

SEQUENCE LISTING

<110> Institute for Research in Biomedicine

<120> NOVEL MALARIA VACCINES AND ANTIBODIES BINDING TO PLASMODIUM
SPOROZOITES

<130> IR01P006W0

<150> US 62/487,266

<151> 2017-04-19

<160> 332

<170> PatentIn version 3.5

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Gln Pro Ala Asp Gly Asn Pro Asp Pro Asn Ala Asn Pro Asn Lys
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Ala Asp Gly Asn Pro Asp Pro Asn Ala Asn Pro Asn Lys
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Pro Ala Asp Gly Asn Pro Asp Pro Asn Ala Asn Pro Asn Lys
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Ala Asp Gly Asn Pro Asp Pro Asn Ala Asn Pro Asn Lys Asn

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Pro Ala Asp Gly Asn Pro Asp Pro Asn Ala Asn Pro Asn Lys Asn
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Met Met Arg Lys Leu Ala Ile Leu Ser Val Ser Ser Phe Leu Phe Val
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20 25 30

Arg Val Leu Asn Glu Leu Asn Tyr Asp Asn Ala Gly Thr Asn Leu Tyr
35 40 45

Asn Glu Leu Glu Met Asn Tyr Tyr Gly Lys Gln Glu Asn Trp Tyr Ser
50 55 60

Leu Lys Lys Asn Ser Arg Ser Leu Gly Glu Asn Asp Asp Gly Asn Asn
65 70 75 80

Glu Asp Asn Glu Lys Leu Arg Lys Pro Lys His Lys Lys Leu Lys Gln
85 90 95

Pro Ala Asp Gly Asn Pro Asp Pro Asn Ala Asn Pro Asn Val Asp Pro
100 105 110

Asn Ala Asn Pro Asn Val Asp Pro Asn Ala Asn Pro Asn Val Asp Pro
115 120 125

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Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro
260 265 270

Asn Lys Asn Asn Gln Gly Asn Gly Gln Gly His Asn Met Pro Asn Asp
275 280 285

Pro Asn Arg Asn Val Asp Glu Asn Ala Asn Ala Asn Ser Ala Val Lys
290 295 300

Asn Asn Asn Asn Glu Glu Pro Ser Asp Lys His Ile Lys Glu Tyr Leu
305 310 315 320

Asn Lys Ile Gln Asn Ser Leu Ser Thr Glu Trp Ser Pro Cys Ser Val
325 330 335

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

Lys Pro Lys Asp Glu Leu Asp Tyr Ala Asn Asp Ile Glu Lys Lys Ile
355 360 365

Cys Lys Met Glu Lys Cys Ser Ser Val Phe Asn Val Val Asn Ser Ser
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Ile Gly Leu Ile Met Val Leu Ser Phe Leu Phe Leu Asn
385 390 395

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<400> 25

Lys Leu Lys Gln Pro
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Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro
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Asn Ala Asn Pro Asn Ala Asn Pro
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<223> 22-110-peptide

<400> 27

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

Asn Tyr Tyr Gly Lys Gln Glu Asn Trp Tyr Ser Leu Lys Lys Asn Ser
35 40 45

Arg Ser Leu Gly Glu Asn Asp Asp Gly Asn Asn Glu Asp Asn Glu Lys
50 55 60

Leu Arg Lys Pro Lys His Lys Lys Leu Lys Gln Pro Ala Asp Gly Asn
65 70 75 80

Pro Asp Pro Asn Ala Asn Pro Asn Val
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<223> MGG1 CDRH1 aa

<400> 28

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

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<400> 31

Ser Ser Asn Ile Gly Asn Asn Tyr

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Gly Thr Trp Asp Ser Ser Leu Ser Ala Gly Val
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<400> 35

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

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

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

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

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr His Cys
85 90 95

Ala Arg Leu Gly Arg Ala Ala Arg Glu Tyr Tyr Tyr Tyr Tyr Met Asp
100 105 110

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

Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
20 25 30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln
65 70 75 80

