SEQUENCE LISTING

<110> UCB BIOPHARMA SPRL

<120> METHODS OF TREATMENT USING ANTI-IL-17A/F ANTIBODIES

<130> PF0044WO

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<170> PatentIn version 3.5

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Gly Phe Thr Phe Ser Asp Tyr Asn Met Ala
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Thr Ile Thr Tyr Glu Gly Arg Asn Thr Tyr Tyr Arg Asp Ser Val Lys
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Gly

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Pro Pro Gln Tyr Tyr Glu Gly Ser Ile Tyr Arg Leu Trp Phe Ala His
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Arg Ala Asp Glu Ser Val Thr Thr Leu Met His
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Leu Val Ser Asn Arg Glu Ser
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Gln Gln Thr Trp Ser Asp Pro Trp Thr
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Arg Ala Asp Glu Ser Val Arg Thr Leu His Met
1   5   10

<210> 8

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Leu Val Ser Asn Ser Glu Ile
1 5

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Asp Glu Ser Val Thr Thr Leu
20 25 30

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

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

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

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

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<220>
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<220>
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<223> Light Chain variable region - CA028_496.g3 (gL57)

<400> 10

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Asp Glu Ser Val Arg Thr Leu
20 25 30

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

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

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

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

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

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<223> Synthetic peptide

<220>
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<223> Heavy chain variable region - CA028_496 and CA028_496.g3 (gH9)

<400> 11

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 Asp Tyr
20 25 30

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

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

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

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

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<220>
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<220>
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<223> Light chain - CA028_496 (w/o signal)

<400> 12

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


Asp Arg Val Thr Ile Thr Cys Arg Ala Asp Glu Ser Val Thr Thr Leu
            20                  25                  30


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


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


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


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


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


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


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

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


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


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


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


Phe Asn Arg Gly Glu Cys
    210


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

<220>
<223>  Synthetic peptide


<220>
<221>  MISC_FEATURE
<223>  Light chain - CA028_496.g3 (w/o signal)

<400>  13

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


Asp Arg Val Thr Ile Thr Cys Arg Ala Asp Glu Ser Val Arg Thr Leu
            20                  25                  30


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


Tyr Leu Val Ser Asn Ser Glu Ile Gly Val Pro Asp Arg Phe Ser Gly
```

```
    50                  55                  60

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

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

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

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys
    210
```

<210> 14
<211> 234
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<220>
<223> Synthetic peptide

<220>
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<223> Light chain - CA028_496.g3 (w/ signal)

<400> 14

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


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


Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Asp Glu Ser
        35                  40                  45


Val Arg Thr Leu Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
    50                  55                  60


Lys Leu Leu Ile Tyr Leu Val Ser Asn Ser Glu Ile Gly Val Pro Asp
65                  70                  75                  80


Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Arg Leu Thr Ile Ser
                85                  90                  95


Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Trp
            100                 105                 110


Ser Asp Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
        115                 120                 125


Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
    130                 135                 140


Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145                 150                 155                 160


Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
                165                 170                 175
```

```
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
            180                 185                 190


Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
        195                 200                 205


His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
    210                 215                 220


Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230


<210>  15
<211>  452
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic peptide


<220>
<221>  MISC_FEATURE
<223>  Heavy chain - CA028_496

<400>  15

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 Asp Tyr
            20                  25                  30


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


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


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

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
        115                 120                 125

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

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

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

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
            180                 185                 190

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys
        195                 200                 205

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

Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu
225                 230                 235                 240

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

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

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

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

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

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser
                325                 330                 335

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

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

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

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

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

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

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

Ser Leu Gly Lys
    450
```

<210> 16

<211> 455
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<220>
<223> Synthetic peptide

<220>
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<223> Heavy chain CA028_496.g3 (w/o signal)

<400> 16

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


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


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


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


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


Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
        115                 120                 125


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

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

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

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
            180                 185                 190

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

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

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
225                 230                 235                 240

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
                245                 250                 255

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

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

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

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

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
                325                 330                 335

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

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


Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
    370                 375                 380


Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
385                 390                 395                 400


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


Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
            420                 425                 430


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


Leu Ser Leu Ser Pro Gly Lys
    450                 455
```

<210> 17
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<223> Synthetic peptide

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<223> Heavy chain - CA8_496.g3 (w/ signal)

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


Val His Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
```

```
            20                  25                  30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
        35                  40                  45

Ser Asp Tyr Asn Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
    50                  55                  60

Glu Trp Val Ala Thr Ile Thr Tyr Glu Gly Arg Asn Thr Tyr Tyr Arg
65                  70                  75                  80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
                85                  90                  95

Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
            100                 105                 110

Tyr Tyr Cys Ala Ser Pro Pro Gln Tyr Tyr Glu Gly Ser Ile Tyr Arg
        115                 120                 125

Leu Trp Phe Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
    130                 135                 140

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
145                 150                 155                 160

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
                165                 170                 175

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
            180                 185                 190

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
        195                 200                 205

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
    210                 215                 220
```

```
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
225                 230                 235                 240


Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
                245                 250                 255


Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
            260                 265                 270


Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
        275                 280                 285


Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
    290                 295                 300


Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
305                 310                 315                 320


Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
                325                 330                 335


His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
            340                 345                 350


Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
        355                 360                 365


Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
    370                 375                 380


Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
385                 390                 395                 400


Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
                405                 410                 415


Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
```

420 425 430

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
435 440 445

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
450 455 460

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470

<210> 18
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<223> Synthetic peptide

