SEQUENCE LISTING

<110> IMMUNOGEN, INC.

<120> ANTI-FOLR1 IMMUNOCONJUGATE DOSING REGIMENS

<130> 2921.050PC03

<140> To be assigned
<141> Herewith

<150> 61/823,317
<151> 2013-05-14

<150> 61/828,586
<151> 2013-05-29

<160> 16

<170> PatentIn version 3.5

<210> 1
<211> 257
<212> PRT
<213> Homo sapiens

<400> 1

```
Met Ala Gln Arg Met Thr Thr Gln Leu Leu Leu Leu Val Trp Val
1               5                  10                  15

Ala Val Val Gly Glu Ala Gln Thr Arg Ile Ala Trp Ala Arg Thr Glu
            20                  25                  30

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

Val Leu Asn Val Pro Leu Cys Lys Glu Asp Cys Glu Gln Trp Trp Glu
    130                 135                 140

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
225 230 235 240

Ala Trp Pro Phe Leu Leu Ser Leu Ala Leu Met Leu Leu Trp Leu Leu
245 250 255

Ser

<210> 2
<211> 771
<212> DNA
<213> Homo sapiens

<400> 2
atggctcagc ggatgacaac acagctgctg ctccttctag tgtgggtggc tgtagtaggg 60

gaggctcaga caaggattgc atgggccagg actgagcttc tcaatgtctg catgaacgcc 120

aagcaccaca aggaaaagcc aggccccgag gacaagttgc atgagcagtg tcgaccctgg 180

aggaagaatg cctgctgttc taccaacacc agccaggaag cccataagga tgtttcctac 240

ctatatagat tcaactggaa ccactgtgga gagatggcac ctgcctgcaa acggcatttc 300

atccaggaca cctgcctcta cgagtgctcc cccaacttgg ggccctggat ccagcaggtg 360

gatcagagct ggcgcaaaga gcgggtactg aacgtgcccc tgtgcaaaga ggactgtgag 420

caatggtggg aagattgtcg cacctcctac acctgcaaga gcaactggca caagggctgg 480

aactggactt cagggtttaa caagtgcgca gtgggagctg cctgccaacc tttccatttc 540

tacttcccca cacccactgt tctgtgcaat gaaatctgga ctcactccta caaggtcagc 600

aactacagcc gagggagtgg ccgctgcatc cagatgtggt tcgacccagc ccagggcaac 660

cccaatgagg aggtggcgag gttctatgct gcagccatga gtggggctgg gccctgggca 720

gcctggcctt tcctgcttag cctggcccta atgctgctgt ggctgctcag c 771

<210> 3
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> huMov19 vHC

<400> 3

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> 4
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> huMov19 vLCv1.00

<400> 4

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

<220>
<223> huMov19 vLCv1.60

<400> 5

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> 6
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> huMov19 vLC CDR1

<400> 6

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

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

<220>
<223> huMov19 vLC CDR2

<400> 7

Arg Ala Ser Asn Leu Glu Ala

1 5

<210> 8
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> huMov19 vLC CDR3

<400> 8

Gln Gln Ser Arg Glu Tyr Pro Tyr Thr
1 5

<210> 9
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> huMov19 vHC CDR1

<400> 9

Gly Tyr Phe Met Asn
1 5

<210> 10
<211> 17
<212> PRT
<213> Artificial Sequence

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

<400> 10

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

Gly

<210> 11
<211> 10
<212> PRT
<213> Artificial Sequence

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

<400> 11

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

<210> 12
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> huMov19 vHC CDR3

<400> 12

Tyr Asp Gly Ser Arg Ala Met Asp Tyr
1 5

<210> 13
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> huMov19 HC amino acid sequence

<400> 13

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> 14
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> huMov19 LCv1.00

<400> 14

```
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> 15
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> huMov19 LCv1.60

<400> 15

```
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> 16
<211> 17
<212> PRT
<213> Artificial Sequence

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

<400> 16

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

Asp