SEQUENCE LISTING

<110> IMMUNOGEN, INC.
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RUI, LINGYUN

<120> ANTIBODIES AND ASSAYS FOR DETECTION OF FOLATE RECEPTOR 1

<130> 2921.044PC03/EKS/CLD

<140> To be assigned
<141> 2014-08-29

<150> 61/940,184
<151> 2014-02-14

<150> 61/875,475
<151> 2013-09-09

<150> 61/872,407
<151> 2013-08-30

<160> 75

<170> PatentIn version 3.5

<210> 1
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Ala Val Val Gly Glu Ala Gln Thr Arg Ile Ala Trp Ala Arg Thr Glu
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Leu Leu Asn Val Cys Met Asn Ala Lys His His Lys Glu Lys Pro Gly
35 40 45

Pro Glu Asp Lys Leu His Glu Gln Cys Arg Pro Trp Arg Lys Asn Ala
50 55 60

Cys Cys Ser Thr Asn Thr Ser Gln Glu Ala His Lys Asp Val Ser Tyr
65 70 75 80

Leu Tyr Arg Phe Asn Trp Asn His Cys Gly Glu Met Ala Pro Ala Cys
85 90 95

Lys Arg His Phe Ile Gln Asp Thr Cys Leu Tyr Glu Cys Ser Pro Asn
100 105 110

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

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Val Leu Asn Val Pro Leu Cys Lys Glu Asp Cys Glu Gln Trp Trp Glu
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Asp Cys Arg Thr Ser Tyr Thr Cys Lys Ser Asn Trp His Lys Gly Trp
145                 150                 155                 160

Asn Trp Thr Ser Gly Phe Asn Lys Cys Ala Val Gly Ala Ala Cys Gln
                165                 170                 175

Pro Phe His Phe Tyr Phe Pro Thr Pro Thr Val Leu Cys Asn Glu Ile
            180                 185                 190

Trp Thr His Ser Tyr Lys Val Ser Asn Tyr Ser Arg Gly Ser Gly Arg
        195                 200                 205

Cys Ile Gln Met Trp Phe Asp Pro Ala Gln Gly Asn Pro Asn Glu Glu
    210                 215                 220

Val Ala Arg Phe Tyr Ala Ala Ala Met Ser Gly Ala Gly Pro Trp Ala
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Ala Trp Pro Phe Leu Leu Ser Leu Ala Leu Met Leu Leu Trp Leu Leu
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Asn Ser Tyr Ile His
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Trp Ile Tyr Pro Glu Ser Leu Asn Thr Gln Tyr Asn Glu Lys Phe Lys
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Ala

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Arg Gly Ile Tyr Tyr Tyr Ser Pro Tyr Ala Leu Asp His
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Lys Ser Ser Lys Ser Leu Leu Asn Ser Asp Gly Phe Thr Tyr Leu Asp
1 5 10 15

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

Ala

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Lys Ser Thr Glu Ser Leu Leu Asn Ser Asp Gly Phe Thr Tyr Leu Asp
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Leu Val Ser Asn His Phe Ser
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Phe Gln Ser Asn Tyr Leu Pro Leu Thr
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Asn Tyr Tyr Ile His
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<223> muFRIHC9-20 VH-CDR2

<400> 16

Trp Ile Tyr Pro Glu Asn Val Asn Val Arg Tyr Asn Asp Lys Phe Lys
1 5 10 15

Ala

<210> 17
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Arg Gly Ile Tyr Tyr Tyr Ser Pro Tyr Ala Met Asp Tyr
1 5 10

<210> 18
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Lys Ser Thr Lys Ser Leu Leu Asn Ser Asp Gly Phe Thr Tyr Leu Asp
1 5 10 15

<210> 19
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<400> 19

Leu Val Ser Asn His Phe Ser
1 5

<210> 20
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<223> muFRIHC9-20 VL-CDR3

