SEQUENCE LISTING

<110> Bayer Pharma AG

<120> Anti-CEACAM6 Antibodies and Uses Thereof

<130> BHC 14 1 064

<160> 186

<170> PatentIn version 3.5

<210> 1
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-1173, h16C3-hIgG1, Heavy Chain

<400> 1

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

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

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

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

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

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

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

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

```
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
    130                 135                 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160

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

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

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

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

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225                 230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

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

```
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400

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

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445

Pro Gly
    450
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<210> 2
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-1173, h16C3-hIgG1, Light Chain

<400> 2

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

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

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

```
Tyr Gly Ala Ser Asn Leu Ala Thr Gly Met Pro Ser Arg Phe Ser Gly
    50                  55                  60

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

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

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

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

Phe Asn Arg Gly Glu Cys
    210
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<210> 3
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-2971, 792.15H12C9, VH

<400> 3

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

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

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

Trp Leu Ala His Ile Trp Trp Asn Asp Asn Lys Tyr Tyr Asn Thr Ala
50 55 60

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

Phe Leu Lys Ile Ala Ser Val Asp Thr Ala Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile Ser Leu Pro Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Thr Leu Thr Val Ser Ser
115

<210> 4
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-2971, 792.15H12C9, HCDR1

<400> 4

Thr Tyr Gly Ile Gly Val Gly
1 5

<210> 5
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-2971, 792.15H12C9, HCDR2

<400> 5

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

<210> 6
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-2971, 792.15H12C9, HCDR3

<400> 6

Ile Ser Leu Pro Tyr Phe Asp Tyr
1   5

<210> 7
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-2971, 792.15H12C9, VL

<400> 7

Asp Ile Val Met Thr Gln Ser Gln Lys Phe 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 Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
        35   40   45

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

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

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

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

<210> 8
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-2971, 792.15H12C9, LCDR1

<400> 8

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

<210> 9
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-2971, 792.15H12C9, LCDR2

<400> 9

Ser Ala Ser Asn Arg Tyr Thr
1 5

<210> 10
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-2971, 792.15H12C9, LCDR3

<400> 10

Gln Gln Tyr Ser Ser Tyr Pro Leu Thr
1 5

<210> 11
<211> 129
<212> PRT

<213> Artificial Sequence

<220>
<223> TPP-2971, 792.15H12C9, Heavy Chain

<400> 11

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

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

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

Trp Leu Ala His Ile Trp Trp Asn Asp Asn Lys Tyr Tyr Asn Thr Ala
50 55 60

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

Phe Leu Lys Ile Ala Ser Val Asp Thr Ala Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile Ser Leu Pro Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro
115 120 125

Leu

<210> 12
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-2971, 792.15H12C9, Light Chain

<400> 12

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Asp Ile Val Met Thr Gln Ser Gln Lys Phe 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 Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
        35                  40                  45


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


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


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


Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Ala Asp Ala Ala
            100                 105                 110


Pro Thr Val Ser Ile Phe Pro Pro Ser Ser
        115                 120


<210>  13
<211>  118
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  TPP-3186, 792.11G2D10, VH

<400>  13

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


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


Gly Ile Gly Val Gly Cys Ile Arg Gln Pro Ser Gly Lys Gly Leu Glu
        35                  40                  45
```

```
Trp Leu Ala His Ile Trp Trp Asn Asp Asn Lys Tyr Tyr Asn Thr Ala
    50                  55                  60


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


Phe Leu Lys Ile Ala Ser Val Asp Thr Ala Asp Thr Ala Thr Tyr Tyr
                85                  90                  95


Cys Ala Arg Ile Ser Leu Pro Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Thr Leu Thr Val Ser Ser
        115


<210>  14
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  TPP-3186, 792.11G2D10, HCDR1

<400>  14

Thr Tyr Gly Ile Gly Val Gly
1               5


<210>  15
<211>  16
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  TPP-3186, 792.11G2D10, HCDR2

<400>  15

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


<210>  16
<211>  8
<212>  PRT
<213>  Artificial Sequence
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<220>
<223> TPP-3186, 792.11G2D10, HCDR3

<400> 16

Ile Ser Leu Pro Tyr Phe Asp Tyr
1   5

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

<220>
<223> TPP-3186, 792.11G2D10, VL

<400> 17

Asp Ile Val Met Thr Gln Ser Gln Lys Phe 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 Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
        35   40   45

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

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

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

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

<210> 18
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3186, 792.11G2D10, LCDR1

<400> 18

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

<210> 19
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3186, 792.11G2D10, LCDR2

<400> 19

Ser Ala Ser Asn Arg Tyr Thr
1   5

<210> 20
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3186, 792.11G2D10, LCDR3

<400> 20

Gln Gln Tyr Ser Ser Tyr Pro Leu Thr
1   5

<210> 21
<211> 129
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3186, 792.11G2D10, Heavy Chain

<400> 21

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

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

```
Gly Ile Gly Val Gly Cys Ile Arg Gln Pro Ser Gly Lys Gly Leu Glu
        35                  40                  45

Trp Leu Ala His Ile Trp Trp Asn Asp Asn Lys Tyr Tyr Asn Thr Ala
    50                  55                  60

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

Phe Leu Lys Ile Ala Ser Val Asp Thr Ala Asp Thr Ala Thr Tyr Tyr
                85                  90                  95

Cys Ala Arg Ile Ser Leu Pro Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro
        115                 120                 125

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

<220>
<223> TPP-3186, 792.11G2D10, Light Chain

<400> 22

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Asp Ile Val Met Thr Gln Ser Gln Lys Phe 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 Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Ser Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
```

```
    50                  55                  60

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

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

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Ala Asp Ala Ala
            100                 105                 110

Pro Thr Val Ser Ile Phe Pro Pro Ser Ser
        115                 120
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<210> 23
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3187, 792.15C4F4, VH

<400> 23

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

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

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

Trp Leu Ala His Ile Trp Trp Asn Asp Asn Lys Tyr Tyr Asn Thr Ala
    50                  55                  60

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

Phe Leu Lys Ile Ala Ser Val Asp Thr Ala Asp Thr Ala Thr Tyr Tyr
                85                  90                  95
```

Cys Ala Arg Ile Ser Leu Pro Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Thr Leu Thr Val Ser Ser
115

<210> 24
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3187, 792.15C4F4, HCDR1

<400> 24

Thr Tyr Gly Ile Gly Val Gly
1 5

<210> 25
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3187, 792.15C4F4, HCDR2

<400> 25

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

<210> 26
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3187, 792.15C4F4, HCDR3

<400> 26

Ile Ser Leu Pro Tyr Phe Asp Tyr
1 5

<210> 27
<211> 107
<212> PRT

<213> Artificial Sequence

<220>
<223> TPP-3187, 792.15C4F4, VL

<400> 27

Asp Ile Val Met Thr Gln Ser Gln Lys Phe 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 Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
35 40 45

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

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

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

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

<210> 28
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3187, 792.15C4F4, LCDR1

<400> 28

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

<210> 29
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3187, 792.15C4F4, LCDR2

<400> 29

Ser Ala Ser Asn Arg Tyr Thr
1   5

<210> 30
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3187, 792.15C4F4, LCDR3

<400> 30

Gln Gln Tyr Asn Asn Tyr Pro Leu Thr
1   5

<210> 31
<211> 129
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3187, 792.15C4F4, Heavy Chain

<400> 31

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

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

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

Trp Leu Ala His Ile Trp Trp Asn Asp Asn Lys Tyr Tyr Asn Thr Ala
    50   55   60

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

Phe Leu Lys Ile Ala Ser Val Asp Thr Ala Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile Ser Leu Pro Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro
115 120 125

Leu

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

<220>
<223> TPP-3187, 792.15C4F4, Light Chain

<400> 32

Asp Ile Val Met Thr Gln Ser Gln Lys Phe 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 Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
35 40 45

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

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

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

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Ala Asp Ala Ala
100 105 110

Pro Thr Val Ser Ile Phe Pro Pro Ser Ser
        115   120

<210> 33
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3308, TPP-2971X1-hIgG2Kappa, VH

<400> 33

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

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

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

Trp Leu Ala His Ile Trp Trp Asn Asp Asn Lys Tyr Tyr Asn Thr Ala
    50   55   60

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

Phe Leu Lys Ile Ala Ser Val Asp Thr Ala Asp Thr Ala Thr Tyr Tyr
                85   90   95

Cys Ala Arg Ile Ser Leu Pro Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
            100   105   110

Thr Leu Thr Val Ser Ser
        115

<210> 34
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3308, TPP-2971X1-hIgG2Kappa, HCDR1

<400> 34

Thr Tyr Gly Ile Gly Val Gly
1   5

<210> 35
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3308, TPP-2971X1-hIgG2Kappa, HCDR2

<400> 35

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

<210> 36
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3308, TPP-2971X1-hIgG2Kappa, HCDR3

<400> 36

Ile Ser Leu Pro Tyr Phe Asp Tyr
1   5

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

<220>
<223> TPP-3308, TPP-2971X1-hIgG2Kappa, VL

<400> 37

Asp Ile Val Met Thr Gln Ser Gln Lys Phe 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 Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
        35   40   45

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

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

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

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

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

<220>
<223> TPP-3308, TPP-2971X1-hIgG2Kappa, LCDR1

<400> 38

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

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

<220>
<223> TPP-3308, TPP-2971X1-hIgG2Kappa, LCDR2

<400> 39

Ser Ala Ser Asn Arg Tyr Thr
1   5

<210> 40
<211> 9
<212> PRT

<213> Artificial Sequence

<220>
<223> TPP-3308, TPP-2971X1-hIgG2Kappa, LCDR3

<400> 40

Gln Gln Tyr Ser Ser Tyr Pro Leu Thr
1 5

<210> 41
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> TPP-3308, TPP-2971X1-hIgG2Kappa, VH

<400> 41
caggtcacac tgaaagagag cggccctggc atcctgcagc ccagccagac cctgagcctg 60

acctgcagct tcagcggctt cagcctgagc acctacggca tcggcgtggg ctggatcaga 120

cagcccagcg gcaaggacct ggaatggctg gcccacatct ggtggaacga caacaagtac 180

tacaacaccg ccctgaagtc ccggctgacc atcagcaagg acaccagcaa caaccaggtg 240

ttcctgaaga tcgccagcgt ggacaccgcc gataccgcca cctactactg cgcccggatc 300

agcctgccct acttcgacta ctggggccag ggcaccaccc tgaccgtgtc ctca 354

<210> 42
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> TPP-3308, TPP-2971X1-hIgG2Kappa, VL

<400> 42
gacatcgtga tgacccagag ccagaaattc atgagcacca gcgtgggcga ccgggtgtcc 60

atcacatgca aggccagcca gaacgtgggc accgccgtgg cctggtatca gcagaagccc 120

ggccagagcc ccaagctgct gatctacagc gccagcaacc ggtacaccgg cgtgcccgac 180

agattcacag gcagcggcag cggcaccgac ttcaccctga ccatcagcaa catgcagagc 240

gaggacctgg ccgactactt ctgccagcag tacagcagct acccccctgac cttcggagcc 300

ggcaccaagc tggaactgaa a 321

<210> 43
<211> 443
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3308, TPP-2971X1-hIgG2Kappa, Heavy Chain

<400> 43

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


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


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


Trp Leu Ala His Ile Trp Trp Asn Asp Asn Lys Tyr Tyr Asn Thr Ala
    50                  55                  60


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


Phe Leu Lys Ile Ala Ser Val Asp Thr Ala Asp Thr Ala Thr Tyr Tyr
                85                  90                  95


Cys Ala Arg Ile Ser Leu Pro Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


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


Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
    130                 135                 140


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


Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
```

```
                165                 170                 175

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

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

Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys
    210                 215                 220

Pro Pro Cys Pro Ala Pro Pro Val Ala 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 His 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 Phe Arg Val Val Ser Val Leu Thr
    290                 295                 300

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

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

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

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
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 Pro Gly
435 440

<210> 44
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3308, TPP-2971X1-hIgG2Kappa, Light Chain

<400> 44

Asp Ile Val Met Thr Gln Ser Gln Lys Phe 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 Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
35 40 45

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

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

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

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

```
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

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

Phe Asn Arg Gly Glu Cys
    210


<210>  45
<211>  1329
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  TPP-3308, TPP-2971X1-hIgG2Kappa, Heavy Chain

<400>  45
caggtcacac tgaaagagag cggccctggc atcctgcagc ccagccagac cctgagcctg       60