<220>
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<400> 18

Gly Cys Cys Ala Thr Cys Cys Ala Gly Cys Thr Gly Ala Cys Cys Cys
1 5 10 15

Ala Gly Ala Gly Cys Cys Cys Thr Thr Cys Cys Thr Cys Thr Cys Thr
20 25 30

Cys Ala Gly Cys Gly Cys Cys Ala Gly Thr Gly Thr Cys Gly Gly Ala
35 40 45

Gly Ala Cys Ala Gly Ala Gly Thr Gly Ala Cys Thr Ala Thr Thr Ala
50 55 60

Cys Cys Thr Gly Cys Ala Gly Gly Gly Cys Thr Gly Ala Cys Gly Ala
65 70 75 80

```
Ala Ala Gly Cys Gly Thr Gly Ala Gly Ala Ala Cys Ala Thr Thr Gly
                85                  90                  95

Ala Thr Gly Cys Ala Cys Thr Gly Gly Thr Ala Cys Cys Ala Ala Cys
            100                 105                 110

Ala Gly Ala Ala Gly Cys Cys Thr Gly Gly Cys Ala Ala Ala Gly Cys
        115                 120                 125

Cys Cys Cys Cys Ala Ala Gly Cys Thr Cys Cys Thr Gly Ala Thr Cys
    130                 135                 140

Thr Ala Thr Cys Thr Gly Gly Thr Thr Thr Cys Cys Ala Ala Thr Thr
145                 150                 155                 160

Cys Gly Gly Ala Gly Ala Thr Thr Gly Gly Ala Gly Thr Cys Cys Cys
                165                 170                 175

Cys Gly Ala Cys Ala Gly Gly Thr Thr Cys Ala Gly Cys Gly Gly Cys
            180                 185                 190

Ala Gly Thr Gly Gly Gly Thr Cys Thr Gly Gly Ala Ala Cys Thr Gly
        195                 200                 205

Ala Cys Thr Thr Thr Cys Gly Cys Cys Thr Gly Ala Cys Ala Ala Thr
    210                 215                 220

Cys Thr Cys Cys Thr Cys Ala Cys Thr Cys Cys Ala Gly Cys Cys Cys
225                 230                 235                 240

Gly Ala Ala Gly Ala Thr Thr Thr Cys Gly Cys Cys Ala Cys Cys Thr
                245                 250                 255

Ala Cys Thr Ala Thr Thr Gly Cys Cys Ala Gly Cys Ala Gly Ala Cys
            260                 265                 270

Thr Thr Gly Gly Ala Gly Cys Gly Ala Cys Cys Cys Thr Thr Gly Gly
        275                 280                 285
```

Ala Cys Ala Thr Thr Thr Gly Gly Ala Cys Ala Gly Gly Gly Cys Ala
290 295 300

Cys Ala Ala Ala Ala Gly Thr Gly Gly Ala Gly Ala Thr Cys Ala Ala
305 310 315 320

Gly

<210> 19
<211> 375
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<220>
<221> MISC_FEATURE
<223> Heavy chain variable region - CA028_496.g3