<400> 20

Phe Gln Ser Asn Tyr Leu Pro Leu Thr
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<400> 21

Asn Xaa Tyr Ile His
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<220>
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Trp Ile Tyr Pro Xaa Xaa Xaa Asn Xaa Xaa Tyr Asn Xaa Lys Phe Lys
1 5 10 15

Ala

<210> 23
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<220>
<223> Composite VH-CDR3

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<220>
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<223> Xaa can be leucine or methionine

<220>
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<400> 23

Arg Gly Ile Tyr Xaa Tyr Ser Pro Tyr Ala Xaa Asp Xaa
1 5 10

<210> 24
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<220>
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Lys Ser Xaa Xaa Ser Leu Leu Asn Ser Asp Gly Phe Thr Tyr Leu Asp
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<210> 25
<211> 7
<212> PRT
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<400> 25

Leu Val Ser Asn His Phe Ser
1 5

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<400> 26

Phe Gln Ser Asn Tyr Leu Pro Leu Thr
1 5

<210> 27
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<220>
<223> muFRIHC2-1 VH Chain

<400> 27

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

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

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

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

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

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

Ala Arg Arg Gly Ile Tyr Tyr Tyr Ser Pro Tyr Ala Leu Asp His Trp
100 105 110

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

<210> 28
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<212> PRT
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<223> muFRIHC2-1 VL Chain

<400> 28

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

Gly Asp Gln Ala Ser Ile Ser Cys Lys Ser Ser Lys Ser Leu Leu Asn
20 25 30

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

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

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

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

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

Lys Arg

<210> 29
<211> 122
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<400> 29

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

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

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

Gly Trp Ile Tyr Pro Gly Ser Phe Asn Val Glu Tyr Asn Glu Lys Phe
50 55 60

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

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

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

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

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

Gly Asp Gln Ala Ser Ile Ser Cys Lys Ser Thr Glu Ser Leu Leu Asn
20 25 30

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

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

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

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

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

Lys Arg

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

<220>
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<400> 31

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

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

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

Gly Trp Ile Tyr Pro Glu Asn Val Asn Val Arg Tyr Asn Asp Lys Phe
50 55 60

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

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

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

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

<210> 32
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> muFRIHC9-20 VL Chain

<400> 32

Ser Asp Val Val Leu Thr Gln Thr Pro Leu Ser Leu Pro Val Asn Leu
1 5 10 15

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

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

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

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

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

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

Lys Arg

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<223> muFRIHC2-1 Full-Length Heavy Chain

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

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

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

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

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

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

Ala Arg Arg Gly Ile Tyr Tyr Tyr Ser Pro Tyr Ala Leu Asp His Trp
            100                 105                 110

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

Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met
    130                 135                 140

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

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

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

Pro Ser Ser Met Arg Pro Ser Glu Thr Val Thr Cys Asn Val Ala His
        195                 200                 205

Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys
    210                 215                 220

Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe
225                 230                 235                 240

Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro
                245                 250                 255

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

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Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr
        275                 280                 285

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

Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys
305                 310                 315                 320

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

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

Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile
        355                 360                 365

Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly
    370                 375                 380

Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asn Thr Asn
385                 390                 395                 400

Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp
                405                 410                 415

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

Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
        435                 440                 445


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

<220>
<223>  muFRIHC2-1 Full-length Light Chain

<400>  34

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

Gly Asp Gln Ala Ser Ile Ser Cys Lys Ser Ser Lys Ser Leu Leu Asn
            20                  25                  30

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

Ser Pro Gln Leu Leu Ile Tyr Leu Val Ser Asn His Phe Ser Gly Val
    50                  55                  60
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Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys
65                  70                  75                  80

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

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

Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser
        115                 120                 125

Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn
    130                 135                 140

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

Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp
                165                 170                 175

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

Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr
        195                 200                 205

Ser Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
    210                 215                 220


