu Leu Asn Pro
20 25 30

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

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

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

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

His Phe Gly Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
100 105 110

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

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180 185 190

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

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> 24
<211> 446
<212> PRT
<213> Artificial

<220>
<223> H7L7, heavy chain humanised construct

<400> 24

```
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 Ile Ser Ala Tyr
            20                  25                  30

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

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

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Glu Gly Asp Val Ala 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 Ser Ser Lys Ser Thr Ser Gly Gly 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 Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        195                 200                 205

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

Cys Pro Pro Cys Pro Ala Pro Glu Leu 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 His Glu Asp Pro Glu Val
            260                 265                 270
```

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
275 280 285

Lys Pro Arg Glu Glu Gln Tyr 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 Ala Leu Pro Ala Pro 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 Arg Asp Glu Leu 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 Lys Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

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

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

<210> 25
<211> 220
<212> PRT
<213> Artificial

<220>
<223> J0L7, light chain humanised construct

<400> 25

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

Asp Arg Val Thr Ile Thr Cys Lys Ser Ser Gln Ser Leu Leu Asn Pro
20 25 30

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

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

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

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

His Phe Gly Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
            100                 105                 110

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

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
    130                 135                 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145                 150                 155                 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
                165                 170                 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
            180                 185                 190

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

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215                 220
```

<210> 26
<211> 446
<212> PRT
<213> Artificial

<220>
<223> J0L7, heavy chain humanised construct

<400> 26

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

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

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

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

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

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

Arg Glu Gly Asp Val Ala 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 Ser Ser Lys Ser Thr Ser Gly Gly 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 Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        195                 200                 205

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

Cys Pro Pro Cys Pro Ala Pro Glu Leu 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 His Glu Asp Pro Glu Val
            260                 265                 270

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285

Lys Pro Arg Glu Glu Gln Tyr 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 Ala Leu Pro Ala Pro 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 Arg Asp Glu Leu 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 Lys Leu Thr Val Asp Lys Ser Arg Trp
                405                 410                 415

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

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


<210>  27
<211>  220
<212>  PRT
<213>  Artificial

<220>
<223>  HOL7, light chain humanised construct

<400>  27

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

Asp Arg Val Thr Ile Thr Cys Lys Ser Ser Gln Ser Leu Leu Asn Pro
            20                  25                  30

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

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

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

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

His Phe Gly Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
            100                 105                 110

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

```
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
    130                 135                 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145                 150                 155                 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
                165                 170                 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
            180                 185                 190

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

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215                 220
```

<210> 28
<211> 446
<212> PRT
<213> Artificial

<220>
<223> HOL7, heavy chain humanised construct

<400> 28

```
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 Ile Ser Ala Tyr
            20                  25                  30

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

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

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Glu Gly Asp Val Ala 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 Ser Ser Lys Ser Thr Ser Gly Gly 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 Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        195                 200                 205

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

Cys Pro Pro Cys Pro Ala Pro Glu Leu 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 His Glu Asp Pro Glu Val
            260                 265                 270

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285

Lys Pro Arg Glu Glu Gln Tyr 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 Ala Leu Pro Ala Pro 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 Arg Asp Glu Leu 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
```

eolf-seql

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

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

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

<210> 29
<211> 220
<212> PRT
<213> Artificial

<220>
<223> H1L1, light chain humanised construct

<400> 29

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

Asp Arg Val Thr Ile Thr Cys Lys Ser Ser Gln Ser Leu Leu Asn Gly
20 25 30

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

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

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

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

His Phe Gly Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
100 105 110

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

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180 185 190

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

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> 30
<211> 446
<212> PRT
<213> Artificial

<220>
<223> H1L1, heavy chain humanised construct

<400> 30

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

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

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

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

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Glu Gly Asp Val Ala 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 Ser Ser Lys Ser Thr Ser Gly Gly 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 Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        195                 200                 205

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

Cys Pro Pro Cys Pro Ala Pro Glu Leu 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 His Glu Asp Pro Glu Val
            260                 265                 270

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285

Lys Pro Arg Glu Glu Gln Tyr 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 Ala Leu Pro Ala Pro 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 Arg Asp Glu Leu 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 Lys Leu Thr Val Asp Lys Ser Arg Trp
                405                 410                 415

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

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

<210> 31
<211> 220
<212> PRT
<213> Artificial

<220>
<223> H5L1, light chain humanised construct

<400> 31

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

Asp Arg Val Thr Ile Thr Cys Lys Ser Ser Gln Ser Leu Leu Asn Gly
            20                  25                  30

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

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

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

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

His Phe Gly Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
            100                 105                 110

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

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
    130                 135                 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145                 150                 155                 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
                165                 170                 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
            180                 185                 190

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

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215                 220
```

<210> 32
<211> 446
<212> PRT
<213> Artificial

<220>

eolf-seql

<223> H5L1, heavy chain humanised construct

<400> 32

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

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

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

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

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Glu Gly Asp Val Ala 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 Ser Ser Lys Ser Thr Ser Gly Gly 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 Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        195                 200                 205

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

Cys Pro Pro Cys Pro Ala Pro Glu Leu 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 His Glu Asp Pro Glu Val
260 265 270

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
275 280 285

Lys Pro Arg Glu Glu Gln Tyr 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 Ala Leu Pro Ala Pro 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 Arg Asp Glu Leu 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 Lys Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

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

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

<210> 33
<211> 220
<212> PRT
<213> Artificial

<220>
<223> J7L1, light chain humanised construct

<400> 33

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

Asp Arg Val Thr Ile Thr Cys Lys Ser Ser Gln Ser Leu Leu Asn Gly
20 25 30

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

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

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

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

His Phe Gly Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
            100                 105                 110

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

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
    130                 135                 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145                 150                 155                 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
                165                 170                 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
            180                 185                 190

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

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215                 220


<210>  34
<211>  446
<212>  PRT
<213>  Artificial

<220>
<223>  J7L1, heavy chain humanised construct

<400>  34

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

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

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

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

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

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

Arg Glu Gly Asp Val Ala 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 Ser Ser Lys Ser Thr Ser Gly Gly 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 Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        195                 200                 205

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

Cys Pro Pro Cys Pro Ala Pro Glu Leu 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 His Glu Asp Pro Glu Val
            260                 265                 270

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285

Lys Pro Arg Glu Glu Gln Tyr 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 Ala Leu Pro Ala Pro 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 Arg Asp Glu Leu 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 Lys Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

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

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

<210> 35
<211> 220
<212> PRT
<213> Artificial

<220>
<223> J11L1, light chain humanised construct

<400> 35

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

Asp Arg Val Thr Ile Thr Cys Lys Ser Ser Gln Ser Leu Leu Asn Gly
20 25 30

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

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

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

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

His Phe Gly Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
100 105 110

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

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
    130                 135                 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145                 150                 155                 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
                165                 170                 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
            180                 185                 190

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

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215                 220
```

<210> 36
<211> 446
<212> PRT
<213> Artificial

<220>
<223> J11L1, heavy chain humanised construct

<400> 36

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

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

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

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

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

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

Arg Glu Gly Asp Val Ala 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 Ser Ser Lys Ser Thr Ser Gly Gly 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 Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        195                 200                 205

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

Cys Pro Pro Cys Pro Ala Pro Glu Leu 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 His Glu Asp Pro Glu Val
            260                 265                 270

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285

Lys Pro Arg Glu Glu Gln Tyr 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 Ala Leu Pro Ala Pro 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 Arg Asp Glu Leu 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 Lys Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

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

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

<210> 37
<211> 220
<212> PRT
<213> Artificial

<220>
<223> J13L1, light chain humanised construct

<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 Lys Ser Ser Gln Ser Leu Leu Asn Gly
20 25 30

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

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

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

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

His Phe Gly Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
100 105 110

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

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180 185 190

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

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> 38
<211> 446
<212> PRT
<213> Artificial

<220>
<223> J13L1, heavy chain humanised construct

<400> 38

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

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

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

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

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

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

Arg Glu Gly Asp Val Ala 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 Ser Ser Lys Ser Thr Ser Gly Gly 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 Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        195                 200                 205

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

Cys Pro Pro Cys Pro Ala Pro Glu Leu 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 His Glu Asp Pro Glu Val
            260                 265                 270

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285

Lys Pro Arg Glu Glu Gln Tyr 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 Ala Leu Pro Ala Pro 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 Arg Asp Glu Leu 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 Lys Leu Thr Val Asp Lys Ser Arg Trp
                405                 410                 415

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

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

<210> 39
<211> 220
<212> PRT
<213> Artificial

<220>
<223> H7L1, light chain humanised construct

<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 Lys Ser Ser Gln Ser Leu Leu Asn Gly
            20                  25                  30

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

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

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

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

His Phe Gly Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
            100                 105                 110

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

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
    130                 135                 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145                 150                 155                 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
                165                 170                 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
            180                 185                 190

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

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215                 220
```

<210> 40
<211> 446

<212> PRT
<213> Artificial

<220>
<223> H7L1, heavy chain humanised construct

<400> 40

```
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 Ile Ser Ala Tyr
            20                  25                  30

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

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

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Glu Gly Asp Val Ala 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 Ser Ser Lys Ser Thr Ser Gly Gly 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 Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        195                 200                 205

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

Cys Pro Pro Cys Pro Ala Pro Glu Leu 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 His Glu Asp Pro Glu Val
            260                 265                 270

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285

Lys Pro Arg Glu Glu Gln Tyr 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 Ala Leu Pro Ala Pro 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 Arg Asp Glu Leu 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 Lys Leu Thr Val Asp Lys Ser Arg Trp
                405                 410                 415

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

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


<210>  41
<211>  220
<212>  PRT
<213>  Artificial

<220>
<223>  JOL1, light chain humanised construct

<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 Lys Ser Ser Gln Ser Leu Leu Asn Gly
            20                  25                  30
```

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

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

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

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

His Phe Gly Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
100 105 110

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

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180 185 190

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

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> 42
<211> 446
<212> PRT
<213> Artificial

<220>
<223> JOL1, heavy chain humanised construct

<400> 42

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

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

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

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

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

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

Arg Glu Gly Asp Val Ala 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 Ser Ser Lys Ser Thr Ser Gly Gly 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 Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        195                 200                 205

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

Cys Pro Pro Cys Pro Ala Pro Glu Leu 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 His Glu Asp Pro Glu Val
            260                 265                 270

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285

Lys Pro Arg Glu Glu Gln Tyr 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 Ala Leu Pro Ala Pro 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 Arg Asp Glu Leu 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 Lys Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

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

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

<210> 43
<211> 220
<212> PRT
<213> Artificial

<220>
<223> H0L1, light chain humanised construct

<400> 43

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

Asp Arg Val Thr Ile Thr Cys Lys Ser Ser Gln Ser Leu Leu Asn Gly
20 25 30

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

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

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

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

His Phe Gly Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
100 105 110

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

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180 185 190

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

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> 44
<211> 446
<212> PRT
<213> Artificial

<220>
<223> HOL1, heavy chain humanised construct

<400> 44

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 Ile Ser Ala Tyr
20 25 30

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

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

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

```
Arg Glu Gly Asp Val Ala 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 Ser Ser Lys Ser Thr Ser Gly Gly 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 Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        195                 200                 205

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

Cys Pro Pro Cys Pro Ala Pro Glu Leu 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 His Glu Asp Pro Glu Val
            260                 265                 270

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285

Lys Pro Arg Glu Glu Gln Tyr 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 Ala Leu Pro Ala Pro 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 Arg Asp Glu Leu 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 Lys Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

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

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

<210> 45
<211> 106
<212> PRT
<213> Human

<400> 45

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
1 5 10 15

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

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
35 40 45

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
50 55 60

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65 70 75 80

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

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 46
<211> 330
<212> PRT
<213> Human

<400> 46

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

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

```
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35                  40                  45

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65                  70                  75                  80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
            100                 105                 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
        115                 120                 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
    130                 135                 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145                 150                 155                 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
                165                 170                 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
            180                 185                 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
        195                 200                 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
    210                 215                 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225                 230                 235                 240

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
                245                 250                 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
            260                 265                 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
        275                 280                 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
    290                 295                 300
```

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 47
<211> 116
<212> PRT
<213> Murine

<400> 47

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

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

Gly Val Asn Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

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

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

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

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

Thr Val Ser Ser
115

<210> 48
<211> 114
<212> PRT
<213> Murine

<400> 48

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

Gln Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Gly
20 25 30

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

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

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

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

His Phe Gly Thr Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
100 105 110

Lys Arg

<210> 49
<211> 446
<212> PRT
<213> Artificial

<220>
<223> IMP731, heavy chain sequence

<400> 49

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

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

Gly Val Asn Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

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

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

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

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

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

Pro Ser Ser Lys Ser Thr Ser Gly Gly 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 Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        195                 200                 205

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

Cys Pro Pro Cys Pro Ala Pro Glu Leu 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 His Glu Asp Pro Glu Val
            260                 265                 270

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285

Lys Pro Arg Glu Glu Gln Tyr 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 Ala Leu Pro Ala Pro 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 Arg Asp Glu Leu 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 Lys Leu Thr Val Asp Lys Ser Arg Trp
                405                 410                 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            420                 425                 430
```

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

<210> 50
<211> 220
<212> PRT
<213> Artificial

<220>
<223> IMP731, light chain sequence

<400> 50

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

Gln Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Gly
20 25 30

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

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

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

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

His Phe Gly Thr Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
100 105 110

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

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180 185 190

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

eolf-seql

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> 51
<211> 417
<212> PRT
<213> Artificial