<400> 19

Gly Ala Gly Gly Thr Thr Cys Ala Gly Cys Thr Cys Gly Thr Thr Gly
1 5 10 15

Ala Ala Thr Cys Cys Gly Gly Ala Gly Gly Cys Gly Gly Ala Cys Thr
20 25 30

Cys Gly Thr Gly Cys Ala Gly Cys Cys Thr Gly Gly Gly Gly Gly Cys
35 40 45

Thr Cys Cys Thr Thr Gly Cys Gly Gly Cys Thr Gly Ala Gly Cys Thr
50 55 60

Gly Cys Gly Cys Thr Gly Cys Cys Ala Gly Thr Gly Gly Cys Thr Thr
65 70 75 80

Cys Ala Cys Thr Thr Thr Cys Ala Gly Cys Gly Ala Thr Thr Ala Cys

```
                85                  90                  95

Ala Ala Thr Ala Thr Gly Gly Cys Cys Thr Gly Gly Gly Thr Gly Cys
            100                 105                 110

Gly Cys Cys Ala Gly Gly Cys Cys Cys Cys Ala Gly Gly Cys Ala Ala
        115                 120                 125

Gly Gly Gly Thr Cys Thr Gly Gly Ala Gly Thr Gly Gly Gly Thr Gly
    130                 135                 140

Gly Cys Cys Ala Cys Ala Ala Thr Thr Ala Cys Cys Thr Ala Thr Gly
145                 150                 155                 160

Ala Gly Gly Gly Cys Ala Gly Ala Ala Ala Cys Ala Cys Thr Thr Ala
                165                 170                 175

Thr Thr Ala Cys Cys Gly Gly Gly Ala Thr Thr Cys Ala Gly Thr Gly
            180                 185                 190

Ala Ala Ala Gly Gly Gly Cys Gly Ala Thr Thr Thr Ala Cys Cys Ala
        195                 200                 205

Thr Cys Ala Gly Cys Ala Gly Gly Gly Ala Thr Ala Ala Thr Gly Cys
    210                 215                 220

Ala Ala Ala Gly Ala Ala Cys Ala Gly Thr Cys Thr Gly Thr Ala Cys
225                 230                 235                 240

Cys Thr Gly Cys Ala Gly Ala Thr Gly Ala Ala Cys Thr Cys Thr Cys
                245                 250                 255

Thr Gly Ala Gly Ala Gly Cys Thr Gly Ala Gly Gly Ala Cys Ala Cys
            260                 265                 270

Cys Gly Cys Thr Gly Thr Cys Thr Ala Cys Thr Ala Thr Thr Gly Thr
        275                 280                 285
```

```
Gly Cys Ala Ala Gly Cys Cys Cys Ala Cys Cys Cys Cys Ala Gly Thr
    290                 295                 300


Ala Cys Thr Ala Thr Gly Ala Gly Gly Gly Cys Thr Cys Ala Ala Thr
305                 310                 315                 320


Cys Thr Ala Cys Ala Gly Ala Thr Thr Gly Thr Gly Gly Thr Thr Thr
                325                 330                 335


Gly Cys Cys Cys Ala Thr Thr Gly Gly Gly Gly Cys Cys Ala Gly Gly
            340                 345                 350


Gly Ala Ala Cys Ala Cys Thr Gly Gly Thr Gly Ala Cys Cys Gly Thr
        355                 360                 365


Cys Thr Cys Gly Ala Gly Cys
    370                 375


<210>  20
<211>  705
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic peptide


<220>
<221>  MISC_FEATURE
<223>  Light chain - CA028_496 (w/ signal)

<400>  20

Ala Thr Gly Thr Cys Ala Gly Thr Thr Cys Cys Cys Ala Cys Ala Cys
1               5                   10                  15


Ala Gly Gly Thr Gly Cys Thr Gly Gly Gly Cys Cys Thr Gly Cys Thr
            20                  25                  30


Thr Cys Thr Gly Thr Thr Gly Thr Gly Gly Cys Thr Cys Ala Cys Cys
        35                  40                  45
```

```
Gly Ala Thr Gly Cys Thr Ala Gly Gly Thr Gly Thr Gly Cys Cys Ala
    50                  55                  60

Thr Cys Cys Ala Gly Cys Thr Gly Ala Cys Cys Cys Ala Gly Ala Gly
65                  70                  75                  80

Cys Cys Cys Thr Thr Cys Cys Thr Cys Thr Cys Thr Cys Ala Gly Cys
                85                  90                  95

Gly Cys Cys Ala Gly Thr Gly Thr Cys Gly Gly Ala Gly Ala Cys Ala
            100                 105                 110

Gly Ala Gly Thr Gly Ala Cys Thr Ala Thr Thr Ala Cys Cys Thr Gly
        115                 120                 125

Cys Ala Gly Gly Gly Cys Thr Gly Ala Cys Gly Ala Ala Ala Gly Cys
    130                 135                 140

Gly Thr Gly Ala Cys Cys Ala Cys Ala Thr Thr Gly Ala Thr Gly Cys
145                 150                 155                 160

Ala Cys Thr Gly Gly Thr Ala Cys Cys Ala Ala Cys Ala Gly Ala Ala
