SEQUENCE LISTING

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<120> ANTI-LGR5 ANTIBODIES AND IMMUNOCONJUGATES

<130> GENE-32548/WO-1/ORD

<150> US 61/618,232
<151> 2012-03-30

<150> US 61/683,048
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<160> 86

<170> PatentIn version 3.5

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<400> 1

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

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

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

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

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

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

Tyr Tyr Ser Thr Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile

100 105 110

Lys Arg

<210> 2
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<220>
<223> Synthetic: huVH1

<400> 2

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

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

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

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

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

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

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

<210> 3
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: mu8E11 light chain variable region

<400> 3

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

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

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

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

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

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

Glu Asp Pro Phe Thr Phe Gly Ser Gly Thr Lys Val Glu Ile Lys Arg
100 105 110

<210> 4
<211> 118
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<213> Artificial Sequence

<220>
<223> Synthetic: mu8E11 heavy chain variable region

<400> 4

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

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

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

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

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

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

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

Thr Leu Lys Val Ser Ser
115

<210> 5

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<223> Synthetic: hu8E11.v1 light chain variable region

<400> 5

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

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

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

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

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

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

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

<210> 6
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<213> Artificial Sequence

<220>
<223> Synthetic: hu8E11.v1 heavy chain variable region

<400> 6

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

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

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

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

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


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


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


Leu Val Thr Val Ser Ser
        115


<210>  7
<211>  112
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<213>  Artificial Sequence

<220>
<223>  Synthetic: hu8E11.v2 light chain variable region

<400>  7

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


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


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


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


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


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


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


<210>  8
<211>  118
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic: hu8E11.v2 heavy chain variable region

<400>  8
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Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15

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

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

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

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

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

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

Leu Val Thr Val Ser Ser
        115
```

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

<220>
<223> Synthetic: hu8E11.v3 light chain variable region

<400> 9

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

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

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

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

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

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

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

<210> 10
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: hu8E11.v3 heavy chain variable region

<400> 10

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

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

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

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

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

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

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

Leu Val Thr Val Ser Ser
115

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

<220>
<223> Synthetic: hu8E11.v4 light chain variable region

<400> 11

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

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

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

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

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

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

Glu Asp Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105                 110
```

<210> 12
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: hu8E11.v4 heavy chain variable region

<400> 12

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

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

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

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

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

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

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

Leu Val Thr Val Ser Ser
115

<210> 13
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: hu8E11.v5 light chain variable region

<400> 13

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

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

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

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

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

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

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

<210> 14
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: hu8E11.v5 heavy chain variable region

<400> 14

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

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

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

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

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

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

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

Leu Val Thr Val Ser Ser
115

<210> 15
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: hu8E11.v6 light chain variable region

<400> 15

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

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

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

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

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

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

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

<210> 16
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: hu8E11.v6 heavy chain variable region

<400> 16

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

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

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

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

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

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

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

Leu Val Thr Val Ser Ser
115

<210> 17
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: hu8E11.v7 light chain variable region

<400> 17

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

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

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

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

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


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


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


<210>  18
<211>  118
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic: hu8E11.v7 heavy chain variable region

<400>  18

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


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


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


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


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


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


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


Leu Val Thr Val Ser Ser
        115


<210>  19
<211>  112
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic: hu8E11.v8 light chain variable region
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<400> 19

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

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

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

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

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

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

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

<210> 20
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: hu8E11.v8 heavy chain variable region

<400> 20

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

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

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

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

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

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

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

Leu Val Thr Val Ser Ser
115

<210> 21
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: mu3G12 light chain variable region

<400> 21

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

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

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

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

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

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

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

Arg

<210> 22
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: mu3G12 heavy chain variable region

<400> 22

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

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

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

Gly Glu Ile Asn Pro Ser Asn Gly Arg Thr Asn Tyr Ile Glu Lys Phe
50 55 60

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

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

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

Val Ser Ser
115

<210> 23
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: mu2H6 light chain variable region

<400> 23

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

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

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

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

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

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

Asp Tyr Ser Phe Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys Arg

<210> 24
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: mu2H6 heavy chain variable region

<400> 24

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

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

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

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

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

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

Ala Arg Gly Gly Ser Thr Met Ile Thr Pro Arg Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 25
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: YW353 light chain variable region

<400> 25

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105
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<210> 26
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: YW353 heavy chain variable region

<400> 26

```
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 Thr Ser Tyr
            20                  25                  30

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

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

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

Thr Val Ser Ser
        115

<210> 27
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: mu8E11 HVR L1

<400> 27

Arg Ala Ser Glu Ser Val Asp Asn Tyr Gly Asn Ser Phe Met His
1   5   10   15

<210> 28
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: mu8E11 HVR L2

<400> 28

Leu Ala Ser Asn Leu Glu Ser
1   5

<210> 29
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: mu8E11 HVR L3

<400> 29

Gln Gln Asn Tyr Glu Asp Pro Phe Thr
1   5

<210> 30
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: mu8E11 HVR H1

<400> 30

Gly Tyr Thr Phe Ser Ala Tyr Trp Ile Glu
1   5   10

<210> 31
<211> 17

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: mu8E11 HVR H2

<400> 31

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

Val

<210> 32
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: mu8E11 HVR H3

<400> 32

Gly Gly His Tyr Gly Ser Leu Asp Tyr
1 5

<210> 33
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Hu8E11 light chain (LC) framework 1 (FR1)

<400> 33

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

Glu Arg Ala Thr Ile Asn Cys
20

<210> 34
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Hu8E11 LC FR2

<400> 34

Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
1 5 10 15

<210> 35

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

<220>
<223> Synthetic: Hu8E11.v1 LC FR3/Hu8E11.v2 LC FR3/Hu8E11.v5 LC FR3/Hu8E11.v6 LC FR3

<400> 35

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

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

<210> 36
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Hu8E11.v3 LC FR3/Hu8E11.v4 LC FR3/Hu8E11.v7 LC FR3/Hu8E11.v8 LC FR3

<400> 36

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr
1 5 10 15

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

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

<220>
<223> Synthetic: Hu8E11 LC FR4

<400> 37

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
1 5 10

<210> 38
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Hu8E11 heavy chain (HC) framework1 (FR1)

<400> 38

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

Ser Val Lys Val Ser Cys Lys Ala Ser
20 25

<210> 39
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Hu8E11 HC FR2

<400> 39

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly
1 5 10

<210> 40
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Hu8E11.v1 HC FR3/Hu8E11.v3 HC FR3

<400> 40

Arg Val Thr Ile Thr Ser Asp Thr Ser Thr Ser Thr Val Tyr Leu Glu
1 5 10 15

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

<210> 41
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Hu8E11.v2 HC FR3/Hu8E11.v4 HC FR3

<400> 41

Arg Ala Thr Phe Thr Ser Asp Thr Ser Thr Ser Thr Val Tyr Leu Glu
1 5 10 15

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

<210> 42
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Hu8E11.v5 HC FR3/Hu8E11.v7 HC FR3

<400> 42

Arg Val Thr Ile Thr Arg Asp Thr Ser Thr Ser Thr Ala Tyr Leu Glu
1 5 10 15

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

<210> 43
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Hu8E11.v6 HC FR3/Hu8E11.v8 HC FR3

<400> 43

Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr Leu Glu
1 5 10 15

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

<210> 44
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: Hu8E11 HC FR4

<400> 44

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
1 5 10

<210> 45
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: mu3G12 HVR L1

<400> 45

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

<210> 46
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic: mu3G12 HVR L2

<400> 46

Lys Val Ser Asn Arg Phe Ser
1 5

<210> 47
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: mu3G12 HVR L3

<400> 47

Ser Gln Ser Thr His Phe Pro Tyr Thr
1 5

<210> 48
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: mu3G12 HVR H1

<400> 48

Val Asp Thr Phe Asn Ser Tyr Trp Met His
1 5 10

<210> 49
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: mu3G12 HVR H2

<400> 49

Glu Ile Asn Pro Ser Asn Gly Arg Thr Asn Tyr Ile Glu Lys Phe Lys
1 5 10 15

Asn

<210> 50
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: mu3G12 HVR H3

<400> 50

Gly Trp Tyr Phe Asp Val
1 5

<210> 51
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: mu2H6 HVR L1

<400> 51

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

Thr

<210> 52
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: mu2H6 HVR L2

<400> 52

Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 53
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: mu2H6 HVR L3

<400> 53

Gln Asn Asp Tyr Ser Phe Pro Phe Thr
1 5

<210> 54
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: mu2H6 HVR H1

<400> 54

Gly Tyr Ser Phe Thr Gly Tyr Thr Met Asn
1 5 10

<210> 55
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: mu2H6 HVR H2

<400> 55

Leu Ile Asn Cys Tyr Asn Gly Gly Thr Asn Tyr Asn Gln Lys Phe Lys
1 5 10 15

Gly

<210> 56
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: mu2H6 HVR H3

<400> 56

Gly Gly Ser Thr Met Ile Thr Pro Arg Phe Ala Tyr
1 5 10

<210> 57
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: YW353 HVR L1

<400> 57

Arg Ala Ser Gln Asp Val Ser Thr Ala Val Ala
1 5 10

<210> 58
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: YW353 HVR L2

<400> 58

Ser Ala Ser Phe Leu Tyr Ser
1 5

<210> 59

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

<220>
<223> Synthetic: YW353 HVR L3

<400> 59

Gln Gln Ser Tyr Thr Thr Pro Pro Thr
1 5

<210> 60
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: YW353 HVR H1

<400> 60

Gly Phe Thr Phe Thr Ser Tyr Ser Ile Ser
1 5 10

<210> 61
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: YW353 HVR H2

<400> 61

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

Gly

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

<220>
<223> Synthetic: YW353 HVR H3

<400> 62

Ala Arg Leu Phe Phe Asp Tyr
1 5

<210> 63
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: hu8E11.v2 light chain

<400> 63

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

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

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

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

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

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

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

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
        115                 120                 125

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
    130                 135                 140

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

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

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

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

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

<210> 64

<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: hu8E11.v2 heavy chain

<400> 64

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


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


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


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


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


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


Ala Arg Gly Gly His Tyr Gly Ser Leu 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 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 Glu Glu Met 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 Lys
        435                 440                 445
```