Thr Gly Asp Glu Ala Asp Tyr Tyr Cys Gly Thr Trp Asp Ser Ser Leu
85 90 95

Ser Ala Gly Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
100 105 110

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<223> MGG1 CDRH2 nuc

<400> 38
attaattgga atggtggtag caca 24

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<212> DNA
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 ctcatTTatg acaataataa gcgaccc 27

<210> 43
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 <223> MGG1 CDRL3 nuc

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 ccagggaagg ggctggagtg ggtctctggt attaattgga atggtggtag cacaggttat 180
 gcagactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
 ctgcaaatga acagtctgag agccgaggac acggccttgt atcactgtgc gagacttggg 300

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<211> 336
<212> DNA
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<223> MGG1 VL nuc

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ccaggaacag cccccaaact cctcatttat gacaataata agcgaccctc agggattcct 180
gaccgattct ctggctccaa gtctggcacg tcagccaccc tgggcatcac cggactccag 240
actggggacg aggccgatta ttactgcggc acatgggata gcagcctgag tgctggagtg 300
ttcggcggag ggaccaagct gaccgtccta ggtcag 336

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Gly Phe Thr Leu Asn Asn Tyr Trp
1 5

<210> 47
<211> 8
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<400> 47

Ile Asn Ile Asp Gly Ser Thr Thr
1 5

<210> 48
<211> 20
<212> PRT
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<220>
<223> MGG2 CDRH3 aa

<400> 48

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

Trp Phe Asp Pro
20

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<223> MGG2 CDRL1 aa

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Pro Gly Pro Val Thr Ser Gly His Tyr
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<210> 51
<211> 9
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<223> MGG2 CDRL2 long aa

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Leu Ile Tyr Asp Thr Ser Asn Lys His
1 5

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<400> 52

Leu Leu Ser Tyr Gly Gly Ala Pro Val
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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 Leu Asn Asn Tyr
20 25 30

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

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

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

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

Ala Lys Gly Ser Ile Lys Ala Gly Gly Phe Trp Ser Gly Tyr Ser Asn
100 105 110

Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

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Gln Ala Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
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Thr Val Thr Leu Thr Cys Asp Ser Asp Pro Gly Pro Val Thr Ser Gly
 20 25 30

His Tyr Pro Tyr Trp Phe Gln Gln Lys Pro Gly Gln Val Pro Arg Thr
 35 40 45

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

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Ala
 65 70 75 80

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

Ala Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 100 105

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<400> 56
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gcaaaggga gtattaaggc cggagggtttt tggagtgggtt actccaactg gttcgacccc

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ctgatttatg ataccagcaa caaacac

27

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<400> 61
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 aagcctggcc aagtccccag gacactgatt tatgatacca gcaacaaaca ctcttgaca 180
 cctgcccggg tttcaggctc cctccttggg ggcaaagctg ccctgaccct ttcgggtgctg 240

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ggcggaggga ccaaactgac cgtcctaa 328

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<220>
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<400> 64

Gly Phe Thr Phe Ser Thr Phe Gly
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<210> 65
<211> 8
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<400> 65

Ile Trp Tyr Asp Gly Ser Ser Lys
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<212> PRT
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<223> MGG3 CDRH3 aa

<400> 66

Val Lys Val Gly Ala Asn Trp Gly Trp Arg Tyr Phe Asp Leu
1 5 10

<210> 67
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<223> MGG3 CDRL1 aa

<400> 67

Gln Ser Leu Leu His Ser Asp Gly Asn Thr Tyr
1 5 10

<210> 68

<400> 68
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<210> 69

<211> 9

<212> PRT

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<220>

<223> MGG3 CDRL2 long aa

<400> 69

Leu Ile Tyr Glu Val Ser Ser Arg Phe
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<210> 70

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<220>

<223> MGG3 CDRL3 aa

<400> 70

Met Gln Gly Ile His Ser Trp Thr
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<212> PRT

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<223> MGG3 VH aa

<400> 71

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

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

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

Ala Val Ile Trp Tyr Asp Gly Ser Ser Lys Tyr His Ala Asp Ser Val
50 55 60

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

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

Val Lys Val Gly Ala Asn Trp Gly Trp Arg Tyr Phe Asp Leu Trp Gly
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser
115 120