                165                 170                 175

Gly Cys Cys Thr Gly Gly Cys Ala Ala Ala Gly Cys Cys Cys Cys Cys
            180                 185                 190

Ala Ala Gly Cys Thr Cys Cys Thr Gly Ala Thr Cys Thr Ala Thr Cys
        195                 200                 205

Thr Gly Gly Thr Thr Thr Cys Cys Ala Ala Thr Cys Gly Gly Gly Ala
    210                 215                 220

Gly Thr Cys Thr Gly Gly Ala Gly Thr Cys Cys Cys Cys Ala Gly Cys
225                 230                 235                 240
```

```
Ala Gly Gly Thr Thr Cys Ala Gly Cys Gly Gly Cys Ala Gly Thr Gly
                245                 250                 255

Gly Gly Thr Cys Thr Gly Gly Ala Ala Cys Thr Gly Ala Cys Thr Thr
            260                 265                 270

Thr Ala Cys Cys Cys Thr Gly Ala Cys Ala Ala Thr Cys Thr Cys Cys
        275                 280                 285

Thr Cys Ala Cys Thr Cys Cys Ala Gly Cys Cys Cys Gly Ala Ala Gly
    290                 295                 300

Ala Thr Thr Thr Cys Gly Cys Cys Ala Cys Cys Thr Ala Cys Thr Ala
305                 310                 315                 320

Thr Thr Gly Cys Cys Ala Gly Cys Ala Gly Ala Cys Thr Thr Gly Gly
                325                 330                 335

Ala Gly Cys Gly Ala Cys Cys Cys Thr Thr Gly Gly Ala Cys Ala Thr
            340                 345                 350

Thr Thr Gly Gly Ala Cys Ala Gly Gly Gly Cys Ala Cys Ala Ala Ala
        355                 360                 365

Ala Gly Thr Gly Gly Ala Gly Ala Thr Cys Ala Ala Gly Cys Gly Thr
    370                 375                 380

Ala Cys Gly Gly Thr Ala Gly Cys Gly Gly Cys Cys Cys Cys Ala Thr
385                 390                 395                 400

Cys Thr Gly Thr Cys Thr Thr Cys Ala Thr Cys Thr Thr Cys Cys Cys
                405                 410                 415

Gly Cys Cys Ala Thr Cys Thr Gly Ala Thr Gly Ala Gly Cys Ala Gly
            420                 425                 430

Thr Thr Gly Ala Ala Ala Thr Cys Thr Gly Gly Ala Ala Cys Thr Gly
        435                 440                 445
```

```
Cys Cys Thr Cys Thr Gly Thr Thr Gly Thr Gly Thr Gly Cys Cys Thr
    450                 455                 460

Gly Cys Thr Gly Ala Ala Thr Ala Ala Cys Thr Thr Cys Thr Ala Thr
465                 470                 475                 480

Cys Cys Cys Ala Gly Ala Gly Ala Gly Gly Cys Cys Ala Ala Ala Gly
                485                 490                 495

Thr Ala Cys Ala Gly Thr Gly Gly Ala Ala Gly Gly Thr Gly Gly Ala
            500                 505                 510

Thr Ala Ala Cys Gly Cys Cys Cys Thr Cys Cys Ala Ala Thr Cys Gly
        515                 520                 525

Gly Gly Thr Ala Ala Cys Thr Cys Cys Cys Ala Gly Gly Ala Gly Ala
    530                 535                 540

Gly Thr Gly Thr Cys Ala Cys Ala Gly Ala Gly Cys Ala Gly Gly Ala
545                 550                 555                 560

Cys Ala Gly Cys Ala Ala Gly Gly Ala Cys Ala Gly Cys Ala Cys Cys
                565                 570                 575

Thr Ala Cys Ala Gly Cys Cys Thr Cys Ala Gly Cys Ala Gly Cys Ala
            580                 585                 590

Cys Cys Cys Thr Gly Ala Cys Gly Cys Thr Gly Ala Gly Cys Ala Ala
        595                 600                 605

Ala Gly Cys Ala Gly Ala Cys Thr Ala Cys Gly Ala Gly Ala Ala Ala
    610                 615                 620

Cys Ala Cys Ala Ala Ala Gly Thr Cys Thr Ala Cys Gly Cys Cys Thr
625                 630                 635                 640
```

```
Gly Cys Gly Ala Ala Gly Thr Cys Ala Cys Cys Cys Ala Thr Cys Ala
                645                 650                 655


Gly Gly Gly Cys Cys Thr Gly Ala Gly Cys Thr Cys Gly Cys Cys Cys
            660                 665                 670


Gly Thr Cys Ala Cys Ala Ala Ala Gly Ala Gly Cys Thr Thr Cys Ala
        675                 680                 685


Ala Cys Ala Gly Gly Gly Gly Ala Gly Ala Gly Thr Gly Thr Thr Ala
    690                 695                 700


Gly
705
```