acctgcagct tcagcggctt cagcctgagc acctacggca tcggcgtggg ctggatcaga      120

cagcccagcg gcaaggacct ggaatggctg gcccacatct ggtggaacga caacaagtac      180

tacaacaccg ccctgaagtc ccggctgacc atcagcaagg acaccagcaa caaccaggtg      240

ttcctgaaga tcgccagcgt ggacaccgcc gataccgcca cctactactg cgcccggatc      300

agcctgccct acttcgacta ctggggccag ggcaccaccc tgaccgtgtc ctcagccagc      360

accaagggcc ccagcgtgtt ccctctggcc ccttgtagca gaagcaccag cgagtctaca      420
```

gccgccctgg gctgcctcgt gaaggactac tttcccgagc ccgtgaccgt gtcctggaac 480

tctggcgctc tgacaagcgg cgtgcacacc tttccagccg tgctgcagag cagcggcctg 540

tactctctga gcagcgtcgt gacagtgccc agcagcaact tcggcaccca gacctacacc 600

tgtaacgtgg accacaagcc cagcaacacc aaggtggaca agaccgtgga acggaagtgc 660

tgcgtggaat gccccccttg tcctgcccct ccagtggctg gcccttccgt gttcctgttc 720

cccccaaagc ccaaggacac cctgatgatc agccggaccc ccgaagtgac ctgcgtggtg 780

gtggatgtgt cccacgagga ccccgaggtg cagttcaatt ggtacgtgga cggcgtggaa 840

gtgcacaacg ccaagaccaa gcccagagag gaacagttca acagcacctt ccgggtggtg 900

tccgtgctga ccgtggtgca tcaggactgg ctgaacggca aagagtacaa gtgcaaggtg 960

tccaacaagg gcctgcctgc ccccatcgag aaaaccatca gcaagaccaa aggccagccc 1020

cgcgagcccc aggtgtacac actgcctcca agccgggaag agatgaccaa gaaccaggtg 1080

tccctgacct gtctcgtgaa aggcttctac ccctccgata tcgccgtgga atgggagagc 1140

aacggccagc ccgagaacaa ctacaagacc acccccccca tgctggacag cgacggctca 1200

ttcttcctgt acagcaagct gacagtggac aagtcccggt ggcagcaggg caacgtgttc 1260

agctgcagcg tgatgcacga ggccctgcac aaccactaca cccagaagtc cctgagcctg 1320

agccctggc 1329

<210> 46
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> TPP-3308, TPP-2971X1-hIgG2Kappa, Light Chain

<400> 46
gacatcgtga tgacccagag ccagaaattc atgagcacca gcgtgggcga ccgggtgtcc 60

atcacatgca aggccagcca gaacgtgggc accgccgtgg cctggtatca gcagaagccc 120

ggccagagcc ccaagctgct gatctacagc gccagcaacc ggtacaccgg cgtgcccgac 180

agattcacag gcagcggcag cggcaccgac ttcaccctga ccatcagcaa catgcagagc 240

gaggacctgg ccgactactt ctgccagcag tacagcagct acccccctgac cttcggagcc 300

ggcaccaagc tggaactgaa acgaaccgtg gccgctccca gcgtgttcat cttcccacct 360

agcgacgagc agctgaagtc cggcacagcc tctgtcgtgt gcctgctgaa caacttctac 420

ccccgcgagg ccaaggtgca gtggaaggtg gacaatgccc tgcagagcgg caacagccag 480

gaaagcgtga ccgagcagga cagcaaggac tccacctaca gcctgagcag caccctgacc 540

ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaagtgac ccaccagggc 600

ctgtctagcc ccgtgaccaa gagcttcaac cggggcgagt gt 642

<210> 47
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3310, TPP-2971HU1-hIgG2Kappa, VH

<400> 47

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

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

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

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

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

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile Ser Leu Pro Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Thr Leu Thr Val Ser Ser
115

<210> 48
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3310, TPP-2971HU1-hIgG2Kappa, HCDR1

<400> 48

Thr Tyr Gly Ile Gly Val Gly
1 5

<210> 49
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3310, TPP-2971HU1-hIgG2Kappa, HCDR2

<400> 49

His Ile Trp Trp Asn Asp Asn Lys Tyr Tyr Ser Thr Ser Leu Lys Thr
1 5 10 15

<210> 50
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3310, TPP-2971HU1-hIgG2Kappa, HCDR3

<400> 50

Ile Ser Leu Pro Tyr Phe Asp Tyr
1 5

<210> 51
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3310, TPP-2971HU1-hIgG2Kappa, VL

<400> 51

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

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

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

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

<210> 52
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3310, TPP-2971HU1-hIgG2Kappa, LCDR1

<400> 52

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

<210> 53
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3310, TPP-2971HU1-hIgG2Kappa, LCDR2

<400> 53

Ser Ala Ser Asn Arg Tyr Thr
1   5

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

<220>
<223> TPP-3310, TPP-2971HU1-hIgG2Kappa, LCDR3

<400> 54

Gln Gln Tyr Ser Ser Tyr Pro Leu Thr
1   5

<210> 55
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> TPP-3310, TPP-2971HU1-hIgG2Kappa, VH

<400> 55
caagtgaccc tgagagagtc cggccctgcc ctcgtgaagc ctacccagac cctgacactg 60

acctgcacct tctccggctt ctccctgtcc acctacggca tcggcgtggg ctggatcaga 120

cagcctcctg gcaaggccct ggaatggctg gctcacatct ggtggaacga caacaagtac 180

tactccacct ccctgaaaac ccggctgacc atctccaagg acacctccaa gaaccaggtg 240

gtgctgacca tgaccaacat ggaccccgtg gacaccgcca cctactactg cgccagaatc 300

tccctgccct acttcgacta ctggggccag ggcaccacac tgaccgtcag ctca 354

<210> 56
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> TPP-3310, TPP-2971HU1-hIgG2Kappa, VL

<400> 56
gatatccagc tgacccagtc ccccagcttc ctgtctgcct ctgtgggcga cagagtgacc 60

atcacatgca aggcctccca gaacgtgggc accgccgtgg cttggtatca gcagaagcct 120

ggcaaggccc ccaagctgct gatctactcc gcctccaacc ggtacaccgg cgtgccctct 180

agattctccg gctctggctc tggcaccgag tttaccctga ccatctccag cctgcagccc 240

gaggacttcg ccacctacta ctgccagcag tactcctcct acccccctgac ctttggcgga 300

ggcaccaagg tggaaatcaa g 321

<210> 57
<211> 443
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3310, TPP-2971HU1-hIgG2Kappa, Heavy Chain

<400> 57

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

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

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

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

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

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile Ser Leu Pro Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

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

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

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

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

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

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

Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys
    210                 215                 220

Pro Pro Cys Pro Ala Pro Pro Val Ala 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 His 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 Phe Arg Val Val Ser Val Leu Thr
    290                 295                 300

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

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

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

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
                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 Pro Gly
        435                 440
```

<210> 58
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3310, TPP-2971HU1-hIgG2Kappa, Light Chain

<400> 58

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

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
```

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

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

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

Phe Asn Arg Gly Glu Cys
    210
```

<210> 59
<211> 1329
<212> DNA
<213> Artificial Sequence

<220>
<223> TPP-3310, TPP-2971HU1-hIgG2Kappa, Heavy Chain

<400> 59
caagtgaccc tgagagagtc cggccctgcc ctcgtgaagc ctacccagac cctgacactg 60

acctgcacct tctccggctt ctccctgtcc acctacggca tcggcgtggg ctggatcaga 120

cagcctcctg gcaaggccct ggaatggctg gctcacatct ggtggaacga caacaagtac 180

tactccacct ccctgaaaac ccggctgacc atctccaagg acacctccaa gaaccaggtg 240

gtgctgacca tgaccaacat ggaccccgtg gacaccgcca cctactactg cgccagaatc 300

tccctgccct acttcgacta ctggggccag ggcaccacac tgaccgtcag ctcagcttcc 360

accaagggcc cctccgtgtt ccctctggcc ccttgctccc ggtccacctc tgagtctacc 420

gccgctctgg gctgcctggt gaaagactac ttccccgagc ccgtgaccgt gtcctggaac 480

tctggcgccc tgacctccgg cgtgcacacc tttccagccg tgctgcagtc ctccggcctg 540

tactccctgt cctccgtggt gacagtgccc tcctccaact tcggcaccca gacctacacc 600

tgtaacgtgg accacaagcc ctccaacacc aaggtggaca agaccgtgga acggaagtgc 660

tgcgtggaat gcccaccctg tcctgctcca cctgtggctg gccccagcgt gttcctgttc 720

cccccaaagc ccaaggacac cctgatgatc tcccggaccc ccgaagtgac ctgcgtggtg 780

gtggacgtgt cccacgagga ccccgaggtg cagttcaatt ggtacgtgga cggcgtggaa 840

gtgcacaacg ccaagaccaa gcccagagag gaacagttca actccacctt ccgggtggtg 900

tccgtgctga ccgtggtgca tcaggactgg ctgaacggca aagagtacaa gtgcaaggtc 960

tccaacaagg gcctgcctgc ccccatcgaa aagaccatca gcaagaccaa gggccagccc 1020

cgcgagcccc aggtgtacac actgcccccc agccgggaag agatgaccaa gaaccaggtg 1080

tccctgacct gtctggtgaa aggcttctac ccctccgaca ttgccgtgga atgggagtcc 1140

aacggacagc ctgagaacaa ctacaagacc acccccccca tgctggactc cgacggctca 1200

ttcttcctgt actccaagct gacagtggac aagtcccggt ggcagcaggg caacgtgttc 1260

tcctgctccg tgatgcacga ggccctgcac aaccactaca cccagaagtc cctgtccctg 1320

agccccggc 1329

<210> 60
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> TPP-3310, TPP-2971HU1-hIgG2Kappa, Light Chain

<400> 60
gatatccagc tgacccagtc ccccagcttc ctgtctgcct ctgtgggcga cagagtgacc 60

atcacatgca aggcctccca gaacgtgggc accgccgtgg cttggtatca gcagaagcct 120

ggcaaggccc ccaagctgct gatctactcc gcctccaacc ggtacaccgg cgtgccctct 180

agattctccg gctctggctc tggcaccgag tttaccctga ccatctccag cctgcagccc 240

gaggacttcg ccacctacta ctgccagcag tactcctcct acccccctgac ctttggcgga 300

ggcaccaagg tggaaatcaa gcggaccgtg gccgctccct ccgtgtttat cttcccaccc 360

tccgacgagc agctgaagtc cggcacagct tccgtcgtgt gcctgctgaa caacttctac 420

ccccgcgagg ccaaggtgca gtggaaggtg gacaacgccc tgcagtccgg caactcccag 480

gaatccgtga ccgagcagga ctccaaggac agcacctact ccctgtcctc caccctgacc 540

ctgtccaagg ccgactacga gaagcacaag gtgtacgcct gcgaagtgac ccaccagggc 600

ctgtctagcc ccgtgaccaa gtctttcaac cggggcgagt gt 642

<210> 61
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3322, TPP-3186X1-hIgG2, VH

<400> 61

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

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

Gly Ile Gly Val Gly Cys Ile Arg Gln Pro Ser Gly Lys Gly Leu Glu
35 40 45

Trp Leu Ala His Ile Trp Trp Asn Asp Asn Lys Tyr Tyr Asn Thr Ala
50 55 60

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

Phe Leu Lys Ile Ala Ser Val Asp Thr Ala Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile Ser Leu Pro Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Thr Leu Thr Val Ser Ser
115

<210> 62
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3322, TPP-3186X1-hIgG2, HCDR1

<400> 62

Thr Tyr Gly Ile Gly Val Gly
1 5

<210> 63
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3322, TPP-3186X1-hIgG2, HCDR2

<400> 63

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

<210> 64
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3322, TPP-3186X1-hIgG2, HCDR3

<400> 64

Ile Ser Leu Pro Tyr Phe Asp Tyr
1 5

<210> 65
<211> 107

<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3322, TPP-3186X1-hIgG2, VL

<400> 65

Asp Ile Val Met Thr Gln Ser Gln Lys Phe 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 Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
35 40 45

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

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

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

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

<210> 66
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3322, TPP-3186X1-hIgG2, LCDR1

<400> 66

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

<210> 67
<211> 7
<212> PRT

<213> Artificial Sequence

<220>
<223> TPP-3322, TPP-3186X1-hIgG2, LCDR2

<400> 67

Ser Ala Ser Asn Arg Tyr Thr
1 5

<210> 68
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3322, TPP-3186X1-hIgG2, LCDR3

<400> 68

Gln Gln Tyr Ser Ser Tyr Pro Leu Thr
1 5

<210> 69
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> TPP-3322, TPP-3186X1-hIgG2, VH

<400> 69
caggtcacac tgaaagagag cggccctggc atcctgcagc ccagccagac cctgagcctg 60

acctgcagct tcagcggctt cagcctgagc acctacggca tcggcgtggg ctgcatcaga 120

cagcccagcg gcaagggcct ggaatggctg gcccacatct ggtggaacga caacaagtac 180

tacaacaccg ccctgaagtc ccggctgacc atcagcaagg acaccagcaa caaccaggtg 240

ttcctgaaga tcgccagcgt ggacaccgcc gataccgcca cctactactg cgcccggatc 300

agcctgccct acttcgacta ctggggccag ggcaccaccc tgaccgtgtc ctca 354

<210> 70
<211> 321
<212> DNA
<213> Artificial Sequence

<220>

<223> TPP-3322, TPP-3186X1-hIgG2, VL

<400> 70
gacatcgtga tgacccagag ccagaaattc atgagcacca gcgtgggcga ccgggtgtcc 60

atcacatgca aggccagcca gaacgtgggc accgccgtgg cctggtatca gcagaagccc 120

ggccagagcc ccaagctgct gatctacagc gccagcaacc ggtacaccgg cgtgcccgac 180

agattcacag gcagcggcag cggcaccgac ttcaccttca ccatcagcaa catgcagagc 240

gaggacctgg ccgactactt ctgccagcag tacagcagct acccccctgac cttcggagcc 300

ggcaccaagc tggaactgaa a 321

<210> 71
<211> 443
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3322, TPP-3186X1-hIgG2, Heavy Chain

<400> 71

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

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

Gly Ile Gly Val Gly Cys Ile Arg Gln Pro Ser Gly Lys Gly Leu Glu
35 40 45

Trp Leu Ala His Ile Trp Trp Asn Asp Asn Lys Tyr Tyr Asn Thr Ala
50 55 60

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

Phe Leu Lys Ile Ala Ser Val Asp Thr Ala Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile Ser Leu Pro Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

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

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
    130                 135                 140

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

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

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

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

Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys
    210                 215                 220

Pro Pro Cys Pro Ala Pro Pro Val Ala 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 His 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 Phe Arg Val Val Ser Val Leu Thr
    290                 295                 300

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

```
Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr
                325                 330                 335

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

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
                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 Pro Gly
        435                 440


<210>  72
<211>  214
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  TPP-3322, TPP-3186X1-hIgG2, Light Chain

<400>  72

Asp Ile Val Met Thr Gln Ser Gln Lys Phe 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 Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
        35                  40                  45
```

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

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

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

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

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

Phe Asn Arg Gly Glu Cys
    210
```

<210> 73
<211> 1329
<212> DNA
<213> Artificial Sequence

<220>
<223> TPP-3322, TPP-3186X1-hIgG2, Heavy Chain

<400> 73
caggtcacac tgaaagagag cggccctggc atcctgcagc ccagccagac cctgagcctg 60

acctgcagct tcagcggctt cagcctgagc acctacggca tcggcgtggg ctgcatcaga 120

cagcccagcg gcaagggcct ggaatggctg gcccacatct ggtggaacga caacaagtac 180

tacaacaccg ccctgaagtc ccggctgacc atcagcaagg acaccagcaa caaccaggtg 240

ttcctgaaga tcgccagcgt ggacaccgcc gataccgcca cctactactg cgcccggatc 300

agcctgccct acttcgacta ctggggccag ggcaccaccc tgaccgtgtc ctcagccagc 360

accaagggcc ccagcgtgtt ccctctggcc ccttgtagca gaagcaccag cgagtctaca 420

gccgccctgg gctgcctcgt gaaggactac tttcccgagc ccgtgaccgt gtcctggaac 480

tctggcgctc tgacaagcgg cgtgcacacc tttccagccg tgctgcagag cagcggcctg 540

tactctctga gcagcgtcgt gacagtgccc agcagcaact tcggcaccca gacctacacc 600

tgtaacgtgg accacaagcc cagcaacacc aaggtggaca agaccgtgga acggaagtgc 660

tgcgtggaat gccccccttg tcctgcccct ccagtggctg gcccttccgt gttcctgttc 720

cccccaaagc ccaaggacac cctgatgatc agccggaccc ccgaagtgac ctgcgtggtg 780

gtggatgtgt cccacgagga ccccgaggtg cagttcaatt ggtacgtgga cggcgtggaa 840

gtgcacaacg ccaagaccaa gcccagagag gaacagttca acagcacctt ccgggtggtg 900

tccgtgctga ccgtggtgca tcaggactgg ctgaacggca aagagtacaa gtgcaaggtg 960

tccaacaagg gcctgcctgc ccccatcgag aaaaccatca gcaagaccaa aggccagccc 1020

cgcgagcccc aggtgtacac actgcctcca agccgggaag agatgaccaa gaaccaggtg 1080

tccctgacct gtctcgtgaa aggcttctac ccctccgata tcgccgtgga atgggagagc 1140

aacggccagc ccgagaacaa ctacaagacc acccccccca tgctggacag cgacggctca 1200

ttcttcctgt acagcaagct gacagtggac aagtcccggt ggcagcaggg caacgtgttc 1260

agctgcagcg tgatgcacga ggccctgcac aaccactaca cccagaagtc cctgagcctg 1320

agccctggc 1329

<210> 74
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> TPP-3322, TPP-3186X1-hIgG2, Light Chain

<400> 74
gacatcgtga tgacccagag ccagaaattc atgagcacca gcgtgggcga ccgggtgtcc 60

atcacatgca aggccagcca gaacgtgggc accgccgtgg cctggtatca gcagaagccc 120

ggccagagcc ccaagctgct gatctacagc gccagcaacc ggtacaccgg cgtgcccgac 180

agattcacag gcagcggcag cggcaccgac ttcaccttca ccatcagcaa catgcagagc 240

gaggacctgg ccgactactt ctgccagcag tacagcagct acccccctgac cttcggagcc 300

ggcaccaagc tggaactgaa acgaaccgtg gccgctccca gcgtgttcat cttcccacct 360

agcgacgagc agctgaagtc cggcacagcc tctgtcgtgt gcctgctgaa caacttctac 420

ccccgcgagg ccaaggtgca gtggaaggtg gacaatgccc tgcagagcgg caacagccag 480

gaaagcgtga ccgagcagga cagcaaggac tccacctaca gcctgagcag caccctgacc 540

ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaagtgac ccaccagggc 600

ctgtctagcc ccgtgaccaa gagcttcaac cggggcgagt gt 642

<210> 75
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3323, TPP-3187X1-hIgG2, VH

<400> 75

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

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

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

Trp Leu Ala His Ile Trp Trp Asn Asp Asn Lys Tyr Tyr Asn Thr Ala
    50   55   60

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


Phe Leu Lys Ile Ala Ser Val Asp Thr Ala Asp Thr Ala Thr Tyr Tyr
                85                  90                  95


Cys Ala Arg Ile Ser Leu Pro Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Thr Leu Thr Val Ser Ser
        115


<210>  76
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  TPP-3323, TPP-3187X1-hIgG2, HCDR1

<400>  76

Thr Tyr Gly Ile Gly Val Gly
1               5


<210>  77
<211>  16
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  TPP-3323, TPP-3187X1-hIgG2, HCDR2

<400>  77

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


<210>  78
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  TPP-3323, TPP-3187X1-hIgG2, HCDR3

<400>  78
```