<210>  35
<211>  446
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  muFRIHC5-7 Full-Length Heavy Chain

<400>  35

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

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

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

Gly Trp Ile Tyr Pro Gly Ser Phe Asn Val Glu Tyr Asn Glu Lys Phe
    50                  55                  60
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```
Lys Ala Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Val Tyr
65                  70                  75                  80

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

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

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

Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met
    130                 135                 140

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

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

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

Pro Ser Ser Met Arg Pro Ser Glu Thr Val Thr Cys Asn Val Ala His
        195                 200                 205

Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys
    210                 215                 220

Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe
225                 230                 235                 240

Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro
                245                 250                 255

Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val
            260                 265                 270

Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr
        275                 280                 285

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

Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys
305                 310                 315                 320

Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser
                325                 330                 335
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Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro
            340                 345                 350


Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile
        355                 360                 365


Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly
    370                 375                 380


Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asn Thr Asn
385                 390                 395                 400


Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp
                405                 410                 415


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


Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
        435                 440                 445


<210>  36
<211>  220
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<213>  Artificial Sequence

<220>
<223>  muFRIHC5-7 Full-Length Light Chain

<400>  36

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


Gly Asp Gln Ala Ser Ile Ser Cys Lys Ser Thr Glu Ser Leu Leu Asn
            20                  25                  30


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


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


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


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


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


Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser
        115                 120                 125
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Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn
130 135 140

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

Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp
165 170 175

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

Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr
195 200 205

Ser Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
210 215 220

<210> 37
<211> 446
<212> PRT
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<220>
<223> muFRIHC9-20 Full-Length Heavy Chain

<400> 37

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

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

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

Gly Trp Ile Tyr Pro Glu Asn Val Asn Val Arg Tyr Asn Asp Lys Phe
50 55 60

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

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

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

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

```
Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met
    130                 135                 140

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

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

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

Pro Ser Ser Met Arg Pro Ser Glu Thr Val Thr Cys Asn Val Ala His
        195                 200                 205

Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys
    210                 215                 220

Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe
225                 230                 235                 240

Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro
                245                 250                 255

Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val
            260                 265                 270

Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr
        275                 280                 285

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

Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys
305                 310                 315                 320

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

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

Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile
        355                 360                 365

Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly
    370                 375                 380

Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asn Thr Asn
385                 390                 395                 400
```

Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp
405 410 415

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

Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
435 440 445

<210> 38
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> muFRIHC9-20 Full-Length Light Chain

<400> 38

Ser Asp Val Val Leu Thr Gln Thr Pro Leu Ser Leu Pro Val Asn Leu
1 5 10 15

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

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

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

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

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

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

Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser
115 120 125

Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn
130 135 140

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

Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp
165 170 175

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

Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr
195 200 205

Ser Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
210 215 220

<210> 39
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> muFRIHC2-1 VH Chain

<400> 39
caggtccaac tgcagcagtc tggacctgag ctggtgaagc ctggggcttc agtgaggata 60

tcctgcaagg cttctggcta caccttcaca aactcctata ttcactgggt gaaaaagagg 120

cctggacagg gacttgagtg gattggatgg atttatcctg aaagtcttaa tactcaatac 180

aatgagaagt tcaaggccaa ggccacactg actgctgaca agtcctccag cacatcctac 240

atgcagctca gcagtctgac ctctgaggac tctgcggtct atttctgtgc aagaaggggt 300

atttattact actctcccta tgctctggac cactggggtc aaggagcctc agtcaccgtc 360

tcctca 366

<210> 40
<211> 342
<212> DNA
<213> Artificial Sequence

<220>
<223> muFRIHC2-1 VL Chain

<400> 40
agtgatgttg ttctgaccca aactccactc tctctgcctg tcaatattgg agatcaagcc 60

tctatctctt gcaagtcttc taagagtctt ctgaatagtg atggattcac ttatttggac 120

tggtacctgc agaagccagg ccagtctcca cagctcctaa tatatttggt ttctaatcat 180

ttttctggag ttccagacag gttcagtggc agtgggtcag gaacagattt cacactcaag 240

atcagcagag tggaggctga ggatttggga gtttattatt gcttccagag taactatctt 300

cctctcacgt tcggaggggg gaccaagctg gaaataaaac gg 342

<210> 41
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> muFRIHC5-7 VH Chain

