SEQUENCE LISTING

<110> AC IMMUNE SA

GENENTECH, INC.

<120> ANTI-TAU ANTIBODIES AND METHODS OF USE

<130> 01147-0007-00PCT

<150> US 62/431,180

<151> 2016-12-07

<160> 624

<170> PatentIn version 3.5

<210> 1

<211> 456

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Human Tau sequence

<400> 1

Met His His His His His His Gly Glu Asn Leu Tyr Phe Gln Gly Ser
1 5 10 15

Ala Glu Pro Arg Gln Glu Phe Glu Val Met Glu Asp His Ala Gly Thr
20 25 30

Tyr Gly Leu Gly Asp Arg Lys Asp Gln Gly Gly Tyr Thr Met His Gln
35 40 45

Asp Gln Glu Gly Asp Thr Asp Ala Gly Leu Lys Glu Ser Pro Leu Gln
50 55 60

Thr Pro Thr Glu Asp Gly Ser Glu Glu Pro Gly Ser Glu Thr Ser Asp
65 70 75 80

Ala Lys Ser Thr Pro Thr Ala Glu Asp Val Thr Ala Pro Leu Val Asp
85 90 95

```
Glu Gly Ala Pro Gly Lys Gln Ala Ala Ala Gln Pro His Thr Glu Ile
            100                 105                 110

Pro Glu Gly Thr Thr Ala Glu Glu Ala Gly Ile Gly Asp Thr Pro Ser
        115                 120                 125

Leu Glu Asp Glu Ala Ala Gly His Val Thr Gln Ala Arg Met Val Ser
    130                 135                 140

Lys Ser Lys Asp Gly Thr Gly Ser Asp Asp Lys Lys Ala Lys Gly Ala
145                 150                 155                 160

Asp Gly Lys Thr Lys Ile Ala Thr Pro Arg Gly Ala Ala Pro Pro Gly
                165                 170                 175

Gln Lys Gly Gln Ala Asn Ala Thr Arg Ile Pro Ala Lys Thr Pro Pro
            180                 185                 190

Ala Pro Lys Thr Pro Pro Ser Ser Gly Glu Pro Pro Lys Ser Gly Asp
        195                 200                 205
```

```
Arg Ser Gly Tyr Ser Ser Pro Gly Ser Pro Gly Thr Pro Gly Ser Arg
    210                 215                 220

Ser Arg Thr Pro Ser Leu Pro Thr Pro Pro Thr Arg Glu Pro Lys Lys
225                 230                 235                 240

Val Ala Val Val Arg Thr Pro Pro Lys Ser Pro Ser Ser Ala Lys Ser
                245                 250                 255

Arg Leu Gln Thr Ala Pro Val Pro Met Pro Asp Leu Lys Asn Val Lys
            260                 265                 270

Ser Lys Ile Gly Ser Thr Glu Asn Leu Lys His Gln Pro Gly Gly Gly
        275                 280                 285

Lys Val Gln Ile Ile Asn Lys Lys Leu Asp Leu Ser Asn Val Gln Ser
    290                 295                 300
```

```
Lys Cys Gly Ser Lys Asp Asn Ile Lys His Val Pro Gly Gly Gly Ser
305                 310                 315                 320

Val Gln Ile Val Tyr Lys Pro Val Asp Leu Ser Lys Val Thr Ser Lys
                325                 330                 335

Cys Gly Ser Leu Gly Asn Ile His His Lys Pro Gly Gly Gly Gln Val
            340                 345                 350

Glu Val Lys Ser Glu Lys Leu Asp Phe Lys Asp Arg Val Gln Ser Lys
        355                 360                 365

Ile Gly Ser Leu Asp Asn Ile Thr His Val Pro Gly Gly Gly Asn Lys
    370                 375                 380

Lys Ile Glu Thr His Lys Leu Thr Phe Arg Glu Asn Ala Lys Ala Lys
385                 390                 395                 400

Thr Asp His Gly Ala Glu Ile Val Tyr Lys Ser Pro Val Val Ser Gly
                405                 410                 415
```

Asp Thr Ser Pro Arg His Leu Ser Asn Val Ser Ser Thr Gly Ser Ile
420 425 430

Asp Met Val Asp Ser Pro Gln Leu Ala Thr Leu Ala Asp Glu Val Ser
435 440 445

Ala Ser Leu Ala Lys Gln Gly Leu
450 455

<210> 2
<211> 23
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Human Tau epitope (2-24)

<400> 2

Ala Glu Pro Arg Gln Glu Phe Glu Val Met Glu Asp His Ala Gly Thr

1 5 10 15

Tyr Gly Leu Gly Asp Arg Lys

20

<210> 3

<211> 456

<212> PRT

<213> Macaca fascicularis

<220>

<221> misc_feature

<223> Cynomolgus monkey Tau sequence

<400> 3

Met His His His His His His Gly Glu Asn Leu Tyr Phe Gln Gly Ser

1 5 10 15

Ala Glu Pro Arg Gln Glu Phe Asp Val Met Glu Asp His Ala Gly Thr

20 25 30

```
Tyr Gly Leu Gly Asp Arg Lys Asp Gln Glu Gly Tyr Thr Met Leu Gln
        35                  40                  45

Asp Gln Glu Gly Asp Thr Asp Ala Gly Leu Lys Glu Ser Pro Leu Gln
    50                  55                  60

Thr Pro Ala Glu Asp Gly Ser Glu Glu Leu Gly Ser Glu Thr Ser Asp
65                  70                  75                  80

Ala Lys Ser Thr Pro Thr Ala Glu Asp Val Thr Ala Pro Leu Val Asp
                85                  90                  95

Glu Arg Ala Pro Gly Glu Gln Ala Ala Ala Gln Pro His Met Glu Ile
            100                 105                 110

Pro Glu Gly Thr Thr Ala Glu Glu Ala Gly Ile Gly Asp Thr Pro Ser
        115                 120                 125
```

```
Leu Glu Asp Glu Ala Ala Gly His Val Thr Gln Ala Arg Met Val Ser
    130                 135                 140

Lys Ser Lys Asp Gly Thr Gly Ser Asp Asp Lys Lys Ala Lys Gly Ala
145                 150                 155                 160

Asp Gly Lys Thr Lys Ile Ala Thr Pro Arg Gly Ala Ala Pro Pro Gly
                165                 170                 175

Gln Lys Gly Gln Ala Asn Ala Thr Arg Ile Pro Ala Lys Thr Pro Pro
            180                 185                 190

Ala Pro Lys Thr Pro Pro Ser Ser Gly Glu Pro Pro Lys Ser Gly Asp
        195                 200                 205

Arg Ser Gly Tyr Ser Ser Pro Gly Ser Pro Gly Thr Pro Gly Ser Arg
    210                 215                 220

Ser Arg Thr Pro Ser Leu Pro Thr Pro Pro Ala Arg Glu Pro Lys Lys
225                 230                 235                 240
```

```
Val Ala Val Val Arg Thr Pro Pro Lys Ser Pro Ser Ser Ala Lys Ser
                245                 250                 255

Arg Leu Gln Thr Ala Pro Val Pro Met Pro Asp Leu Lys Asn Val Lys
            260                 265                 270

Ser Lys Ile Gly Ser Thr Glu Asn Leu Lys His Gln Pro Gly Gly Gly
        275                 280                 285

Lys Val Gln Ile Ile Asn Lys Lys Leu Asp Leu Ser Asn Val Gln Ser
    290                 295                 300

Lys Cys Gly Ser Lys Asp Asn Ile Lys His Val Pro Gly Gly Gly Ser
305                 310                 315                 320

Val Gln Ile Val Tyr Lys Pro Val Asp Leu Ser Lys Val Thr Ser Lys
                325                 330                 335
```

```
Cys Gly Ser Leu Gly Asn Ile His His Lys Pro Gly Gly Gly Gln Val
            340                 345                 350

Glu Val Lys Ser Glu Lys Leu Asp Phe Lys Asp Arg Val Gln Ser Lys
        355                 360                 365

Ile Gly Ser Leu Asp Asn Ile Thr His Val Pro Gly Gly Gly Asn Lys
    370                 375                 380

Lys Ile Glu Thr His Lys Leu Thr Phe Arg Glu Asn Ala Lys Ala Lys
385                 390                 395                 400

Thr Asp His Gly Ala Glu Ile Val Tyr Lys Ser Pro Val Val Ser Gly
                405                 410                 415

Asp Thr Ser Pro Arg His Leu Ser Asn Val Ser Ser Thr Gly Ser Ile
            420                 425                 430

Asp Met Val Asp Ser Pro Gln Leu Ala Thr Leu Ala Asp Glu Val Ser
        435                 440                 445
```

Ala Ser Leu Ala Lys Gln Gly Leu

450 455

<210> 4

<211> 23

<212> PRT

<213> Macaca fascicularis

<220>

<221> misc_feature

<223> Cynomolgus monkey Tau epitope (2-24)

<400> 4

Ala Glu Pro Arg Gln Glu Phe Asp Val Met Glu Asp His Ala Gly Thr

1 5 10 15

Tyr Gly Leu Gly Asp Arg Lys

20

<210> 5

<400> 5

000

<210> 6

<400> 6

000

<210> 7

<400> 7

000

<210> 8

<400> 8

000

<210> 9

<400> 9

000

<210> 10

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 37D3-H9 heavy chain variable region (VH)

<400> 10

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

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

Gly Met Ser Trp Val Arg Gln Thr Pro Asp Lys Arg Leu Glu Trp Val
35 40 45

Ala Thr Ile Asn Ser Gly Gly Thr Tyr Thr Tyr Tyr Pro Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys

85 90 95

Ala Asn Ser Tyr Ser Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser

100 105 110

Val Thr Val Ser Ser

115

<210> 11

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 37D3-H9 light chain variable region (VL)

<400> 11

Asp Asp Leu Leu Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly

1 5 10 15

Asp Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser

20 25 30

Asn Gly Asn Thr Tyr Phe Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser

35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro

50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile

65 70 75 80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly

85 90 95

Ser Leu Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

100 105 110

<210> 12

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 37D3-H9 HVR-H1

<400> 12

Ser Tyr Gly Met Ser
1 5

<210> 13

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 37D3-H9 HVR-H2

<400> 13

Thr Ile Asn Ser Gly Gly Thr Tyr Thr Tyr Tyr Pro Asp Ser Val Lys

1 5 10 15

Gly

<210> 14

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 37D3-H9 HVR-H3

<400> 14

Ser Tyr Ser Gly Ala Met Asp Tyr

1 5

<210> 15

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 37D3-H9 HVR-L1

<400> 15

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Phe Glu
1 5 10 15

<210> 16

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 37D3-H9 HVR-L2

<400> 16

Lys Val Ser Asn Arg Phe Ser
1 5

<210> 17

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 37D3-H9 HVR-L3

<400> 17

Phe Gln Gly Ser Leu Val Pro Trp Thr
1 5

<210> 18

<400> 18
000

<210> 19

<400> 19
000

<210> 20

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 37D3-H9b heavy chain variable region (VH)

<400> 20

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

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

Gly Met Ser Trp Val Arg Gln Thr Pro Asp Lys Arg Leu Glu Trp Val
35 40 45

Ala Thr Ile Asn Ser Gly Gly Thr Tyr Thr Tyr Tyr Pro Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys

85 90 95

Ala Asn Ser Tyr Ser Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser

100 105 110

Val Thr Val Ser Ser

115

<210> 21

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 37D3-H9b light chain variable region (VL)

<400> 21

Glu Asp Leu Leu Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly

1 5 10 15

Asp Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser

20 25 30

Asn Gly Asn Thr Tyr Phe Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser

35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro

50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile

65 70 75 80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly

85 90 95

Ser Leu Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

100 105 110

<210> 22

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 37D3-H9b HVR-H1

<400> 22

Ser Tyr Gly Met Ser

1 5

<210> 23

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 37D3-H9b HVR-H2

<400> 23

Thr Ile Asn Ser Gly Gly Thr Tyr Thr Tyr Tyr Pro Asp Ser Val Lys

1 5 10 15

Gly

<210> 24

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 37D3-H9b HVR-H3

<400> 24

Ser Tyr Ser Gly Ala Met Asp Tyr
1 5

<210> 25

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 37D3-H9b HVR-L1

<400> 25

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Phe Glu

1 5 10 15

<210> 26

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 37D3-H9b HVR-L2

<400> 26

Lys Val Ser Asn Arg Phe Ser

1 5

<210> 27

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 37D3-H9b HVR-L3

<400> 27

Phe Gln Gly Ser Leu Val Pro Trp Thr
1 5

<210> 28

<400> 28
000

<210> 29

<400> 29
000

<210> 30
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: 11E10-B8 heavy chain variable region (VH)

<400> 30

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

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

Gly Met Ser Trp Val Arg Gln Thr Pro Asp Lys Arg Leu Glu Trp Val
        35                  40                  45

Ala Thr Ile Ser Gly Gly Gly Ser Tyr Thr Tyr Tyr Pro Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65                  70                  75                  80