<220>
<223> Recombinant human LAG-3-ECD-His6

<400> 51

Leu Gln Pro Gly Ala Glu Val Pro Val Val Trp Ala Gln Glu Gly Ala
1 5 10 15

Pro Ala Gln Leu Pro Cys Ser Pro Thr Ile Pro Leu Gln Asp Leu Ser
20 25 30

Leu Leu Arg Arg Ala Gly Val Thr Trp Gln His Gln Pro Asp Ser Gly
35 40 45

Pro Pro Ala Ala Ala Pro Gly His Pro Leu Ala Pro Gly Pro His Pro
50 55 60

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

Ser Val Gly Pro Gly Gly Leu Arg Ser Gly Arg Leu Pro Leu Gln Pro
85 90 95

Arg Val Gln Leu Asp Glu Arg Gly Arg Gln Arg Gly Asp Phe Ser Leu
100 105 110

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

Val His Leu Arg Asp Arg Ala Leu Ser Cys Arg Leu Arg Leu Arg Leu
130 135 140

Gly Gln Ala Ser Met Thr Ala Ser Pro Pro Gly Ser Leu Arg Ala Ser
145 150 155 160

Asp Trp Val Ile Leu Asn Cys Ser Phe Ser Arg Pro Asp Arg Pro Ala
165 170 175

Ser Val His Trp Phe Arg Asn Arg Gly Gln Gly Arg Val Pro Val Arg
180 185 190

Glu Ser Pro His His His Leu Ala Glu Ser Phe Leu Phe Leu Pro Gln
195 200 205

Val Ser Pro Met Asp Ser Gly Pro Trp Gly Cys Ile Leu Thr Tyr Arg
210 215 220

```
Asp Gly Phe Asn Val Ser Ile Met Tyr Asn Leu Thr Val Leu Gly Leu
225                 230                 235                 240

Glu Pro Pro Thr Pro Leu Thr Val Tyr Ala Gly Ala Gly Ser Arg Val
                245                 250                 255

Gly Leu Pro Cys Arg Leu Pro Ala Gly Val Gly Thr Arg Ser Phe Leu
            260                 265                 270

Thr Ala Lys Trp Thr Pro Pro Gly Gly Gly Pro Asp Leu Leu Val Thr
        275                 280                 285

Gly Asp Asn Gly Asp Phe Thr Leu Arg Leu Glu Asp Val Ser Gln Ala
    290                 295                 300

Gln Ala Gly Thr Tyr Thr Cys His Ile His Leu Gln Glu Gln Gln Leu
305                 310                 315                 320

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

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

Ser Gly Gln Glu Arg Phe Val Trp Ser Ser Leu Asp Thr Pro Ser Gln
        355                 360                 365

Arg Ser Phe Ser Gly Pro Trp Leu Glu Ala Gln Glu Ala Gln Leu Leu
    370                 375                 380

Ser Gln Pro Trp Gln Cys Gln Leu Tyr Gln Gly Glu Arg Leu Leu Gly
385                 390                 395                 400

Ala Ala Val Tyr Phe Thr Glu Leu Ser Ser Pro His His His His His
                405                 410                 415

His
```

<210> 52
<211> 417
<212> PRT
<213> Artificial

<220>
<223> Recombinant cynomolgus macaque LAG-3 ECD-His6

<400> 52

```
Pro Gln Pro Gly Ala Glu Ile Ser Val Val Trp Ala Gln Glu Gly Ala
1               5                   10                  15
```

```
Pro Ala Gln Leu Pro Cys Ser Pro Thr Ile Pro Leu Gln Asp Leu Ser
            20                  25                  30

Leu Leu Arg Arg Ala Gly Val Thr Trp Gln His Gln Pro Asp Ser Gly
        35                  40                  45

Pro Pro Ala Pro Ala Pro Gly His Pro Pro Ala Pro Gly His Arg Pro
    50                  55                  60

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

Ser Val Gly Pro Gly Gly Leu Arg Ser Gly Arg Leu Pro Leu Gln Pro
                85                  90                  95

Arg Val Gln Leu Asp Glu Arg Gly Arg Gln Arg Gly Asp Phe Ser Leu
            100                 105                 110

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

Val His Leu Arg Asp Arg Ala Leu Ser Cys Arg Leu Arg Leu Arg Val
    130                 135                 140

Gly Gln Ala Ser Met Thr Ala Ser Pro Pro Gly Ser Leu Arg Thr Ser
145                 150                 155                 160

Asp Trp Val Ile Leu Asn Cys Ser Phe Ser Arg Pro Asp Arg Pro Ala
                165                 170                 175

Ser Val His Trp Phe Arg Ser Arg Gly Gln Gly Arg Val Pro Val Gln
            180                 185                 190

Gly Ser Pro His His His Leu Ala Glu Ser Phe Leu Phe Leu Pro His
        195                 200                 205

Val Gly Pro Met Asp Ser Gly Leu Trp Gly Cys Ile Leu Thr Tyr Arg
    210                 215                 220

Asp Gly Phe Asn Val Ser Ile Met Tyr Asn Leu Thr Val Leu Gly Leu
225                 230                 235                 240

Glu Pro Ala Thr Pro Leu Thr Val Tyr Ala Gly Ala Gly Ser Arg Val
                245                 250                 255

Glu Leu Pro Cys Arg Leu Pro Pro Ala Val Gly Thr Gln Ser Phe Leu
            260                 265                 270

Thr Ala Lys Trp Ala Pro Pro Gly Gly Gly Pro Asp Leu Leu Val Ala
        275                 280                 285
```

Gly Asp Asn Gly Asp Phe Thr Leu Arg Leu Glu Asp Val Ser Gln Ala
290 295 300

Gln Ala Gly Thr Tyr Ile Cys His Ile Arg Leu Gln Gly Gln Gln Leu
305 310 315 320

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

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

Ser Gly Gln Glu His Phe Val Trp Ser Pro Leu Asn Thr Pro Ser Gln
355 360 365

Arg Ser Phe Ser Gly Pro Trp Leu Glu Ala Gln Glu Ala Gln Leu Leu
370 375 380

Ser Gln Pro Trp Gln Cys Gln Leu His Gln Gly Glu Arg Leu Leu Gly
385 390 395 400

Ala Ala Val Tyr Phe Thr Glu Leu Ser Ser Pro His His His His His
405 410 415

His

<210> 53
<211> 417
<212> PRT
<213> Artificial

<220>
<223> Recombinant baboon LAG-3 ECD-His6

<400> 53

Pro Gln Pro Gly Ala Glu Ile Ser Val Val Trp Ala Gln Glu Gly Ala
1 5 10 15

Pro Ala Gln Leu Pro Cys Ser Pro Thr Ile Pro Leu Gln Asp Leu Ser
20 25 30

Leu Leu Arg Arg Ala Gly Val Thr Trp Gln His Gln Pro Asp Ser Gly
35 40 45

Pro Pro Ala Pro Ala Pro Gly His Pro Pro Ala Pro Gly His Arg Pro
50 55 60

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

Ser Val Gly Pro Gly Gly Leu Arg Ser Gly Arg Leu Pro Leu Gln Pro
85 90 95

```
Arg Val Gln Leu Asp Glu Arg Gly Arg Gln Arg Gly Asp Phe Ser Leu
            100                 105                 110

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

Val His Leu Arg Asp Arg Ala Leu Ser Cys Arg Leu Arg Leu Arg Val
    130                 135                 140

Gly Gln Ala Ser Met Thr Ala Ser Pro Pro Gly Ser Leu Arg Thr Ser
145                 150                 155                 160

Asp Trp Val Ile Leu Asn Cys Ser Phe Ser Arg Pro Asp Arg Pro Ala
                165                 170                 175

Ser Val His Trp Phe Arg Ser Arg Gly Gln Gly Gln Val Pro Val Gln
            180                 185                 190

Glu Ser Pro His His His Leu Ala Glu Ser Phe Leu Phe Leu Pro His
        195                 200                 205

Val Gly Pro Met Asp Ser Gly Leu Trp Gly Cys Ile Leu Thr Tyr Arg
    210                 215                 220

Asp Gly Phe Asn Val Ser Ile Met Tyr Asn Leu Thr Val Leu Gly Leu
225                 230                 235                 240

Glu Pro Thr Thr Pro Leu Thr Val Tyr Ala Gly Ala Gly Ser Arg Val
                245                 250                 255

Glu Leu Pro Cys Arg Leu Pro Pro Ala Val Gly Thr Gln Ser Phe Leu
            260                 265                 270

Thr Ala Lys Trp Ala Pro Pro Gly Gly Gly Pro Asp Leu Leu Val Val
        275                 280                 285

Gly Asp Asn Gly Asn Phe Thr Leu Arg Leu Glu Asp Val Ser Gln Ala
    290                 295                 300

Gln Ala Gly Thr Tyr Ile Cys His Ile Arg Leu Gln Gly Gln Gln Leu
305                 310                 315                 320

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

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

Ser Gly Gln Glu Arg Phe Val Trp Ser Pro Leu Asn Thr Pro Ser Gln
        355                 360                 365
```

Arg Ser Phe Ser Gly Pro Trp Leu Glu Ala Gln Glu Ala Gln Leu Leu
370 375 380

Ser Gln Pro Trp Gln Cys Gln Leu His Gln Gly Glu Arg Leu Leu Gly
385 390 395 400

Ala Ala Val Tyr Phe Thr Glu Leu Ser Ser Pro His His His His His
405 410 415

His

<210> 54
<211> 19
<212> PRT
<213> Murine

<400> 54

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

Val His Ser

<210> 55
<211> 20
<212> PRT
<213> Murine

<400> 55

Met Glu Ser Gln Thr Gln Val Leu Met Phe Leu Leu Leu Trp Val Ser
1 5 10 15

Gly Ala Cys Ala
20

<210> 56
<211> 16
<212> PRT
<213> Human

<400> 56

Met Pro Leu Leu Leu Leu Leu Pro Leu Leu Trp Ala Gly Ala Leu Ala
1 5 10 15

<210> 57
<211> 51
<212> DNA
<213> Artificial

<220>
<223> H5L7, CDRL1 (Kabat defined)

<400> 57

aagagcagcc agagcctgct gaaccccagc aaccagaaga actacctggc c 51

<210> 58
<211> 21
<212> DNA
<213> Murine

<400> 58
ttcgcctcta ccagggattc c 21

<210> 59
<211> 27
<212> DNA
<213> Murine

<400> 59
ctgcagcact tcggcacccc tcccact 27

<210> 60
<211> 342
<212> DNA
<213> Artificial

<220>
<223> H5L7, VL

<400> 60
gacatccaga tgacccagag cccctctagc ctcagcgcca gcgtgggcga cagggtgacc 60

atcacctgca agagcagcca gagcctgctg aaccccagca accagaagaa ctacctggcc 120

tggtaccagc agaaacccgg caaggccccc aagctgctgg tctacttcgc ctctaccagg 180

gattccggcg tccccagcag gttcagcggc agcggcagcg gcaccgactt cacactgacc 240

atcagcagcc tgcagcccga ggacttcgcc acctactact gcctgcagca cttcggcacc 300

cctcccactt ttggccaggg caccaagctg gagattaagc gt 342

<210> 61
<211> 660
<212> DNA
<213> Artificial

<220>
<223> H5L7, light chain humanised construct

<400> 61
gacatccaga tgacccagag cccctctagc ctcagcgcca gcgtgggcga cagggtgacc 60

atcacctgca agagcagcca gagcctgctg aaccccagca accagaagaa ctacctggcc 120

tggtaccagc agaaacccgg caaggccccc aagctgctgg tctacttcgc ctctaccagg 180

gattccggcg tccccagcag gttcagcggc agcggcagcg gcaccgactt cacactgacc 240

atcagcagcc tgcagcccga ggacttcgcc acctactact gcctgcagca cttcggcacc 300

cctcccactt ttggccaggg caccaagctg gagattaagc gtacggtggc cgcccccagc 360

gtgttcatct tcccccccag cgatgagcag ctgaagagcg gcaccgccag cgtggtgtgt 420

ctgctgaaca acttctaccc ccgggaggcc aaggtgcagt ggaaggtgga caatgccctg 480

cagagcggca acagccagga gagcgtgacc gagcaggaca gcaaggactc cacctacagc 540

ctgagcagca ccctgaccct gagcaaggcc gactacgaga agcacaaggt gtacgcctgt 600

gaggtgaccc accagggcct gtccagcccc gtgaccaaga gcttcaaccg gggcgagtgc 660

<210> 62
<211> 15
<212> DNA
<213> Murine

<400> 62
gcctacggcg tcaac 15

<210> 63
<211> 48
<212> DNA
<213> Artificial

<220>
<223> H5L7, CDRH2 (Kabat defined)

