SEQUENCE LISTING

<110> Halozyme, Inc. et al.

<120> MODIFIED ANTI-EPIDERMAL GROWTH FACTOR
RECEPTOR ANTIBODIES AND METHODS OF USE THEREOF

<130> 33320.03118.US01/3118

<140> Not Yet Assigned
<141> Herewith

<150> US 61/960,253
<151> 2013-09-12

<160> 394

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Cetuximab A119 R216 heavy chain

<220>
<221> DOMAIN
<222> (1)...(119)
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<220>
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<222> (120)...(217)
<223> CH1

<220>
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<222> (218)...(232)
<223> hinge region

<220>
<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

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

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

<210> 2
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Cetuximab A119 heavy chain variable domain

<400> 2

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

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


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

<220>
<223> Cetuximab A100 LELK104-107 A213 light chain


<220>
<221> DOMAIN
<222> (1)...(107)
<223> variable domain

<220>
<221> DOMAIN
<222> (108)...(213)
<223> constant domain

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


<210> 4
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Cetuximab A100 LELK104-107 light chain variable
      domain
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<400> 4
Asp Ile Leu Leu Thr Gln Ser Pro Val Ile Leu Ser Val Ser Pro Gly
 1   5   10   15
Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
            20   25   30
Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
        35   40   45
Lys Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Ser Val Glu Ser
65   70   75   80
Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
                85   90   95
Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
            100   105

<210> 5
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> Cetuximab A119 R216 Ins222PKS heavy chain

<220>
<221> DOMAIN
<222> (1)...(119)
<223> variable domain

<220>
<221> DOMAIN
<222> (120)...(217)
<223> CH1

<220>
<221> DOMAIN
<222> (218)...(235)
<223> hinge region

<220>
<221> DOMAIN
<222> (236)...(345)
<223> CH2

<220>
<221> DOMAIN
<222> (346)...(452)
<223> CH3

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

```
        115                 120                 125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205
Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Pro Lys Ser
    210                 215                 220
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
225                 230                 235                 240
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                245                 250                 255
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            260                 265                 270
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
        275                 280                 285
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
    290                 295                 300
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
305                 310                 315                 320
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
                325                 330                 335
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            340                 345                 350
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
        355                 360                 365
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    370                 375                 380
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
385                 390                 395                 400
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
                405                 410                 415
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
            420                 425                 430
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
        435                 440                 445
Ser Pro Gly Lys
    450


<210> 6
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Cetuximab S119 K216 heavy chain


<220>
<221> DOMAIN
<222> (1)...(119)
<223> variable domain

<220>
<221> DOMAIN
<222> (120)...(217)
<223> CH1

<220>
<221> DOMAIN
<222> (218)...(232)
<223> hinge region
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<220>
<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 6
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Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
 1               5                  10                  15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
            20                  25                  30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50                  55                  60
Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65                  70                  75                  80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
                85                  90                  95
Arg Ala Leu Thr Tyr Tyr Asp Tyr Glu Phe Ala Tyr Trp Gly Gln Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
```

435 440 445
Lys

<210> 7
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Cetuximab S119 heavy chain variable domain

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

<210> 8
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Cetuximab Q100 VEIK104-107 EC213-214 light chain

<220>
<221> DOMAIN
<222> (1)...(107)
<223> variable domain

<220>
<221> DOMAIN
<222> (108)...(214)
<223> constant domain

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

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


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

<220>
<223> Cetuximab Q100 VEIK104-107 light chain variable
      domain


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


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

<220>
<223> Cetuximab Q100 LELK104-107 A213 light chain


<220>
<221> DOMAIN
<222> (1)...(107)
<223> variable domain

<220>
<221> DOMAIN
<222> (108)...(213)
<223> constant domain

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

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


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

<220>
<223> Cetuximab Q100 LELK104-107 light chain variable
      domain


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


<210> 12
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Cetuximab A119 R216 E358 M360 heavy chain

<220>
<221> DOMAIN
<222> (1)...(119)
<223> variable domain

<220>
<221> DOMAIN
<222> (120)...(217)
<223> CH1
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<220>
<221> DOMAIN
<222> (218)...(232)
<223> hinge region

<220>
<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 12

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

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
405 410 415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445
Lys

<210> 13
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Cetuximab A100 LELK104-107 EC213-214 light chain

<220>
<221> DOMAIN
<222> (1)...(107)
<223> variable domain

<220>
<221> DOMAIN
<222> (108)...(214)
<223> constant domain

<400> 13
Asp Ile Leu Leu Thr Gln Ser Pro Val Ile Leu Ser Val Ser Pro Gly
1 5 10 15
Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
20 25 30
Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
35 40 45
Lys Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Ser Val Glu Ser
65 70 75 80
Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
85 90 95
Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Val Ala Ala
100 105 110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205
Phe Asn Arg Gly Glu Cys
210

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

<220>
<223> Humanized Cetuximab (H225) heavy chain variable domain

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

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

<220>
<223> Humanized Cetuximab (H225) light chain variable
      domain

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

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

<220>
<223> Humanized Cetuximab (Hu225) Heavy Chain Variable
      domain

<400> 16
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Leu Thr Asn Tyr
            20   25   30
Gly Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu
        35   40   45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50   55   60
Ser Arg Leu Thr Ile Asn Lys Asp Asn Ser Lys Asn Thr Val Tyr Leu

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

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

<220>
<223> Humanized Cetuximab (Hu225) Light Chain Variable domain

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

<210> 18
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> Cetuximab S119 K216 Heavy Chain with Flag Tag

<220>
<221> DOMAIN
<222> (1)...(119)
<223> variable domain

<220>
<221> DOMAIN
<222> (120)...(449)
<223> constant domain

<220>
<221> PEPTIDE
<222> (450)...(457)
<223> Flag tag

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

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


<210> 19
<211> 330
<212> PRT
<213> Homo sapiens

<220>
<223> human IgG1


<220>
<221> DOMAIN
<222> (1)...(98)
<223> CH1

<220>
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<221> DOMAIN
<222> (99)...(113)
<223> hinge region

<220>
<221> DOMAIN
<222> (114)...(223)
<223> CH2

<220>
<221> DOMAIN
<222> (224)...(328)
<223> CH3

<400> 19
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> 20
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Cetuximab R216 heavy chain constant domain

<220>
<221> DOMAIN
<222> (1)...(98)
<223> CH1

<220>
<221> DOMAIN
<222> (99)...(113)
<223> hinge region

<220>
<221> DOMAIN
<222> (114)...(223)
<223> CH2

<220>
<221> DOMAIN
<222> (224)...(328)
<223> CH3

<400> 20
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
Arg 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> 21
<211> 333
<212> PRT

<213> Artificial Sequence

<220>
<223> Cetuximab R216 Ins222PKS heavy chain constant domain

<220>
<221> DOMAIN
<222> (1)...(98)
<223> CH1

<220>
<221> DOMAIN
<222> (99)...(116)
<223> hinge region

<220>
<221> DOMAIN
<222> (117)...(226)
<223> CH2

<220>
<221> DOMAIN
<222> (227)...(331)
<223> CH3

<400> 21

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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
Arg Val Glu Pro Lys Ser Pro Lys Ser Cys Asp Lys Thr His Thr Cys
            100                 105                 110
Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
        115                 120                 125
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
    130                 135                 140
Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
145                 150                 155                 160
Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
                165                 170                 175
Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
            180                 185                 190
Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
        195                 200                 205
Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
    210                 215                 220
Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
225                 230                 235                 240
Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
                245                 250                 255
Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
            260                 265                 270
Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
        275                 280                 285
Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
    290                 295                 300
Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
305                 310                 315                 320
```

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 22
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Cetuximab K216 heavy chain constant domain

<220>
<221> DOMAIN
<222> (1)...(98)
<223> CH1

<220>
<221> DOMAIN
<222> (99)...(113)
<223> hinge region

<220>
<221> DOMAIN
<222> (114)...(223)
<223> CH2

<220>
<221> DOMAIN
<222> (224)...(328)
<223> CH3

<400> 22
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> 23
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Cetuximab R216 E358 M360 heavy chain constant
      domain


<220>
<221> DOMAIN
<222> (1)...(98)
<223> CH1

<220>
<221> DOMAIN
<222> (99)...(113)
<223> hinge region

<220>
<221> DOMAIN
<222> (114)...(223)
<223> CH2

<220>
<221> DOMAIN
<222> (224)...(328)
<223> CH3

<400> 23
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
Arg 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 Glu Glu
225                 230                 235                 240
Met 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> 24
<211> 326
<212> PRT
<213> Homo sapiens

<220>
<223> human IgG2

<220>
<221> DOMAIN
<222> (1)...(98)
<223> CH1

<220>
<221> DOMAIN
<222> (99)...(110)
<223> hinge region

<220>
<221> DOMAIN
<222> (111)...(219)
<223> CH2

<220>
<221> DOMAIN
<222> (220)...(326)
<223> CH3

<400> 24
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
 1               5                  10                  15
Ser Thr Ser Glu Ser 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 Asn Phe Gly Thr Gln Thr
65                  70                  75                  80
Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95
Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
            100                 105                 110
Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
        115                 120                 125
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
    130                 135                 140
Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
145                 150                 155                 160
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
                165                 170                 175
```

```
Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp
            180                 185                 190
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
        195                 200                 205
Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu
    210                 215                 220
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
225                 230                 235                 240
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
                245                 250                 255
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
            260                 265                 270
Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
        275                 280                 285
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
    290                 295                 300
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
305                 310                 315                 320
Ser Leu Ser Pro Gly Lys
                325


<210> 25
<211> 377
<212> PRT
<213> Homo sapiens

<220>
<223> human IgG3


<220>
<221> DOMAIN
<222> (1)...(98)
<223> CH1

<220>
<221> DOMAIN
<222> (99)...(160)
<223> hinge region

<220>
<221> DOMAIN
<222> (161)...(270)
<223> CH2

<220>
<221> DOMAIN
<222> (271)...(376)
<223> CH3

<400> 25
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
 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 Thr Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95
Arg Val Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro
            100                 105                 110
Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg
        115                 120                 125
```

```
Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys
    130                 135                 140
Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
145                 150                 155                 160
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                165                 170                 175
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            180                 185                 190
Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Lys Trp Tyr
        195                 200                 205
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    210                 215                 220
Gln Tyr Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Leu His
225                 230                 235                 240
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                245                 250                 255
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln
            260                 265                 270
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
        275                 280                 285
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    290                 295                 300
Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu Asn Asn
305                 310                 315                 320
Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
                325                 330                 335
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile
            340                 345                 350
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln
        355                 360                 365
Lys Ser Leu Ser Leu Ser Pro Gly Lys
    370                 375
```

<210> 26
<211> 327
<212> PRT
<213> Homo sapiens

<220>
<223> human IgG4

<220>
<221> DOMAIN
<222> (1)...(98)
<223> CH1

<220>
<221> DOMAIN
<222> (99)...(110)
<223> hinge region

<220>
<221> DOMAIN
<222> (111)...(220)
<223> CH2

<220>
<221> DOMAIN
<222> (221)...(327)
<223> CH3

<400> 26

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

<210> 27
<211> 231
<212> PRT
<213> Homo sapiens

<220>
<223> human IgG1 Fc

<400> 27

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

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


<210> 28
<211> 232
<212> PRT
<213> Homo sapiens

<220>
<223> human IgG1 native C-terminus of Fc domain


<400> 28
Glu Pro Arg Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 1               5                  10                  15
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20                  25                  30
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35                  40                  45
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95
Asp Trp Leu Asn Gly Lys Asp Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100                 105                 110
Leu Pro Ala Pro Met Gln Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115                 120                 125
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Arg
145                 150                 155                 160
His Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220
Ser Leu Ser Leu Ser Pro Gly Lys
225                 230


<210> 29
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> Cetuximab A119 R216 E358 M360 heavy chain DNA



<220>
<221> V_region
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<222> (1)...(357)

<220>
<221> C_region
<222> (358)...(1347)

<400> 29
caggtgcagc tgaagcagtc aggacctggc ctagtgcagc cctcacagag cctgtccatc 60
acctgcacag tctctggttt ctcattaact aactatggtg tacactgggt tcgccagtct 120
ccaggaaagg gtctggagtg gctgggagtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagact gagcatcaac aaggacaatt ccaagagcca agttttcttt 240
aaaatgaaca gtctgcaatc taatgacaca gccatatatt actgtgccag agccctcacc 300
tactatgatt acgagtttgc ttactggggc caagggactc tggtcactgt ctctgcagcc 360
tccaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480
aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540
ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600
atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagagagt tgagcccaaa 660
tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 720
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780
gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960
tacaagtgca aggtctccaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1020
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggaggagatg 1080
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200
gactccgacg gctccttctt cctctatagc aagctcaccg tggacaagag caggtggcag 1260
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320
aagagcctct ccctgtcccc gggtaaa   1347

<210> 30
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> Cetuximab A100 LELK104-107 EC213-214 light chain
      DNA

<220>
<221> V_region
<222> (1)...(321)

<220>
<221> C_region
<222> (322)...(642)

<400> 30
gacatcttgc tgactcagtc tccagtcatc ctgtctgtga gtccaggaga aagagtcagt 60
ttctcctgca gggccagtca gagtattggc acaaacatac actggtatca gcaaagaaca 120
aatggttctc caaggcttct cataaagtat gcttctgagt ctatctctgg gatcccttcc 180
aggtttagtg gcagtggatc agggacagat tttactctta gcatcaacag tgtggagtct 240
gaagatattg cagattatta ctgtcaacaa aataataact ggccaaccac gttcggtgct 300
gggaccaagc tggagctgaa acgaactgtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt   642

<210> 31
<211> 107
<212> PRT
<213> Homo sapiens

<220>

<223> human kappa light chain constant domain

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

<210> 32
<211> 104
<212> PRT
<213> Homo sapiens

<220>
<223> human lambda light chain constant domain

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

<210> 33
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Cetuximab A213 kappa light chain constant domain

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

Pro Val Thr Lys Ser Phe Asn Arg Gly Ala
100 105

<210> 34
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Cetuximab EC213-214 light chain constant domain

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

<210> 35
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Cetuximab CDRH1

<400> 35
Asn Tyr Gly Val His
1 5

<210> 36
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Cetuximab CDRH2

<400> 36
Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr Ser
1 5 10 15

<210> 37
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Cetuximab CDRH3

<400> 37

Ala Leu Thr Tyr Tyr Asp Tyr Glu Phe Ala Tyr
 1   5   10

<210> 38
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Cetuximab CDRL1

<400> 38
Arg Ala Ser Gln Ser Ile Gly Thr Asn Ile His
 1   5   10

<210> 39
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Cetuximab CDRL2

<400> 39
Tyr Ala Ser Glu Ser Ile Ser
 1   5

<210> 40
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Cetuximab CDRL3

<400> 40
Gln Gln Asn Asn Asn Trp Pro Thr Thr
 1   5

<210> 41
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Heavy chain signal sequence

<400> 41
Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly
 1   5   10   15
Val Gln Cys

<210> 42
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Light chain signal sequence

<400> 42
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
 1   5   10   15
Leu Pro Gly Ala Lys Cys
            20

<210> 43
<211> 1210
<212> PRT
<213> Homo sapiens

<220>
<223> epidermal growth factor receptor (EGFR)

<400> 43
Met Arg Pro Ser Gly Thr Ala Gly Ala Ala Leu Leu Ala Leu Leu Ala
 1   5   10   15
Ala Leu Cys Pro Ala Ser Arg Ala Leu Glu Glu Lys Lys Val Cys Gln
            20   25   30
Gly Thr Ser Asn Lys Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe
        35   40   45
Leu Ser Leu Gln Arg Met Phe Asn Asn Cys Glu Val Val Leu Gly Asn
    50   55   60
Leu Glu Ile Thr Tyr Val Gln Arg Asn Tyr Asp Leu Ser Phe Leu Lys
65   70   75   80
Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val
                85   90   95
Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Met Tyr
            100   105   110
Tyr Glu Asn Ser Tyr Ala Leu Ala Val Leu Ser Asn Tyr Asp Ala Asn
        115   120   125
Lys Thr Gly Leu Lys Glu Leu Pro Met Arg Asn Leu Gln Glu Ile Leu
    130   135   140
His Gly Ala Val Arg Phe Ser Asn Asn Pro Ala Leu Cys Asn Val Glu
145   150   155   160
Ser Ile Gln Trp Arg Asp Ile Val Ser Ser Asp Phe Leu Ser Asn Met
                165   170   175
Ser Met Asp Phe Gln Asn His Leu Gly Ser Cys Gln Lys Cys Asp Pro
            180   185   190
Ser Cys Pro Asn Gly Ser Cys Trp Gly Ala Gly Glu Glu Asn Cys Gln
        195   200   205
Lys Leu Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser Gly Arg Cys Arg
    210   215   220
Gly Lys Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys
225   230   235   240
Thr Gly Pro Arg Glu Ser Asp Cys Leu Val Cys Arg Lys Phe Arg Asp
                245   250   255
Glu Ala Thr Cys Lys Asp Thr Cys Pro Pro Leu Met Leu Tyr Asn Pro
            260   265   270
Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys Tyr Ser Phe Gly
        275   280   285
Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val Val Thr Asp His
    290   295   300
Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu
305   310   315   320
Asp Gly Val Arg Lys Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val
                325   330   335
Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn
            340   345   350
Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp
        355   360   365
Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr
    370   375   380
Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu
385   390   395   400

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Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp
                405                 410                 415
Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln
            420                 425                 430
His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu
        435                 440                 445
Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser
    450                 455                 460
Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu
465                 470                 475                 480
Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu
                485                 490                 495
Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro
            500                 505                 510
Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn
        515                 520                 525
Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu Leu Glu Gly
    530                 535                 540
Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro
545                 550                 555                 560
Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro
                565                 570                 575
Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val
            580                 585                 590
Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp
        595                 600                 605
Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys
    610                 615                 620
Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro Thr Asn Gly
625                 630                 635                 640
Pro Lys Ile Pro Ser Ile Ala Thr Gly Met Val Gly Ala Leu Leu Leu
                645                 650                 655
Leu Leu Val Val Ala Leu Gly Ile Gly Leu Phe Met Arg Arg Arg His
            660                 665                 670
Ile Val Arg Lys Arg Thr Leu Arg Arg Leu Leu Gln Glu Arg Glu Leu
        675                 680                 685
Val Glu Pro Leu Thr Pro Ser Gly Glu Ala Pro Asn Gln Ala Leu Leu
    690                 695                 700
Arg Ile Leu Lys Glu Thr Glu Phe Lys Lys Ile Lys Val Leu Gly Ser
705                 710                 715                 720
Gly Ala Phe Gly Thr Val Tyr Lys Gly Leu Trp Ile Pro Glu Gly Glu
                725                 730                 735
Lys Val Lys Ile Pro Val Ala Ile Lys Glu Leu Arg Glu Ala Thr Ser
            740                 745                 750
Pro Lys Ala Asn Lys Glu Ile Leu Asp Glu Ala Tyr Val Met Ala Ser
        755                 760                 765
Val Asp Asn Pro His Val Cys Arg Leu Leu Gly Ile Cys Leu Thr Ser
    770                 775                 780
Thr Val Gln Leu Ile Thr Gln Leu Met Pro Phe Gly Cys Leu Leu Asp
785                 790                 795                 800
Tyr Val Arg Glu His Lys Asp Asn Ile Gly Ser Gln Tyr Leu Leu Asn
                805                 810                 815
Trp Cys Val Gln Ile Ala Lys Gly Met Asn Tyr Leu Glu Asp Arg Arg
            820                 825                 830
Leu Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Lys Thr Pro
        835                 840                 845
Gln His Val Lys Ile Thr Asp Phe Gly Leu Ala Lys Leu Leu Gly Ala
    850                 855                 860
Glu Glu Lys Glu Tyr His Ala Glu Gly Gly Lys Val Pro Ile Lys Trp
865                 870                 875                 880
Met Ala Leu Glu Ser Ile Leu His Arg Ile Tyr Thr His Gln Ser Asp
                885                 890                 895
Val Trp Ser Tyr Gly Val Thr Val Trp Glu Leu Met Thr Phe Gly Ser
            900                 905                 910
Lys Pro Tyr Asp Gly Ile Pro Ala Ser Glu Ile Ser Ser Ile Leu Glu
        915                 920                 925
Lys Gly Glu Arg Leu Pro Gln Pro Pro Ile Cys Thr Ile Asp Val Tyr
    930                 935                 940
```

```
Met Ile Met Val Lys Cys Trp Met Ile Asp Ala Asp Ser Arg Pro Lys
945                 950                 955                 960
Phe Arg Glu Leu Ile Ile Glu Phe Ser Lys Met Ala Arg Asp Pro Gln
                965                 970                 975
Arg Tyr Leu Val Ile Gln Gly Asp Glu Arg Met His Leu Pro Ser Pro
            980                 985                 990
Thr Asp Ser Asn Phe Tyr Arg Ala Leu Met Asp Glu Glu Asp Met Asp
        995                 1000                1005
Asp Val Val Asp Ala Asp Glu Tyr Leu Ile Pro Gln Gln Gly Phe Phe
    1010                1015                1020
Ser Ser Pro Ser Thr Ser Arg Thr Pro Leu Leu Ser Ser Leu Ser Ala
1025                1030                1035                1040
Thr Ser Asn Asn Ser Thr Val Ala Cys Ile Asp Arg Asn Gly Leu Gln
                1045                1050                1055
Ser Cys Pro Ile Lys Glu Asp Ser Phe Leu Gln Arg Tyr Ser Ser Asp
            1060                1065                1070
Pro Thr Gly Ala Leu Thr Glu Asp Ser Ile Asp Asp Thr Phe Leu Pro
        1075                1080                1085
Val Pro Glu Tyr Ile Asn Gln Ser Val Pro Lys Arg Pro Ala Gly Ser
    1090                1095                1100
Val Gln Asn Pro Val Tyr His Asn Gln Pro Leu Asn Pro Ala Pro Ser
1105                1110                1115                1120
Arg Asp Pro His Tyr Gln Asp Pro His Ser Thr Ala Val Gly Asn Pro
                1125                1130                1135
Glu Tyr Leu Asn Thr Val Gln Pro Thr Cys Val Asn Ser Thr Phe Asp
            1140                1145                1150
Ser Pro Ala His Trp Ala Gln Lys Gly Ser His Gln Ile Ser Leu Asp
        1155                1160                1165
Asn Pro Asp Tyr Gln Gln Asp Phe Phe Pro Lys Glu Ala Lys Pro Asn
    1170                1175                1180
Gly Ile Phe Lys Gly Ser Thr Ala Glu Asn Ala Glu Tyr Leu Arg Val
1185                1190                1195                1200
Ala Pro Gln Ser Ser Glu Phe Ile Gly Ala
                1205                1210
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<210> 44
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> His tag

<400> 44
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His His His His His His
 1               5
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<210> 45
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Flag tag

<400> 45
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Asp Tyr Lys Asp Asp Asp Asp Lys
 1               5
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<210> 46
<211> 15
<212> PRT
<213> Artificial Sequence