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

Ala Val Ser Tyr Asp Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
```

100 105 110

Val Thr Val Ser Ser

115

<210> 31

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 11E10-B8 light chain variable region (VL)

<400> 31

Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly

1 5 10 15

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser

20 25 30

Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser

35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro

50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile

65 70 75 80

Ser Arg Val Glu Ala Glu Asp Leu Gly Leu Tyr Tyr Cys Phe Gln Gly

85 90 95

Ser His Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

100 105 110

<210> 32

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 11E10-B8 HVR-H1

<400> 32

Ser Tyr Gly Met Ser
1 5

<210> 33

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 11E10-B8 HVR-H2

<400> 33

Thr Ile Ser Gly Gly Gly Ser Tyr Thr Tyr Tyr Pro Asp Ser Val Lys
1 5 10 15

Gly

<210> 34

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 11E10-B8 HVR-H3

<400> 34

Ser Tyr Asp Gly Ala Met Asp Tyr
1 5

<210> 35

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 11E10-B8 HVR-L1

<400> 35

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu
1 5 10 15

<210> 36

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 11E10-B8 HVR-L2

<400> 36

Lys Val Ser Asn Arg Phe Ser
1 5

<210> 37

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 11E10-B8 HVR-L3

<400> 37

Phe Gln Gly Ser His Val Pro Trp Thr

1 5

<210> 38

<400> 38

000

<210> 39

<400> 39

000

<210> 40

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 54C1-H11 and 61E7-C4 heavy chain variable region (VH)

<400> 40

Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys Pro Gly Gly

1 5 10 15

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

Gly Met Ser Trp Val Arg Gln Thr Pro Asp Lys Arg Leu Asp Trp Val
35 40 45

Ala Thr Ile Ser Ser Gly Gly Asn Tyr Thr Tyr Tyr Pro Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80

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

Ala Ser Ser Tyr Ser Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
100 105 110

Val Thr Val Ser Ser

115

<210> 41

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 54C1-H11 and 61E7-C4 light chain variable region (VL)

<400> 41

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

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser
20 25 30

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

Pro Lys Leu Leu Ile Tyr Thr Val Ser Asn Arg Phe Ser Gly Val Pro

50 55 60

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

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

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

<210> 42

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 54C1-H11 and 61E7-C4 HVR-H1

<400> 42

Ser Tyr Gly Met Ser

1 5

<210> 43

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 54C1-H11 and 61E7-C4 HVR-H2

<400> 43

Thr Ile Ser Ser Gly Gly Asn Tyr Thr Tyr Tyr Pro Asp Ser Val Lys

1 5 10 15

Gly

<210> 44

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 54C1-H11 and 61E7-C4 HVR-H3

<400> 44

Ser Tyr Ser Gly Ala Met Asp Tyr
1 5

<210> 45

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 54C1-H11 and 61E7-C4 HVR-L1

<400> 45

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu
1 5 10 15

<210> 46

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 54C1-H11 and 61E7-C4 HVR-L2

<400> 46

Thr Val Ser Asn Arg Phe Ser
1 5

<210> 47

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 54C1-H11 and 61E7-C4 HVR-L3

<400> 47

Phe Gln Gly Ser His Val Pro Trp Thr
1 5

<210> 48

<400> 48

000

<210> 49

<400> 49

000

<210> 50

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 3A4-H4 heavy chain variable region (VH)

<400> 50

Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys Pro Gly Gly

1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Gly Met Ser Trp Val Arg Gln Thr Pro Asp Lys Arg Leu Glu Trp Val
35 40 45

Ala Thr Ile Ser Ser Gly Gly Thr Tyr Thr Tyr Tyr Pro Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Phe Cys
85 90 95

Ala Thr Ser Tyr Asp Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
100 105 110

Val Thr Val Ser Ser
115

<210> 51

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 3A4-H4 light chain variable region (VL)

<400> 51

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

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Asn Ile Val His Ser
20 25 30

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

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile

65 70 75 80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly

85 90 95

Thr Leu Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

100 105 110

<210> 52

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 3A4-H4 HVR-H1

<400> 52

Ser Tyr Gly Met Ser

1 5

<210> 53

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 3A4-H4 HVR-H2

<400> 53

Thr Ile Ser Ser Gly Gly Thr Tyr Thr Tyr Tyr Pro Asp Ser Val Lys
1 5 10 15

Gly

<210> 54

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 3A4-H4 HVR-H3

<400> 54

Ser Tyr Asp Gly Ala Met Asp Tyr

1 5

<210> 55

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 3A4-H4 HVR-L1

<400> 55

Arg Ser Ser Gln Asn Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu

1 5 10 15

<210> 56

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 3A4-H4 HVR-L2

<400> 56

Lys Val Ser Asn Arg Phe Ser
1 5

<210> 57

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 3A4-H4 HVR-L3

<400> 57

Phe Gln Gly Thr Leu Val Pro Trp Thr
1 5

<210> 58

<400> 58

000

<210> 59

<400> 59

000

<210> 60

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 19H6-F7 heavy chain variable region (VH)

<400> 60

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

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

Gly Met Ser Trp Val Arg Gln Thr Pro Asp Lys Arg Leu Glu Trp Val
35 40 45

Ala Thr Ile Ser Ser Gly Gly Thr Tyr Thr Tyr Tyr Pro Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80

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

Ala Pro Ser Tyr Asp Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
100 105 110

Val Thr Val Ser Ser
115

<210> 61
<211> 112
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic: 19H6-F7 light chain variable region (VL)

<400> 61

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

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser
20 25 30

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

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly

85 90 95

Ser Leu Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

100 105 110

<210> 62

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 19H6-F7 HVR-H1

<400> 62

Ser Tyr Gly Met Ser

1 5

<210> 63

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 19H6-F7 HVR-H2

<400> 63

Thr Ile Ser Ser Gly Gly Thr Tyr Thr Tyr Tyr Pro Asp Ser Val Lys
1 5 10 15

Gly

<210> 64

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 19H6-F7 HVR-H3

<400> 64

Ser Tyr Asp Gly Ala Met Asp Tyr
1 5

<210> 65

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 19H6-F7 HVR-L1

<400> 65

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu
1 5 10 15

<210> 66

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 19H6-F7 HVR-L2

<400> 66

Lys Val Ser Asn Arg Phe Ser

1 5

<210> 67

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 19H6-F7 HVR-L3

<400> 67

Phe Gln Gly Ser Leu Val Pro Trp Thr

1 5

<210> 68

<400> 68

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<210> 69

<400> 69

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<210> 70

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 94B2-C1 heavy chain variable region (VH)

<400> 70

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

Ser Met Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Leu Thr Gly Tyr
20 25 30

Thr Met Asn Trp Val Lys Gln Ser His Gly Lys Asn Leu Glu Trp Ile
35 40 45

Gly Leu Ile Ser Pro Tyr Asn Gly Val Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Asn Thr Ala Tyr
65 70 75 80

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

Ala Arg Gln Gly Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
100 105 110

Ala

<210> 71
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: 94B2-C1 light chain variable region (VL)

<400> 71

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

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

Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro Gly Gln Ser
        35                  40                  45

Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
    50                  55                  60

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

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Trp Gln Gly
                85                  90                  95

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

<210> 72

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 94B2-C1 HVR-H1

<400> 72

Gly Tyr Thr Met Asn

1 5

<210> 73

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 94B2-C1 HVR-H2

<400> 73

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

Gly

<210> 74
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: 94B2-C1 HVR-H3

<400> 74

Gln Gly Ala Tyr
1

<210> 75
<211> 16
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 94B2-C1 HVR-L1

<400> 75

Lys Ser Ser Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn
1 5 10 15

<210> 76

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 94B2-C1 HVR-L2

<400> 76

Leu Val Ser Lys Leu Asp Ser
1 5

<210> 77

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 94B2-C1 HVR-L3

<400> 77

Trp Gln Gly Thr His Phe Pro Trp Thr
1 5

<210> 78

<400> 78
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<210> 79

<400> 79
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<210> 80

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 125B11-H3 heavy chain variable region (VH)

<400> 80

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

Ser Met Lys Leu Ser Cys Val Ala Ser Arg Phe Ile Phe Ser Asn Tyr
20 25 30

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

Ala Gln Ile Arg Leu Lys Ser Asp Asn Tyr Ala Thr His Tyr Ala Glu
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ser
65 70 75 80

Val Tyr Leu Gln Met Asn Asn Leu Arg Ala Glu Asp Thr Gly Ile Tyr
85 90 95

Tyr Cys Thr Gly Gly Thr Thr Tyr Trp Gly Gln Gly Thr Thr Leu Thr
100 105 110

Val Ser Ser
115

<210> 81
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: 125B11-H3 light chain variable region (VL)

<400> 81

Asp Ile Val Met Thr Gln Ser Gln Lys Phe Leu Ser Thr Ser Val Gly
1 5 10 15

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

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

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

Asn Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asp Met Gln Ser
65 70 75 80

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

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 82

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 125B11-H3 HVR-H1

<400> 82

Asn Tyr Trp Met Asn
1 5

<210> 83

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 125B11-H3 HVR-H2

<400> 83

Gln Ile Arg Leu Lys Ser Asp Asn Tyr Ala Thr His Tyr Ala Glu Ser
1 5 10 15

Val Lys Gly

<210> 84

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 125B11-H3 HVR-H3

<400> 84

Gly Thr Thr Tyr
1

<210> 85

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 125B11-H3 HVR-L1

<400> 85

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

<210> 86

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 125B11-H3 HVR-L2

<400> 86

Ser Ala Ser Ile Arg Tyr Thr
1 5

<210> 87

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 125B11-H3 HVR-L3

<400> 87

Gln Gln Phe Arg Thr Tyr Pro Tyr Thr
1 5

<210> 88

<400> 88
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<210> 89

<400> 89
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<210> 90
<211> 115
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic: 113F5-F7 heavy chain variable region (VH)

<400> 90

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

Ser Met Arg Leu Ser Cys Val Ala Ser Glu Phe Thr Phe Ser Asn Tyr
20 25 30

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

Ala Gln Ile Arg Leu Lys Ser Asp Asn Tyr Ala Thr His Tyr Ala Glu
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Ala Ser Asn Phe Ser
65 70 75 80

Val Tyr Leu Gln Met Asn Asn Leu Arg Ala Glu Asp Thr Gly Ile Tyr
85 90 95

Tyr Cys Thr Gly Gly Thr Ser Tyr Trp Gly Gln Gly Thr Thr Leu Thr
100 105 110

Val Ser Ser
115

<210> 91
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: 113F5-F7 light chain variable region (VL)

<400> 91

Asp Ile Val Met Thr Gln Ser Gln Lys Ile Met Ser Thr Ser Val Gly
1 5 10 15

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

Val Ala Trp Tyr Gln Gln Arg Pro Gly His Ser Pro Lys Leu Leu Ile
35 40 45

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

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

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

Thr Phe Gly Val Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 92
<211> 5
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic: 113F5-F7 HVR-H1

<400> 92

Asn Tyr Trp Met Asn
1 5

<210> 93

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 113F5-F7 HVR-H2

<400> 93

Gln Ile Arg Leu Lys Ser Asp Asn Tyr Ala Thr His Tyr Ala Glu Ser
1 5 10 15

Val Lys Gly

<210> 94

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 113F5-F7 HVR-H3

<400> 94

Gly Thr Ser Tyr
1

<210> 95

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 113F5-F7 HVR-L1

<400> 95

Lys Ala Ser Gln Asn Val Gly Thr Ala Val Ala

1 5 10

<210> 96

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 113F5-F7 HVR-L2

<400> 96

Ser Ala Ser Arg Arg Phe Ser

1 5

<210> 97

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 113F5-F7 HVR-L3

<400> 97

Gln Gln Phe Ser Thr Tyr Pro Tyr Thr

1 5

<210> 98

<400> 98

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<210> 99

<400> 99

000

<210> 100

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 26C1-B11 heavy chain variable region (VH)

<400> 100

Glu Val His Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Ser Gly Ala

1 5 10 15

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Tyr

20 25 30

Tyr Met Tyr Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile

35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Phe Pro Lys Phe

50 55 60

Gln Gly Lys Ala Thr Met Thr Ala Asp Thr Ser Ser Lys Thr Ala Tyr

65 70 75 80

Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Asn Ala Trp Arg Ala Arg Ala Thr Asn Ser Ala Leu Asp Tyr Trp Gly

100 105 110

Gln Gly Thr Ser Val Thr Val Ser Ser
115 120

<210> 101
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: 26C1-B11 light chain variable region (VL)

<400> 101

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

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

Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Arg Arg Pro Gly Gln Ser
35 40 45

Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Trp Gln Gly
85 90 95

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

<210> 102
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: 26C1-B11 HVR-H1

<400> 102

Asp Tyr Tyr Met Tyr

1 5

<210> 103

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 26C1-B11 HVR-H2

<400> 103

Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Phe Pro Lys Phe Gln

1 5 10 15

Gly

<210> 104

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 26C1-B11 HVR-H3

<400> 104

Trp Arg Ala Arg Ala Thr Asn Ser Ala Leu Asp Tyr
1 5 10

<210> 105

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 26C1-B11 HVR-L1

<400> 105

Lys Ser Ser Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn
1 5 10 15

<210> 106

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 26C1-B11 HVR-L2

<400> 106

Leu Val Ser Lys Leu Asp Ser
1 5

<210> 107

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 26C1-B11 HVR-L3

<400> 107

Trp Gln Gly Thr His Phe Pro Trp Thr
1 5

<210> 108

<400> 108

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<210> 109

<400> 109

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<210> 110

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 26C1-C8 heavy chain variable region (VH)

<400> 110

Glu Val His Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Ser Gly Ala

1 5 10 15

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Tyr

20 25 30

Tyr Met Tyr Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile

35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Phe Pro Lys Phe

50 55 60

Gln Gly Lys Ala Thr Met Thr Ala Asp Thr Ser Ser Lys Thr Ala Tyr

65 70 75 80

Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Asn Ala Trp Arg Ala Arg Ala Thr Asn Ser Ala Leu Asp Tyr Trp Gly

100 105 110

Gln Gly Thr Ser Val Thr Val Ser Ser

115 120

<210> 111

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 26C1-C8 light chain variable region (VL)

<400> 111

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

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

Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Arg Arg Pro Gly Gln Ser
35 40 45

Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Trp Gln Gly
85 90 95

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

<210> 112
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: 26C1-C8 HVR-H1

<400> 112

Asp Tyr Tyr Met Tyr
1 5

<210> 113

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 26C1-C8 HVR-H2

<400> 113

Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Phe Pro Lys Phe Gln
1 5 10 15

Gly

<210> 114

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 26C1-C8 HVR-H3

<400> 114

Trp Arg Ala Arg Ala Thr Asn Ser Ala Leu Asp Tyr
1 5 10

<210> 115

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 26C1-C8 HVR-L1

<400> 115

Lys Ser Ser Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn
1 5 10 15

<210> 116

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 26C1-C8 HVR-L2

<400> 116

Leu Val Ser Lys Leu Asp Ser
1 5

<210> 117

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 26C1-C8 HVR-L3

<400> 117

Trp Gln Gly Thr His Phe Pro Trp Thr
1 5

<210> 118

<400> 118

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<210> 119

<400> 119

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<210> 120

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 30G1-B2 heavy chain variable region (VH)

<400> 120

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala

1 5 10 15

Ser Val Thr Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr

20 25 30

Glu Met Tyr Trp Val Lys Gln Thr Pro Val His Gly Leu Glu Trp Ile

35 40 45

Gly Ala Ile Asp Pro Glu Thr Gly Asp Thr Ala Tyr Asn Gln Lys Phe

50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Asn Thr Ala Tyr

65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys

85 90 95

Ile Arg Gln Tyr Gly Asn Trp Phe Pro Tyr Trp Gly Gln Gly Thr Leu

100 105 110

Val Thr Val Ser Ala

115

<210> 121

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 30G1-B2 light chain variable region (VL)

<400> 121

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

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ala
20 25 30

Asn Gly Asn Thr Tyr Leu His Trp Phe Leu Gln Lys Pro Gly Leu Ser
35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

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

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

<210> 122

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 30G1-B2 HVR-H1

<400> 122

Asp Tyr Glu Met Tyr
1 5

<210> 123

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 30G1-B2 HVR-H2

<400> 123

Ala Ile Asp Pro Glu Thr Gly Asp Thr Ala Tyr Asn Gln Lys Phe Lys
1 5 10 15

Gly

<210> 124

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 30G1-B2 HVR-H3

<400> 124

Gln Tyr Gly Asn Trp Phe Pro Tyr

1 5

<210> 125

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 30G1-B2 HVR-L1

<400> 125

Arg Ser Ser Gln Ser Leu Val His Ala Asn Gly Asn Thr Tyr Leu His

1 5 10 15

<210> 126

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 30G1-B2 HVR-L2

<400> 126

Lys Val Ser Asn Arg Phe Ser

1 5

<210> 127

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 30G1-B2 HVR-L3

<400> 127

Ser Gln Ser Thr His Val Pro Phe Thr

1 5

<210> 128

<400> 128

000

<210> 129

<400> 129

000

<210> 130

<211> 114

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 66F5-A1 heavy chain variable region (VH)

<400> 130

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

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

Glu Met Asn Trp Val Lys Gln Thr Pro Val His Gly Leu Glu Trp Ile
35 40 45

Gly Ala Ile Asp Pro Glu Asn Gly Gly Thr Ala Tyr Asn Gln Lys Phe

50 55 60

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

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

Ser Gly Pro His Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val
100 105 110

Ser Ser

<210> 131

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 66F5-A1 light chain variable region (VL)

<400> 131

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

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

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

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

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

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

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

Lys

<210> 132
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: 66F5-A1 HVR-H1