<400> 41
caggtccaac tgcagcagtc tggacctgag gtggtgaagc ctggggcttc agtgaggata 60

tcctgcaagg cttctggcta caccttcaca aactactata tacactgggt gaagcagagg 120

cctggacagg gacttgagtg gattggatgg atttatcctg gaagttttaa tgttgagtac 180

aatgagaagt tcaaggccaa ggccacactg actgcagaca aatcctccag cacagtctac 240

atgcaactca gcagcctgac ctctgaggac tctgcggtct atttctgtgc aagaaggggt 300

atttatttct actctcccta tgctttggac tactggggtc aaggagcctc agtcaccgtc 360

tcctca 366

<210> 42
<211> 342
<212> DNA
<213> Artificial Sequence

<220>
<223> muFRIHC5-7 VL Chain

<400> 42
agtgatgttg ttctgaccca aactccactc tctctgcctg tcaatattgg agatcaagcc 60

tctatctctt gcaagtctac tgagagtctt ctgaatagtg atggattcac ttatttggac 120

tggtacctgc agaagccagg ccagtctcca cagctcctaa tatatttggt ttctaatcat 180

ttttctggag ttccagacag gttcagtggc agtgggtcag gaacagattt cacactcaag 240

atcagcagag tggaggctga ggatttggga gtttattatt gcttccagag taactatctt 300

cctctcacgt tcggaggggg gaccaagctg gaagtaaaac gg 342

<210> 43
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> muFRIHC9-20 VH Chain