<400> 63
atgatctggg acgacggcag caccgactac gacagcgccc tgaagagc 48

<210> 64
<211> 24
<212> DNA
<213> Murine

<400> 64
gagggcgacg tggccttcga ttac 24

<210> 65
<211> 348
<212> DNA
<213> Artificial

<220>
<223> H5L7, VH

<400> 65
caggtgcagc tccaggagag cggccccggc ctggtgaagc ctagcgagac cctgagcctg 60

acctgcaccg tgagcggctt ctccctgacc gcctacggcg tcaactggat caggcagccc 120

cccggcaaag gcctggagtg gattgggatg atctgggacg acggcagcac cgactacgac 180

agcgccctga agagcagggt gaccatcagc gtggacacca gcaagaacca gttcagcctg 240

aagctgagca gcgtgactgc cgccgacacc gccgtctatt actgcgccag ggagggcgac 300

gtggccttcg attactgggg ccagggcaca ctagtgaccg tgtccagc 348

<210> 66
<211> 1338
<212> DNA
<213> Artificial

<220>
<223> H5L7, heavy chain humanised construct

<400> 66

caggtgcagc tccaggagag cggccccggc ctggtgaagc ctagcgagac cctgagcctg 60

acctgcaccg tgagcggctt ctccctgacc gcctacggcg tcaactggat caggcagccc 120

cccggcaaag gcctggagtg gattgggatg atctgggacg acggcagcac cgactacgac 180

agcgccctga agagcagggt gaccatcagc gtggacacca gcaagaacca gttcagcctg 240

aagctgagca gcgtgactgc cgccgacacc gccgtctatt actgcgccag ggagggcgac 300

gtggccttcg attactgggg ccagggcaca ctagtgaccg tgtccagcgc cagcaccaag 360

ggccccagcg tgttccccct ggccccccagc agcaagagca ccagcggcgg cacagccgcc 420

ctgggctgcc tggtgaagga ctacttcccc gaaccggtga ccgtgtcctg gaacagcgga 480

gccctgacca gcggcgtgca caccttcccc gccgtgctgc agagcagcgg cctgtacagc 540

ctgagcagcg tggtgaccgt gcccagcagc agcctgggca cccagaccta catctgtaac 600

gtgaaccaca agcccagcaa caccaaggtg gacaagaagg tggagcccaa gagctgtgac 660

aagacccaca cctgcccccc ctgccctgcc cccgagctgc tgggaggccc cagcgtgttc 720

ctgttccccc ccaagcctaa ggacaccctg atgatcagca gaaccccga ggtgacctgt 780

gtggtggtgg atgtgagcca cgaggaccct gaggtgaagt tcaactggta cgtggacggc 840

gtggaggtgc acaatgccaa gaccaagccc agggaggagc agtacaacag cacctaccgg 900

gtggtgtccg tgctgaccgt gctgcaccag gattggctga acggcaagga gtacaagtgt 960

aaggtgtcca acaaggccct gcctgccccct atcgagaaaa ccatcagcaa ggccaagggc 1020

cagcccagag agccccaggt gtacaccctg ccccctagca gagatgagct gaccaagaac 1080

caggtgtccc tgacctgcct ggtgaagggc ttctacccca gcgacatcgc cgtggagtgg 1140

gagagcaacg gccagcccga gaacaactac aagaccaccc cccctgtgct ggacagcgat 1200

ggcagcttct tcctgtacag caagctgacc gtggacaaga gcagatggca gcagggcaac 1260

gtgttcagct gctccgtgat gcacgaggcc ctgcacaatc actacaccca gaagagcctg 1320

agcctgtccc ctggcaag 1338

<210> 67
<211> 660
<212> DNA
<213> Artificial

<220>
<223> H1L7, light chain humanised construct

<400> 67
gacatccaga tgacccagag cccctctagc ctcagcgcca gcgtgggcga cagggtgacc 60

atcacctgca agagcagcca gagcctgctg aaccccagca accagaagaa ctacctggcc 120

tggtaccagc agaaacccgg caaggccccc aagctgctgg tctacttcgc ctctaccagg 180

gattccggcg tccccagcag gttcagcggc agcggcagcg gcaccgactt cacactgacc 240

atcagcagcc tgcagcccga ggacttcgcc acctactact gcctgcagca cttcggcacc 300

cctcccactt ttggccaggg caccaagctg gagattaagc gtacggtggc cgcccccagc 360

gtgttcatct tccccccag cgatgagcag ctgaagagcg gcaccgccag cgtggtgtgt 420

ctgctgaaca acttctaccc ccgggaggcc aaggtgcagt ggaaggtgga caatgccctg 480

cagagcggca acagccagga gagcgtgacc gagcaggaca gcaaggactc cacctacagc 540

ctgagcagca ccctgaccct gagcaaggcc gactacgaga agcacaaggt gtacgcctgt 600

gaggtgaccc accagggcct gtccagcccc gtgaccaaga gcttcaaccg gggcgagtgc 660

<210> 68
<211> 1338
<212> DNA
<213> Artificial

<220>
<223> H1L7, heavy chain humanised construct

<400> 68
caggtgcagc tccaggagag cggccccggc ctggtgaagc ctagcgagac cctgagcctg 60

acctgcaccg tgagcggctt ctccctgacc gcctacggcg tcaactggat caggcagccc 120

cccggcaaag gcctggagtg gattgggatg atctgggacg acggcagcac cgactacaac 180

agcgccctga agagcagggt gaccatcagc gtggacacca gcaagaacca gttcagcctg 240

aagctgagca gcgtgactgc cgccgacacc gccgtctatt actgcgccag ggagggcgac 300

gtggccttcg attactgggg ccagggcaca ctagtgaccg tgtccagcgc cagcaccaag 360

ggccccagcg tgttccccct ggccccagc agcaagagca ccagcggcgg cacagccgcc 420

ctgggctgcc tggtgaagga ctacttcccc gaaccggtga ccgtgtcctg gaacagcgga 480

gccctgacca gcggcgtgca caccttcccc gccgtgctgc agagcagcgg cctgtacagc 540

ctgagcagcg tggtgaccgt gcccagcagc agcctgggca cccagaccta catctgtaac 600

gtgaaccaca agcccagcaa caccaaggtg gacaagaagg tggagcccaa gagctgtgac 660

aagacccaca cctgcccccc ctgccctgcc cccgagctgc tgggaggccc cagcgtgttc 720

ctgttccccc ccaagcctaa ggacaccctg atgatcagca gaaccccga ggtgacctgt 780

gtggtggtgg atgtgagcca cgaggaccct gaggtgaagt tcaactggta cgtggacggc 840

gtggaggtgc acaatgccaa gaccaagccc agggaggagc agtacaacag cacctaccgg 900

gtggtgtccg tgctgaccgt gctgcaccag gattggctga acggcaagga gtacaagtgt 960

aaggtgtcca acaaggccct gcctgccccc atcgagaaaa ccatcagcaa ggccaagggc 1020

cagcccagag agccccaggt gtacaccctg ccccctagca gagatgagct gaccaagaac 1080

caggtgtccc tgacctgcct ggtgaagggc ttctacccca gcgacatcgc cgtggagtgg 1140

gagagcaacg gccagcccga gaacaactac aagaccaccc cccctgtgct ggacagcgat 1200

ggcagcttct tcctgtacag caagctgacc gtggacaaga gcagatggca gcagggcaac 1260

gtgttcagct gctccgtgat gcacgaggcc ctgcacaatc actacaccca gaagagcctg 1320

agcctgtccc ctggcaag 1338

<210> 69

<211> 660
<212> DNA
<213> Artificial

<220>
<223> J7L7, light chain humanised construct

<400> 69
gacatccaga tgacccagag cccctctagc ctcagcgcca gcgtgggcga cagggtgacc 60

atcacctgca agagcagcca gagcctgctg aaccccagca accagaagaa ctacctggcc 120

tggtaccagc agaaacccgg caaggccccc aagctgctgg tctacttcgc ctctaccagg 180

gattccggcg tccccagcag gttcagcggc agcggcagcg gcaccgactt cacactgacc 240

atcagcagcc tgcagcccga ggacttcgcc acctactact gcctgcagca cttcggcacc 300

cctcccactt ttggccaggg caccaagctg gagattaagc gtacggtggc cgcccccagc 360

gtgttcatct tcccccccag cgatgagcag ctgaagagcg gcaccgccag cgtggtgtgt 420

ctgctgaaca acttctaccc ccgggaggcc aaggtgcagt ggaaggtgga caatgccctg 480

cagagcggca acagccagga gagcgtgacc gagcaggaca gcaaggactc cacctacagc 540

ctgagcagca ccctgaccct gagcaaggcc gactacgaga agcacaaggt gtacgcctgt 600

gaggtgaccc accagggcct gtccagcccc gtgaccaaga gcttcaaccg gggcgagtgc 660

<210> 70
<211> 1338
<212> DNA
<213> Artificial

<220>
<223> J7L7, heavy chain humanised construct

<400> 70
caggtgcagc tcgtgcagag cggggccgaa gtcaagaaac ccggcagctc cgtgaaggtg 60

agctgcaagg ccagcggctt ctctctcact gcctacggcg tgaactgggt gaggcaggct 120

cccggccagg gcctggagtg gatgggcatg atctgggacg acggcagcac cgactacaac 180

agcgccctga agagcagggt gaccatcacc gccgacaaga gcaccagcac cgcctacatg 240

gaactgagca gcctgaggag cgaggacacc gccgtgtact attgcgccag ggagggcgac 300

gtggccttcg attactgggg ccagggcaca ctagtgaccg tgtccagcgc cagcaccaag 360

ggccccagcg tgttccccct ggccccccagc agcaagagca ccagcggcgg cacagccgcc 420

ctgggctgcc tggtgaagga ctacttcccc gaaccggtga ccgtgtcctg gaacagcgga 480

gccctgacca gcggcgtgca caccttcccc gccgtgctgc agagcagcgg cctgtacagc 540

ctgagcagcg tggtgaccgt gcccagcagc agcctgggca cccagaccta catctgtaac 600

gtgaaccaca agcccagcaa caccaaggtg gacaagaagg tggagcccaa gagctgtgac 660

aagacccaca cctgcccccc ctgccctgcc cccgagctgc tgggaggccc cagcgtgttc 720

ctgttccccc ccaagcctaa ggacaccctg atgatcagca gaaccccga ggtgacctgt 780

gtggtggtgg atgtgagcca cgaggaccct gaggtgaagt tcaactggta cgtggacggc 840

gtggaggtgc acaatgccaa gaccaagccc agggaggagc agtacaacag cacctaccgg 900

gtggtgtccg tgctgaccgt gctgcaccag gattggctga acggcaagga gtacaagtgt 960

aaggtgtcca acaaggccct gcctgccccc atcgagaaaa ccatcagcaa ggccaagggc 1020

cagcccagag agccccaggt gtacaccctg ccccctagca gagatgagct gaccaagaac 1080

caggtgtccc tgacctgcct ggtgaagggc ttctacccca gcgacatcgc cgtggagtgg 1140

gagagcaacg gccagcccga gaacaactac aagaccaccc cccctgtgct ggacagcgat 1200

ggcagcttct tcctgtacag caagctgacc gtggacaaga gcagatggca gcagggcaac 1260

gtgttcagct gctccgtgat gcacgaggcc ctgcacaatc actacaccca gaagagcctg 1320

agcctgtccc ctggcaag 1338

<210> 71
<211> 660
<212> DNA
<213> Artificial

<220>
<223> H4L7, light chain humanised construct

<400> 71
gacatccaga tgacccagag cccctctagc ctcagcgcca gcgtgggcga cagggtgacc 60

atcacctgca agagcagcca gagcctgctg aaccccagca accagaagaa ctacctggcc 120

tggtaccagc agaaacccgg caaggccccc aagctgctgg tctacttcgc ctctaccagg 180

gattccggcg tccccagcag gttcagcggc agcggcagcg gcaccgactt cacactgacc 240

atcagcagcc tgcagcccga ggacttcgcc acctactact gcctgcagca cttcggcacc 300

cctcccactt ttggccaggg caccaagctg gagattaagc gtacggtggc cgcccccagc 360

gtgttcatct tcccccccag cgatgagcag ctgaagagcg gcaccgccag cgtggtgtgt 420

ctgctgaaca acttctaccc ccgggaggcc aaggtgcagt ggaaggtgga caatgccctg 480

cagagcggca acagccagga gagcgtgacc gagcaggaca gcaaggactc cacctacagc 540

ctgagcagca ccctgaccct gagcaaggcc gactacgaga agcacaaggt gtacgcctgt 600

gaggtgaccc accagggcct gtccagcccc gtgaccaaga gcttcaaccg gggcgagtgc 660

<210> 72
<211> 1338
<212> DNA
<213> Artificial

<220>
<223> H4L7, heavy chain humanised construct

<400> 72
caggtgcagc tccaggagag cggccccggc ctggtgaagc ctagcgagac cctgagcctg 60

acctgcaccg tgagcggctt ctccctgacc gcctacggcg tcaactggat caggcagccc 120

cccggcaaag gcctggagtg gctggggatg atctgggacg acggcagcac cgactacaac 180

agcgccctga agagcaggct gaccatcagc aaggacaaca gcaagaacca ggtgagcctg 240

aagctgagca gcgtgactgc cgccgacacc gccgtctatt actgcgccag ggagggcgac 300

gtggccttcg attactgggg ccagggcaca ctagtgaccg tgtccagcgc cagcaccaag 360

ggccccagcg tgttcccccc ggcccccagc agcaagagca ccagcggcgg cacagccgcc 420

ctgggctgcc tggtgaagga ctacttcccc gaaccggtga ccgtgtcctg gaacagcgga 480

gccctgacca gcggcgtgca caccttcccc gccgtgctgc agagcagcgg cctgtacagc 540

ctgagcagcg tggtgaccgt gcccagcagc agcctgggca cccagaccta catctgtaac 600

gtgaaccaca agcccagcaa caccaaggtg gacaagaagg tggagcccaa gagctgtgac 660

aagacccaca cctgcccccc ctgccctgcc cccgagctgc tgggaggccc cagcgtgttc 720

ctgttccccc ccaagcctaa ggacaccctg atgatcagca gaacccccga ggtgacctgt 780