<210> 65
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: YW353 light chain

<400> 65

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Ser 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 Phe Leu Tyr 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 Ser Tyr Thr Thr Pro Pro
                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> 66
<211> 446

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: YW353 heavy chain

<400> 66

```
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 Thr Ser Tyr
            20                  25                  30

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

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

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

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

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

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

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

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

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

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

```
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
225                 230                 235                 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                245                 250                 255

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

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

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

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

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

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

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

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

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

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

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

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

<210> 67
<211> 907
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Human LgR5 precursor; LGR5_human NP_003658; signal sequence = amino acids 1-21

<400> 67

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

Gln Leu Ala Thr Gly Gly Ser Ser Pro Arg Ser Gly Val Leu Leu Arg
            20                  25                  30

Gly Cys Pro Thr His Cys His Cys Glu Pro Asp Gly Arg Met Leu Leu
        35                  40                  45

Arg Val Asp Cys Ser Asp Leu Gly Leu Ser Glu Leu Pro Ser Asn Leu
    50                  55                  60

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

Leu Leu Pro Asn Pro Leu Pro Ser Leu Arg Phe Leu Glu Glu Leu Arg
                85                  90                  95

Leu Ala Gly Asn Ala Leu Thr Tyr Ile Pro Lys Gly Ala Phe Thr Gly
            100                 105                 110

Leu Tyr Ser Leu Lys Val Leu Met Leu Gln Asn Asn Gln Leu Arg His
        115                 120                 125

Val Pro Thr Glu Ala Leu Gln Asn Leu Arg Ser Leu Gln Ser Leu Arg
    130                 135                 140

Leu Asp Ala Asn His Ile Ser Tyr Val Pro Pro Ser Cys Phe Ser Gly
145                 150                 155                 160

Leu His Ser Leu Arg His Leu Trp Leu Asp Asp Asn Ala Leu Thr Glu
                165                 170                 175

Ile Pro Val Gln Ala Phe Arg Ser Leu Ser Ala Leu Gln Ala Met Thr
            180                 185                 190

Leu Ala Leu Asn Lys Ile His His Ile Pro Asp Tyr Ala Phe Gly Asn
        195                 200                 205

Leu Ser Ser Leu Val Val Leu His Leu His Asn Asn Arg Ile His Ser
    210                 215                 220
```

```
Leu Gly Lys Lys Cys Phe Asp Gly Leu His Ser Leu Glu Thr Leu Asp
225                 230                 235                 240

Leu Asn Tyr Asn Asn Leu Asp Glu Phe Pro Thr Ala Ile Arg Thr Leu
                245                 250                 255

Ser Asn Leu Lys Glu Leu Gly Phe His Ser Asn Asn Ile Arg Ser Ile
            260                 265                 270

Pro Glu Lys Ala Phe Val Gly Asn Pro Ser Leu Ile Thr Ile His Phe
        275                 280                 285

Tyr Asp Asn Pro Ile Gln Phe Val Gly Arg Ser Ala Phe Gln His Leu
    290                 295                 300

Pro Glu Leu Arg Thr Leu Thr Leu Asn Gly Ala Ser Gln Ile Thr Glu
305                 310                 315                 320

Phe Pro Asp Leu Thr Gly Thr Ala Asn Leu Glu Ser Leu Thr Leu Thr
                325                 330                 335

Gly Ala Gln Ile Ser Ser Leu Pro Gln Thr Val Cys Asn Gln Leu Pro
            340                 345                 350

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

Ser Phe Ser Val Cys Gln Lys Leu Gln Lys Ile Asp Leu Arg His Asn
    370                 375                 380

Glu Ile Tyr Glu Ile Lys Val Asp Thr Phe Gln Gln Leu Leu Ser Leu
385                 390                 395                 400

Arg Ser Leu Asn Leu Ala Trp Asn Lys Ile Ala Ile Ile His Pro Asn
                405                 410                 415

Ala Phe Ser Thr Leu Pro Ser Leu Ile Lys Leu Asp Leu Ser Ser Asn
            420                 425                 430

Leu Leu Ser Ser Phe Pro Ile Thr Gly Leu His Gly Leu Thr His Leu
        435                 440                 445

Lys Leu Thr Gly Asn His Ala Leu Gln Ser Leu Ile Ser Ser Glu Asn
    450                 455                 460

Phe Pro Glu Leu Lys Val Ile Glu Met Pro Tyr Ala Tyr Gln Cys Cys
465                 470                 475                 480
```

```
Ala Phe Gly Val Cys Glu Asn Ala Tyr Lys Ile Ser Asn Gln Trp Asn
                485                 490                 495

Lys Gly Asp Asn Ser Ser Met Asp Asp Leu His Lys Lys Asp Ala Gly
            500                 505                 510

Met Phe Gln Ala Gln Asp Glu Arg Asp Leu Glu Asp Phe Leu Leu Asp
        515                 520                 525

Phe Glu Glu Asp Leu Lys Ala Leu His Ser Val Gln Cys Ser Pro Ser
    530                 535                 540

Pro Gly Pro Phe Lys Pro Cys Glu His Leu Leu Asp Gly Trp Leu Ile
545                 550                 555                 560

Arg Ile Gly Val Trp Thr Ile Ala Val Leu Ala Leu Thr Cys Asn Ala
                565                 570                 575

Leu Val Thr Ser Thr Val Phe Arg Ser Pro Leu Tyr Ile Ser Pro Ile
            580                 585                 590

Lys Leu Leu Ile Gly Val Ile Ala Ala Val Asn Met Leu Thr Gly Val
        595                 600                 605

Ser Ser Ala Val Leu Ala Gly Val Asp Ala Phe Thr Phe Gly Ser Phe
    610                 615                 620

Ala Arg His Gly Ala Trp Trp Glu Asn Gly Val Gly Cys His Val Ile
625                 630                 635                 640

Gly Phe Leu Ser Ile Phe Ala Ser Glu Ser Ser Val Phe Leu Leu Thr
                645                 650                 655

Leu Ala Ala Leu Glu Arg Gly Phe Ser Val Lys Tyr Ser Ala Lys Phe
            660                 665                 670

Glu Thr Lys Ala Pro Phe Ser Ser Leu Lys Val Ile Ile Leu Leu Cys
        675                 680                 685

Ala Leu Leu Ala Leu Thr Met Ala Ala Val Pro Leu Leu Gly Gly Ser
    690                 695                 700

Lys Tyr Gly Ala Ser Pro Leu Cys Leu Pro Leu Pro Phe Gly Glu Pro
705                 710                 715                 720