<210> 21
<211> 645
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<220>
<221> MISC_FEATURE
<223> Light chain - CA028_496.g3 (w/o signal)

<400> 21

```
Gly Cys Cys Ala Thr Cys Cys Ala Gly Cys Thr Gly Ala Cys Cys Cys
1               5                   10                  15


Ala Gly Ala Gly Cys Cys Cys Thr Thr Cys Cys Thr Cys Thr Cys Thr
            20                  25                  30


Cys Ala Gly Cys Gly Cys Cys Ala Gly Thr Gly Thr Cys Gly Gly Ala
        35                  40                  45


Gly Ala Cys Ala Gly Ala Gly Thr Gly Ala Cys Thr Ala Thr Thr Ala
    50                  55                  60
```

```
Cys Cys Thr Gly Cys Ala Gly Gly Gly Cys Thr Gly Ala Cys Gly Ala
65                  70                  75                  80

Ala Ala Gly Cys Gly Thr Gly Ala Gly Ala Ala Cys Ala Thr Thr Gly
                85                  90                  95

Ala Thr Gly Cys Ala Cys Thr Gly Gly Thr Ala Cys Cys Ala Ala Cys
            100                 105                 110

Ala Gly Ala Ala Gly Cys Cys Thr Gly Gly Cys Ala Ala Ala Gly Cys
        115                 120                 125

Cys Cys Cys Cys Ala Ala Gly Cys Thr Cys Cys Thr Gly Ala Thr Cys
    130                 135                 140

Thr Ala Thr Cys Thr Gly Gly Thr Thr Thr Cys Cys Ala Ala Thr Thr
145                 150                 155                 160

Cys Gly Gly Ala Gly Ala Thr Thr Gly Gly Ala Gly Thr Cys Cys Cys
                165                 170                 175

Cys Gly Ala Cys Ala Gly Gly Thr Thr Cys Ala Gly Cys Gly Gly Cys
            180                 185                 190

Ala Gly Thr Gly Gly Gly Thr Cys Thr Gly Gly Ala Ala Cys Thr Gly
        195                 200                 205

Ala Cys Thr Thr Thr Cys Gly Cys Cys Thr Gly Ala Cys Ala Ala Thr
    210                 215                 220

Cys Thr Cys Cys Thr Cys Ala Cys Thr Cys Cys Ala Gly Cys Cys Cys
225                 230                 235                 240

Gly Ala Ala Gly Ala Thr Thr Thr Cys Gly Cys Cys Ala Cys Cys Thr
                245                 250                 255

Ala Cys Thr Ala Thr Thr Gly Cys Cys Ala Gly Cys Ala Gly Ala Cys
```

```
            260                 265                 270

Thr Thr Gly Gly Ala Gly Cys Gly Ala Cys Cys Cys Thr Thr Gly Gly
        275                 280                 285

Ala Cys Ala Thr Thr Thr Gly Gly Ala Cys Ala Gly Gly Gly Cys Ala
    290                 295                 300

Cys Ala Ala Ala Ala Gly Thr Gly Gly Ala Gly Ala Thr Cys Ala Ala
305                 310                 315                 320

Gly Cys Gly Thr Ala Cys Gly Gly Thr Ala Gly Cys Gly Gly Cys Cys
                325                 330                 335

Cys Cys Ala Thr Cys Thr Gly Thr Cys Thr Thr Cys Ala Thr Cys Thr
            340                 345                 350

Thr Cys Cys Cys Gly Cys Cys Ala Thr Cys Thr Gly Ala Thr Gly Ala
        355                 360                 365

Gly Cys Ala Gly Thr Thr Gly Ala Ala Ala Thr Cys Thr Gly Gly Ala
    370                 375                 380

Ala Cys Thr Gly Cys Cys Thr Cys Thr Gly Thr Thr Gly Thr Gly Thr
385                 390                 395                 400

Gly Cys Cys Thr Gly Cys Thr Gly Ala Ala Thr Ala Ala Cys Thr Thr
                405                 410                 415

Cys Thr Ala Thr Cys Cys Cys Ala Gly Ala Gly Ala Gly Gly Cys Cys
            420                 425                 430

Ala Ala Ala Gly Thr Ala Cys Ala Gly Thr Gly Gly Ala Ala Gly Gly
        435                 440                 445

Thr Gly Gly Ala Thr Ala Ala Cys Gly Cys Cys Cys Thr Cys Cys Ala
    450                 455                 460
```

```
Ala Thr Cys Gly Gly Gly Thr Ala Ala Cys Thr Cys Cys Cys Ala Gly
465                 470                 475                 480


Gly Ala Gly Ala Gly Thr Gly Thr Cys Ala Cys Ala Gly Ala Gly Cys
                485                 490                 495


Ala Gly Gly Ala Cys Ala Gly Cys Ala Ala Gly Gly Ala Cys Ala Gly
            500                 505                 510


Cys Ala Cys Cys Thr Ala Cys Ala Gly Cys Cys Thr Cys Ala Gly Cys
        515                 520                 525


Ala Gly Cys Ala Cys Cys Cys Thr Gly Ala Cys Gly Cys Thr Gly Ala
    530                 535                 540


Gly Cys Ala Ala Ala Gly Cys Ala Gly Ala Cys Thr Ala Cys Gly Ala
545                 550                 555                 560


Gly Ala Ala Ala Cys Ala Cys Ala Ala Ala Gly Thr Cys Thr Ala Cys
                565                 570                 575


Gly Cys Cys Thr Gly Cys Gly Ala Ala Gly Thr Cys Ala Cys Cys Cys
            580                 585                 590


Ala Thr Cys Ala Gly Gly Gly Cys Cys Thr Gly Ala Gly Cys Thr Cys
        595                 600                 605


Gly Cys Cys Cys Gly Thr Cys Ala Cys Ala Ala Ala Gly Ala Gly Cys
    610                 615                 620


Thr Thr Cys Ala Ala Cys Ala Gly Gly Gly Gly Ala Gly Ala Gly Thr
625                 630                 635                 640


Gly Thr Thr Ala Gly
                645
```