<400> 132

Asp Tyr Glu Met Asn
1 5

<210> 133
<211> 17
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 66F5-A1 HVR-H2

<400> 133

Ala Ile Asp Pro Glu Asn Gly Gly Thr Ala Tyr Asn Gln Lys Phe Lys
1 5 10 15

Gly

<210> 134

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 66F5-A1 HVR-H3

<400> 134

Pro His Phe Asp Tyr

1 5

<210> 135

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 66F5-A1 HVR-L1

<400> 135

Lys Ser Ser Gln Ser Leu Leu Asn Ser Ser Thr Gln Lys Asn Tyr Leu

1 5 10 15

Ala

<210> 136

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 66F5-A1 HVR-L2

<400> 136

Phe Ala Ser Thr Arg Glu Ser
1 5

<210> 137

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 66F5-A1 HVR-L3

<400> 137

Gln Gln His Tyr Ser Thr Pro Tyr Thr
1 5

<210> 138

<400> 138

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<210> 139

<400> 139

000

<210> 140

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 123E9-A1 heavy chain variable region (VH)

<400> 140

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

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

Tyr Met Lys Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile

35 40 45

Gly Asp Ile Asp Pro Asn Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe

50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr

65 70 75 80

Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Ser Ala Gly Phe Gly Asp Ser Phe Ser Phe Trp Gly Leu Gly

100 105 110

Thr Leu Val Thr Val Ser Ala

115

<210> 141

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 123E9-A1 light chain variable region (VL)

<400> 141

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

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser
20 25 30

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

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

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

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

<210> 142

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 123E9-A1 HVR-H1

<400> 142

Asp Tyr Tyr Met Lys
1 5

<210> 143

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 123E9-A1 HVR-H2

<400> 143

Asp Ile Asp Pro Asn Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe Lys
1 5 10 15

Gly

<210> 144

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 123E9-A1 HVR-H3

<400> 144

Ser Ala Gly Phe Gly Asp Ser Phe Ser Phe

1 5 10

<210> 145

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 123E9-A1 HVR-L1

<400> 145

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu

1 5 10 15

<210> 146

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 123E9-A1 HVR-L2

<400> 146

Lys Val Ser Asn Arg Phe Ser

1 5

<210> 147

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 123E9-A1 HVR-L3

<400> 147

Phe Gln Gly Ser His Val Pro Pro Thr

1 5

<210> 148

<400> 148

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<210> 149

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<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 15C6-A7 heavy chain variable region (VH)

<400> 150

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

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

Tyr Met Lys Trp Val Lys Gln Ser Asn Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Asp Leu Asp Pro Tyr Thr Gly Gly Ala Asn Tyr Asn Gln Lys Phe

50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met His Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Arg Gly Tyr Gly Asp Ser Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ala
115

<210> 151
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<213> Artificial Sequence

<220>
<223> Synthetic: 15C6-A7 light chain variable region (VL)

<400> 151

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

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Asn Ile Val His Ser
20 25 30

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

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

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

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

<210> 152
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: 15C6-A7 HVR-H1

<400> 152

Asp Tyr Tyr Met Lys
1 5

<210> 153
<211> 17
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<213> Artificial Sequence

<220>
<223> Synthetic: 15C6-A7 HVR-H2

<400> 153

Asp Leu Asp Pro Tyr Thr Gly Gly Ala Asn Tyr Asn Gln Lys Phe Lys
1 5 10 15

Gly

<210> 154
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: 15C6-A7 HVR-H3

<400> 154

Ser Arg Gly Tyr Gly Asp Ser Phe Ala Tyr
1 5 10

<210> 155

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 15C6-A7 HVR-L1

<400> 155

Arg Ser Ser Gln Asn Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu
1 5 10 15

<210> 156

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 15C6-A7 HVR-L2

<400> 156

Lys Val Ser Asn Arg Phe Ser
1 5

<210> 157

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 15C6-A7 HVR-L3

<400> 157

Phe Gln Gly Ser His Val Pro Pro Thr
1 5

<210> 158

<400> 158
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<210> 159

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<210> 160

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 19F8-B1 heavy chain variable region (VH)

<400> 160

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

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

Tyr Met Lys Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Asp Leu Asn Pro Asn Asn Gly Gly Thr Leu Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Gln Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr

65 70 75 80

Met Gln Phe Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Ser Ala Gly Tyr Gly Asp Ser Phe Ala Tyr Trp Gly Gln Gly

100 105 110

Thr Leu Val Thr Val Ser Ala

115

<210> 161

<211> 112

<212> PRT

<213> Artificial Sequence

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<223> Synthetic: 19F8-B1 light chain variable region (VL)

<400> 161

Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly

1 5 10 15

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Asn Ile Val His Ser

20 25 30

Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser

35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro

50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile

65 70 75 80

Ser Arg Val Glu Ala Glu Asp Leu Gly Ile Tyr Phe Cys Phe Gln Gly

85 90 95

Ser His Val Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

100 105 110

<210> 162

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 19F8-B1 HVR-H1

<400> 162

Asp Tyr Tyr Met Lys
1 5

<210> 163

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 19F8-B1 HVR-H2

<400> 163

Asp Leu Asn Pro Asn Asn Gly Gly Thr Leu Tyr Asn Gln Lys Phe Lys

1 5 10 15

Gly

<210> 164

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 19F8-B1 HVR-H3

<400> 164

Ser Ala Gly Tyr Gly Asp Ser Phe Ala Tyr

1 5 10

<210> 165

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 19F8-B1 HVR-L1

<400> 165

Arg Ser Ser Gln Asn Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu
1 5 10 15

<210> 166

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 19F8-B1 HVR-L2

<400> 166

Lys Val Ser Asn Arg Phe Ser
1 5

<210> 167

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 19F8-B1 HVR-L3

<400> 167

Phe Gln Gly Ser His Val Pro Pro Thr
1 5

<210> 168

<400> 168
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<210> 169

<400> 169
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<210> 170
<211> 119
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic: 24A11-D5 heavy chain variable region (VH)

<400> 170

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

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

Tyr Met Lys Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Asp Leu Asn Pro Lys Asn Gly Gly Ile Ile Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Gln Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Phe Tyr Cys

85 90 95

Ala Arg Ser Gly Gly Tyr Gly Asp Ser Phe Ala Tyr Trp Gly Gln Gly

100 105 110

Thr Leu Val Thr Val Ser Ala

115

<210> 171

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 24A11-D5 light chain variable region (VL)

<400> 171

Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly

1 5 10 15

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Asn Ile Val His Ser

20 25 30

Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser

35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro

50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile

65 70 75 80

Ser Arg Val Glu Ala Glu Asp Leu Gly Ile Tyr Phe Cys Phe Gln Gly

85 90 95

Ser His Val Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

100 105 110

<210> 172

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 24A11-D5 HVR-H1

<400> 172

Asp Tyr Tyr Met Lys
1 5

<210> 173

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 24A11-D5 HVR-H2

<400> 173

Asp Leu Asn Pro Lys Asn Gly Gly Ile Ile Tyr Asn Gln Lys Phe Lys
1 5 10 15

Gly

<210> 174

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 24A11-D5 HVR-H3

<400> 174

Ser Gly Gly Tyr Gly Asp Ser Phe Ala Tyr
1 5 10

<210> 175

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 24A11-D5 HVR-L1

<400> 175

Arg Ser Ser Gln Asn Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu

1 5 10 15

<210> 176

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 24A11-D5 HVR-L2

<400> 176

Lys Val Ser Asn Arg Phe Ser

1 5

<210> 177

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 24A11-D5 HVR-L3

<400> 177

Phe Gln Gly Ser His Val Pro Pro Thr
1 5

<210> 178

<400> 178
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<210> 179

<400> 179
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<210> 180
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: 126F11-G11 heavy chain variable region (VH)

<400> 180

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

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

Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
        35                  40                  45

Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Ser Lys Phe
    50                  55                  60

Gln Gly Lys Ala Thr Ile Thr Thr Asp Thr Ser Ser Asn Thr Ala Tyr
65                  70                  75                  80

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

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

Ser Ser

<210> 181

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 126F11-G11 light chain variable region (VL)

<400> 181

Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly

1 5 10 15

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser

20 25 30

Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser

35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro

50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile

65 70 75 80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly

85 90 95

Ser His Val Pro Pro Ala Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

100 105 110

<210> 182

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 126F11-G11 HVR-H1

<400> 182

Asp Asp Tyr Met His
1 5

<210> 183
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: 126F11-G11 HVR-H2

<400> 183

Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Ser Lys Phe Gln
1 5 10 15

Gly

<210> 184

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 126F11-G11 HVR-H3

<400> 184

Phe Ala Tyr Gly Tyr
1 5

<210> 185

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 126F11-G11 HVR-L1

<400> 185

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu
1 5 10 15

<210> 186

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 126F11-G11 HVR-L2

<400> 186

Lys Val Ser Asn Arg Phe Ser
1 5

<210> 187

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 126F11-G11 HVR-L3

<400> 187

Phe Gln Gly Ser His Val Pro Pro Ala

1 5

<210> 188

<400> 188

000

<210> 189

<400> 189

000

<210> 190

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 89F4-A1 heavy chain variable region (VH)

<400> 190

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Lys Gly

1 5 10 15

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

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

Ala Arg Ile Arg Ser Lys Ser Asn Asn Tyr Ala Ala Tyr Phe Ala Asp
50 55 60

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

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

Tyr Cys Val Ser Gly Gly Asn Tyr Val Pro Phe Ala Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ala

115 120

<210> 191

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 89F4-A1 light chain variable region (VL)

<400> 191

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

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Phe Tyr Ser
20 25 30

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

Ser Pro Lys Leu Leu Ile Ser Trp Ala Ser Thr Arg Glu Ser Gly Val

50 55 60

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

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

Tyr Leu Ser Ser Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 192

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 89F4-A1 HVR-H1

<400> 192

Thr Tyr Ala Met Asn

1 5

<210> 193

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 89F4-A1 HVR-H2

<400> 193

Arg Ile Arg Ser Lys Ser Asn Asn Tyr Ala Ala Tyr Phe Ala Asp Ser

1 5 10 15

Val Lys Asp

<210> 194

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 89F4-A1 HVR-H3

<400> 194

Gly Gly Asn Tyr Val Pro Phe Ala Tyr
1 5

<210> 195

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 89F4-A1 HVR-L1

<400> 195

Lys Ser Ser Gln Ser Val Phe Tyr Ser Ser Glu Gln Arg Asn Tyr Leu
1 5 10 15

Ala

<210> 196

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 89F4-A1 HVR-L2

<400> 196

Trp Ala Ser Thr Arg Glu Ser

1 5

<210> 197

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 89F4-A1 HVR-L3

<400> 197

His Gln Tyr Leu Ser Ser Phe Thr

1 5

<210> 198

<400> 198

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<210> 199

<400> 199

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<210> 200

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 93A8-D2 heavy chain variable region (VH)

<400> 200

Glu Val Gln Leu Gln Gln Ser Gly Pro Val Leu Val Lys Pro Gly Ala

1 5 10 15

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

Tyr Val Asn Trp Val Lys Gln Ser His Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Leu Ile Asn Pro Asn Asn Gly Arg Thr Ser Tyr Asn Gln Asn Phe
50 55 60

Asn Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Phe
65 70 75 80

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

Thr Arg Glu Gly Gly Thr Gly Tyr Trp Gly Gln Gly Thr Thr Leu Ser
100 105 110

Val Ser Ser

<210> 201

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 93A8-D2 light chain variable region (VL)

<400> 201

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

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

Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro

50 55 60

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

Ser Arg Val Ala Ala Glu Asp Leu Gly Val Tyr Tyr Cys Trp Gln Gly
85 90 95

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

<210> 202

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 93A8-D2 HVR-H1

<400> 202

Asp Tyr Tyr Val Asn

1 5

<210> 203

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 93A8-D2 HVR-H2

<400> 203

Leu Ile Asn Pro Asn Asn Gly Arg Thr Ser Tyr Asn Gln Asn Phe Asn

1 5 10 15

Asp

<210> 204

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 93A8-D2 HVR-H3

<400> 204

Glu Gly Gly Thr Gly Tyr
1 5

<210> 205

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 93A8-D2 HVR-L1

<400> 205

Lys Ser Ser Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn
1 5 10 15

<210> 206

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 93A8-D2 HVR-L2

<400> 206

Leu Val Ser Lys Leu Asp Ser
1 5

<210> 207

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 93A8-D2 HVR-L3

<400> 207

Trp Gln Gly Thr His Phe Pro Arg Thr
1 5

<210> 208

<400> 208

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<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 14F5-D9 heavy chain variable region (VH)

<400> 210

Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Ser Asp Phe

20 25 30

Tyr Met Glu Trp Val Arg Gln Ser Pro Gly Lys Arg Leu Glu Trp Ile
35 40 45

Ala Ala Ser Lys Asn Lys Ala Asn Asp Tyr Thr Thr Glu Tyr Asn Ala
50 55 60

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

Leu Tyr Leu Gln Met Asn Ala Leu Arg Ala Glu Asp Thr Ala Ile Tyr
85 90 95

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

Gly Thr Leu Val Thr Val Ser Ala
115 120

<210> 211

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 14F5-D9 light chain variable region (VL)

<400> 211

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

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

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

Pro Lys Leu Leu Ile Tyr Lys Val Phe Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile

65 70 75 80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser

85 90 95

Thr Leu Val Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys

100 105 110

<210> 212

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 14F5-D9 HVR-H1

<400> 212

Asp Phe Tyr Met Glu

1 5

<210> 213

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 14F5-D9 HVR-H2

<400> 213

Ala Ser Lys Asn Lys Ala Asn Asp Tyr Thr Thr Glu Tyr Asn Ala Ser
1 5 10 15

Val Lys Asp

<210> 214

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 14F5-D9 HVR-H3

<400> 214

Asp Ala Leu Gly Thr Val Phe Ala Tyr

1 5

<210> 215

<211> 16

<212> PRT

<213> Artificial Sequence

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<223> Synthetic: 14F5-D9 HVR-L1

<400> 215

Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His

1 5 10 15

<210> 216

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 14F5-D9 HVR-L2

<400> 216

Lys Val Phe Asn Arg Phe Ser
1 5

<210> 217

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 14F5-D9 HVR-L3

<400> 217

Ser Gln Ser Thr Leu Val Pro Leu Thr
1 5

<210> 218

<400> 218

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<210> 219

<400> 219

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<210> 220

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 73H6-B8 heavy chain variable region (VH)

<400> 220

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

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

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

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

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

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

Arg Gln Gly Gly Phe Ile Thr Thr Ala Tyr Tyr Ala Met Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Ser Val Thr Val Ser Ser
115 120

<210> 221
<211> 112
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic: 73H6-B8 light chain variable region (VL)

<400> 221

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

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

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

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

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

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Lys Gln

85 90 95

Ser Tyr Asn Leu Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

100 105 110

<210> 222

<211> 5

<212> PRT

<213> Artificial Sequence

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<223> Synthetic: 73H6-B8 HVR-H1

<400> 222

Ser Tyr Gly Val His

1 5

<210> 223

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 73H6-B8 HVR-H2

<400> 223

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

<210> 224

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 73H6-B8 HVR-H3

<400> 224

Gln Gly Gly Phe Ile Thr Thr Ala Tyr Tyr Ala Met Asp Tyr
1 5 10

<210> 225

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 73H6-B8 HVR-L1

<400> 225

Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 226

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 73H6-B8 HVR-L2

<400> 226

Trp Ala Ser Thr Arg Glu Ser

1 5

<210> 227

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 73H6-B8 HVR-L3

<400> 227

Lys Gln Ser Tyr Asn Leu Tyr Thr

1 5

<210> 228

<400> 228

000

<210> 229

<400> 229

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<210> 230

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 22G7-C9 heavy chain variable region (VH)

<400> 230

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

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

Ser Ile His Trp Val Lys Gln Ala Pro Gly Glu Gly Leu Lys Trp Met
35 40 45

Gly Trp Ile Asn Thr Glu Thr Gly Glu Pro Ser Tyr Ala Asp Asp Phe
50 55 60

Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Phe
65 70 75 80

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

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

Gly Thr Ser Val Thr Val Ser Ser
115 120

<210> 231
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: 22G7-C9 light chain variable region (VL)

<400> 231

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

Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
            20                  25                  30

Ser Tyr Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45

Lys Leu Leu Ile Lys Tyr Ala Ser Asn Leu Glu Ser Gly Val Pro Ala
    50                  55                  60

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

Pro Val Glu Glu Glu Asp Thr Ala Thr Tyr Tyr Cys Gln His Ser Trp
                85                  90                  95

Glu Leu Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
```