gtggtggtgg atgtgagcca cgaggaccct gaggtgaagt tcaactggta cgtggacggc 840

gtggaggtgc acaatgccaa gaccaagccc agggaggagc agtacaacag cacctaccgg 900

gtggtgtccg tgctgaccgt gctgcaccag gattggctga acggcaagga gtacaagtgt 960

aaggtgtcca acaaggccct gcctgccccc atcgagaaaa ccatcagcaa ggccaagggc 1020

cagcccagag agccccaggt gtacaccctg ccccctagca gagatgagct gaccaagaac 1080

caggtgtccc tgacctgcct ggtgaagggc ttctacccca gcgacatcgc cgtggagtgg 1140

gagagcaacg gccagcccga gaacaactac aagaccaccc cccctgtgct ggacagcgat 1200

ggcagcttct tcctgtacag caagctgacc gtggacaaga gcagatggca gcagggcaac 1260

gtgttcagct gctccgtgat gcacgaggcc ctgcacaatc actacaccca gaagagcctg 1320

agcctgtccc ctggcaag 1338

<210> 73
<211> 660
<212> DNA
<213> Artificial

<220>
<223> J11L7, light chain humanised construct

<400> 73
gacatccaga tgacccagag cccctctagc ctcagcgcca gcgtgggcga cagggtgacc 60

atcacctgca agagcagcca gagcctgctg aaccccagca accagaagaa ctacctggcc 120

tggtaccagc agaaacccgg caaggccccc aagctgctgg tctacttcgc ctctaccagg 180

gattccggcg tccccagcag gttcagcggc agcggcagcg gcaccgactt cacactgacc 240

atcagcagcc tgcagcccga ggacttcgcc acctactact gcctgcagca cttcggcacc 300

cctcccactt ttggccaggg caccaagctg gagattaagc gtacggtggc cgcccccagc 360

gtgttcatct tcccccccag cgatgagcag ctgaagagcg gcaccgccag cgtggtgtgt 420

ctgctgaaca acttctaccc ccgggaggcc aaggtgcagt ggaaggtgga caatgccctg 480

cagagcggca acagccagga gagcgtgacc gagcaggaca gcaaggactc cacctacagc 540

ctgagcagca ccctgaccct gagcaaggcc gactacgaga agcacaaggt gtacgcctgt 600

gaggtgaccc accagggcct gtccagcccc gtgaccaaga gcttcaaccg gggcgagtgc 660

<210> 74
<211> 1338
<212> DNA
<213> Artificial

<220>
<223> J11L7, heavy chain humanised construct

<400> 74
caggtgcagc tcgtgcagag cggggccgaa gtcaagaaac ccggcagctc cgtgaaggtg 60

agctgcaagg ccagcggctt ctctctcact gcctacggcg tgaactgggt gaggcaggct 120

cccggccagg gcctggagtg gatgggcatg atctgggacg acggcagcac cgactacgac 180

agcgccctga agagcagggt gaccatcacc gccgacaaga gcaccagcac cgcctacatg 240

gaactgagca gcctgaggag cgaggacacc gccgtgtact attgcgccag ggagggcgac 300

gtggccttcg attactgggg ccagggcaca ctagtgaccg tgtccagcgc cagcaccaag 360

ggccccagcg tgttcccccc ggcccccagc agcaagagca ccagcggcgg cacagccgcc 420

ctgggctgcc tggtgaagga ctacttcccc gaaccggtga ccgtgtcctg gaacagcgga 480

gccctgacca gcggcgtgca caccttcccc gccgtgctgc agagcagcgg cctgtacagc 540

ctgagcagcg tggtgaccgt gcccagcagc agcctgggca cccagaccta catctgtaac 600

gtgaaccaca agcccagcaa caccaaggtg gacaagaagg tggagcccaa gagctgtgac 660

aagacccaca cctgcccccc ctgccctgcc cccgagctgc tgggaggccc cagcgtgttc 720

ctgttccccc ccaagcctaa ggacaccctg atgatcagca gaaccccga ggtgacctgt 780

gtggtggtgg atgtgagcca cgaggaccct gaggtgaagt tcaactggta cgtggacggc 840

gtggaggtgc acaatgccaa gaccaagccc agggaggagc agtacaacag cacctaccgg 900

gtggtgtccg tgctgaccgt gctgcaccag gattggctga acggcaagga gtacaagtgt 960

aaggtgtcca acaaggccct gcctgccccc atcgagaaaa ccatcagcaa ggccaagggc 1020

cagcccagag agccccaggt gtacaccctg cccccctagca gagatgagct gaccaagaac 1080

caggtgtccc tgacctgcct ggtgaagggc ttctacccca gcgacatcgc cgtggagtgg 1140

gagagcaacg gccagcccga gaacaactac aagaccaccc cccctgtgct ggacagcgat 1200

ggcagcttct tcctgtacag caagctgacc gtggacaaga gcagatggca gcagggcaac 1260

gtgttcagct gctccgtgat gcacgaggcc ctgcacaatc actacaccca gaagagcctg 1320

agcctgtccc ctggcaag 1338

<210> 75
<211> 660
<212> DNA
<213> Artificial

<220>
<223> H2L7, light chain humanised construct

<400> 75

gacatccaga tgacccagag cccctctagc ctcagcgcca gcgtgggcga cagggtgacc 60

atcacctgca agagcagcca gagcctgctg aaccccagca accagaagaa ctacctggcc 120

tggtaccagc agaaacccgg caaggccccc aagctgctgg tctacttcgc ctctaccagg 180

gattccggcg tccccagcag gttcagcggc agcggcagcg gcaccgactt cacactgacc 240

atcagcagcc tgcagcccga ggacttcgcc acctactact gcctgcagca cttcggcacc 300

cctcccactt ttggccaggg caccaagctg gagattaagc gtacggtggc cgcccccagc 360

gtgttcatct tcccccccag cgatgagcag ctgaagagcg gcaccgccag cgtggtgtgt 420

ctgctgaaca acttctaccc ccgggaggcc aaggtgcagt ggaaggtgga caatgccctg 480

cagagcggca acagccagga gagcgtgacc gagcaggaca gcaaggactc cacctacagc 540

ctgagcagca ccctgaccct gagcaaggcc gactacgaga agcacaaggt gtacgcctgt 600

gaggtgaccc accagggcct gtccagcccc gtgaccaaga gcttcaaccg gggcgagtgc 660

<210> 76
<211> 1338
<212> DNA
<213> Artificial

<220>
<223> H2L7, heavy chain humanised construct

<400> 76
caggtgcagc tccaggagag cggccccggc ctggtgaagc ctagcgagac cctgagcctg 60

acctgcaccg tgagcggctt ctccctgacc gcctacggcg tcaactggat caggcagccc 120

cccggcaaag gcctggagtg gattgggatg atctgggacg acggcagcac cgactacaac 180

agcgccctga agagcagggt gaccatcagc aaggacaaca gcaagaacca ggtgagcctg 240

aagctgagca gcgtgactgc cgccgacacc gccgtctatt actgcgccag ggagggcgac 300

gtggccttcg attactgggg ccagggcaca ctagtgaccg tgtccagcgc cagcaccaag 360

ggccccagcg tgttccccct ggccccagc agcaagagca ccagcggcgg cacagccgcc 420

ctgggctgcc tggtgaagga ctacttcccc gaaccggtga ccgtgtcctg gaacagcgga 480

gccctgacca gcggcgtgca caccttcccc gccgtgctgc agagcagcgg cctgtacagc 540

ctgagcagcg tggtgaccgt gcccagcagc agcctgggca cccagaccta catctgtaac 600

gtgaaccaca agcccagcaa caccaaggtg gacaagaagg tggagcccaa gagctgtgac 660

aagacccaca cctgcccccc ctgccctgcc cccgagctgc tgggaggccc cagcgtgttc 720

ctgttccccc ccaagcctaa ggacaccctg atgatcagca gaaccccga ggtgacctgt 780

gtggtggtgg atgtgagcca cgaggaccct gaggtgaagt tcaactggta cgtggacggc 840

gtggaggtgc acaatgccaa gaccaagccc agggaggagc agtacaacag cacctaccgg 900

gtggtgtccg tgctgaccgt gctgcaccag gattggctga acggcaagga gtacaagtgt 960

aaggtgtcca acaaggccct gcctgccccc atcgagaaaa ccatcagcaa ggccaagggc 1020

cagcccagag agccccaggt gtacaccctg ccccctagca gagatgagct gaccaagaac 1080

caggtgtccc tgacctgcct ggtgaagggc ttctacccca gcgacatcgc cgtggagtgg 1140

gagagcaacg gccagcccga gaacaactac aagaccaccc cccctgtgct ggacagcgat 1200

ggcagcttct tcctgtacag caagctgacc gtggacaaga gcagatggca gcagggcaac 1260

gtgttcagct gctccgtgat gcacgaggcc ctgcacaatc actacaccca gaagagcctg 1320

agcctgtccc ctggcaag 1338

<210> 77
<211> 660
<212> DNA
<213> Artificial

<220>
<223> J13L7, light chain humanised construct

<400> 77
gacatccaga tgacccagag cccctctagc ctcagcgcca gcgtgggcga cagggtgacc 60

atcacctgca agagcagcca gagcctgctg aaccccagca accagaagaa ctacctggcc 120

tggtaccagc agaaacccgg caaggccccc aagctgctgg tctacttcgc ctctaccagg 180

gattccggcg tccccagcag gttcagcggc agcggcagcg gcaccgactt cacactgacc 240

atcagcagcc tgcagcccga ggacttcgcc acctactact gcctgcagca cttcggcacc 300

cctcccactt ttggccaggg caccaagctg gagattaagc gtacggtggc cgcccccagc 360

gtgttcatct tcccccccag cgatgagcag ctgaagagcg gcaccgccag cgtggtgtgt 420

ctgctgaaca acttctaccc ccgggaggcc aaggtgcagt ggaaggtgga caatgccctg 480

cagagcggca acagccagga gagcgtgacc gagcaggaca gcaaggactc cacctacagc 540

ctgagcagca ccctgaccct gagcaaggcc gactacgaga agcacaaggt gtacgcctgt 600

gaggtgaccc accagggcct gtccagcccc gtgaccaaga gcttcaaccg gggcgagtgc 660

<210> 78
<211> 1338
<212> DNA
<213> Artificial

<220>
<223> J13L7, heavy chain humanised construct

<400> 78
caggtgcagc tcgtgcagag cggggccgaa gtcaagaaac ccggcagctc cgtgaaggtg 60

agctgcaagg ccagcggcgg caccttcagc gcctacggcg tgaactgggt gaggcaggct 120

cccggccagg gcctggagtg gatgggcatg atctgggacg acggcagcac cgactacgac 180

agcgccctga agagcagggt gaccatcacc gccgacaaga gcaccagcac cgcctacatg 240

gaactgagca gcctgaggag cgaggacacc gccgtgtact attgcgccag ggagggcgac 300

gtggccttcg attactgggg ccagggcaca ctagtgaccg tgtccagcgc cagcaccaag 360

ggccccagcg tgttcccccc ggcccccagc agcaagagca ccagcggcgg cacagccgcc 420

ctgggctgcc tggtgaagga ctacttcccc gaaccggtga ccgtgtcctg gaacagcgga 480

gccctgacca gcggcgtgca caccttcccc gccgtgctgc agagcagcgg cctgtacagc 540

ctgagcagcg tggtgaccgt gcccagcagc agcctgggca cccagaccta catctgtaac 600

gtgaaccaca agcccagcaa caccaaggtg gacaagaagg tggagcccaa gagctgtgac 660

aagacccaca cctgcccccc ctgccctgcc cccgagctgc tgggaggccc cagcgtgttc 720

ctgttccccc ccaagcctaa ggacaccctg atgatcagca gaaccccga ggtgacctgt 780

gtggtggtgg atgtgagcca cgaggaccct gaggtgaagt tcaactggta cgtggacggc 840

gtggaggtgc acaatgccaa gaccaagccc agggaggagc agtacaacag cacctaccgg 900

gtggtgtccg tgctgaccgt gctgcaccag gattggctga acggcaagga gtacaagtgt 960

aaggtgtcca acaaggccct gcctgccccc atcgagaaaa ccatcagcaa ggccaagggc 1020

cagcccagag agccccaggt gtacaccctg ccccctagca gagatgagct gaccaagaac 1080

caggtgtccc tgacctgcct ggtgaagggc ttctacccca gcgacatcgc cgtggagtgg 1140

gagagcaacg gccagcccga gaacaactac aagaccaccc cccctgtgct ggacagcgat 1200

ggcagcttct tcctgtacag caagctgacc gtggacaaga gcagatggca gcagggcaac 1260

gtgttcagct gctccgtgat gcacgaggcc ctgcacaatc actacaccca gaagagcctg 1320

agcctgtccc ctggcaag 1338

<210> 79
<211> 660
<212> DNA
<213> Artificial

<220>
<223> H7L7, light chain humanised construct

<400> 79
gacatccaga tgacccagag cccctctagc ctcagcgcca gcgtgggcga cagggtgacc 60

atcacctgca agagcagcca gagcctgctg aaccccagca accagaagaa ctacctggcc 120

tggtaccagc agaaacccgg caaggccccc aagctgctgg tctacttcgc ctctaccagg 180

gattccggcg tccccagcag gttcagcggc agcggcagcg gcaccgactt cacactgacc 240

atcagcagcc tgcagcccga ggacttcgcc acctactact gcctgcagca cttcggcacc 300

cctcccactt ttggccaggg caccaagctg gagattaagc gtacggtggc cgcccccagc 360

gtgttcatct tcccccccag cgatgagcag ctgaagagcg gcaccgccag cgtggtgtgt 420

ctgctgaaca acttctaccc ccgggaggcc aaggtgcagt ggaaggtgga caatgccctg 480

cagagcggca acagccagga gagcgtgacc gagcaggaca gcaaggactc cacctacagc 540

ctgagcagca ccctgaccct gagcaaggcc gactacgaga agcacaaggt gtacgcctgt 600

gaggtgaccc accagggcct gtccagcccc gtgaccaaga gcttcaaccg gggcgagtgc 660

<210> 80
<211> 1338
<212> DNA
<213> Artificial

<220>