<210> 22

<211> 705
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<220>
<221> MISC_FEATURE
<223> Light chain - CA028_496.g3 (w/ signal)

<400> 22

```
Ala Thr Gly Thr Cys Ala Gly Thr Thr Cys Cys Cys Ala Cys Ala Cys
1               5                   10                  15


Ala Gly Gly Thr Gly Cys Thr Gly Gly Gly Cys Cys Thr Gly Cys Thr
            20                  25                  30


Thr Cys Thr Gly Thr Thr Gly Thr Gly Gly Cys Thr Cys Ala Cys Cys
        35                  40                  45


Gly Ala Thr Gly Cys Thr Ala Gly Gly Thr Gly Thr Gly Cys Cys Ala
    50                  55                  60


Thr Cys Cys Ala Gly Cys Thr Gly Ala Cys Cys Cys Ala Gly Ala Gly
65                  70                  75                  80


Cys Cys Cys Thr Thr Cys Cys Thr Cys Thr Cys Thr Cys Ala Gly Cys
                85                  90                  95


Gly Cys Cys Ala Gly Thr Gly Thr Cys Gly Gly Ala Gly Ala Cys Ala
            100                 105                 110


Gly Ala Gly Thr Gly Ala Cys Thr Ala Thr Thr Ala Cys Cys Thr Gly
        115                 120                 125


Cys Ala Gly Gly Gly Cys Thr Gly Ala Cys Gly Ala Ala Ala Gly Cys
    130                 135                 140
```

```
Gly Thr Gly Ala Gly Ala Ala Cys Ala Thr Thr Gly Ala Thr Gly Cys
145                 150                 155                 160


Ala Cys Thr Gly Gly Thr Ala Cys Cys Ala Ala Cys Ala Gly Ala Ala
                165                 170                 175


Gly Cys Cys Thr Gly Gly Cys Ala Ala Ala Gly Cys Cys Cys Cys Cys
            180                 185                 190


Ala Ala Gly Cys Thr Cys Cys Thr Gly Ala Thr Cys Thr Ala Thr Cys
        195                 200                 205


Thr Gly Gly Thr Thr Thr Cys Cys Ala Ala Thr Thr Cys Gly Gly Ala
    210                 215                 220


Gly Ala Thr Thr Gly Gly Ala Gly Thr Cys Cys Cys Cys Gly Ala Cys
225                 230                 235                 240


Ala Gly Gly Thr Thr Cys Ala Gly Cys Gly Gly Cys Ala Gly Thr Gly
                245                 250                 255


Gly Gly Thr Cys Thr Gly Gly Ala Ala Cys Thr Gly Ala Cys Thr Thr
            260                 265                 270


Thr Cys Gly Cys Cys Thr Gly Ala Cys Ala Ala Thr Cys Thr Cys Cys
        275                 280                 285


Thr Cys Ala Cys Thr Cys Cys Ala Gly Cys Cys Cys Gly Ala Ala Gly
    290                 295                 300


Ala Thr Thr Thr Cys Gly Cys Cys Ala Cys Cys Thr Ala Cys Thr Ala
305                 310                 315                 320


Thr Thr Gly Cys Cys Ala Gly Cys Ala Gly Ala Cys Thr Thr Gly Gly
                325                 330                 335


Ala Gly Cys Gly Ala Cys Cys Cys Thr Thr Gly Gly Ala Cys Ala Thr
            340                 345                 350
```

```
Thr Thr Gly Gly Ala Cys Ala Gly Gly Gly Cys Ala Cys Ala Ala Ala
        355                 360                 365

Ala Gly Thr Gly Gly Ala Gly Ala Thr Cys Ala Ala Gly Cys Gly Thr
    370                 375                 380

Ala Cys Gly Gly Thr Ala Gly Cys Gly Gly Cys Cys Cys Cys Ala Thr
385                 390                 395                 400

Cys Thr Gly Thr Cys Thr Thr Cys Ala Thr Cys Thr Thr Cys Cys Cys
                405                 410                 415

Gly Cys Cys Ala Thr Cys Thr Gly Ala Thr Gly Ala Gly Cys Ala Gly
            420                 425                 430

Thr Thr Gly Ala Ala Ala Thr Cys Thr Gly Gly Ala Ala Cys Thr Gly
        435                 440                 445

Cys Cys Thr Cys Thr Gly Thr Thr Gly Thr Gly Thr Gly Cys Cys Thr
    450                 455                 460

Gly Cys Thr Gly Ala Ala Thr Ala Ala Cys Thr Thr Cys Thr Ala Thr
465                 470                 475                 480

Cys Cys Cys Ala Gly Ala Gly Ala Gly Gly Cys Cys Ala Ala Ala Gly
                485                 490                 495

Thr Ala Cys Ala Gly Thr Gly Gly Ala Ala Gly Gly Thr Gly Gly Ala
            500                 505                 510

Thr Ala Ala Cys Gly Cys Cys Cys Thr Cys Cys Ala Ala Thr Cys Gly
        515                 520                 525

Gly Gly Thr Ala Ala Cys Thr Cys Cys Cys Ala Gly Gly Ala Gly Ala
    530                 535                 540
```

```
Gly Thr Gly Thr Cys Ala Cys Ala Gly Ala Gly Cys Ala Gly Gly Ala
545                 550                 555                 560


Cys Ala Gly Cys Ala Ala Gly Gly Ala Cys Ala Gly Cys Ala Cys Cys
                565                 570                 575


Thr Ala Cys Ala Gly Cys Cys Thr Cys Ala Gly Cys Ala Gly Cys Ala
            580                 585                 590


Cys Cys Cys Thr Gly Ala Cys Gly Cys Thr Gly Ala Gly Cys Ala Ala
        595                 600                 605


Ala Gly Cys Ala Gly Ala Cys Thr Ala Cys Gly Ala Gly Ala Ala Ala
    610                 615                 620


Cys Ala Cys Ala Ala Ala Gly Thr Cys Thr Ala Cys Gly Cys Cys Thr