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<400> 72

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1 5 10 15

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

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

Pro Gln Leu Leu Ile Tyr Glu Val Ser Ser 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 Asp Asp Val Gly Val Tyr Tyr Cys Met Gln Gly
85 90 95

Ile His Ser Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

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<400> 73

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 <400> 80
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 tcctgtgcag cctctggatt caccttcagt acctttggca tgcactgggt ccgccaggct 120
 ccaggcaagg ggctggagtg ggtggcagtc atctggtatg atggaagtag taaataccat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagag cacgctgtat	240
ctgcaaatga acagcctgag agctgaggac acggctatgt attactgtgt gaaagtcgga	300
gctaactggg gatggaggta cttcgatctc tggggccgtg gcaccctggt caccgtctcc	360
tcag	364

<210> 81
 <211> 334
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MGG3 VL nuc

<400> 81	
gatattgtga tgaccagac tccactctct ctgtccgtca cccctggaca gccggcctcc	60
atctcctgca agtctagtca gagcctccta catagtgatg gaaacaccta tttgtcttgg	120
tacctgcaga agccaggcca gtctccacag ctctgatct atgaagtttc cagccggttc	180
tctggagtgc cagataggtt cagcggcagc gggtcaggga cagatttcac actgaaaatc	240
agccgggtgg aggctgacga tgttgggggt tactactgca tgcaaggcat acactcgtgg	300
acgttcggcc aagggaacaa ggtggaaatc aaac	334

<210> 82
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MGG4 CDRH1 aa

<400> 82

Gly	Phe	Arg	Phe	Ser	Asp	Tyr	Gly
1				5			

<210> 83
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MGG4 CDRH2 aa

<400> 83

Ile Trp Tyr Asp Gly Ser Asn Glu
1 5

<210> 84

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> MGG4 CDRH3 aa

<400> 84

Ala Lys Leu Leu Val Gly Ile Thr Thr Asp Val Phe Asp Val
1 5 10

<210> 85

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> MGG4 CDRL1 aa

<400> 85

Gln Ser Val Leu Ser Ser Ser Asn Asn Lys Asn Tyr
1 5 10

<210> 86

<400> 86

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<210> 87

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> MGG4 CDRL2 long aa

<400> 87

Leu Ile Tyr Trp Ala Ser Thr Arg Glu
1 5

<210> 88
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> MGG4 CDRL3 aa

<400> 88

Gln Gln Tyr Tyr Thr Ala Ser Pro Phe
1 5

<210> 89
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> MGG4 VH aa

<400> 89

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

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

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

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

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

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

Ala Lys Leu Leu Val Gly Ile Thr Thr Asp Val Phe Asp Val Trp Gly
100 105 110

Gln Gly Thr Val Val Thr Val Ser Ser
115 120

<210> 90
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> MGG4 VL aa

<400> 90

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 Ser Ser Gln Ser Val Leu Ser Ser
20 25 30

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

Lys

<210> 91
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> MGG4 CDRH1 nuc

<400> 91
ggattcaggt tcagtgacta tggc 24

<210> 92
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> MGG4 CDRH2 nuc

<400> 92
atatggtatg atggaagtaa tgaa 24

<210> 93
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> MGG4 CDRH3 nuc

<400> 93
gcgaaactac tagtgggaat tactactgat gtttttgatg tc 42

<210> 94
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> MGG4 CDRL1 nuc

<400> 94
cagagtgttt tatccagctc caacaataag aactac 36

<210> 95

<400> 95
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<210> 96
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> MGG4 CDRL2 long nuc