<220>

<223> (Gly4Ser)3 Linker

<400> 46
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1   5   10   15

<210> 47
<211> 4136
<212> DNA
<213> Artificial Sequence

<220>
<223> Cetuximab heavy chain S119 K216/light chain Q100
      VEIK104-107 EC213-214 DNA

<220>
<221> sig_peptide
<222> (1109)...(1174)
<223> light chain signal sequence

<220>
<221> V_region
<222> (1175)...(1495)
<223> light chain variable domain

<220>
<221> C_region
<222> (1496)...(1816)
<223> light chain constant domain

<220>
<221> RBS
<222> (1859)...(2433)
<223> IRES

<220>
<221> sig_peptide
<222> (2447)...(2503)
<223> heavy chain signal sequence

<220>
<221> V_region
<222> (2504)...(2860)
<223> heavy chain variable domain

<220>
<221> C_region
<222> (2861)...(3850)
<223> heavy chain constant domain

<220>
<221> misc_feature
<222> (3851)...(3874)
<223> Flag tag

<400> 47
tcaatattgg ccattagcca tattattcat tggttatata gcataaatca atattggcta 60
ttggccattg catacgttgt atctatatca taatatgtac atttatattg gctcatgtcc 120
aatatgaccg ccatgttggc attgattatt gactagttat taatagtaat caattacggg 180
gtcattagtt catagcccat atatggagtt ccgcgttaca taacttacgg taaatggccc 240
gcctggctga ccgcccaacg acccccgccc attgacgtca ataatgacgt atgttcccat 300
agtaacgcca atagggactt tccattgacg tcaatgggtg gagtatttac ggtaaactgc 360

ccacttggca gtacatcaag tgtatcatat gccaagtccg ccccctattg acgtcaatga 420
cggtaaatgg cccgcctggc attatgccca gtacatgacc ttacgggact ttcctacttg 480
gcagtacatc tacgtattag tcatcgctat taccatggtg atgcggtttt ggcagtacac 540
caattggcgt ggatagcggt ttgactcacg gggatttcca agtctccacc ccattgacgt 600
caatgggagt ttgttttggc accaaaatca acgggacttt ccaaaatgtc gtaacaactg 660
cgatcgcccg ccccgttgac gcaaatgggc ggtaggcgtg tacggtggga ggtctatata 720
agcagagctc gtttagtgaa ccgtcagatc actagaagct ttattgcggt agtttatcac 780
agttaaattg ctaacgcagt cagtgcttct gacacaacag tctcgaactt aagctgcagt 840
gactctctta aggtagcctt gcagaagttg gtcgtgaggc actgggcagg taagtatcaa 900
ggttacaaga caggtttaag gtgaccaata gaaactgggc ttgtcgagac agagaagact 960
cttgcgtttc tgataggcac ctattggtct tactgacatc cactttgcct ttctctccac 1020
aggtgtccac tcccagttca attacagctc ttaaggctag agtacttaat acgactcact 1080
ataggctagt ctcgtcgacg agactagcat ggacatgagg gtccccgctc agctcctggg 1140
gctcctgctg ctctggctcc caggtgccaa gtgtgacatc ttgctgactc agtctccagt 1200
catcctgtct gtgagtccag gagaaagagt cagtttctcc tgcagggcca gtcagagtat 1260
tggcacaaac atacactggt atcagcaaag aacaaatggt tctccaaggc ttctcataaa 1320
gtatgcttct gagtctatct ctgggatccc ttccaggttt agtggcagtg gatcagggac 1380
agattttact cttagcatca acagtgtgga gtctgaagat attgcagatt attactgtca 1440
acaaaataat aactggccaa ccacgttcgg ccaagggacc aaggtggaaa tcaaacgtac 1500
ggtggctgca ccatctgtct tcatcttccc gccatctgat gagcagttga aatctggaac 1560
tgcctctgtt gtgtgcctgc tgaataactt ctatcccaga gaggccaaag tacagtggaa 1620
ggtggataac gccctccaat cgggtaactc ccaggagagt gtcacagagc aggacagcaa 1680
ggacagcacc tacagcctca gcagcaccct gacgctgagc aaagcagact acgagaaaca 1740
caaagtctac gcctgcgaag tcacccatca gggcctgagc tcgcccgtca caaagagctt 1800
caacagggga gagtgttgac tcgaggcgcg ccgagcatgc atctagggcg gccaattccg 1860
cccctctccc ccccccccc taacgttact ggccgaagcc gcttggaata aggccggtgt 1920
gcgtttgtct atatgttatt ttccaccata ttgccgtctt ttggcaatgt gagggcccgg 1980
aaacctggcc ctgtcttctt gacgagcatt cctaggggtc tttcccctct cgccaaagga 2040
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tgcggccaaa agccacgtgt ataagataca cctgcaaagg cggcacaacc ccagtgccac 2220
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gacgtggttt tcctttgaaa aacacgatga taatatggcc acaaccatgg agtttgggct 2460
gagctggctt tttcttgtgg ctattttaaa aggtgtccag tgtcaggtgc agctgaagca 2520
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tttctcatta actaactatg gtgtacactg ggttcgccag tctccaggaa agggtctgga 2640
gtggctggga gtgatatgga gtggtggaaa cacagactat aatacacctt tcacatccag 2700
actgagcatc aacaaggaca attccaagag ccaagttttc tttaaaatga acagtctgca 2760
atctaatgac acagccatat attactgtgc cagagccctc acctactatg attacgagtt 2820
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ggtcttcccc ctggcaccct cctccaagag cacctctggg ggcacagcgg ccctgggctg 2940
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cagcggcgtg cacaccttcc cggctgtcct acagtcctca ggactctact ccctcagcag 3060
cgtggtgacc gtgccctcca gcagcttggg cacccagacc tacatctgca acgtgaatca 3120
caagcccagc aacaccaagg tggacaagaa agttgagccc aaatcttgtg acaaaactca 3180
cacatgccca ccgtgcccag cacctgaact cctgggggga ccgtcagtct tcctcttccc 3240
cccaaaaccc aaggacaccc tcatgatctc ccggaccccc gaggtcacat gcgtggtggt 3300
ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg tacgtggacg gcgtggaggt 3360
gcataatgcc aagacaaagc cgcgggagga gcagtacaac agcacgtacc gtgtggtcag 3420
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caacaaagcc ctcccagccc ccatcgagaa aaccatctcc aaagccaaag ggcagccccg 3540
agaaccacag gtgtacaccc tgccccatc ccgggatgag ctgaccaaga accaggtcag 3600
cctgacctgc ctggtcaaag gcttctatcc cagcgacatc gccgtggagt gggagagcaa 3660
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atgctccgtg atgcatgagg ctctgcacaa ccactacacg cagaagagcc tctccctgtc 3840
tccgggtaaa gattacaagg atgacgacga taagtgagcg gccgcttccc tttagtgagg 3900
gttaatgctt cgagcagaca tgataagata cattgatgag tttggacaaa ccacaactag 3960
aatgcagtga aaaaaatgct ttatttgtga aatttgtgat gctattgctt tatttgtaac 4020
cattataagc tgcaataaac aagttaacaa caacaattgc attcatttta tgtttcaggt 4080
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<210> 48
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> Cetuximab heavy chain S119 K216 DNA

<220>
<221> V_region
<222> (1)...(357)

<220>
<221> C_region
<222> (358)...(1347)

<400> 48
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ccaggaaagg gtctggagtg gctgggagtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagact gagcatcaac aaggacaatt ccaagagcca agttttcttt 240
aaaatgaaca gtctgcaatc taatgacaca gccatatatt actgtgccag agccctcacc 300
tactatgatt acgagtttgc ttactggggc cagggaacgc tggtcaccgt cagctcagcc 360
tccaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480
aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540
ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600
atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 660
tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 720
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780
gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960
tacaagtgca aggtcagcaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1020
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1080
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320
aagagcctct ccctgtctcc gggtaaa   1347

<210> 49
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Cetuximab heavy chain S119 variable domain DNA

<400> 49
caggtgcagc tgaagcagtc aggacctggc ctagtgcagc cctcacagag cctgtccatc 60
acctgcacag tctctggttt ctcattaact aactatggtg tacactgggt tcgccagtct 120
ccaggaaagg gtctggagtg gctgggagtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagact gagcatcaac aaggacaatt ccaagagcca agttttcttt 240
aaaatgaaca gtctgcaatc taatgacaca gccatatatt actgtgccag agccctcacc 300
tactatgatt acgagtttgc ttactggggc cagggaacgc tggtcaccgt cagctca   357

<210> 50
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> Cetuximab Q100 VEIK104-107 EC213-214 light chain
DNA

<220>
<221> V_region
<222> (1)...(321)

<220>
<221> C_region
<222> (322)...(642)

<400> 50
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ttctcctgca gggccagtca gagtattggc acaaacatac actggtatca gcaaagaaca 120
aatggttctc caaggcttct cataaagtat gcttctgagt ctatctctgg gatcccttcc 180
aggtttagtg gcagtggatc agggacagat tttactctta gcatcaacag tgtggagtct 240
gaagatattg cagattatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagg tggaaatcaa acgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt   642

<210> 51
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Cetuximab Q100 VEIK104-107 EC213-214 light chain
variable domain DNA

<400> 51
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ttctcctgca gggccagtca gagtattggc acaaacatac actggtatca gcaaagaaca 120
aatggttctc caaggcttct cataaagtat gcttctgagt ctatctctgg gatcccttcc 180
aggtttagtg gcagtggatc agggacagat tttactctta gcatcaacag tgtggagtct 240
gaagatattg cagattatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagg tggaaatcaa a   321

<210> 52
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> HC-Y104D/Q111P control heavy chain nucleic acid
S119

<220>
<221> V_region
<222> (1)...(357)

<220>
<221> C_region
<222> (358)...(1347)

<220>
<221> variation
<222> 312
<223> n = t or c

<400> 52
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ccaggaaagg gtctggagtg gctgggagtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagact gagcatcaac aaggacaatt ccaagagcca agttttcttt 240
aaaatgaaca gtctgcaatc taatgacaca gccatatatt actgtgccag agccctcacc 300
tactatgatg angagtttgc ttactggggc cctggaacgc tggtcaccgt cagctcagcc 360
tccaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480

aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540
ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600
atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 660
tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 720
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780
gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960
tacaagtgca aggtcagcaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1020
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1080
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320
aagagcctct ccctgtctcc gggtaaa 1347

<210> 53
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-Y104D/Q111P control heavy chain amino acid S119

<220>
<221> DOMAIN
<222> (1)...(119)
<223> variable domain

<220>
<221> DOMAIN
<222> (120)...(217)
<223> CH1

<220>
<221> DOMAIN
<222> (218)...(232)
<223> hinge region

<220>
<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 53
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
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Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
            20   25   30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
        35   40   45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50   55   60
Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65   70   75   80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
                85   90   95
Arg Ala Leu Thr Tyr Tyr Asp Asp Glu Phe Ala Tyr Trp Gly Pro Gly
            100   105   110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115   120   125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu

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    130                 135                 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
Lys
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<210> 54
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> DP-h3, 7 heavy chain nucleic acid S119

<220>
<221> V_region
<222> (1)...(357)

<220>
<221> C_region
<222> (358)...(1347)

<400> 54
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actggacaag ggcttgagtg gatgggtgtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagatt caccatctcc agagatgatt caaagaacac ggcgtatctg 240
caaatgaaca gcctgaaaac cgaggacacg gccgtgtatt actgtgccag agccctcacc 300
tactatgatg atgagtttgc ttactggggc cctggaacgc tggtcaccgt cagctcagcc 360

tccaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480
aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540
ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600
atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 660
tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 720
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780
gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960
tacaagtgca aggtcagcaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1020
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1080
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320
aagagcctct ccctgtctcc gggtaaa 1347

<210> 55
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> DP-h3, 7 heavy chain amino acid S119

<220>
<221> DOMAIN
<222> (1)...(119)
<223> variable domain

<220>
<221> DOMAIN
<222> (120)...(217)
<223> CH1

<220>
<221> DOMAIN
<222> (218)...(232)
<223> hinge region

<220>
<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

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

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            100                 105                 110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
Lys
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<210> 56
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> D-h3, 7 heavy chain nucleic acid S119

<220>
<221> V_region
<222> (1)...(357)

<220>
<221> C_region
<222> (358)...(1347)

<220>
<221> variation
<222> 312

<223> n = t or c

<400> 56
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actggacaag ggcttgagtg gatgggtgtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagatt caccatctcc agagatgatt caaagaacac ggcgtatctg 240
caaatgaaca gcctgaaaac cgaggacacg gccgtgtatt actgtgccag agccctcacc 300
tactatgatg angagtttgc ttactggggc cagggaacgc tggtcaccgt cagctcagcc 360
tccaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480
aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540
ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600
atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 660
tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 720
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780
gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960
tacaagtgca aggtcagcaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1020
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1080
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320
aagagcctct ccctgtctcc gggtaaa 1347

<210> 57
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> D-h3, 7 heavy chain amino acid S119

<220>
<221> DOMAIN
<222> (1)...(119)
<223> variable domain

<220>
<221> DOMAIN
<222> (120)...(217)
<223> CH1

<220>
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<222> (218)...(232)
<223> hinge region

<220>
<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 57
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
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Thr Val Lys Ile Ser Cys Lys Val Ser Gly Phe Ser Leu Thr Asn Tyr
            20   25   30

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Gly Val His Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Glu Trp Met
        35                  40                  45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50                  55                  60
Ser Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu
65                  70                  75                  80
Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95
Arg Ala Leu Thr Tyr Tyr Asp Asp Glu Phe Ala Tyr Trp Gly Gln Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
Lys
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<210> 58
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> E-h3, 7 heavy chain nucleic acid S119

<220>
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<222> (1)...(357)

<220>
<221> C_region
<222> (358)...(1347)

<220>
<221> variation
<222> 312
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actggacaag ggcttgagtg gatgggtgtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagatt caccatctcc agagatgatt caaagaacac ggcgtatctg 240
caaatgaaca gcctgaaaac cgaggacacg gccgtgtatt actgtgccag agccctcacc 300
tactatgatg angagtttgc ttactggggc cagggaacgc tggtcaccgt cagctcagcc 360
tccaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480
aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540
ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600
atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 660
tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 720
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780
gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960
tacaagtgca aggtcagcaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1020
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1080
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320
aagagcctct ccctgtctcc gggtaaa   1347

<210> 59
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> E-h3, 7 heavy chain amino acid S119

<220>
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<220>
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<223> CH1

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<220>
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<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN

<222> (343)...(449)
<223> CH3

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

<210> 60
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
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S119

<220>
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<222> 312
<223> n = a or g

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tcctgcaagg tttctggttt ctcattaact aactatggtg tacactgggt gcgacaggcc 120
actggacaag ggcttgagtg gatgggtgtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagatt caccatctcc agagatgatt caaagaacac ggcgtatctg 240
caaatgaaca gcctgaaaac cgaggacacg gccgtgtatt actgtgccag agccctcacc 300
tactatgatg angagtttgc ttactggggc cagggaacgc tggtcaccgt cagctca 357

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

<220>
<223> E-h3, 7 heavy chain variable domain amino acid
S119

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

<210> 62
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> E-h3, 7 heavy chain variable domain nucleic acid
A119

<220>
<221> variation
<222> 312
<223> n = a or g

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gaggtccagc tggtacagtc tggggctgag gtgaagaagc ctggggctac agtgaaaatc 60
tcctgcaagg tttctggttt ctcattaact aactatggtg tacactgggt gcgacaggcc 120

actggacaag ggcttgagtg gatgggtgtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagatt caccatctcc agagatgatt caaagaacac ggcgtatctg 240
caaatgaaca gcctgaaaac cgaggacacg gccgtgtatt actgtgccag agccctcacc 300
tactatgatg angagtttgc ttactggggc cagggaacgc tggtcaccgt cagcgca 357

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

<220>
<223> E-h3, 7 heavy chain variable domain amino acid
A119

<400> 63
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Thr Val Lys Ile Ser Cys Lys Val Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30
Gly Val His Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
50 55 60
Ser Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu
65 70 75 80
Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Gln Gly
100 105 110
Thr Leu Val Thr Val Ser Ala
115

<210> 64
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> FDP-h3, 7, 11, 15 heavy chain nucleic acid S119

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<220>
<221> C_region
<222> (358)...(1347)

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actggacaag ggcttgagtg gatgggtgtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagatt caccatctcc agagatgatt caaagaacac ggcgtatctg 240
caaatgaaca gcctgaaaac cgaggacacg gccgtgtatt actgtgccag agccctcacc 300
tactatgatg atgagtttgc ttactggggc cctggaacgc tggtcaccgt cagctcagcc 360
tccaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480
aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540
ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600
atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 660
tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 720
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780
gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960

tacaagtgca aggtcagcaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1020
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1080
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320
aagagcctct ccctgtctcc gggtaaa 1347

<210> 65
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> FDP-h3, 7, 11, 15 heavy chain amino acid S119

<220>
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<223> variable domain

<220>
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<222> (120)...(217)
<223> CH1

<220>
<221> DOMAIN
<222> (218)...(232)
<223> hinge region

<220>
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<222> (233)...(342)
<223> CH2

<220>
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<222> (343)...(447)
<223> CH3

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

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        195                 200                 205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
Lys
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<210> 66
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<220>
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<220>
<221> C_region
<222> (358)...(1347)

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ccaggaaagg gtctggagtg gctgggagtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagact gagcatcaac aaggacaatt ccaagagcca agttttcttt 240
aaaatgaaca gtctgcaatc taatgacaca gccatatatt actgtgccag agccctcacc 300
tactatgatg angagtttgc ttactggggc cagggaacgc tggtcaccgt cagctcagcc 360
tccaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480
aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540
ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600

atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 660
tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 720
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780
gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960
tacaagtgca aggtcagcaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1020
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1080
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320
aagagcctct ccctgtctcc gggtaaa 1347

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<220>
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<223> CH1

<220>
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<222> (218)...(232)
<223> hinge region

<220>
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<222> (233)...(342)
<223> CH2

<220>
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<223> CH3

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

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

<210> 68
<211> 357
<212> DNA
<213> Artificial Sequence

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nucleic acid S119

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<221> variation
<222> 312
<223> n = t or c

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ccaggaaagg gtctggagtg gctgggagtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagact gagcatcaac aaggacaatt ccaagagcca agttttcttt 240
aaaatgaaca gtctgcaatc taatgacaca gccatatatt actgtgccag agccctcacc 300
tactatgatg angagtttgc ttactggggc cagggaacgc tggtcaccgt cagctca 357

<210> 69
<211> 119
<212> PRT

<213> Artificial Sequence

<220>
<223> HC-Y104D control heavy chain variable domain amino acid S119

<400> 69
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
 1   5   10   15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
            20   25   30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
        35   40   45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50   55   60
Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65   70   75   80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
                85   90   95
Arg Ala Leu Thr Tyr Tyr Asp Asp Glu Phe Ala Tyr Trp Gly Gln Gly
            100   105   110
Thr Leu Val Thr Val Ser Ser
        115

<210> 70
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-Y104D control heavy chain variable domain amino acid A119

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

<210> 71
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> HC-Y104E heavy chain nucleic acid S119

<220>
<221> V_region
<222> (1)...(357)

<220>
<221> C_region
<222> (358)...(1347)

<220>
<221> variation
<222> 312
<223> n = a or g

<400> 71
caggtgcagc tgaagcagtc aggacctggc ctagtgcagc cctcacagag cctgtccatc 60
acctgcacag tctctggttt ctcattaact aactatggtg tacactgggt tcgccagtct 120
ccaggaaagg gtctggagtg gctgggagtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagact gagcatcaac aaggacaatt ccaagagcca agttttcttt 240
aaaatgaaca gtctgcaatc taatgacaca gccatatatt actgtgccag agccctcacc 300
tactatgatg angagtttgc ttactggggc cagggaacgc tggtcaccgt cagctcagcc 360
tccaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480
aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540
ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600
atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 660
tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 720
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780
gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960
tacaagtgca aggtcagcaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1020
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1080
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320
aagagcctct ccctgtctcc gggtaaa 1347

<210> 72
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-Y104E heavy chain amino acid S119

<220>
<221> DOMAIN
<222> (1)...(119)
<223> variable domain

<220>
<221> DOMAIN
<222> (120)...(217)
<223> CH1

<220>
<221> DOMAIN
<222> (218)...(232)
<223> hinge region

<220>
<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 72
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
 1   5   10   15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
            20   25   30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
        35   40   45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50   55   60
Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65   70   75   80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
                85   90   95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Gln Gly
            100   105   110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115   120   125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130   135   140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145   150   155   160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165   170   175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180   185   190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195   200   205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210   215   220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225   230   235   240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245   250   255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260   265   270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275   280   285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290   295   300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305   310   315   320
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325   330   335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340   345   350
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355   360   365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370   375   380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385   390   395   400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405   410   415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420   425   430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435   440   445
Lys

<210> 73
<211> 357
<212> DNA
<213> Artificial Sequence

<220>

<223> HC-Y104E heavy chain variable domain nucleic acid
S119

<220>
<221> variation
<222> 312
<223> n = a or g

<400> 73
caggtgcagc tgaagcagtc aggacctggc ctagtgcagc cctcacagag cctgtccatc 60
acctgcacag tctctggttt ctcattaact aactatggtg tacactgggt tcgccagtct 120
ccaggaaagg gtctggagtg gctgggagtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagact gagcatcaac aaggacaatt ccaagagcca agttttcttt 240
aaaatgaaca gtctgcaatc taatgacaca gccatatatt actgtgccag agccctcacc 300
tactatgatg angagtttgc ttactggggc cagggaacgc tggtcaccgt cagctca 357

<210> 74
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-Y104E heavy chain variable domain amino acid
S119

<400> 74
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
1 5 10 15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
50 55 60
Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65 70 75 80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
85 90 95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Gln Gly
100 105 110
Thr Leu Val Thr Val Ser Ser
115

<210> 75
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-Y104E heavy chain variable domain amino acid
A119

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

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Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Gln Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ala
        115


<210> 76
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-Y104E/HC-Q111P heavy chain amino acid S119


<220>
<221> DOMAIN
<222> (1)...(119)
<223> variable domain

<220>
<221> DOMAIN
<222> (120)...(217)
<223> CH1

<220>
<221> DOMAIN
<222> (218)...(232)
<223> hinge region

<220>
<221> DOMAIN
<222> (233)...(342)
<223> CH2


<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 76
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
 1               5                  10                  15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
            20                  25                  30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50                  55                  60
Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65                  70                  75                  80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
                85                  90                  95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Pro Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205
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Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
Lys



<210> 77
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-Y104E/HC-Q111P heavy chain variable domain
      amino acid S119


<400> 77
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
 1               5                  10                  15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
            20                  25                  30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50                  55                  60
Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65                  70                  75                  80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
                85                  90                  95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Pro Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ser
        115