<223> H7L7, heavy chain humanised construct

<400> 80
caggtgcagc tccaggagag cggccccggc ctggtgaagc ctagcgagac cctgagcctg 60

acctgcaccg tgagcggcgg ctccatcagc gcctacggcg tcaactggat caggcagccc 120

cccggcaaag gcctggagtg gattgggatg atctgggacg acggcagcac cgactacgac 180

agcgccctga agagcagggt gaccatcagc gtggacacca gcaagaacca gttcagcctg 240

aagctgagca gcgtgactgc cgccgacacc gccgtctatt actgcgccag ggagggcgac 300

gtggccttcg attactgggg ccagggcaca ctagtgaccg tgtccagcgc cagcaccaag 360

ggccccagcg tgttcccccc ggcccccagc agcaagagca ccagcggcgg cacagccgcc 420

ctgggctgcc tggtgaagga ctacttcccc gaaccggtga ccgtgtcctg gaacagcgga 480

gccctgacca gcggcgtgca caccttcccc gccgtgctgc agagcagcgg cctgtacagc 540

ctgagcagcg tggtgaccgt gcccagcagc agcctgggca cccagaccta catctgtaac 600

gtgaaccaca agcccagcaa caccaaggtg gacaagaagg tggagcccaa gagctgtgac 660

aagacccaca cctgcccccc ctgccctgcc cccgagctgc tgggaggccc cagcgtgttc 720

ctgttccccc ccaagcctaa ggacaccctg atgatcagca gaaccccga ggtgacctgt 780

gtggtggtgg atgtgagcca cgaggaccct gaggtgaagt tcaactggta cgtggacggc 840

gtggaggtgc acaatgccaa gaccaagccc agggaggagc agtacaacag cacctaccgg 900

gtggtgtccg tgctgaccgt gctgcaccag gattggctga acggcaagga gtacaagtgt 960

aaggtgtcca acaaggccct gcctgccccc atcgagaaaa ccatcagcaa ggccaagggc 1020

cagcccagag agccccaggt gtacaccctg ccccctagca gagatgagct gaccaagaac 1080

caggtgtccc tgacctgcct ggtgaagggc ttctacccca gcgacatcgc cgtggagtgg 1140

gagagcaacg gccagcccga gaacaactac aagaccaccc cccctgtgct ggacagcgat 1200

ggcagcttct tcctgtacag caagctgacc gtggacaaga gcagatggca gcagggcaac 1260

gtgttcagct gctccgtgat gcacgaggcc ctgcacaatc actacaccca gaagagcctg 1320

agcctgtccc ctggcaag 1338

<210> 81
<211> 660
<212> DNA
<213> Artificial

<220>
<223> JOL7, light chain humanised construct

<400> 81
gacatccaga tgacccagag cccctctagc ctcagcgcca gcgtgggcga cagggtgacc 60

atcacctgca agagcagcca gagcctgctg aaccccagca accagaagaa ctacctggcc 120

tggtaccagc agaaacccgg caaggccccc aagctgctgg tctacttcgc ctctaccagg 180

gattccggcg tccccagcag gttcagcggc agcggcagcg gcaccgactt cacactgacc 240

atcagcagcc tgcagcccga ggacttcgcc acctactact gcctgcagca cttcggcacc 300

cctcccactt ttggccaggg caccaagctg gagattaagc gtacggtggc cgcccccagc 360

gtgttcatct tccccccccag cgatgagcag ctgaagagcg gcaccgccag cgtggtgtgt 420

ctgctgaaca acttctaccc ccgggaggcc aaggtgcagt ggaaggtgga caatgccctg 480

cagagcggca acagccagga gagcgtgacc gagcaggaca gcaaggactc cacctacagc 540

ctgagcagca ccctgaccct gagcaaggcc gactacgaga agcacaaggt gtacgcctgt 600

gaggtgaccc accagggcct gtccagcccc gtgaccaaga gcttcaaccg gggcgagtgc 660

<210> 82
<211> 1338
<212> DNA
<213> Artificial

<220>
<223> JOL7, heavy chain humanised construct

<400> 82
caggtgcagc tcgtgcagag cggggccgaa gtcaagaaac ccggcagctc cgtgaaggtg 60

agctgcaagg ccagcggcgg caccttcagc gcctacggcg tgaactgggt gaggcaggct 120

cccggccagg gcctggagtg gatgggcatg atctgggacg acggcagcac cgactacaac 180

agcgccctga agagcagggt gaccatcacc gccgacaaga gcaccagcac cgcctacatg 240

gaactgagca gcctgaggag cgaggacacc gccgtgtact attgcgccag ggagggcgac 300

gtggccttcg attactgggg ccagggcaca ctagtgaccg tgtccagcgc cagcaccaag 360

ggccccagcg tgttccccct ggccccccagc agcaagagca ccagcggcgg cacagccgcc 420

ctgggctgcc tggtgaagga ctacttcccc gaaccggtga ccgtgtcctg gaacagcgga 480

gccctgacca gcggcgtgca caccttcccc gccgtgctgc agagcagcgg cctgtacagc 540

ctgagcagcg tggtgaccgt gcccagcagc agcctgggca cccagaccta catctgtaac 600

gtgaaccaca agcccagcaa caccaaggtg gacaagaagg tggagcccaa gagctgtgac 660

aagacccaca cctgcccccc ctgccctgcc cccgagctgc tgggaggccc cagcgtgttc 720

ctgttccccc ccaagcctaa ggacaccctg atgatcagca gaaccccga ggtgacctgt 780

gtggtggtgg atgtgagcca cgaggaccct gaggtgaagt tcaactggta cgtggacggc 840

gtggaggtgc acaatgccaa gaccaagccc agggaggagc agtacaacag cacctaccgg 900

gtggtgtccg tgctgaccgt gctgcaccag gattggctga acggcaagga gtacaagtgt 960

aaggtgtcca acaaggccct gcctgccccct atcgagaaaa ccatcagcaa ggccaagggc 1020

cagcccagag agccccaggt gtacaccctg ccccctagca gagatgagct gaccaagaac 1080

caggtgtccc tgacctgcct ggtgaagggc ttctacccca gcgacatcgc cgtggagtgg 1140

gagagcaacg gccagcccga gaacaactac aagaccaccc cccctgtgct ggacagcgat 1200

ggcagcttct tcctgtacag caagctgacc gtggacaaga gcagatggca gcagggcaac 1260

gtgttcagct gctccgtgat gcacgaggcc ctgcacaatc actacaccca gaagagcctg 1320

agcctgtccc ctggcaag 1338

<210> 83
<211> 660
<212> DNA
<213> Artificial

<220>
<223> HOL7, light chain humanised construct

<400> 83
gacatccaga tgacccagag cccctctagc ctcagcgcca gcgtgggcga cagggtgacc 60

atcacctgca agagcagcca gagcctgctg aaccccagca accagaagaa ctacctggcc 120

tggtaccagc agaaacccgg caaggccccc aagctgctgg tctacttcgc ctctaccagg 180

gattccggcg tccccagcag gttcagcggc agcggcagcg gcaccgactt cacactgacc 240

atcagcagcc tgcagcccga ggacttcgcc acctactact gcctgcagca cttcggcacc 300

cctcccactt ttggccaggg caccaagctg gagattaagc gtacggtggc cgcccccagc 360

gtgttcatct tcccccccag cgatgagcag ctgaagagcg gcaccgccag cgtggtgtgt 420

ctgctgaaca acttctaccc ccgggaggcc aaggtgcagt ggaaggtgga caatgccctg 480

cagagcggca acagccagga gagcgtgacc gagcaggaca gcaaggactc cacctacagc 540

ctgagcagca ccctgaccct gagcaaggcc gactacgaga agcacaaggt gtacgcctgt 600

gaggtgaccc accagggcct gtccagcccc gtgaccaaga gcttcaaccg gggcgagtgc 660

<210> 84
<211> 1338
<212> DNA
<213> Artificial

<220>
<223> HOL7, heavy chain humanised construct

<400> 84
caggtgcagc tccaggagag cggccccggc ctggtgaagc ctagcgagac cctgagcctg 60

acctgcaccg tgagcggcgg ctccatcagc gcctacggcg tcaactggat caggcagccc 120

cccggcaaag gcctggagtg gattgggatg atctgggacg acggcagcac cgactacaac 180

agcgccctga agagcagggt gaccatcagc gtggacacca gcaagaacca gttcagcctg 240

aagctgagca gcgtgactgc cgccgacacc gccgtctatt actgcgccag ggagggcgac 300

gtggccttcg attactgggg ccagggcaca ctagtgaccg tgtccagcgc cagcaccaag 360

ggccccagcg tgttcccccc ggcccccagc agcaagagca ccagcggcgg cacagccgcc 420

ctgggctgcc tggtgaagga ctacttcccc gaaccggtga ccgtgtcctg gaacagcgga 480

gccctgacca gcggcgtgca caccttcccc gccgtgctgc agagcagcgg cctgtacagc 540

ctgagcagcg tggtgaccgt gcccagcagc agcctgggca cccagaccta catctgtaac 600

gtgaaccaca agcccagcaa caccaaggtg gacaagaagg tggagcccaa gagctgtgac 660

aagacccaca cctgcccccc ctgccctgcc cccgagctgc tgggaggccc cagcgtgttc 720

ctgttccccc ccaagcctaa ggacaccctg atgatcagca gaacccccga ggtgacctgt 780

gtggtggtgg atgtgagcca cgaggaccct gaggtgaagt tcaactggta cgtggacggc 840

gtggaggtgc acaatgccaa gaccaagccc agggaggagc agtacaacag cacctaccgg 900

gtggtgtccg tgctgaccgt gctgcaccag gattggctga acggcaagga gtacaagtgt 960

aaggtgtcca acaaggccct gcctgccccc atcgagaaaa ccatcagcaa ggccaagggc 1020

cagcccagag agccccaggt gtacaccctg ccccctagca gagatgagct gaccaagaac 1080

caggtgtccc tgacctgcct ggtgaagggc ttctacccca gcgacatcgc cgtggagtgg 1140

gagagcaacg gccagcccga gaacaactac aagaccaccc cccctgtgct ggacagcgat 1200

ggcagcttct tcctgtacag caagctgacc gtggacaaga gcagatggca gcagggcaac 1260

gtgttcagct gctccgtgat gcacgaggcc ctgcacaatc actacaccca gaagagcctg 1320

agcctgtccc ctggcaag 1338

<210> 85
<211> 660
<212> DNA
<213> Artificial

<220>
<223> H1L1, light chain humanised construct

<400> 85
gacatccaga tgacccagag cccctctagc ctcagcgcca gcgtgggcga cagggtgacc 60

atcacctgca agagcagcca gagcctgctg aacggcagca accagaagaa ctacctggcc 120

tggtaccagc agaaacccgg caaggccccc aagctgctgg tctacttcgc ctctaccagg 180

gattccggcg tccccagcag gttcagcggc agcggcagcg gcaccgactt cacactgacc 240

atcagcagcc tgcagcccga ggacttcgcc acctactact gcctgcagca cttcggcacc 300

cctcccactt ttggccaggg caccaagctg gagattaagc gtacggtggc cgcccccagc 360

gtgttcatct tccccccccag cgatgagcag ctgaagagcg gcaccgccag cgtggtgtgt 420

ctgctgaaca acttctaccc ccgggaggcc aaggtgcagt ggaaggtgga caatgccctg 480

cagagcggca acagccagga gagcgtgacc gagcaggaca gcaaggactc cacctacagc 540

ctgagcagca ccctgaccct gagcaaggcc gactacgaga agcacaaggt gtacgcctgt 600

gaggtgaccc accagggcct gtccagcccc gtgaccaaga gcttcaaccg gggcgagtgc 660

<210> 86
<211> 1338
<212> DNA
<213> Artificial

<220>
<223> H1L1, heavy chain humanised construct

<400> 86
caggtgcagc tccaggagag cggccccggc ctggtgaagc ctagcgagac cctgagcctg 60

acctgcaccg tgagcggctt ctccctgacc gcctacggcg tcaactggat caggcagccc 120

cccggcaaag gcctggagtg gattgggatg atctgggacg acggcagcac cgactacaac 180

agcgccctga agagcagggt gaccatcagc gtggacacca gcaagaacca gttcagcctg 240

aagctgagca gcgtgactgc cgccgacacc gccgtctatt actgcgccag ggagggcgac 300

gtggccttcg attactgggg ccagggcaca ctagtgaccg tgtccagcgc cagcaccaag 360

ggccccagcg tgttccccct ggcccccagc agcaagagca ccagcggcgg cacagccgcc 420

ctgggctgcc tggtgaagga ctacttcccc gaaccggtga ccgtgtcctg gaacagcgga 480

gccctgacca gcggcgtgca caccttcccc gccgtgctgc agagcagcgg cctgtacagc 540

ctgagcagcg tggtgaccgt gcccagcagc agcctgggca cccagaccta catctgtaac 600

gtgaaccaca agcccagcaa caccaaggtg gacaagaagg tggagcccaa gagctgtgac 660

aagacccaca cctgcccccc ctgccctgcc cccgagctgc tgggaggccc cagcgtgttc 720

ctgttccccc ccaagcctaa ggacaccctg atgatcagca gaaccccga ggtgacctgt 780

gtggtggtgg atgtgagcca cgaggaccct gaggtgaagt tcaactggta cgtggacggc 840

gtggaggtgc acaatgccaa gaccaagccc agggaggagc agtacaacag cacctaccgg 900

gtggtgtccg tgctgaccgt gctgcaccag gattggctga acggcaagga gtacaagtgt 960

aaggtgtcca acaaggccct gcctgccccc atcgagaaaa ccatcagcaa ggccaagggc 1020

cagcccagag agccccaggt gtacaccctg ccccctagca gagatgagct gaccaagaac 1080

caggtgtccc tgacctgcct ggtgaagggc ttctacccca gcgacatcgc cgtggagtgg 1140

gagagcaacg gccagcccga gaacaactac aagaccaccc cccctgtgct ggacagcgat 1200

ggcagcttct tcctgtacag caagctgacc gtggacaaga gcagatggca gcagggcaac 1260

gtgttcagct gctccgtgat gcacgaggcc ctgcacaatc actacaccca gaagagcctg 1320

agcctgtccc ctggcaag 1338