Ile Ser Leu Pro Tyr Phe Asp Tyr
1   5

<210> 79
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3323, TPP-3187X1-hIgG2, VL

<400> 79

Asp Ile Val Met Thr Gln Ser Gln Lys Phe 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 Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
        35   40   45

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

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

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

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

<210> 80
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3323, TPP-3187X1-hIgG2, LCDR1

<400> 80

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

<210> 81
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3323, TPP-3187X1-hIgG2, LCDR2

<400> 81

Ser Ala Ser Asn Arg Tyr Thr
1 5

<210> 82
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3323, TPP-3187X1-hIgG2, LCDR3

<400> 82

Gln Gln Tyr Asn Asn Tyr Pro Leu Thr
1 5

<210> 83
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> TPP-3323, TPP-3187X1-hIgG2, VH

<400> 83
caagtgaccc tgaaagagtc cggccctggc atcctgcagc cttcccagac cctgtccctg 60

acctgctcct tctccggctt ctccctgacc acctacggca tcggcgtggg ctggatcaga 120

cagccttctg gcaagggcct ggaatggctg gcccacatct ggtggaacga caacaagtac 180

tacaacaccg ccctgaagtc ccggctgacc atctccaagg acacctccaa caaccaggtg 240

ttcctgaaga tcgcctccgt ggacaccgcc gataccgcca cctactactg cgcccggatc 300

tccctgccct acttcgacta ttggggccag ggcaccaccc tgaccgtcag ctca 354

<210> 84
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> TPP-3323, TPP-3187X1-hIgG2, VL

<400> 84
gacatcgtga tgacccagtc ccagaaattc atgtccacct ccgtgggcga ccgggtgtcc 60

atcacatgca aggcctctca gaacgtgggc accgccgtgg cctggtatca gcagaagcct 120

ggccagtccc ccaagctgct gatctactcc gcctccaacc ggtacaccgg cgtgcccgat 180

agattcaccg gctctggctc tggcaccgac ttcaccctga ccatctccaa catgcagtcc 240

gaggacctgg ccgactactt ctgccagcag tacaacaact acccccctgac cttcggcgct 300

ggcaccaagc tggaactgaa g 321

<210> 85
<211> 443
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3323, TPP-3187X1-hIgG2, Heavy Chain

<400> 85

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

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

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

Trp Leu Ala His Ile Trp Trp Asn Asp Asn Lys Tyr Tyr Asn Thr Ala
50 55 60

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

```
Phe Leu Lys Ile Ala Ser Val Asp Thr Ala Asp Thr Ala Thr Tyr Tyr
                85                  90                  95

Cys Ala Arg Ile Ser Leu Pro Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

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

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
    130                 135                 140

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

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

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

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

Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys
    210                 215                 220

Pro Pro Cys Pro Ala Pro Pro Val Ala 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 His 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 Phe Arg Val Val Ser Val Leu Thr
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```
    290                 295                 300

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

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

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

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
                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 Pro Gly
        435                 440


<210>  86
<211>  214
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  TPP-3323, TPP-3187X1-hIgG2, Light Chain

<400>  86

Asp Ile Val Met Thr Gln Ser Gln Lys Phe 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 Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
        35                  40                  45

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

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

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

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

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

Phe Asn Arg Gly Glu Cys
    210
```

<210> 87

<211> 1329
<212> DNA
<213> Artificial Sequence

<220>
<223> TPP-3323, TPP-3187X1-hIgG2, Heavy Chain

<400> 87
caagtgaccc tgaaagagtc cggccctggc atcctgcagc cttcccagac cctgtccctg 60

acctgctcct tctccggctt ctccctgacc acctacggca tcggcgtggg ctggatcaga 120

cagccttctg gcaagggcct ggaatggctg gcccacatct ggtggaacga caacaagtac 180

tacaacaccg ccctgaagtc ccggctgacc atctccaagg acacctccaa caaccaggtg 240

ttcctgaaga tcgcctccgt ggacaccgcc gataccgcca cctactactg cgcccggatc 300

tccctgccct acttcgacta ttggggccag ggcaccaccc tgaccgtcag ctcagcttcc 360

accaagggcc cctccgtgtt ccctctggcc ccttgctccc ggtccacctc tgagtctacc 420

gccgctctgg gctgcctggt gaaagactac ttccccgagc ccgtgaccgt gtcctggaac 480

tctggcgccc tgacctccgg cgtgcacacc tttccagccg tgctgcagtc ctccggcctg 540

tactccctgt cctccgtggt gacagtgccc tcctccaact tcggcaccca gacctacacc 600

tgtaacgtgg accacaagcc ctccaacacc aaggtggaca agaccgtgga acggaagtgc 660

tgcgtggaat gcccaccctg tcctgctcca cctgtggctg gccccagcgt gttcctgttc 720

cccccaaagc ccaaggacac cctgatgatc tcccggaccc ccgaagtgac ctgcgtggtg 780

gtggacgtgt cccacgagga ccccgaggtg cagttcaatt ggtacgtgga cggcgtggaa 840

gtgcacaacg ccaagaccaa gcccagagag gaacagttca actccacctt ccgggtggtg 900

tccgtgctga ccgtggtgca tcaggactgg ctgaacggca aagagtacaa gtgcaaggtc 960

tccaacaagg gcctgcctgc ccccatcgaa aagaccatca gcaagaccaa gggccagccc 1020

cgcgagcccc aggtgtacac actgcccccc agccgggaag agatgaccaa gaaccaggtg 1080

tccctgacct gtctggtgaa aggcttctac ccctccgaca ttgccgtgga atgggagtcc 1140

aacggacagc ctgagaacaa ctacaagacc acccccccca tgctggactc cgacggctca 1200

ttcttcctgt actccaagct gacagtggac aagtcccggt ggcagcaggg caacgtgttc 1260

tcctgctccg tgatgcacga ggccctgcac aaccactaca cccagaagtc cctgtccctg 1320

agccccggc 1329

<210> 88
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> TPP-3323, TPP-3187X1-hIgG2, Light Chain

<400> 88
gacatcgtga tgacccagtc ccagaaattc atgtccacct ccgtgggcga ccgggtgtcc 60

atcacatgca aggcctctca gaacgtgggc accgccgtgg cctggtatca gcagaagcct 120

ggccagtccc ccaagctgct gatctactcc gcctccaacc ggtacaccgg cgtgcccgat 180

agattcaccg gctctggctc tggcaccgac ttcaccctga ccatctccaa catgcagtcc 240

gaggacctgg ccgactactt ctgccagcag tacaacaact acccccctgac cttcggcgct 300

ggcaccaagc tggaactgaa gagaaccgtg gccgctccct ccgtgtttat cttcccaccc 360

tccgacgagc agctgaagtc cggcacagct tccgtcgtgt gcctgctgaa caacttctac 420

ccccgcgagg ccaaggtgca gtggaaggtg gacaacgccc tgcagtccgg caactcccag 480

gaatccgtga ccgagcagga ctccaaggac agcacctact ccctgtcctc taccctgacc 540

ctgtccaagg ccgattacga gaagcacaag gtgtacgcct gcgaagtgac ccaccagggc 600

ctgtctagcc ccgtgaccaa gtctttcaac cggggcgagt gt 642

<210> 89
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3688, h16C3-hIgG2Kappa, Heavy Chain

<400> 89

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

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

Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met

```
        35                  40                  45

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

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

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

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

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

Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
    130                 135                 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160

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

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

Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His
        195                 200                 205

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

Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala 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 Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
        275                 280                 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser
    290                 295                 300

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

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

Ser Lys Thr 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 Met 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
        435                 440                 445
```

<210> 90
<211> 214
<212> PRT

<213> Artificial Sequence

<220>
<223> TPP-3688, h16C3-hIgG2Kappa, Light Chain

<400> 90

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 Gln Ala Ser Glu Asn Ile Tyr Gly Ala
20 25 30

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

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

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

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

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

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

Phe Asn Arg Gly Glu Cys
210

<210> 91
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3705, 090E-M007-A09-Mat1-hIgG2-hIgG2Kappa, VH

<400> 91

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

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

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

Ser Trp Ile Ser Phe Ser Gly Gly Asn Thr Gly Tyr Ala 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 Arg Ala Thr Gly Tyr Ser Ser Pro Trp Tyr Leu Asp Pro Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 92

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

<220>
<223> TPP-3705, 090E-M007-A09-Mat1-hIgG2-hIgG2Kappa, HCDR1

<400> 92

Leu Tyr Gln Met His
1 5

<210> 93
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3705, 090E-M007-A09-Mat1-hIgG2-hIgG2Kappa, HCDR2

<400> 93

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

Gly

<210> 94
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3705, 090E-M007-A09-Mat1-hIgG2-hIgG2Kappa, HCDR3

<400> 94

Ala Thr Gly Tyr Ser Ser Pro Trp Tyr Leu Asp Pro
1 5 10

<210> 95
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3705, 090E-M007-A09-Mat1-hIgG2-hIgG2Kappa, VL

<400> 95

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 Gln Ala Ser His Glu Ile Asp Asn Tyr
20 25 30

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

Tyr Asp Ala Tyr Trp Leu Lys 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 Ile Ala Thr Tyr Tyr Cys Gln Gly Tyr Asp Asp Leu Ser Val
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys
100 105

<210> 96
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3705, 090E-M007-A09-Mat1-hIgG2-hIgG2Kappa, LCDR1

<400> 96

Gln Ala Ser His Glu Ile Asp Asn Tyr Leu Asn
1 5 10

<210> 97
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3705, 090E-M007-A09-Mat1-hIgG2-hIgG2Kappa, LCDR2

<400> 97

Asp Ala Tyr Trp Leu Lys Thr
1   5

<210> 98
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3705, 090E-M007-A09-Mat1-hIgG2-hIgG2Kappa, LCDR3

<400> 98

Gln Gly Tyr Asp Asp Leu Ser Val Thr
1   5

<210> 99
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> TPP-3705, 090E-M007-A09-Mat1-hIgG2-hIgG2Kappa, VH

<400> 99
gaagtgcagc tggtggaatc cggcggaggc ctggtgcagc ctggcggatc tctgagactg 60

tcttgtgccg cctccggctt caccttcagc ctgtaccaga tgcactgggt gcgacaggcc 120

cctggcaagg gactggaatg ggtgtcctgg atctccttct ccggcggcaa taccggctac 180

gccgactccg tgaagggccg gttcaccatc tcccgggaca actccaagaa caccctgtac 240

ctgcagatga actccctgcg ggccgaggac accgccgtgt actactgtgc tagagccacc 300

ggctactcct ccccctggta tctggatcct tggggccagg gcacactcgt gaccgtcagc 360

tca 363

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

<220>
<223> TPP-3705, 090E-M007-A09-Mat1-hIgG2-hIgG2Kappa, VL

<400> 100
gacatccaga tgacccagag cccttccagc ctgtccgcct ctgtgggcga cagagtgacc 60

atcacctgtc aggcctccca cgagatcgac aactacctga actggtatca gcagaagccc 120

ggcaaggccc ccaagctgct gatctacgat gcctactggc tgaaaaccgg cgtgccctcc 180

agattctccg gctctggctc tggcaccgac tttaccctga ccatctccag cctgcagccc 240

gaggatatcg ccacctacta ttgtcagggc tacgacgacc tgtccgtgac ctttggcgga 300

ggcaccaagg tggacatcaa g 321

<210> 101
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3705, 090E-M007-A09-Mat1-hIgG2-hIgG2Kappa, Heavy Chain

<400> 101

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

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

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

Ser Trp Ile Ser Phe Ser Gly Gly Asn Thr Gly Tyr Ala 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 Arg Ala Thr Gly Tyr Ser Ser Pro Trp Tyr Leu Asp Pro Trp Gly
100 105 110

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

```
Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
    130                 135                 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160

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

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

Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His
        195                 200                 205

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

Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala 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 Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
        275                 280                 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser
    290                 295                 300

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

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

```
Ser Lys Thr 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 Met 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
        435                 440                 445


<210>  102
<211>  214
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  TPP-3705, 090E-M007-A09-Mat1-hIgG2-hIgG2Kappa, Light Chain

<400>  102

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 Gln Ala Ser His Glu Ile Asp Asn Tyr
            20                  25                  30

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

Tyr Asp Ala Tyr Trp Leu Lys 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 Ile Ala Thr Tyr Tyr Cys Gln Gly Tyr Asp Asp Leu Ser Val
                85                  90                  95


Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala Ala
            100                 105                 110


Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125


Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140


Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160


Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175


Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190


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


Phe Asn Arg Gly Glu Cys
    210


<210>  103
<211>  1338
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  TPP-3705, 090E-M007-A09-Mat1-hIgG2-hIgG2Kappa, Heavy Chain

<400>  103
gaagtgcagc tggtggaatc cggcggaggc ctggtgcagc ctggcggatc tctgagactg       60

tcttgtgccg cctccggctt caccttcagc ctgtaccaga tgcactgggt gcgacaggcc      120
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cctggcaagg gactggaatg ggtgtcctgg atctccttct ccggcggcaa taccggctac 180

gccgactccg tgaagggccg gttcaccatc tcccgggaca actccaagaa caccctgtac 240

ctgcagatga actccctgcg ggccgaggac accgccgtgt actactgtgc tagagccacc 300

ggctactcct ccccctggta tctggatcct tggggccagg gcacactcgt gaccgtcagc 360

tcagcttcca ccaagggccc ctccgtgttc cctctggccc cttgctcccg gtccacctct 420

gagtctaccg ccgctctggg ctgcctggtg aaagactact tccccgagcc cgtgaccgtg 480

tcctggaact ctggcgccct gacctccggc gtgcacacct ttccagccgt gctgcagtcc 540

tccggcctgt actccctgtc ctccgtggtg acagtgccct cctccaactt cggcacccag 600

acctacacct gtaacgtgga ccacaagccc tccaacacca aggtggacaa gaccgtggaa 660

cggaagtgct gcgtggaatg cccaccctgt cctgctccac ctgtggctgg ccccagcgtg 720

ttcctgttcc ccccaaagcc caaggacacc ctgatgatct cccggacccc cgaagtgacc 780

tgcgtggtgg tggacgtgtc ccacgaggac cccgaggtgc agttcaattg gtacgtggac 840

ggcgtggaag tgcacaacgc caagaccaag cccagagagg aacagttcaa ctccaccttc 900

cgggtggtgt ccgtgctgac cgtggtgcat caggactggc tgaacggcaa agagtacaag 960

tgcaaggtct ccaacaaggg cctgcctgcc cccatcgaaa agaccatcag caagaccaag 1020

ggccagcccc gcgagcccca ggtgtacaca ctgccccca gccgggaaga gatgaccaag 1080

aaccaggtgt ccctgacctg tctggtgaaa ggcttctacc cctccgacat tgccgtggaa 1140

tgggagtcca acggacagcc tgagaacaac tacaagacca ccccccccat gctggactcc 1200

gacggctcat tcttcctgta ctccaagctg acagtggaca agtcccggtg gcagcagggc 1260

aacgtgttct cctgctccgt gatgcacgag gccctgcaca accactacac ccagaagtcc 1320

ctgtccctga gccccggc 1338

<210> 104
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> TPP-3705, 090E-M007-A09-Mat1-hIgG2-hIgG2Kappa, Light Chain