<210> 78
<211> 119
<212> PRT
<213> Artificial Sequence
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<220>
<223> HC-Y104E/HC-Q111P heavy chain variable domain
amino acid A119

<400> 78
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
 1   5   10   15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
            20   25   30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
        35   40   45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50   55   60
Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65   70   75   80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
                85   90   95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Pro Gly
            100   105   110
Thr Leu Val Thr Val Ser Ala
        115

<210> 79
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-S25C/HC-Y104E heavy chain amino acid S119

<220>
<221> DOMAIN
<222> (1)...(119)
<223> variable domain

<220>
<221> DOMAIN
<222> (120)...(217)
<223> CH1

<220>
<221> DOMAIN
<222> (218)...(232)
<223> hinge region

<220>
<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 79
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
 1   5   10   15
Ser Leu Ser Ile Thr Cys Thr Val Cys Gly Phe Ser Leu Thr Asn Tyr
            20   25   30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
        35   40   45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50   55   60

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

<210> 80
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-S25C/HC-Y104E heavy chain variable domain amino acid S119

<400> 80

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


<210> 81
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-S25C/HC-Y104E heavy chain variable domain amino
      acid A119


<400> 81
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
 1               5                  10                  15
Ser Leu Ser Ile Thr Cys Thr Val Cys Gly Phe Ser Leu Thr Asn Tyr
            20                  25                  30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50                  55                  60
Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65                  70                  75                  80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
                85                  90                  95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Gln Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ala
        115


<210> 82
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-S53G/HC-Y104E heavy chain amino acid S119



<220>
<221> DOMAIN
<222> (1)...(119)
<223> variable domain

<220>
<221> DOMAIN
<222> (120)...(217)
<223> CH1

<220>
<221> DOMAIN
<222> (218)...(232)
<223> hinge region

<220>
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<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 82

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Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
 1               5                  10                  15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
            20                  25                  30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45
Gly Val Ile Trp Gly Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50                  55                  60
Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65                  70                  75                  80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
                85                  90                  95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Gln Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
Lys
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<210> 83
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-S53G/HC-Y104E heavy chain variable domain amino acid S119

<400> 83
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
 1   5   10   15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
            20   25   30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
        35   40   45
Gly Val Ile Trp Gly Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50   55   60
Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65   70   75   80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
                85   90   95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Gln Gly
            100   105   110
Thr Leu Val Thr Val Ser Ser
        115

<210> 84
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-S53G/HC-Y104E heavy chain variable domain amino acid A119

<400> 84
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
 1   5   10   15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
            20   25   30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
        35   40   45
Gly Val Ile Trp Gly Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50   55   60
Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65   70   75   80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
                85   90   95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Gln Gly
            100   105   110
Thr Leu Val Thr Val Ser Ala
        115

<210> 85
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-S53G/HC-Y104E/HC-Q111P heavy chain amino acid

S119

<220>
<221> DOMAIN
<222> (1)...(119)
<223> variant domain

<220>
<221> DOMAIN
<222> (120)...(217)
<223> CH1

<220>
<221> DOMAIN
<222> (218)...(232)
<223> hinge region

<220>
<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 85

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

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

<210> 86
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-S53G/HC-Y104E/HC-Q111P heavy chain variable domain amino acid S119

<400> 86
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
1 5 10 15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45
Gly Val Ile Trp Gly Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
50 55 60
Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65 70 75 80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
85 90 95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Pro Gly
100 105 110
Thr Leu Val Thr Val Ser Ser
115

<210> 87
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-S53G/HC-Y104E/HC-Q111P heavy chain variable domain amino acid A119

<400> 87
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
1 5 10 15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

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


<210> 88
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-S25V/HC-Y104E heavy chain amino acid S119


<220>
<221> DOMAIN
<222> (1)...(119)
<223> variable domain

<220>
<221> DOMAIN
<222> (120)...(217)
<223> CH1

<220>
<221> DOMAIN
<222> (218)...(232)
<223> hinge region

<220>
<221> DOMAIN
<222> (233)...(342)
<223> CH2


<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 88
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
 1                  5                  10                  15
Ser Leu Ser Ile Thr Cys Thr Val Val Gly Phe Ser Leu Thr Asn Tyr
            20                  25                  30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50                  55                  60
Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65                  70                  75                  80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
                85                  90                  95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Gln Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160
```

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

<210> 89
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-S25V/HC-Y104E heavy chain variable domain amino acid S119

<400> 89

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

<210> 90
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-S25V/HC-Y104E heavy chain variable domain amino acid A119

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

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

<220>
<223> HC-S25V/HC-Y104E/HC-Q111P heavy chain amino acid S119

<220>
<221> DOMAIN
<222> (1)...(119)
<223> variable domain

<220>
<221> DOMAIN
<222> (120)...(217)
<223> CH1

<220>
<221> DOMAIN
<222> (218)...(232)
<223> hinge region

<220>
<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 91
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln

```
 1               5                  10                  15
Ser Leu Ser Ile Thr Cys Thr Val Val Gly Phe Ser Leu Thr Asn Tyr
            20                  25                  30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50                  55                  60
Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65                  70                  75                  80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
                85                  90                  95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Pro Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
Lys
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<210> 92
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-S25V/HC-Y104E/HC-Q111P heavy chain variable domain amino acid S119

<400> 92
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
 1   5   10   15
Ser Leu Ser Ile Thr Cys Thr Val Val Gly Phe Ser Leu Thr Asn Tyr
            20   25   30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
        35   40   45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50   55   60
Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65   70   75   80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
                85   90   95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Pro Gly
            100   105   110
Thr Leu Val Thr Val Ser Ser
        115

<210> 93
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-S25V/HC-Y104E/HC-Q111P heavy chain variable
      domain amino acid A119

<400> 93
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
 1   5   10   15
Ser Leu Ser Ile Thr Cys Thr Val Val Gly Phe Ser Leu Thr Asn Tyr
            20   25   30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
        35   40   45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50   55   60
Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65   70   75   80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
                85   90   95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Pro Gly
            100   105   110
Thr Leu Val Thr Val Ser Ala
        115

<210> 94
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-S25V/HC-S53G/HC-Y104E heavy chain amino acid
      S119

<220>
<221> DOMAIN
<222> (1)...(119)
<223> variable domain

<220>
<221> DOMAIN
<222> (120)...(217)
<223> CH1

<220>
<221> DOMAIN
<222> (218)...(232)
<223> hinge region

<220>
<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 94

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

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
405 410 415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445
Lys

<210> 95
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-S25V/HC-S53G/HC-Y104E heavy chain variable domain amino acid S119

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

<210> 96
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-S25V/HC-S53G/HC-Y104E heavy chain variable domain amino acid A119

<400> 96
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
1 5 10 15
Ser Leu Ser Ile Thr Cys Thr Val Val Gly Phe Ser Leu Thr Asn Tyr
20 25 30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45
Gly Val Ile Trp Gly Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
50 55 60
Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65 70 75 80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
85 90 95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Gln Gly
100 105 110
Thr Leu Val Thr Val Ser Ala
115

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

<220>
<223> HC-S25V/HC-S53G/HC-Y104E/HC-Q111P heavy chain
amino acid S119

<220>
<221> DOMAIN
<222> (1)...(119)
<223> variable domain

<220>
<221> DOMAIN
<222> (120)...(217)
<223> CH1

<220>
<221> DOMAIN
<222> (218)...(232)
<223> hinge region

<220>
<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

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

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

<210> 98
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-S25V/HC-S53G/HC-Y104E/HC-Q111P heavy chain
variable domain amino acid S119

<400> 98
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
1 5 10 15
Ser Leu Ser Ile Thr Cys Thr Val Val Gly Phe Ser Leu Thr Asn Tyr
20 25 30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45
Gly Val Ile Trp Gly Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
50 55 60
Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65 70 75 80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
85 90 95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Pro Gly
100 105 110
Thr Leu Val Thr Val Ser Ser
115

<210> 99
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-S25V/HC-S53G/HC-Y104E/HC-Q111P heavy chain
variable domain amino acid A119

<400> 99
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
 1   5   10   15
Ser Leu Ser Ile Thr Cys Thr Val Val Gly Phe Ser Leu Thr Asn Tyr
            20   25   30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
        35   40   45
Gly Val Ile Trp Gly Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50   55   60
Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65   70   75   80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
                85   90   95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Pro Gly
            100   105   110
Thr Leu Val Thr Val Ser Ala
        115

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

<220>
<223> HC-T30F/HC-Y104E heavy chain amino acid S119

<220>
<221> DOMAIN
<222> (1)...(119)
<223> variable domain

<220>
<221> DOMAIN
<222> (120)...(217)
<223> CH1

<220>
<221> DOMAIN
<222> (218)...(232)
<223> hinge region

<220>
<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

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

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

<210> 101
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-T30F/HC-Y104E heavy chain variable domain amino acid S119

<400> 101

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

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

<210> 102
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-T30F/HC-Y104E heavy chain variable domain amino acid A119

<400> 102
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
1 5 10 15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Phe Asn Tyr
20 25 30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
50 55 60
Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65 70 75 80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
85 90 95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Gln Gly
100 105 110
Thr Leu Val Thr Val Ser Ala
115

<210> 103
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-T30F/HC-Y104E/HC-Q111P heavy chain amino acid S119

<220>
<221> DOMAIN
<222> (1)...(119)
<223> variable domain

<220>
<221> DOMAIN
<222> (120)...(217)
<223> CH1

<220>
<221> DOMAIN
<222> (218)...(232)
<223> hinge region

<220>
<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>

<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 103
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
 1   5   10   15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Phe Asn Tyr
            20   25   30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
        35   40   45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50   55   60
Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65   70   75   80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
                85   90   95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Pro Gly
            100   105   110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115   120   125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130   135   140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145   150   155   160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165   170   175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180   185   190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195   200   205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210   215   220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225   230   235   240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245   250   255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260   265   270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275   280   285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290   295   300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305   310   315   320
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325   330   335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340   345   350
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355   360   365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370   375   380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385   390   395   400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405   410   415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420   425   430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435   440   445
Lys

<210> 104
<211> 119
<212> PRT

<213> Artificial Sequence

<220>
<223> HC-T30F/HC-Y104E/HC-Q111P heavy chain variable
domain amino acid S119

<400> 104
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
1 5 10 15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Phe Asn Tyr
20 25 30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
50 55 60
Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65 70 75 80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
85 90 95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Pro Gly
100 105 110
Thr Leu Val Thr Val Ser Ser
115

<210> 105
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-T30F/HC-Y104E/HC-Q111P heavy chain variable
domain amino acid A119

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

<210> 106
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-T30F/HC-S53G/HC-Y104E heavy chain amino acid
S119

<220>
<221> DOMAIN
<222> (1)...(119)

<223> variable domain

<220>
<221> DOMAIN
<222> (120)...(217)
<223> CH1

<220>
<221> DOMAIN
<222> (218)...(232)
<223> hinge region

<220>
<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 106
```
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
 1               5                  10                  15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Phe Asn Tyr
            20                  25                  30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45
Gly Val Ile Trp Gly Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50                  55                  60
Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65                  70                  75                  80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
                85                  90                  95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Gln Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350
```

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

<210> 107
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-T30F/HC-S53G/HC-Y104E heavy chain variable domain amino acid S119

<400> 107

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

<210> 108
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-T30F/HC-S53G/HC-Y104E heavy chain variable domain amino acid A119

<400> 108

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

Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Gln Gly
100 105 110
Thr Leu Val Thr Val Ser Ala
115

<210> 109
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-T30F/HC-S53G/HC-Y104E/HC-Q111P heavy chain amino acid S119

<220>
<221> DOMAIN
<222> (1)...(119)
<223> variable domain

<220>
<221> DOMAIN
<222> (120)...(217)
<223> CH1

<220>
<221> DOMAIN
<222> (218)...(232)
<223> hinge region

<220>
<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 109
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
1 5 10 15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Phe Asn Tyr
20 25 30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45
Gly Val Ile Trp Gly Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
50 55 60
Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65 70 75 80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
85 90 95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Pro Gly
100 105 110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
130 135 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro

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

<210> 110
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-T30F/HC-S53G/HC-Y104E/HC-Q111P heavy chain variable domain amino acid S119

<400> 110

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

<210> 111
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-T30F/HC-S53G/HC-Y104E/HC-Q111P heavy chain
variable domain amino acid A119

<400> 111
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
1 5 10 15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Phe Asn Tyr
20 25 30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45
Gly Val Ile Trp Gly Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
50 55 60
Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65 70 75 80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
85 90 95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Pro Gly
100 105 110
Thr Leu Val Thr Val Ser Ala
115

<210> 112
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-D72L/HC-Y104E heavy chain amino acid S119

<220>
<221> DOMAIN
<222> (1)...(119)
<223> variable domain

<220>
<221> DOMAIN
<222> (120)...(217)
<223> CH1

<220>
<221> DOMAIN
<222> (218)...(232)
<223> hinge region

<220>
<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 112
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
1 5 10 15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr

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

<210> 113
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-D72L/HC-Y104E heavy chain variable domain amino acid S119

<400> 113

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Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
 1               5                  10                  15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
            20                  25                  30
```

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

<210> 114
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-D72L/HC-Y104E heavy chain variable domain amino acid A119

<400> 114
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
1 5 10 15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
50 55 60
Ser Arg Leu Ser Ile Asn Lys Leu Asn Ser Lys Ser Gln Val Phe Phe
65 70 75 80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
85 90 95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Gln Gly
100 105 110
Thr Leu Val Thr Val Ser Ala
115

<210> 115
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-D72L/HC-Y104E/HC-Q111P heavy chain amino acid S119

<220>
<221> DOMAIN
<222> (1)...(119)
<223> variable domain

<220>
<221> DOMAIN
<222> (120)...(217)
<223> CH1

<220>
<221> DOMAIN
<222> (218)...(232)
<223> hinge region

<220>
<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 115

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

<210> 116
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-D72L/HC-Y104E/HC-Q111P heavy chain variable domain amino acid S119

<400> 116
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
 1   5   10   15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
            20   25   30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
        35   40   45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50   55   60
Ser Arg Leu Ser Ile Asn Lys Leu Asn Ser Lys Ser Gln Val Phe Phe
65   70   75   80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
                85   90   95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Pro Gly
            100   105   110
Thr Leu Val Thr Val Ser Ser
        115

<210> 117
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-D72L/HC-Y104E/HC-Q111P heavy chain variable domain amino acid A119

<400> 117
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
 1   5   10   15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
            20   25   30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
        35   40   45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50   55   60
Ser Arg Leu Ser Ile Asn Lys Leu Asn Ser Lys Ser Gln Val Phe Phe
65   70   75   80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
                85   90   95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Pro Gly
            100   105   110
Thr Leu Val Thr Val Ser Ala
        115

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

<220>

<223> HC-S53G/HC-D72L/HC-Y104E heavy chain amino acid
S119

<220>
<223> variable domain

<220>
<221> DOMAIN
<222> (120)...(217)
<223> CH1

<220>
<221> DOMAIN
<222> (218)...(232)
<223> hinge region

<220>
<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 118
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Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
 1               5                  10                  15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
            20                  25                  30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45
Gly Val Ile Trp Gly Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50                  55                  60
Ser Arg Leu Ser Ile Asn Lys Leu Asn Ser Lys Ser Gln Val Phe Phe
65                  70                  75                  80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
                85                  90                  95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Gln Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
```

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

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

<220>
<223> HC-S53G/HC-D72L/HC-Y104E heavy chain variable domain amino acid S119

<400> 119
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
1 5 10 15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45
Gly Val Ile Trp Gly Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
50 55 60
Ser Arg Leu Ser Ile Asn Lys Leu Asn Ser Lys Ser Gln Val Phe Phe
65 70 75 80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
85 90 95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Gln Gly
100 105 110
Thr Leu Val Thr Val Ser Ser
115

<210> 120
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-S53G/HC-D72L/HC-Y104E heavy chain variable domain amino acid A119

<400> 120
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
1 5 10 15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45
Gly Val Ile Trp Gly Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr

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


<210> 121
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-S53G/HC-D72L/HC-Y104E/HC-Q111P heavy chain
      amino acid S119


<220>
<221> DOMAIN
<222> (1)...(119)
<223> variable domain

<220>
<221> DOMAIN
<222> (120)...(217)
<223> CH1

<220>
<221> DOMAIN
<222> (218)...(232)
<223> hinge region

<220>
<221> DOMAIN
<222> (233)...(342)
<223> CH2


<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 121
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
 1               5                  10                  15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
            20                  25                  30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45
Gly Val Ile Trp Gly Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50                  55                  60
Ser Arg Leu Ser Ile Asn Lys Leu Asn Ser Lys Ser Gln Val Phe Phe
65                  70                  75                  80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
                85                  90                  95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Pro Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160
```

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

<210> 122
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-S53G/HC-D72L/HC-Y104E/HC-Q111P heavy chain variable domain amino acid S119

<400> 122

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

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

<220>
<223> HC-S53G/HC-D72L/HC-Y104E/HC-Q111P heavy chain
variable domain amino acid A119

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

<210> 124
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> LC-I29S light chain amino acid Q100 VEIK104-107
EC213-214

<220>
<221> DOMAIN
<222> (1)...(107)
<223> variable domain

<220>
<221> DOMAIN
<222> (108)...(214)
<223> constant domain

<400> 124
Asp Ile Leu Leu Thr Gln Ser Pro Val Ile Leu Ser Val Ser Pro Gly
1 5 10 15
Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Ser Ser Gly Thr Asn
20 25 30
Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
35 40 45
Lys Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Ser Val Glu Ser
65 70 75 80
Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

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

<210> 125
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> LC-I29S light chain variable domain amino acid
Q100 VEIK104-107

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

<210> 126
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> LC-I29S light chain variable domain amino acid
A100 LELK104-107

<400> 126
Asp Ile Leu Leu Thr Gln Ser Pro Val Ile Leu Ser Val Ser Pro Gly
1 5 10 15
Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Ser Ser Gly Thr Asn
20 25 30
Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
35 40 45
Lys Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Ser Val Glu Ser
65 70 75 80
Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
85 90 95
Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105

<210> 127
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> LC-I29S light chain variable domain amino acid
Q100 LELK104-107

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

<210> 128
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> EP-h1, 2, 4, 5, 6, 8 heavy chain nucleic acid S119

<220>
<221> variation
<222> 312
<223> n = a or g

<220>
<221> V_region
<222> (1)...(357)

<220>
<221> C_region
<222> (358)...(1347)

<400> 128
caggtacagc tgcagcagtc aggtccagga ctggtgaagc cctcgcagac cctctcactc 60
acctgtgcca tctctggttt ctcattaact aactatggtg tacactggat ccgccagccc 120
ccagggaagg ggctggagtg gattggtgtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagatt caccatctcc agagatgatt caaagaacac ggcgtatctg 240
caaatgaaca gcctgaaaac cgaggacacg gccgtgtatt actgtgccag agccctcacc 300
tactatgatg angagtttgc ttactggggc cctggaacgc tggtcaccgt cagctcagcc 360
tccaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480
aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540
ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600
atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 660
tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 720
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780
gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960
tacaagtgca aggtcagcaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1020

gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1080
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320
aagagcctct ccctgtctcc gggtaaa 1347

<210> 129
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> EP-h1, 2, 4, 5, 6, 8 heavy chain amino acid S119

<220>
<221> DOMAIN
<222> (1)...(119)
<223> variable domain

<220>
<221> DOMAIN
<222> (120)...(217)
<223> CH1

<220>
<221> DOMAIN
<222> (218)...(232)
<223> hinge region

<220>
<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 129
Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1   5   10   15
Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Phe Ser Leu Thr Asn Tyr
            20   25   30
Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
        35   40   45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50   55   60
Ser Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu
65   70   75   80
Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85   90   95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Pro Gly
            100   105   110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115   120   125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130   135   140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145   150   155   160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165   170   175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180   185   190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro

```
        195                 200                 205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
Lys
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<210> 130
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> EP-h1, 2, 4, 5, 6, 8 heavy chain variable domain
nucleic acid S119

<220>
<221> variation
<222> 312
<223> n = a or g

<400> 130
caggtacagc tgcagcagtc aggtccagga ctggtgaagc cctcgcagac cctctcactc 60
acctgtgcca tctctggttt ctcattaact aactatggtg tacactggat ccgccagccc 120
ccagggaagg ggctggagtg gattggtgtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagatt caccatctcc agagatgatt caaagaacac ggcgtatctg 240
caaatgaaca gcctgaaaac cgaggacacg gccgtgtatt actgtgccag agccctcacc 300
tactatgatg angagtttgc ttactggggc cctggaacgc tggtcaccgt cagctca 357

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

<220>
<223> EP-h1, 2, 4, 5, 6, 8 heavy chain variable domain
amino acid S119

<400> 131
Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1   5   10   15
Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Phe Ser Leu Thr Asn Tyr
            20   25   30
Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
        35   40   45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50   55   60
Ser Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu
65   70   75   80
Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85   90   95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Pro Gly
            100   105   110
Thr Leu Val Thr Val Ser Ser
        115

<210> 132
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> EP-h1, 2, 4, 5, 6, 8 heavy chain variable domain
      nucleic acid A119

<220>
<221> variation
<222> 312
<223> n = a or g

<400> 132
caggtacagc tgcagcagtc aggtccagga ctggtgaagc cctcgcagac cctctcactc 60
acctgtgcca tctctggttt ctcattaact aactatggtg tacactggat ccgccagccc 120
ccagggaagg ggctggagtg gattggtgtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagatt caccatctcc agagatgatt caaagaacac ggcgtatctg 240
caaatgaaca gcctgaaaac cgaggacacg gccgtgtatt actgtgccag agccctcacc 300
tactatgatg angagtttgc ttactggggc cctggaacgc tggtcaccgt cagcgca   357

<210> 133
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> EP-h1, 2, 4, 5, 6, 8 heavy chain variable domain
      amino acid A119

<400> 133
Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1   5   10   15
Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Phe Ser Leu Thr Asn Tyr
            20   25   30
Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
        35   40   45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50   55   60
Ser Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu
65   70   75   80
Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85   90   95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Pro Gly
            100   105   110
Thr Leu Val Thr Val Ser Ala

115

<210> 134
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> EP-h3, 7 heavy chain nucleic acid S119

<220>
<221> variation
<222> 312
<223> n = a or g

<220>
<221> V_region
<222> (1)...(357)

<220>
<221> C_region
<222> (358)...(1347)

<400> 134
gaggtccagc tggtacagtc tggggctgag gtgaagaagc ctggggctac agtgaaaatc 60
tcctgcaagg tttctggttt ctcattaact aactatggtg tacactgggt gcgacaggcc 120
actggacaag ggcttgagtg gatgggtgtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagatt caccatctcc agagatgatt caaagaacac ggcgtatctg 240
caaatgaaca gcctgaaaac cgaggacacg gccgtgtatt actgtgccag agccctcacc 300
tactatgatg angagtttgc ttactggggc cctggaacgc tggtcaccgt cagctcagcc 360
tccaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480
aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540
ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600
atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 660
tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 720
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780
gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960
tacaagtgca aggtcagcaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1020
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1080
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320
aagagcctct ccctgtctcc gggtaaa 1347