625                 630                 635                 640


Gly Cys Gly Ala Ala Gly Thr Cys Ala Cys Cys Cys Ala Thr Cys Ala
                645                 650                 655


Gly Gly Gly Cys Cys Thr Gly Ala Gly Cys Thr Cys Gly Cys Cys Cys
            660                 665                 670


Gly Thr Cys Ala Cys Ala Ala Ala Gly Ala Gly Cys Thr Thr Cys Ala
        675                 680                 685


Ala Cys Ala Gly Gly Gly Gly Ala Gly Ala Gly Thr Gly Thr Thr Ala
    690                 695                 700


Gly
705


<210>  23
<211>  2020
<212>  DNA
<213>  Artificial Sequence

<220>
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<223> Synthetic polynucleotide

<220>
<221> misc_feature
<223> Heavy chain CA028_496 (w/ signal)

<400> 23
atggaatggt cctgggtctt cctgtttttc ctttctgtca caaccggggt gcacagcgag 60

gttcagctcg ttgaatccgg aggcggactc gtgcagcctg ggggctcctt gcggctgagc 120

tgcgctgcca gtggcttcac tttcagcgat tacaatatgg cctgggtgcg ccaggcccca 180

ggcaagggtc tggagtgggt ggccacaatt acctatgagg gcagaaacac ttattaccgg 240

gattcagtga aagggcgatt taccatcagc agggataatg caaagaacag tctgtacctg 300

cagatgaact ctctgagagc tgaggacacc gctgtctact attgtgcaag cccaccccag 360

tactatgagg gctcaatcta cagattgtgg tttgcccatt ggggccaggg aacactggtg 420

accgtctcga gcgcttctac aaagggccca tccgtcttcc ccctggcgcc ctgctccagg 480

agcacctccg agagcacagc cgccctgggc tgcctggtca aggactactt ccccgaaccg 540

gtgacggtgt cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc 600

ctacagtcct caggactcta ctccctcagc agcgtggtga ccgtgccctc cagcagcttg 660

ggcacgaaga cctacacctg caacgtagat cacaagccca gcaacaccaa ggtggacaag 720

agagttggtg agaggccagc acagggaggg agggtgtctg ctggaagcca ggctcagccc 780

tcctgcctgg acgcaccccg gctgtgcagc cccagcccag ggcagcaagg catgccccat 840

ctgtctcctc acccggaggc ctctgaccac cccactcatg cccagggaga gggtcttctg 900

gatttttcca ccaggctccg ggcagccaca ggctggatgc ccctacccca ggccctgcgc 960

atacaggggc aggtgctgcg ctcagacctg ccaagagcca tatccgggag gaccctgccc 1020

ctgacctaag cccaccccaa aggccaaact ctccactccc tcagctcaga caccttctct 1080

cctcccagat ctgagtaact cccaatcttc tctctgcaga gtccaaatat ggtcccccat 1140

gcccaccatg cccaggtaag ccaacccagg cctcgccctc agctcaagg cgggacaggt 1200

gccctagagt agcctgcatc cagggacagg ccccagccgg gtgctgacgc atccacctcc 1260

atctcttcct cagcacctga gttcctgggg ggaccatcag tcttcctgtt ccccccaaaa 1320

cccaaggaca ctctcatgat ctcccggacc cctgaggtca cgtgcgtggt ggtggacgtg 1380

agccaggaag accccgaggt ccagttcaac tggtacgtgg atggcgtgga ggtgcataat 1440

gccaagacaa agccgcggga ggagcagttc aacagcacgt accgtgtggt cagcgtcctc 1500

accgtcctgc accaggactg gctgaacggc aaggagtaca agtgcaaggt ctccaacaaa 1560

ggcctcccgt cctccatcga gaaaaccatc tccaaagcca aaggtgggac ccacggggtg 1620

cgagggccac atggacagag gtcagctcgg cccaccctct gccctgggag tgaccgctgt 1680

gccaacctct gtccctacag ggcagccccg agagccacag gtgtacaccc tgcccccatc 1740

ccaggaggag atgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctaccc 1800

cagcgacatc gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac 1860

gcctcccgtg ctggactccg acggctcctt cttcctctac agcaggctaa ccgtggacaa 1920

gagcaggtgg caggagggga atgtcttctc atgctccgtg atgcatgagg ctctgcacaa 1980

ccactacaca cagaagagcc tctccctgtc tctgggtaaa 2020

<210> 24
<211> 1365
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<220>
<221> misc_feature
<223> Heavy chain - CA028_496.g3 (w/ exons, w/o signal)

<400> 24
gaggttcagc tcgttgaatc cggaggcgga ctcgtgcagc ctgggggctc cttgcggctg 60

agctgcgctg ccagtggctt cactttcagc gattacaata tggcctgggt gcgccaggcc 120

ccaggcaagg gtctggagtg ggtggccaca attacctatg agggcagaaa cacttattac 180

cgggattcag tgaaagggcg atttaccatc agcagggata atgcaaagaa cagtctgtac 240

ctgcagatga actctctgag agctgaggac accgctgtct actattgtgc aagcccaccc 300

cagtactatg agggctcaat ctacagattg tggtttgccc attggggcca gggaacactg 360

gtgaccgtct cgagcgcttc tacaaagggc ccatcggtct tccccctggc accctcctcc 420

aagagcacct ctgggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa 480

ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct 540

gtcctacagt cctcaggact ctactccctc agcagcgtgg tgaccgtgcc ctccagcagc 600

ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtcgac 660

aagaaagttg agcccaaatc ttgtgacaaa actcacacat gcccaccgtg cccagcacct 720

gaactcctgg ggggaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 780

atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 840

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 900

gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 960

tggctgaatg gcaaggagta caagtgcaag gtctccaaca aagccctccc agcccccatc 1020

gagaaaacca tctccaaagc caaagcgcag ccccgagaac cacaggtgta caccctgccc 1080

ccatcccggg atgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 1140

tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag 1200

accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg 1260

gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1320

cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtaaa 1365

<210> 25
<211> 1422