Ser Thr Met Gly Tyr Met Val Ala Leu Ile Leu Leu Asn Ser Leu Cys
                725                 730                 735
```

```
Phe Leu Met Met Thr Ile Ala Tyr Thr Lys Leu Tyr Cys Asn Leu Asp
            740                 745                 750

Lys Gly Asp Leu Glu Asn Ile Trp Asp Cys Ser Met Val Lys His Ile
        755                 760                 765

Ala Leu Leu Leu Phe Thr Asn Cys Ile Leu Asn Cys Pro Val Ala Phe
    770                 775                 780

Leu Ser Phe Ser Ser Leu Ile Asn Leu Thr Phe Ile Ser Pro Glu Val
785                 790                 795                 800

Ile Lys Phe Ile Leu Leu Val Val Val Pro Leu Pro Ala Cys Leu Asn
                805                 810                 815

Pro Leu Leu Tyr Ile Leu Phe Asn Pro His Phe Lys Glu Asp Leu Val
            820                 825                 830

Ser Leu Arg Lys Gln Thr Tyr Val Trp Thr Arg Ser Lys His Pro Ser
        835                 840                 845

Leu Met Ser Ile Asn Ser Asp Asp Val Glu Lys Gln Ser Cys Asp Ser
    850                 855                 860

Thr Gln Ala Leu Val Thr Phe Thr Ser Ser Ser Ile Thr Tyr Asp Leu
865                 870                 875                 880

Pro Pro Ser Ser Val Pro Ser Pro Ala Tyr Pro Val Thr Glu Ser Cys
                885                 890                 895

His Leu Ser Ser Val Ala Phe Val Pro Cys Leu
            900                 905
```

<210> 68
<211> 886
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Human LgR5 mature, without signal sequence; amino acids 22 to 907

<400> 68

```
Gly Ser Ser Pro Arg Ser Gly Val Leu Leu Arg Gly Cys Pro Thr His
1               5                   10                  15

Cys His Cys Glu Pro Asp Gly Arg Met Leu Leu Arg Val Asp Cys Ser
```

```
            20                  25                  30

Asp Leu Gly Leu Ser Glu Leu Pro Ser Asn Leu Ser Val Phe Thr Ser
        35                  40                  45

Tyr Leu Asp Leu Ser Met Asn Asn Ile Ser Gln Leu Leu Pro Asn Pro
    50                  55                  60

Leu Pro Ser Leu Arg Phe Leu Glu Glu Leu Arg Leu Ala Gly Asn Ala
65                  70                  75                  80

Leu Thr Tyr Ile Pro Lys Gly Ala Phe Thr Gly Leu Tyr Ser Leu Lys
                85                  90                  95

Val Leu Met Leu Gln Asn Asn Gln Leu Arg His Val Pro Thr Glu Ala
            100                 105                 110

Leu Gln Asn Leu Arg Ser Leu Gln Ser Leu Arg Leu Asp Ala Asn His
        115                 120                 125

Ile Ser Tyr Val Pro Pro Ser Cys Phe Ser Gly Leu His Ser Leu Arg
    130                 135                 140

His Leu Trp Leu Asp Asp Asn Ala Leu Thr Glu Ile Pro Val Gln Ala
145                 150                 155                 160

Phe Arg Ser Leu Ser Ala Leu Gln Ala Met Thr Leu Ala Leu Asn Lys
                165                 170                 175

Ile His His Ile Pro Asp Tyr Ala Phe Gly Asn Leu Ser Ser Leu Val
            180                 185                 190

Val Leu His Leu His Asn Asn Arg Ile His Ser Leu Gly Lys Lys Cys
        195                 200                 205

Phe Asp Gly Leu His Ser Leu Glu Thr Leu Asp Leu Asn Tyr Asn Asn
    210                 215                 220

Leu Asp Glu Phe Pro Thr Ala Ile Arg Thr Leu Ser Asn Leu Lys Glu
225                 230                 235                 240

Leu Gly Phe His Ser Asn Asn Ile Arg Ser Ile Pro Glu Lys Ala Phe
                245                 250                 255

Val Gly Asn Pro Ser Leu Ile Thr Ile His Phe Tyr Asp Asn Pro Ile
            260                 265                 270
```

```
Gln Phe Val Gly Arg Ser Ala Phe Gln His Leu Pro Glu Leu Arg Thr
        275                 280                 285

Leu Thr Leu Asn Gly Ala Ser Gln Ile Thr Glu Phe Pro Asp Leu Thr
    290                 295                 300

Gly Thr Ala Asn Leu Glu Ser Leu Thr Leu Thr Gly Ala Gln Ile Ser
305                 310                 315                 320

Ser Leu Pro Gln Thr Val Cys Asn Gln Leu Pro Asn Leu Gln Val Leu
                325                 330                 335

Asp Leu Ser Tyr Asn Leu Leu Glu Asp Leu Pro Ser Phe Ser Val Cys
            340                 345                 350

Gln Lys Leu Gln Lys Ile Asp Leu Arg His Asn Glu Ile Tyr Glu Ile
        355                 360                 365

Lys Val Asp Thr Phe Gln Gln Leu Leu Ser Leu Arg Ser Leu Asn Leu
    370                 375                 380

Ala Trp Asn Lys Ile Ala Ile Ile His Pro Asn Ala Phe Ser Thr Leu
385                 390                 395                 400

Pro Ser Leu Ile Lys Leu Asp Leu Ser Ser Asn Leu Leu Ser Ser Phe
                405                 410                 415

Pro Ile Thr Gly Leu His Gly Leu Thr His Leu Lys Leu Thr Gly Asn
            420                 425                 430

His Ala Leu Gln Ser Leu Ile Ser Ser Glu Asn Phe Pro Glu Leu Lys
        435                 440                 445

Val Ile Glu Met Pro Tyr Ala Tyr Gln Cys Cys Ala Phe Gly Val Cys
    450                 455                 460

Glu Asn Ala Tyr Lys Ile Ser Asn Gln Trp Asn Lys Gly Asp Asn Ser
465                 470                 475                 480

Ser Met Asp Asp Leu His Lys Lys Asp Ala Gly Met Phe Gln Ala Gln
                485                 490                 495

Asp Glu Arg Asp Leu Glu Asp Phe Leu Leu Asp Phe Glu Glu Asp Leu
            500                 505                 510

Lys Ala Leu His Ser Val Gln Cys Ser Pro Ser Pro Gly Pro Phe Lys
        515                 520                 525
```

```
Pro Cys Glu His Leu Leu Asp Gly Trp Leu Ile Arg Ile Gly Val Trp
    530                 535                 540

Thr Ile Ala Val Leu Ala Leu Thr Cys Asn Ala Leu Val Thr Ser Thr
545                 550                 555                 560

Val Phe Arg Ser Pro Leu Tyr Ile Ser Pro Ile Lys Leu Leu Ile Gly
                565                 570                 575

Val Ile Ala Ala Val Asn Met Leu Thr Gly Val Ser Ser Ala Val Leu
            580                 585                 590

Ala Gly Val Asp Ala Phe Thr Phe Gly Ser Phe Ala Arg His Gly Ala
        595                 600                 605

Trp Trp Glu Asn Gly Val Gly Cys His Val Ile Gly Phe Leu Ser Ile
    610                 615                 620

Phe Ala Ser Glu Ser Ser Val Phe Leu Leu Thr Leu Ala Ala Leu Glu
625                 630                 635                 640

Arg Gly Phe Ser Val Lys Tyr Ser Ala Lys Phe Glu Thr Lys Ala Pro
                645                 650                 655

Phe Ser Ser Leu Lys Val Ile Ile Leu Leu Cys Ala Leu Leu Ala Leu
            660                 665                 670

Thr Met Ala Ala Val Pro Leu Leu Gly Gly Ser Lys Tyr Gly Ala Ser
        675                 680                 685

Pro Leu Cys Leu Pro Leu Pro Phe Gly Glu Pro Ser Thr Met Gly Tyr
    690                 695                 700

Met Val Ala Leu Ile Leu Leu Asn Ser Leu Cys Phe Leu Met Met Thr
705                 710                 715                 720

Ile Ala Tyr Thr Lys Leu Tyr Cys Asn Leu Asp Lys Gly Asp Leu Glu
                725                 730                 735

Asn Ile Trp Asp Cys Ser Met Val Lys His Ile Ala Leu Leu Leu Phe
            740                 745                 750