<210> 135
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> EP-h3, 7 heavy chain amino acid S119

<220>
<221> DOMAIN
<222> (1)...(119)
<223> variable domain

<220>
<221> DOMAIN
<222> (120)...(217)
<223> CH1

<220>
<221> DOMAIN
<222> (218)...(232)
<223> hinge region

<220>
<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

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

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
405 410 415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445
Lys

<210> 136
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> EP-h3, 7 heavy chain variable domain nucleic acid
S119

<220>
<221> variation
<222> 312
<223> n = a or g

<220>
<221> V_region
<222> (1)...(357)

<220>
<221> C_region
<222> (358)...(1347)

<400> 136
gaggtccagc tggtacagtc tggggctgag gtgaagaagc ctggggctac agtgaaaatc 60
tcctgcaagg tttctggttt ctcattaact aactatggtg tacactgggt gcgacaggcc 120
actggacaag ggcttgagtg gatgggtgtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagatt caccatctcc agagatgatt caaagaacac ggcgtatctg 240
caaatgaaca gcctgaaaac cgaggacacg gccgtgtatt actgtgccag agccctcacc 300
tactatgatg angagtttgc ttactggggc cctggaacgc tggtcaccgt cagctca 357

<210> 137
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> EP-h3, 7 heavy chain variable domain amino acid
S119

<400> 137
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Thr Val Lys Ile Ser Cys Lys Val Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30
Gly Val His Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
50 55 60
Ser Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu
65 70 75 80
Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Pro Gly
100 105 110
Thr Leu Val Thr Val Ser Ser
115

<210> 138
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> EP-h3, 7 heavy chain variable domain nucleic acid
A119

<220>
<221> variation
<222> 312
<223> n = a or g

<400> 138
gaggtccagc tggtacagtc tggggctgag gtgaagaagc ctggggctac agtgaaaatc 60
tcctgcaagg tttctggttt ctcattaact aactatggtg tacactgggt gcgacaggcc 120
actggacaag ggcttgagtg gatgggtgtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagatt caccatctcc agagatgatt caaagaacac ggcgtatctg 240
caaatgaaca gcctgaaaac cgaggacacg gccgtgtatt actgtgccag agccctcacc 300
tactatgatg angagtttgc ttactggggc cctggaacgc tggtcaccgt cagcgca 357

<210> 139
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> EP-h3, 7 heavy chain variable domain amino acid
A119

<400> 139
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Thr Val Lys Ile Ser Cys Lys Val Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30
Gly Val His Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
50 55 60
Ser Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu
65 70 75 80
Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Pro Gly
100 105 110
Thr Leu Val Thr Val Ser Ala
115

<210> 140
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> EP-h9, 12, 14 heavy chain nucleic acid S119

<220>
<221> variation
<222> 312
<223> n = a or g

<220>
<221> V_region
<222> (1)...(357)

<220>
<221> C_region
<222> (358)...(1347)

<400> 140
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tcctgcaagg tttctggttt ctcattaact aactatggtg tacactggat caggcagtcc 120
ccatcgagag gccttgagtg gctgggtgtg atatggagtg gtggaaatac agactataat 180
acacctttca catccagact caccatctcc aaggacacct ccaaaaacca ggtggtcctt 240
acaatgacca acatggaccc tgtggacaca gccacgtatt actgtgccag agccctcacc 300
tactatgatg angagtttgc ttactggggc cctggaacgc tggtcaccgt cagctcagcc 360
tccaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480
aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540
ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600
atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 660
tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 720
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780
gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960
tacaagtgca aggtcagcaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1020
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1080
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320
aagagcctct ccctgtctcc gggtaaa 1347

<210> 141
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> EP-h9, 12, 14 heavy chain amino acid S119

<220>
<221> DOMAIN
<222> (1)...(119)
<223> variable domain

<220>
<221> DOMAIN
<222> (120)...(217)
<223> CH1

<220>
<221> DOMAIN
<222> (218)...(232)
<223> hinge region

<220>
<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 141
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1   5   10   15
Thr Val Lys Ile Ser Cys Lys Val Ser Gly Phe Ser Leu Thr Asn Tyr
            20   25   30
Gly Val His Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu Trp Leu
        35   40   45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50   55   60
Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val Val Leu
65   70   75   80
Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala
                85   90   95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Pro Gly
            100   105   110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115   120   125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130   135   140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145   150   155   160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165   170   175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180   185   190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195   200   205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210   215   220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225   230   235   240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245   250   255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260   265   270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275   280   285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290   295   300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305   310   315   320
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325   330   335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340   345   350
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355   360   365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370   375   380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385   390   395   400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405   410   415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420   425   430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435   440   445
Lys

<210> 142
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> EP-h9, 12, 14 heavy chain variable domain nucleic

acid S119

<220>
<221> variation
<222> 312
<223> n = a or g

<400> 142
gaggtccagc tggtacagtc tggggctgag gtgaagaagc ctggggctac agtgaaaatc 60
tcctgcaagg tttctggttt ctcattaact aactatggtg tacactggat caggcagtcc 120
ccatcgagag gccttgagtg gctgggtgtg atatggagtg gtggaaatac agactataat 180
acacctttca catccagact caccatctcc aaggacacct ccaaaaacca ggtggtcctt 240
acaatgacca acatggaccc tgtggacaca gccacgtatt actgtgccag agccctcacc 300
tactatgatg angagtttgc ttactggggc cctggaacgc tggtcaccgt cagctca 357

<210> 143
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> EP-h9, 12, 14 heavy chain variable domain amino
acid S119

<400> 143
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Thr Val Lys Ile Ser Cys Lys Val Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30
Gly Val His Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu Trp Leu
35 40 45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
50 55 60
Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val Val Leu
65 70 75 80
Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala
85 90 95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Pro Gly
100 105 110
Thr Leu Val Thr Val Ser Ser
115

<210> 144
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> EP-h9, 12, 14 heavy chain variable domain nucleic
acid A119

<220>
<221> variation
<222> 312
<223> n = a or g

<400> 144
gaggtccagc tggtacagtc tggggctgag gtgaagaagc ctggggctac agtgaaaatc 60
tcctgcaagg tttctggttt ctcattaact aactatggtg tacactggat caggcagtcc 120
ccatcgagag gccttgagtg gctgggtgtg atatggagtg gtggaaatac agactataat 180
acacctttca catccagact caccatctcc aaggacacct ccaaaaacca ggtggtcctt 240
acaatgacca acatggaccc tgtggacaca gccacgtatt actgtgccag agccctcacc 300
tactatgatg angagtttgc ttactggggc cctggaacgc tggtcaccgt cagcgca 357

<210> 145
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> EP-h9, 12, 14 heavy chain variable domain amino
acid A119

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

<210> 146
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> EP-h10, 13 heavy chain nucleic acid S119

<220>
<221> variation
<222> 312
<223> n = a or g

<220>
<221> V_region
<222> (1)...(357)

<220>
<221> C_region
<222> (358)...(1347)

<400> 146
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tcctgcaagg tttctggttt ctcattaact aactatggtg tacactggat ccgccagccc 120
ccagggaagg ggctggagtg gattggtgtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagatt caccatctcc agagacaacg ccaagaactc actgtatctg 240
caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgccag agccctcacc 300
tactatgatg angagtttgc ttactggggc cctggaacgc tggtcaccgt cagctcagcc 360
tccaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480
aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540
ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600
atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 660
tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 720
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780
gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900

acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960
tacaagtgca aggtcagcaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1020
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1080
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320
aagagcctct ccctgtctcc gggtaaa 1347

<210> 147
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> EP-h10, 13 heavy chain amino acid S119

<220>
<221> DOMAIN
<222> (1)...(119)
<223> variable domain

<220>
<221> DOMAIN
<222> (120)...(217)
<223> CH1

<220>
<221> DOMAIN
<222> (218)...(232)
<223> hinge region

<220>
<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 147
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1   5   10   15
Thr Val Lys Ile Ser Cys Lys Val Ser Gly Phe Ser Leu Thr Asn Tyr
            20   25   30
Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
        35   40   45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50   55   60
Ser Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65   70   75   80
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85   90   95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Pro Gly
            100   105   110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115   120   125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130   135   140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145   150   155   160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165   170   175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser

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            180                 185                 190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
Lys
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<210> 148
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> EP-h10, 13 heavy chain variable domain nucleic acid S119

<220>
<221> variation
<222> 312
<223> n = a or g

<400> 148
gaggtccagc tggtacagtc tggggctgag gtgaagaagc ctggggctac agtgaaaatc 60
tcctgcaagg tttctggttt ctcattaact aactatggtg tacactggat ccgccagccc 120
ccagggaagg ggctggagtg gattggtgtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagatt caccatctcc agagacaacg ccaagaactc actgtatctg 240
caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgccag agccctcacc 300
tactatgatg angagtttgc ttactggggc cctggaacgc tggtcaccgt cagctca   357

<210> 149
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> EP-h10, 13 heavy chain variable domain amino acid S119

<400> 149
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1   5   10   15
Thr Val Lys Ile Ser Cys Lys Val Ser Gly Phe Ser Leu Thr Asn Tyr
            20   25   30
Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
        35   40   45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50   55   60
Ser Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65   70   75   80
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85   90   95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Pro Gly
            100   105   110
Thr Leu Val Thr Val Ser Ser
        115

<210> 150
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> EP-h10, 13 heavy chain variable domain nucleic
      acid A119

<220>
<221> variation
<222> 312
<223> n = a or g

<400> 150
gaggtccagc tggtacagtc tggggctgag gtgaagaagc ctggggctac agtgaaaatc 60
tcctgcaagg tttctggttt ctcattaact aactatggtg tacactggat ccgccagccc 120
ccagggaagg ggctggagtg gattggtgtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagatt caccatctcc agagacaacg ccaagaactc actgtatctg 240
caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgccag agccctcacc 300
tactatgatg angagtttgc ttactggggc cctggaacgc tggtcaccgt cagcgca   357

<210> 151
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> EP-h10, 13 heavy chain variable domain amino acid
      A119

<400> 151
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1   5   10   15
Thr Val Lys Ile Ser Cys Lys Val Ser Gly Phe Ser Leu Thr Asn Tyr
            20   25   30
Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
        35   40   45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50   55   60
Ser Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65   70   75   80
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85   90   95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Pro Gly

100 105 110
Thr Leu Val Thr Val Ser Ala
115

<210> 152
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> EP-h1, 3 light chain nucleic acid Q100 VEIK

<220>
<221> V_region
<222> (1)...(321)

<220>
<221> C_region
<222> (322)...(642)

<400> 152
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atcacttgca gggccagtca gagtattggc acaaacatac actggtacca gcagaaacct 120
ggccaggctc ccaggctcct catctattat gcttctgagt ctatctctgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
gaagattttg caacttatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagg tggaaatcaa acgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 153
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> EP-h1, 3 light chain amino acid Q100 VEIK

<220>
<221> DOMAIN
<222> (1)...(107)
<223> variable domain

<220>
<221> DOMAIN
<222> (108)...(214)
<223> constant domain

<400> 153
Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
20 25 30
Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala

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

<210> 154
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> EP-h1, 3 light chain variable domain nucleic acid
Q100 VEIK

<400> 154
gccatccagt tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgca gggccagtca gagtattggc acaaacatac actggtacca gcagaaacct 120
ggccaggctc ccaggctcct catctattat gcttctgagt ctatctctgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
gaagattttg caacttatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagg tggaaatcaa a 321

<210> 155
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> EP-h1, 3 light chain variable domain amino acid
Q100 VEIK

<400> 155
Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
20 25 30
Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 156
<211> 107
<212> PRT
<213> Artificial Sequence

<220>

<223> EP-h1, 3 light chain variable domain amino acid
A100 LELK

<400> 156
Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
            20   25   30
Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35   40   45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
                85   90   95
Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
            100   105

<210> 157
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> EP-h1, 3 light chain variable domain nucleic acid
Q100 LELK

<400> 157
gccatccagt tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgca gggccagtca gagtattggc acaaacatac actggtacca gcagaaacct 120
ggccaggctc ccaggctcct catctattat gcttctgagt ctatctctgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
gaagattttg caacttatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagc tggagctgaa a   321

<210> 158
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> EP-h1, 3 light chain variable domain amino acid
Q100 LELK

<400> 158
Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
            20   25   30
Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35   40   45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Leu Lys
            100   105

<210> 159
<211> 642

<212> DNA
<213> Artificial Sequence

<220>
<223> EP-h2 light chain nucleic acid Q100 VEIK

<220>
<221> V_region
<222> (1)...(321)

<220>
<221> C_region
<222> (322)...(642)

<400> 159
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atcacttgca gggccagtca gagtattggc acaaacatac actggtacct gcagaagcca 120
gggcagtctc cacagctcct gatctattat gcttctgagt ctatctctgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
gaagattttg caacttatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagg tggaaatcaa acgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 160
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> EP-h2 light chain amino acid Q100 VEIK

<220>
<221> DOMAIN
<222> (1)...(107)
<223> variable domain

<220>
<221> DOMAIN
<222> (108)...(214)
<223> constant domain

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

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205
Phe Asn Arg Gly Glu Cys
210

<210> 161
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> EP-h2 light chain variable domain nucleic acid Q100 VEIK

<400> 161
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atcacttgca gggccagtca gagtattggc acaaacatac actggtacct gcagaagcca 120
gggcagtctc cacagctcct gatctattat gcttctgagt ctatctctgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
gaagattttg caacttatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagg tggaaatcaa a 321

<210> 162
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> EP-h2 light chain variable domain amino acid Q100 VEIK

<400> 162
Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
20 25 30
Ile His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile
35 40 45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 163
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> EP-h2 light chain variable domain amino acid A100 LELK

<400> 163
Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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

<210> 164
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> EP-h2 light chain variable domain nucleic acid
      Q100 LELK

<400> 164
gccatccagt tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgca gggccagtca gagtattggc acaaacatac actggtacct gcagaagcca 120
gggcagtctc cacagctcct gatctattat gcttctgagt ctatctctgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
gaagattttg caacttatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagc tggagctgaa a   321

<210> 165
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> EP-h2 light chain variable domain amino acid Q100
      LELK

<400> 165
Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
            20   25   30
Ile His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile
        35   40   45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Leu Lys
            100   105

<210> 166
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> EP-h4 light chain nucleic acid Q100 VEIK

<220>
<221> V_region
<222> (1)...(321)
<223> variable domain

<220>
<221> C_region
<222> (322)...(642)
<223> constant domain

<400> 166
gccatccagt tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgca gggccagtca gagtattggc acaaacatac actggtatca gcagaaacca 120
gggaaagctc ctaagctcct gatctattat gcttctgagt ctatctctgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
gaagattttg caacttatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagg tggaaatcaa acgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 167
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> EP-h4 light chain amino acid Q100 VEIK

<220>
<221> DOMAIN
<222> (1)...(107)
<223> variable domain

<220>
<221> DOMAIN
<222> (108)...(214)
<223> constant domain

<400> 167
Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
            20   25   30
Ile His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100   105   110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115   120   125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130   135   140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145   150   155   160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165   170   175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180   185   190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser

195 200 205
Phe Asn Arg Gly Glu Cys
210

<210> 168
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> EP-h4 light chain variable domain nucleic acid Q100 VEIK

<400> 168
gccatccagt tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgca gggccagtca gagtattggc acaaacatac actggtatca gcagaaacca 120
gggaaagctc ctaagctcct gatctattat gcttctgagt ctatctctgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
gaagattttg caacttatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagg tggaaatcaa a 321

<210> 169
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> EP-h4 light chain variable domain amino acid Q100 VEIK

<400> 169
Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
20 25 30
Ile His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 170
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> EP-h4 light chain variable domain amino acid A100 LELK

<400> 170
Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
20 25 30
Ile His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly

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


<210> 171
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> EP-h4 light chain variable domain nucleic acid
      Q100 LELK


<400> 171
gccatccagt tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgca gggccagtca gagtattggc acaaacatac actggtatca gcagaaacca 120
gggaaagctc ctaagctcct gatctattat gcttctgagt ctatctctgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
gaagattttg caacttatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagc tggagctgaa a                                           321

<210> 172
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> EP-h4 light chain variable domain amino acid Q100
      LELK


<400> 172
Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
            20                  25                  30
Ile His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
                85                  90                  95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Leu Lys
            100                 105


<210> 173
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> EP-h5 light chain nucleic acid Q100 VEIK


<220>
<221> V_region
<222> (1)...(321)
<223> variable domain
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<220>
<221> C_region
<222> (322)...(642)
<223> constant domain

<400> 173
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgca gggccagtca gagtattggc acaaacatac actggtacca gcagaaacct 120
ggccaggctc ccaggctcct catctattat gcttctgagt ctatctctgg gatcccagac 180
aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag actggagcct 240
gaagattttg cagtgtatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagg tggaaatcaa acgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 174
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> EP-h5 light chain amino acid Q100 VEIK

<220>
<221> DOMAIN
<222> (1)...(107)
<223> variable domain

<220>
<221> DOMAIN
<222> (108)...(214)
<223> constant domain

<400> 174
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
            20   25   30
Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35   40   45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Asp Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
65   70   75   80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100   105   110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115   120   125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130   135   140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145   150   155   160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165   170   175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180   185   190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195   200   205
Phe Asn Arg Gly Glu Cys
    210

<210> 175
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> EP-h5 light chain variable domain nucleic acid
Q100 VEIK

<400> 175
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgca gggccagtca gagtattggc acaaacatac actggtacca gcagaaacct 120
ggccaggctc ccaggctcct catctattat gcttctgagt ctatctctgg gatcccagac 180
aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag actggagcct 240
gaagattttg cagtgtatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagg tggaaatcaa a 321

<210> 176
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> EP-h5 light chain variable domain amino acid Q100
VEIK

<220>
<221> DOMAIN
<222> (1)...(107)
<223> variable domain

<220>
<221> DOMAIN
<222> (108)...(214)
<223> constant domain

<400> 176
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
20 25 30
Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Asp Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
65 70 75 80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 177
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> EP-h5 light chain variable domain amino acid A100
LELK

<400> 177
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
            20                  25                  30
Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35                  40                  45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Asp Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
65                  70                  75                  80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
                85                  90                  95
Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
            100                 105
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<210> 178
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> EP-h5 light chain variable domain nucleic acid Q100 LELK

<400> 178
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgca gggccagtca gagtattggc acaaacatac actggtacca gcagaaacct 120
ggccaggctc ccaggctcct catctattat gcttctgagt ctatctctgg gatcccagac 180
aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag actggagcct 240
gaagattttg cagtgtatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagc tggagctgaa a 321

<210> 179
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> EP-h5 light chain variable domain amino acid Q100 LELK

<400> 179
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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
            20                  25                  30
Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35                  40                  45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Asp Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
65                  70                  75                  80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
                85                  90                  95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Leu Lys
            100                 105
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<210> 180
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> EP-h6, 7, 9 light chain nucleic acid Q100 VEIK

<220>
<221> V_region
<222> (1)...(321)
<223> variable domain

<220>
<221> C_region
<222> (322)...(642)
<223> constant domain

<400> 180
gccatccagt tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgca gggccagtca gagtattggc acaaacatac actggtacct gcagaagcca 120
gggcagtctc cacagctcct gatctattat gcttctgagt ctatctctgg gatcccagac 180
aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag actggagcct 240
gaagattttg cagtgtatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagg tggaaatcaa acgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 181
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> EP-h6, 7, 9 light chain amino acid Q100 VEIK

<220>
<221> DOMAIN
<222> (1)...(107)
<223> variable domain

<220>
<221> DOMAIN
<222> (108)...(214)
<223> constant domain

<400> 181
Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
            20   25   30
Ile His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile
        35   40   45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Asp Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
65   70   75   80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100   105   110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115   120   125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130   135   140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145   150   155   160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165   170   175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180   185   190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser

195 200 205
Phe Asn Arg Gly Glu Cys
210

<210> 182
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> EP-h6, 7, 9 light chain variable domain nucleic acid Q100 VEIK

<400> 182
gccatccagt tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgca gggccagtca gagtattggc acaaacatac actggtacct gcagaagcca 120
gggcagtctc cacagctcct gatctattat gcttctgagt ctatctctgg gatcccagac 180
aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag actggagcct 240
gaagattttg cagtgtatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagg tggaaatcaa a 321

<210> 183
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> EP-h6, 7, 9 light chain variable domain amino acid Q100 VEIK

<400> 183
Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
20 25 30
Ile His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile
35 40 45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Asp Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
65 70 75 80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 184
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> EP-h6, 7, 9 light chain variable domain amino acid A100 LELK

<400> 184
Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
20 25 30
Ile His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile
35 40 45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Asp Arg Phe Ser Gly

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


<210> 185
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> EP-h6, 7, 9 light chain variable domain nucleic
      acid Q100 LELK


<400> 185
gccatccagt tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgca gggccagtca gagtattggc acaaacatac actggtacct gcagaagcca 120
gggcagtctc cacagctcct gatctattat gcttctgagt ctatctctgg gatcccagac 180
aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag actggagcct 240
gaagattttg cagtgtatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagc tggagctgaa a                                           321

<210> 186
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> EP-h6, 7, 9 light chain variable domain amino acid
      Q100 LELK


<400> 186
Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
            20                  25                  30
Ile His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile
        35                  40                  45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Asp Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
65                  70                  75                  80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
                85                  90                  95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Leu Lys
            100                 105


<210> 187
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> EP-h8 light chain nucleic acid Q100 VEIK


<220>
<221> V_region
<222> (1)...(321)

<220>
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<221> C_region
<222> (322)...(642)

<400> 187
gccatccagt tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgca gggccagtca gagtattggc acaaacatac actggtacca gcagaaacct 120
ggccaggctc ccaggctcct catctattat gcttctgagt ctatctctgg gatcccagcc 180
aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct 240
gaagattttg cagtttatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagg tggaaatcaa acgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 188
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> EP-h8 light chain amino acid Q100 VEIK

<220>
<221> DOMAIN
<222> (1)...(107)
<223> variable domain

<220>
<221> DOMAIN
<222> (108)...(214)
<223> constant domain

<400> 188
Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
            20   25   30
Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35   40   45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65   70   75   80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100   105   110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115   120   125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130   135   140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145   150   155   160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165   170   175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180   185   190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195   200   205
Phe Asn Arg Gly Glu Cys
    210

<210> 189
<211> 321

<212> DNA
<213> Artificial Sequence

<220>
<223> EP-h8 light chain variable domain nucleic acid
Q100 VEIK

<400> 189
gccatccagt tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgca gggccagtca gagtattggc acaaacatac actggtacca gcagaaacct 120
ggccaggctc ccaggctcct catctattat gcttctgagt ctatctctgg gatcccagcc 180
aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct 240
gaagattttg cagtttatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagg tggaaatcaa a 321

<210> 190
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> EP-h8 light chain variable domain amino acid Q100
VEIK