<400> 96
ctcatttact gggcatctac ccgggaa 27

<210> 97
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> MGG4 CDRL3 nuc

<400> 97
cagcaatatt atactgcttc cccatt 26

<210> 98
<211> 364
<212> DNA
<213> Artificial Sequence

<220>
<223> MGG4 VH nuc

<400> 98
caggtgcagc tgggtggagtc tggggggaggc gtgggtccagc ctgggaggtc cctgagactc 60
tcctgtgcag cctctggatt caggttcagt gactatggca tgcactgggt ccgccaggct 120
ccgggcaagg ggctggagtg ggtggcactt atatggtatg atggaagtaa tgaatcctat 180
ttagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacactgtat 240
ctgcaaatga acaacctgag aactgaggac acggctgtgt attactgtgc gaaactacta 300
gtgggaatta ctactgatgt ttttgatgtc tggggccaag ggacagtggc caccgtctct 360
tcag 364

<210> 99
<211> 340
<212> DNA
<213> Artificial Sequence

<220>
<223> MGG4 VL nuc

<400> 99
gacatcgtga tgaccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60
atcaactgca ggtccagcca gagtgtttta tccagctcca acaataagaa ctacttagct 120

tggtaccagc	acaaaccacg	acagcctcct	aaactgctca	tttactgggc	atctaccg	180
gaatccgggg	tccctgaccg	attcagtggc	agcgggtctg	ggacagattt	cactctcacc	240
atcagcagcc	tgcaggctga	agatgtggca	gtttattact	gtcagcaata	ttatactgct	300
tccccatttt	tcggcggagg	gaccaaggta	gagatcaaac			340

<210>	100
<211>	8
<212>	PRT
<213>	Artificial Sequence

<220>
<223> MGG8 CDRH1 aa

$\langle 400 \rangle$ 100

Gly Phe Met Ile Ser Gly Ser Val
1 5

<210>	101
<211>	10
<212>	PRT
<213>	Artificial Sequence

<220>
<223> MGG8 CDRH2 aa

<400> 101

Ile Arg Asp Lys Ala Asn Asn Glu Ala Thr
1 5 10

<210>	102
<211>	14
<212>	PRT
<213>	Artificial Sequence

<220>
<223> MGG8 CDRH3 aa

$\langle 400 \rangle$ 102

Thr Arg Gly Ile Ile Val Gly Asp Thr Trp His Phe Asp Pro
1 5 10

<210> 103

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

<220>
<223> MGG8 CDRL1 aa

<400> 103

Glu	Ser	Leu	Leu	Arg	Ser	Asp	Gly	Lys	Thr	Tyr
1				5					10	

<210> 104

<400> 104
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<210> 105
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> MGG8 CDRL2 long aa

<400> 105

Leu	Met	Tyr	Glu	Val	Ser	Lys	Arg	Phe
1				5				

<210> 106
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> MGG8 CDRL3 aa

<400> 106

Met	Gln	Ser	Ile	Gln	Leu	Val	Thr
1				5			

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

<220>
<223> MGG8 VH aa

<400> 107

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

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Met Ile Ser Gly Ser
20 25 30

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

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

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

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

Tyr Cys Thr Arg Gly Ile Ile Val Gly Asp Thr Trp His Phe Asp Pro
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 108

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> MGG8 VL aa

<400> 108

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

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

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

Pro Gln Leu Leu Met Tyr Glu Val Ser Lys 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 Thr Asp Asp Val Gly Ile Tyr Tyr Cys Met Gln Ser
85 90 95

Ile Gln Leu Val Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 109
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> MGG8 CDRH1 nuc

<400> 109
gggttcatga tcagtggctc tggt 24

<210> 110
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> MGG8 CDRH2 nuc

<400> 110
attagagaca aagctaacaa tgaggcgaca 30

<210> 111
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> MGG8 CDRH3 nuc

<400> 111

acgaggggta tcatagtagg tgacacctgg cacttcgacc cc 42

<210> 112
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> MGG8 CDRL1 nuc

<400> 112
gagagcctcc tgagaagcga tggaaagacc ta 32

<210> 113

<400> 113
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<210> 114
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> MGG8 CDRL2 long nuc