Thr Asn Cys Ile Leu Asn Cys Pro Val Ala Phe Leu Ser Phe Ser Ser
        755                 760                 765

Leu Ile Asn Leu Thr Phe Ile Ser Pro Glu Val Ile Lys Phe Ile Leu
    770                 775                 780
```

Leu Val Val Val Pro Leu Pro Ala Cys Leu Asn Pro Leu Leu Tyr Ile
785 790 795 800

Leu Phe Asn Pro His Phe Lys Glu Asp Leu Val Ser Leu Arg Lys Gln
805 810 815

Thr Tyr Val Trp Thr Arg Ser Lys His Pro Ser Leu Met Ser Ile Asn
820 825 830

Ser Asp Asp Val Glu Lys Gln Ser Cys Asp Ser Thr Gln Ala Leu Val
835 840 845

Thr Phe Thr Ser Ser Ser Ile Thr Tyr Asp Leu Pro Pro Ser Ser Val
850 855 860

Pro Ser Pro Ala Tyr Pro Val Thr Glu Ser Cys His Leu Ser Ser Val
865 870 875 880

Ala Phe Val Pro Cys Leu
885

<210> 69
<211> 875
<212> PRT
<213> M. cynomolgus

<220>
<221> misc_feature
<223> Cynomolgus monkey LgR5 partial sequence, predicted; predicted to correspond to amino acids 33 to 907 of full-length precursor

<400> 69

Gly Cys Pro Thr His Cys His Cys Glu Pro Asp Gly Arg Met Leu Leu
1 5 10 15

Arg Val Asp Cys Ser Asp Leu Gly Leu Ser Glu Leu Pro Ser Asn Leu
20 25 30

Ser Val Phe Thr Ser Tyr Leu Asp Leu Ser Met Asn Asn Ile Ser Gln
35 40 45

Leu Leu Pro Asn Pro Leu Pro Ser Leu Arg Phe Leu Glu Glu Leu Arg
50 55 60

Leu Ala Gly Asn Ala Leu Thr Tyr Ile Pro Lys Gly Ala Phe Thr Gly
65 70 75 80

```
Leu Tyr Ser Leu Lys Val Leu Met Leu Gln Asn Asn Gln Leu Arg Gln
                85                  90                  95

Val Pro Thr Glu Ala Leu Gln Asn Leu Arg Ser Leu Gln Ser Leu Arg
            100                 105                 110

Leu Asp Ala Asn His Ile Ser Tyr Val Pro Pro Ser Cys Phe Ser Gly
        115                 120                 125

Leu His Ser Leu Arg His Leu Trp Leu Asp Asp Asn Ala Leu Thr Glu
    130                 135                 140

Ile Pro Val Gln Ala Phe Arg Ser Leu Ser Ala Leu Gln Ala Met Thr
145                 150                 155                 160

Leu Ala Leu Asn Lys Ile His His Ile Pro Asp Tyr Ala Phe Gly Asn
                165                 170                 175

Leu Ser Ser Leu Val Val Leu His Leu His Asn Asn Arg Ile His Ser
            180                 185                 190

Leu Gly Lys Lys Cys Phe Asp Gly Leu His Ser Leu Glu Thr Leu Asp
        195                 200                 205

Leu Asn Tyr Asn Asn Leu Asp Glu Phe Pro Thr Ala Ile Arg Thr Leu
    210                 215                 220

Ser Asn Leu Lys Glu Leu Gly Phe His Ser Asn Asn Ile Arg Ser Ile
225                 230                 235                 240

Pro Glu Lys Ala Phe Val Gly Asn Pro Ser Leu Ile Thr Ile His Phe
                245                 250                 255

Tyr Asp Asn Pro Ile Gln Phe Val Gly Arg Ser Ala Phe Gln His Leu
            260                 265                 270

Pro Glu Leu Arg Thr Leu Thr Leu Asn Gly Ala Ser Gln Ile Thr Glu
        275                 280                 285

Phe Pro Asp Leu Thr Gly Thr Ala Asn Leu Glu Ser Leu Thr Leu Thr
    290                 295                 300

Gly Ala Gln Ile Ser Ser Leu Pro Gln Thr Val Cys Asn Gln Leu Pro
305                 310                 315                 320

Asn Leu Gln Val Leu Asp Leu Ser Tyr Asn Leu Leu Glu Asp Leu Pro
                325                 330                 335
```

```
Ser Phe Ser Val Cys Gln Lys Leu Gln Lys Ile Asp Leu Arg His Asn
            340                 345                 350

Glu Ile Tyr Glu Ile Lys Val Asp Thr Phe Gln Gln Leu Leu Ser Leu
        355                 360                 365

Arg Ser Leu Asn Leu Ala Trp Asn Lys Ile Ala Ile Ile His Pro Asn
    370                 375                 380

Ala Phe Ser Thr Leu Pro Ser Leu Ile Lys Leu Asp Leu Ser Ser Asn
385                 390                 395                 400

Leu Leu Ser Ser Phe Pro Val Thr Gly Leu His Gly Leu Thr His Leu
                405                 410                 415

Lys Leu Thr Gly Asn His Ala Leu Gln Ser Leu Ile Ser Ser Glu Asn
            420                 425                 430

Phe Pro Glu Leu Lys Ile Ile Glu Met Pro Tyr Ala Tyr Gln Cys Cys
        435                 440                 445

Ala Phe Gly Val Cys Glu Asn Ala Tyr Lys Ile Ser Asn Gln Trp Asn
    450                 455                 460

Lys Gly Asp Asn Ser Ser Met Asp Asp Leu His Lys Lys Asp Ala Gly
465                 470                 475                 480

Met Phe Gln Val Gln Asp Glu Arg Asp Leu Glu Asp Phe Leu Leu Asp
                485                 490                 495

Phe Glu Glu Asp Leu Lys Ala Leu His Ser Val Gln Cys Ser Pro Ser
            500                 505                 510

Pro Gly Pro Phe Lys Pro Cys Glu His Leu Leu Asp Gly Trp Leu Ile
        515                 520                 525

Arg Ile Gly Val Trp Thr Ile Ala Val Leu Ala Leu Thr Cys Asn Ala
    530                 535                 540

Leu Val Thr Ser Thr Val Phe Arg Ser Pro Leu Tyr Ile Ser Pro Ile
545                 550                 555                 560

Lys Leu Leu Ile Gly Val Ile Ala Val Val Asn Met Leu Thr Gly Val
                565                 570                 575

Ser Ser Ala Val Leu Ala Gly Val Asp Ala Phe Thr Phe Gly Ser Phe
            580                 585                 590
```

```
Ala Arg His Gly Ala Trp Trp Glu Asn Gly Val Gly Cys Gln Val Ile
        595                 600                 605

Gly Phe Leu Ser Ile Phe Ala Ser Glu Ser Ser Val Phe Leu Leu Thr
    610                 615                 620

Leu Ala Ala Leu Glu Arg Gly Phe Ser Val Lys Cys Ser Ala Lys Phe
625                 630                 635                 640

Glu Thr Lys Ala Pro Phe Ser Ser Leu Lys Val Ile Ile Leu Leu Cys
                645                 650                 655

Ala Leu Leu Ala Leu Thr Met Ala Ala Val Pro Leu Leu Gly Gly Ser
            660                 665                 670

Glu Tyr Gly Ala Ser Pro Leu Cys Leu Pro Leu Pro Phe Gly Glu Pro
        675                 680                 685

Ser Thr Thr Gly Tyr Met Val Ala Leu Ile Leu Leu Asn Ser Leu Cys
    690                 695                 700

Phe Leu Met Met Thr Ile Ala Tyr Thr Lys Leu Tyr Cys Asn Leu Asp
705                 710                 715                 720

Lys Gly Asp Leu Glu Asn Ile Trp Asp Cys Ser Met Val Lys His Ile
                725                 730                 735

Ala Leu Leu Leu Phe Thr Asn Cys Ile Leu Tyr Cys Pro Val Ala Phe
            740                 745                 750

Leu Ser Phe Ser Ser Leu Leu Asn Leu Thr Phe Ile Ser Pro Glu Val
        755                 760                 765

Ile Lys Phe Ile Leu Leu Val Ile Val Pro Leu Pro Ala Cys Leu Asn
    770                 775                 780

Pro Leu Leu Tyr Ile Leu Phe Asn Pro His Phe Lys Glu Asp Leu Val
785                 790                 795                 800