<400> 104

gacatccaga tgacccagag cccttccagc ctgtccgcct ctgtgggcga cagagtgacc 60

atcacctgtc aggcctccca cgagatcgac aactacctga actggtatca gcagaagccc 120

ggcaaggccc ccaagctgct gatctacgat gcctactggc tgaaaaccgg cgtgccctcc 180

agattctccg gctctggctc tggcaccgac tttaccctga ccatctccag cctgcagccc 240

gaggatatcg ccacctacta ttgtcagggc tacgacgacc tgtccgtgac ctttggcgga 300

ggcaccaagg tggacatcaa gcggacagtg gccgctccct ccgtgtttat cttcccaccc 360

tccgacgagc agctgaagtc cggcacagct tccgtcgtgt gcctgctgaa caacttctac 420

ccccgcgagg ccaaggtgca gtggaaagtg gataacgccc tgcagtccgg caactcccag 480

gaatccgtga ccgagcagga ctccaaggac agcacctact ccctgtcctc caccctgacc 540

ctgtccaagg ccgactacga gaagcacaag gtgtacgcct gcgaagtgac ccaccagggc 600

ctgtctagcc ccgtgaccaa gtctttcaac cggggcgagt gt 642

<210> 105
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3707, 090E-M007-A09-Mat2-hIgG2-hIgG2Kappa, VH

<400> 105

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

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

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

Ser Trp Ile Ser Phe Ser Gly Gly Asn Thr Gly Tyr Ala 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 Arg Ala Thr Gly Tyr Ser Ser Pro Trp Tyr Leu Asp Pro Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  106
<211>  5
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  TPP-3707, 090E-M007-A09-Mat2-hIgG2-hIgG2Kappa, HCDR1

<400>  106

Leu Tyr Gln Met His
1               5


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

<220>
<223>  TPP-3707, 090E-M007-A09-Mat2-hIgG2-hIgG2Kappa, HCDR2

<400>  107

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


Gly



<210>  108
<211>  12
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  TPP-3707, 090E-M007-A09-Mat2-hIgG2-hIgG2Kappa, HCDR3

<400>  108
```

Ala Thr Gly Tyr Ser Ser Pro Trp Tyr Leu Asp Pro
1 5 10

<210> 109
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3707, 090E-M007-A09-Mat2-hIgG2-hIgG2Kappa, VL

<400> 109

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 Gln Ala Ser His Glu Ile Asp Asn Tyr
20 25 30

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

Tyr Asp Ala Tyr Trp Ser Lys 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 Ile Ala Thr Tyr Tyr Cys Gln Gly Tyr Asp Asp Leu Ser Val
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys
100 105

<210> 110
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3707, 090E-M007-A09-Mat2-hIgG2-hIgG2Kappa, LCDR1

<400> 110

Gln Ala Ser His Glu Ile Asp Asn Tyr Leu Asn
1   5   10

<210> 111
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3707, 090E-M007-A09-Mat2-hIgG2-hIgG2Kappa, LCDR2

<400> 111

Asp Ala Tyr Trp Ser Lys Thr
1   5

<210> 112
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3707, 090E-M007-A09-Mat2-hIgG2-hIgG2Kappa, LCDR3

<400> 112

Gln Gly Tyr Asp Asp Leu Ser Val Thr
1   5

<210> 113
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> TPP-3707, 090E-M007-A09-Mat2-hIgG2-hIgG2Kappa, VH

<400> 113
gaagtgcagc tggtggaatc cggcggaggc ctggtgcagc ctggcggatc tctgagactg   60

tcttgtgccg cctccggctt caccttcagc ctgtaccaga tgcactgggt gcgacaggcc   120

cctggcaagg gactggaatg ggtgtcctgg atctccttct ccggcggcaa taccggctac   180

gccgactccg tgaagggccg gttcaccatc tcccgggaca actccaagaa caccctgtac   240

ctgcagatga actccctgcg ggccgaggac accgccgtgt actactgtgc tagagccacc   300

ggctactcct ccccctggta tctggatcct tggggccagg gcacactcgt gaccgtcagc   360

tca 363

<210> 114
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> TPP-3707, 090E-M007-A09-Mat2-hIgG2-hIgG2Kappa, VL

<400> 114
gacatccaga tgacccagag cccttccagc ctgtccgcct ctgtgggcga cagagtgacc 60

atcacctgtc aggcctccca cgagatcgac aactacctga actggtatca gcagaagccc 120

ggcaaggccc ccaagctgct gatctacgac gcctactggt ccaagaccgg cgtgccctcc 180

agattctccg gctctggctc tggcaccgac tttaccctga ccatctccag cctgcagccc 240

gaggatatcg ccacctacta ttgtcagggc tacgacgacc tgtccgtgac ctttggcgga 300

ggcaccaagg tggacatcaa g 321

<210> 115
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3707, 090E-M007-A09-Mat2-hIgG2-hIgG2Kappa, Heavy Chain

<400> 115

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

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

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

Ser Trp Ile Ser Phe Ser Gly Gly Asn Thr Gly Tyr Ala 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 Arg Ala Thr Gly Tyr Ser Ser Pro Trp Tyr Leu Asp Pro Trp Gly
            100                 105                 110

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

Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
    130                 135                 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160

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

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

Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His
        195                 200                 205

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

Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala 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 Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
        275                 280                 285
```

```
Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser
    290                 295                 300

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

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

Ser Lys Thr 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 Met 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
        435                 440                 445
```

<210> 116
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3707, 090E-M007-A09-Mat2-hIgG2-hIgG2Kappa, Light Chain

<400> 116

```
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 Gln Ala Ser His Glu Ile Asp Asn Tyr
            20                  25                  30

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

Tyr Asp Ala Tyr Trp Ser Lys 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 Ile Ala Thr Tyr Tyr Cys Gln Gly Tyr Asp Asp Leu Ser Val
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

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

Phe Asn Arg Gly Glu Cys
    210
```

<210> 117
<211> 1338
<212> DNA
<213> Artificial Sequence

<220>
<223> TPP-3707, 090E-M007-A09-Mat2-hIgG2-hIgG2Kappa, Heavy Chain

<400> 117
gaagtgcagc tggtggaatc cggcggaggc ctggtgcagc ctggcggatc tctgagactg 60

tcttgtgccg cctccggctt caccttcagc ctgtaccaga tgcactgggt gcgacaggcc 120

cctggcaagg gactggaatg ggtgtcctgg atctccttct ccggcggcaa taccggctac 180

gccgactccg tgaagggccg gttcaccatc tcccgggaca actccaagaa caccctgtac 240

ctgcagatga actccctgcg ggccgaggac accgccgtgt actactgtgc tagagccacc 300

ggctactcct ccccctggta tctggatcct tggggccagg gcacactcgt gaccgtcagc 360

tcagcttcca ccaagggccc ctccgtgttc cctctggccc cttgctcccg gtccacctct 420

gagtctaccg ccgctctggg ctgcctggtg aaagactact tccccgagcc cgtgaccgtg 480

tcctggaact ctggcgccct gacctccggc gtgcacacct ttccagccgt gctgcagtcc 540

tccggcctgt actccctgtc ctccgtggtg acagtgccct cctccaactt cggcacccag 600

acctacacct gtaacgtgga ccacaagccc tccaacacca aggtggacaa gaccgtggaa 660

cggaagtgct gcgtggaatg cccaccctgt cctgctccac ctgtggctgg ccccagcgtg 720

ttcctgttcc ccccaaagcc caaggacacc ctgatgatct cccggacccc cgaagtgacc 780

tgcgtggtgg tggacgtgtc ccacgaggac cccgaggtgc agttcaattg gtacgtggac 840

ggcgtggaag tgcacaacgc caagaccaag cccagagagg aacagttcaa ctccaccttc 900

cgggtggtgt ccgtgctgac cgtggtgcat caggactggc tgaacggcaa agagtacaag 960

tgcaaggtct ccaacaaggg cctgcctgcc cccatcgaaa agaccatcag caagaccaag 1020

ggccagcccc gcgagcccca ggtgtacaca ctgccccccа gccgggaaga gatgaccaag 1080

aaccaggtgt ccctgacctg tctggtgaaa ggcttctacc cctccgacat tgccgtggaa 1140

tgggagtcca acggacagcc tgagaacaac tacaagacca ccccccccat gctggactcc 1200

gacggctcat tcttcctgta ctccaagctg acagtggaca agtcccggtg gcagcagggc 1260

aacgtgttct cctgctccgt gatgcacgag gccctgcaca accactacac ccagaagtcc 1320

ctgtccctga gccccggc 1338

<210> 118
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> TPP-3707, 090E-M007-A09-Mat2-hIgG2-hIgG2Kappa, Light Chain

<400> 118
gacatccaga tgacccagag cccttccagc ctgtccgcct ctgtgggcga cagagtgacc 60

atcacctgtc aggcctccca cgagatcgac aactacctga actggtatca gcagaagccc 120

ggcaaggccc ccaagctgct gatctacgac gcctactggt ccaagaccgg cgtgccctcc 180

agattctccg gctctggctc tggcaccgac tttaccctga ccatctccag cctgcagccc 240

gaggatatcg ccacctacta ttgtcagggc tacgacgacc tgtccgtgac ctttggcgga 300

ggcaccaagg tggacatcaa gcggacagtg gccgctccct ccgtgtttat cttcccaccc 360

tccgacgagc agctgaagtc cggcacagct tccgtcgtgt gcctgctgaa caacttctac 420

ccccgcgagg ccaaggtgca gtggaaagtg gataacgccc tgcagtccgg caactcccag 480

gaatccgtga ccgagcagga ctccaaggac agcacctact ccctgtcctc caccctgacc 540

ctgtccaagg ccgactacga gaagcacaag gtgtacgcct gcgaagtgac ccaccagggc 600

ctgtctagcc ccgtgaccaa gtctttcaac cggggcgagt gt 642

<210> 119
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3714, TPP-2971HU2-hIgG2Kappa, VH

<400> 119

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

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

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

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

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

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
                85                  90                  95

Cys Ala Arg Ile Ser Leu Pro Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser
        115
```

<210> 120
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3714, TPP-2971HU2-hIgG2Kappa, HCDR1

<400> 120

```
Thr Tyr Gly Ile Gly Val Gly
1               5
```

<210> 121
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3714, TPP-2971HU2-hIgG2Kappa, HCDR2

<400> 121

```
His Ile Trp Trp Asn Asp Asn Lys Tyr Tyr Ser Thr Ser Leu Lys Thr
1               5                   10                  15
```

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

<220>
<223> TPP-3714, TPP-2971HU2-hIgG2Kappa, HCDR3

<400> 122

Ile Ser Leu Pro Tyr Phe Asp Tyr
1 5

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

<220>
<223> TPP-3714, TPP-2971HU2-hIgG2Kappa, VL

<400> 123

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

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

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

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

<210> 124

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

<220>
<223> TPP-3714, TPP-2971HU2-hIgG2Kappa, LCDR1

<400> 124

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

<210> 125
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3714, TPP-2971HU2-hIgG2Kappa, LCDR2

<400> 125

Ser Ala Ser Asn Arg Tyr Thr
1 5

<210> 126
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3714, TPP-2971HU2-hIgG2Kappa, LCDR3

<400> 126

Gln Gln Tyr Ser Ser Tyr Pro Leu Thr
1 5

<210> 127
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> TPP-3714, TPP-2971HU2-hIgG2Kappa, VH

<400> 127
caagtgaccc tgagagagtc cggccctgcc ctcgtgaagc ctacccagac cctgacactg 60

acctgcacct tctccggctt ctccctgtcc acctacggca tcggcgtggg ctggatcaga 120

cagcctcctg gcaaggccct ggaatggctg gctcacatct ggtggaacga caacaagtac 180

tactccacct ccctgaaaac ccggctgacc atctccaagg acacctccaa gaaccaggtg 240

gtgctgacca tgaccaacat ggaccccgtg gacaccgcca cctactactg cgccagaatc 300

tccctgccct acttcgacta ctggggccag ggcacactcg tgaccgtcag ctca 354

<210> 128
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> TPP-3714, TPP-2971HU2-hIgG2Kappa, VL

<400> 128
gatatccagc tgacccagtc ccccagcttc ctgtctgcct ctgtgggcga cagagtgacc 60

atcacatgca aggcctccca gaacgtgggc accgccgtgg cttggtatca gcagaagcct 120

ggcaaggccc ccaagctgct gatctactcc gcctccaacc ggtacaccgg cgtgccctct 180

agattctccg gctctggctc tggcaccgag tttaccctga ccatctccag cctgcagccc 240

gaggacttcg ccacctacta ctgccagcag tactcctcct acccccctgac ctttggcgga 300

ggcaccaagg tggaaatcaa g 321

<210> 129
<211> 443
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3714, TPP-2971HU2-hIgG2Kappa, Heavy Chain

<400> 129

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

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

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

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

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

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
                85                  90                  95

Cys Ala Arg Ile Ser Leu Pro Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

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

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
    130                 135                 140

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

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

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

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

Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys
    210                 215                 220

Pro Pro Cys Pro Ala Pro Pro Val Ala 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 His 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 Phe Arg Val Val Ser Val Leu Thr
    290                 295                 300

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

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

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

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
                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 Pro Gly
        435                 440
```

<210> 130
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3714, TPP-2971HU2-hIgG2Kappa, Light Chain

<400> 130

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

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80

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

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100   105   110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115   120   125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130   135   140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145   150   155   160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165   170   175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180   185   190

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

Phe Asn Arg Gly Glu Cys
210

<210> 131
<211> 1329
<212> DNA
<213> Artificial Sequence

<220>
<223> TPP-3714, TPP-2971HU2-hIgG2Kappa, Heavy Chain

<400> 131
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acctgcacct tctccggctt ctccctgtcc acctacggca tcggcgtggg ctggatcaga 120

cagcctcctg gcaaggccct ggaatggctg gctcacatct ggtggaacga caacaagtac 180

tactccacct ccctgaaaac ccggctgacc atctccaagg acacctccaa gaaccaggtg 240

gtgctgacca tgaccaacat ggaccccgtg gacaccgcca cctactactg cgccagaatc 300

tccctgccct acttcgacta ctggggccag ggcacactcg tgaccgtcag ctcagcttcc 360

accaagggcc cctccgtgtt ccctctggcc ccttgctccc ggtccacctc tgagtctacc 420

gccgctctgg gctgcctggt gaaagactac ttccccgagc ccgtgaccgt gtcctggaac 480

tctggcgccc tgacctccgg cgtgcacacc tttccagccg tgctgcagtc ctccggcctg 540

tactccctgt cctccgtggt gacagtgccc tcctccaact tcggcaccca gacctacacc 600

tgtaacgtgg accacaagcc ctccaacacc aaggtggaca agaccgtgga acggaagtgc 660

tgcgtggaat gcccaccctg tcctgctcca cctgtggctg gccccagcgt gttcctgttc 720

cccccaaagc ccaaggacac cctgatgatc tcccggaccc ccgaagtgac ctgcgtggtg 780

gtggacgtgt cccacgagga ccccgaggtg cagttcaatt ggtacgtgga cggcgtggaa 840

gtgcacaacg ccaagaccaa gcccagagag gaacagttca actccacctt ccgggtggtg 900

tccgtgctga ccgtggtgca tcaggactgg ctgaacggca aagagtacaa gtgcaaggtc 960

tccaacaagg gcctgcctgc ccccatcgaa aagaccatca gcaagaccaa gggccagccc 1020

cgcgagcccc aggtgtacac actgcccccc agccgggaag agatgaccaa gaaccaggtg 1080

tccctgacct gtctggtgaa aggcttctac ccctccgaca ttgccgtgga atgggagtcc 1140

aacggacagc ctgagaacaa ctacaagacc acccccccca tgctggactc cgacggctca 1200

ttcttcctgt actccaagct gacagtggac aagtcccggt ggcagcaggg caacgtgttc 1260

tcctgctccg tgatgcacga ggccctgcac aaccactaca cccagaagtc cctgtccctg 1320

agccccggc 1329

<210> 132
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> TPP-3714, TPP-2971HU2-hIgG2Kappa, Light Chain