<400> 43
caggtccaac tgcagcagtc tggacctgac ctggtgaagc ctggggcttc agtgaggata 60

tcctgcaagg cttctggctt caccttcaca aactactata tacactgggt gaagcagagg 120

cctggacagg gacttgagtg gattggatgg atttatcctg aaaatgttaa tgttaggtac 180

aatgacaagt tcaaggccaa ggccacactg actgcagaca aatcctccag cacagcctac 240

atgcagctca gcagcctgac ctctgaggac tctgcggtct atttctgtgc aagaaggggt 300

atttattact actctcccta tgctatggac tactggggtc aaggagcctc agtcaccgtc 360

tcctca 366

<210> 44
<211> 342
<212> DNA
<213> Artificial Sequence

<220>
<223> muFRIHC9-20 VL Chain

<400> 44
agtgatgttg ttctgaccca aactccactc tctctgcctg tcaatcttgg agatcaagcc 60

tctatctctt gcaagtctac taagagtctt ctgaatagtg atggattcac ttatttggac 120

tggtacctgc agaagccagg ccagtctcca cagctcctaa tatatttggt ttctaatcat 180

ttttctggag ttccagacag gttcagtggc agtgggtcag gaacagattt caccctcaag 240

atcagcagag tggaggctga ggatttggga gtttattatt gcttccagag taactatctt 300

cctctcacgt tcggaggggg gaccaagctg gaaataaaac gg 342

<210> 45
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> huMov19 vHC

<400> 45

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

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

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

Gly Arg Ile His Pro Tyr Asp Gly Asp Thr Phe Tyr Asn Gln Lys Phe
50 55 60

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

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

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

Thr Val Thr Val Ser Ser
115

<210> 46
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> huMov19 vLCv1.00

<400> 46

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

Gln Pro Ala Ile Ile Ser Cys Lys Ala Ser Gln Ser Val Ser Phe Ala
20 25 30

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

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

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

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

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

<210> 47
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> huMov19 vLCv1.60

<400> 47

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

Gln Pro Ala Ile Ile Ser Cys Lys Ala Ser Gln Ser Val Ser Phe Ala
20 25 30

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

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

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

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

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

<210> 48
<211> 15
<212> PRT
<213> Artificial Sequence

<220>

<223> huMov19 vLC CDR1

<400> 48

Lys Ala Ser Gln Ser Val Ser Phe Ala Gly Thr Ser Leu Met His
1 5 10 15

<210> 49
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> huMov19 vLC CDR2

<400> 49

Arg Ala Ser Asn Leu Glu Ala
1 5

<210> 50
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> huMov19 vLC CDR3

<400> 50

Gln Gln Ser Arg Glu Tyr Pro Tyr Thr
1 5

<210> 51
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> huMov19 vHC CDR1

<400> 51

Gly Tyr Phe Met Asn
1 5

<210> 52
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> huMov19 vHC CDR2 - Kabat Defined

<400> 52

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

Gly

<210> 53
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> huMov19 vHC CDR2 - Abm Defined

<400> 53

Arg Ile His Pro Tyr Asp Gly Asp Thr Phe
1 5 10

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

<220>
<223> huMov19 vHC CDR3

<400> 54

Tyr Asp Gly Ser Arg Ala Met Asp Tyr
1 5

<210> 55
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> huMov19 HC amino acid sequence

<400> 55

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

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

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

Gly Arg Ile His Pro Tyr Asp Gly Asp Thr Phe Tyr Asn Gln Lys Phe
50 55 60

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

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

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

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

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

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

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

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

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

<210> 56
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> huMov19 LCv1.00

<400> 56

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

Gln Pro Ala Ile Ile Ser Cys Lys Ala Ser Gln Ser Val Ser Phe Ala
20 25 30

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

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

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

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

Glu Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu 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> 57
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> huMov19 LCv1.60

<400> 57

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

Gln Pro Ala Ile Ile Ser Cys Lys Ala Ser Gln Ser Val Ser Phe Ala
20 25 30

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

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

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

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

Glu Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu 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> 58
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> muMov19 vHC CDR2 - Kabat Defined

<400> 58

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

Asp

<210> 59
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> FRIHC2-1 Resurfaced or Grafted Light Chain v1.0 CDR1

<400> 59

Arg Ser Ser Arg Ser Leu Leu Asn Ser Asp Gly Phe Thr Tyr Leu Asp
1 5 10 15

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

<220>
<223> FRIHC2-1 Resurfaced Heavy Chain CDR2

<400> 60

Trp Ile Tyr Pro Glu Ser Leu Asn Thr Gln
1 5 10

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

<220>
<223> FRIHC2-1 Resurfaced HC CDR2

<400> 61

Trp Ile Tyr Pro Glu Ser Leu Asn Thr Gln Tyr Asn Gln Lys Phe Gln
1 5 10 15

Gly

<210> 62
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> huFRIHC2-1 (resurfaced) VH Chain

<400> 62

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

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

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

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

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

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

Ala Arg Arg Gly Ile Tyr Tyr Tyr Ser Pro Tyr Ala Leu Asp His Trp
100 105 110

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

<210> 63
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> huFRIHC2-1 v. 1.0 (resurfaced) VL Chain

<400> 63

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

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Arg Ser Leu Leu Asn Ser
20 25 30

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

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

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

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

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

Arg

<210> 64
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> huFRIHC2-1 v. 1.01 (resurfaced) VL Chain

<400> 64

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

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

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

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

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

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

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

Arg

<210> 65
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> huFRIHC2-1 (grafted) VH Chain