<210> 87
<211> 660
<212> DNA
<213> Artificial

<220>
<223> H5L1, light chain humanised construct

<400> 87
gacatccaga tgacccagag cccctctagc ctcagcgcca gcgtgggcga cagggtgacc 60

atcacctgca agagcagcca gagcctgctg aacggcagca accagaagaa ctacctggcc 120

tggtaccagc agaaacccgg caaggccccc aagctgctgg tctacttcgc ctctaccagg 180

gattccggcg tccccagcag gttcagcggc agcggcagcg gcaccgactt cacactgacc 240

atcagcagcc tgcagcccga ggacttcgcc acctactact gcctgcagca cttcggcacc 300

cctcccactt ttggccaggg caccaagctg gagattaagc gtacggtggc cgcccccagc 360

gtgttcatct tccccccccag cgatgagcag ctgaagagcg gcaccgccag cgtggtgtgt 420

ctgctgaaca acttctaccc ccgggaggcc aaggtgcagt ggaaggtgga caatgccctg 480

cagagcggca acagccagga gagcgtgacc gagcaggaca gcaaggactc cacctacagc 540

ctgagcagca ccctgaccct gagcaaggcc gactacgaga agcacaaggt gtacgcctgt 600

gaggtgaccc accagggcct gtccagcccc gtgaccaaga gcttcaaccg gggcgagtgc 660

<210> 88
<211> 1338
<212> DNA
<213> Artificial

<220>
<223> H5L1, heavy chain humanised construct

<400> 88
caggtgcagc tccaggagag cggccccggc ctggtgaagc ctagcgagac cctgagcctg 60

acctgcaccg tgagcggctt ctccctgacc gcctacggcg tcaactggat caggcagccc 120

cccggcaaag gcctggagtg gattgggatg atctgggacg acggcagcac cgactacgac 180

agcgccctga agagcagggt gaccatcagc gtggacacca gcaagaacca gttcagcctg 240

aagctgagca gcgtgactgc cgccgacacc gccgtctatt actgcgccag ggagggcgac 300

gtggccttcg attactgggg ccagggcaca ctagtgaccg tgtccagcgc cagcaccaag 360

ggccccagcg tgttccccct ggccccccagc agcaagagca ccagcggcgg cacagccgcc 420

ctgggctgcc tggtgaagga ctacttcccc gaaccggtga ccgtgtcctg gaacagcgga 480

gccctgacca gcggcgtgca caccttcccc gccgtgctgc agagcagcgg cctgtacagc 540

ctgagcagcg tggtgaccgt gcccagcagc agcctgggca cccagaccta catctgtaac 600

gtgaaccaca agcccagcaa caccaaggtg gacaagaagg tggagcccaa gagctgtgac 660

aagacccaca cctgcccccc ctgccctgcc cccgagctgc tgggaggccc cagcgtgttc 720

ctgttccccc ccaagcctaa ggacaccctg atgatcagca gaaccccga ggtgacctgt 780

gtggtggtgg atgtgagcca cgaggaccct gaggtgaagt tcaactggta cgtggacggc 840

gtggaggtgc acaatgccaa gaccaagccc agggaggagc agtacaacag cacctaccgg 900

gtggtgtccg tgctgaccgt gctgcaccag gattggctga acggcaagga gtacaagtgt 960

aaggtgtcca acaaggccct gcctgccccct atcgagaaaa ccatcagcaa ggccaagggc 1020

cagcccagag agccccaggt gtacaccctg ccccctagca gagatgagct gaccaagaac 1080

caggtgtccc tgacctgcct ggtgaagggc ttctacccca gcgacatcgc cgtggagtgg 1140

gagagcaacg gccagcccga gaacaactac aagaccaccc cccctgtgct ggacagcgat 1200

ggcagcttct tcctgtacag caagctgacc gtggacaaga gcagatggca gcagggcaac 1260

gtgttcagct gctccgtgat gcacgaggcc ctgcacaatc actacaccca gaagagcctg 1320

agcctgtccc ctggcaag 1338

<210> 89
<211> 660
<212> DNA
<213> Artificial

<220>
<223> J7L1, light chain humanised construct

<400> 89
gacatccaga tgacccagag cccctctagc ctcagcgcca gcgtgggcga cagggtgacc 60

atcacctgca agagcagcca gagcctgctg aacggcagca accagaagaa ctacctggcc 120

tggtaccagc agaaacccgg caaggccccc aagctgctgg tctacttcgc ctctaccagg 180

gattccggcg tccccagcag gttcagcggc agcggcagcg gcaccgactt cacactgacc 240

atcagcagcc tgcagcccga ggacttcgcc acctactact gcctgcagca cttcggcacc 300

cctcccactt ttggccaggg caccaagctg gagattaagc gtacggtggc cgcccccagc 360

gtgttcatct tcccccccag cgatgagcag ctgaagagcg gcaccgccag cgtggtgtgt 420

ctgctgaaca acttctaccc ccgggaggcc aaggtgcagt ggaaggtgga caatgccctg 480

cagagcggca acagccagga gagcgtgacc gagcaggaca gcaaggactc cacctacagc 540

ctgagcagca ccctgaccct gagcaaggcc gactacgaga agcacaaggt gtacgcctgt 600

gaggtgaccc accagggcct gtccagcccc gtgaccaaga gcttcaaccg gggcgagtgc 660

<210> 90
<211> 1338
<212> DNA
<213> Artificial

<220>
<223> J7L1, heavy chain humanised construct

<400> 90
caggtgcagc tcgtgcagag cggggccgaa gtcaagaaac ccggcagctc cgtgaaggtg 60

agctgcaagg ccagcggctt ctctctcact gcctacggcg tgaactgggt gaggcaggct 120

cccggccagg gcctggagtg gatgggcatg atctgggacg acggcagcac cgactacaac 180

agcgccctga agagcagggt gaccatcacc gccgacaaga gcaccagcac cgcctacatg 240

gaactgagca gcctgaggag cgaggacacc gccgtgtact attgcgccag ggagggcgac 300

gtggccttcg attactgggg ccagggcaca ctagtgaccg tgtccagcgc cagcaccaag 360

ggccccagcg tgttccccct ggccccccagc agcaagagca ccagcggcgg cacagccgcc 420

ctgggctgcc tggtgaagga ctacttcccc gaaccggtga ccgtgtcctg gaacagcgga 480

gccctgacca gcggcgtgca caccttcccc gccgtgctgc agagcagcgg cctgtacagc 540

ctgagcagcg tggtgaccgt gcccagcagc agcctgggca cccagaccta catctgtaac 600

gtgaaccaca agcccagcaa caccaaggtg gacaagaagg tggagcccaa gagctgtgac 660

aagacccaca cctgcccccc ctgccctgcc cccgagctgc tgggaggccc cagcgtgttc 720

ctgttccccc ccaagcctaa ggacaccctg atgatcagca gaaccccga ggtgacctgt 780

gtggtggtgg atgtgagcca cgaggaccct gaggtgaagt tcaactggta cgtggacggc 840

gtggaggtgc acaatgccaa gaccaagccc agggaggagc agtacaacag cacctaccgg 900

gtggtgtccg tgctgaccgt gctgcaccag gattggctga acggcaagga gtacaagtgt 960

aaggtgtcca acaaggccct gcctgcccct atcgagaaaa ccatcagcaa ggccaagggc 1020

cagcccagag agccccaggt gtacaccctg ccccctagca gagatgagct gaccaagaac 1080

caggtgtccc tgacctgcct ggtgaagggc ttctacccca gcgacatcgc cgtggagtgg 1140

gagagcaacg gccagcccga gaacaactac aagaccaccc cccctgtgct ggacagcgat 1200

ggcagcttct tcctgtacag caagctgacc gtggacaaga gcagatggca gcagggcaac 1260

gtgttcagct gctccgtgat gcacgaggcc ctgcacaatc actacaccca gaagagcctg 1320

agcctgtccc ctggcaag 1338

<210> 91
<211> 660
<212> DNA
<213> Artificial

<220>
<223> J11L1, light chain humanised construct

<400> 91
gacatccaga tgacccagag cccctctagc ctcagcgcca gcgtgggcga cagggtgacc 60

atcacctgca agagcagcca gagcctgctg aacggcagca accagaagaa ctacctggcc 120

tggtaccagc agaaacccgg caaggccccc aagctgctgg tctacttcgc ctctaccagg 180

gattccggcg tccccagcag gttcagcggc agcggcagcg gcaccgactt cacactgacc 240

atcagcagcc tgcagcccga ggacttcgcc acctactact gcctgcagca cttcggcacc 300

cctcccactt ttggccaggg caccaagctg gagattaagc gtacggtggc cgcccccagc 360

gtgttcatct tcccccccag cgatgagcag ctgaagagcg gcaccgccag cgtggtgtgt 420

ctgctgaaca acttctaccc ccgggaggcc aaggtgcagt ggaaggtgga caatgccctg 480

cagagcggca acagccagga gagcgtgacc gagcaggaca gcaaggactc cacctacagc 540

ctgagcagca ccctgaccct gagcaaggcc gactacgaga agcacaaggt gtacgcctgt 600

gaggtgaccc accagggcct gtccagcccc gtgaccaaga gcttcaaccg gggcgagtgc 660

<210> 92
<211> 1338
<212> DNA
<213> Artificial

<220>
<223> J11L1, heavy chain humanised construct

<400> 92
caggtgcagc tcgtgcagag cggggccgaa gtcaagaaac ccggcagctc cgtgaaggtg 60

agctgcaagg ccagcggctt ctctctcact gcctacggcg tgaactgggt gaggcaggct 120

cccggccagg gcctggagtg gatgggcatg atctgggacg acggcagcac cgactacgac 180

agcgccctga agagcagggt gaccatcacc gccgacaaga gcaccagcac cgcctacatg 240

gaactgagca gcctgaggag cgaggacacc gccgtgtact attgcgccag ggagggcgac 300

gtggccttcg attactgggg ccagggcaca ctagtgaccg tgtccagcgc cagcaccaag 360

ggccccagcg tgttcccccct ggcccccagc agcaagagca ccagcggcgg cacagccgcc 420

ctgggctgcc tggtgaagga ctacttcccc gaaccggtga ccgtgtcctg gaacagcgga 480

gccctgacca gcggcgtgca caccttcccc gccgtgctgc agagcagcgg cctgtacagc 540

ctgagcagcg tggtgaccgt gcccagcagc agcctgggca cccagaccta catctgtaac 600

gtgaaccaca agcccagcaa caccaaggtg gacaagaagg tggagcccaa gagctgtgac 660

aagacccaca cctgcccccc ctgccctgcc cccgagctgc tgggaggccc cagcgtgttc 720

ctgttccccc ccaagcctaa ggacaccctg atgatcagca gaacccccga ggtgacctgt 780

gtggtggtgg atgtgagcca cgaggaccct gaggtgaagt tcaactggta cgtggacggc 840

gtggaggtgc acaatgccaa gaccaagccc agggaggagc agtacaacag cacctaccgg 900

gtggtgtccg tgctgaccgt gctgcaccag gattggctga acggcaagga gtacaagtgt 960

aaggtgtcca acaaggccct gcctgccccct atcgagaaaa ccatcagcaa ggccaagggc 1020

cagcccagag agccccaggt gtacaccctg ccccctagca gagatgagct gaccaagaac 1080

caggtgtccc tgacctgcct ggtgaagggc ttctacccca gcgacatcgc cgtggagtgg 1140

gagagcaacg gccagcccga gaacaactac aagaccaccc cccctgtgct ggacagcgat 1200

ggcagcttct tcctgtacag caagctgacc gtggacaaga gcagatggca gcagggcaac 1260

gtgttcagct gctccgtgat gcacgaggcc ctgcacaatc actacaccca gaagagcctg 1320

agcctgtccc ctggcaag 1338

<210> 93
<211> 660
<212> DNA
<213> Artificial

<220>
<223> J13L1, light chain humanised construct

<400> 93
gacatccaga tgacccagag cccctctagc ctcagcgcca gcgtgggcga cagggtgacc 60

atcacctgca agagcagcca gagcctgctg aacggcagca accagaagaa ctacctggcc 120

tggtaccagc agaaacccgg caaggccccc aagctgctgg tctacttcgc ctctaccagg 180

gattccggcg tccccagcag gttcagcggc agcggcagcg gcaccgactt cacactgacc 240

atcagcagcc tgcagcccga ggacttcgcc acctactact gcctgcagca cttcggcacc 300

cctcccactt ttggccaggg caccaagctg gagattaagc gtacggtggc cgcccccagc 360

gtgttcatct tcccccccag cgatgagcag ctgaagagcg gcaccgccag cgtggtgtgt 420

ctgctgaaca acttctaccc ccgggaggcc aaggtgcagt ggaaggtgga caatgccctg 480

cagagcggca acagccagga gagcgtgacc gagcaggaca gcaaggactc cacctacagc 540

ctgagcagca ccctgaccct gagcaaggcc gactacgaga agcacaaggt gtacgcctgt 600

gaggtgaccc accagggcct gtccagcccc gtgaccaaga gcttcaaccg gggcgagtgc 660

<210> 94

<211> 1338
<212> DNA
<213> Artificial

<220>
<223> J13L1, heavy chain humanised construct

<400> 94
caggtgcagc tcgtgcagag cggggccgaa gtcaagaaac ccggcagctc cgtgaaggtg 60

agctgcaagg ccagcggcgg caccttcagc gcctacggcg tgaactgggt gaggcaggct 120

cccggccagg gcctggagtg gatgggcatg atctgggacg acggcagcac cgactacgac 180

agcgccctga agagcagggt gaccatcacc gccgacaaga gcaccagcac cgcctacatg 240

gaactgagca gcctgaggag cgaggacacc gccgtgtact attgcgccag ggagggcgac 300

gtggccttcg attactgggg ccagggcaca ctagtgaccg tgtccagcgc cagcaccaag 360

ggccccagcg tgttcccccc ggcccccagc agcaagagca ccagcggcgg cacagccgcc 420

ctgggctgcc tggtgaagga ctacttcccc gaaccggtga ccgtgtcctg gaacagcgga 480

gccctgacca gcggcgtgca caccttcccc gccgtgctgc agagcagcgg cctgtacagc 540