<400> 190
Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
20 25 30
Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 191
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> EP-h8 light chain variable domain amino acid A100
LELK

<400> 191
Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
20 25 30
Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
85 90 95
Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105

<210> 192
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> EP-h8 light chain variable domain nucleic acid
Q100 LELK

<400> 192
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atcacttgca gggccagtca gagtattggc acaaacatac actggtacca gcagaaacct 120
ggccaggctc ccaggctcct catctattat gcttctgagt ctatctctgg gatcccagcc 180
aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct 240
gaagattttg cagtttatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagc tggagctgaa a 321

<210> 193
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> EP-h8 light chain variable domain amino acid Q100
LELK

<400> 193
Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
20 25 30
Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
85 90 95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Leu Lys
100 105

<210> 194
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> EP-h10, 12 light chain nucleic acid Q100 VEIK

<220>
<221> V_region
<222> (1)...(321)

<220>
<221> C_region
<222> (322)...(642)

<400> 194
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ctctcctgca gggccagtca gagtattggc acaaacatac actggtatca gcagaaacca 120
gggaaagctc ctaagctcct gatctattat gcttctgagt ctatctctgg gatcccagac 180

aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag actggagcct 240
gaagattttg cagtgtatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagg tggaaatcaa acgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 195
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> EP-h10, 12 light chain amino acid Q100 VEIK

<220>
<221> DOMAIN
<222> (1)...(107)
<223> variable domain

<220>
<221> DOMAIN
<222> (108)...(214)
<223> constant domain

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

<210> 196
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> EP-h10, 12 light chain variable domain nucleic
      acid Q100 VEIK

<400> 196
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ctctcctgca gggccagtca gagtattggc acaaacatac actggtatca gcagaaacca 120
gggaaagctc ctaagctcct gatctattat gcttctgagt ctatctctgg gatcccagac 180
aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag actggagcct 240
gaagattttg cagtgtatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagg tggaaatcaa a 321

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

<220>
<223> EP-h10, 12 light chain variable domain amino acid
Q100 VEIK

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

<210> 198
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> EP-h10, 12 light chain variable domain amino acid
A100 LELK

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

<210> 199
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> EP-h10, 12 light chain variable domain nucleic acid Q100 LELK

<400> 199
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ctctcctgca gggccagtca gagtattggc acaaacatac actggtatca gcagaaacca 120
gggaaagctc ctaagctcct gatctattat gcttctgagt ctatctctgg gatcccagac 180
aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag actggagcct 240
gaagattttg cagtgtatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagc tggagctgaa a 321

<210> 200
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> EP-h10, 12 light chain variable domain amino acid Q100 LELK

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

<210> 201
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> EP-h13, 14 light chain nucleic acid Q100 VEIK

<220>
<221> V_region
<222> (1)...(321)

<220>
<221> C_region
<222> (322)...(642)

<400> 201
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ctctcctgca gggccagtca gagtattggc acaaacatac actggtacca gcagaaacct 120
ggccaggctc ccaggctcct catctattat gcttctgagt ctatctctgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240
gatgattttg caacttatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagg tggaaatcaa acgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 202
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> EP-h13, 14 light chain amino acid Q100 VEIK

<220>
<221> DOMAIN
<222> (1)...(107)
<223> variable domain

<220>
<221> DOMAIN
<222> (108)...(214)
<223> constant domain

<400> 202
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1   5   10   15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
            20   25   30
Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35   40   45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100   105   110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115   120   125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130   135   140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145   150   155   160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165   170   175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180   185   190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195   200   205
Phe Asn Arg Gly Glu Cys
    210

<210> 203
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> EP-h13, 14 light chain variable domain nucleic
      acid Q100 VEIK

<400> 203
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ctctcctgca gggccagtca gagtattggc acaaacatac actggtacca gcagaaacct 120
ggccaggctc ccaggctcct catctattat gcttctgagt ctatctctgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240
gatgattttg caacttatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagg tggaaatcaa a   321

<210> 204
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> EP-h13, 14 light chain variable domain amino acid
Q100 VEIK

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

<210> 205
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> EP-h13, 14 light chain variable domain amino acid
A100 LELK

<400> 205
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
20 25 30
Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
85 90 95
Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105

<210> 206
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> EP-h13, 14 light chain variable domain nucleic
acid Q100 LELK

<400> 206
gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtattggc acaaacatac actggtacca gcagaaacct 120

ggccaggctc ccaggctcct catctattat gcttctgagt ctatctctgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240
gatgattttg caacttatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagc tggagctgaa a 321

<210> 207
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> EP-h13, 14 light chain variable domain amino acid
Q100 LELK

<400> 207
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
20 25 30
Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
85 90 95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Leu Lys
100 105

<210> 208
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> FEP-h1, 19, 20, 21 heavy chain nucleic acid S119

<220>
<221> variation
<222> 312
<223> n = a or g

<220>
<221> V_region
<222> (1)...(357)

<220>
<221> C_region
<222> (358)...(1347)

<400> 208
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tcctgcaagg tttctggttt ctcattattt aactatggtg tacactggat ccgccagccc 120
ccagggaagg ggctggagtg gattggtgtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240
caaatgaaca gcctgagagc cgaggacacg gccgtgtatt actgtgccag agccctcacc 300
tactatgatg angagtttgc ttactggggc cctggaacgc tggtcaccgt cagctcagcc 360
tccaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480
aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540
ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600
atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 660
tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 720
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780

gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960
tacaagtgca aggtcagcaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1020
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1080
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320
aagagcctct ccctgtctcc gggtaaa 1347

<210> 209
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h1, 19, 20, 21 heavy chain amino acid S119

<220>
<221> DOMAIN
<222> (1)...(119)
<223> variable domain

<220>
<221> DOMAIN
<222> (120)...(217)
<223> CH1

<220>
<221> DOMAIN
<222> (218)...(232)
<223> hinge region

<220>
<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 209
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1   5   10   15
Thr Val Lys Ile Ser Cys Lys Val Ser Gly Phe Ser Leu Phe Asn Tyr
            20   25   30
Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
        35   40   45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50   55   60
Ser Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65   70   75   80
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85   90   95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Pro Gly
            100   105   110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115   120   125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130   135   140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145   150   155   160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu

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                165                 170                 175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
Lys
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<210> 210
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> FEP-h1, 19, 20, 21 heavy chain variable domain
nucleic acid S119

<220>
<221> variation
<222> 312
<223> n = a or g

<400> 210
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tcctgcaagg tttctggttt ctcattattt aactatggtg tacactggat ccgccagccc 120
ccagggaagg ggctggagtg gattggtgtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240
caaatgaaca gcctgagagc cgaggacacg gccgtgtatt actgtgccag agccctcacc 300
tactatgatg angagtttgc ttactggggc cctggaacgc tggtcaccgt cagctca 357

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

<220>

<223> FEP-h1, 19, 20, 21 heavy chain variable domain
amino acid S119

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

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

<220>
<223> FEP-h1, 19, 20, 21 heavy chain variable domain
nucleic acid A119

<220>
<221> variation
<222> 312
<223> n = a or g

<400> 212
gaggtccagc tggtacagtc tggggctgag gtgaagaagc ctggggctac agtgaaaatc 60
tcctgcaagg tttctggttt ctcattattt aactatggtg tacactggat ccgccagccc 120
ccagggaagg ggctggagtg gattggtgtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240
caaatgaaca gcctgagagc cgaggacacg gccgtgtatt actgtgccag agccctcacc 300
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<210> 213
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h1, 19, 20, 21 heavy chain variable domain
amino acid A119

<400> 213
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1   5   10   15
Thr Val Lys Ile Ser Cys Lys Val Ser Gly Phe Ser Leu Phe Asn Tyr
            20   25   30
Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
        35   40   45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50   55   60
Ser Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65   70   75   80
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala

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

<210> 214
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> FEP-h2 heavy chain nucleic acid S119

<220>
<221> variation
<222> 312
<223> n = a or g

<220>
<221> V_region
<222> (1)...(357)

<220>
<221> C_region
<222> (368)...(1347)

<400> 214
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tcctgcaagg tttctggttt ctcattattt aactatggtg tacactgggt gcgacaggct 120
cgtggacaac gccttgagtg gataggtgtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagatt caccatctcc agagatgatt caaagaacac ggcgtatctg 240
caaatgaaca gcctgaaaac cgaggacacg gccgtgtatt actgtgccag agccctcacc 300
tactatgatg angagtttgc ttactggggc cctggaacgc tggtcaccgt cagctcagcc 360
tccaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480
aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540
ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600
atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 660
tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 720
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780
gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960
tacaagtgca aggtcagcaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1020
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1080
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320
aagagcctct ccctgtctcc gggtaaa 1347

<210> 215
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h2 heavy chain amino acid S119

<220>
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<222> (1)...(119)
<223> variable domain

<220>
<221> DOMAIN
<222> (120)...(217)
<223> CH1

<220>
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<222> (218)...(232)
<223> hinge region

<220>
<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 215

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

<210> 216
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> FEP-h2 heavy chain variable domain nucleic acid S119

<220>
<221> variation
<222> 312
<223> n = a or g

<400> 216
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tcctgcaagg tttctggttt ctcattattt aactatggtg tacactgggt gcgacaggct 120
cgtggacaac gccttgagtg gataggtgtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagatt caccatctcc agagatgatt caaagaacac ggcgtatctg 240
caaatgaaca gcctgaaaac cgaggacacg gccgtgtatt actgtgccag agccctcacc 300
tactatgatg angagtttgc ttactggggc cctggaacgc tggtcaccgt cagctca 357

<210> 217
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h2 heavy chain variable domain amino acid S119

<400> 217
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Thr Val Lys Ile Ser Cys Lys Val Ser Gly Phe Ser Leu Phe Asn Tyr
20 25 30
Gly Val His Trp Val Arg Gln Ala Arg Gly Gln Arg Leu Glu Trp Ile
35 40 45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
50 55 60
Ser Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu
65 70 75 80
Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Pro Gly
100 105 110
Thr Leu Val Thr Val Ser Ser
115

<210> 218
<211> 357
<212> DNA

<213> Artificial Sequence

<220>
<223> FEP-h2 heavy chain variable domain nucleic acid
A119

<220>
<221> variation
<222> 312
<223> n = a or g

<400> 218
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tcctgcaagg tttctggttt ctcattattt aactatggtg tacactgggt gcgacaggct 120
cgtggacaac gccttgagtg gataggtgtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagatt caccatctcc agagatgatt caaagaacac ggcgtatctg 240
caaatgaaca gcctgaaaac cgaggacacg gccgtgtatt actgtgccag agccctcacc 300
tactatgatg angagtttgc ttactggggc cctggaacgc tggtcaccgt cagcgca 357

<210> 219
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h2 heavy chain variable domain amino acid A119

<400> 219
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1   5   10   15
Thr Val Lys Ile Ser Cys Lys Val Ser Gly Phe Ser Leu Phe Asn Tyr
            20   25   30
Gly Val His Trp Val Arg Gln Ala Arg Gly Gln Arg Leu Glu Trp Ile
        35   40   45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50   55   60
Ser Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu
65   70   75   80
Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85   90   95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Pro Gly
            100   105   110
Thr Leu Val Thr Val Ser Ala
        115

<210> 220
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> FEP-h3, 7, 11, 15 heavy chain nucleic acid S119

<220>
<221> variation
<222> 312
<223> n = a or g

<220>
<221> V_region
<222> (1)...(357)

<220>
<221> C_region

<222> (358)...(1347)

<400> 220
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actggacaag ggcttgagtg gatgggtgtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagatt caccatctcc agagatgatt caaagaacac ggcgtatctg 240
caaatgaaca gcctgaaaac cgaggacacg gccgtgtatt actgtgccag agccctcacc 300
tactatgatg angagtttgc ttactggggc cctggaacgc tggtcaccgt cagctcagcc 360
tccaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480
aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540
ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600
atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 660
tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 720
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780
gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960
tacaagtgca aggtcagcaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1020
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1080
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320
aagagcctct ccctgtctcc gggtaaa 1347

<210> 221
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h3, 7, 11, 15 heavy chain amino acid S119

<220>
<221> DOMAIN
<222> (1)...(119)
<223> variable domain

<220>
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<222> (120)...(217)
<223> CH1

<220>
<221> DOMAIN
<222> (218)...(232)
<223> hinge region

<220>
<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 221
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1   5   10   15
Thr Val Lys Ile Ser Cys Lys Val Ser Gly Phe Ser Leu Phe Asn Tyr
            20   25   30
Gly Val His Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Glu Trp Met

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        35                  40                  45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50                  55                  60
Ser Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu
65                  70                  75                  80
Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Pro Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
Lys
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<210> 222
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> FEP-h3, 7, 11, 15 heavy chain variable domain
nucleic acid S119

<220>
<221> variation
<222> 312

<223> n = a or g

<400> 222
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tcctgcaagg tttctggttt ctcattattt aactatggtg tacactgggt gcgacaggcc 120
actggacaag ggcttgagtg gatgggtgtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagatt caccatctcc agagatgatt caaagaacac ggcgtatctg 240
caaatgaaca gcctgaaaac cgaggacacg gccgtgtatt actgtgccag agccctcacc 300
tactatgatg angagtttgc ttactggggc cctggaacgc tggtcaccgt cagctca 357

<210> 223
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h3, 7, 11, 15 heavy chain variable domain
amino acid S119

<400> 223
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Thr Val Lys Ile Ser Cys Lys Val Ser Gly Phe Ser Leu Phe Asn Tyr
20 25 30
Gly Val His Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
50 55 60
Ser Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu
65 70 75 80
Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Pro Gly
100 105 110
Thr Leu Val Thr Val Ser Ser
115

<210> 224
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> FEP-h3, 7, 11, 15 heavy chain variable domain
nucleic acid A119

<220>
<221> variation
<222> 312
<223> n = a or g

<400> 224
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tcctgcaagg tttctggttt ctcattattt aactatggtg tacactgggt gcgacaggcc 120
actggacaag ggcttgagtg gatgggtgtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagatt caccatctcc agagatgatt caaagaacac ggcgtatctg 240
caaatgaaca gcctgaaaac cgaggacacg gccgtgtatt actgtgccag agccctcacc 300
tactatgatg angagtttgc ttactggggc cctggaacgc tggtcaccgt cagcgca 357

<210> 225
<211> 119
<212> PRT
<213> Artificial Sequence

<220>

<223> FEP-h3, 7, 11, 15 heavy chain variable domain
amino acid A119

<400> 225
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1   5   10   15
Thr Val Lys Ile Ser Cys Lys Val Ser Gly Phe Ser Leu Phe Asn Tyr
            20   25   30
Gly Val His Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Glu Trp Met
        35   40   45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50   55   60
Ser Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu
65   70   75   80
Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85   90   95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Pro Gly
            100   105   110
Thr Leu Val Thr Val Ser Ala
        115

<210> 226
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> FEP-h4, 8, 12, 16 heavy chain nucleic acid S119

<220>
<221> variation
<222> 312
<223> n = a or g

<220>
<221> V_region
<222> (1)...(357)

<220>
<221> C_region
<222> (358)...(1347)

<400> 226
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ccatcgagag gccttgagtg gctgggtgtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagact caccatctcc aaggacacct ccaaaaacca ggtggtcctt 240
acaatgacca acatggaccc tgtggacaca gccacgtatt actgtgccag agccctcacc 300
tactatgatg angagtttgc ttactggggc cctggaacgc tggtcaccgt cagctcagcc 360
tccaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480
aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540
ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600
atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 660
tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 720
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780
gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960
tacaagtgca aggtcagcaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1020
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1080
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320

aagagcctct ccctgtctcc gggtaaa 1347

<210> 227
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h4, 8, 12, 16 heavy chain amino acid S119

<220>
<221> DOMAIN
<222> (1)...(119)
<223> variable domain

<220>
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<222> (120)...(217)
<223> CH1

<220>
<221> DOMAIN
<222> (218)...(232)
<223> hinge region

<220>
<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 227
Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
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Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Phe Ser Leu Phe Asn Tyr
            20   25   30
Gly Val His Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu Trp Leu
        35   40   45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50   55   60
Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val Val Leu
65   70   75   80
Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala
                85   90   95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Pro Gly
            100   105   110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115   120   125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130   135   140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145   150   155   160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165   170   175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180   185   190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195   200   205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210   215   220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225   230   235   240

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

<210> 228
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> FEP-h4, 8, 12, 16 heavy chain variable domain
nucleic acid S119

<220>
<221> variation
<222> 312
<223> n = a or g

<400> 228
caggtacagc tgcagcagtc aggtccagga ctggtgaagc cctcgcagac cctctcactc 60
acctgtgcca tctctggttt ctcattattt aactatggtg tacactggat caggcagtcc 120
ccatcgagag gccttgagtg gctgggtgtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagact caccatctcc aaggacacct ccaaaaacca ggtggtcctt 240
acaatgacca acatggaccc tgtggacaca gccacgtatt actgtgccag agccctcacc 300
tactatgatg angagtttgc ttactggggc cctggaacgc tggtcaccgt cagctca 357

<210> 229
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h4, 8, 12, 16 heavy chain variable domain
amino acid S119

<400> 229
Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15
Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Phe Ser Leu Phe Asn Tyr
20 25 30

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


<210> 230
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> FEP-h4, 8, 12, 16 heavy chain variable domain
      nucleic acid A119


<220>
<221> variation
<222> 312
<223> n = a or g

<400> 230
caggtacagc tgcagcagtc aggtccagga ctggtgaagc cctcgcagac cctctcactc 60
acctgtgcca tctctggttt ctcattattt aactatggtg tacactggat caggcagtcc 120
ccatcgagag gccttgagtg gctgggtgtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagact caccatctcc aaggacacct ccaaaaacca ggtggtcctt 240
acaatgacca acatggaccc tgtggacaca gccacgtatt actgtgccag agccctcacc 300
tactatgatg angagtttgc ttactggggc cctggaacgc tggtcaccgt cagcgca    357

<210> 231
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h4, 8, 12, 16 heavy chain variable domain
      amino acid A119


<400> 231
Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1               5                  10                  15
Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Phe Ser Leu Phe Asn Tyr
            20                  25                  30
Gly Val His Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu Trp Leu
        35                  40                  45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50                  55                  60
Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val Val Leu
65                  70                  75                  80
Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala
                85                  90                  95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Pro Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ala
        115


<210> 232
<211> 1347
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<212> DNA
<213> Artificial Sequence

<220>
<223> FEP-h5, 9, 13, 17 heavy chain nucleic acid S119

<220>
<221> variation
<222> 312
<223> n = a or g

<220>
<221> V_region
<222> (1)...(357)

<220>
<221> C_region
<222> (358)...(1347)

<400> 232
gaggtccagc tggtacagtc tggggctgag gtgaagaagc ctggggctac agtgaaaatc 60
tcctgcaagg tttctggttt ttcattattt aactatggtg tacactggat ccgccagccc 120
ccagggaagg ggctggagtg gattggtgtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240
caaatgaaca gcctgagagc cgaggacacg gccgtgtatt actgtgccag agccctcacc 300
tactatgatg angagtttgc ttactggggc cctggaacgc tggtcaccgt cagctcagcc 360
tccaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480
aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540
ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600
atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 660
tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 720
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780
gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960
tacaagtgca aggtcagcaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1020
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1080
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320
aagagcctct ccctgtctcc gggtaaa 1347

<210> 233
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h5, 9, 13, 17 heavy chain amino acid S119

<220>
<221> DOMAIN
<222> (1)...(119)
<223> variable domain

<220>
<221> DOMAIN
<222> (120)...(217)
<223> CH1

<220>
<221> DOMAIN
<222> (218)...(232)
<223> hinge region

<220>
<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 233
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Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1               5                  10                  15
Thr Val Lys Ile Ser Cys Lys Val Ser Gly Phe Ser Leu Phe Asn Tyr
            20                  25                  30
Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
        35                  40                  45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50                  55                  60
Ser Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65                  70                  75                  80
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Pro Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
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435 440 445
Lys

<210> 234
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> FEP-h5, 9, 13, 17 heavy chain variable domain
nucleic acid S119

<220>
<221> variation
<222> 312
<223> n = a or g

<400> 234
gaggtccagc tggtacagtc tggggctgag gtgaagaagc ctggggctac agtgaaaatc 60
tcctgcaagg tttctggttt ttcattattt aactatggtg tacactggat ccgccagccc 120
ccagggaagg ggctggagtg gattggtgtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240
caaatgaaca gcctgagagc cgaggacacg gccgtgtatt actgtgccag agccctcacc 300
tactatgatg angagtttgc ttactggggc cctggaacgc tggtcaccgt cagctca 357

<210> 235
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h5, 9, 13, 17 heavy chain variable domain
amino acid S119

<400> 235
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Thr Val Lys Ile Ser Cys Lys Val Ser Gly Phe Ser Leu Phe Asn Tyr
20 25 30
Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
50 55 60
Ser Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Pro Gly
100 105 110
Thr Leu Val Thr Val Ser Ser
115

<210> 236
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> FEP-h5, 9, 13, 17 heavy chain variable domain
nucleic acid A119

<220>

<221> variation
<222> 312
<223> n = a or g

<400> 236
gaggtccagc tggtacagtc tggggctgag gtgaagaagc ctggggctac agtgaaaatc 60
tcctgcaagg tttctggttt ttcattattt aactatggtg tacactggat ccgccagccc 120
ccagggaagg ggctggagtg gattggtgtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240
caaatgaaca gcctgagagc cgaggacacg gccgtgtatt actgtgccag agccctcacc 300
tactatgatg angagtttgc ttactggggc cctggaacgc tggtcaccgt cagcgca 357

<210> 237
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h5, 9, 13, 17 heavy chain variable domain
amino acid A119

<400> 237
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Thr Val Lys Ile Ser Cys Lys Val Ser Gly Phe Ser Leu Phe Asn Tyr
20 25 30
Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
50 55 60
Ser Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Pro Gly
100 105 110
Thr Leu Val Thr Val Ser Ala
115

<210> 238
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> FEP-h6 heavy chain nucleic acid S119

<220>
<221> variation
<222> 312
<223> n = a or g

<220>
<221> V_region
<222> (1)...(357)

<220>
<221> C_region
<222> (358)...(1347)

<400> 238
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tcctgcaagg tttctggttt ctcattattt aactatggtg tacactggat caggcagtcc 120
ccatcgagag gccttgagtg gctgggtgtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc cgaggacacg gccgtgtatt actgtgccag agccctcacc 300
tactatgatg angagtttgc ttactggggc cctggaacgc tggtcaccgt cagctcagcc 360
tccaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480
aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540
ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600
atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 660
tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 720
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780
gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960
tacaagtgca aggtcagcaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1020
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1080
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320
aagagcctct ccctgtctcc gggtaaa 1347

<210> 239
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h6 heavy chain amino acid S119