100 105 110

<210> 232

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 22G7-C9 HVR-H1

<400> 232

Asp Cys Ser Ile His
1 5

<210> 233

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 22G7-C9 HVR-H2

<400> 233

Trp Ile Asn Thr Glu Thr Gly Glu Pro Ser Tyr Ala Asp Asp Phe Lys
1 5 10 15

Gly

<210> 234
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: 22G7-C9 HVR-H3

<400> 234

Ala Tyr Tyr Arg Tyr Asp Gly Ala Leu Asp Tyr
1 5 10

<210> 235
<211> 15
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 22G7-C9 HVR-L1

<400> 235

Arg Ala Ser Gln Ser Val Ser Thr Ser Ser Tyr Ser Tyr Met His
1 5 10 15

<210> 236

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 22G7-C9 HVR-L2

<400> 236

Tyr Ala Ser Asn Leu Glu Ser
1 5

<210> 237

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 22G7-C9 HVR-L3

<400> 237

Gln His Ser Trp Glu Leu Pro Trp Thr
1 5

<210> 238

<400> 238
000

<210> 239

<400> 239
000

<210> 240

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 7A11-C12 heavy chain variable region (VH)

<400> 240

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

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

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

Gly Trp Ile Asn Thr Asn Thr Gly Glu Pro Thr Tyr Ala Glu Glu Phe
50 55 60

Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Leu Gln Ile Asp Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys
85 90 95

Ala Arg Gly Thr Val Ser Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ala
115

<210> 241
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: 7A11-C12 light chain variable region (VL)

<400> 241

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

Asp His Ala Ser Ile Ser Cys Arg Ser Ser Gln Asn Leu Val His Ser
20 25 30

Asp Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

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

Thr His Val Ile Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 242

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 7A11-C12 HVR-H1

<400> 242

Asn Tyr Gly Met Asn
1 5

<210> 243

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 7A11-C12 HVR-H2

<400> 243

Trp Ile Asn Thr Asn Thr Gly Glu Pro Thr Tyr Ala Glu Glu Phe Lys
1 5 10 15

Gly

<210> 244

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 7A11-C12 HVR-H3

<400> 244

Gly Thr Val Ser Phe Pro Tyr
1 5

<210> 245

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 7A11-C12 HVR-L1

<400> 245

Arg Ser Ser Gln Asn Leu Val His Ser Asp Gly Asn Thr Tyr Leu His
1 5 10 15

<210> 246

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 7A11-C12 HVR-L2

<400> 246

Lys Val Ser Asn Arg Phe Ser
1 5

<210> 247

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 7A11-C12 HVR-L3

<400> 247

Ser Gln Ser Thr His Val Ile Phe Thr
1 5

<210> 248

<400> 248
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<210> 249

<400> 249
000

<210> 250
<211> 115
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic: 12A10-E8 heavy chain variable region (VH)

<400> 250

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

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

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

Gly Trp Ile Asn Met Tyr Thr Gly Glu Pro Thr Tyr Gly Asp Asp Phe
50 55 60

Lys Gly Arg Phe Val Phe Ser Leu Glu Thr Ser Val Ser Thr Val Tyr
65 70 75 80

Leu Gln Ile Asn Asn Leu Lys Lys Glu Asp Thr Ala Thr Phe Phe Cys
85 90 95

Ala Arg Gly Gly Arg Pro Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr
100 105 110

Val Ser Ser
115

<210> 251
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: 12A10-E8 light chain variable region (VL)

<400> 251

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

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser
20 25 30

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

Pro Lys Leu Leu Ile Tyr Lys Val Phe Asn Arg Phe Ser Gly Val Pro
50 55 60

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

Asn Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Leu Gln Gly
85 90 95

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

<210> 252
<211> 5
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic: 12A10-E8 HVR-H1

<400> 252

Asn Tyr Gly Met Asn
1 5

<210> 253

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 12A10-E8 HVR-H2

<400> 253

Trp Ile Asn Met Tyr Thr Gly Glu Pro Thr Tyr Gly Asp Asp Phe Lys
1 5 10 15

Gly

<210> 254

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 12A10-E8 HVR-H3

<400> 254

Gly Gly Arg Pro Asp Tyr
1 5

<210> 255

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 12A10-E8 HVR-L1

<400> 255

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu

1 5 10 15

<210> 256

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 1 2A10-E8 HVR-L2

<400> 256

Lys Val Phe Asn Arg Phe Ser
1 5

<210> 257

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 12A10-E8 HVR-L3

<400> 257

Leu Gln Gly Ser His Val Pro Tyr Thr

1 5

<210> 258

<400> 258

000

<210> 259

<400> 259

000

<210> 260

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 55E7-F11 heavy chain variable region (VH)

<400> 260

Glu Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Met Lys Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Asn Tyr

20 25 30

Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val

35 40 45

Ala Gln Ile Arg Leu Lys Ser Asp Asn Tyr Ala Thr His Tyr Ala Glu

50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ser

65 70 75 80

Val Tyr Leu Gln Met Asn Asn Leu Arg Ala Glu Asp Thr Gly Ile Tyr

85 90 95

Tyr Cys Ala Gly Tyr Phe Tyr Gly Gly Tyr Phe Asp Val Trp Gly Thr

100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 261

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 55E7-F11 light chain variable region (VL)

<400> 261

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

Lys Lys Ile Thr Ile Thr Cys Ser Ala Ser Ser Ser Ile Ser Ser Asn
20 25 30

Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Phe Ser Pro Lys Leu Leu
35 40 45

Ile Tyr Arg Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Gly Thr Met Glu
65 70 75 80

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

Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 262
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: 55E7-F11 HVR-H1

<400> 262

Asn Tyr Trp Met Asn

1 5

<210> 263

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 55E7-F11 HVR-H2

<400> 263

Gln Ile Arg Leu Lys Ser Asp Asn Tyr Ala Thr His Tyr Ala Glu Ser

1 5 10 15

Val Lys Gly

<210> 264

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 55E7-F11 HVR-H3

<400> 264

Tyr Phe Tyr Gly Gly Tyr Phe Asp Val
1 5

<210> 265

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 55E7-F11 HVR-L1

<400> 265

Ser Ala Ser Ser Ser Ile Ser Ser Asn Tyr Leu His
1 5 10

<210> 266

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 55E7-F11 HVR-L2

<400> 266

Arg Thr Ser Asn Leu Ala Ser
1 5

<210> 267

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 55E7-F11 HVR-L3

<400> 267

Gln Gln Gly Ser Ser Leu Pro Phe Thr
1 5

<210> 268

<400> 268

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<210> 269

<400> 269

000

<210> 270

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 52F6-F11 heavy chain variable region (VH)

<400> 270

Gln Val Gln Leu Gln Gln Ser Gly Thr Glu Leu Ala Lys Pro Gly Ala

1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr His Tyr

20 25 30

Trp Met His Trp Ile Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile

35 40 45

Gly Tyr Ile Tyr Pro Thr Asn Asp Tyr Thr Lys Tyr Asn Gln Asn Phe

50 55 60

Arg Asp Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Asn Ser Ala Tyr

65 70 75 80

Met Gln Leu Asn Ser Leu Thr Tyr Glu Asp Ser Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Ala Gly Asn Arg Val Phe Asp Phe Trp Gly Gln Gly Thr Thr

100 105 110

Leu Thr Val Ser Ser

115

<210> 271

<211> 109

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 52F6-F11 light chain variable region (VL)

<400> 271

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

Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Phe Ala Asn Trp Val Gln Glu Lys Pro Asp His Leu Phe Thr Gly
35 40 45

Leu Ile Gly Gly Thr Asn Asn Arg Ala Pro Gly Val Pro Ala Arg Phe
50 55 60

Ser Gly Ser Leu Ile Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

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

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 272
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: 52F6-F11 HVR-H1

<400> 272

His Tyr Trp Met His
1 5

<210> 273

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 52F6-F11 HVR-H2

<400> 273

Tyr Ile Tyr Pro Thr Asn Asp Tyr Thr Lys Tyr Asn Gln Asn Phe Arg
1 5 10 15

Asp

<210> 274

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 52F6-F11 HVR-H3

<400> 274

Ala Gly Asn Arg Val Phe Asp Phe
1 5

<210> 275
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: 52F6-F11 HVR-L1

<400> 275

Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Phe Ala Asn
1 5 10

<210> 276
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic: 52F6-F11 HVR-L2

<400> 276

Gly Thr Asn Asn Arg Ala Pro
1 5

<210> 277

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: 52F6-F11 HVR-L3

<400> 277

Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 278

<400> 278

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<210> 279

<400> 279

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<210> 280

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v1 heavy chain variable region (VH)

<400> 280

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 Leu Ile Phe Arg Ser Tyr

20 25 30

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Thr Ile Asn Ser Gly Gly Thr Tyr Thr Tyr Tyr Pro Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Asn Ser Tyr Ser Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu

100 105 110

Val Thr Val Ser Ser

115

<210> 281

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v1 light chain variable region (VL)

<400> 281

Glu Asp 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 Ser Ser Gln Ser Ile Val His Ser
20 25 30

Asn Gly Asn Thr Tyr Phe Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ser
35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

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

Ser Leu Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 282
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Hu37D3-H9.v1 HVR-H1

<400> 282

Ser Tyr Gly Met Ser
1 5

<210> 283
<211> 17
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v1 HVR-H2

<400> 283

Thr Ile Asn Ser Gly Gly Thr Tyr Thr Tyr Tyr Pro Asp Ser Val Lys
1 5 10 15

Gly

<210> 284

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v1 HVR-H3

<400> 284

Ser Tyr Ser Gly Ala Met Asp Tyr

1 5

<210> 285

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v1 HVR-L1

<400> 285

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Phe Glu

1 5 10 15

<210> 286

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v1 HVR-L2

<400> 286

Lys Val Ser Asn Arg Phe Ser

1 5

<210> 287

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v1 HVR-L3

<400> 287

Phe Gln Gly Ser Leu Val Pro Trp Thr

1 5

<210> 288

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v1 IgG1 heavy chain

<400> 288

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 Leu Ile Phe Arg Ser Tyr
20 25 30

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

Ala Thr Ile Asn Ser Gly Gly Thr Tyr Thr Tyr Tyr Pro Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

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

```
Ala Asn Ser Tyr Ser Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110

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

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
    130                 135                 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145                 150                 155                 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
                165                 170                 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
            180                 185                 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
```

195 200 205

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His

210 215 220

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val

225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr

245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu

260 265 270

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys

275 280 285

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser

290 295 300

```
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305                 310                 315                 320

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

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
            340                 345                 350

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
        355                 360                 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
    370                 375                 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385                 390                 395                 400

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
```

405 410 415

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu

420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

435 440 445

<210> 289

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v1 IgG1 light chain

<400> 289

Glu Asp 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 Ser Ser Gln Ser Ile Val His Ser

20 25 30

Asn Gly Asn Thr Tyr Phe Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ser

35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro

50 55 60

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile

65 70 75 80

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly

85 90 95

Ser Leu Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu

115 120 125

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

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

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

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

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

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

<210> 290

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v5 heavy chain variable region (VH)

<400> 290

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 Leu Ile Phe Arg Ser Tyr
20 25 30

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

Ala Thr Ile Asn Ser Gly Gly Thr Tyr Thr Tyr Tyr Pro Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Asn Ser Tyr Ser Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu

100 105 110

Val Thr Val Ser Ser

115

<210> 291

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v5 light chain variable region (VL)

<400> 291

Glu Asp Val Leu Thr Gln Thr Pro Leu Ser Leu Pro Val Thr Pro Gly

1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser

20 25 30

Asn Gly Asn Thr Tyr Phe Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser

35 40 45

Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro

50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile

65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Phe Gln Gly

85 90 95

Ser Leu Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

100 105 110

<210> 292

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v5 HVR-H1

<400> 292

Ser Tyr Gly Met Ser
1 5

<210> 293

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v5 HVR-H2

<400> 293

Thr Ile Asn Ser Gly Gly Thr Tyr Thr Tyr Tyr Pro Asp Ser Val Lys

1 5 10 15

Gly

<210> 294

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v5 HVR-H3

<400> 294

Ser Tyr Ser Gly Ala Met Asp Tyr

1 5

<210> 295

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v5 HVR-L1

<400> 295

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Phe Glu
1 5 10 15

<210> 296

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v5 HVR-L2

<400> 296

Lys Val Ser Asn Arg Phe Ser
1 5

<210> 297

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v5 HVR-L3

<400> 297

Phe Gln Gly Ser Leu Val Pro Trp Thr
1 5

<210> 298

<400> 298
000

<210> 299

<400> 299
000

<210> 300
<211> 113
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic: Hu94B2.v105 heavy chain variable region (VH)

<400> 300

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

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

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

Gly Leu Ile Ser Pro Tyr Asn Gly Val Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Arg Ala Thr Leu Thr Val Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Leu Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Gln Gly Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser

100 105 110

Ser

<210> 301

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu94B2.v105 light chain variable region (VL)

<400> 301

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Thr Pro Gly

1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser

20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Lys Pro Gly Gln Ser

35 40 45

Pro Gln Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro

50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile

65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly

85 90 95

Thr His Phe Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

100 105 110

<210> 302

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu94B2.v105 HVR-H1

<400> 302

Gly Tyr Thr Met Asn
1 5

<210> 303

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu94B2.v105 HVR-H2

<400> 303

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

Gly

<210> 304

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu94B2.v105 HVR-H3

<400> 304

Gln Gly Ala Tyr
1

<210> 305

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu94B2.v105 HVR-L1

<400> 305

Lys Ser Ser Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn

1 5 10 15

<210> 306

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu94B2.v105 HVR-L2

<400> 306

Leu Val Ser Lys Leu Asp Ser

1 5

<210> 307

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu94B2.v105 HVR-L3

<400> 307

Trp Gln Gly Thr His Phe Pro Trp Thr
1 5

<210> 308

<400> 308
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<210> 309

<400> 309
000

<210> 310
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: hu125B11.v17 heavy chain variable region (VH)

<400> 310

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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 Arg Phe Ile Phe Ser Asn Tyr
            20                  25                  30

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

Ala Gln Ile Arg Leu Lys Ser Asp Asn Tyr Ala Thr His Tyr Ala Glu
    50                  55                  60

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

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
                85                  90                  95

Tyr Cys Thr Gly Gly Thr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
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100 105 110

Val Ser Ser

115

<210> 311

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu125B11.v17 light chain variable region (VH)

<400> 311

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Ala

20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Lys Leu Leu Ile

35 40 45

Tyr Ser Ala Ser Ile Arg Tyr Thr 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 Phe Cys Gln Gln Phe Arg Thr Tyr Pro Tyr

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

100 105

<210> 312

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu125B11.v17 HVR-H1

<400> 312

Asn Tyr Trp Met Asn
1 5

<210> 313

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu125B11.v17 HVR-H2

<400> 313

Gln Ile Arg Leu Lys Ser Asp Asn Tyr Ala Thr His Tyr Ala Glu Ser
1 5 10 15

Val Lys Gly

<210> 314

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu125B11.v17 HVR-H3

<400> 314

Gly Thr Thr Tyr
1

<210> 315

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu125B11.v17 HVR-L1

<400> 315

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

<210> 316

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu125B11.v17 HVR-L2

<400> 316

Ser Ala Ser Ile Arg Tyr Thr

1 5

<210> 317

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu125B11.v17 HVR-L3

<400> 317

Gln Gln Phe Arg Thr Tyr Pro Tyr Thr

1 5

<210> 318

<400> 318

000

<210> 319

<400> 319

000

<210> 320

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu125B11.v26 heavy chain variable region (VH)

<400> 320

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 Arg Phe Ile Phe Ser Asn Tyr
20 25 30

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

Ala Gln Ile Arg Leu Lys Ser Asp Asn Tyr Ala Thr His Tyr Ala Glu
50 55 60

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

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Thr Gly Gly Thr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser

115

<210> 321

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu125B11.v26 light chain variable region (VH)

<400> 321

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

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

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Ile Arg Tyr Thr 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 Phe Cys Gln Gln Phe Arg Thr Tyr Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 322