<400> 65

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

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

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

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

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

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

Ala Arg Arg Gly Ile Tyr Tyr Tyr Ser Pro Tyr Ala Leu Asp His Trp
            100                 105                 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
        115                 120                 125
```

<210> 66
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> huFRIHC2-1 v. 1.0 (grafted) VL Chain

<400> 66

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

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Arg Ser Leu Leu Asn Ser
            20                  25                  30

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

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

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

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

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

<210> 67
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> huFRIHC2-1 v. 1.01 (grafted) VL Chain

<400> 67

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

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

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

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

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

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

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

<210> 68
<211> 442
<212> PRT
<213> Artificial Sequence

<220>
<223> muhuMov19 Full-Length Heavy Chain

<400> 68

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

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

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

```
Gly Arg Ile His Pro Tyr Asp Gly Asp Thr Phe Tyr Asn Gln Lys Phe
    50                  55                  60

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

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

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

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

Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu Gly
    130                 135                 140

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

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

Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser Ser Met
            180                 185                 190

Arg Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala Ser Ser
        195                 200                 205

Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Cys Lys Pro
    210                 215                 220

Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe Pro Pro
225                 230                 235                 240

Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr Cys
                245                 250                 255

Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln Phe Ser Trp
            260                 265                 270

Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Gln Pro Arg Glu
        275                 280                 285

Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro Ile Met
    290                 295                 300

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

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

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

Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asp Phe Phe
        355                 360                 365

Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu
    370                 375                 380

Asn Tyr Lys Asn Thr Gln Pro Ile Met Asn Thr Asn Gly Ser Tyr Phe
385                 390                 395                 400

Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala Gly Asn
                405                 410                 415

Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His His Thr
            420                 425                 430

Glu Lys Ser Leu Ser His Ser Pro Gly Lys
        435                 440
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<210> 69
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> muhuMov19 Full-Length Light Chain

<400> 69

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

Gln Pro Ala Ile Ile Ser Cys Lys Ala Ser Gln Ser Val Ser Phe Ala
            20                  25                  30

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

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

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

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

Glu Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
            100                 105                 110
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Thr Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln
115 120 125