<400> 132
gatatccagc tgacccagtc ccccagcttc ctgtctgcct ctgtgggcga cagagtgacc 60

atcacatgca aggcctccca gaacgtgggc accgccgtgg cttggtatca gcagaagcct 120

ggcaaggccc ccaagctgct gatctactcc gcctccaacc ggtacaccgg cgtgccctct 180

agattctccg gctctggctc tggcaccgag tttaccctga ccatctccag cctgcagccc 240

gaggacttcg ccacctacta ctgccagcag tactcctcct acccccctgac ctttggcgga 300

ggcaccaagg tggaaatcaa gcggaccgtg gccgctccct ccgtgtttat cttcccaccc 360

tccgacgagc agctgaagtc cggcacagct tccgtcgtgt gcctgctgaa caacttctac 420

ccccgcgagg ccaaggtgca gtggaaggtg gacaacgccc tgcagtccgg caactcccag 480

gaatccgtga ccgagcagga ctccaaggac agcacctact ccctgtcctc caccctgacc 540

ctgtccaagg ccgactacga gaagcacaag gtgtacgcct gcgaagtgac ccaccagggc 600

ctgtctagcc ccgtgaccaa gtctttcaac cggggcgagt gt 642

<210> 133
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3820, 3187HU1-hIgG2Kappa, VH

<400> 133

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


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


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


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


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


Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
                85                  90                  95


Cys Ala Arg Ile Ser Leu Pro Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210>  134
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  TPP-3820, 3187HU1-hIgG2Kappa, HCDR1

<400>  134

Thr Tyr Gly Ile Gly Val Gly
1               5


<210>  135
<211>  16
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  TPP-3820, 3187HU1-hIgG2Kappa, HCDR2
```

<400> 135

His Ile Trp Trp Asn Asp Asn Lys Tyr Tyr Ser Thr Ser Leu Lys Thr
1 5 10 15

<210> 136
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3820, 3187HU1-hIgG2Kappa, HCDR3

<400> 136

Ile Ser Leu Pro Tyr Phe Asp Tyr
1 5

<210> 137
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3820, 3187HU1-hIgG2Kappa, VL

<400> 137

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

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

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

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

<210> 138
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3820, 3187HU1-hIgG2Kappa, LCDR1

<400> 138

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

<210> 139
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3820, 3187HU1-hIgG2Kappa, LCDR2

<400> 139

Ser Ala Ser Asn Arg Tyr Thr
1 5

<210> 140
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3820, 3187HU1-hIgG2Kappa, LCDR3

<400> 140

Gln Gln Tyr Asn Asn Tyr Pro Leu Thr
1 5

<210> 141
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> TPP-3820, 3187HU1-hIgG2Kappa, VH

<400> 141
caagtgaccc tgagagagtc cggccctgcc ctcgtgaagc ctacccagac cctgacactg 60

acctgcacct tcagcggctt cagcctgacc acctacggca tcggcgtggg ctggatcaga 120

cagcctcctg gcaagggcct ggaatggctg gcccacatct ggtggaacga caacaagtac 180

tacagcacca gcctgaaaac ccggctgacc atcagcaagg acaccagcaa gaaccaggtg 240

gtgctgacca tgaccaacat ggaccccgtg gacaccgcca cctactactg cgccagaatc 300

agcctgccct acttcgacta ctggggccag ggcaccctcg tgacagtgtc atca 354

<210> 142
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> TPP-3820, 3187HU1-hIgG2Kappa, VL

<400> 142
gatatccagc tgacccagag ccccagcttt ctgagcgcca gcgtgggcga cagagtgacc 60

atcacatgca aggccagcca gaacgtgggc acagccgtgg cctggtatca gcagaagcct 120

ggcaaggccc ccaagctgct gatctacagc gccagcaacc ggtacaccgg cgtgcccagc 180

agattttctg gcagcggctc cggcaccgag ttcaccctga caatcagcag cctgcagccc 240

gaggacttcg ccacctacta ctgccagcag tacaacaact acccccctgac cttcggcgga 300

ggcaccaagg tggaaattaa a 321

<210> 143
<211> 443
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3820, 3187HU1-hIgG2Kappa, Heavy Chain

<400> 143

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

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

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

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

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

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
                85                  90                  95

Cys Ala Arg Ile Ser Leu Pro Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

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

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
    130                 135                 140

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

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

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

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

Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys
    210                 215                 220

Pro Pro Cys Pro Ala Pro Pro Val Ala 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 His 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 Phe Arg Val Val Ser Val Leu Thr
    290                 295                 300

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

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

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

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
                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 Pro Gly
        435                 440
```

<210> 144
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3820, 3187HU1-hIgG2Kappa, Light Chain

<400> 144

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

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

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

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser

165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

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

Phe Asn Arg Gly Glu Cys
210

<210> 145
<211> 1329
<212> DNA
<213> Artificial Sequence

<220>
<223> TPP-3820, 3187HU1-hIgG2Kappa, Heavy Chain

<400> 145
caagtgaccc tgagagagtc cggccctgcc ctcgtgaagc ctacccagac cctgacactg 60

acctgcacct tcagcggctt cagcctgacc acctacggca tcggcgtggg ctggatcaga 120

cagcctcctg gcaagggcct ggaatggctg gcccacatct ggtggaacga caacaagtac 180

tacagcacca gcctgaaaac ccggctgacc atcagcaagg acaccagcaa gaaccaggtg 240

gtgctgacca tgaccaacat ggaccccgtg gacaccgcca cctactactg cgccagaatc 300

agcctgccct acttcgacta ctggggccag ggcaccctcg tgacagtgtc atcagccagc 360

accaagggcc ccagcgtgtt ccctctggcc ccttgtagca gaagcaccag cgagtctaca 420

gccgccctgg gctgcctcgt gaaggactac tttcccgagc ccgtgaccgt gtcctggaac 480

tctggcgctc tgacaagcgg cgtgcacacc tttccagccg tgctgcagag cagcggcctg 540

tactctctga gcagcgtcgt gacagtgccc agcagcaact tcggcaccca gacctacacc 600

tgtaacgtgg accacaagcc cagcaacacc aaggtggaca agaccgtgga acggaagtgc 660

tgcgtggaat gccccccttg tcctgcccct ccagtggctg gcccttccgt gttcctgttc 720

cccccaaagc ccaaggacac cctgatgatc agccggaccc ccgaagtgac ctgcgtggtg 780

gtggatgtgt cccacgagga ccccgaggtg cagttcaatt ggtacgtgga cggcgtggaa 840

gtgcacaacg ccaagaccaa gcccagagag gaacagttca acagcacctt ccgggtggtg 900

tccgtgctga ccgtggtgca tcaggactgg ctgaacggca aagagtacaa gtgcaaggtg 960

tccaacaagg gcctgcctgc ccccatcgag aaaaccatca gcaagaccaa aggccagccc 1020

cgcgagcccc aggtgtacac actgcctcca agccgggaag agatgaccaa gaaccaggtg 1080

tccctgacct gtctcgtgaa aggcttctac ccctccgata tcgccgtgga atgggagagc 1140

aacggccagc ccgagaacaa ctacaagacc acccccccca tgctggacag cgacggctca 1200

ttcttcctgt acagcaagct gacagtggac aagtcccggt ggcagcaggg caacgtgttc 1260

agctgcagcg tgatgcacga ggccctgcac aaccactaca cccagaagtc cctgagcctg 1320

agccctggc 1329

<210> 146
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> TPP-3820, 3187HU1-hIgG2Kappa, Light Chain

<400> 146
gatatccagc tgacccagag ccccagcttt ctgagcgcca gcgtgggcga cagagtgacc 60

atcacatgca aggccagcca gaacgtgggc acagccgtgg cctggtatca gcagaagcct 120

ggcaaggccc ccaagctgct gatctacagc gccagcaacc ggtacaccgg cgtgcccagc 180

agattttctg gcagcggctc cggcaccgag ttcaccctga caatcagcag cctgcagccc 240

gaggacttcg ccacctacta ctgccagcag tacaacaact acccccctgac cttcggcgga 300

ggcaccaagg tggaaattaa acgaaccgtg gccgctccca gcgtgttcat cttcccacct 360

agcgacgagc agctgaagtc cggcacagcc tctgtcgtgt gcctgctgaa caacttctac 420

ccccgcgagg ccaaggtgca gtggaaggtg gacaatgccc tgcagagcgg caacagccag 480

gaaagcgtga ccgagcagga cagcaaggac tccacctaca gcctgagcag caccctgacc 540

ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaagtgac ccaccagggc 600

ctgtctagcc ccgtgaccaa gagcttcaac cggggcgagt gt 642

<210> 147
<211> 118
<212> PRT

<213> Artificial Sequence

<220>
<223> TPP-3821, 3187HU2-hIgG2Kappa, VH

<400> 147

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

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

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

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

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

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile Ser Leu Pro Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 148
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3821, 3187HU2-hIgG2Kappa, HCDR1

<400> 148

Thr Tyr Gly Ile Gly Val Gly
1 5

<210> 149
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3821, 3187HU2-hIgG2Kappa, HCDR2

<400> 149

His Ile Trp Trp Asn Asp Asn Lys Tyr Tyr Ser Thr Ser Leu Lys Thr
1 5 10 15

<210> 150
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3821, 3187HU2-hIgG2Kappa, HCDR3

<400> 150

Ile Ser Leu Pro Tyr Phe Asp Tyr
1 5

<210> 151
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3821, 3187HU2-hIgG2Kappa, VL

<400> 151

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

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

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

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

<210> 152
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3821, 3187HU2-hIgG2Kappa, LCDR1

<400> 152

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

<210> 153
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3821, 3187HU2-hIgG2Kappa, LCDR2

<400> 153

Ser Ala Ser Asn Arg Tyr Thr
1 5

<210> 154
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3821, 3187HU2-hIgG2Kappa, LCDR3

<400> 154

Gln Gln Tyr Asn Asn Tyr Pro Leu Thr
1 5

<210> 155
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> TPP-3821, 3187HU2-hIgG2Kappa, VH

<400> 155
caggtcacac tgagagagtc cggccctgcc ctggtgaaac ccacccagac cctgaccctg 60

acatgcacct tcagcggctt cagcctgagc acctacggca tcggcgtggg ctggatcaga 120

cagccccctg gcaaggccct ggaatggctg gcccacatct ggtggaacga caacaagtac 180

tacagcacca gcctgaaaac ccggctgacc atcagcaagg acaccagcaa gaaccaggtg 240

gtgctgacca tgaccaacat ggaccccgtg gacaccgcca cctactactg cgcccggatc 300

agcctgccct acttcgacta ctggggccag ggcaccctgg tgaccgtgtc ctca 354

<210> 156
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> TPP-3821, 3187HU2-hIgG2Kappa, VL

<400> 156
gatatccagc tgacccagag ccccagcttt ctgagcgcca gcgtgggcga cagagtgacc 60

atcacatgca aggccagcca gaacgtgggc acagccgtgg cctggtatca gcagaagcct 120

ggcaaggccc ccaagctgct gatctacagc gccagcaacc ggtacaccgg cgtgcccagc 180

agattttctg gcagcggctc cggcaccgag ttcaccctga caatcagcag cctgcagccc 240

gaggacttcg ccacctacta ctgccagcag tacaacaact acccccctgac cttcggcgga 300

ggcaccaagg tggaaattaa a 321

<210> 157
<211> 443
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-3821, 3187HU2-hIgG2Kappa, Heavy Chain

<400> 157

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

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

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

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

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

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
                85                  90                  95

Cys Ala Arg Ile Ser Leu Pro Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

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

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
    130                 135                 140

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

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

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

Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
        195                 200                 205
```

```
Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys
    210                 215                 220

Pro Pro Cys Pro Ala Pro Pro Val Ala 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 His 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 Phe Arg Val Val Ser Val Leu Thr
    290                 295                 300

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

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

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

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
                405                 410                 415
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```
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 Pro Gly
        435                 440


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

<220>
<223>  TPP-3821, 3187HU2-hIgG2Kappa, Light Chain

<400>  158

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


Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


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


Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110


Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125


Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140
```

```
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160


Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175


Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190


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


Phe Asn Arg Gly Glu Cys
    210


<210>  159
<211>  1329
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  TPP-3821, 3187HU2-hIgG2Kappa, Heavy Chain