ctgagcagcg tggtgaccgt gcccagcagc agcctgggca cccagaccta catctgtaac 600

gtgaaccaca agcccagcaa caccaaggtg gacaagaagg tggagcccaa gagctgtgac 660

aagacccaca cctgcccccc ctgccctgcc cccgagctgc tgggaggccc cagcgtgttc 720

ctgttccccc ccaagcctaa ggacaccctg atgatcagca gaacccccga ggtgacctgt 780

gtggtggtgg atgtgagcca cgaggaccct gaggtgaagt tcaactggta cgtggacggc 840

gtggaggtgc acaatgccaa gaccaagccc agggaggagc agtacaacag cacctaccgg 900

gtggtgtccg tgctgaccgt gctgcaccag gattggctga acggcaagga gtacaagtgt 960

aaggtgtcca acaaggccct gcctgccccc atcgagaaaa ccatcagcaa ggccaagggc 1020

cagcccagag agccccaggt gtacaccctg ccccctagca gagatgagct gaccaagaac 1080

caggtgtccc tgacctgcct ggtgaagggc ttctacccca gcgacatcgc cgtggagtgg 1140

gagagcaacg gccagcccga gaacaactac aagaccaccc cccctgtgct ggacagcgat 1200

ggcagcttct tcctgtacag caagctgacc gtggacaaga gcagatggca gcagggcaac 1260

gtgttcagct gctccgtgat gcacgaggcc ctgcacaatc actacaccca gaagagcctg 1320

agcctgtccc ctggcaag 1338

<210> 95
<211> 660
<212> DNA
<213> Artificial

<220>
<223> H7L1, light chain humanised construct

<400> 95
gacatccaga tgacccagag cccctctagc ctcagcgcca gcgtgggcga cagggtgacc 60

atcacctgca agagcagcca gagcctgctg aacggcagca accagaagaa ctacctggcc 120

tggtaccagc agaaacccgg caaggccccc aagctgctgg tctacttcgc ctctaccagg 180

gattccggcg tccccagcag gttcagcggc agcggcagcg gcaccgactt cacactgacc 240

atcagcagcc tgcagcccga ggacttcgcc acctactact gcctgcagca cttcggcacc 300

cctcccactt ttggccaggg caccaagctg gagattaagc gtacggtggc cgcccccagc 360

gtgttcatct tccccccccag cgatgagcag ctgaagagcg gcaccgccag cgtggtgtgt 420

ctgctgaaca acttctaccc ccgggaggcc aaggtgcagt ggaaggtgga caatgccctg 480

cagagcggca acagccagga gagcgtgacc gagcaggaca gcaaggactc cacctacagc 540

ctgagcagca ccctgaccct gagcaaggcc gactacgaga agcacaaggt gtacgcctgt 600

gaggtgaccc accagggcct gtccagcccc gtgaccaaga gcttcaaccg gggcgagtgc 660

<210> 96
<211> 1338
<212> DNA
<213> Artificial

<220>
<223> H7L1, heavy chain humanised construct

<400> 96
caggtgcagc tccaggagag cggccccggc ctggtgaagc ctagcgagac cctgagcctg 60

acctgcaccg tgagcggcgg ctccatcagc gcctacggcg tcaactggat caggcagccc 120

cccggcaaag gcctggagtg gattgggatg atctgggacg acggcagcac cgactacgac 180

agcgccctga agagcagggt gaccatcagc gtggacacca gcaagaacca gttcagcctg 240

aagctgagca gcgtgactgc cgccgacacc gccgtctatt actgcgccag ggagggcgac 300

gtggccttcg attactgggg ccagggcaca ctagtgaccg tgtccagcgc cagcaccaag 360

ggccccagcg tgttccccct ggcccccagc agcaagagca ccagcggcgg cacagccgcc 420

ctgggctgcc tggtgaagga ctacttcccc gaaccggtga ccgtgtcctg gaacagcgga 480

gccctgacca gcggcgtgca caccttcccc gccgtgctgc agagcagcgg cctgtacagc 540

ctgagcagcg tggtgaccgt gcccagcagc agcctgggca cccagaccta catctgtaac 600

gtgaaccaca agcccagcaa caccaaggtg gacaagaagg tggagcccaa gagctgtgac 660

aagacccaca cctgcccccc ctgccctgcc cccgagctgc tgggaggccc cagcgtgttc 720

ctgttccccc ccaagcctaa ggacaccctg atgatcagca gaacccccga ggtgacctgt 780

gtggtggtgg atgtgagcca cgaggaccct gaggtgaagt tcaactggta cgtggacggc 840

gtggaggtgc acaatgccaa gaccaagccc agggaggagc agtacaacag cacctaccgg 900

gtggtgtccg tgctgaccgt gctgcaccag gattggctga acggcaagga gtacaagtgt 960

aaggtgtcca acaaggccct gcctgccccct atcgagaaaa ccatcagcaa ggccaagggc 1020

cagcccagag agccccaggt gtacaccctg ccccctagca gagatgagct gaccaagaac 1080

caggtgtccc tgacctgcct ggtgaagggc ttctacccca gcgacatcgc cgtggagtgg 1140

gagagcaacg gccagcccga gaacaactac aagaccaccc cccctgtgct ggacagcgat 1200

ggcagcttct tcctgtacag caagctgacc gtggacaaga gcagatggca gcagggcaac 1260

gtgttcagct gctccgtgat gcacgaggcc ctgcacaatc actacaccca gaagagcctg 1320

agcctgtccc ctggcaag 1338

<210> 97
<211> 660
<212> DNA
<213> Artificial

<220>
<223> JOL1, light chain humanised construct

<400> 97
gacatccaga tgacccagag cccctctagc ctcagcgcca gcgtgggcga cagggtgacc 60

atcacctgca agagcagcca gagcctgctg aacggcagca accagaagaa ctacctggcc 120

tggtaccagc agaaacccgg caaggccccc aagctgctgg tctacttcgc ctctaccagg 180

gattccggcg tccccagcag gttcagcggc agcggcagcg gcaccgactt cacactgacc 240

atcagcagcc tgcagcccga ggacttcgcc acctactact gcctgcagca cttcggcacc 300

cctcccactt ttggccaggg caccaagctg gagattaagc gtacggtggc cgcccccagc 360

gtgttcatct tccccccccag cgatgagcag ctgaagagcg gcaccgccag cgtggtgtgt 420

ctgctgaaca acttctaccc ccgggaggcc aaggtgcagt ggaaggtgga caatgccctg 480

cagagcggca acagccagga gagcgtgacc gagcaggaca gcaaggactc cacctacagc 540

ctgagcagca ccctgaccct gagcaaggcc gactacgaga agcacaaggt gtacgcctgt 600

gaggtgaccc accagggcct gtccagcccc gtgaccaaga gcttcaaccg gggcgagtgc 660

<210> 98
<211> 1338
<212> DNA
<213> Artificial

<220>
<223> JOL1, heavy chain humanised construct

<400> 98
caggtgcagc tcgtgcagag cggggccgaa gtcaagaaac ccggcagctc cgtgaaggtg 60

agctgcaagg ccagcggcgg caccttcagc gcctacggcg tgaactgggt gaggcaggct 120

cccggccagg gcctggagtg gatgggcatg atctgggacg acggcagcac cgactacaac 180

agcgccctga agagcagggt gaccatcacc gccgacaaga gcaccagcac cgcctacatg 240

gaactgagca gcctgaggag cgaggacacc gccgtgtact attgcgccag ggagggcgac 300

gtggccttcg attactgggg ccagggcaca ctagtgaccg tgtccagcgc cagcaccaag 360

ggccccagcg tgttccccct ggcccccagc agcaagagca ccagcggcgg cacagccgcc 420

ctgggctgcc tggtgaagga ctacttcccc gaaccggtga ccgtgtcctg gaacagcgga 480

gccctgacca gcggcgtgca caccttcccc gccgtgctgc agagcagcgg cctgtacagc 540

ctgagcagcg tggtgaccgt gcccagcagc agcctgggca cccagaccta catctgtaac 600

gtgaaccaca agcccagcaa caccaaggtg gacaagaagg tggagcccaa gagctgtgac 660

aagacccaca cctgcccccc ctgccctgcc cccgagctgc tgggaggccc cagcgtgttc 720

ctgttccccc ccaagcctaa ggacaccctg atgatcagca gaacccccga ggtgacctgt 780

gtggtggtgg atgtgagcca cgaggaccct gaggtgaagt tcaactggta cgtggacggc 840

gtggaggtgc acaatgccaa gaccaagccc agggaggagc agtacaacag cacctaccgg 900

gtggtgtccg tgctgaccgt gctgcaccag gattggctga acggcaagga gtacaagtgt 960

aaggtgtcca acaaggccct gcctgccccc atcgagaaaa ccatcagcaa ggccaagggc 1020

cagcccagag agccccaggt gtacaccctg ccccctagca gagatgagct gaccaagaac 1080

caggtgtccc tgacctgcct ggtgaagggc ttctacccca gcgacatcgc cgtggagtgg 1140

gagagcaacg gccagcccga gaacaactac aagaccaccc cccctgtgct ggacagcgat 1200

ggcagcttct tcctgtacag caagctgacc gtggacaaga gcagatggca gcagggcaac 1260

gtgttcagct gctccgtgat gcacgaggcc ctgcacaatc actacaccca gaagagcctg 1320

agcctgtccc ctggcaag 1338

<210> 99
<211> 660
<212> DNA
<213> Artificial

<220>
<223> HOL1, light chain humanised construct

<400> 99
gacatccaga tgacccagag cccctctagc ctcagcgcca gcgtgggcga cagggtgacc 60

atcacctgca agagcagcca gagcctgctg aacggcagca accagaagaa ctacctggcc 120

tggtaccagc agaaacccgg caaggccccc aagctgctgg tctacttcgc ctctaccagg 180

gattccggcg tccccagcag gttcagcggc agcggcagcg gcaccgactt cacactgacc 240

atcagcagcc tgcagcccga ggacttcgcc acctactact gcctgcagca cttcggcacc 300

cctcccactt ttggccaggg caccaagctg gagattaagc gtacggtggc cgcccccagc 360

gtgttcatct tccccccccag cgatgagcag ctgaagagcg gcaccgccag cgtggtgtgt 420

ctgctgaaca acttctaccc ccgggaggcc aaggtgcagt ggaaggtgga caatgccctg 480

cagagcggca acagccagga gagcgtgacc gagcaggaca gcaaggactc cacctacagc 540

ctgagcagca ccctgaccct gagcaaggcc gactacgaga agcacaaggt gtacgcctgt 600

gaggtgaccc accagggcct gtccagcccc gtgaccaaga gcttcaaccg gggcgagtgc 660

<210> 100
<211> 1338
<212> DNA
<213> Artificial

<220>
<223> HOL1, heavy chain humanised construct

<400> 100

caggtgcagc tccaggagag cggccccggc ctggtgaagc ctagcgagac cctgagcctg 60

acctgcaccg tgagcggcgg ctccatcagc gcctacggcg tcaactggat caggcagccc 120

cccggcaaag gcctggagtg gattgggatg atctgggacg acggcagcac cgactacaac 180

agcgccctga agagcagggt gaccatcagc gtggacacca gcaagaacca gttcagcctg 240

aagctgagca gcgtgactgc cgccgacacc gccgtctatt actgcgccag ggagggcgac 300

gtggccttcg attactgggg ccagggcaca ctagtgaccg tgtccagcgc cagcaccaag 360

ggccccagcg tgttccccct ggccccccagc agcaagagca ccagcggcgg cacagccgcc 420

ctgggctgcc tggtgaagga ctacttcccc gaaccggtga ccgtgtcctg gaacagcgga 480

gccctgacca gcggcgtgca caccttcccc gccgtgctgc agagcagcgg cctgtacagc 540

ctgagcagcg tggtgaccgt gcccagcagc agcctgggca cccagaccta catctgtaac 600

gtgaaccaca agcccagcaa caccaaggtg gacaagaagg tggagcccaa gagctgtgac 660

aagacccaca cctgcccccc ctgccctgcc cccgagctgc tgggaggccc cagcgtgttc 720

ctgttccccc ccaagcctaa ggacaccctg atgatcagca gaaccccga ggtgacctgt 780

gtggtggtgg atgtgagcca cgaggaccct gaggtgaagt tcaactggta cgtggacggc 840

gtggaggtgc acaatgccaa gaccaagccc agggaggagc agtacaacag cacctaccgg 900

gtggtgtccg tgctgaccgt gctgcaccag gattggctga acggcaagga gtacaagtgt 960

aaggtgtcca acaaggccct gcctgccccct atcgagaaaa ccatcagcaa ggccaagggc 1020

cagcccagag agccccaggt gtacaccctg ccccctagca gagatgagct gaccaagaac 1080

caggtgtccc tgacctgcct ggtgaagggc ttctacccca gcgacatcgc cgtggagtgg 1140

gagagcaacg gccagcccga gaacaactac aagaccaccc cccctgtgct ggacagcgat 1200

ggcagcttct tcctgtacag caagctgacc gtggacaaga gcagatggca gcagggcaac 1260

gtgttcagct gctccgtgat gcacgaggcc ctgcacaatc actacaccca gaagagcctg 1320

agcctgtccc ctggcaag 1338

<210> 101
<211> 318
<212> DNA
<213> Human

<400> 101
acggtggccg cccccagcgt gttcatcttc ccccccagcg atgagcagct gaagagcggc 60

accgccagcg tggtgtgtct gctgaacaac ttctaccccc gggaggccaa ggtgcagtgg 120

aaggtggaca atgccctgca gagcggcaac agccaggaga gcgtgaccga gcaggacagc 180

aaggactcca cctacagcct gagcagcacc ctgaccctga gcaaggccga ctacgagaag 240

cacaaggtgt acgcctgtga ggtgacccac cagggcctgt ccagccccgt gaccaagagc 300

ttcaaccggg gcgagtgc 318

<210> 102
<211> 990

<212> DNA
<213> Human

<400> 102
gccagcacca agggccccag cgtgttcccc ctggccccca gcagcaagag caccagcggc 60

ggcacagccg ccctgggctg cctggtgaag gactacttcc ccgaaccggt gaccgtgtcc 120

tggaacagcg gagccctgac cagcggcgtg cacaccttcc ccgccgtgct gcagagcagc 180