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

Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln
145 150 155 160

Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr
165 170 175

Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg
180 185 190

His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro
195 200 205

Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
210 215

<210> 70
<211> 452
<212> DNA
<213> Artificial Sequence

<220>
<223> huFRIHC2-1 (resurfaced) VH Chain

<400> 70
aagcttgcca ccatgggttg gagctgcatt atccttttcc ttgtggctac agctactggc 60

gttcactctc aggtacaatt ggttcagtca ggagccgagg tcgtaaagcc cggtgccagt 120

gtgaagatct catgcaaggc aagcggttat acttttacaa actcttacat tcattgggtg 180

aaaaagcggc ccggccaggg tctcgaatgg atcggctgga tctacccaga aagtctgaac 240

actcaataca accagaagtt tcagggtaag gcaactctca ctgccgacaa gagctctagc 300

acaagctata tgcagttgtc tagtttgaca agcgaggata gcgcagttta cttttgtgct 360

cggcgtggta tttattacta ctcaccttat gctctggatc actggggaca gggtgcctct 420

gttaccgttt ccagtgcatc caccaagggc cc 452

<210> 71
<211> 452
<212> DNA
<213> Artificial Sequence

<220>
<223> huFRIHC2-1 (grafted) VH Chain

<400> 71
aagcttgcca ccatgggctg gagctgcata atcctcttcc tcgtagctac cgccactggg 60

gtgcattctc aagtacagtt ggtgcagtcc ggagctgaag tcaagaagcc aggggcttct 120

gttaaggtga gctgtaaggc ttccggatat accttcacaa acagttatat ccattgggtg 180

aggcaagctc caggccaggg tctcgaatgg atgggatgga tctaccccga gagtctgaac 240

acccagtaca acgagaagtt caaggcacgt gtgaccatga caagagacac ctccatcagt 300

acagcctata tggaattgag ccgtctcaga agtgatgata cagcagtgta ctactgcgcc 360

aggcggggca tctactacta cagcccatac gctctcgacc actggggaca aggaacactg 420

gtaaccgtaa gctcagcttc tacaaagggc cc 452

<210> 72
<211> 411
<212> DNA
<213> Artificial Sequence

<220>
<223> huFRIHC2-1 v. 1.0 (resurfaced) VL Chain

<400> 72
gaattcgcca ccatgggttg gtcatgtata atacttttcc tggtagctac tgctactggt 60

gtgcattcag atgtggtgct gactcagtca cccttgtctc tcccagtcaa tcttgggcag 120

ccagcatcta tcagctgccg aagcagcagg tctctcctga actccgatgg ctttacttat 180

cttgactggt atctccagaa gccaggacag tccccccggc tgctcatcta cctggtttct 240

aatcatttta gtggcgtccc tgaccgcttc tctgggagtg gaagtgggac cgattttaca 300

ctgaagatct ccagggtcga agctgaggac cttggggttt actactgttt ccagagcaac 360

taccttccct tgacattcgg ccagggaacc aagctggaaa tcaagcgtac g 411

<210> 73
<211> 411
<212> DNA
<213> Artificial Sequence

<220>
<223> huFRIHC2-1 v. 1.01 (resurfaced) VL Chain

<400> 73
gaattcgcca ccatgggttg gtcttgtatc attctgttcc tggtcgccac tgccacagga 60

gttcactcag acgtggtact cacacaatct ccccttccc tgcctgtgaa cctgggacag 120

ccagcctcaa tcagttgcaa gagctctaaa tctctgctca atagcgatgg ctttacctac 180

ttggattggt acctccagaa gcccggccag tctcctcggc tcctgattta ccttgtttca 240

aatcactttt caggcgtgcc tgaccggttc tccggatctg gctcagggac agacttcacc 300

ctgaagatct cccgcgtcga ggcagaggat ctcggcgtgt attactgttt ccaaagtaac 360

tacctgccat tgacttttgg acaaggaact aaactggaaa tcaaacgtac g 411

<210> 74
<211> 411
<212> DNA
<213> Artificial Sequence

<220>

<223> huFRIHC2-1 v. 1.0 (grafted) VL Chain

<400> 74
gaattcgcca ccatgggatg gagttgtatt attctgttct tggtcgctac tgcaacaggc 60

gttcattctg acatcgtaat gacccagaca cctctgagtc tgagtgtcac tcccggccag 120

cccgcctcta tttcatgtcg tagctctcgc tccctgctca attccgacgg ttttacctac 180

ttggactggt atcttcagaa acctgggcag agccctcagc ttctgatcta tctggtgtcc 240

aatcacttca gtggcgtccc agaccgattt tccggaagcg gaagcggaac cgactttacc 300

ctgaagatat cccgcgtcga agcagaggac gtgggcgtgt attattgctt tcaaagcaat 360

tacttgccat tgactttcgg acaaggcaca aaactggaga ttaagcgtac g 411

<210> 75
<211> 411
<212> DNA
<213> Artificial Sequence

<220>
<223> huFRIHC2-1 v. 1.01 (grafted) VL Chain

<400> 75
gaattcgcca ccatgggctg gtcatgcatc atactgttcc tggtggctac agcaaccggg 60

gtgcacagcg atattgttat gacacagaca ccactgagtt tgtcagtgac ccccggccag 120

ccagcctcta tatcctgcaa gtcctcaaaa agtctcctga atagcgatgg ctttacctac 180

ctcgactggt atcttcagaa gcccggtcaa agccctcagc tgctgatata tctggtgtct 240

aaccatttta gcggagtccc cgaccgcttt tcaggctccg gcagtggcac cgacttcacc 300

cttaagattt ctcgcgtgga ggctgaagat gtaggggtct actactgttt ccagtcaaac 360

tacctgccac tgacctttgg tcaaggcact aagctcgaaa ttaagcgtac g 411