Ser Leu Gly Lys Gln Thr Tyr Phe Trp Thr Arg Ser Lys His Pro Ser
                805                 810                 815

Leu Met Ser Ile Asn Ser Asp Asp Val Glu Lys Gln Ser Cys Asp Ser
            820                 825                 830

Thr Gln Ala Leu Val Thr Phe Thr Ser Ser Ser Ile Ala Tyr Asp Leu
```

835 840 845

Pro Pro Ser Ser Val Pro Ser Pro Ala Tyr Pro Val Thr Glu Ser Cys
850 855 860

His Leu Ser Ser Val Ala Phe Val Pro Cys Leu
865 870 875

<210> 70
<211> 907
<212> PRT
<213> Rattus sp.

<220>
<221> misc_feature
<223> Rat LgR5 precursor; LGR5_rat NP_001100254; signal sequence = amino acids 1-21

<400> 70

Met Asp Thr Ser Arg Val Arg Met Leu Leu Ser Leu Leu Ala Leu Leu
1 5 10 15

Gln Leu Val Ala Ala Gly Ser Pro Pro Arg Pro Asp Thr Met Pro Arg
20 25 30

Gly Cys Pro Ser Tyr Cys His Cys Glu Leu Asp Gly Arg Met Leu Leu
35 40 45

Arg Val Asp Cys Ser Asp Leu Gly Leu Ser Glu Leu Pro Ser Asn Leu
50 55 60

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

Leu Pro Ala Ser Leu Leu His Arg Leu Arg Phe Leu Glu Glu Leu Arg
85 90 95

Leu Ala Gly Asn Ala Leu Thr His Ile Pro Lys Gly Ala Phe Ala Gly
100 105 110

Leu His Ser Leu Lys Val Leu Met Leu Gln Asn Asn Gln Leu Arg Gln
115 120 125

Val Pro Glu Glu Ala Leu Gln Asn Leu Arg Ser Leu Gln Ser Leu Arg
130 135 140

Leu Asp Ala Asn His Ile Ser Tyr Val Pro Pro Ser Cys Phe Ser Gly
145 150 155 160

```
Leu His Ser Leu Arg His Leu Trp Leu Asp Asp Asn Ala Leu Thr Asp
                165                 170                 175

Val Pro Val Gln Ala Phe Arg Ser Leu Ser Ala Leu Gln Ala Met Thr
            180                 185                 190

Leu Ala Leu Asn Lys Ile His His Ile Ala Asp His Ala Phe Gly Asn
        195                 200                 205

Leu Ser Ser Leu Val Val Leu His Leu His Asn Asn Arg Ile His Ser
    210                 215                 220

Leu Gly Lys Lys Cys Phe Asp Gly Leu His Ser Leu Glu Thr Leu Asp
225                 230                 235                 240

Leu Asn Tyr Asn Asn Leu Asp Glu Phe Pro Thr Ala Ile Lys Thr Leu
                245                 250                 255

Ser Asn Leu Lys Glu Leu Gly Phe His Ser Asn Asn Ile Arg Ser Ile
            260                 265                 270

Pro Glu Arg Ala Phe Val Gly Asn Pro Ser Leu Ile Thr Ile His Phe
        275                 280                 285

Tyr Asp Asn Pro Ile Gln Phe Val Gly Ile Ser Ala Phe Gln His Leu
    290                 295                 300

Pro Glu Leu Arg Thr Leu Thr Leu Asn Gly Ala Ser Gln Ile Thr Glu
305                 310                 315                 320

Phe Pro Asp Leu Thr Gly Thr Ala Thr Leu Glu Ser Leu Thr Leu Thr
                325                 330                 335

Gly Ala Lys Ile Ser Ser Leu Pro Gln Thr Val Cys Asp Gln Leu Pro
            340                 345                 350

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

Ser Leu Ser Gly Cys Gln Lys Leu Gln Lys Ile Asp Leu Arg His Asn
    370                 375                 380

Glu Ile Tyr Glu Ile Lys Gly Gly Thr Phe Gln Gln Leu Phe Asn Leu
385                 390                 395                 400

Arg Ser Leu Asn Leu Ala Arg Asn Lys Ile Ala Ile Ile His Pro Asn
                405                 410                 415
```

```
Ala Phe Ser Thr Leu Pro Ser Leu Ile Lys Leu Asp Leu Ser Ser Asn
            420                 425                 430

Leu Leu Ser Ser Phe Pro Val Thr Gly Leu His Gly Leu Thr His Leu
        435                 440                 445

Lys Leu Thr Gly Asn Arg Ala Leu Gln Ser Leu Ile Pro Ser Ala Asn
    450                 455                 460

Phe Pro Glu Leu Lys Ile Ile Glu Met Pro Tyr Ala Tyr Gln Cys Cys
465                 470                 475                 480

Ala Phe Gly Gly Cys Glu Asn Val Tyr Lys Ile Pro Asn Gln Trp Asn
                485                 490                 495

Lys Asp Asp Ser Ser Ser Val Asp Asp Leu Arg Lys Lys Asp Ala Gly
            500                 505                 510

Leu Phe Gln Val Gln Asp Glu Arg Asp Leu Glu Asp Phe Leu Leu Asp
        515                 520                 525

Phe Glu Glu Asp Leu Lys Val Leu His Ser Val Gln Cys Ser Pro Pro
    530                 535                 540

Pro Gly Pro Phe Lys Pro Cys Glu His Leu Phe Gly Ser Trp Leu Ile
545                 550                 555                 560

Arg Ile Gly Val Trp Thr Thr Ala Val Leu Ala Leu Ser Cys Asn Ala
                565                 570                 575

Leu Val Ala Phe Thr Val Phe Arg Thr Pro Leu Tyr Ile Ser Ser Ile
            580                 585                 590

Lys Leu Leu Ile Gly Val Ile Ala Val Val Asp Ile Leu Met Gly Val
        595                 600                 605

Ser Ser Ala Ile Leu Ala Val Val Asp Thr Phe Thr Phe Gly Ser Phe
    610                 615                 620

Ala Gln His Gly Ala Trp Trp Glu Gly Gly Ile Gly Cys Gln Ile Val
625                 630                 635                 640

Gly Phe Leu Ser Ile Phe Ala Ser Glu Ser Ser Val Phe Leu Leu Thr
                645                 650                 655

Leu Ala Ala Leu Glu Arg Gly Phe Ser Val Lys Cys Ser Ser Lys Phe
```

660 665 670

Glu Met Lys Ala Pro Leu Ser Ser Leu Lys Ala Ile Ile Leu Leu Cys
675 680 685

Val Leu Leu Ala Leu Thr Ile Ala Thr Val Pro Leu Leu Gly Gly Ser
690 695 700

Glu Tyr Asn Ala Ser Pro Leu Cys Leu Pro Leu Pro Phe Gly Glu Pro
705 710 715 720

Ser Thr Thr Gly Tyr Met Val Ala Leu Val Leu Leu Asn Ser Leu Cys
725 730 735

Phe Leu Ile Met Thr Ile Ala Tyr Thr Arg Leu Tyr Cys Ser Leu Glu
740 745 750

Lys Gly Glu Leu Glu Asn Leu Trp Asp Cys Ser Met Val Lys His Thr
755 760 765

Ala Leu Leu Leu Phe Thr Asn Cys Ile Leu Tyr Cys Pro Val Ala Phe
770 775 780

Leu Ser Phe Ser Ser Leu Leu Asn Leu Thr Phe Ile Ser Pro Glu Val
785 790 795 800

Ile Lys Phe Ile Leu Leu Val Ile Val Pro Leu Pro Ala Cys Leu Asn
805 810 815

Pro Leu Leu Tyr Ile Val Phe Asn Pro His Phe Lys Glu Asp Met Gly
820 825 830

Ser Leu Gly Lys Gln Thr Arg Phe Trp Thr Arg Ala Lys His Pro Ser
835 840 845

Leu Leu Ser Ile Asn Ser Asp Asp Val Glu Lys Arg Ser Cys Asp Ser
850 855 860

Thr Gln Ala Leu Val Ser Phe Thr His Ala Ser Ile Ala Tyr Asp Leu
865 870 875 880

Pro Ser Asp Ser Gly Ser Ser Pro Ala Tyr Pro Met Thr Glu Ser Cys
885 890 895

His Leu Ser Ser Val Ala Phe Val Pro Cys Leu
900 905

<210> 71
<211> 886
<212> PRT
<213> Rattus sp.

<220>
<221> misc_feature
<223> Rat LgR5 mature, without signal sequence; amino acids 22 to 907

<400> 71

Gly Ser Pro Pro Arg Pro Asp Thr Met Pro Arg Gly Cys Pro Ser Tyr
1 5 10 15

Cys His Cys Glu Leu Asp Gly Arg Met Leu Leu Arg Val Asp Cys Ser
20 25 30

Asp Leu Gly Leu Ser Glu Leu Pro Ser Asn Leu Ser Val Phe Thr Ser
35 40 45

Tyr Leu Asp Leu Ser Met Asn Asn Ile Ser Gln Leu Pro Ala Ser Leu
50 55 60

Leu His Arg Leu Arg Phe Leu Glu Glu Leu Arg Leu Ala Gly Asn Ala
65 70 75 80

Leu Thr His Ile Pro Lys Gly Ala Phe Ala Gly Leu His Ser Leu Lys
85 90 95

Val Leu Met Leu Gln Asn Asn Gln Leu Arg Gln Val Pro Glu Glu Ala
100 105 110

Leu Gln Asn Leu Arg Ser Leu Gln Ser Leu Arg Leu Asp Ala Asn His
115 120 125

Ile Ser Tyr Val Pro Pro Ser Cys Phe Ser Gly Leu His Ser Leu Arg
130 135 140

His Leu Trp Leu Asp Asp Asn Ala Leu Thr Asp Val Pro Val Gln Ala
145 150 155 160

Phe Arg Ser Leu Ser Ala Leu Gln Ala Met Thr Leu Ala Leu Asn Lys
165 170 175

Ile His His Ile Ala Asp His Ala Phe Gly Asn Leu Ser Ser Leu Val
180 185 190

Val Leu His Leu His Asn Asn Arg Ile His Ser Leu Gly Lys Lys Cys
195 200 205