<400> 114
ctgatgtatg aagtttccaa gcgcttc 27

<210> 115
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> MGG8 CDRL3 nuc

<400> 115
atgcaaagta tacagcttgt gact 24

<210> 116
<211> 370
<212> DNA
<213> Artificial Sequence

<220>
<223> MGG8 VH nuc

<400> 116

gaagtgcagc tggaggagtc cgggggaggc ctggtccagc ctgggggggc cctgaaactc	60
tcctgtgcag cctctgggtt catgatcagt ggctctgttc tacactgggt ccgccaggcc	120
tccgggaaag ggctggagtg gcttggccgt attagagaca aagctaaca tgaggcgaca	180
gcatatgcag cgtcggtgaa aggcagggtc accatctcca gagatgattc aaaggacacg	240
acatatctgc aaatgaacag cctgagaatc gaggacacgg ccgtgtatta ctgtacgagg	300
ggtatcatag taggtgacac ctggcacttc gaccctggg gccagggaac cctggtcacc	360
gtctcctcag	370

<210> 117
 <211> 334
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MGG8 VL nuc

<400> 117	
gatattgtga tgaccagac tccactctct ctgtccgtca cccctggaca gacggcctcc	60
atctcctgca agtctagtga gaggctcctg agaagcgatg gaaagacctt cttgtattgg	120
tatctgcaga agccaggcca gtctccacag ctctgatgt atgaagtttc caagcgcttc	180
tctggagtg cagatagggt cagtggcagc gggtcaggaa cagattttac actgaaaatc	240
agccgggtgg agactgatga tgttggcatt tattactgca tgcaaagtat acagcttgtg	300
actttcggcc aagggaacaa ggtggaaatc aaac	334

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

<220>
 <223> MGH1 CDRH1 aa

<400> 118

Gly Tyr Thr Phe Thr Asp Tyr Tyr
1 5

<210> 119
 <211> 8

<212> PRT
<213> Artificial Sequence

<220>
<223> MGH1 CDRH2 aa

<400> 119

Ile Asn Pro Tyr Ile Gly Val Ser
1 5

<210> 120
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> MGH1 CDRH3 aa

<400> 120

Ala Ala Cys Ser Asn Val Gly Cys Tyr Val Tyr
1 5 10

<210> 121
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> MGH1 CDRL1 aa

<400> 121

Gln Ser Leu Val Tyr Ser Asp Gly Asn Thr Tyr
1 5 10

<210> 122

<400> 122
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<210> 123
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> MGH1 CDRL2 long aa

<400> 123

Leu Ile Tyr Lys Val Ser Asn Arg Asp
1 5

<210> 124

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> MGH1 CDRL3 aa

<400> 124

Met Gln Gly Thr His Trp Pro Asp Thr
1 5

<210> 125

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> MGH1 VH aa

<400> 125

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

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

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

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

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

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

Ala Ala Cys Ser Asn Val Gly Cys Tyr Val Tyr Trp Gly Gln Gly Ser
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 126
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> MGH1 VL aa

<400> 126

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

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Ser
20 25 30

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

Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Arg Asp 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 Ala Ile Tyr Phe Cys Met Gln Gly
85 90 95

Thr His Trp Pro Asp Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 127
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> MGH1 CDRH1 nuc

<400> 127
ggatacacgt tcaccgacta ctat

24

<210> 128
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> MGH1 CDRH2 nuc

<400> 128
atcaatcctt acattggtgt ctca

24

<210> 129
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> MGH1 CDRH3 nuc

<400> 129
gcggccttgta gtaacgttgg ctgctacgtc tat

33

<210> 130
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> MGH1 CDRL1 nuc

<400> 130
caaagtctcg tgtacagtga tggaaacacc tac

33

<210> 131

<400> 131
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<210> 132
<211> 27
<212> DNA
<213> Artificial Sequence