<400>  159
caggtcacac tgagagagtc cggccctgcc ctggtgaaac ccacccagac cctgaccctg       60

acatgcacct tcagcggctt cagcctgagc acctacggca tcggcgtggg ctggatcaga      120

cagccccctg gcaaggccct ggaatggctg gcccacatct ggtggaacga caacaagtac      180

tacagcacca gcctgaaaac ccggctgacc atcagcaagg acaccagcaa gaaccaggtg      240

gtgctgacca tgaccaacat ggaccccgtg gacaccgcca cctactactg cgcccggatc      300

agcctgccct acttcgacta ctggggccag ggcaccctgg tgaccgtgtc ctcagccagc      360

accaagggcc ccagcgtgtt ccctctggcc ccttgtagca gaagcaccag cgagtctaca      420

gccgccctgg gctgcctcgt gaaggactac tttcccgagc ccgtgaccgt gtcctggaac      480

tctggcgctc tgacaagcgg cgtgcacacc tttccagccg tgctgcagag cagcggcctg      540

tactctctga gcagcgtcgt gacagtgccc agcagcaact tcggcaccca gacctacacc      600

tgtaacgtgg accacaagcc cagcaacacc aaggtggaca agaccgtgga acggaagtgc      660
```

tgcgtggaat gccccccttg tcctgcccct ccagtggctg gcccttccgt gttcctgttc 720

cccccaaagc ccaaggacac cctgatgatc agccggaccc ccgaagtgac ctgcgtggtg 780

gtggatgtgt cccacgagga ccccgaggtg cagttcaatt ggtacgtgga cggcgtggaa 840

gtgcacaacg ccaagaccaa gcccagagag gaacagttca acagcacctt ccgggtggtg 900

tccgtgctga ccgtggtgca tcaggactgg ctgaacggca aagagtacaa gtgcaaggtg 960

tccaacaagg gcctgcctgc ccccatcgag aaaaccatca gcaagaccaa aggccagccc 1020

cgcgagcccc aggtgtacac actgcctcca agccgggaag agatgaccaa gaaccaggtg 1080

tccctgacct gtctcgtgaa aggcttctac ccctccgata tcgccgtgga atgggagagc 1140

aacggccagc ccgagaacaa ctacaagacc acccccccca tgctggacag cgacggctca 1200

ttcttcctgt acagcaagct gacagtggac aagtcccggt ggcagcaggg caacgtgttc 1260

agctgcagcg tgatgcacga ggccctgcac aaccactaca cccagaagtc cctgagcctg 1320

agccctggc 1329

<210> 160
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> TPP-3821, 3187HU2-hIgG2Kappa, Light Chain

<400> 160
gatatccagc tgacccagag ccccagcttt ctgagcgcca gcgtgggcga cagagtgacc 60

atcacatgca aggccagcca gaacgtgggc acagccgtgg cctggtatca gcagaagcct 120

ggcaaggccc ccaagctgct gatctacagc gccagcaacc ggtacaccgg cgtgcccagc 180

agattttctg gcagcggctc cggcaccgag ttcaccctga caatcagcag cctgcagccc 240

gaggacttcg ccacctacta ctgccagcag tacaacaact acccccctgac cttcggcgga 300

ggcaccaagg tggaaattaa acgaaccgtg gccgctccca gcgtgttcat cttcccacct 360

agcgacgagc agctgaagtc cggcacagcc tctgtcgtgt gcctgctgaa caacttctac 420

ccccgcgagg ccaaggtgca gtggaaggtg gacaatgccc tgcagagcgg caacagccag 480

gaaagcgtga ccgagcagga cagcaaggac tccacctaca gcctgagcag caccctgacc 540

ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaagtgac ccaccagggc 600

ctgtctagcc ccgtgaccaa gagcttcaac cggggcgagt gt 642

<210> 161
<211> 532
<212> PRT
<213> Macaca mulatta (Rhesus monkey)

<400> 161

Gln Leu Thr Ile Glu Ser Arg Pro Phe Asn Val Ala Glu Gly Lys Glu
1 5 10 15

Val Leu Leu Leu Ala His Asn Leu Pro Gln Asn Leu Ile Gly Phe Asn
20 25 30

Trp Tyr Lys Gly Glu Arg Val Asp Ala Lys Arg Leu Ile Val Ala Tyr
35 40 45

Val Ile Glu Thr Gln Gln Thr Thr Pro Gly Pro Ala His Ser Gly Arg
50 55 60

Glu Thr Val Tyr Ser Asn Ala Ser Leu Leu Ile Gln Asn Val Thr Gln
65 70 75 80

Asn Asp Thr Gly Ser Tyr Thr Leu Gln Val Ile Lys Gly Asp Leu Val
85 90 95

Asn Glu Glu Ala Thr Gly Arg Phe Trp Val Tyr Pro Glu Leu Pro Lys
100 105 110

Pro Tyr Ile Thr Ser Asn Asn Ser Asn Pro Val Glu Asp Lys Asp Ala
115 120 125

Val Asp Phe Thr Cys Glu Pro Asp Ile His Ser Thr Thr Tyr Leu Trp
130 135 140

Trp Val Asn Asp Gln Ser Leu Pro Val Ser Pro Arg Leu Gln Leu Ser
145 150 155 160

Asn Gly Asn Arg Thr Leu Thr Leu Leu Ser Val Lys Arg Asn Asp Ala
165 170 175

```
Gly Ala Tyr Glu Cys Glu Ile Gln Asn Pro Val Ser Ala Asn Leu Ser
            180                 185                 190

Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Val Pro Thr Ile
        195                 200                 205

Ser Pro Ser Asn Ser Asn Tyr Arg Pro Gly Glu Asn Leu Asn Leu Ser
    210                 215                 220

Cys His Ala Ala Ser Asn Pro Thr Ala Gln Tyr Ser Trp Phe Val Asn
225                 230                 235                 240

Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn Ile Thr
                245                 250                 255

Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala Tyr Asn Ser Ala Thr
            260                 265                 270

Gly Leu Asn Arg Thr Thr Val Met Met Ile Thr Val Ser Gly Ile Glu
        275                 280                 285

Gly Arg Asp Met Asp Thr Gly Pro Lys Ser Cys Asp Lys Thr His Thr
    290                 295                 300

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
305                 310                 315                 320

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                325                 330                 335

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            340                 345                 350

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        355                 360                 365

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    370                 375                 380
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```
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
385                 390                 395                 400


Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
                405                 410                 415


Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            420                 425                 430


Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
        435                 440                 445


Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    450                 455                 460


Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
465                 470                 475                 480


Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                485                 490                 495


Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            500                 505                 510


Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys His His
        515                 520                 525


His His His His
    530


<210>  162
<211>  292
<212>  PRT
<213>  Homo sapiens

<400>  162

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


Val Leu Leu Leu Ala His Asn Leu Pro Gln Asn Arg Ile Gly Tyr Ser
```

```
            20                  25                  30

Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Ser Leu Ile Val Gly Tyr
        35                  40                  45

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

Glu Thr Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Val Thr Gln
65                  70                  75                  80

Asn Asp Thr Gly Phe Tyr Thr Leu Gln Val Ile Lys Ser Asp Leu Val
                85                  90                  95

Asn Glu Glu Ala Thr Gly Gln Phe His Val Tyr Pro Glu Leu Pro Lys
            100                 105                 110

Pro Ser Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys Asp Ala
        115                 120                 125

Val Ala Phe Thr Cys Glu Pro Glu Val Gln Asn Thr Thr Tyr Leu Trp
    130                 135                 140

Trp Val Asn Gly Gln Ser Leu Pro Val Ser Pro Arg Leu Gln Leu Ser
145                 150                 155                 160

Asn Gly Asn Met Thr Leu Thr Leu Leu Ser Val Lys Arg Asn Asp Ala
                165                 170                 175

Gly Ser Tyr Glu Cys Glu Ile Gln Asn Pro Ala Ser Ala Asn Arg Ser
            180                 185                 190

Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp Gly Pro Thr Ile
        195                 200                 205

Ser Pro Ser Lys Ala Asn Tyr Arg Pro Gly Glu Asn Leu Asn Leu Ser
    210                 215                 220

Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe Ile Asn
225                 230                 235                 240
```

```
Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn Ile Thr
                245                 250                 255


Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His Asn Ser Ala Thr
            260                 265                 270


Gly Leu Asn Arg Thr Thr Val Thr Met Ile Thr Val Ser Gly His His
        275                 280                 285


His His His His
    290


<210>  163
<211>  404
<212>  PRT
<213>  Homo sapiens

<400>  163

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


Val Leu Leu Leu Val His Asn Leu Pro Gln Gln Leu Phe Gly Tyr Ser
            20                  25                  30


Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Val Gly Tyr
        35                  40                  45


Ala Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Asn Ser Gly Arg
    50                  55                  60


Glu Thr Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Val Thr Gln
65                  70                  75                  80


Asn Asp Thr Gly Phe Tyr Thr Leu Gln Val Ile Lys Ser Asp Leu Val
                85                  90                  95


Asn Glu Glu Ala Thr Gly Gln Phe His Val Tyr Pro Glu Leu Pro Lys
            100                 105                 110
```

```
Pro Ser Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys Asp Ala
        115                 120                 125

Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Thr Thr Tyr Leu Trp
    130                 135                 140

Trp Ile Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln Leu Ser
145                 150                 155                 160

Asn Gly Asn Arg Thr Leu Thr Leu Leu Ser Val Thr Arg Asn Asp Thr
                165                 170                 175

Gly Pro Tyr Glu Cys Glu Ile Gln Asn Pro Val Ser Ala Asn Arg Ser
            180                 185                 190

Asp Pro Val Thr Leu Asn Val Thr Tyr Gly Pro Asp Thr Pro Thr Ile
        195                 200                 205

Ser Pro Ser Asp Thr Tyr Tyr Arg Pro Gly Ala Asn Leu Ser Leu Ser
    210                 215                 220

Cys Tyr Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Leu Ile Asn
225                 230                 235                 240

Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn Ile Thr
                245                 250                 255

Val Asn Asn Ser Gly Ser Tyr Thr Cys His Ala Asn Asn Ser Val Thr
            260                 265                 270

Gly Cys Asn Arg Thr Thr Val Lys Thr Ile Ile Val Thr Glu Leu Ser
        275                 280                 285

Pro Val Val Ala Lys Pro Gln Ile Lys Ala Ser Lys Thr Thr Val Thr
    290                 295                 300

Gly Asp Lys Asp Ser Val Asn Leu Thr Cys Ser Thr Asn Asp Thr Gly
305                 310                 315                 320

Ile Ser Ile Arg Trp Phe Phe Lys Asn Gln Ser Leu Pro Ser Ser Glu
```

```
                325                 330                 335

Arg Met Lys Leu Ser Gln Gly Asn Thr Thr Leu Ser Ile Asn Pro Val
            340                 345                 350

Lys Arg Glu Asp Ala Gly Thr Tyr Trp Cys Glu Val Phe Asn Pro Ile
        355                 360                 365

Ser Lys Asn Gln Ser Asp Pro Ile Met Leu Asn Val Asn Tyr Asn Ala
    370                 375                 380

Leu Pro Gln Glu Asn Gly Leu Ser Pro Gly His His His His His His
385                 390                 395                 400

His His His His
```

<210> 164
<211> 657
<212> PRT
<213> Homo sapiens

<400> 164

```
Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly Lys Glu
1               5                   10                  15

Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly Tyr Ser
            20                  25                  30

Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile Gly Tyr
        35                  40                  45

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

Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile Ile Gln
65                  70                  75                  80

Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp Leu Val
                85                  90                  95
```

```
Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu Pro Lys
            100                 105                 110

Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys Asp Ala
        115                 120                 125

Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr Leu Trp
    130                 135                 140

Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln Leu Ser
145                 150                 155                 160

Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn Asp Ser
                165                 170                 175

Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg Arg Ser
            180                 185                 190

Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro Thr Ile
        195                 200                 205

Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn Leu Ser
    210                 215                 220

Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe Val Asn
225                 230                 235                 240

Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn Ile Thr
                245                 250                 255

Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser Asp Thr
            260                 265                 270

Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala Glu Pro
        275                 280                 285

Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu Asp Glu
    290                 295                 300
```

```
Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr Thr Tyr
305                 310                 315                 320

Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
                325                 330                 335

Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr Arg Asn
            340                 345                 350

Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser Val Asp
        355                 360                 365

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

Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn Leu Ser
385                 390                 395                 400

Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Leu
                405                 410                 415

Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile Ser Asn
            420                 425                 430

Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn Asn Ser
        435                 440                 445

Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val Ser Ala
    450                 455                 460

Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu
465                 470                 475                 480

Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln Asn Thr
                485                 490                 495

Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser Pro Arg
            500                 505                 510

Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr
```

```
        515                 520                 525

Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser Val Ser
    530                 535                 540

Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly Pro Asp
545                 550                 555                 560

Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly Ala Asn
                565                 570                 575

Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln Tyr Ser
            580                 585                 590

Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu Phe Ile
        595                 600                 605

Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe Val Ser
    610                 615                 620

Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile Thr Val
625                 630                 635                 640

Ser Ala Ser Gly Thr Ser Pro Gly Leu Ser Ala His His His His His
                645                 650                 655

His
```

<210> 165
<211> 532
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-1790, hCeacam6-WT-Fc-6xHis

<400> 165

```
Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly Lys Glu
1               5                   10                  15
```

```
Val Leu Leu Leu Ala His Asn Leu Pro Gln Asn Arg Ile Gly Tyr Ser
            20                  25                  30

Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Ser Leu Ile Val Gly Tyr
        35                  40                  45

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

Glu Thr Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Val Thr Gln
65                  70                  75                  80

Asn Asp Thr Gly Phe Tyr Thr Leu Gln Val Ile Lys Ser Asp Leu Val
                85                  90                  95

Asn Glu Glu Ala Thr Gly Gln Phe His Val Tyr Pro Glu Leu Pro Lys
            100                 105                 110

Pro Ser Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys Asp Ala
        115                 120                 125

Val Ala Phe Thr Cys Glu Pro Glu Val Gln Asn Thr Thr Tyr Leu Trp
    130                 135                 140

Trp Val Asn Gly Gln Ser Leu Pro Val Ser Pro Arg Leu Gln Leu Ser
145                 150                 155                 160

Asn Gly Asn Met Thr Leu Thr Leu Leu Ser Val Lys Arg Asn Asp Ala
                165                 170                 175

Gly Ser Tyr Glu Cys Glu Ile Gln Asn Pro Ala Ser Ala Asn Arg Ser
            180                 185                 190

Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp Gly Pro Thr Ile
        195                 200                 205

Ser Pro Ser Lys Ala Asn Tyr Arg Pro Gly Glu Asn Leu Asn Leu Ser
    210                 215                 220

Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe Ile Asn
```

```
225                 230                 235                 240

Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn Ile Thr
                245                 250                 255

Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His Asn Ser Ala Thr
            260                 265                 270

Gly Leu Asn Arg Thr Thr Val Thr Met Ile Thr Val Ser Gly Ile Glu
        275                 280                 285

Gly Arg Asp Met Asp Thr Gly Pro Lys Ser Cys Asp Lys Thr His Thr
    290                 295                 300

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
305                 310                 315                 320

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                325                 330                 335

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            340                 345                 350

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        355                 360                 365

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    370                 375                 380

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
385                 390                 395                 400

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
                405                 410                 415

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            420                 425                 430

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
        435                 440                 445
```

```
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    450                 455                 460

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
465                 470                 475                 480

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                485                 490                 495

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            500                 505                 510

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys His His
        515                 520                 525

His His His His
    530


<210>  166
<211>  532
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  TPP-1791, hCeacam6-Dom1-MacMul-Xa-Fc-His

<400>  166

Gln Leu Thr Ile Glu Ser Arg Pro Phe Asn Val Ala Glu Gly Lys Glu
1               5                   10                  15

Val Leu Leu Leu Ala His Asn Leu Pro Gln Asn Leu Ile Gly Phe Asn
            20                  25                  30

Trp Tyr Lys Gly Glu Arg Val Asp Ala Lys Arg Leu Ile Val Ala Tyr
        35                  40                  45

Val Ile Glu Thr Gln Gln Thr Thr Pro Gly Pro Ala His Ser Gly Arg
    50                  55                  60

Glu Thr Val Tyr Ser Asn Ala Ser Leu Leu Ile Gln Asn Val Thr Gln
```

```
65                  70                  75                  80

Asn Asp Thr Gly Ser Tyr Thr Leu Gln Val Ile Lys Gly Asp Leu Val
                85                  90                  95

Asn Glu Glu Ala Thr Gly Arg Phe Trp Val Tyr Pro Glu Leu Pro Lys
            100                 105                 110

Pro Ser Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys Asp Ala
        115                 120                 125

Val Ala Phe Thr Cys Glu Pro Glu Val Gln Asn Thr Thr Tyr Leu Trp
    130                 135                 140

Trp Val Asn Gly Gln Ser Leu Pro Val Ser Pro Arg Leu Gln Leu Ser
145                 150                 155                 160

Asn Gly Asn Met Thr Leu Thr Leu Leu Ser Val Lys Arg Asn Asp Ala
                165                 170                 175

Gly Ser Tyr Glu Cys Glu Ile Gln Asn Pro Ala Ser Ala Asn Arg Ser
            180                 185                 190

Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp Gly Pro Thr Ile
        195                 200                 205

Ser Pro Ser Lys Ala Asn Tyr Arg Pro Gly Glu Asn Leu Asn Leu Ser
    210                 215                 220

Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe Ile Asn
225                 230                 235                 240

Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn Ile Thr
                245                 250                 255

Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His Asn Ser Ala Thr
            260                 265                 270

Gly Leu Asn Arg Thr Thr Val Thr Met Ile Thr Val Ser Gly Ile Glu
        275                 280                 285
```

```
Gly Arg Asp Met Asp Thr Gly Pro Lys Ser Cys Asp Lys Thr His Thr
    290                 295                 300