```
Phe Asp Gly Leu His Ser Leu Glu Thr Leu Asp Leu Asn Tyr Asn Asn
    210                 215                 220

Leu Asp Glu Phe Pro Thr Ala Ile Lys Thr Leu Ser Asn Leu Lys Glu
225                 230                 235                 240

Leu Gly Phe His Ser Asn Asn Ile Arg Ser Ile Pro Glu Arg Ala Phe
                245                 250                 255

Val Gly Asn Pro Ser Leu Ile Thr Ile His Phe Tyr Asp Asn Pro Ile
            260                 265                 270

Gln Phe Val Gly Ile Ser Ala Phe Gln His Leu Pro Glu Leu Arg Thr
        275                 280                 285

Leu Thr Leu Asn Gly Ala Ser Gln Ile Thr Glu Phe Pro Asp Leu Thr
    290                 295                 300

Gly Thr Ala Thr Leu Glu Ser Leu Thr Leu Thr Gly Ala Lys Ile Ser
305                 310                 315                 320

Ser Leu Pro Gln Thr Val Cys Asp Gln Leu Pro Asn Leu Gln Val Leu
                325                 330                 335

Asp Leu Ser Tyr Asn Leu Leu Glu Asp Leu Pro Ser Leu Ser Gly Cys
            340                 345                 350

Gln Lys Leu Gln Lys Ile Asp Leu Arg His Asn Glu Ile Tyr Glu Ile
        355                 360                 365

Lys Gly Gly Thr Phe Gln Gln Leu Phe Asn Leu Arg Ser Leu Asn Leu
    370                 375                 380

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

Pro Ser Leu Ile Lys Leu Asp Leu Ser Ser Asn Leu Leu Ser Ser Phe
                405                 410                 415

Pro Val Thr Gly Leu His Gly Leu Thr His Leu Lys Leu Thr Gly Asn
            420                 425                 430

Arg Ala Leu Gln Ser Leu Ile Pro Ser Ala Asn Phe Pro Glu Leu Lys
        435                 440                 445

Ile Ile Glu Met Pro Tyr Ala Tyr Gln Cys Cys Ala Phe Gly Gly Cys
    450                 455                 460
```

```
Glu Asn Val Tyr Lys Ile Pro Asn Gln Trp Asn Lys Asp Asp Ser Ser
465                 470                 475                 480

Ser Val Asp Asp Leu Arg Lys Lys Asp Ala Gly Leu Phe Gln Val Gln
                485                 490                 495

Asp Glu Arg Asp Leu Glu Asp Phe Leu Leu Asp Phe Glu Glu Asp Leu
            500                 505                 510

Lys Val Leu His Ser Val Gln Cys Ser Pro Pro Pro Gly Pro Phe Lys
        515                 520                 525

Pro Cys Glu His Leu Phe Gly Ser Trp Leu Ile Arg Ile Gly Val Trp
    530                 535                 540

Thr Thr Ala Val Leu Ala Leu Ser Cys Asn Ala Leu Val Ala Phe Thr
545                 550                 555                 560

Val Phe Arg Thr Pro Leu Tyr Ile Ser Ser Ile Lys Leu Leu Ile Gly
                565                 570                 575

Val Ile Ala Val Val Asp Ile Leu Met Gly Val Ser Ser Ala Ile Leu
            580                 585                 590

Ala Val Val Asp Thr Phe Thr Phe Gly Ser Phe Ala Gln His Gly Ala
        595                 600                 605

Trp Trp Glu Gly Gly Ile Gly Cys Gln Ile Val Gly Phe Leu Ser Ile
    610                 615                 620

Phe Ala Ser Glu Ser Ser Val Phe Leu Leu Thr Leu Ala Ala Leu Glu
625                 630                 635                 640

Arg Gly Phe Ser Val Lys Cys Ser Ser Lys Phe Glu Met Lys Ala Pro
                645                 650                 655

Leu Ser Ser Leu Lys Ala Ile Ile Leu Leu Cys Val Leu Leu Ala Leu
            660                 665                 670

Thr Ile Ala Thr Val Pro Leu Leu Gly Gly Ser Glu Tyr Asn Ala Ser
        675                 680                 685

Pro Leu Cys Leu Pro Leu Pro Phe Gly Glu Pro Ser Thr Thr Gly Tyr
    690                 695                 700

Met Val Ala Leu Val Leu Leu Asn Ser Leu Cys Phe Leu Ile Met Thr
```

705 710 715 720

Ile Ala Tyr Thr Arg Leu Tyr Cys Ser Leu Glu Lys Gly Glu Leu Glu
725 730 735

Asn Leu Trp Asp Cys Ser Met Val Lys His Thr Ala Leu Leu Leu Phe
740 745 750

Thr Asn Cys Ile Leu Tyr Cys Pro Val Ala Phe Leu Ser Phe Ser Ser
755 760 765

Leu Leu Asn Leu Thr Phe Ile Ser Pro Glu Val Ile Lys Phe Ile Leu
770 775 780

Leu Val Ile Val Pro Leu Pro Ala Cys Leu Asn Pro Leu Leu Tyr Ile
785 790 795 800

Val Phe Asn Pro His Phe Lys Glu Asp Met Gly Ser Leu Gly Lys Gln
805 810 815

Thr Arg Phe Trp Thr Arg Ala Lys His Pro Ser Leu Leu Ser Ile Asn
820 825 830

Ser Asp Asp Val Glu Lys Arg Ser Cys Asp Ser Thr Gln Ala Leu Val
835 840 845

Ser Phe Thr His Ala Ser Ile Ala Tyr Asp Leu Pro Ser Asp Ser Gly
850 855 860

Ser Ser Pro Ala Tyr Pro Met Thr Glu Ser Cys His Leu Ser Ser Val
865 870 875 880

Ala Phe Val Pro Cys Leu
885

<210> 72
<211> 907
<212> PRT
<213> Mus musculus

<220>
<221> misc_feature
<223> Mouse LgR5 precursor; LGR5_mouse NP_034325; signal sequence = amino acids 1-21

<400> 72

Met Asp Thr Ser Cys Val His Met Leu Leu Ser Leu Leu Ala Leu Leu
1 5 10 15

```
Gln Leu Val Ala Ala Gly Ser Ser Pro Gly Pro Asp Ala Ile Pro Arg
            20                  25                  30

Gly Cys Pro Ser His Cys His Cys Glu Leu Asp Gly Arg Met Leu Leu
        35                  40                  45

Arg Val Asp Cys Ser Asp Leu Gly Leu Ser Glu Leu Pro Ser Asn Leu
    50                  55                  60