<220>
<221> DOMAIN
<222> (1)...(119)
<223> variable domain

<220>
<221> DOMAIN
<222> (120)...(217)
<223> CH1

<220>
<221> DOMAIN
<222> (218)...(232)
<223> hinge region

<220>
<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 239
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1   5   10   15
Thr Val Lys Ile Ser Cys Lys Val Ser Gly Phe Ser Leu Phe Asn Tyr
            20   25   30
Gly Val His Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu Trp Leu
        35   40   45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50   55   60
Ser Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65   70   75   80
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85   90   95

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Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Pro Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
Lys
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<210> 240
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> FEP-h6 heavy chain variable domain nucleic acid
S119

<220>
<221> variation
<222> 312
<223> n = a or g

<400> 240
gaggtccagc tggtacagtc tggggctgag gtgaagaagc ctggggctac agtgaaaatc 60
tcctgcaagg tttctggttt ctcattattt aactatggtg tacactggat caggcagtcc 120
ccatcgagag gccttgagtg gctgggtgtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc cgaggacacg gccgtgtatt actgtgccag agccctcacc 300
tactatgatg angagtttgc ttactggggc cctggaacgc tggtcaccgt cagctca 357

<210> 241
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h6 heavy chain variable domain amino acid S119

<400> 241
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1   5   10   15
Thr Val Lys Ile Ser Cys Lys Val Ser Gly Phe Ser Leu Phe Asn Tyr
            20   25   30
Gly Val His Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu Trp Leu
        35   40   45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50   55   60
Ser Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65   70   75   80
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85   90   95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Pro Gly
            100   105   110
Thr Leu Val Thr Val Ser Ser
        115

<210> 242
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> FEP-h6 heavy chain variable domain nucleic acid
      A119

<220>
<221> variation
<222> 312
<223> n = a or g

<220>
<221> V_region
<222> (1)...(357)

<220>
<221> C_region
<222> (358)...(1347)

<400> 242
gaggtccagc tggtacagtc tggggctgag gtgaagaagc ctggggctac agtgaaaatc 60
tcctgcaagg tttctggttt ctcattattt aactatggtg tacactggat caggcagtcc 120
ccatcgagag gccttgagtg gctgggtgtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240
caaatgaaca gcctgagagc cgaggacacg gccgtgtatt actgtgccag agccctcacc 300
tactatgatg angagtttgc ttactggggc cctggaacgc tggtcaccgt cagcgca 357

<210> 243
<211> 119
<212> PRT
<213> Artificial Sequence

<220>

<223> FEP-h6 heavy chain variable domain amino acid A119

<400> 243
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1   5   10   15
Thr Val Lys Ile Ser Cys Lys Val Ser Gly Phe Ser Leu Phe Asn Tyr
            20   25   30
Gly Val His Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu Trp Leu
        35   40   45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50   55   60
Ser Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65   70   75   80
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85   90   95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Pro Gly
            100   105   110
Thr Leu Val Thr Val Ser Ala
        115

<210> 244
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> FEP-h10, 14, 18 heavy chain nucleic acid S119

<220>
<221> variation
<222> 312
<223> n = a or g

<220>
<221> V_region
<222> (1)...(357)

<220>
<221> C_region
<222> (358)...(1347)

<400> 244
gaggtccagc tggtacagtc tggggctgag gtgaagaagc ctggggctac agtgaaaatc 60
tcctgcaagg tttctggttt ctcattattt aactatggtg tacactggat ccgccagccc 120
ccagggaagg ggctggagtg gattggtgtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagatt caccatctcc agagatgatt caaagaacac ggcgtatctg 240
caaatgaaca gcctgaaaac cgaggacacg gccgtgtatt actgtgccag agccctcacc 300
tactatgatg angagtttgc ttactggggc cctggaacgc tggtcaccgt cagctcagcc 360
tccaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480
aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540
ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600
atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 660
tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 720
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780
gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960
tacaagtgca aggtcagcaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1020
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1080
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320
aagagcctct ccctgtctcc gggtaaa   1347

<210> 245
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h10, 14, 18 heavy chain amino acid S119

<220>
<221> DOMAIN
<222> (1)...(119)
<223> variable domain

<220>
<221> DOMAIN
<222> (120)...(217)
<223> CH1

<220>
<221> DOMAIN
<222> (218)...(232)
<223> hinge region

<220>
<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

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

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

<210> 246
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> FEP-h10, 14, 18 heavy chain variable domain nucleic acid S119

<220>
<221> variation
<222> 312
<223> n = a or g

<400> 246
gaggtccagc tggtacagtc tggggctgag gtgaagaagc ctggggctac agtgaaaatc 60
tcctgcaagg tttctggttt ctcattattt aactatggtg tacactggat ccgccagccc 120
ccagggaagg ggctggagtg gattggtgtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagatt caccatctcc agagatgatt caaagaacac ggcgtatctg 240
caaatgaaca gcctgaaaac cgaggacacg gccgtgtatt actgtgccag agccctcacc 300
tactatgatg angagtttgc ttactggggc cctggaacgc tggtcaccgt cagctca 357

<210> 247
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h10, 14, 18 heavy chain variable domain amino acid S119

<400> 247
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Thr Val Lys Ile Ser Cys Lys Val Ser Gly Phe Ser Leu Phe Asn Tyr
20 25 30

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

<210> 248
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> FEP-h10, 14, 18 heavy chain variable domain
      nucleic acid A119

<220>
<221> variation
<222> 312
<223> n = a or g

<400> 248
gaggtccagc tggtacagtc tggggctgag gtgaagaagc ctggggctac agtgaaaatc 60
tcctgcaagg tttctggttt ctcattattt aactatggtg tacactggat ccgccagccc 120
ccagggaagg ggctggagtg gattggtgtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagatt caccatctcc agagatgatt caaagaacac ggcgtatctg 240
caaatgaaca gcctgaaaac cgaggacacg gccgtgtatt actgtgccag agccctcacc 300
tactatgatg angagtttgc ttactggggc cctggaacgc tggtcaccgt cagcgca   357

<210> 249
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h10, 14, 18 heavy chain variable domain amino
      acid A119

<400> 249
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1   5   10   15
Thr Val Lys Ile Ser Cys Lys Val Ser Gly Phe Ser Leu Phe Asn Tyr
            20   25   30
Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
        35   40   45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50   55   60
Ser Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu
65   70   75   80
Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85   90   95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Pro Gly
            100   105   110
Thr Leu Val Thr Val Ser Ala
        115

<210> 250
<211> 642

<212> DNA
<213> Artificial Sequence

<220>
<223> FEP-h1, 2 light chain nucleic acid Q100 VEIK

<220>
<221> V_region
<222> (1)...(321)

<220>
<221> C_region
<222> (322)...(642)

<400> 250
gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtattggc acaaacatac actggtacca gcagaaacct 120
ggccaggctc ccaggctcct catctattat gcttctgagt ctatctctgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240
gatgattttg caacttatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagg tggaaatcaa acgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 251
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h1, 2 light chain amino acid Q100 VEIK

<220>
<221> DOMAIN
<222> (1)...(107)
<223> variable domain

<220>
<221> DOMAIN
<222> (108)...(214)
<223> constant domain

<400> 251
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1   5   10   15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
            20   25   30
Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35   40   45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100   105   110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115   120   125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130   135   140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145   150   155   160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205
Phe Asn Arg Gly Glu Cys
210

<210> 252
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> FEP-h1, 2 light chain variable domain nucleic acid
Q100 VEIK

<400> 252
gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtattggc acaaacatac actggtacca gcagaaacct 120
ggccaggctc ccaggctcct catctattat gcttctgagt ctatctctgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240
gatgattttg caacttatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagg tggaaatcaa a 321

<210> 253
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h1, 2 light chain variable domain amino acid
Q100 VEIK

<400> 253
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
20 25 30
Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 254
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h1, 2 light chain variable domain amino acid
A100 LELK

<400> 254
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

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

<210> 255
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> FEP-h1, 2 light chain variable domain nucleic acid
      Q100 LELK

<400> 255
gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtattggc acaaacatac actggtacca gcagaaacct 120
ggccaggctc ccaggctcct catctattat gcttctgagt ctatctctgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240
gatgattttg caacttatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagc tggagctgaa a   321

<210> 256
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h1, 2 light chain variable domain amino acid
      Q100 LELK

<400> 256
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1   5   10   15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
            20   25   30
Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35   40   45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Leu Lys
            100   105

<210> 257
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> FEP-h3, 4 light chain nucleic acid Q100 VEIK

<220>
<221> V_region
<222> (1)...(321)

<220>
<221> C_region
<222> (322)...(642)

<400> 257
gccatccagt tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgca gggccagtca gagtattggc acaaacatac actggtacct gcagaagcca 120
gggcagtctc cacagctcct gatctattat gcttctgagt ctatctctgg gatcccagac 180
aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag actggagcct 240
gaagattttg cagtgtatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagg tggaaatcaa acgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt   642

<210> 258
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h3, 4 light chain amino acid Q100 VEIK

<220>
<221> DOMAIN
<222> (1)...(107)
<223> variable domain

<220>
<221> DOMAIN
<222> (108)...(214)
<223> constant domain

<400> 258
Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
            20   25   30
Ile His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile
        35   40   45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Asp Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
65   70   75   80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100   105   110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115   120   125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130   135   140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145   150   155   160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165   170   175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180   185   190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195   200   205
Phe Asn Arg Gly Glu Cys

210

<210> 259
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> FEP-h3, 4 light chain variable domain nucleic acid
Q100 VEIK

<400> 259
gccatccagt tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgca gggccagtca gagtattggc acaaacatac actggtacct gcagaagcca 120
gggcagtctc cacagctcct gatctattat gcttctgagt ctatctctgg gatcccagac 180
aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag actggagcct 240
gaagattttg cagtgtatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagg tggaaatcaa a 321

<210> 260
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h3, 4 light chain variable domain amino acid
Q100 VEIK

<400> 260
Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
20 25 30
Ile His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile
35 40 45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Asp Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
65 70 75 80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 261
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h3, 4 light chain variable domain amino acid
A100 LELK

<400> 261
Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
20 25 30
Ile His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile
35 40 45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Asp Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro

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

<210> 262
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> FEP-h3, 4 light chain variable domain nucleic acid
Q100 LELK

<400> 262
gccatccagt tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgca gggccagtca gagtattggc acaaacatac actggtacct gcagaagcca 120
gggcagtctc cacagctcct gatctattat gcttctgagt ctatctctgg gatcccagac 180
aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag actggagcct 240
gaagattttg cagtgtatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagc tggagctgaa a 321

<210> 263
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h3, 4 light chain variable domain amino acid
Q100 LELK

<400> 263
Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
20 25 30
Ile His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile
35 40 45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Asp Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
65 70 75 80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
85 90 95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Leu Lys
100 105

<210> 264
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> FEP-h5 light chain nucleic acid Q100 VEIK

<220>
<221> V_region
<222> (1)...(321)

<220>
<221> C_region
<222> (322)...(642)

<400> 264
gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtattggc acaaacatac actggtatca gcagaaacca 120
gggaaagctc ctaagctcct gatctattat gcttctgagt ctatctctgg gatcccagac 180
aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag actggagcct 240
gaagattttg cagtgtatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagg tggaaatcaa acgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 265
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h5 light chain amino acid Q100 VEIK

<220>
<221> DOMAIN
<222> (1)...(107)
<223> variable domain

<220>
<221> DOMAIN
<222> (108)...(214)
<223> constant domain

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

<210> 266
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> FEP-h5 light chain variable domain nucleic acid
Q100 VEIK

<400> 266
gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtattggc acaaacatac actggtatca gcagaaacca 120
gggaaagctc ctaagctcct gatctattat gcttctgagt ctatctctgg gatcccagac 180
aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag actggagcct 240
gaagattttg cagtgtatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagg tggaaatcaa a 321

<210> 267
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h5 light chain variable domain amino acid Q100
VEIK

<400> 267
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
20 25 30
Ile His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Asp Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
65 70 75 80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 268
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h5 light chain variable domain amino acid A100
LELK

<400> 268
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
20 25 30
Ile His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Asp Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
65 70 75 80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
85 90 95
Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105

<210> 269
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> FEP-h5 light chain variable domain nucleic acid
Q100 LELK

<400> 269
gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtattggc acaaacatac actggtatca gcagaaacca 120
gggaaagctc ctaagctcct gatctattat gcttctgagt ctatctctgg gatcccagac 180
aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag actggagcct 240
gaagattttg cagtgtatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagc tggagctgaa a 321

<210> 270
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h5 light chain variable domain amino acid Q100
LELK

<400> 270
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1   5   10   15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
            20   25   30
Ile His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Asp Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
65   70   75   80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Leu Lys
            100   105

<210> 271
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> FEP-h6, 7, 8 light chain nucleic acid Q100 VEIK

<220>
<221> V_region
<222> (1)...(321)

<220>
<221> C_region
<222> (322)...(642)

<400> 271
gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtattggc acaaacatac actggtacca gcagaaacct 120
ggccaggctc ccaggctcct catctattat gcttctgagt ctatctctgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
gaagattttg caacttatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300

gggaccaagg tggaaatcaa acgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 272
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h6, 7, 8 light chain amino acid Q100 VEIK

<220>
<221> DOMAIN
<222> (1)...(107)
<223> variable domain

<220>
<221> DOMAIN
<222> (108)...(214)
<223> constant domain

<400> 272
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1   5   10   15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
            20   25   30
Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35   40   45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100   105   110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115   120   125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130   135   140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145   150   155   160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165   170   175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180   185   190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195   200   205
Phe Asn Arg Gly Glu Cys
    210

<210> 273
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> FEP-h6, 7, 8 light chain variable domain nucleic
      acid Q100 VEIK

<400> 273

gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtattggc acaaacatac actggtacca gcagaaacct 120
ggccaggctc ccaggctcct catctattat gcttctgagt ctatctctgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
gaagattttg caacttatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagg tggaaatcaa a 321

<210> 274
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h6, 7, 8 light chain variable domain amino
acid Q100 VEIK

<400> 274
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
20 25 30
Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 275
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h6, 7, 8 light chain variable domain amino
acid A100 LELK

<400> 275
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
20 25 30
Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
85 90 95
Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105

<210> 276
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> FEP-h6, 7, 8 light chain variable domain nucleic

acid Q100 LELK

<400> 276
gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtattggc acaaacatac actggtacca gcagaaacct 120
ggccaggctc ccaggctcct catctattat gcttctgagt ctatctctgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
gaagattttg caacttatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagc tggagctgaa a 321

<210> 277
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h6, 7, 8 light chain variable domain amino
acid Q100 LELK

<400> 277
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
20 25 30
Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
85 90 95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Leu Lys
100 105

<210> 278
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> FEP-h9, 10, 11, 12, 20 light chain nucleic acid
Q100 VEIK

<220>
<221> V_region
<222> (1)...(321)

<220>
<221> C_region
<222> (322)...(642)

<400> 278
gccatccagt tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgca gggccagtca gagtattggc acaaacatac actggtacca gcagaaacct 120
ggccaggctc ccaggctcct catctattat gcttctgagt ctatctctgg gatcccacct 180
cgattcagtg gcagcgggtc tgggacagac ttcactctca ccatcagcag actggagcct 240
gaagattttg cagtgtatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagg tggaaatcaa acgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 279
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h9, 10, 11, 12, 20 light chain amino acid
Q100 VEIK

<220>
<221> DOMAIN
<222> (1)...(107)
<223> variable domain

<220>
<221> DOMAIN
<222> (108)...(214)
<223> constant domain

<400> 279
Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
20 25 30
Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Pro Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
65 70 75 80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205
Phe Asn Arg Gly Glu Cys
210

<210> 280
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> FEP-h9, 10, 11, 12, 20 light chain variable
domain nucleic acid Q100 VEIK

<400> 280
gccatccagt tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgca gggccagtca gagtattggc acaaacatac actggtacca gcagaaacct 120
ggccaggctc ccaggctcct catctattat gcttctgagt ctatctctgg gatcccacct 180
cgattcagtg gcagcgggtc tgggacagac ttcactctca ccatcagcag actggagcct 240
gaagattttg cagtgtatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300

gggaccaagg tggaaatcaa a 321

<210> 281
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h9, 10, 11, 12, 20 light chain variable
domain amino acid Q100 VEIK

<400> 281
Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
20 25 30
Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Pro Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
65 70 75 80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 282
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h9, 10, 11, 12, 20 light chain variable
domain amino acid A100 LELK

<400> 282
Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
20 25 30
Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Pro Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
65 70 75 80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
85 90 95
Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105

<210> 283
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> FEP-h9, 10, 11, 12, 20 light chain variable
domain nucleic acid Q100 LELK

<400> 283
gccatccagt tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgca gggccagtca gagtattggc acaaacatac actggtacca gcagaaacct 120
ggccaggctc ccaggctcct catctattat gcttctgagt ctatctctgg gatcccacct 180
cgattcagtg gcagcgggtc tgggacagac ttcactctca ccatcagcag actggagcct 240
gaagattttg cagtgtatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagc tggagctgaa a 321

<210> 284
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h9, 10, 11, 12, 20 light chain variable
domain amino acid Q100 LELK

<400> 284
Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
20 25 30
Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Pro Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
65 70 75 80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
85 90 95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Leu Lys
100 105

<210> 285
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> FEP-h13, 14, 15, 16, 21 light chain nucleic acid
Q100 VEIK

<220>
<221> V_region
<222> (1)...(321)

<220>
<221> C_region
<222> (322)...(642)

<400> 285
gccatccagt tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgca gggccagtca gagtattggc acaaacatac actggtacca gcagaaacct 120
ggccaggctc ccaggctcct catctattat gcttctgagt ctatctctgg gatcccagac 180
aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag actggagcct 240
gaagattttg cagtgtatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagg tggaaatcaa acgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 286
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h13, 14, 15, 16, 21 light chain amino acid
Q100 VEIK

<220>
<221> DOMAIN
<222> (1)...(107)
<223> variable domain

<220>
<221> DOMAIN
<222> (108)...(214)
<223> constant domain

<400> 286
Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
20 25 30
Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Asp Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
65 70 75 80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205
Phe Asn Arg Gly Glu Cys
210

<210> 287
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> FEP-h13, 14, 15, 16, 21 light chain variable
domain nucleic acid Q100 VEIK

<400> 287
gccatccagt tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgca gggccagtca gagtattggc acaaacatac actggtacca gcagaaacct 120
ggccaggctc ccaggctcct catctattat gcttctgagt ctatctctgg gatcccagac 180
aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag actggagcct 240
gaagattttg cagtgtatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagg tggaaatcaa a 321

<210> 288
<211> 107
<212> PRT

<213> Artificial Sequence

<220>
<223> FEP-h13, 14, 15, 16, 21 light chain variable
domain amino acid Q100 VEIK

<400> 288
Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
            20   25   30
Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35   40   45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Asp Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
65   70   75   80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 289
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h13, 14, 15, 16, 21 light chain variable
domain amino acid A100 LELK

<400> 289
Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
            20   25   30
Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35   40   45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Asp Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
65   70   75   80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
                85   90   95
Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
            100   105

<210> 290
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> FEP-h13, 14, 15, 16, 21 light chain variable
domain nucleic acid Q100 LELK

<400> 290
gccatccagt tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgca gggccagtca gagtattggc acaaacatac actggtacca gcagaaacct 120
ggccaggctc ccaggctcct catctattat gcttctgagt ctatctctgg gatcccagac 180
aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag actggagcct 240
gaagattttg cagtgtatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagc tggagctgaa a   321

<210> 291
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h13, 14, 15, 16, 21 light chain variable
domain amino acid Q100 LELK

<400> 291
Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
            20   25   30
Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35   40   45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Asp Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
65   70   75   80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Leu Lys
            100   105

<210> 292
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> FEP-h17 light chain nucleic acid Q100 VEIK

<220>
<221> V_region
<222> (1)...(321)

<220>
<221> C_region
<222> (322)...(642)

<400> 292
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ggccaggctc ccaggctcct catctattat gcttctgagt ctatctctgg gatcccagcc 180
aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct 240
gaagattttg cagtttatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagg tggaaatcaa acgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt   642

<210> 293
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h17 light chain amino acid Q100 VEIK

<220>

<221> DOMAIN
<222> (1)...(107)
<223> variable domain

<220>
<221> DOMAIN
<222> (108)...(214)
<223> constant domain

<400> 293
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1   5   10   15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
            20   25   30
Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35   40   45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65   70   75   80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100   105   110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115   120   125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130   135   140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145   150   155   160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165   170   175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180   185   190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195   200   205
Phe Asn Arg Gly Glu Cys
    210

<210> 294
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> FEP-h17 light chain variable domain nucleic acid
      Q100 VEIK

<400> 294
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ggccaggctc ccaggctcct catctattat gcttctgagt ctatctctgg gatcccagcc 180
aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct 240
gaagattttg cagtttatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagg tggaaatcaa a   321

<210> 295
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h17 light chain variable domain amino acid
      Q100 VEIK

<400> 295
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1   5   10   15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
            20   25   30
Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35   40   45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65   70   75   80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 296
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h17 light chain variable domain amino acid
      A100 LELK

<400> 296
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1   5   10   15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
            20   25   30
Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35   40   45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65   70   75   80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
                85   90   95
Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
            100   105

<210> 297
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> FEP-h17 light chain variable domain nucleic acid
      Q100 LELK

<400> 297
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ggccaggctc ccaggctcct catctattat gcttctgagt ctatctctgg gatcccagcc 180
aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct 240
gaagattttg cagtttatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagc tggagctgaa a   321

<210> 298
<211> 107
<212> PRT
<213> Artificial Sequence

<220>

<223> FEP-h17 light chain variable domain amino acid Q100 LELK

<400> 298

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 1               5                  10                  15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
            20                  25                  30
Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35                  40                  45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65                  70                  75                  80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
                85                  90                  95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Leu Lys
            100                 105
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<210> 299
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> FEP-h18, 19 light chain nucleic acid Q100 VEIK

<220>
<221> V_region
<222> (1)...(321)

<220>
<221> C_region
<222> (322)...(642)

<400> 299

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gggcagtctc cacagctcct gatctattat gcttctgagt ctatctctgg gatcccagac 180
aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag actggagcct 240
gaagattttg cagtgtatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagg tggaaatcaa acgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt                    642
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<210> 300
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h18, 19 light chain amino acid Q100 VEIK

<220>
<221> DOMAIN
<222> (1)...(107)
<223> variable domain

<220>
<221> DOMAIN
<222> (108)...(214)

<223> constant domain

<400> 300
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 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
            20   25   30
Ile His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile
        35   40   45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Asp Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
65   70   75   80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100   105   110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115   120   125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130   135   140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145   150   155   160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165   170   175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180   185   190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195   200   205
Phe Asn Arg Gly Glu Cys
    210

<210> 301
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> FEP-h18, 19 light chain variable domain nucleic
      acid Q100 VEIK

<400> 301
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aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag actggagcct 240
gaagattttg cagtgtatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagg tggaaatcaa a   321

<210> 302
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h18, 19 light chain variable domain amino acid
      Q100 VEIK

<400> 302
Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
            20   25   30
Ile His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile
        35   40   45