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu125B11.v26 HVR-H1

<400> 322

Asn Tyr Trp Met Asn

1 5

<210> 323

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu125B11.v26 HVR-H2

<400> 323

Gln Ile Arg Leu Lys Ser Asp Asn Tyr Ala Thr His Tyr Ala Glu Ser

1 5 10 15

Val Lys Gly

<210> 324

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu125B11.v26 HVR-H3

<400> 324

Gly Thr Thr Tyr

1

<210> 325

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu125B11.v26 HVR-L1

<400> 325

Lys Ala Ser Gln Asn Val Gly Thr Ala Val Ala

1 5 10

<210> 326

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu125B11.v26 HVR-L2

<400> 326

Ser Ala Ser Ile Arg Tyr Thr
1 5

<210> 327

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu125B11.v26 HVR-L3

<400> 327

Gln Gln Phe Arg Thr Tyr Pro Tyr Thr
1 5

<210> 328

<400> 328

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<210> 329

<400> 329

000

<210> 330

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu125B11.v28 heavy chain variable region (VH)

<400> 330

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 Arg Phe Ile Phe Ser Asn Tyr

20 25 30

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

Ala Gln Ile Arg Leu Lys Ser Asp Asn Tyr Ala Thr His Tyr Ala Glu
50 55 60

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

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Thr Gly Gly Thr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 331

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu125B11.v28 light chain variable region (VH)

<400> 331

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

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

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Ile Arg Tyr Thr 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 Phe Arg Thr Tyr Pro Tyr

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

100 105

<210> 332

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu125B11.v28 HVR-H1

<400> 332

Asn Tyr Trp Met Asn

1 5

<210> 333

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu125B11.v28 HVR-H2

<400> 333

Gln Ile Arg Leu Lys Ser Asp Asn Tyr Ala Thr His Tyr Ala Glu Ser
1 5 10 15

Val Lys Gly

<210> 334

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu125B11.v28 HVR-H3

<400> 334

Gly Thr Thr Tyr

1

<210> 335

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu125B11.v28 HVR-L1

<400> 335

Lys Ala Ser Gln Asn Val Gly Thr Ala Val Ala

1 5 10

<210> 336

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu125B11.v28 HVR-L2

<400> 336

Ser Ala Ser Ile Arg Tyr Thr
1 5

<210> 337

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu125B11.v28 HVR-L3

<400> 337

Gln Gln Phe Arg Thr Tyr Pro Tyr Thr
1 5

<210> 338

<400> 338

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<210> 339

<400> 339

000

<210> 340

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v28.A4 heavy chain variable region (VH)

<400> 340

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 Leu Ile Phe Arg Ser Tyr
20 25 30

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

Ala Thr Ile Asn Ser Gly Gly Thr Tyr Thr Tyr Tyr Pro Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

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

Ala Asn Ser Tyr Ser Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 341
<211> 112
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v28.A4 light chain variable region (VL)

<400> 341

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

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser
20 25 30

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

Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Phe Gln Gly

85 90 95

Ser Leu Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

100 105 110

<210> 342

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v28.A4 HVR-H1

<400> 342

Ser Tyr Gly Met Ser

1 5

<210> 343

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v28.A4 HVR-H2

<400> 343

Thr Ile Asn Ser Gly Gly Thr Tyr Thr Tyr Tyr Pro Asp Ser Val Lys
1 5 10 15

Gly

<210> 344

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v28.A4 HVR-H3

<400> 344

Ser Tyr Ser Gly Ala Met Asp Tyr
1 5

<210> 345

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v28.A4 HVR-L1

<400> 345

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu

1 5 10 15

<210> 346

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v28.A4 HVR-L2

<400> 346

Lys Val Ser Asn Arg Phe Ser

1 5

<210> 347

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v28.A4 HVR-L3

<400> 347

Phe Gln Gly Ser Leu Val Pro Trp Thr

1 5

<210> 348

<211> 444

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v28.A4 IgG4-S228P.YTE heavy chain

<400> 348

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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 Leu Ile Phe Arg Ser Tyr
            20                  25                  30

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

Ala Thr Ile Asn Ser Gly Gly Thr Tyr Thr Tyr Tyr Pro Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

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

Ala Asn Ser Tyr Ser Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu
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100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu

115 120 125

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys

130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser

145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser

165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser

180 185 190

Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn

195 200 205

Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro
210 215 220

Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe
225 230 235 240

Pro Pro Lys Pro Lys Asp Thr Leu Tyr Ile Thr Arg Glu Pro Glu Val
245 250 255

Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
260 265 270

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

Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
290 295 300

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val

305 310 315 320

Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
325 330 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln
340 345 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
355 360 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
370 375 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
385 390 395 400

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

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

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440

<210> 349
<211> 219
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Hu37D3-H9.v28.A4 IgG4-S228P.YTE light chain

<400> 349

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

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser
20 25 30

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

Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Phe Gln Gly
85 90 95

Ser Leu Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

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

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe

130 135 140

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

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

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

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

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

<210> 350

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Unstressed control (mean, n=9)

<400> 350

Glu Asp Leu His Ser Asn Gly Asn Thr Tyr Phe Leu
1 5 10

<210> 351

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3-H9.v5

<400> 351

Glu Asp Leu His Ser Asn Gly Asn Thr Tyr Phe Leu
1 5 10

<210> 352

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3-H9.v5.1

<400> 352

Glu Asp Leu His Ser Asn Ala Asn Thr Tyr Phe Leu
1 5 10

<210> 353

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3-H9.v5.2

<400> 353

Glu Asp Leu His Ser Ser Gly Asn Thr Tyr Phe Leu
1 5 10

<210> 354

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3-H9.v5.3

<400> 354

Glu Asp Leu His Ser Asp Gly Asn Thr Tyr Phe Leu
1 5 10

<210> 355

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3-H9.v5.4

<400> 355

Glu Asp Leu His Ser Gln Gly Asn Thr Tyr Phe Leu

1 5 10

<210> 356

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3-H9.v5.5

<400> 356

Glu Asp Leu His Ser Glu Gly Asn Thr Tyr Phe Leu
1 5 10

<210> 357

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3-H9.v5.6

<400> 357

Glu Asp Leu His Ser Ala Gly Asn Thr Tyr Phe Leu

1 5 10

<210> 358

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3-H9.v5.7

<400> 358

Glu Asp Leu His Ser Asn Gly Asp Thr Tyr Phe Leu

1 5 10

<210> 359

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3-H9.v5.8

<400> 359

Glu Asp Leu His Ser Asn Gly Gln Thr Tyr Phe Leu
1 5 10

<210> 360

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3-H9.v5.9

<400> 360

Glu Asp Leu His Ser Asn Gly Glu Thr Tyr Phe Leu
1 5 10

<210> 361

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3-H9.v5.10

<400> 361

Glu Asp Leu His Ser Asn Gly Ala Thr Tyr Phe Leu
1 5 10

<210> 362

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3-H9.v5.11

<400> 362

Glu Asp Leu His Ser Asn Gly Ser Thr Tyr Phe Leu
1 5 10

<210> 363

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v28

<400> 363

Asp Asp Leu His Ser Asn Gly Asn Thr Tyr Phe Leu
1 5 10

<210> 364

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v28.A2

<400> 364

Asp Asp Leu His Ser Asn Gly Asn Thr Tyr Phe His
1 5 10

<210> 365

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v28.A4

<400> 365

Asp Asp Leu His Ser Asn Gly Asn Thr Tyr Leu Leu
1 5 10

<210> 366

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v28.A6

<400> 366

Asp Asp Leu His Ser Asn Gly Asn Thr Tyr Leu His
1 5 10

<210> 367

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v28.A8

<400> 367

Asp Asp Met His Ser Asn Gly Asn Thr Tyr Phe Leu
1 5 10

<210> 368

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v28.A10

<400> 368

Asp Asp Met His Ser Asn Gly Asn Thr Tyr Phe His

1 5 10

<210> 369

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v28.A12

<400> 369

Asp Asp Met His Ser Asn Gly Asn Thr Tyr Leu Leu

1 5 10

<210> 370

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v28.A14

<400> 370

Asp Asp Met His Ser Asn Gly Asn Thr Tyr Leu His

1 5 10

<210> 371

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v28.A16

<400> 371

Asp Val Leu His Ser Asn Gly Asn Thr Tyr Phe Leu

1 5 10

<210> 372

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v28.A18

<400> 372

Asp Val Leu His Ser Asn Gly Asn Thr Tyr Phe His
1 5 10

<210> 373

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v28.A20

<400> 373

Asp Val Leu His Ser Asn Gly Asn Thr Tyr Leu Leu
1 5 10

<210> 374

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v28.A22

<400> 374

Asp Val Leu His Ser Asn Gly Asn Thr Tyr Leu His
1 5 10

<210> 375

<211> 12

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<220>

<223> Synthetic: hu37D3.v28.A24

<400> 375

Asp Val Met His Ser Asn Gly Asn Thr Tyr Phe Leu
1 5 10

<210> 376

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v28.A26

<400> 376

Asp Val Met His Ser Asn Gly Asn Thr Tyr Phe His
1 5 10

<210> 377

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v28.A28

<400> 377

Asp Val Met His Ser Asn Gly Asn Thr Tyr Leu Leu
1 5 10

<210> 378

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v28.A30

<400> 378

Asp Val Met His Ser Asn Gly Asn Thr Tyr Leu His
1 5 10

<210> 379

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v28.B1

<400> 379

Asp Asp Leu His Ser Ile Gly Asn Thr Phe Phe Leu
1 5 10

<210> 380

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v28.B2

<400> 380

Asp Asp Leu His Ser Met Gly Asn Thr Phe Phe Leu
1 5 10

<210> 381

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v28.B3

<400> 381

Asp Asp Leu His Ser Gln Gly Asn Thr Trp Phe Leu

1 5 10

<210> 382

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v28.B4

<400> 382

Asp Asp Leu His Ser Gln Gly Asn Thr His Phe Leu

1 5 10

<210> 383

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v28.B6

<400> 383

Asp Asp Leu His Ser Asp Gly Asn Thr Arg Phe Leu

1 5 10

<210> 384

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v28.B7

<400> 384

Asp Asp Leu His Ser Asp Gly Asn Thr Lys Phe Leu

1 5 10

<210> 385

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v28.B8

<400> 385

Asp Asp Leu His Ser Glu Gly Asn Thr Arg Phe Leu
1 5 10

<210> 386

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v28.C1

<400> 386

Asp Asp Leu His Ser Asn Asn Asn Thr Tyr Phe Leu
1 5 10

<210> 387

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v28.C2

<400> 387

Asp Asp Leu His Ser Asn Asp Asn Thr Tyr Phe Leu
1 5 10

<210> 388

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v28.D1

<400> 388

Asp Asp Leu His Ala Asn Gly Asn Thr Tyr Phe Leu
1 5 10

<210> 389

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Unstressed control (mean, n=9)

<400> 389

Glu Asp Leu His Ser Asn Gly Asn Thr Tyr Phe Leu
1 5 10

<210> 390

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v28.E1

<400> 390

Asp Asp Leu Asn Ser Asn Gly Asn Thr Tyr Phe Leu
1 5 10

<210> 391

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v28.E2

<400> 391

Asp Asp Leu Gln Ser Asn Gly Asn Thr Tyr Phe Leu
1 5 10

<210> 392

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v28.E3

<400> 392

Asp Asp Leu Asp Ser Asp Gly Asn Thr Tyr Phe Leu
1 5 10

<210> 393

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v28.F1

<400> 393

Asp Asp Leu His Ser Asn Thr Asn Thr Tyr Phe Leu
1 5 10

<210> 394

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v28.F2

<400> 394

Asp Asp Leu His Thr Asn Gly Asn Thr Tyr Phe Leu

1 5 10

<210> 395

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v28.F3

<400> 395

Asp Asp Leu His Thr Asn Ala Asn Thr Tyr Phe Leu

1 5 10

<210> 396

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v28.51

<400> 396

Glu Asp Leu His Ser His Gly Asn Thr Tyr Phe Leu

1 5 10

<210> 397

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v28.52

<400> 397

Glu Asp Leu His Ser Lys Gly Asn Thr Tyr Phe Leu

1 5 10

<210> 398

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v28.53

<400> 398

Glu Asp Leu His Ser Arg Gly Asn Thr Tyr Phe Leu
1 5 10

<210> 399

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v28.54

<400> 399

Glu Asp Leu His Ser Leu Gly Asn Thr Tyr Phe Leu
1 5 10

<210> 400

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v28.55

<400> 400

Asp Asp Leu His Ser Asn Gln Asn Thr Tyr Phe Leu
1 5 10

<210> 401

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v28.56

<400> 401

Asp Asp Leu His Ser Asn Tyr Asn Thr Tyr Phe Leu
1 5 10

<210> 402

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v28.57

<400> 402

Asp Asp Leu His Ser Asn Phe Asn Thr Tyr Phe Leu
1 5 10

<210> 403

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v29.1

<400> 403

Glu Asp Leu His Ser Asn Gly Asp Thr Tyr Phe Leu
1 5 10

<210> 404

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v29.2

<400> 404

Glu Asp Leu His Ser Asn Gly Gln Thr Tyr Phe Leu
1 5 10

<210> 405

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v29.3

<400> 405

Glu Asp Leu His Ser Asn Gly Glu Thr Tyr Phe Leu
1 5 10

<210> 406

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v29.4

<400> 406

Glu Asp Leu His Ser Asn Gly Ala Thr Tyr Phe Leu
1 5 10

<210> 407

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v29.5

<400> 407

Glu Asp Leu His Ser Asn Gly His Thr Tyr Phe Leu

1 5 10

<210> 408

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v29.6

<400> 408

Glu Asp Leu His Ser Asn Gly Lys Thr Tyr Phe Leu
1 5 10

<210> 409

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v29.7

<400> 409

Glu Asp Leu His Ser Asn Gly Leu Thr Tyr Phe Leu

1 5 10

<210> 410

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v29.8

<400> 410

Glu Asp Leu His Ser Asn Ala Asp Thr Tyr Phe Leu

1 5 10

<210> 411

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v29.9

<400> 411

Glu Asp Leu His Ser Asn Ala Gln Thr Tyr Phe Leu
1 5 10

<210> 412
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: hu37D3.v29.10

<400> 412

Glu Asp Leu His Ser Asn Ala Glu Thr Tyr Phe Leu
1 5 10

<210> 413
<211> 12
<212> PRT
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<220>

<223> Synthetic: hu37D3.v29.11

<400> 413

Glu Asp Leu His Ser Asn Ala Ala Thr Tyr Phe Leu
1 5 10

<210> 414

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v29.12

<400> 414

Glu Asp Leu His Ser Asn Ala His Thr Tyr Phe Leu
1 5 10

<210> 415

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v29.13

<400> 415

Glu Asp Leu His Ser Asn Ala Lys Thr Tyr Phe Leu
1 5 10

<210> 416

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3.v29.14

<400> 416

Glu Asp Leu His Ser Asn Ala Leu Thr Tyr Phe Leu
1 5 10

<210> 417

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3-H9.v30.1

<400> 417

Asp Asp Leu His Ser Gly Gly Asn Thr Tyr Phe Leu
1 5 10

<210> 418

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3-H9.v30.2

<400> 418

Asp Asp Leu His Ser Thr Gly Asn Thr Tyr Phe Leu
1 5 10

<210> 419

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3-H9.v30.3

<400> 419

Asp Asp Leu His Ser Val Gly Asn Thr Tyr Phe Leu
1 5 10

<210> 420

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3-H9.v30.4

<400> 420

Asp Asp Leu His Ser Leu Gly Asn Thr Tyr Phe Leu

1 5 10

<210> 421

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3-H9.v30.5

<400> 421

Asp Asp Leu His Ser Ile Gly Asn Thr Tyr Phe Leu

1 5 10

<210> 422

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3-H9.v30.6

<400> 422

Asp Asp Leu His Ser Pro Gly Asn Thr Tyr Phe Leu

1 5 10

<210> 423

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3-H9.v30.7

<400> 423

Asp Asp Leu His Ser Phe Gly Asn Thr Tyr Phe Leu

1 5 10

<210> 424

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3-H9.v30.8

<400> 424

Asp Asp Leu His Ser Tyr Gly Asn Thr Tyr Phe Leu
1 5 10

<210> 425
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: hu37D3-H9.v30.9

<400> 425

Asp Asp Leu His Ser His Gly Asn Thr Tyr Phe Leu
1 5 10

<210> 426
<211> 12
<212> PRT
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<220>