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

Leu Pro Ala Ser Leu Leu His Arg Leu Cys Phe Leu Glu Glu Leu Arg
                85                  90                  95

Leu Ala Gly Asn Ala Leu Thr His Ile Pro Lys Gly Ala Phe Thr Gly
            100                 105                 110

Leu His Ser Leu Lys Val Leu Met Leu Gln Asn Asn Gln Leu Arg Gln
        115                 120                 125

Val Pro Glu Glu Ala Leu Gln Asn Leu Arg Ser Leu Gln Ser Leu Arg
    130                 135                 140

Leu Asp Ala Asn His Ile Ser Tyr Val Pro Pro Ser Cys Phe Ser Gly
145                 150                 155                 160

Leu His Ser Leu Arg His Leu Trp Leu Asp Asp Asn Ala Leu Thr Asp
                165                 170                 175

Val Pro Val Gln Ala Phe Arg Ser Leu Ser Ala Leu Gln Ala Met Thr
            180                 185                 190

Leu Ala Leu Asn Lys Ile His His Ile Ala Asp Tyr Ala Phe Gly Asn
        195                 200                 205

Leu Ser Ser Leu Val Val Leu His Leu His Asn Asn Arg Ile His Ser
    210                 215                 220

Leu Gly Lys Lys Cys Phe Asp Gly Leu His Ser Leu Glu Thr Leu Asp
225                 230                 235                 240

Leu Asn Tyr Asn Asn Leu Asp Glu Phe Pro Thr Ala Ile Lys Thr Leu
                245                 250                 255

Ser Asn Leu Lys Glu Leu Gly Phe His Ser Asn Asn Ile Arg Ser Ile
            260                 265                 270
```

```
Pro Glu Arg Ala Phe Val Gly Asn Pro Ser Leu Ile Thr Ile His Phe
        275                 280                 285

Tyr Asp Asn Pro Ile Gln Phe Val Gly Val Ser Ala Phe Gln His Leu
    290                 295                 300

Pro Glu Leu Arg Thr Leu Thr Leu Asn Gly Ala Ser His Ile Thr Glu
305                 310                 315                 320

Phe Pro His Leu Thr Gly Thr Ala Thr Leu Glu Ser Leu Thr Leu Thr
                325                 330                 335

Gly Ala Lys Ile Ser Ser Leu Pro Gln Ala Val Cys Asp Gln Leu Pro
            340                 345                 350

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

Ser Leu Ser Gly Cys Gln Lys Leu Gln Lys Ile Asp Leu Arg His Asn
    370                 375                 380

Glu Ile Tyr Glu Ile Lys Gly Ser Thr Phe Gln Gln Leu Phe Asn Leu
385                 390                 395                 400

Arg Ser Leu Asn Leu Ala Trp Asn Lys Ile Ala Ile Ile His Pro Asn
                405                 410                 415

Ala Phe Ser Thr Leu Pro Ser Leu Ile Lys Leu Asp Leu Ser Ser Asn
            420                 425                 430

Leu Leu Ser Ser Phe Pro Val Thr Gly Leu His Gly Leu Thr His Leu
        435                 440                 445

Lys Leu Thr Gly Asn Arg Ala Leu Gln Ser Leu Ile Pro Ser Ala Asn
    450                 455                 460

Phe Pro Glu Leu Lys Ile Ile Glu Met Pro Ser Ala Tyr Gln Cys Cys
465                 470                 475                 480

Ala Phe Gly Gly Cys Glu Asn Val Tyr Lys Ile Ser Asn Gln Trp Asn
                485                 490                 495

Lys Asp Asp Gly Asn Ser Val Asp Asp Leu His Lys Lys Asp Ala Gly
            500                 505                 510

Leu Phe Gln Val Gln Asp Glu Arg Asp Leu Glu Asp Phe Leu Leu Asp
```

515 520 525

Phe Glu Glu Asp Leu Lys Ala Leu His Ser Val Gln Cys Ser Pro Ser
530 535 540

Pro Gly Pro Phe Lys Pro Cys Glu His Leu Phe Gly Ser Trp Leu Ile
545 550 555 560

Arg Ile Gly Val Trp Thr Thr Ala Val Leu Ala Leu Ser Cys Asn Ala
565 570 575

Leu Val Ala Leu Thr Val Phe Arg Thr Pro Leu Tyr Ile Ser Ser Ile
580 585 590

Lys Leu Leu Ile Gly Val Ile Ala Val Val Asp Ile Leu Met Gly Val
595 600 605

Ser Ser Ala Val Leu Ala Ala Val Asp Ala Phe Thr Phe Gly Arg Phe
610 615 620

Ala Gln His Gly Ala Trp Trp Glu Asp Gly Ile Gly Cys Gln Ile Val
625 630 635 640

Gly Phe Leu Ser Ile Phe Ala Ser Glu Ser Ser Ile Phe Leu Leu Thr
645 650 655

Leu Ala Ala Leu Glu Arg Gly Phe Ser Val Lys Cys Ser Ser Lys Phe
660 665 670

Glu Val Lys Ala Pro Leu Phe Ser Leu Arg Ala Ile Val Leu Leu Cys
675 680 685

Val Leu Leu Ala Leu Thr Ile Ala Thr Ile Pro Leu Leu Gly Gly Ser
690 695 700

Lys Tyr Asn Ala Ser Pro Leu Cys Leu Pro Leu Pro Phe Gly Glu Pro
705 710 715 720

Ser Thr Thr Gly Tyr Met Val Ala Leu Val Leu Leu Asn Ser Leu Cys
725 730 735

Phe Leu Ile Met Thr Ile Ala Tyr Thr Lys Leu Tyr Cys Ser Leu Glu
740 745 750

Lys Gly Glu Leu Glu Asn Leu Trp Asp Cys Ser Met Val Lys His Ile
755 760 765

Ala Leu Leu Leu Phe Ala Asn Cys Ile Leu Tyr Cys Pro Val Ala Phe
770 775 780

Leu Ser Phe Ser Ser Leu Leu Asn Leu Thr Phe Ile Ser Pro Asp Val
785 790 795 800

Ile Lys Phe Ile Leu Leu Val Ile Val Pro Leu Pro Ser Cys Leu Asn
805 810 815

Pro Leu Leu Tyr Ile Val Phe Asn Pro His Phe Lys Glu Asp Met Gly
820 825 830

Ser Leu Gly Lys His Thr Arg Phe Trp Met Arg Ser Lys His Ala Ser
835 840 845

Leu Leu Ser Ile Asn Ser Asp Asp Val Glu Lys Arg Ser Cys Glu Ser
850 855 860

Thr Gln Ala Leu Val Ser Phe Thr His Ala Ser Ile Ala Tyr Asp Leu
865 870 875 880

Pro Ser Thr Ser Gly Ala Ser Pro Ala Tyr Pro Met Thr Glu Ser Cys
885 890 895

His Leu Ser Ser Val Ala Phe Val Pro Cys Leu
900 905

<210> 73
<211> 886
<212> PRT
<213> Mus musculus

<220>
<221> misc_feature
<223> Mouse LgR5 mature, without signal sequence; amino acids 22 to 907

<400> 73

Gly Ser Ser Pro Gly Pro Asp Ala Ile Pro Arg Gly Cys Pro Ser His
1 5 10 15

Cys His Cys Glu Leu Asp Gly Arg Met Leu Leu Arg Val Asp Cys Ser
20 25 30

Asp Leu Gly Leu Ser Glu Leu Pro Ser Asn Leu Ser Val Phe Thr Ser
35 40 45

Tyr Leu Asp Leu Ser Met Asn Asn Ile Ser Gln Leu Pro Ala Ser Leu
50 55 60

```
Leu His Arg Leu Cys Phe Leu Glu Glu Leu Arg Leu Ala Gly Asn Ala
65                  70                  75                  80

Leu Thr His Ile Pro Lys Gly Ala Phe Thr Gly Leu His Ser Leu Lys
                85                  90                  95

Val Leu Met Leu Gln Asn Asn Gln Leu Arg Gln Val Pro Glu Glu Ala
            100                 105                 110

Leu Gln Asn Leu Arg Ser Leu Gln Ser Leu Arg Leu Asp Ala Asn His
        115                 120                 125

Ile Ser Tyr Val Pro Pro Ser Cys Phe Ser Gly Leu His Ser Leu Arg
    130                 135                 140