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

<210> 303
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h18, 19 light chain variable domain amino acid
      A100 LELK

<400> 303
Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
            20   25   30
Ile His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile
        35   40   45
Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Asp Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
65   70   75   80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
                85   90   95
Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
            100   105

<210> 304
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> FEP-h18, 19 light chain variable domain nucleic
      acid Q100 LELK

<400> 304
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gggcagtctc cacagctcct gatctattat gcttctgagt ctatctctgg gatcccagac 180
aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag actggagcct 240
gaagattttg cagtgtatta ctgtcaacaa aataataact ggccaaccac gttcggccaa 300
gggaccaagc tggagctgaa a   321

<210> 305
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> FEP-h18, 19 light chain variable domain amino acid
      Q100 LELK

<400> 305
Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15

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


<210> 306
<211> 8345
<212> DNA
<213> Artificial Sequence

<220>
<223> pcDNA3-Erbitux-LC-IRES-HC-WT


<220>
<221> sig_peptide
<222> (1126)...(1191)
<223> light chain signal sequence

<220>
<221> V_region
<222> (1192)...(1512)
<223> light chain variable domain

<220>
<221> C_region
<222> (1513)...(1833)
<223> light chain constant domain

<220>
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<223> IRES


<220>
<221> sig_peptide
<222> (2464)...(2520)
<223> heavy chain signal sequence


<220>
<221> V_region
<222> (2521)...(2877)
<223> heavy chain variable domain


<220>
<221> C_region
<222> (2878)...(3867)
<223> heavy chain constan domain


<220>
<221> misc_feature
<222> (3868)...(3891)
<223> Flag tag

<400> 306
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<211> 449
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<213> Artificial Sequence

<220>
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<220>
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<220>
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<220>
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<400> 315
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Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50                  55                  60
Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65                  70                  75                  80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
                85                  90                  95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Gln Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175
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Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
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Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
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Lys
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<210> 316
<211> 119
<212> PRT
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<220>
<223> HC-F27G/HC-Y104E heavy chain variable domain amino acid S119

<400> 316

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Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50                  55                  60
Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65                  70                  75                  80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
                85                  90                  95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Gln Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ser
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<210> 317

<211> 119
<212> PRT
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<220>
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 1   5   10   15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Gly Ser Leu Thr Asn Tyr
            20   25   30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
        35   40   45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50   55   60
Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65   70   75   80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
                85   90   95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Gln Gly
            100   105   110
Thr Leu Val Thr Val Ser Ala
        115

<210> 318
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
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<223> CH3

<400> 318
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Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Gly Ser Leu Thr Asn Tyr

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Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50                  55                  60
Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65                  70                  75                  80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
                85                  90                  95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Pro Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
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<210> 319
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<220>
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            20   25   30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
        35   40   45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50   55   60
Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65   70   75   80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
                85   90   95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Pro Gly
            100   105   110
Thr Leu Val Thr Val Ser Ser
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      domain amino acid A119

<400> 320
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Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Gly Ser Leu Thr Asn Tyr
            20   25   30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
        35   40   45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50   55   60
Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65   70   75   80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
                85   90   95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Pro Gly
            100   105   110
Thr Leu Val Thr Val Ser Ala
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<210> 321
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<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> hinge region

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<223> CH2

<220>
<221> DOMAIN
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<223> CH3

<400> 321

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

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445
Lys

<210> 322
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-F27G/HC-S53G/HC-Y104E heavy chain variable domain amino acid S119

<400> 322
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
1 5 10 15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Gly Ser Leu Thr Asn Tyr
20 25 30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45
Gly Val Ile Trp Gly Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
50 55 60
Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65 70 75 80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
85 90 95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Gln Gly
100 105 110
Thr Leu Val Thr Val Ser Ser
115

<210> 323
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-F27G/HC-S53G/HC-Y104E heavy chain variable domain amino acid A119

<400> 323
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
1 5 10 15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Gly Ser Leu Thr Asn Tyr
20 25 30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45
Gly Val Ile Trp Gly Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
50 55 60
Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65 70 75 80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
85 90 95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Gln Gly
100 105 110
Thr Leu Val Thr Val Ser Ala
115

<210> 324
<211> 449

<212> PRT
<213> Artificial Sequence

<220>
<223> HC-F27G/HC-S53G/HC-Y104E/HC-Q111P heavy chain
amino acid S119

<220>
<221> DOMAIN
<222> (1)...(119)
<223> variable domain

<220>
<221> DOMAIN
<222> (120)...(217)
<223> CH1

<220>
<221> DOMAIN
<222> (218)...(232)
<223> hinge region

<220>
<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 324

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

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

<210> 325
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-F27G/HC-S53G/HC-Y104E/HC-Q111P heavy chain
variable domain amino acid S119

<400> 325
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
1 5 10 15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Gly Ser Leu Thr Asn Tyr
20 25 30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45
Gly Val Ile Trp Gly Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
50 55 60
Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65 70 75 80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
85 90 95
Arg Ala Leu Thr Tyr Tyr Asp Glu Glu Phe Ala Tyr Trp Gly Pro Gly
100 105 110
Thr Leu Val Thr Val Ser Ser
115

<210> 326
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-F27G/HC-S53G/HC-Y104E/HC-Q111P heavy chain
variable domain amino acid A119

<400> 326
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln

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


<210> 327
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 327
Gly Gly Ser Ser Arg Ser Ser Ser Ser Gly Gly Gly Gly Ser Gly Gly
 1               5                  10                  15
Gly Gly



<210> 328
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 328
Gly Ser Gly Arg Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1               5                  10                  15


<210> 329
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 329
Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr
 1               5                  10


<210> 330
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 330
Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr Gln
```

1 5 10 15

<210> 331
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 331
Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Val Asp
1 5 10

<210> 332
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 332
Gly Ser Thr Ser Gly Ser Gly Lys Ser Ser Glu Gly Lys Gly
1 5 10

<210> 333
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 333
Lys Glu Ser Gly Ser Val Ser Ser Glu Gln Leu Ala Gln Phe Arg Ser
1 5 10 15
Leu Asp

<210> 334
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 334
Glu Ser Gly Ser Val Ser Ser Glu Glu Leu Ala Phe Arg Ser Leu Asp
1 5 10 15

<210> 335
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> c-Myc

<400> 335
Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
1 5 10

<210> 336
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> HA

<400> 336
Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
 1   5

<210> 337
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> VSV-G

<400> 337
Tyr Thr Asp Ile Glu Met Asn Arg Leu Gly Lys
 1   5   10

<210> 338
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> HSV

<400> 338
Gln Pro Glu Leu Ala Pro Glu Asp Pro Glu Asp
 1   5   10

<210> 339
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> V5

<400> 339
Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr
 1   5   10

<210> 340
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Poly Arg

<400> 340
Arg Arg Arg Arg Arg
 1   5

<210> 341

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

<220>
<223> Strep-tag-II

<400> 341
Trp Ser His Pro Gln Phe Glu Lys
 1   5

<210> 342
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> S tag

<400> 342
Lys Glu Thr Ala Ala Ala Lys Phe Glu Arg Gln His Met Asp Ser
 1   5   10   15

<210> 343
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> 3x FLAG tag

<400> 343
Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His Asp Ile Asp Tyr
 1   5   10   15
Lys Asp Asp Asp Asp Lys
            20

<210> 344
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> HAT

<400> 344
Lys Asp His Leu Ile His Asn Val His Lys Glu Phe His Ala His Ala
 1   5   10   15
His Asn Lys

<210> 345
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> SBP

<400> 345
Met Asp Glu Lys Thr Thr Gly Trp Arg Gly Gly His Val Val Glu Gly
 1   5   10   15
Leu Ala Gly Glu Leu Glu Gln Leu Arg Ala Arg Leu Glu His His Pro
            20   25   30

Gln Gly Gln Arg Glu Pro
        35

<210> 346
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 346
Gly Gly Gly Gly Ser
 1   5

<210> 347
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 347
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1   5   10

<210> 348
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 348
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 1   5   10   15
Gly Gly Gly Ser
            20

<210> 349
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 349
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 1   5   10   15
Gly Gly Gly Ser Gly Gly Gly Gly Ser
            20   25

<210> 350
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Modified Pseudomonas endotoxin sorting signal
            (Xaa-Asp-Glu-Leu)n, where n = 1-6

<220>
<221> REPEAT
<222> (1)...(4)
<223> occurring 1, 2, 3, 4, 5, or 6 times

<220>
<221> VARIANT
<222> (1)...(1)
<223> Xaa = Lys or Arg

<220>
<221> VARIANT
<222> (5)...(5)
<223> Xaa = Lys or Arg

<220>
<221> VARIANT
<222> (9)...(9)
<223> Xaa = Lys or Arg

<220>
<221> VARIANT
<222> (13)...(13)
<223> Xaa = Lys or Arg

<220>
<221> VARIANT
<222> (17)...(17)
<223> Xaa = Lys or Arg

<220>
<221> VARIANT
<222> (21)...(21)
<223> Xaa = Lys or Arg

<220>
<221> VARIANT
<222> (5)...(24)
<223> these amino acids can be present or absent

<400> 350
Xaa Asp Glu Leu Xaa Asp Glu Leu Xaa Asp Glu Leu Xaa Asp Glu Leu
 1   5   10   15
Xaa Asp Glu Leu Xaa Asp Glu Leu
            20

<210> 351
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Ala-Leu-Ala-Ala Peptide linker

<400> 351
Ala Leu Ala Ala
 1

<210> 352
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-S25C/HC-Y104D heavy chain amino acid S119

<220>
<221> DOMAIN
<222> (1)...(119)
<223> variable domain

<220>
<221> DOMAIN
<222> (120)...(217)
<223> CH1

<220>
<221> DOMAIN
<222> (218)...(232)
<223> hinge region

<220>
<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 352
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Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
 1               5                  10                  15
Ser Leu Ser Ile Thr Cys Thr Val Cys Gly Phe Ser Leu Thr Asn Tyr
            20                  25                  30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50                  55                  60
Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65                  70                  75                  80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
                85                  90                  95
Arg Ala Leu Thr Tyr Tyr Asp Asp Glu Phe Ala Tyr Trp Gly Gln Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
```

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

<210> 353
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-S53G/HC-Y104D heavy chain amino acid S119

<220>
<221> DOMAIN
<222> (1)...(119)
<223> variable domain

<220>
<221> DOMAIN
<222> (120)...(217)
<223> CH1

<220>
<221> DOMAIN
<222> (218)...(232)
<223> hinge region

<220>
<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 353
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
1 5 10 15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30

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

<210> 354
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-S53G/HC-Y104D/HC-Q111P heavy chain amino acid S119

<220>
<221> DOMAIN

<222> (1)...(119)
<223> variable domain

<220>
<221> DOMAIN
<222> (120)...(217)
<223> CH1

<220>
<221> DOMAIN
<222> (218)...(232)
<223> hinge region

<220>
<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 354
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
 1   5   10   15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
            20   25   30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
        35   40   45
Gly Val Ile Trp Gly Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50   55   60
Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65   70   75   80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
                85   90   95
Arg Ala Leu Thr Tyr Tyr Asp Asp Glu Phe Ala Tyr Trp Gly Pro Gly
            100   105   110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115   120   125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130   135   140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145   150   155   160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165   170   175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180   185   190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195   200   205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210   215   220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225   230   235   240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245   250   255
Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser His Glu Asp
            260   265   270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275   280   285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290   295   300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305   310   315   320
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325   330   335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr

```
            340                 345                 350
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
Lys
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<210> 355
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<220>
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<220>
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<220>
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<222> (233)...(342)
<223> CH2

<220>
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<222> (343)...(449)
<223> CH3

<400> 355

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

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        115                 120                 125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
Lys
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<210> 356
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-S25V/HC-Y104D/HC-Q111P heavy chain amino acid
S119

<220>
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<223> CH1

<220>
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<223> hinge region

<220>
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<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 356
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Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
 1               5                  10                  15
Ser Leu Ser Ile Thr Cys Thr Val Val Gly Phe Ser Leu Thr Asn Tyr
            20                  25                  30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50                  55                  60
Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65                  70                  75                  80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
                85                  90                  95
Arg Ala Leu Thr Tyr Tyr Asp Asp Glu Phe Ala Tyr Trp Gly Pro Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430
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Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435   440   445
Lys

<210> 357
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-S25V/HC-S53G/HC-Y104D heavy chain amino acid
      S119

<220>
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<223> CH1

<220>
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<223> hinge region

<220>
<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 357
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
 1   5   10   15
Ser Leu Ser Ile Thr Cys Thr Val Val Gly Phe Ser Leu Thr Asn Tyr
            20   25   30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
        35   40   45
Gly Val Ile Trp Gly Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50   55   60
Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65   70   75   80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
                85   90   95
Arg Ala Leu Thr Tyr Tyr Asp Asp Glu Phe Ala Tyr Trp Gly Gln Gly
            100   105   110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115   120   125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130   135   140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145   150   155   160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165   170   175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180   185   190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro

```
        195                 200                 205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
Lys
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<210> 358
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-S25V/HC-S53G/HC-Y104D/HC-Q111P heavy chain
amino acid S119

<220>
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<220>
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<223> CH1

<220>
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<223> hinge region

<220>
<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN

<222> (343)...(449)
<223> CH3

<400> 358
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
 1   5   10   15
Ser Leu Ser Ile Thr Cys Thr Val Val Gly Phe Ser Leu Thr Asn Tyr
            20   25   30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
        35   40   45
Gly Val Ile Trp Gly Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50   55   60
Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65   70   75   80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
                85   90   95
Arg Ala Leu Thr Tyr Tyr Asp Asp Glu Phe Ala Tyr Trp Gly Pro Gly
            100   105   110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115   120   125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130   135   140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145   150   155   160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165   170   175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180   185   190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195   200   205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210   215   220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225   230   235   240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245   250   255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260   265   270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275   280   285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290   295   300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305   310   315   320
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325   330   335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340   345   350
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355   360   365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370   375   380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385   390   395   400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405   410   415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420   425   430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435   440   445
Lys

<210> 359
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<212> PRT
<213> Artificial Sequence

<220>
<223> HC-T30F/HC-Y104D heavy chain amino acid S119

<220>
<221> DOMAIN
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<222> (120)...(217)
<223> CH1

<220>
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<223> hinge region

<220>
<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
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<222> (343)...(449)
<223> CH3

<400> 359
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Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
 1               5                  10                  15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Phe Asn Tyr
            20                  25                  30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50                  55                  60
Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65                  70                  75                  80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
                85                  90                  95
Arg Ala Leu Thr Tyr Tyr Asp Asp Glu Phe Ala Tyr Trp Gly Gln Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285
```

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

<210> 360
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-T30F/HC-Y104D/HC-Q111P heavy chain amino acid
S119

<220>
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<220>
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<223> CH1

<220>
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<222> (218)...(232)
<223> hinge region

<220>
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<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 360
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
1 5 10 15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Phe Asn Tyr
20 25 30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr

```
    50                  55                  60
Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65                  70                  75                  80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
                85                  90                  95
Arg Ala Leu Thr Tyr Tyr Asp Asp Glu Phe Ala Tyr Trp Gly Pro Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
Lys
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<210> 361
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-T30F/HC-S53G/HC-Y104D heavy chain amino acid S119

<220>
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<223> CH1

<220>
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<223> hinge region

<220>
<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 361

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

```
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
Lys
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<210> 362
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-T30F/HC-S53G/HC-Y104D/HC-Q111P heavy chain amino acid S119

<220>
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<220>
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<223> CH1

<220>
<221> DOMAIN
<222> (218)...(232)
<223> hinge region

<220>
<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 362

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

```
    130                 135                 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
Lys



<210> 363
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-D72L/HC-Y104D heavy chain amino acid S119


<220>
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<220>
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<222> (218)...(232)
<223> hinge region

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<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
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<222> (343)...(449)
<223> CH3

<400> 363

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

<210> 364
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
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S119

<220>
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<220>
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<223> hinge region

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<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 364
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
 1   5   10   15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
            20   25   30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
        35   40   45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50   55   60
Ser Arg Leu Ser Ile Asn Lys Leu Asn Ser Lys Ser Gln Val Phe Phe
65   70   75   80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
                85   90   95
Arg Ala Leu Thr Tyr Tyr Asp Asp Glu Phe Ala Tyr Trp Gly Pro Gly
            100   105   110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115   120   125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130   135   140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145   150   155   160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165   170   175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180   185   190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195   200   205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210   215   220

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



<210> 365
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-S53G/HC-D72L/HC-Y104D heavy chain amino acid
      S119


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<220>
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<223> CH1

<220>
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<222> (218)...(232)
<223> hinge region

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<222> (233)...(342)
<223> CH2


<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3
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<400> 365
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
 1   5   10   15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
            20   25   30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
        35   40   45
Gly Val Ile Trp Gly Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50   55   60
Ser Arg Leu Ser Ile Asn Lys Leu Asn Ser Lys Ser Gln Val Phe Phe
65   70   75   80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
                85   90   95
Arg Ala Leu Thr Tyr Tyr Asp Asp Glu Phe Ala Tyr Trp Gly Gln Gly
            100   105   110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115   120   125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130   135   140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145   150   155   160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165   170   175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180   185   190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195   200   205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210   215   220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225   230   235   240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245   250   255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260   265   270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275   280   285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290   295   300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305   310   315   320
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325   330   335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340   345   350
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355   360   365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370   375   380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385   390   395   400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405   410   415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420   425   430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435   440   445
Lys

<210> 366
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-S53G/HC-D72L/HC-Y104D/HC-Q111P heavy chain

amino acid S119

<220>
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<223> CH1

<220>
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<223> hinge region

<220>
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<220>
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<223> CH3

<400> 366

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

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

<210> 367
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-F27G/HC-Y104D heavy chain amino acid S119

<220>
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<220>
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<223> CH1

<220>
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<222> (218)...(232)
<223> hinge region

<220>
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<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 367
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
1 5 10 15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Gly Ser Leu Thr Asn Tyr
20 25 30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
50 55 60
Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65 70 75 80

```
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
                85                  90                  95
Arg Ala Leu Thr Tyr Tyr Asp Asp Glu Phe Ala Tyr Trp Gly Gln Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
Lys
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<210> 368
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> HC-F27G/HC-Y104D/HC-Q111P heavy chain amino acid S119

<220>
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<223> CH1

<220>
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<222> (218)...(232)
<223> hinge region

<220>
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<223> CH2

<220>
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<222> (343)...(449)
<223> CH3

<400> 368

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

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

<210> 369
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> hinge region

<220>
<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 369
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
1 5 10 15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Gly Ser Leu Thr Asn Tyr
20 25 30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45
Gly Val Ile Trp Gly Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
50 55 60
Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65 70 75 80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
85 90 95
Arg Ala Leu Thr Tyr Tyr Asp Asp Glu Phe Ala Tyr Trp Gly Gln Gly
100 105 110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
130 135 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

```
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
Lys
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<210> 370
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
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amino acid S119

<220>
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<220>
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<223> CH1

<220>
<221> DOMAIN
<222> (218)...(232)
<223> hinge region

<220>
<221> DOMAIN
<222> (233)...(342)

<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 370

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Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
 1               5                  10                  15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Gly Ser Leu Thr Asn Tyr
            20                  25                  30
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45
Gly Val Ile Trp Gly Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50                  55                  60
Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65                  70                  75                  80
Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
                85                  90                  95
Arg Ala Leu Thr Tyr Tyr Asp Asp Glu Phe Ala Tyr Trp Gly Pro Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
Lys
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<210> 371
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> DP-h1, 2, 4, 5, 6, 8 heavy chain nucleic acid S119

<220>
<221> V_region
<222> (1)...(357)

<220>
<221> C_region
<222> (358)...(1347)

<400> 371
caggtacagc tgcagcagtc aggtccagga ctggtgaagc cctcgcagac cctctcactc 60
acctgtgcca tctctggttt ctcattaact aactatggtg tacactggat ccgccagccc 120
ccagggaagg ggctggagtg gattggtgtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagatt caccatctcc agagatgatt caaagaacac ggcgtatctg 240
caaatgaaca gcctgaaaac cgaggacacg gccgtgtatt actgtgccag agccctcacc 300
tactatgatg atgagtttgc ttactggggc cctggaacgc tggtcaccgt cagctcagcc 360
tccaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480
aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540
ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600
atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 660
tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 720
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780
gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960
tacaagtgca aggtcagcaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1020
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1080
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320
aagagcctct ccctgtctcc gggtaaa 1347

<210> 372
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> DP-h1, 2, 4, 5, 6, 8 heavy chain amino acid S119

<220>
<221> DOMAIN
<222> (1)...(119)
<223> variable domain

<220>
<221> DOMAIN
<222> (120)...(217)
<223> CH1

<220>
<221> DOMAIN
<222> (218)...(232)
<223> hinge region

<220>

<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 372

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Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1               5                  10                  15
Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Phe Ser Leu Thr Asn Tyr
            20                  25                  30
Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
        35                  40                  45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50                  55                  60
Ser Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu
65                  70                  75                  80
Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95
Arg Ala Leu Thr Tyr Tyr Asp Asp Glu Phe Ala Tyr Trp Gly Pro Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
Lys
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<210> 373
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> DP-h9, 12, 14 heavy chain nucleic acid S119

<220>
<221> V_region
<222> (1)...(357)

<220>
<221> C_region
<222> (358)...(1347)

<400> 373
gaggtccagc tggtacagtc tggggctgag gtgaagaagc ctggggctac agtgaaaatc 60
tcctgcaagg tttctggttt ctcattaact aactatggtg tacactggat caggcagtcc 120
ccatcgagag gccttgagtg gctgggtgtg atatggagtg gtggaaatac agactataat 180
acacctttca catccagact caccatctcc aaggacacct ccaaaaacca ggtggtcctt 240
acaatgacca acatggaccc tgtggacaca gccacgtatt actgtgccag agccctcacc 300
tactatgatg atgagtttgc ttactggggc cctggaacgc tggtcaccgt cagctcagcc 360
tccaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480
aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540
ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600
atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 660
tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 720
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780
gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960
tacaagtgca aggtcagcaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1020
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1080
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320
aagagcctct ccctgtctcc gggtaaa 1347

<210> 374
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> DP-h9, 12, 14 heavy chain amino acid S119

<220>
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<222> (1)...(119)
<223> variable domain

<220>
<221> DOMAIN
<222> (120)...(217)
<223> CH1

<220>
<221> DOMAIN
<222> (218)...(232)
<223> hinge region

<220>

<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 374

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Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1               5                  10                  15
Thr Val Lys Ile Ser Cys Lys Val Ser Gly Phe Ser Leu Thr Asn Tyr
            20                  25                  30
Gly Val His Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu Trp Leu
        35                  40                  45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50                  55                  60
Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val Val Leu
65                  70                  75                  80
Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala
                85                  90                  95
Arg Ala Leu Thr Tyr Tyr Asp Asp Glu Phe Ala Tyr Trp Gly Pro Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
Lys
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<210> 375
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> DP-h10, 13 heavy chain nucleic acid S119

<220>
<221> V_region
<222> (1)...(357)