<223> Synthetic: hu37D3-H9.v30.10

<400> 426

Asp Asp Leu His Ser Lys Gly Asn Thr Tyr Phe Leu
1 5 10

<210> 427

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3-H9.v30.11

<400> 427

Asp Asp Leu His Ser Arg Gly Asn Thr Tyr Phe Leu
1 5 10

<210> 428

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3-H9.v31.1

<400> 428

Asp Asp Leu His Ser Asn Ala Gly Thr Tyr Phe Leu
1 5 10

<210> 429

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3-H9.v31.2

<400> 429

Asp Asp Leu His Ser Asn Ala Val Thr Tyr Phe Leu
1 5 10

<210> 430

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3-H9.v31.3

<400> 430

Asp Asp Leu His Ser Asn Ala Ile Thr Tyr Phe Leu
1 5 10

<210> 431

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3-H9.v31.4

<400> 431

Asp Asp Leu His Ser Asn Ala Pro Thr Tyr Phe Leu
1 5 10

<210> 432

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3-H9.v31.5

<400> 432

Asp Asp Leu His Ser Asn Ala Phe Thr Tyr Phe Leu
1 5 10

<210> 433

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3-H9.v31.6

<400> 433

Asp Asp Leu His Ser Asn Ala Tyr Thr Tyr Phe Leu

1 5 10

<210> 434

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3-H9.v31.7

<400> 434

Asp Asp Leu His Ser Asn Ala Arg Thr Tyr Phe Leu

1 5 10

<210> 435

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3-H9.v31.8

<400> 435

Asp Asp Leu His Ser Asn Ala Asn Val Tyr Phe Leu

1 5 10

<210> 436

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3-H9.v31.9

<400> 436

Asp Asp Leu His Ser Asn Ala Asn Ile Tyr Phe Leu

1 5 10

<210> 437

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3-H9.v31.10

<400> 437

Asp Asp Leu His Ser Asn Ala Asn Pro Tyr Phe Leu
1 5 10

<210> 438
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: hu37D3-H9.v31.11

<400> 438

Asp Asp Leu His Ser Asn Ala Asn Phe Tyr Phe Leu
1 5 10

<210> 439
<211> 12
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3-H9.v31.12

<400> 439

Asp Asp Leu His Ser Asn Ala Asn Tyr Tyr Phe Leu
1 5 10

<210> 440

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3-H9.v31.13

<400> 440

Asp Asp Leu His Ser Asn Ala Asn Asn Tyr Phe Leu
1 5 10

<210> 441

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu37D3-H9.v31.14

<400> 441

Asp Asp Leu His Ser Asn Ala Asn Arg Tyr Phe Leu
1 5 10

<210> 442

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu125B11-H3.LC1

<400> 442

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

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Ala

20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Lys Leu Leu Ile

35 40 45

Tyr Ser Ala Ser Ile Arg Tyr Thr 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 Phe Cys Gln Gln Phe Arg Thr Tyr Pro Tyr

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

100 105

<210> 443

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu125B11-H3.LC2

<400> 443

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

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

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Ile Arg Tyr Thr 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 Phe Cys Gln Gln Phe Arg Thr Tyr Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 444
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: hu125B11-H3.LC3

<400> 444

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

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

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

Tyr Ser Ala Ser Ile Arg Tyr Thr 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 Phe Arg Thr Tyr Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 445
<211> 107
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic: hu125B11-H3.LC4

<400> 445

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

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

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Ile Arg Tyr Thr 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 Phe Arg Thr Tyr Pro Tyr

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

100 105

<210> 446

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu125B11-H3.HC1

<400> 446

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 Arg Phe Ile Phe Ser Asn Tyr

20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Gln Ile Arg Leu Lys Ser Asp Asn Tyr Ala Thr His Tyr Ala Glu
50 55 60

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

Val Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Thr Gly Gly Thr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 447

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu125B11-H3.HC2

<400> 447

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 Arg Phe Ile Phe Ser Asn Tyr
20 25 30

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

Ala Gln Ile Arg Leu Lys Ser Asp Asn Tyr Ala Thr His Tyr Ala Glu
50 55 60

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

Val Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Thr Gly Gly Thr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 448
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: hu125B11-H3.HC3

<400> 448

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 Arg Phe Ile Phe Ser Asn Tyr
20 25 30

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

Ala Gln Ile Arg Leu Lys Ser Asp Asn Tyr Ala Thr His Tyr Ala Glu
50 55 60

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

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Thr Gly Gly Thr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser

115

<210> 449

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu125B11-H3.HC4

<400> 449

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 Arg Phe Ile Phe Ser Asn Tyr
20 25 30

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

Ala Gln Ile Arg Leu Lys Ser Asp Asn Tyr Ala Thr His Tyr Ala Glu

50 55 60

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

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Thr Gly Gly Thr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 450
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: hu125B11-H3.HC5

<400> 450

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 Arg Phe Ile Phe Ser Asn Tyr
20 25 30

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

Ala Gln Ile Arg Leu Lys Ser Asp Asn Tyr Ala Thr His Tyr Ala Glu
50 55 60

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

Val Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Thr Gly Gly Thr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 451
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: hu125B11-H3.HC6

<400> 451

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 Arg Phe Ile Phe Ser Asn Tyr
20 25 30

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

Ala Gln Ile Arg Leu Lys Ser Asp Asn Tyr Ala Thr His Tyr Ala Glu
50 55 60

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

Val Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Thr Gly Gly Thr Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 452

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu94B2.HC1

<400> 452

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

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

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

Gly Leu Ile Ser Pro Tyr Asn Gly Val Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Arg Ala Thr Leu Thr Val Asp Lys Ser Thr Ser Thr Ala Tyr

65 70 75 80

Leu Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Gln Gly Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser

100 105 110

Ser

<210> 453

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu94B2.HC2

<400> 453

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala

1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Leu Thr Gly Tyr

20 25 30

Thr Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile

35 40 45

Gly Leu Ile Ser Pro Tyr Asn Gly Val Thr Ser Tyr Asn Gln Lys Phe

50 55 60

Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser Thr Ala Tyr

65 70 75 80

Leu Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Gln Gly Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser

100 105 110

Ser

<210> 454

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu94B2.HC3

<400> 454

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

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

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

Gly Leu Ile Ser Pro Tyr Asn Gly Val Thr Ser Tyr Asn Gln Lys Phe
50 55 60

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

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

Ala Arg Gln Gly Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
100 105 110

Ser

<210> 455
<211> 113
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic: Hu94B2.HC4

<400> 455

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

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

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

Gly Leu Ile Ser Pro Tyr Asn Gly Val Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Arg Ala Thr Leu Thr Arg Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Leu Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Gln Gly Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser

100 105 110

Ser

<210> 456

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu94B2.HC5

<400> 456

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala

1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Leu Thr Gly Tyr

20 25 30

Thr Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile

35 40 45

Gly Leu Ile Ser Pro Tyr Asn Gly Val Thr Ser Tyr Asn Gln Lys Phe

50 55 60

Lys Gly Arg Ala Thr Leu Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr

65 70 75 80

Leu Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Gln Gly Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser

100 105 110

Ser

<210> 457

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu94B2.HC6

<400> 457

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

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

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

Gly Leu Ile Ser Pro Tyr Asn Gly Val Thr Ser Tyr Asn Gln Lys Phe
50 55 60

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

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

Ala Arg Gln Gly Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
100 105 110

Ser

<210> 458
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Hu94B2.HC7

<400> 458

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

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

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

Gly Leu Ile Ser Pro Tyr Asn Gly Val Thr Ser Tyr Asn Gln Lys Phe
    50                  55                  60

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

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

Ala Arg Gln Gly Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
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100 105 110

Ser

<210> 459

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu94B2.HC8

<400> 459

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala

1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Leu Thr Gly Tyr

20 25 30

Thr Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile

35 40 45

Gly Leu Ile Ser Pro Tyr Asn Gly Val Thr Ser Tyr Asn Gln Lys Phe

50 55 60

Lys Gly Arg Val Thr Ile Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr

65 70 75 80

Leu Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Gln Gly Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser

100 105 110

Ser

<210> 460

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu94B2.LC9

<400> 460

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

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

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

Pro Gln Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly
85 90 95

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

<210> 461

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu94B2.LC10

<400> 461

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

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

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

Pro Gln Leu Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly
85 90 95

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

<210> 462
<211> 112
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic: Hu94B2.LC11

<400> 462

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

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

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

Pro Gln Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly

85 90 95

Thr His Phe Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

100 105 110

<210> 463

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu94B2.LC12

<400> 463

Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Thr Pro Gly

1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser

20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Tyr Leu Gln Lys Pro Gly Gln Ser

35 40 45

Pro Gln Leu Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro

50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile

65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly

85 90 95

Thr His Phe Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

100 105 110

<210> 464

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu94B2.LC13

<400> 464

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

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

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

Pro Gln Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly
85 90 95

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

<210> 465

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu94B2.LC14

<400> 465

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

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

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

Pro Gln Leu Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly
85 90 95

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

<210> 466
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Hu94B2.LC15

<400> 466

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

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

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

Pro Gln Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
    50                  55                  60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly
                85                  90                  95