His Leu Trp Leu Asp Asp Asn Ala Leu Thr Asp Val Pro Val Gln Ala
145                 150                 155                 160

Phe Arg Ser Leu Ser Ala Leu Gln Ala Met Thr Leu Ala Leu Asn Lys
                165                 170                 175

Ile His His Ile Ala Asp Tyr Ala Phe Gly Asn Leu Ser Ser Leu Val
            180                 185                 190

Val Leu His Leu His Asn Asn Arg Ile His Ser Leu Gly Lys Lys Cys
        195                 200                 205

Phe Asp Gly Leu His Ser Leu Glu Thr Leu Asp Leu Asn Tyr Asn Asn
    210                 215                 220

Leu Asp Glu Phe Pro Thr Ala Ile Lys Thr Leu Ser Asn Leu Lys Glu
225                 230                 235                 240

Leu Gly Phe His Ser Asn Asn Ile Arg Ser Ile Pro Glu Arg Ala Phe
                245                 250                 255

Val Gly Asn Pro Ser Leu Ile Thr Ile His Phe Tyr Asp Asn Pro Ile
            260                 265                 270

Gln Phe Val Gly Val Ser Ala Phe Gln His Leu Pro Glu Leu Arg Thr
        275                 280                 285

Leu Thr Leu Asn Gly Ala Ser His Ile Thr Glu Phe Pro His Leu Thr
    290                 295                 300

Gly Thr Ala Thr Leu Glu Ser Leu Thr Leu Thr Gly Ala Lys Ile Ser
305                 310                 315                 320
```

```
Ser Leu Pro Gln Ala Val Cys Asp Gln Leu Pro Asn Leu Gln Val Leu
                325                 330                 335

Asp Leu Ser Tyr Asn Leu Leu Glu Asp Leu Pro Ser Leu Ser Gly Cys
            340                 345                 350

Gln Lys Leu Gln Lys Ile Asp Leu Arg His Asn Glu Ile Tyr Glu Ile
        355                 360                 365

Lys Gly Ser Thr Phe Gln Gln Leu Phe Asn Leu Arg Ser Leu Asn Leu
    370                 375                 380

Ala Trp Asn Lys Ile Ala Ile Ile His Pro Asn Ala Phe Ser Thr Leu
385                 390                 395                 400

Pro Ser Leu Ile Lys Leu Asp Leu Ser Ser Asn Leu Leu Ser Ser Phe
                405                 410                 415

Pro Val Thr Gly Leu His Gly Leu Thr His Leu Lys Leu Thr Gly Asn
            420                 425                 430

Arg Ala Leu Gln Ser Leu Ile Pro Ser Ala Asn Phe Pro Glu Leu Lys
        435                 440                 445

Ile Ile Glu Met Pro Ser Ala Tyr Gln Cys Cys Ala Phe Gly Gly Cys
    450                 455                 460

Glu Asn Val Tyr Lys Ile Ser Asn Gln Trp Asn Lys Asp Asp Gly Asn
465                 470                 475                 480

Ser Val Asp Asp Leu His Lys Lys Asp Ala Gly Leu Phe Gln Val Gln
                485                 490                 495

Asp Glu Arg Asp Leu Glu Asp Phe Leu Leu Asp Phe Glu Glu Asp Leu
            500                 505                 510

Lys Ala Leu His Ser Val Gln Cys Ser Pro Ser Pro Gly Pro Phe Lys
        515                 520                 525

Pro Cys Glu His Leu Phe Gly Ser Trp Leu Ile Arg Ile Gly Val Trp
    530                 535                 540

Thr Thr Ala Val Leu Ala Leu Ser Cys Asn Ala Leu Val Ala Leu Thr
545                 550                 555                 560

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

565 570 575

Val Ile Ala Val Val Asp Ile Leu Met Gly Val Ser Ser Ala Val Leu
580 585 590

Ala Ala Val Asp Ala Phe Thr Phe Gly Arg Phe Ala Gln His Gly Ala
595 600 605

Trp Trp Glu Asp Gly Ile Gly Cys Gln Ile Val Gly Phe Leu Ser Ile
610 615 620

Phe Ala Ser Glu Ser Ser Ile Phe Leu Leu Thr Leu Ala Ala Leu Glu
625 630 635 640

Arg Gly Phe Ser Val Lys Cys Ser Ser Lys Phe Glu Val Lys Ala Pro
645 650 655

Leu Phe Ser Leu Arg Ala Ile Val Leu Leu Cys Val Leu Leu Ala Leu
660 665 670

Thr Ile Ala Thr Ile Pro Leu Leu Gly Gly Ser Lys Tyr Asn Ala Ser
675 680 685

Pro Leu Cys Leu Pro Leu Pro Phe Gly Glu Pro Ser Thr Thr Gly Tyr
690 695 700

Met Val Ala Leu Val Leu Leu Asn Ser Leu Cys Phe Leu Ile Met Thr
705 710 715 720

Ile Ala Tyr Thr Lys Leu Tyr Cys Ser Leu Glu Lys Gly Glu Leu Glu
725 730 735

Asn Leu Trp Asp Cys Ser Met Val Lys His Ile Ala Leu Leu Leu Phe
740 745 750

Ala Asn Cys Ile Leu Tyr Cys Pro Val Ala Phe Leu Ser Phe Ser Ser
755 760 765

Leu Leu Asn Leu Thr Phe Ile Ser Pro Asp Val Ile Lys Phe Ile Leu
770 775 780

Leu Val Ile Val Pro Leu Pro Ser Cys Leu Asn Pro Leu Leu Tyr Ile
785 790 795 800

Val Phe Asn Pro His Phe Lys Glu Asp Met Gly Ser Leu Gly Lys His
805 810 815

Thr Arg Phe Trp Met Arg Ser Lys His Ala Ser Leu Leu Ser Ile Asn
820 825 830

Ser Asp Asp Val Glu Lys Arg Ser Cys Glu Ser Thr Gln Ala Leu Val
835 840 845

Ser Phe Thr His Ala Ser Ile Ala Tyr Asp Leu Pro Ser Thr Ser Gly
850 855 860

Ala Ser Pro Ala Tyr Pro Met Thr Glu Ser Cys His Leu Ser Ser Val
865 870 875 880

Ala Phe Val Pro Cys Leu
885

<210> 74
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: hu8E11.v2 V205C cysteine engineered light chain (Igk)

<400> 74

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

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

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

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

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

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

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

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
115 120 125

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

130 135 140

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

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

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

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

Cys Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 75
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: hu8E11.v2 A118C cysteine engineered heavy chain (IgG1)

<400> 75

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

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

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

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

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

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

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

Leu Val Thr Val Ser Ser Cys 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 Glu Glu Met 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 Lys
435 440 445

<210> 76
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: hu8E11.v2 S400C cysteine engineered heavy chain (IgG1)

<400> 76

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

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

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

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

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

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

Ala Arg Gly Gly His Tyr Gly Ser Leu 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 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 Glu Glu Met 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

Cys 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 Lys
435 440 445

<210> 77
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: YW353 V205C cysteine engineered light chain (Igk)

<400> 77

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Ser 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 Phe Leu Tyr 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 Ser Tyr Thr Thr Pro Pro
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 Cys Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 78
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: YW353 A118C cysteine engineered heavy chain (IgG1)

<400> 78

```
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 Thr Ser Tyr
            20                  25                  30

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

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

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

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

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

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

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

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

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

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

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

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                245                 250                 255

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

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

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

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

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

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

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

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

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

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

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

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

<210> 79
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: YW353 S400C cysteine engineered heavy chain (IgG1)

<400> 79

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 Thr Ser Tyr
20 25 30

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

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

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

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

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

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

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

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

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

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

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

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                245                 250                 255

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

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

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

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

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

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

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

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

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

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

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


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

<210> 80
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: V205C cysteine engineered light chain constant region (Igk)

<400> 80

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


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


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


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


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


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


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

<210> 81
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: A118C cysteine engineered heavy chain constant region (IgG1)

<400> 81

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 82
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic: S400C cysteine engineered heavy chain constant region
       (IgG1)

<400> 82

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 83
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic: primer

<400> 83
accaactgca tcctaaactg 20

<210> 84

<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic: primer

<400> 84
accgagtttc acctcagctc 20

<210> 85
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic: primer

<400> 85
acattgccct gttgctcttc 20

<210> 86
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic: primer

<400> 86
actgctctga tatactcaat c 21