<220>
<221> C_region
<222> (358)...(1347)

<400> 375
gaggtccagc tggtacagtc tggggctgag gtgaagaagc ctggggctac agtgaaaatc 60
tcctgcaagg tttctggttt ctcattaact aactatggtg tacactggat ccgccagccc 120
ccagggaagg ggctggagtg gattggtgtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagatt caccatctcc agagacaacg ccaagaactc actgtatctg 240
caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgccag agccctcacc 300
tactatgatg atgagtttgc ttactggggc cctggaacgc tggtcaccgt cagctcagcc 360
tccaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480
aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540
ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600
atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 660
tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 720
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780
gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960
tacaagtgca aggtcagcaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1020
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1080
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320
aagagcctct ccctgtctcc gggtaaa 1347

<210> 376
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> DP-h10, 13 heavy chain amino acid S119

<220>
<221> DOMAIN
<222> (1)...(119)
<223> variable domain

<220>
<221> DOMAIN
<222> (120)...(217)
<223> CH1

<220>
<221> DOMAIN
<222> (218)...(232)
<223> hinge region

<220>

<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 376

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Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1               5                  10                  15
Thr Val Lys Ile Ser Cys Lys Val Ser Gly Phe Ser Leu Thr Asn Tyr
            20                  25                  30
Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
        35                  40                  45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50                  55                  60
Ser Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65                  70                  75                  80
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95
Arg Ala Leu Thr Tyr Tyr Asp Asp Glu Phe Ala Tyr Trp Gly Pro Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
Lys
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<210> 377
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> FDP-h1, 19, 20, 21 heavy chain nucleic acid S119

<220>
<221> V_region
<222> (1)...(357)

<220>
<221> C_region
<222> (358)...(1347)

<400> 377
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tcctgcaagg tttctggttt ctcattattt aactatggtg tacactggat ccgccagccc 120
ccagggaagg ggctggagtg gattggtgtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240
caaatgaaca gcctgagagc cgaggacacg gccgtgtatt actgtgccag agccctcacc 300
tactatgatg atgagtttgc ttactggggc cctggaacgc tggtcaccgt cagctcagcc 360
tccaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480
aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540
ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600
atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 660
tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 720
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780
gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960
tacaagtgca aggtcagcaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1020
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1080
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320
aagagcctct ccctgtctcc gggtaaa 1347

<210> 378
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> FDP-h1, 19, 20, 21 heavy chain amino acid S119

<220>
<221> DOMAIN
<222> (1)...(119)
<223> variable domain

<220>
<221> DOMAIN
<222> (120)...(217)
<223> CH1

<220>
<221> DOMAIN
<222> (218)...(232)
<223> hinge region

<220>

<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 378

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Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1               5                  10                  15
Thr Val Lys Ile Ser Cys Lys Val Ser Gly Phe Ser Leu Phe Asn Tyr
            20                  25                  30
Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
        35                  40                  45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50                  55                  60
Ser Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65                  70                  75                  80
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95
Arg Ala Leu Thr Tyr Tyr Asp Asp Glu Phe Ala Tyr Trp Gly Pro Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
Lys
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<210> 379
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> FDP-h2 heavy chain nucleic acid S119

<220>
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<222> (1)...(357)

<220>
<221> C_region
<222> (358)...(1347)

<400> 379
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tcctgcaagg tttctggttt ctcattattt aactatggtg tacactgggt gcgacaggct 120
cgtggacaac gccttgagtg gataggtgtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagatt caccatctcc agagatgatt caaagaacac ggcgtatctg 240
caaatgaaca gcctgaaaac cgaggacacg gccgtgtatt actgtgccag agccctcacc 300
tactatgatg atgagtttgc ttactggggc cctggaacgc tggtcaccgt cagctcagcc 360
tccaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480
aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540
ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600
atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 660
tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 720
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780
gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960
tacaagtgca aggtcagcaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1020
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1080
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320
aagagcctct ccctgtctcc gggtaaa 1347

<210> 380
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> FDP-h2 heavy chain amino acid S119

<220>
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<223> variable domain

<220>
<221> DOMAIN
<222> (120)...(217)
<223> CH1

<220>
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<222> (218)...(232)
<223> hinge region

<220>

<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
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<222> (343)...(449)
<223> CH3

<400> 380

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Thr Val Lys Ile Ser Cys Lys Val Ser Gly Phe Ser Leu Phe Asn Tyr
            20                  25                  30
Gly Val His Trp Val Arg Gln Ala Arg Gly Gln Arg Leu Glu Trp Ile
        35                  40                  45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50                  55                  60
Ser Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu
65                  70                  75                  80
Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95
Arg Ala Leu Thr Tyr Tyr Asp Asp Glu Phe Ala Tyr Trp Gly Pro Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
Lys
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<210> 381
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> FDP-h4, 8, 12, 16 heavy chain nucleic acid S119

<220>
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<222> (1)...(357)

<220>
<221> C_region
<222> (358)...(1347)

<400> 381
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ccatcgagag gccttgagtg gctgggtgtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagact caccatctcc aaggacacct ccaaaaacca ggtggtcctt 240
acaatgacca acatggaccc tgtggacaca gccacgtatt actgtgccag agccctcacc 300
tactatgatg atgagtttgc ttactggggc cctggaacgc tggtcaccgt cagctcagcc 360
tccaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480
aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540
ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600
atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 660
tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 720
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780
gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960
tacaagtgca aggtcagcaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1020
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1080
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320
aagagcctct ccctgtctcc gggtaaa 1347

<210> 382
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> FDP-h4, 8, 12, 16 heavy chain amino acid S119

<220>
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<223> variable domain

<220>
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<222> (120)...(217)
<223> CH1

<220>
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<222> (218)...(232)
<223> hinge region

<220>

<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 382

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Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1               5                  10                  15
Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Phe Ser Leu Phe Asn Tyr
            20                  25                  30
Gly Val His Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu Trp Leu
        35                  40                  45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50                  55                  60
Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val Val Leu
65                  70                  75                  80
Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala
                85                  90                  95
Arg Ala Leu Thr Tyr Tyr Asp Asp Glu Phe Ala Tyr Trp Gly Pro Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
Lys
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<210> 383
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> FDP-h5, 9, 13, 17 heavy chain nucleic acid S119

<220>
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<222> (1)...(357)

<220>
<221> C_region
<222> (358)...(1347)

<400> 383
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tcctgcaagg tttctggttt ttcattattt aactatggtg tacactggat ccgccagccc 120
ccagggaagg ggctggagtg gattggtgtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240
caaatgaaca gcctgagagc cgaggacacg gccgtgtatt actgtgccag agccctcacc 300
tactatgatg atgagtttgc ttactggggc cctggaacgc tggtcaccgt cagctcagcc 360
tccaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480
aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540
ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600
atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 660
tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 720
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780
gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960
tacaagtgca aggtcagcaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1020
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1080
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320
aagagcctct ccctgtctcc gggtaaa 1347

<210> 384
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> FDP-h5, 9, 13, 17 heavy chain amino acid S119

<220>
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<223> variable domain

<220>
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<222> (120)...(217)
<223> CH1

<220>
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<222> (218)...(232)
<223> hinge region

<220>

<221> DOMAIN
<222> (233)...(342)
<223> CH3

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 384

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Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1               5                  10                  15
Thr Val Lys Ile Ser Cys Lys Val Ser Gly Phe Ser Leu Phe Asn Tyr
            20                  25                  30
Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
        35                  40                  45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50                  55                  60
Ser Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65                  70                  75                  80
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95
Arg Ala Leu Thr Tyr Tyr Asp Asp Glu Phe Ala Tyr Trp Gly Pro Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
Lys
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<210> 385
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> FDP-h6 heavy chain nucleic acid S119

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<220>
<221> C_region
<222> (358)...(1347)

<400> 385
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ccatcgagag gccttgagtg gctgggtgtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240
caaatgaaca gcctgagagc cgaggacacg gccgtgtatt actgtgccag agccctcacc 300
tactatgatg atgagtttgc ttactggggc cctggaacgc tggtcaccgt cagctcagcc 360
tccaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480
aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540
ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600
atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 660
tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 720
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780
gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960
tacaagtgca aggtcagcaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1020
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1080
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320
aagagcctct ccctgtctcc gggtaaa 1347

<210> 386
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> FDP-h6 heavy chain amino acid S119

<220>
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<223> variable domain

<220>
<221> DOMAIN
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<223> CH1

<220>
<221> DOMAIN
<222> (218)...(232)
<223> hinge region

<220>

<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 386

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Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1               5                  10                  15
Thr Val Lys Ile Ser Cys Lys Val Ser Gly Phe Ser Leu Phe Asn Tyr
            20                  25                  30
Gly Val His Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu Trp Leu
        35                  40                  45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50                  55                  60
Ser Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65                  70                  75                  80
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95
Arg Ala Leu Thr Tyr Tyr Asp Asp Glu Phe Ala Tyr Trp Gly Pro Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
Lys
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<210> 387
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> FDP-h10, 14, 18 heavy chain nucleic acid S119

<220>
<221> V_region
<222> (1)...(357)

<220>
<221> C_region
<222> (358)...(1347)

<400> 387
gaggtccagc tggtacagtc tggggctgag gtgaagaagc ctggggctac agtgaaaatc 60
tcctgcaagg tttctggttt ctcattattt aactatggtg tacactggat ccgccagccc 120
ccagggaagg ggctggagtg gattggtgtg atatggagtg gtggaaacac agactataat 180
acacctttca catccagatt caccatctcc agagatgatt caaagaacac ggcgtatctg 240
caaatgaaca gcctgaaaac cgaggacacg gccgtgtatt actgtgccag agccctcacc 300
tactatgatg atgagtttgc ttactggggc cctggaacgc tggtcaccgt cagctcagcc 360
tccaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480
aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540
ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600
atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 660
tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 720
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780
gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960
tacaagtgca aggtcagcaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1020
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1080
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320
aagagcctct ccctgtctcc gggtaaa 1347

<210> 388
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> FDP-h10, 14, 18 heavy chain amino acid S119

<220>
<221> DOMAIN
<222> (1)...(119)
<223> variable domain

<220>
<221> DOMAIN
<222> (120)...(217)
<223> CH1

<220>
<221> DOMAIN
<222> (218)...(232)
<223> hinge region

<220>

<221> DOMAIN
<222> (233)...(342)
<223> CH2

<220>
<221> DOMAIN
<222> (343)...(449)
<223> CH3

<400> 388

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Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1               5                  10                  15
Thr Val Lys Ile Ser Cys Lys Val Ser Gly Phe Ser Leu Phe Asn Tyr
            20                  25                  30
Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
        35                  40                  45
Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50                  55                  60
Ser Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu
65                  70                  75                  80
Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95
Arg Ala Leu Thr Tyr Tyr Asp Asp Glu Phe Ala Tyr Trp Gly Pro Gly
            100                 105                 110
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
Lys
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<210> 389
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> Bryodin

<400> 389
Asp Val Ser Phe Arg Leu Ser Gly Ala Thr Thr Thr Ser Tyr Gly Val
 1   5   10   15
Phe Ile Lys Asn Leu Arg Glu Ala Leu Pro Tyr Glu Arg Lys Val Tyr
            20   25   30
Asn Ile Pro Leu Leu Arg Ser Ser Ile Ser Gly Arg Tyr Thr Leu Leu
        35   40   45
His Leu Thr Asn Tyr Ala Asp Glu Thr Ile Ser Val Ala Val Asp Val
    50   55   60
Thr Asn Val Tyr Ile Met Gly Tyr Leu Ala Gly Asp Val Ser Tyr Phe
65   70   75   80
Phe Asn Glu Ala Ser Ala Thr Glu Ala Ala Lys Phe Val Phe Lys Asp
                85   90   95
Ala Lys Lys Lys Val Thr Leu Pro Tyr Ser Gly Asn Tyr Glu Arg Leu
            100   105   110
Gln Thr Ala Ala Gly Lys Ile Arg Glu Asn Ile Pro Leu Gly Leu Pro
        115   120   125
Ala Leu Asp Ser Ala Ile Thr Thr Leu Tyr Tyr Tyr Thr Ala Ser Ser
    130   135   140
Ala Ala Ser Ala Leu Leu Val Leu Ile Gln Ser Thr Ala Glu Ser Ala
145   150   155   160
Arg Tyr Lys Phe Ile Glu Gln Gln Ile Gly Lys Arg Val Asp Lys Thr
                165   170   175
Phe Leu Pro Ser Leu Ala Thr Ile Ser Leu Glu Asn Asn Trp Ser Ala
            180   185   190
Leu Ser Lys Gln Ile Gln Ile Ala Ser Thr Asn Asn Gly Gln Phe Glu
        195   200   205
Ser Pro Val Val Leu Ile Asp Gly Asn Asn Gln Arg Val Ser Ile Thr
    210   215   220
Asn Ala Ser Ala Arg Val Val Thr Ser Asn Ile Ala Leu Leu Leu Asn
225   230   235   240
Arg Asn Asn Ile Ala
                245

<210> 390
<211> 274
<212> PRT
<213> Artificial Sequence

<220>
<223> Saporin-6

<400> 390
Val Thr Ser Ile Thr Leu Asp Leu Val Asn Pro Thr Ala Gly Gln Tyr
 1   5   10   15
Ser Ser Phe Val Asp Lys Ile Arg Asn Asn Val Lys Asp Pro Asn Leu
            20   25   30
Lys Tyr Gly Gly Thr Asp Ile Ala Val Ile Pro Pro Ser Lys Glu Lys
        35   40   45
Phe Leu Arg Ile Asn Phe Gln Ser Ser Arg Gly Thr Val Ser Leu Gly
    50   55   60
Leu Lys Arg Asp Asn Leu Tyr Val Val Ala Tyr Leu Ala Met Asp Asn
65   70   75   80
Thr Asn Val Asn Arg Ala Tyr Tyr Phe Arg Ser Glu Ile Thr Ser Ala
                85   90   95

```
Glu Ser Thr Ala Leu Phe Pro Glu Ala Thr Thr Ala Asn Gln Lys Ala
            100                 105                 110
Leu Glu Tyr Thr Glu Asp Tyr Gln Ser Ile Glu Lys Asn Ala Gln Ile
        115                 120                 125
Thr Gln Gly Asp Gln Ser Arg Lys Glu Leu Gly Leu Gly Ile Asp Leu
    130                 135                 140
Leu Ser Thr Ser Met Glu Ala Val Asn Lys Lys Ala Arg Val Val Lys
145                 150                 155                 160
Asp Glu Ala Arg Phe Leu Leu Ile Ala Ile Gln Met Thr Ala Glu Ala
                165                 170                 175
Ala Arg Phe Arg Tyr Ile Gln Asn Leu Val Ile Lys Asn Phe Pro Asn
            180                 185                 190
Lys Phe Asn Ser Glu Asn Lys Val Ile Gln Phe Glu Val Asn Trp Lys
        195                 200                 205
Lys Ile Ser Thr Ala Ile Tyr Gly Asp Ala Lys Asn Gly Val Phe Asn
    210                 215                 220
Lys Asp Tyr Asp Phe Gly Phe Gly Lys Val Arg Gln Val Lys Asp Leu
225                 230                 235                 240
Gln Met Gly Leu Leu Met Tyr Leu Gly Lys Pro Lys Ser Ser Asn Glu
                245                 250                 255
Ala Asn Ser Thr Val Arg His Tyr Gly Pro Leu Lys Pro Thr Leu Leu
            260                 265                 270
Ile Thr
```

<210> 391
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-Viral Protein MAP

<400> 391

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

<210> 392
<211> 293
<212> PRT
<213> Artificial Sequence

<220>
<223> Shiga Toxin A-Chain

<400> 392
Lys Glu Phe Thr Leu Asp Phe Ser Thr Ala Lys Thr Tyr Val Asp Ser
 1   5   10   15
Leu Asn Val Ile Arg Ser Ala Ile Gly Thr Pro Leu Gln Thr Ile Ser
            20   25   30
Ser Gly Gly Thr Ser Leu Leu Met Ile Asp Ser Gly Thr Gly Asp Asn
        35   40   45
Leu Phe Ala Val Asp Val Arg Gly Ile Asp Pro Glu Glu Gly Arg Phe
    50   55   60
Asn Asn Leu Arg Leu Ile Val Glu Arg Asn Asn Leu Tyr Val Thr Gly
65   70   75   80
Phe Val Asn Arg Thr Asn Asn Val Phe Tyr Arg Phe Ala Asp Phe Ser
                85   90   95
His Val Thr Phe Pro Gly Thr Thr Ala Val Thr Leu Ser Gly Asp Ser
            100   105   110
Ser Tyr Thr Thr Leu Gln Arg Val Ala Gly Ile Ser Arg Thr Gly Met
        115   120   125
Gln Ile Asn Arg His Ser Leu Thr Thr Ser Tyr Leu Asp Leu Met Ser
    130   135   140
His Ser Gly Thr Ser Leu Thr Gln Ser Val Ala Arg Ala Met Leu Arg
145   150   155   160
Phe Val Thr Val Thr Ala Glu Ala Leu Arg Phe Arg Gln Ile Gln Arg
                165   170   175
Gly Phe Arg Thr Thr Leu Asp Asp Leu Ser Gly Arg Ser Tyr Val Met
            180   185   190
Thr Ala Glu Asp Val Asp Leu Thr Leu Asn Trp Gly Arg Leu Ser Ser
        195   200   205
Val Leu Pro Asp Tyr His Gly Gln Asp Ser Val Arg Val Gly Arg Ile
    210   215   220
Ser Phe Gly Ser Ile Asn Ala Ile Leu Gly Ser Val Ala Leu Ile Leu
225   230   235   240
Asn Cys His His His Ala Ser Arg Val Ala Arg Met Ala Ser Asp Glu
                245   250   255
Phe Pro Ser Met Cys Pro Ala Asp Gly Arg Val Arg Gly Ile Thr His
            260   265   270
Asn Lys Ile Leu Trp Asp Ser Ser Thr Leu Gly Ala Ile Leu Met Arg
        275   280   285
Arg Thr Ile Ser Ser
    290

<210> 393
<211> 319
<212> PRT
<213> Artificial Sequence

<220>
<223> Shiga-Like Toxin Subunit A (Verotoxin 2)

<400> 393
Met Lys Cys Ile Leu Phe Lys Trp Val Leu Cys Leu Leu Leu Gly Phe
 1   5   10   15
Ser Ser Val Ser Tyr Ser Arg Glu Phe Thr Ile Asp Phe Ser Thr Gln
            20   25   30
Gln Ser Tyr Val Ser Ser Leu Asn Ser Ile Arg Thr Glu Ile Ser Thr
        35   40   45
Pro Leu Glu His Ile Ser Gln Gly Thr Thr Ser Val Ser Val Ile Asn
    50   55   60
His Thr Pro Pro Gly Ser Tyr Phe Ala Val Asp Ile Arg Gly Leu Asp

65 70 75 80
Val Tyr Gln Ala Arg Phe Asp His Leu Arg Leu Ile Ile Glu Gln Asn
85 90 95
Asn Leu Tyr Val Ala Gly Phe Val Asn Thr Ala Thr Asn Thr Phe Tyr
100 105 110
Arg Phe Ser Asp Phe Thr His Ile Ser Val Pro Gly Val Thr Thr Val
115 120 125
Ser Met Thr Thr Asp Ser Ser Tyr Thr Thr Leu Gln Arg Val Ala Ala
130 135 140
Leu Glu Arg Ser Gly Met Gln Ile Ser Arg His Ser Leu Val Ser Ser
145 150 155 160
Tyr Leu Ala Leu Met Glu Phe Ser Gly Asn Thr Met Thr Arg Asp Ala
165 170 175
Ser Arg Ala Val Leu Arg Phe Val Thr Val Thr Ala Glu Ala Leu Arg
180 185 190
Phe Arg Gln Ile Gln Arg Glu Phe Arg Gln Ala Leu Ser Glu Thr Ala
195 200 205
Pro Val Tyr Thr Met Thr Pro Gly Asp Val Asp Leu Thr Leu Asn Trp
210 215 220
Gly Arg Ile Ser Asn Val Leu Pro Glu Tyr Arg Gly Glu Asp Gly Val
225 230 235 240
Arg Val Gly Arg Ile Ser Phe Asn Asn Ile Ser Ala Ile Leu Gly Thr
245 250 255
Val Ala Val Ile Leu Asn Cys His His Gln Gly Ala Arg Ser Val Arg
260 265 270
Ala Val Asn Glu Glu Ser Gln Pro Glu Cys Gln Ile Thr Gly Asp Arg
275 280 285
Pro Val Ile Lys Ile Asn Asn Thr Leu Trp Glu Ser Asn Thr Ala Ala
290 295 300
Ala Phe Leu Asn Arg Lys Ser Gln Phe Leu Tyr Thr Thr Gly Lys
305 310 315

<210> 394
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> Trichosanthin

<400> 394
Asp Val Ser Phe Arg Leu Ser Gly Ala Thr Ser Ser Ser Tyr Gly Val
1 5 10 15
Phe Ile Ser Asn Leu Arg Lys Ala Leu Pro Asn Glu Arg Lys Leu Tyr
20 25 30
Asp Ile Pro Leu Leu Arg Ser Ser Leu Pro Gly Ser Gln Arg Tyr Ala
35 40 45
Leu Ile His Leu Thr Asn Tyr Ala Asp Glu Thr Ile Ser Val Ala Ile
50 55 60
Asp Val Thr Asn Val Tyr Ile Met Gly Tyr Arg Ala Gly Asp Thr Ser
65 70 75 80
Tyr Phe Phe Asn Glu Ala Ser Ala Thr Glu Ala Ala Lys Tyr Val Phe
85 90 95
Lys Asp Ala Met Arg Lys Val Thr Leu Pro Tyr Ser Gly Asn Tyr Glu
100 105 110
Arg Leu Gln Thr Ala Ala Gly Lys Ile Arg Glu Asn Ile Pro Leu Gly
115 120 125
Leu Pro Ala Leu Asp Ser Ala Ile Thr Thr Leu Phe Tyr Tyr Asn Ala
130 135 140
Asn Ser Ala Ala Ser Ala Leu Met Val Leu Ile Gln Ser Thr Ser Glu
145 150 155 160
Ala Ala Arg Tyr Lys Phe Ile Glu Gln Gln Ile Gly Lys Arg Val Asp
165 170 175
Lys Thr Phe Leu Pro Ser Leu Ala Ile Ile Ser Leu Glu Asn Ser Trp
180 185 190
Ser Ala Leu Ser Lys Gln Ile Gln Ile Ala Ser Thr Asn Asn Gly Gln
195 200 205

```
Phe Glu Ser Pro Val Val Leu Ile Asn Ala Gln Asn Gln Arg Val Thr
    210                 215                 220
Ile Thr Asn Val Asp Ala Gly Val Val Thr Ser Asn Ile Ala Leu Leu
225                 230                 235                 240
Leu Asn Arg Asn Asn Met Ala
                245
```