Thr His Phe Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
```

100 105 110

<210> 467

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu94B2.LC16

<400> 467

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

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

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

Pro Gln Leu Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro

50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly
85 90 95

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

<210> 468

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v5.1 HVR-L1

<400> 468

Arg Ser Ser Gln Ser Ile Val His Ser Asn Ala Asn Thr Tyr Phe Glu

1 5 10 15

<210> 469

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v5.2 HVR-L1

<400> 469

Arg Ser Ser Gln Ser Ile Val His Ser Ser Gly Asn Thr Tyr Phe Glu

1 5 10 15

<210> 470

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v5.3 HVR-L1

<400> 470

Arg Ser Ser Gln Ser Ile Val His Ser Asp Gly Asn Thr Tyr Phe Glu
1 5 10 15

<210> 471
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Hu37D3-H9.v5.4 HVR-L1

<400> 471

Arg Ser Ser Gln Ser Ile Val His Ser Gln Gly Asn Thr Tyr Phe Glu
1 5 10 15

<210> 472
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Hu37D3-H9.v5.5 HVR-L1

<400> 472

Arg Ser Ser Gln Ser Ile Val His Ser Glu Gly Asn Thr Tyr Phe Glu
1 5 10 15

<210> 473

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v5.6 HVR-L1

<400> 473

Arg Ser Ser Gln Ser Ile Val His Ser Ala Gly Asn Thr Tyr Phe Glu
1 5 10 15

<210> 474

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v5.7 HVR-L1

<400> 474

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asp Thr Tyr Phe Glu
1 5 10 15

<210> 475

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v5.8 HVR-L1

<400> 475

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Gln Thr Tyr Phe Glu
1 5 10 15

<210> 476

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v5.9 HVR-L1

<400> 476

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Glu Thr Tyr Phe Glu
1 5 10 15

<210> 477

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v5.10 HVR-L1

<400> 477

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Ala Thr Tyr Phe Glu
1 5 10 15

<210> 478

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v5.11 HVR-L1

<400> 478

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Ser Thr Tyr Phe Glu
1 5 10 15

<210> 479

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v28 HVR-L1

<400> 479

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Phe Glu
1 5 10 15

<210> 480

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v28.A2 HVR-L1

<400> 480

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Phe Glu
1 5 10 15

<210> 481

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v28.A4 HVR-L1

<400> 481

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu

1 5 10 15

<210> 482

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v28.A6 HVR-L1

<400> 482

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu

1 5 10 15

<210> 483

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v28.A8 HVR-L1

<400> 483

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Phe Glu

1 5 10 15

<210> 484

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v28.A10 HVR-L1

<400> 484

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Phe Glu

1 5 10 15

<210> 485

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v28.A12 HVR-L1

<400> 485

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu
1 5 10 15

<210> 486

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v28.A14 HVR-L1

<400> 486

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu
1 5 10 15

<210> 487

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v28.A16 HVR-L1

<400> 487

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Phe Glu
1 5 10 15

<210> 488

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v28.A18 HVR-L1

<400> 488

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Phe Glu
1 5 10 15

<210> 489

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v28.A20 HVR-L1

<400> 489

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu
1 5 10 15

<210> 490

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v28.A22 HVR-L1

<400> 490

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu
1 5 10 15

<210> 491

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v28.A24 HVR-L1

<400> 491

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Phe Glu
1 5 10 15

<210> 492

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v28.A26 HVR-L1

<400> 492

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Phe Glu
1 5 10 15

<210> 493

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v28.A28 HVR-L1

<400> 493

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu
1 5 10 15

<210> 494

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v28.A30 HVR-L1

<400> 494

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu

1 5 10 15

<210> 495

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v28.B1 HVR-L1

<400> 495

Arg Ser Ser Gln Ser Ile Val His Ser Ile Gly Asn Thr Phe Phe Glu

1 5 10 15

<210> 496

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v28.B2 HVR-L1

<400> 496

Arg Ser Ser Gln Ser Ile Val His Ser Met Gly Asn Thr Phe Phe Glu
1 5 10 15

<210> 497

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v28.B3 HVR-L1

<400> 497

Arg Ser Ser Gln Ser Ile Val His Ser Gln Gly Asn Thr Trp Phe Glu
1 5 10 15

<210> 498

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v28.B4 HVR-L1

<400> 498

Arg Ser Ser Gln Ser Ile Val His Ser Gln Gly Asn Thr His Phe Glu
1 5 10 15

<210> 499

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v28.B6 HVR-L1

<400> 499

Arg Ser Ser Gln Ser Ile Val His Ser Asp Gly Asn Thr Arg Phe Glu
1 5 10 15

<210> 500

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v28.B7 HVR-L1

<400> 500

Arg Ser Ser Gln Ser Ile Val His Ser Asp Gly Asn Thr Lys Phe Glu
1 5 10 15

<210> 501

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v28.B8 HVR-L1

<400> 501

Arg Ser Ser Gln Ser Ile Val His Ser Glu Gly Asn Thr Arg Phe Glu
1 5 10 15

<210> 502

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v28.C1 HVR-L1

<400> 502

Arg Ser Ser Gln Ser Ile Val His Ser Asn Asn Asn Thr Tyr Phe Glu
1 5 10 15

<210> 503

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v28.C2 HVR-L1

<400> 503

Arg Ser Ser Gln Ser Ile Val His Ser Asn Asp Asn Thr Tyr Phe Glu
1 5 10 15

<210> 504

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v28.D1 HVR-L1

<400> 504

Arg Ser Ser Gln Ser Ile Val His Ala Asn Gly Asn Thr Tyr Phe Glu
1 5 10 15

<210> 505

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v28.E1 HVR-L1

<400> 505

Arg Ser Ser Gln Ser Ile Val Asn Ser Asn Gly Asn Thr Tyr Phe Glu
1 5 10 15

<210> 506

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v28.E2 HVR-L1

<400> 506

Arg Ser Ser Gln Ser Ile Val Gln Ser Asn Gly Asn Thr Tyr Phe Glu
1 5 10 15

<210> 507

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v28.E3 HVR-L1

<400> 507

Arg Ser Ser Gln Ser Ile Val Asp Ser Asp Gly Asn Thr Tyr Phe Glu

1 5 10 15

<210> 508

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v28.F1 HVR-L1

<400> 508

Arg Ser Ser Gln Ser Ile Val His Ser Asn Thr Asn Thr Tyr Phe Glu

1 5 10 15

<210> 509

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v28.F2 HVR-L1

<400> 509

Arg Ser Ser Gln Ser Ile Val His Thr Asn Gly Asn Thr Tyr Phe Glu
1 5 10 15

<210> 510

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v28.F3 HVR-L1

<400> 510

Arg Ser Ser Gln Ser Ile Val His Thr Asn Ala Asn Thr Tyr Phe Glu
1 5 10 15

<210> 511

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v28.51 HVR-L1

<400> 511

Arg Ser Ser Gln Ser Ile Val His Ser His Gly Asn Thr Tyr Phe Glu
1 5 10 15

<210> 512
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Hu37D3.v28.52 HVR-L1

<400> 512

Arg Ser Ser Gln Ser Ile Val His Ser Lys Gly Asn Thr Tyr Phe Glu
1 5 10 15

<210> 513
<211> 16
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v28.53 HVR-L1

<400> 513

Arg Ser Ser Gln Ser Ile Val His Ser Arg Gly Asn Thr Tyr Phe Glu
1 5 10 15

<210> 514

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v28.54 HVR-L1

<400> 514

Arg Ser Ser Gln Ser Ile Val His Ser Leu Gly Asn Thr Tyr Phe Glu
1 5 10 15

<210> 515

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v28.55 HVR-L1

<400> 515

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gln Asn Thr Tyr Phe Glu
1 5 10 15

<210> 516

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v28.56 HVR-L1

<400> 516

Arg Ser Ser Gln Ser Ile Val His Ser Asn Tyr Asn Thr Tyr Phe Glu
1 5 10 15

<210> 517

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v28.57 HVR-L1

<400> 517

Arg Ser Ser Gln Ser Ile Val His Ser Asn Phe Asn Thr Tyr Phe Glu
1 5 10 15

<210> 518

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v29.1 HVR-L1

<400> 518

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asp Thr Tyr Phe Glu
1 5 10 15

<210> 519

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v29.2 HVR-L1

<400> 519

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Gln Thr Tyr Phe Glu
1 5 10 15

<210> 520

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v29.3 HVR-L1

<400> 520

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Glu Thr Tyr Phe Glu

1 5 10 15

<210> 521

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v29.4 HVR-L1

<400> 521

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Ala Thr Tyr Phe Glu

1 5 10 15

<210> 522

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v29.5 HVR-L1

<400> 522

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly His Thr Tyr Phe Glu
1 5 10 15

<210> 523
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Hu37D3.v29.6 HVR-L1

<400> 523

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Lys Thr Tyr Phe Glu
1 5 10 15

<210> 524
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Hu37D3.v29.7 HVR-L1

<400> 524

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Leu Thr Tyr Phe Glu
1 5 10 15

<210> 525

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v29.8 HVR-L1

<400> 525

Arg Ser Ser Gln Ser Ile Val His Ser Asn Ala Asp Thr Tyr Phe Glu
1 5 10 15

<210> 526

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v29.9 HVR-L1

<400> 526

Arg Ser Ser Gln Ser Ile Val His Ser Asn Ala Gln Thr Tyr Phe Glu
1 5 10 15

<210> 527

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v29.10 HVR-L1

<400> 527

Arg Ser Ser Gln Ser Ile Val His Ser Asn Ala Glu Thr Tyr Phe Glu
1 5 10 15

<210> 528

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v29.11 HVR-L1

<400> 528

Arg Ser Ser Gln Ser Ile Val His Ser Asn Ala Ala Thr Tyr Phe Glu
1 5 10 15

<210> 529

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v29.12 HVR-L1

<400> 529

Arg Ser Ser Gln Ser Ile Val His Ser Asn Ala His Thr Tyr Phe Glu
1 5 10 15

<210> 530

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v29.13 HVR-L1

<400> 530

Arg Ser Ser Gln Ser Ile Val His Ser Asn Ala Lys Thr Tyr Phe Glu
1 5 10 15

<210> 531

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v29.14 HVR-L1

<400> 531

Arg Ser Ser Gln Ser Ile Val His Ser Asn Ala Leu Thr Tyr Phe Glu
1 5 10 15

<210> 532

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v30.1 HVR-L1

<400> 532

Arg Ser Ser Gln Ser Ile Val His Ser Gly Gly Asn Thr Tyr Phe Glu
1 5 10 15

<210> 533

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v30.2 HVR-L1

<400> 533

Arg Ser Ser Gln Ser Ile Val His Ser Thr Gly Asn Thr Tyr Phe Glu

1 5 10 15

<210> 534

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v30.3 HVR-L1

<400> 534

Arg Ser Ser Gln Ser Ile Val His Ser Val Gly Asn Thr Tyr Phe Glu

1 5 10 15

<210> 535

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v30.4 HVR-L1

<400> 535

Arg Ser Ser Gln Ser Ile Val His Ser Leu Gly Asn Thr Tyr Phe Glu

1 5 10 15

<210> 536

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v30.5 HVR-L1

<400> 536

Arg Ser Ser Gln Ser Ile Val His Ser Ile Gly Asn Thr Tyr Phe Glu

1 5 10 15

<210> 537

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v30.6 HVR-L1

<400> 537

Arg Ser Ser Gln Ser Ile Val His Ser Pro Gly Asn Thr Tyr Phe Glu
1 5 10 15

<210> 538

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v30.7 HVR-L1

<400> 538

Arg Ser Ser Gln Ser Ile Val His Ser Phe Gly Asn Thr Tyr Phe Glu
1 5 10 15

<210> 539

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v30.8 HVR-L1

<400> 539

Arg Ser Ser Gln Ser Ile Val His Ser Tyr Gly Asn Thr Tyr Phe Glu
1 5 10 15

<210> 540

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v30.9 HVR-L1

<400> 540

Arg Ser Ser Gln Ser Ile Val His Ser His Gly Asn Thr Tyr Phe Glu
1 5 10 15

<210> 541

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v30.10 HVR-L1

<400> 541

Arg Ser Ser Gln Ser Ile Val His Ser Lys Gly Asn Thr Tyr Phe Glu
1 5 10 15

<210> 542

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v30.11 HVR-L1

<400> 542

Arg Ser Ser Gln Ser Ile Val His Ser Arg Gly Asn Thr Tyr Phe Glu
1 5 10 15

<210> 543

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v31.1 HVR-L1

<400> 543

Arg Ser Ser Gln Ser Ile Val His Ser Asn Ala Gly Thr Tyr Phe Glu
1 5 10 15

<210> 544

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v31.2 HVR-L1

<400> 544

Arg Ser Ser Gln Ser Ile Val His Ser Asn Ala Val Thr Tyr Phe Glu
1 5 10 15

<210> 545

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v31.3 HVR-L1

<400> 545

Arg Ser Ser Gln Ser Ile Val His Ser Asn Ala Ile Thr Tyr Phe Glu
1 5 10 15

<210> 546

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v31.4 HVR-L1

<400> 546

Arg Ser Ser Gln Ser Ile Val His Ser Asn Ala Pro Thr Tyr Phe Glu

1 5 10 15

<210> 547

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v31.5 HVR-L1

<400> 547

Arg Ser Ser Gln Ser Ile Val His Ser Asn Ala Phe Thr Tyr Phe Glu
1 5 10 15

<210> 548

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v31.6 HVR-L1

<400> 548

Arg Ser Ser Gln Ser Ile Val His Ser Asn Ala Tyr Thr Tyr Phe Glu

1 5 10 15

<210> 549

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v31.7 HVR-L1

<400> 549

Arg Ser Ser Gln Ser Ile Val His Ser Asn Ala Arg Thr Tyr Phe Glu

1 5 10 15

<210> 550

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v31.8 HVR-L1

<400> 550

Arg Ser Ser Gln Ser Ile Val His Ser Asn Ala Asn Val Tyr Phe Glu
1 5 10 15

<210> 551

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v31.9 HVR-L1

<400> 551

Arg Ser Ser Gln Ser Ile Val His Ser Asn Ala Asn Ile Tyr Phe Glu
1 5 10 15

<210> 552

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v31.10 HVR-L1

<400> 552

Arg Ser Ser Gln Ser Ile Val His Ser Asn Ala Asn Pro Tyr Phe Glu
1 5 10 15

<210> 553

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v31.11 HVR-L1

<400> 553

Arg Ser Ser Gln Ser Ile Val His Ser Asn Ala Asn Phe Tyr Phe Glu
1 5 10 15

<210> 554

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v31.12 HVR-L1

<400> 554

Arg Ser Ser Gln Ser Ile Val His Ser Asn Ala Asn Tyr Tyr Phe Glu
1 5 10 15

<210> 555

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v31.13 HVR-L1

<400> 555

Arg Ser Ser Gln Ser Ile Val His Ser Asn Ala Asn Asn Tyr Phe Glu
1 5 10 15

<210> 556

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v31.14 HVR-L1

<400> 556

Arg Ser Ser Gln Ser Ile Val His Ser Asn Ala Asn Arg Tyr Phe Glu
1 5 10 15

<210> 557

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Human Tau 7-24 peptide

<400> 557

Glu Phe Glu Val Met Glu Asp His Ala Gly Thr Tyr Gly Leu Gly Asp
1 5 10 15

Arg Lys

<210> 558

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Human Tau 7-20 peptide

<400> 558

Glu Phe Glu Val Met Glu Asp His Ala Gly Thr Tyr Gly Leu
1 5 10

<210> 559

<400> 559

000

<210> 560

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v39 heavy chain variable region (VH)

<400> 560

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 Leu Ile Phe Arg Ser Tyr
20 25 30

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

Ala Thr Ile Asn Ser Gly Gly Thr Tyr Thr Tyr Tyr Pro Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

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

Ala Asn Ser Tyr Ser Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 561
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Hu37D3.v39 light chain variable region (VL)

<400> 561

Glu Asp 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 Ser Ser Gln Ser Ile Val His Ser
            20                  25                  30

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

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
    50                  55                  60

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

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

Ser Leu Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105                 110
```

<210> 562

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v39 HVR-H1

<400> 562

Ser Tyr Gly Met Ser
1 5

<210> 563

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v39 HVR-H2

<400> 563

Thr Ile Asn Ser Gly Gly Thr Tyr Thr Tyr Tyr Pro Asp Ser Val Lys
1 5 10 15

Gly

<210> 564

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v39 HVR-H3

<400> 564

Ser Tyr Ser Gly Ala Met Asp Tyr

1 5

<210> 565

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v39 HVR-L1

<400> 565

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu
1 5 10 15

<210> 566

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v39 HVR-L2

<400> 566

Lys Val Ser Asn Arg Phe Ser
1 5

<210> 567

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v39 HVR-L3

<400> 567

Phe Gln Gly Ser Leu Val Pro Trp Thr
1 5

<210> 568

<211> 444

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v39 IgG4-S228P.YTE heavy chain

<400> 568

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 Leu Ile Phe Arg Ser Tyr
20 25 30

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

Ala Thr Ile Asn Ser Gly Gly Thr Tyr Thr Tyr Tyr Pro Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

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

Ala Asn Ser Tyr Ser Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110

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

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys

130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser

145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser

165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser

180 185 190

Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn

195 200 205

Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro

210 215 220

Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe

225 230 235 240

Pro Pro Lys Pro Lys Asp Thr Leu Tyr Ile Thr Arg Glu Pro Glu Val
245 250 255

Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
260 265 270

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

Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
290 295 300

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305 310 315 320

Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
325 330 335

```
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln
            340                 345                 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
        355                 360                 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
    370                 375                 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
385                 390                 395                 400

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

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

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440
```

<210> 569

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v39 IgG4-S228P.YTE light chain

<400> 569

Glu Asp 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 Ser Ser Gln Ser Ile Val His Ser
20 25 30

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

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

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

Ser Leu Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105                 110

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

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

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

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser

165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu

180 185 190

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

195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys

210 215

<210> 570

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v40 heavy chain variable region (VH)

<400> 570

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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 Leu Ile Phe Arg Ser Tyr
            20                  25                  30

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

Ala Thr Ile Asn Ser Gly Gly Thr Tyr Thr Tyr Tyr Pro Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

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

Ala Asn Ser Tyr Ser Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110
```

Val Thr Val Ser Ser
115

<210> 571
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Hu37D3.v40 light chain variable region (VL)

<400> 571

Glu Asp 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 Ser Ser Gln Ser Ile Val His Ser
20 25 30

Asn Thr Asn Thr Tyr Phe Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ser
35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

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

Ser Leu Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 572
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Hu37D3.v40 HVR-H1

<400> 572

Ser Tyr Gly Met Ser
1 5

<210> 573

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v40 HVR-H2

<400> 573

Thr Ile Asn Ser Gly Gly Thr Tyr Thr Tyr Tyr Pro Asp Ser Val Lys
1 5 10 15

Gly

<210> 574

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v40 HVR-H3

<400> 574

Ser Tyr Ser Gly Ala Met Asp Tyr
1 5

<210> 575

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v40 HVR-L1

<400> 575

Arg Ser Ser Gln Ser Ile Val His Ser Asn Thr Asn Thr Tyr Phe Glu
1 5 10 15

<210> 576

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v40 HVR-L2

<400> 576

Lys Val Ser Asn Arg Phe Ser
1 5

<210> 577

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v40 HVR-L3

<400> 577

Phe Gln Gly Ser Leu Val Pro Trp Thr
1 5

<210> 578

<211> 444

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v40 IgG4-S228P.YTE heavy chain

<400> 578

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 Leu Ile Phe Arg Ser Tyr
20 25 30

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

Ala Thr Ile Asn Ser Gly Gly Thr Tyr Thr Tyr Tyr Pro Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

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

Ala Asn Ser Tyr Ser Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

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

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145 150 155 160

```
Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
                165                 170                 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
            180                 185                 190

Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
        195                 200                 205

Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro
    210                 215                 220

Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe
225                 230                 235                 240

Pro Pro Lys Pro Lys Asp Thr Leu Tyr Ile Thr Arg Glu Pro Glu Val
                245                 250                 255

Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
            260                 265                 270
```

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

Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
    290                 295                 300

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305                 310                 315                 320

Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
                325                 330                 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln
            340                 345                 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
        355                 360                 365
```

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro

370 375 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser

385 390 395 400

Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu

405 410 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His

420 425 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys

435 440

<210> 579

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v40 IgG4-S228P.YTE light chain

<400> 579

Glu Asp 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 Ser Ser Gln Ser Ile Val His Ser
20 25 30

Asn Thr Asn Thr Tyr Phe Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ser
35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

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

Ser Leu Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

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

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

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

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

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

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

195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys

210 215

<210> 580

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v41 heavy chain variable region (VH)

<400> 580

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 Leu Ile Phe Arg Ser Tyr

20 25 30

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Thr Ile Asn Ser Gly Gly Thr Tyr Thr Tyr Tyr Pro Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Asn Ser Tyr Ser Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu

100 105 110

Val Thr Val Ser Ser

115

<210> 581

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v41 light chain variable region (VL)

<400> 581

Glu Asp 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 Ser Ser Gln Ser Ile Val His Ser
20 25 30

Asn Gly Gln Thr Tyr Phe Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ser
35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

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

Ser Leu Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 582
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Hu37D3.v41 HVR-H1

<400> 582

Ser Tyr Gly Met Ser
1 5

<210> 583
<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v41 HVR-H2

<400> 583

Thr Ile Asn Ser Gly Gly Thr Tyr Thr Tyr Tyr Pro Asp Ser Val Lys
1 5 10 15

Gly

<210> 584

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v41 HVR-H3

<400> 584

Ser Tyr Ser Gly Ala Met Asp Tyr

1 5

<210> 585

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v41 HVR-L1

<400> 585

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Gln Thr Tyr Phe Glu

1 5 10 15

<210> 586

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v41 HVR-L2

<400> 586

Lys Val Ser Asn Arg Phe Ser
1 5

<210> 587

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v41 HVR-L3

<400> 587

Phe Gln Gly Ser Leu Val Pro Trp Thr
1 5

<210> 588

<211> 444

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v41 IgG4-S228P.YTE heavy chain

<400> 588

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 Leu Ile Phe Arg Ser Tyr
20 25 30