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
305                 310                 315                 320

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                325                 330                 335

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            340                 345                 350

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        355                 360                 365

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    370                 375                 380

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
385                 390                 395                 400

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
                405                 410                 415

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            420                 425                 430

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
        435                 440                 445

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    450                 455                 460

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
465                 470                 475                 480

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                485                 490                 495
```

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            500   505   510

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys His His
        515   520   525

His His His His
    530

<210> 167
<211> 532
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-1792, hCeacam6-Dom2-MacMul-Xa-Fc-His

<400> 167

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

Val Leu Leu Leu Ala His Asn Leu Pro Gln Asn Arg Ile Gly Tyr Ser
            20   25   30

Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Ser Leu Ile Val Gly Tyr
        35   40   45

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

Glu Thr Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Val Thr Gln
65   70   75   80

Asn Asp Thr Gly Phe Tyr Thr Leu Gln Val Ile Lys Ser Asp Leu Val
                85   90   95

Asn Glu Glu Ala Thr Gly Gln Phe His Val Tyr Pro Glu Leu Pro Lys
            100   105   110

Pro Tyr Ile Thr Ser Asn Asn Ser Asn Pro Val Glu Asp Lys Asp Ala
        115   120   125

```
Val Asp Phe Thr Cys Glu Pro Asp Ile His Ser Thr Thr Tyr Leu Trp
    130                 135                 140

Trp Val Asn Asp Gln Ser Leu Pro Val Ser Pro Arg Leu Gln Leu Ser
145                 150                 155                 160

Asn Gly Asn Arg Thr Leu Thr Leu Leu Ser Val Lys Arg Asn Asp Ala
                165                 170                 175

Gly Ala Tyr Glu Cys Glu Ile Gln Asn Pro Val Ser Ala Asn Leu Ser
            180                 185                 190

Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Gly Pro Thr Ile
        195                 200                 205

Ser Pro Ser Lys Ala Asn Tyr Arg Pro Gly Glu Asn Leu Asn Leu Ser
    210                 215                 220

Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe Ile Asn
225                 230                 235                 240

Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn Ile Thr
                245                 250                 255

Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His Asn Ser Ala Thr
            260                 265                 270

Gly Leu Asn Arg Thr Thr Val Thr Met Ile Thr Val Ser Gly Ile Glu
        275                 280                 285

Gly Arg Asp Met Asp Thr Gly Pro Lys Ser Cys Asp Lys Thr His Thr
    290                 295                 300

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
305                 310                 315                 320

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                325                 330                 335
```

```
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            340                 345                 350

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        355                 360                 365

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    370                 375                 380

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
385                 390                 395                 400

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
                405                 410                 415

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            420                 425                 430

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
        435                 440                 445

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    450                 455                 460

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
465                 470                 475                 480

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                485                 490                 495

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            500                 505                 510

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys His His
        515                 520                 525

His His His His
    530
```

<210> 168
<211> 532
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-1793, hCeacam6-Dom3-MacMul-Xa-Fc-His

<400> 168

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

Val Leu Leu Leu Ala His Asn Leu Pro Gln Asn Arg Ile Gly Tyr Ser
20 25 30

Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Ser Leu Ile Val Gly Tyr
35 40 45

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

Glu Thr Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Val Thr Gln
65 70 75 80

Asn Asp Thr Gly Phe Tyr Thr Leu Gln Val Ile Lys Ser Asp Leu Val
85 90 95

Asn Glu Glu Ala Thr Gly Gln Phe His Val Tyr Pro Glu Leu Pro Lys
100 105 110

Pro Ser Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys Asp Ala
115 120 125

Val Ala Phe Thr Cys Glu Pro Glu Val Gln Asn Thr Thr Tyr Leu Trp
130 135 140

Trp Val Asn Gly Gln Ser Leu Pro Val Ser Pro Arg Leu Gln Leu Ser
145 150 155 160

Asn Gly Asn Met Thr Leu Thr Leu Leu Ser Val Lys Arg Asn Asp Ala
165 170 175

```
Gly Ser Tyr Glu Cys Glu Ile Gln Asn Pro Ala Ser Ala Asn Arg Ser
            180                 185                 190

Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp Val Pro Thr Ile
        195                 200                 205

Ser Pro Ser Asn Ser Asn Tyr Arg Pro Gly Glu Asn Leu Asn Leu Ser
    210                 215                 220

Cys His Ala Ala Ser Asn Pro Thr Ala Gln Tyr Ser Trp Phe Val Asn
225                 230                 235                 240

Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn Ile Thr
                245                 250                 255

Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala Tyr Asn Ser Ala Thr
            260                 265                 270

Gly Leu Asn Arg Thr Thr Val Met Met Ile Thr Val Ser Gly Ile Glu
        275                 280                 285

Gly Arg Asp Met Asp Thr Gly Pro Lys Ser Cys Asp Lys Thr His Thr
    290                 295                 300

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
305                 310                 315                 320

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                325                 330                 335

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            340                 345                 350

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        355                 360                 365

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    370                 375                 380
```

```
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
385                 390                 395                 400

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
                405                 410                 415

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            420                 425                 430

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
        435                 440                 445

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    450                 455                 460

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
465                 470                 475                 480

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                485                 490                 495

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            500                 505                 510

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys His His
        515                 520                 525

His His His His
    530
```

<210> 169
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-1794, hCeacam6-Dom1-8xHis (E.coli)

<400> 169

```
Met Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly Lys
1               5                   10                  15
```

```
Glu Val Leu Leu Leu Ala His Asn Leu Pro Gln Asn Arg Ile Gly Tyr
            20                  25                  30

Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Ser Leu Ile Val Gly
        35                  40                  45

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

Arg Glu Thr Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Val Thr
65                  70                  75                  80

Gln Asn Asp Thr Gly Phe Tyr Thr Leu Gln Val Ile Lys Ser Asp Leu
                85                  90                  95

Val Asn Glu Glu Ala Thr Gly Gln Phe His Val Tyr Pro Gly Ser Gly
            100                 105                 110

Ser His His His His His His His His
        115                 120
```

<210> 170
<211> 533
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-2443, cyno CEACAM-6-Xa-Fc-His

<400> 170

```
Gln Leu Thr Ile Glu Ser Arg Pro Phe Asn Val Ala Glu Gly Lys Glu
1               5                   10                  15

Val Leu Leu Leu Ala His Asn Leu Pro Gln Asn Thr Leu Gly Phe Asn
            20                  25                  30

Trp Tyr Lys Gly Glu Arg Val Asp Ala Lys Arg Leu Ile Val Ala Tyr
        35                  40                  45

Val Ile Gly Thr Gln Gln Thr Thr Pro Gly Pro Ala His Ser Gly Arg
    50                  55                  60
```

```
Glu Met Ile Tyr Ser Asn Ala Ser Leu Leu Ile Gln Asn Val Thr Gln
65                  70                  75                  80

Asn Asp Thr Gly Ser Tyr Thr Leu Gln Ala Ile Lys Glu Asp Leu Val
                85                  90                  95

Thr Glu Glu Ala Thr Gly Arg Phe Trp Val Tyr Pro Glu Leu Pro Lys
            100                 105                 110

Pro Tyr Ile Thr Ser Asn Asn Ser Asn Pro Val Glu Asp Lys Asp Ala
        115                 120                 125

Val Asp Phe Thr Cys Glu Pro Asp Ile His Ser Thr Thr Tyr Leu Trp
    130                 135                 140

Trp Val Asn Asp Gln Ser Leu Pro Val Ser Pro Arg Leu Gln Leu Ser
145                 150                 155                 160

Asn Gly Asn Arg Thr Leu Thr Leu Leu Ser Val Lys Arg Asn Asp Ala
                165                 170                 175

Gly Ala Tyr Glu Cys Glu Ile Gln Asn Pro Val Ser Ala Asn Leu Ser
            180                 185                 190

Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Val Pro Thr Ile
        195                 200                 205

Ser Pro Ser Asn Ser Asn Tyr Arg Pro Gly Glu Asn Leu Asn Leu Ser
    210                 215                 220

Cys His Ala Ala Ser Asn Pro Thr Ala Gln Tyr Ser Trp Phe Val Asn
225                 230                 235                 240

Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn Ile Thr
                245                 250                 255

Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala Tyr Asn Ser Ala Thr
            260                 265                 270
```

```
Gly Leu Asn Arg Thr Thr Val Met Met Ile Thr Val Ser Gly Ser Ile
        275                 280                 285

Glu Gly Arg Asp Met Asp Thr Gly Pro Lys Ser Cys Asp Lys Thr His
    290                 295                 300

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
305                 310                 315                 320

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
                325                 330                 335

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
            340                 345                 350

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
        355                 360                 365

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
    370                 375                 380

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
385                 390                 395                 400

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
                405                 410                 415

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
            420                 425                 430

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
        435                 440                 445

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
    450                 455                 460

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
465                 470                 475                 480
```

```
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
                485                 490                 495


Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
            500                 505                 510


His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys His
        515                 520                 525


His His His His His
    530


<210>  171
<211>  356
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  TPP-2452, cynomolgus Ceacam6-Dom1-Xa-Fc-His

<400>  171

Gln Leu Thr Ile Glu Ser Arg Pro Phe Asn Val Ala Glu Gly Lys Glu
1               5                   10                  15


Val Leu Leu Leu Ala His Asn Leu Pro Gln Asn Thr Leu Gly Phe Asn
            20                  25                  30


Trp Tyr Lys Gly Glu Arg Val Asp Ala Lys Arg Leu Ile Val Ala Tyr
        35                  40                  45


Val Ile Gly Thr Gln Gln Thr Thr Pro Gly Pro Ala His Ser Gly Arg
    50                  55                  60


Glu Met Ile Tyr Ser Asn Ala Ser Leu Leu Ile Gln Asn Val Thr Gln
65                  70                  75                  80


Asn Asp Thr Gly Ser Tyr Thr Leu Gln Ala Ile Lys Glu Asp Leu Val
                85                  90                  95


Thr Glu Glu Ala Thr Gly Arg Phe Trp Val Tyr Pro Glu Leu Ile Glu
            100                 105                 110
```

```
Gly Arg Asp Met Asp Thr Gly Pro Lys Ser Cys Asp Lys Thr His Thr
        115                 120                 125

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
    130                 135                 140

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
145                 150                 155                 160

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
                165                 170                 175

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
            180                 185                 190

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
        195                 200                 205

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
    210                 215                 220

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
225                 230                 235                 240

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

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
            260                 265                 270

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
        275                 280                 285

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
    290                 295                 300

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
305                 310                 315                 320
```

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
                325   330   335

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys His His
            340   345   350

His His His His
        355

<210> 172
<211> 127
<212> PRT
<213> Homo sapiens

<400> 172

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

Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly Tyr Ser
            20   25   30

Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Ser Leu Ile Val Gly Tyr
        35   40   45

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

Glu Thr Ile Tyr Thr Asn Ala Ser Leu Leu Ile Gln Asn Val Thr Gln
65   70   75   80

Asn Asp Ile Gly Phe Tyr Thr Leu Gln Val Ile Lys Ser Asp Leu Val
                85   90   95

Asn Glu Glu Ala Thr Gly Gln Phe His Val Tyr Gln Glu Asn Ala Pro
            100   105   110

Gly Leu Pro Val Gly Ala Val Ala Gly His His His His His His
        115   120   125

<210> 173
<211> 526

<212> PRT
<213> Homo sapiens

<400> 173

```
Met Gly His Leu Ser Ala Pro Leu His Arg Val Arg Val Pro Trp Gln
1               5                  10                  15


Gly Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
            20                  25                  30


Thr Ala Gln Leu Thr Thr Glu Ser Met Pro Phe Asn Val Ala Glu Gly
        35                  40                  45


Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln Gln Leu Phe Gly
    50                  55                  60


Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Val
65                  70                  75                  80


Gly Tyr Ala Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Asn Ser
                85                  90                  95


Gly Arg Glu Thr Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Val
            100                 105                 110


Thr Gln Asn Asp Thr Gly Phe Tyr Thr Leu Gln Val Ile Lys Ser Asp
        115                 120                 125


Leu Val Asn Glu Glu Ala Thr Gly Gln Phe His Val Tyr Pro Glu Leu
    130                 135                 140


Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys
145                 150                 155                 160


Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Thr Thr Tyr
                165                 170                 175


Leu Trp Trp Ile Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
            180                 185                 190
```

```
Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Leu Ser Val Thr Arg Asn
        195                 200                 205

Asp Thr Gly Pro Tyr Glu Cys Glu Ile Gln Asn Pro Val Ser Ala Asn
    210                 215                 220

Arg Ser Asp Pro Val Thr Leu Asn Val Thr Tyr Gly Pro Asp Thr Pro
225                 230                 235                 240

Thr Ile Ser Pro Ser Asp Thr Tyr Tyr Arg Pro Gly Ala Asn Leu Ser
                245                 250                 255

Leu Ser Cys Tyr Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Leu
            260                 265                 270

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

Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys His Ala Asn Asn Ser
    290                 295                 300

Val Thr Gly Cys Asn Arg Thr Thr Val Lys Thr Ile Ile Val Thr Glu
305                 310                 315                 320

Leu Ser Pro Val Val Ala Lys Pro Gln Ile Lys Ala Ser Lys Thr Thr
                325                 330                 335

Val Thr Gly Asp Lys Asp Ser Val Asn Leu Thr Cys Ser Thr Asn Asp
            340                 345                 350

Thr Gly Ile Ser Ile Arg Trp Phe Phe Lys Asn Gln Ser Leu Pro Ser
        355                 360                 365

Ser Glu Arg Met Lys Leu Ser Gln Gly Asn Thr Thr Leu Ser Ile Asn
    370                 375                 380

Pro Val Lys Arg Glu Asp Ala Gly Thr Tyr Trp Cys Glu Val Phe Asn
385                 390                 395                 400

Pro Ile Ser Lys Asn Gln Ser Asp Pro Ile Met Leu Asn Val Asn Tyr
```

```
                405                 410                 415

Asn Ala Leu Pro Gln Glu Asn Gly Leu Ser Pro Gly Ala Ile Ala Gly
            420                 425                 430

Ile Val Ile Gly Val Val Ala Leu Val Ala Leu Ile Ala Val Ala Leu
        435                 440                 445

Ala Cys Phe Leu His Phe Gly Lys Thr Gly Arg Ala Ser Asp Gln Arg
    450                 455                 460

Asp Leu Thr Glu His Lys Pro Ser Val Ser Asn His Thr Gln Asp His
465                 470                 475                 480

Ser Asn Asp Pro Pro Asn Lys Met Asn Glu Val Thr Tyr Ser Thr Leu
                485                 490                 495

Asn Phe Glu Ala Gln Gln Pro Thr Gln Pro Thr Ser Ala Ser Pro Ser
            500                 505                 510

Leu Thr Ala Thr Glu Ile Ile Tyr Ser Glu Val Lys Lys Gln
        515                 520                 525


<210>  174
<211>  300
<212>  PRT
<213>  Homo sapiens

<400>  174

Met Glu Ile Pro Met Gly Thr Gln Gly Cys Phe Ser Lys Ser Leu Leu
1               5                   10                  15

Leu Ser Ala Ser Ile Leu Val Leu Trp Met Leu Gln Gly Ser Gln Ala
            20                  25                  30

Ala Leu Tyr Ile Gln Lys Ile Pro Glu Gln Pro Gln Lys Asn Gln Asp
        35                  40                  45

Leu Leu Leu Ser Val Gln Gly Val Pro Asp Thr Phe Gln Asp Phe Asn
    50                  55                  60
```