ggcctgtaca gcctgagcag cgtggtgacc gtgcccagca gcagcctggg cacccagacc 240

tacatctgta acgtgaacca caagcccagc aacaccaagg tggacaagaa ggtggagccc 300

aagagctgtg acaagaccca cacctgcccc ccctgccctg cccccgagct gctgggaggc 360

cccagcgtgt tcctgttccc ccccaagcct aaggacaccc tgatgatcag cagaaccccc 420

gaggtgacct gtgtggtggt ggatgtgagc cacgaggacc ctgaggtgaa gttcaactgg 480

tacgtggacg gcgtggaggt gcacaatgcc aagaccaagc ccagggagga gcagtacaac 540

agcacctacc gggtggtgtc cgtgctgacc gtgctgcacc aggattggct gaacggcaag 600

gagtacaagt gtaaggtgtc caacaaggcc ctgcctgccc ctatcgagaa aaccatcagc 660

aaggccaagg gccagcccag agagccccag gtgtacaccc tgcccccctag cagagatgag 720

ctgaccaaga accaggtgtc cctgacctgc ctggtgaagg gcttctaccc cagcgacatc 780

gccgtggagt gggagagcaa cggccagccc gagaacaact acaagaccac ccccccctgtg 840

ctggacagcg atggcagctt cttcctgtac agcaagctga ccgtggacaa gagcagatgg 900

cagcagggca acgtgttcag ctgctccgtg atgcacgagg ccctgcacaa tcactacacc 960

cagaagagcc tgagcctgtc ccctggcaag 990

<210> 103
<211> 348
<212> DNA
<213> Murine

<400> 103
caggtgcagc tgaaggagtc aggtcctggc ctggtggcgc cctcacagag cctgtccatc 60

acatgcaccg tctcagggtt ctcattaacc gcctatggtg taaactgggt tcgccagcct 120

ccaggaaagg gtctggagtg gctgggaatg atatgggatg atggaagcac agactataat 180

tcagctctca aatccagact gagcatcagt aaggacaact ccaagagcca agttttctta 240

aaaatgaaca gtctgcaaac tgatgacaca gccaggtact actgtgccag agaaggggac 300

gtagcctttg actactgggg ccaaggcacc actctcacag tctcctca 348

<210> 104
<211> 342
<212> DNA
<213> Murine

<400> 104
gacattgtga tgacacagtc tccctcctcc ctggctgtgt cagtaggaca gaaggtcact 60

atgagctgca agtccagtca gagcctttta aatggtagca atcaaaagaa ctacttggcc 120

tggtaccagc agaaaccagg acagtctcct aaacttctgg tatactttgc atccactagg 180

gattctgggg tccctgatcg cttcataggc agtggatctg ggacagattt cactcttacc 240

atcagcagtg tgcaggctga agacctggca gattacttct gtctgcaaca ttttggcact 300

cctccgacgt tcggtggagg caccaaactg gaaatcaaac gg 342

<210> 105
<211> 1338
<212> DNA
<213> Artificial

<220>
<223> IMP731, heavy chain sequence

<400> 105
caggtgcagc tgaaggagtc aggtcctggc ctggtggcgc cctcacagag cctgtccatc 60

acatgcaccg tctcagggtt ctcattaacc gcctatggtg taaactgggt tcgccagcct 120

ccaggaaagg gtctggagtg gctgggaatg atatgggatg atggaagcac agactataat 180

tcagctctca aatccagact gagcatcagt aaggacaact ccaagagcca agttttctta 240

aaaatgaaca gtctgcaaac tgatgacaca gccaggtact actgtgccag agaaggggac 300

gtagcctttg actactgggg ccaaggcacc actctcacag tctcctcagc tagcaccaag 360

ggcccatcgg tcttcccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 420

ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 480

gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc 540

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 600

gtgaatcaca agcccagcaa caccaaggtg gacaagaaag ttgagcccaa atcttgtgac 660

aaaactcaca catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc 720

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 780

gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 840

gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt 900

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 960

aaggtctcca acaaagccct cccagccccc atcgagaaaa ccatctccaa agccaaaggg 1020

cagccccgag aaccacaggt gtacaccctg cccccatccc gggatgagct gaccaagaac 1080

caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1140

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1260

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1320

tccctgtctc cgggtaaa 1338

<210> 106
<211> 660
<212> DNA

<213> Artificial

<220>
<223> IMP731, light chain sequence

<400> 106
gacattgtga tgacacagtc tccctcctcc ctggctgtgt cagtaggaca gaaggtcact 60

atgagctgca agtccagtca gagcctttta aatggtagca atcaaaagaa ctacttggcc 120

tggtaccagc agaaaccagg acagtctcct aaacttctgg tatactttgc atccactagg 180

gattctgggg tccctgatcg cttcataggc agtggatctg ggacagattt cactcttacc 240

atcagcagtg tgcaggctga agacctggca gattacttct gtctgcaaca ttttggcact 300

cctccgacgt tcggtggagg caccaaactg gaaatcaaac ggaccgtggc tgcaccatct 360

gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc 420

ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgccctc 480

caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 540

ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600

gaagtcaccc atcagggcct gagttcgccc gtcacaaaga gcttcaacag gggagagtgt 660

<210> 107
<211> 1251
<212> DNA
<213> Artificial

<220>
<223> Recombinant human LAG-3-ECD-His6

<400> 107
ctccagccag gggctgaggt cccggtggtg tgggcccagg agggggctcc tgcccagctc 60

ccctgcagcc ccacaatccc cctccaggat ctcagccttc tgcgaagagc aggggtcact 120

tggcagcatc agccagacag tggcccgccc gctgccgccc ccggccatcc cctggccccc 180

ggccctcacc cggcggcgcc ctcctcctgg gggcccaggc cccgccgcta cacggtgctg 240

agcgtgggtc ccggaggcct gcgcagcggg aggctgcccc tgcagccccg cgtccagctg 300

gatgagcgcg gccggcagcg cggggacttc tcgctatggc tgcgcccagc ccggcgcgcg 360

gacgccggcg agtaccgcgc cgcggtgcac ctcagggacc gcgccctctc ctgccgcctc 420

cgtctgcgcc tgggccaggc ctcgatgact gccagccccc caggatctct cagagcctcc 480

gactgggtca ttttgaactg ctccttcagc cgccctgacc gcccagcctc tgtgcattgg 540

ttccggaacc ggggccaggg ccgagtccct gtccgggagt ccccccatca ccacttagcg 600

gaaagcttcc tcttcctgcc ccaagtcagc cccatggact ctgggccctg gggctgcatc 660

ctcacctaca gagatggctt caacgtctcc atcatgtata acctcactgt tctgggtctg 720

gagcccccaa ctcccttgac agtgtacgct ggagcaggtt ccagggtggg gctgccctgc 780

cgcctgcctg ctggtgtggg gacccggtct ttcctcactg ccaagtggac tcctcctggg 840

ggaggccctg acctcctggt gactggagac aatggcgact ttacccttcg actagaggat 900

gtgagccagg cccaggctgg gacctacacc tgccatatcc atctgcagga acagcagctc 960

aatgccactg tcacattggc aatcatcaca gtgactccca aatcctttgg gtcacctgga 1020

tccctgggga agctgctttg tgaggtgact ccagtatctg gacaagaacg ctttgtgtgg 1080

agctctctgg acaccccatc ccagaggagt ttctcaggac cttggctgga ggcacaggag 1140

gcccagctcc tttcccagcc ttggcaatgc cagctgtacc agggggagag gcttcttgga 1200

gcagcagtgt acttcacaga gctgtctagc ccacaccacc atcatcacca t 1251

<210> 108
<211> 1251
<212> DNA
<213> Artificial

<220>
<223> Recombinant cynomolgus macaque LAG-3 ECD-His6

<400> 108
ccccagccag gggctgagat ctcggtggtg tgggcccagg agggggctcc tgcccagctc 60

ccctgcagcc ccacaatccc cctccaggat ctcagccttc tgcgaagagc aggggtcact 120

tggcagcatc aaccagacag tggcccgccc gctcccgccc ccggccaccc cccggccccc 180

ggccatcgcc cggcggcgcc ctactcttgg gggcccaggc cccgccgcta cacagtgctg 240

agcgtgggtc ctggaggcct gcgcagcggg aggctgcccc tgcagccccg cgtccagctg 300

gatgagcgcg gccggcagcg cggggacttc tcgctgtggc tgcgcccagc ccggcgcgcg 360

gacgccggcg agtaccgcgc cacggtgcac ctcagggacc gcgccctctc ctgccgcctt 420

cgtctgcgcg tgggccaggc ctcgatgact gccagccccc cagggtctct caggacctct 480

gactgggtca ttttgaactg ctccttcagc cgccctgacc gcccagcctc tgtgcattgg 540

ttccggagcc gtggccaggg ccgagtccct gtccaggggt ccccccatca ccacttagcg 600

gaaagcttcc tcttcctgcc ccatgtcggc cccatggact ctgggctctg gggctgcatc 660

ctcacctaca gagatggctt caatgtctcc atcatgtata acctcactgt tctgggtctg 720

gagcccgcaa ctcccttgac agtgtacgct ggagcaggtt ccagggtgga gctgccctgc 780

cgcctgcctc ctgctgtggg gacccagtct ttccttactg ccaagtgggc tcctcctggg 840

ggaggccctg acctcctggt ggctggagac aatggcgact ttacccttcg actagaggat 900

gtaagccagg cccaggctgg gacctacatc tgccatatcc gtctacaggg acagcagctc 960

aatgccactg tcacattggc aatcatcaca gtgactccca aatcctttgg gtcacctggc 1020

tccctgggga agctgctttg tgaggtgact ccagcatctg gacaagaaca ctttgtgtgg 1080

agccccctga acaccccatc ccagaggagt ttctcaggac catggctgga ggcccaggaa 1140

gcccagctcc tttcccagcc ttggcaatgc cagctgcacc agggggagag gcttcttgga 1200

gcagcagtat acttcacaga actgtctagc ccacaccacc atcatcacca t 1251

<210> 109
<211> 1251
<212> DNA

<213> Artificial

<220>
<223> Recombinant baboon LAG-3 ECD-His6

<400> 109
ccccagccag gggctgagat ctcggtggtg tgggcccagg agggggctcc tgcccagctc 60

ccctgcagcc ccacaatccc cctccaggat ctcagccttc tgcgaagagc aggggtcact 120

tggcagcatc aaccagacag tggcccgccc gctcccgccc ccggccaccc cccggccccc 180

ggccatcgcc cggcggcgcc ctactcttgg gggcccaggc cccgccgcta cacagtgctg 240

agcgtgggtc ctggaggcct gcgcagcggg aggctgcccc tgcagccccg cgtccagctg 300

gatgagcgcg gccggcagcg cggggacttc tcgctgtggc tgcgcccagc ccggcgcgcg 360

gacgccggcg agtaccgcgc cacggtgcac ctcagggacc gcgccctctc ctgccgcctt 420

cgtctgcgcg tgggccaggc ctcgatgact gccagccccc cagggtctct caggacctct 480

gactgggtca ttttgaactg ctccttcagc cgccctgacc gcccagcctc tgtgcattgg 540

ttccggagcc gtggccaggg ccaagtccct gtccaggagt ccccccatca ccacttagcg 600

gaaagcttcc tcttcctgcc ccatgtcggc cccatggact ctgggctctg gggctgcatc 660

ctcacctaca gagatggctt caatgtctcc atcatgtata acctcactgt tctgggtctg 720

gagcccacaa ctcccttgac agtgtacgct ggagcaggtt ccagggtgga gctgccctgc 780

cgcctgcctc ctgctgtggg gacccagtct ttccttactg ccaagtgggc tcctcctggg 840

ggaggccctg acctcctggt ggttggagac aatggcaact ttacccttcg actagaggat 900

gtaagccagg cccaggctgg gacctacatc tgccatatcc gtctacaggg acagcagctc 960

aatgccactg tcacattggc aatcatcaca gtgactccca aatcctttgg gtcacctggc 1020

tccctgggga agctgctttg tgaggtgact ccagcatctg gacaagaacg ctttgtgtgg 1080

agccccctga acaccccatc ccagaggagt ttctcaggac cgtggctgga ggcccaggaa 1140

gcccagctcc tttcccagcc ttggcaatgc cagctgcacc agggggagag gcttcttgga 1200

gcagcagtat acttcacaga actgtctagc ccacaccacc atcatcacca t 1251

<210> 110
<211> 57
<212> DNA
<213> Murine

<400> 110
atgggctgga gctgcatcat cctgttcctg gtggccaccg ctaccggagt gcacagc 57

<210> 111
<211> 60
<212> DNA
<213> Murine

<400> 111
atggaatcac agacccaggt cctcatgttt cttctgctct gggtatctgg tgcctgtgca 60

<210> 112

<211> 48
<212> DNA
<213> Human

<400> 112
atgccgctgc tgctactgct gcccctgctg tgggcagggg cgctagct 48