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<220>
<221> misc_feature
<223> Heavy chain - CA028_496.g3 (w/ signal and exons)

<400> 25
atggaatggt cctgggtctt cctgtttttc ctttctgtca caaccggggt gcacagcgag 60

gttcagctcg ttgaatccgg aggcggactc gtgcagcctg ggggctcctt gcggctgagc 120

tgcgctgcca gtggcttcac tttcagcgat tacaatatgg cctgggtgcg ccaggcccca 180

ggcaagggtc tggagtgggt ggccacaatt acctatgagg gcagaaacac ttattaccgg 240

gattcagtga aagggcgatt taccatcagc agggataatg caaagaacag tctgtacctg 300

cagatgaact ctctgagagc tgaggacacc gctgtctact attgtgcaag cccaccccag 360

tactatgagg gctcaatcta cagattgtgg tttgcccatt ggggccaggg aacactggtg 420

accgtctcga gcgcttctac aaagggccca tcggtcttcc ccctggcacc ctcctccaag 480

agcacctctg ggggcacagc ggccctgggc tgcctggtca aggactactt ccccgaaccg 540

gtgacggtgt cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc 600

ctacagtcct caggactcta ctccctcagc agcgtggtga ccgtgccctc cagcagcttg 660

ggcacccaga cctacatctg caacgtgaat cacaagccca gcaacaccaa ggtcgacaag 720

aaagttgagc ccaaatcttg tgacaaaact cacacatgcc caccgtgccc agcacctgaa 780

ctcctggggg gaccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgatc 840

tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc 900

aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag 960

gagcagtaca acagcacgta ccgtgtggtc agcgtcctca ccgtcctgca ccaggactgg 1020

ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc ccccatcgag 1080

aaaaccatct ccaaagccaa agcgcagccc cgagaaccac aggtgtacac cctgccccca 1140

tcccgggatg agctgaccaa gaaccaggtc agcctgacct gcctggtcaa aggcttctat 1200

cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1260

acgcctcccg tgctggactc cgacggctcc ttcttcctct acagcaagct caccgtggac 1320

aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 1380

aaccactaca cgcagaagag cctctccctg tctccgggta aa 1422

<210> 26
<211> 1422
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<220>
<221> misc_feature
<223> Heavy chain - CA028_496.g3 (w/ signal)

<400> 26
atggaatggt cctgggtctt cctgtttttc ctttctgtca caaccggggt gcacagcgag 60

gttcagctcg ttgaatccgg aggcggactc gtgcagcctg ggggctcctt gcggctgagc 120

tgcgctgcca gtggcttcac tttcagcgat tacaatatgg cctgggtgcg ccaggcccca 180

ggcaagggtc tggagtgggt ggccacaatt acctatgagg gcagaaacac ttattaccgg 240

gattcagtga aagggcgatt taccatcagc agggataatg caaagaacag tctgtacctg 300

cagatgaact ctctgagagc tgaggacacc gctgtctact attgtgcaag cccaccccag 360

tactatgagg gctcaatcta cagattgtgg tttgcccatt ggggccaggg aacactggtg 420

accgtctcga gcgcttctac aaagggccca tcggtcttcc ccctggcacc ctcctccaag 480

agcacctctg ggggcacagc ggccctgggc tgcctggtca aggactactt ccccgaaccg 540

gtgacggtgt cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc 600

ctacagtcct caggactcta ctccctcagc agcgtggtga ccgtgccctc cagcagcttg 660

ggcacccaga cctacatctg caacgtgaat cacaagccca gcaacaccaa ggtcgacaag 720

aaagttgagc ccaaatcttg tgacaaaact cacacatgcc caccgtgccc agcacctgaa 780

ctcctggggg gaccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgatc 840

tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc 900

aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag 960

gagcagtaca acagcacgta ccgtgtggtc agcgtcctca ccgtcctgca ccaggactgg 1020

ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc ccccatcgag 1080

aaaaccatct ccaaagccaa agcgcagccc cgagaaccac aggtgtacac cctgccccca 1140

tcccgggatg agctgaccaa gaaccaggtc agcctgacct gcctggtcaa aggcttctat 1200

cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1260

acgcctcccg tgctggactc cgacggctcc ttcttcctct acagcaagct caccgtggac 1320

aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 1380

aaccactaca cgcagaagag cctctccctg tctccgggta aa 1422

<210> 27
<211> 132
<212> PRT
<213> Homo sapiens

<400> 27

Gly Ile Thr Ile Pro Arg Asn Pro Gly Cys Pro Asn Ser Glu Asp Lys
1 5 10 15

Asn Phe Pro Arg Thr Val Met Val Asn Leu Asn Ile His Asn Arg Asn
20 25 30

Thr Asn Thr Asn Pro Lys Arg Ser Ser Asp Tyr Tyr Asn Arg Ser Thr
35 40 45

Ser Pro Trp Asn Leu His Arg Asn Glu Asp Pro Glu Arg Tyr Pro Ser
50 55 60

Val Ile Trp Glu Ala Lys Cys Arg His Leu Gly Cys Ile Asn Ala Asp
65 70 75 80

Gly Asn Val Asp Tyr His Met Asn Ser Val Pro Ile Gln Gln Glu Ile
85 90 95

Leu Val Leu Arg Arg Glu Pro Pro His Cys Pro Asn Ser Phe Arg Leu
100 105 110

Glu Lys Ile Leu Val Ser Val Gly Cys Thr Cys Val Thr Pro Ile Val

115 120 125

His His Val Ala
130

<210> 28
<211> 133
<212> PRT
<213> Homo sapiens

<400> 28

Arg Lys Ile Pro Lys Val Gly His Thr Phe Phe Gln Lys Pro Glu Ser
1 5 10 15

Cys Pro Pro Val Pro Gly Gly Ser Met Lys Leu Asp Ile Gly Ile Ile
20 25 30

Asn Glu Asn Gln Arg Val Ser Met Ser Arg Asn Ile Glu Ser Arg Ser
35 40 45

Thr Ser Pro Trp Asn Tyr Thr Val Thr Trp Asp Pro Asn Arg Tyr Pro
50 55 60

Ser Glu Val Val Gln Ala Gln Cys Arg Asn Leu Gly Cys Ile Asn Ala
65 70 75 80

Gln Gly Lys Glu Asp Ile Ser Met Asn Ser Val Pro Ile Gln Gln Glu
85 90 95

Thr Leu Val Val Arg Arg Lys His Gln Gly Cys Ser Val Ser Phe Gln
100 105 110

Leu Glu Lys Val Leu Val Thr Val Gly Cys Thr Cys Val Thr Pro Val
115 120 125

Ile His His Val Gln
130