```
Trp Tyr Leu Gly Glu Glu Thr Tyr Gly Gly Thr Arg Leu Phe Thr Tyr
65                  70                  75                  80

Ile Pro Gly Ile Gln Arg Pro Gln Arg Asp Gly Ser Ala Met Gly Gln
                85                  90                  95

Arg Asp Ile Val Gly Phe Pro Asn Gly Ser Met Leu Leu Arg Arg Ala
            100                 105                 110

Gln Pro Thr Asp Ser Gly Thr Tyr Gln Val Ala Ile Thr Ile Asn Ser
        115                 120                 125

Glu Trp Thr Met Lys Ala Lys Thr Glu Val Gln Val Ala Glu Lys Asn
    130                 135                 140

Lys Glu Leu Pro Ser Thr His Leu Pro Thr Asn Ala Gly Ile Leu Ala
145                 150                 155                 160

Ala Thr Ile Ile Gly Ser Leu Ala Ala Gly Ala Leu Leu Ile Ser Cys
                165                 170                 175

Ile Ala Tyr Leu Leu Val Thr Arg Asn Trp Arg Gly Gln Ser His Arg
            180                 185                 190

Leu Pro Ala Pro Arg Gly Gln Gly Ser Leu Ser Ile Leu Cys Ser Ala
        195                 200                 205

Val Ser Pro Val Pro Ser Val Thr Pro Ser Thr Trp Met Ala Thr Thr
    210                 215                 220

Glu Lys Pro Glu Leu Gly Pro Ala His Asp Ala Gly Asp Asn Asn Ile
225                 230                 235                 240

Tyr Glu Val Met Pro Ser Pro Val Leu Leu Val Ser Pro Ile Ser Asp
                245                 250                 255

Thr Arg Ser Ile Asn Pro Ala Arg Pro Leu Pro Thr Pro Pro His Leu
            260                 265                 270
```

Gln Ala Glu Pro Glu Asn His Gln Tyr Gln Gln Asp Leu Leu Asn Pro
        275   280   285

Asp Pro Ala Pro Tyr Cys Gln Leu Val Pro Thr Ser
    290   295   300

<210> 175
<211> 252
<212> PRT
<213> Homo sapiens

<400> 175

Met Gly Pro Pro Ser Ala Ser Pro His Arg Glu Cys Ile Pro Trp Gln
1   5   10   15

Gly Leu Leu Leu Thr Ala Ser Leu Leu Asn Phe Trp Asn Pro Pro Thr
            20   25   30

Thr Ala Lys Leu Thr Ile Glu Ser Met Pro Leu Ser Val Ala Glu Gly
        35   40   45

Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
    50   55   60

Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Ser Leu Ile Val
65   70   75   80

Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Ala Ala Tyr Ser
                85   90   95

Gly Arg Glu Thr Ile Tyr Thr Asn Ala Ser Leu Leu Ile Gln Asn Val
            100   105   110

Thr Gln Asn Asp Ile Gly Phe Tyr Thr Leu Gln Val Ile Lys Ser Asp
        115   120   125

Leu Val Asn Glu Glu Ala Thr Gly Gln Phe His Val Tyr Gln Glu Asn
    130   135   140

Ala Pro Gly Leu Pro Val Gly Ala Val Ala Gly Ile Val Thr Gly Val
145   150   155   160

```
Leu Val Gly Val Ala Leu Val Ala Ala Leu Val Cys Phe Leu Leu Leu
                165                 170                 175

Ala Lys Thr Gly Arg Thr Ser Ile Gln Arg Asp Leu Lys Glu Gln Gln
            180                 185                 190

Pro Gln Ala Leu Ala Pro Gly Arg Gly Pro Ser His Ser Ser Ala Phe
        195                 200                 205

Ser Met Ser Pro Leu Ser Thr Ala Gln Ala Pro Leu Pro Asn Pro Arg
    210                 215                 220

Thr Ala Ala Ser Ile Tyr Glu Glu Leu Leu Lys His Asp Thr Asn Ile
225                 230                 235                 240

Tyr Cys Arg Met Asp His Lys Ala Glu Val Ala Ser
                245                 250


<210>  176
<211>  702
<212>  PRT
<213>  Homo sapiens

<400>  176

Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile Pro Trp Gln
1               5                   10                  15

Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
            20                  25                  30

Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
        35                  40                  45

Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
    50                  55                  60

Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
65                  70                  75                  80
```

```
Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
                85                  90                  95

Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
            100                 105                 110

Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
        115                 120                 125

Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
    130                 135                 140

Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
145                 150                 155                 160

Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
                165                 170                 175

Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
            180                 185                 190

Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
        195                 200                 205

Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
    210                 215                 220

Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
225                 230                 235                 240

Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
                245                 250                 255

Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
            260                 265                 270

Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
        275                 280                 285

Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser
```

```
    290                 295                 300

Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala
305                 310                 315                 320

Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu
                325                 330                 335

Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr
            340                 345                 350

Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
        355                 360                 365

Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr
    370                 375                 380

Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Lys Leu Ser
385                 390                 395                 400

Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp
                405                 410                 415

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

Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser
        435                 440                 445

Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
    450                 455                 460

Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn
465                 470                 475                 480

Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val
                485                 490                 495

Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro
            500                 505                 510
```

```
Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln
        515                 520                 525

Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser
    530                 535                 540

Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn
545                 550                 555                 560

Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser
                565                 570                 575

Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly
            580                 585                 590

Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly
        595                 600                 605

Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln
    610                 615                 620

Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
625                 630                 635                 640

Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
                645                 650                 655

Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile
            660                 665                 670

Thr Val Ser Ala Ser Gly Thr Ser Pro Gly Leu Ser Ala Gly Ala Thr
        675                 680                 685

Val Gly Ile Met Ile Gly Val Leu Val Gly Val Ala Leu Ile
    690                 695                 700
```

<210> 177
<211> 344
<212> PRT

<213> Macaca fascicularis (Cynomolgus monkey)

<400> 177

```
Met Gly Pro Pro Ser Ala Pro Pro Cys Arg Ile Cys Val Pro Trp Lys
1               5                  10                  15


Glu Val Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Ser Pro Pro Thr
            20                  25                  30


Thr Ala Gln Leu Thr Ile Glu Ser Arg Pro Phe Asn Val Ala Glu Gly
        35                  40                  45


Lys Glu Val Leu Leu Leu Ala His Asn Leu Pro Gln Asn Thr Leu Gly
    50                  55                  60


Phe Asn Trp Tyr Lys Gly Glu Arg Val Asp Ala Lys Arg Leu Ile Val
65                  70                  75                  80


Ala Tyr Val Ile Gly Thr Gln Gln Thr Thr Pro Gly Pro Ala His Ser
                85                  90                  95


Gly Arg Glu Met Ile Tyr Ser Asn Ala Ser Leu Leu Ile Gln Asn Val
            100                 105                 110


Thr Gln Asn Asp Thr Gly Ser Tyr Thr Leu Gln Ala Ile Lys Glu Asp
        115                 120                 125


Leu Val Thr Glu Glu Ala Thr Gly Arg Phe Trp Val Tyr Pro Glu Leu
    130                 135                 140


Pro Lys Pro Tyr Ile Thr Ser Asn Asn Ser Asn Pro Val Glu Asp Lys
145                 150                 155                 160


Asp Ala Val Asp Phe Thr Cys Glu Pro Asp Ile His Ser Thr Thr Tyr
                165                 170                 175


Leu Trp Trp Val Asn Asp Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
            180                 185                 190


Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Leu Ser Val Lys Arg Asn
```

```
        195                 200                 205

Asp Ala Gly Ala Tyr Glu Cys Glu Ile Gln Asn Pro Val Ser Ala Asn
    210                 215                 220

Leu Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Val Pro
225                 230                 235                 240

Thr Ile Ser Pro Ser Asn Ser Asn Tyr Arg Pro Gly Glu Asn Leu Asn
                245                 250                 255

Leu Ser Cys His Ala Ala Ser Asn Pro Thr Ala Gln Tyr Ser Trp Phe
            260                 265                 270

Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
        275                 280                 285

Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala Tyr Asn Ser
    290                 295                 300

Ala Thr Gly Leu Asn Arg Thr Thr Val Met Met Ile Thr Val Ser Gly
305                 310                 315                 320

Ser Ala Pro Gly Leu Ser Ala Val Ala Thr Val Gly Ile Met Ile Gly
                325                 330                 335

Val Leu Ala Arg Val Ala Leu Ile
            340


<210>  178
<211>  349
<212>  PRT
<213>  Homo sapiens

<400>  178

Met Gly Pro Ile Ser Ala Pro Ser Cys Arg Trp Arg Ile Pro Trp Gln
1               5                   10                  15

Gly Leu Leu Leu Thr Ala Ser Leu Phe Thr Phe Trp Asn Pro Pro Thr
            20                  25                  30
```

```
Thr Ala Gln Leu Thr Ile Glu Ala Val Pro Ser Asn Ala Ala Glu Gly
        35                  40                  45

Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln Asp Pro Arg Gly
    50                  55                  60

Tyr Asn Trp Tyr Lys Gly Glu Thr Val Asp Ala Asn Arg Arg Ile Ile
65                  70                  75                  80

Gly Tyr Val Ile Ser Asn Gln Gln Ile Thr Pro Gly Pro Ala Tyr Ser
                85                  90                  95

Asn Arg Glu Thr Ile Tyr Pro Asn Ala Ser Leu Leu Met Arg Asn Val
            100                 105                 110

Thr Arg Asn Asp Thr Gly Ser Tyr Thr Leu Gln Val Ile Lys Leu Asn
        115                 120                 125

Leu Met Ser Glu Glu Val Thr Gly Gln Phe Ser Val His Pro Glu Thr
    130                 135                 140

Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys
145                 150                 155                 160

Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asn Thr Thr Tyr
                165                 170                 175

Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
            180                 185                 190

Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Leu Ser Val Thr Arg Asn
        195                 200                 205

Asp Val Gly Pro Tyr Glu Cys Glu Ile Gln Asn Pro Ala Ser Ala Asn
    210                 215                 220

Phe Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
225                 230                 235                 240
```

```
Thr Ile Ser Pro Ser Asp Thr Tyr Tyr His Ala Gly Val Asn Leu Asn
                245                 250                 255

Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ser Gln Tyr Ser Trp Ser
            260                 265                 270

Val Asn Gly Thr Phe Gln Gln Tyr Thr Gln Lys Leu Phe Ile Pro Asn
        275                 280                 285

Ile Thr Thr Lys Asn Ser Gly Ser Tyr Ala Cys His Thr Thr Asn Ser
    290                 295                 300

Ala Thr Gly Arg Asn Arg Thr Thr Val Arg Met Ile Thr Val Ser Asp
305                 310                 315                 320

Ala Leu Val Gln Gly Ser Ser Pro Gly Leu Ser Ala Arg Ala Thr Val
                325                 330                 335

Ser Ile Met Ile Gly Val Leu Ala Arg Val Ala Leu Ile
            340                 345


<210>  179
<211>  344
<212>  PRT
<213>  Homo sapiens

<400>  179

Met Gly Pro Pro Ser Ala Pro Pro Cys Arg Leu His Val Pro Trp Lys
1               5                   10                  15

Glu Val Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
            20                  25                  30

Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
        35                  40                  45

Lys Glu Val Leu Leu Leu Ala His Asn Leu Pro Gln Asn Arg Ile Gly
    50                  55                  60

Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Ser Leu Ile Val
65                  70                  75                  80
```

```
Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
                85                  90                  95

Gly Arg Glu Thr Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Val
            100                 105                 110

Thr Gln Asn Asp Thr Gly Phe Tyr Thr Leu Gln Val Ile Lys Ser Asp
        115                 120                 125

Leu Val Asn Glu Glu Ala Thr Gly Gln Phe His Val Tyr Pro Glu Leu
    130                 135                 140

Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys
145                 150                 155                 160

Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Val Gln Asn Thr Thr Tyr
                165                 170                 175

Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
            180                 185                 190

Leu Ser Asn Gly Asn Met Thr Leu Thr Leu Leu Ser Val Lys Arg Asn
        195                 200                 205

Asp Ala Gly Ser Tyr Glu Cys Glu Ile Gln Asn Pro Ala Ser Ala Asn
    210                 215                 220

Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp Gly Pro
225                 230                 235                 240

Thr Ile Ser Pro Ser Lys Ala Asn Tyr Arg Pro Gly Glu Asn Leu Asn
                245                 250                 255

Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
            260                 265                 270

Ile Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
        275                 280                 285
```

Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His Asn Ser
290 295 300

Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Met Ile Thr Val Ser Gly
305 310 315 320

Ser Ala Pro Val Leu Ser Ala Val Ala Thr Val Gly Ile Thr Ile Gly
325 330 335

Val Leu Ala Arg Val Ala Leu Ile
340

<210> 180
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Macaca fascicularis CEACAM6-Domain 1-His

<400> 180

Met Gln Leu Thr Ile Glu Ser Arg Pro Phe Asn Val Ala Glu Gly Lys
1 5 10 15

Glu Val Leu Leu Leu Ala His Asn Leu Pro Gln Asn Thr Leu Gly Phe
20 25 30

Asn Trp Tyr Lys Gly Glu Arg Val Asp Ala Lys Arg Leu Ile Val Ala
35 40 45

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

Arg Glu Met Ile Tyr Ser Asn Ala Ser Leu Leu Ile Gln Asn Val Thr
65 70 75 80

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

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

Ser Gly Ser His His His His His His His His
        115   120

<210> 181
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-5468 - Heavy Chain

<400> 181

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

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

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

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

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

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
                85   90   95

Cys Ala Arg Ile Ser Leu Pro Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
            100   105   110

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

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

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn

```
145                 150                 155                 160

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

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

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

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

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
225                 230                 235                 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245                 250                 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            260                 265                 270

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

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
    290                 295                 300

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

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

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

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

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

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

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

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

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

<210> 182
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-5468 - Light Chain

<400> 182

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

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Ser Tyr Pro Leu

```
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

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

Phe Asn Arg Gly Glu Cys
    210


<210>  183
<211>  225
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  APP-1574 - Heavy Chain (Fab)

<400>  183

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

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

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

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

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

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
                85                  90                  95

Cys Ala Arg Ile Ser Leu Pro Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

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

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

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

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

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

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

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

His
225
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Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe 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 Asn Arg Tyr Thr Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


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


Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110


Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125


Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140


Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160


Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175
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Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180   185   190

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

Phe Asn Arg Gly Glu Cys
    210

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Met Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly Lys
1   5   10   15

Glu Val Leu Leu Leu Ala His Asn Leu Pro Gln Asn Arg Leu Gly Tyr
            20   25   30

Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Ser Leu Ile Val Gly
        35   40   45

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

Arg Glu Thr Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Val Thr
65   70   75   80

Gln Asn Asp Thr Gly Phe Tyr Thr Leu Gln Val Ile Lys Ser Asp Leu
                85   90   95

Val Asn Glu Glu Ala Thr Gly Gln Phe His Val Tyr Pro Gly Ser Gly
            100   105   110

Ser His His His His His His His His
        115   120

<210> 186
<211> 121
<212> PRT
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<220>
<223> TPP-8698, hCEACAM6-Domain 1-His - I30F

<400> 186

Met Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly Lys
1 5 10 15

Glu Val Leu Leu Leu Ala His Asn Leu Pro Gln Asn Arg Phe Gly Tyr
20 25 30

Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Ser Leu Ile Val Gly
35 40 45

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

Arg Glu Thr Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Val Thr
65 70 75 80

Gln Asn Asp Thr Gly Phe Tyr Thr Leu Gln Val Ile Lys Ser Asp Leu
85 90 95

Val Asn Glu Glu Ala Thr Gly Gln Phe His Val Tyr Pro Gly Ser Gly
100 105 110

Ser His His His His His His His His
115 120