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

Ala Thr Ile Asn Ser Gly Gly Thr Tyr Thr Tyr Tyr Pro Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

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

```
Ala Asn Ser Tyr Ser Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110

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

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
    130                 135                 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145                 150                 155                 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
                165                 170                 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
            180                 185                 190
```

Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
195 200 205

Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro
210 215 220

Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe
225 230 235 240

Pro Pro Lys Pro Lys Asp Thr Leu Tyr Ile Thr Arg Glu Pro Glu Val
245 250 255

Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
260 265 270

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

Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
290 295 300

```
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305                 310                 315                 320

Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
                325                 330                 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln
            340                 345                 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
        355                 360                 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
    370                 375                 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
385                 390                 395                 400
```

Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu

405 410 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His

420 425 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys

435 440

<210> 589

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3.v41 IgG4-S228P.YTE light chain

<400> 589

Glu Asp 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 Ser Ser Gln Ser Ile Val His Ser
            20                  25                  30

Asn Gly Gln Thr Tyr Phe Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ser
        35                  40                  45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
    50                  55                  60

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

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

Ser Leu Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105                 110

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

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

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

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

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

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

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

<210> 590

<211> 444

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v1 IgG4 heavy chain

<400> 590

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 Leu Ile Phe Arg Ser Tyr
20 25 30

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

Ala Thr Ile Asn Ser Gly Gly Thr Tyr Thr Tyr Tyr Pro Asp Ser Val
50 55 60

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

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

Ala Asn Ser Tyr Ser Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110

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

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
    130                 135                 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145                 150                 155                 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
                165                 170                 175
```

```
Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
            180                 185                 190

Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
        195                 200                 205

Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro
    210                 215                 220

Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe
225                 230                 235                 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
                245                 250                 255

Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
            260                 265                 270
```

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

Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
    290                 295                 300

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305                 310                 315                 320

Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
                325                 330                 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln
            340                 345                 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
        355                 360                 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
    370                 375                 380
```

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
385 390 395 400

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

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

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440

<210> 591
<211> 219
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Hu37D3-H9.v1 IgG4 light chain

<400> 591

Glu Asp 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 Ser Ser Gln Ser Ile Val His Ser
20 25 30

Asn Gly Asn Thr Tyr Phe Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ser
35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

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

```
Ser Leu Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105                 110

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

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

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

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

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

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

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys

210 215

<210> 592

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: MAPT(10-24)

<400> 592

Val Met Glu Asp His Ala Gly Thr Tyr Gly Leu Gly Asp Arg Lys

1 5 10 15

<210> 593

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: MAPT(2-24)

<400> 593

Ala Glu Pro Arg Gln Glu Phe Glu Val Met Glu Asp His Ala Gly Thr
1 5 10 15

Tyr Gly Leu Gly Asp Arg Lys
20

<210> 594
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: MAPT(2-34)

<400> 594

Ala Glu Pro Arg Gln Glu Phe Glu Val Met Glu Asp His Ala Gly Thr
1 5 10 15

Tyr Gly Leu Gly Asp Arg Lys Asp Gln Gly Gly Tyr Thr Met His Gln

20 25 30

Asp

<210> 595

<211> 35

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: MAPT(10-44)

<400> 595

Val Met Glu Asp His Ala Gly Thr Tyr Gly Leu Gly Asp Arg Lys Asp

1 5 10 15

Gln Gly Gly Tyr Thr Met His Gln Asp Gln Glu Gly Asp Thr Asp Ala

20 25 30

Gly Leu Lys

35

<210> 596

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: MAPT(2-24)Y18A

<400> 596

Ala Glu Pro Arg Gln Glu Phe Glu Val Met Glu Asp His Ala Gly Thr

1 5 10 15

Ala Gly Leu Gly Asp Arg Lys

20

<210> 597

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: MAPT(2-24)L20A

<400> 597

Ala Glu Pro Arg Gln Glu Phe Glu Val Met Glu Asp His Ala Gly Thr
1 5 10 15

Tyr Gly Ala Gly Asp Arg Lys
20

<210> 598

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu113F5-F7.LC1

<400> 598

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

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

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

Tyr Ser Ala Ser Arg Arg Phe 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 Phe Cys Gln Gln Phe Ser Thr Tyr Pro Tyr
                85                  90                  95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105
```

<210> 599

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu113F5-F7.LC2

<400> 599

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

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

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Arg Arg Phe 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 Phe Cys Gln Gln Phe Ser Thr Tyr Pro Tyr

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

100 105

<210> 600

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu113F5-F7.LC3

<400> 600

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Ala

20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Lys Leu Leu Ile

35 40 45

Tyr Ser Ala Ser Arg Arg Phe 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 Phe Ser Thr Tyr Pro Tyr

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

100 105

<210> 601

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: hu113F5-F7.LC4

<400> 601

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

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

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Arg Arg Phe 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 Phe Ser Thr Tyr Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 602
<211> 443
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Hu37D3-H9.v28.A4 IgG4-S228P.YTE des-K heavy chain

<400> 602

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 Leu Ile Phe Arg Ser Tyr
20 25 30

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

Ala Thr Ile Asn Ser Gly Gly Thr Tyr Thr Tyr Tyr Pro Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

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

Ala Asn Ser Tyr Ser Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110

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

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys

130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser

145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser

165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser

180 185 190

Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn

195 200 205

Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro

210 215 220

Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe

225 230 235 240

```
Pro Pro Lys Pro Lys Asp Thr Leu Tyr Ile Thr Arg Glu Pro Glu Val
                245                 250                 255

Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
            260                 265                 270

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

Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
    290                 295                 300

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305                 310                 315                 320

Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
                325                 330                 335
```

```
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln
            340                 345                 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
        355                 360                 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
    370                 375                 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
385                 390                 395                 400

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

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

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
        435                 440
```

<210> 603

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v76 heavy chain variable region (VH)

<400> 603

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 Leu Ile Phe Arg Ser Tyr
20 25 30

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

Ala Thr Ile Asn Ser Gly Gly Thr Arg Thr Tyr Tyr Pro Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

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

Ala Asn Ser Tyr Ser Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 604
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Hu37D3-H9.v76 light chain variable region (VL)

<400> 604

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

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser
20 25 30

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

Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Phe Gln Gly
85 90 95

Thr Leu Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

100 105 110

<210> 605

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v76 HVR-H1; Hu37D3-H9.v83 HVR-H1;

Hu37D3-H9.v93 HVR-H1

<400> 605

Ser Tyr Gly Met Ser

1 5

<210> 606

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v76 HVR-H2; Hu37D3-H9.v83 HVR-H2;

Hu37D3-H9.v93 HVR-H2

<400> 606

Thr Ile Asn Ser Gly Gly Thr Arg Thr Tyr Tyr Pro Asp Ser Val Lys
1 5 10 15

Gly

<210> 607

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v76 HVR-H3; Hu37D3-H9.v83 HVR-H3;

Hu37D3-H9.v93 HVR-H3

<400> 607

Ser Tyr Ser Gly Ala Met Asp Tyr
1 5

<210> 608

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v76 HVR-L1; Hu37D3-H9.v83 HVR-L1;
Hu37D3-H9.v93 HVR-L1

<400> 608

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu
1 5 10 15

<210> 609

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v76 HVR-L2; Hu37D3-H9.v83 HVR-L2;
Hu37D3-H9.v93 HVR-L2

<400> 609

Lys Val Ser Asn Arg Phe Ser
1 5

<210> 610
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Hu37D3-H9.v76 HVR-L3; Hu37D3-H9.v83 HVR-L3;
Hu37D3-H9.v93 HVR-L3

<400> 610

Phe Gln Gly Thr Leu Val Pro Trp Thr
1 5

<210> 611
<211> 444
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v76 IgG4-S228P.YTE heavy chain

<400> 611

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 Leu Ile Phe Arg Ser Tyr
20 25 30

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

Ala Thr Ile Asn Ser Gly Gly Thr Arg Thr Tyr Tyr Pro Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

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

```
Ala Asn Ser Tyr Ser Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110

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

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
    130                 135                 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145                 150                 155                 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
                165                 170                 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
            180                 185                 190
```

```
Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
        195                 200                 205

Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro
    210                 215                 220

Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe
225                 230                 235                 240

Pro Pro Lys Pro Lys Asp Thr Leu Tyr Ile Thr Arg Glu Pro Glu Val
                245                 250                 255

Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
            260                 265                 270

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

Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
    290                 295                 300
```

```
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305                 310                 315                 320

Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
                325                 330                 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln
            340                 345                 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
        355                 360                 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
    370                 375                 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
385                 390                 395                 400
```

Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu

405 410 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His

420 425 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys

435 440

<210> 612

<211> 443

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v76 IgG4-S228P.YTE des-K heavy chain

<400> 612

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 Leu Ile Phe Arg Ser Tyr

20 25 30

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Thr Ile Asn Ser Gly Gly Thr Arg Thr Tyr Tyr Pro Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Asn Ser Tyr Ser Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu

100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu

115 120 125

```
Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
    130                 135                 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145                 150                 155                 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
                165                 170                 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
            180                 185                 190

Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
        195                 200                 205

Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro
    210                 215                 220
```

```
Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe
225                 230                 235                 240

Pro Pro Lys Pro Lys Asp Thr Leu Tyr Ile Thr Arg Glu Pro Glu Val
                245                 250                 255

Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
            260                 265                 270

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

Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
    290                 295                 300

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305                 310                 315                 320

Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
                325                 330                 335
```

```
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln
            340                 345                 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
        355                 360                 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
    370                 375                 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
385                 390                 395                 400

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

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

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly

435 440

<210> 613

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v76 IgG4-S228P.YTE light chain

<400> 613

Asp Asp Leu Leu Thr Gln Thr Pro Leu Ser Leu Pro Val Thr Pro Gly

1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser

20 25 30

Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser

35 40 45

```
Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
    50                  55                  60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Phe Gln Gly
                85                  90                  95

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

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

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

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

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

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

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

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

<210> 614
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Hu37D3-H9.v83 heavy chain variable region (VH)

<400> 614

Glu Val Gln Leu Leu 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 Leu Ile Phe Arg Ser Tyr
20 25 30

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

Ala Thr Ile Asn Ser Gly Gly Thr Arg Thr Tyr Tyr Pro Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

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

Ala Asn Ser Tyr Ser Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu

100 105 110

Val Thr Val Ser Ser

115

<210> 615

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v83 light chain variable region (VL)

<400> 615

Asp Asp Leu Leu Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly

1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser

20 25 30

Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Gln Gln Arg Pro Gly Gln Ser

35 40 45

Pro Arg Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro

50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile

65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Phe Gln Gly

85 90 95

Thr Leu Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

100 105 110

<210> 616

<211> 444

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v83 IgG4-S228P.YTE heavy chain

<400> 616

Glu Val Gln Leu Leu 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 Leu Ile Phe Arg Ser Tyr
20 25 30

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

Ala Thr Ile Asn Ser Gly Gly Thr Arg Thr Tyr Tyr Pro Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

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

```
Ala Asn Ser Tyr Ser Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110

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

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
    130                 135                 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145                 150                 155                 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
                165                 170                 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
            180                 185                 190
```

Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
195 200 205

Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro
210 215 220

Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe
225 230 235 240

Pro Pro Lys Pro Lys Asp Thr Leu Tyr Ile Thr Arg Glu Pro Glu Val
245 250 255

Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
260 265 270

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

Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
290 295 300

```
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305                 310                 315                 320

Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
                325                 330                 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln
            340                 345                 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
        355                 360                 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
    370                 375                 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
385                 390                 395                 400
```

Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu

405 410 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His

420 425 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys

435 440

<210> 617

<211> 443

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v83 IgG4-S228P.YTE des-K heavy chain

<400> 617

Glu Val Gln Leu Leu 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 Leu Ile Phe Arg Ser Tyr
            20                  25                  30

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

Ala Thr Ile Asn Ser Gly Gly Thr Arg Thr Tyr Tyr Pro Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

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

Ala Asn Ser Tyr Ser Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110

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

```
Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
    130                 135                 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145                 150                 155                 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
                165                 170                 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
            180                 185                 190

Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
        195                 200                 205

Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro
    210                 215                 220
```

```
Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe
225                 230                 235                 240

Pro Pro Lys Pro Lys Asp Thr Leu Tyr Ile Thr Arg Glu Pro Glu Val
                245                 250                 255

Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
            260                 265                 270

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

Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
    290                 295                 300

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305                 310                 315                 320

Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
                325                 330                 335
```

```
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln
            340                 345                 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
        355                 360                 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
    370                 375                 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
385                 390                 395                 400

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

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

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly

435 440

<210> 618

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v83 IgG4-S228P.YTE light chain

<400> 618

Asp Asp Leu Leu Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly

1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser

20 25 30

Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Gln Gln Arg Pro Gly Gln Ser

35 40 45

```
Pro Arg Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
    50                  55                  60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Phe Gln Gly
                85                  90                  95

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

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

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

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

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

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

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

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

<210> 619
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Hu37D3-H9.v93 heavy chain variable region (VH)

<400> 619

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 Leu Ile Phe Arg Ser Tyr
20 25 30

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

Ala Thr Ile Asn Ser Gly Gly Thr Arg Thr Tyr Tyr Pro Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

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

Ala Asn Ser Tyr Ser Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu

100 105 110

Val Thr Val Ser Ser

115

<210> 620

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v93 light chain variable region (VL)

<400> 620

Glu Asp Leu 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 Ser Ser Gln Ser Ile Val His Ser

20 25 30

Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ser

35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro

50 55 60

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile

65 70 75 80

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly

85 90 95

Thr Leu Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

100 105 110

<210> 621

<211> 444

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v93 IgG4-S228P.YTE heavy chain

<400> 621

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 Leu Ile Phe Arg Ser Tyr
20 25 30

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

Ala Thr Ile Asn Ser Gly Gly Thr Arg Thr Tyr Tyr Pro Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

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

```
Ala Asn Ser Tyr Ser Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110

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

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
    130                 135                 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145                 150                 155                 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
                165                 170                 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
            180                 185                 190
```

Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
195 200 205

Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro
210 215 220

Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe
225 230 235 240

Pro Pro Lys Pro Lys Asp Thr Leu Tyr Ile Thr Arg Glu Pro Glu Val
245 250 255

Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
260 265 270

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

Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
290 295 300

```
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305                 310                 315                 320

Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
                325                 330                 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln
            340                 345                 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
        355                 360                 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
    370                 375                 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
385                 390                 395                 400
```

Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu

405 410 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His

420 425 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys

435 440

<210> 622

<211> 443

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v93 IgG4-S228P.YTE des-K heavy chain

<400> 622

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 Leu Ile Phe Arg Ser Tyr

20 25 30

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Thr Ile Asn Ser Gly Gly Thr Arg Thr Tyr Tyr Pro Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Asn Ser Tyr Ser Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu

100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu

115 120 125

```
Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
    130                 135                 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145                 150                 155                 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
                165                 170                 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
            180                 185                 190

Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
        195                 200                 205

Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro
    210                 215                 220
```

```
Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe
225                 230                 235                 240

Pro Pro Lys Pro Lys Asp Thr Leu Tyr Ile Thr Arg Glu Pro Glu Val
                245                 250                 255

Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
            260                 265                 270

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

Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
    290                 295                 300

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305                 310                 315                 320

Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
                325                 330                 335
```

```
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln
            340                 345                 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
        355                 360                 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
    370                 375                 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
385                 390                 395                 400

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

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

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly

435 440

<210> 623

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic: Hu37D3-H9.v93 IgG4-S228P.YTE light chain

<400> 623

Glu Asp Leu 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 Ser Ser Gln Ser Ile Val His Ser

20 25 30

Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ser

35 40 45

```
Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
    50                  55                  60

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

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

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

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

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

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

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

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

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

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

<210> 624
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: N-terminally biotinylated peptide

<400> 624

Ala Glu Pro Arg Gln Glu Phe Glu Val Met Glu Asp His Ala Gly Thr
1 5 10 15

Tyr Gly Leu Gly Asp Arg Lys
20