<220>

<223> MGH1 CDRL2 long nuc

<400> 132
ctaatttata aggttttctaa tcgggac 27

<210> 133
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> MGH1 CDRL3 nuc

<400> 133
atgcaaggta cacactggcc tgacact 27

<210> 134
<211> 355
<212> DNA
<213> Artificial Sequence

<220>
<223> MGH1 VH nuc

<400> 134
caggtgcagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgagagtc 60
tcctgcaaga catctggata cacgttcacc gactactatg tccactgggt gcgacaggcc 120
ccaggacacg ggcttgagtg catgggctgg atcaatcctt acattggtgt ctcaaagtat 180
gcacagaagt ttcagggcag ggtcaccttg accagggaca cgtccatcag cacagcctac 240
atggaaatta gcaggctaac atctgacgac acggccgtct attactgtgc ggcttgtagt 300
aacgttggct gctacgtcta ttggggccag ggatcgctgg tcaccgtctc ctacg 355

<210> 135
<211> 337
<212> DNA
<213> Artificial Sequence

<220>
<223> MGH1 VL nuc

<400> 135
gatgttgta tgactcagtc tccactctcc ctgcccgtca cccttggaca gccggcctcc 60
atctcctgca ggtctagtca aagtctcgtg tacagtgatg gaaacaccta cttgaattgg 120

tttcagcaga ggccaggcca atctccaagg cgcctaattt ataaggtttc taatcgggac	180
tctgggggtcc cagacagatt cagcggcagt gggtcaggca ctgatttcac actgaaaatc	240
agcaggggtgg aggctgagga tgttgcgatt tattttctgca tgcaaggtag acactggcct	300
gacacttttg gccaggggac caaactggag atcaaac	337

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

<220>
 <223> MGH2 CDRH1 aa

<400> 136

Gly Phe Ser Phe Ser Ser Tyr Ala
1 5

<210> 137
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MGH2 CDRH2 aa

<400> 137

Thr Arg Tyr Asp Gly Ser Asn Lys
1 5

<210> 138
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MGH2 CDRH3 aa

<400> 138

Ala Lys Val Gly Asp Gly Thr Val Ala Gly Thr Ile Asp Tyr
1 5 10

<210> 139
 <211> 11

<212> PRT
<213> Artificial Sequence

<220>
<223> MGH2 CDRL1 aa

<400> 139

Gln Ser Leu Val Tyr Ser Asp Gly Asn Thr Tyr
1 5 10

<210> 140

<400> 140
000

<210> 141
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> MGH2 CDRL2 long aa

<400> 141

Leu Ile Tyr Lys Val Ser Asn Arg Asp
1 5

<210> 142
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> MGH2 CDRL3 aa

<400> 142

Met Gln Gly Thr His Trp Trp Thr
1 5

<210> 143
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> MGH2 VH aa

<400> 143

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

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

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

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

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

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

Ala Lys Val Gly Asp Gly Thr Val Ala Gly Thr Ile Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 144

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> MGH2 VL aa

<400> 144

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

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Ser
20 25 30

Asp Gly Asn Thr Tyr Leu Asn Trp Tyr Gln Gln Arg Pro Gly Gln Ser

35

40

45

Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Arg Asp 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 Met Gln Gly
 85 90 95

Thr His Trp Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105 110

<210> 145
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MGH2 CDRH1 nuc

<400> 145
 ggtttcagct tcagtagtta tgcc

24

<210> 146
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MGH2 CDRH2 nuc

<400> 146
 acacggatatg atggaagtaa taag

24

<210> 147
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MGH2 CDRH3 nuc

<400> 147
 gcgaaagtgg gggacgggac agtggctggt actattgact a

41

<210> 148
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> MGH2 CDRL1 nuc

 <400> 148
 caaagcctcg tatatagtga tggaaacacc tac 33

 <210> 149

 <400> 149
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 <210> 150
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> MGH2 CDRL2 long nuc

 <400> 150
 ctaatttata aggtttctaa tcgggac 27

 <210> 151
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> MGH2 CDRL3 nuc

 <400> 151
 atgcaaggta cacactggtg gacg 24

 <210> 152
 <211> 364
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> MGH2 VH nuc

 <400> 152
 caggtgcagc tgggtggagtc tggggggaggc gtggtccagc ctgggggggtc cctgagactc 60

tcctgtacag cgtctggttt cagcttcagt agttatgcca tgcactgggt ccgccaggct	120
ccaggcaagg gactggagtg ggtggcatat acacggtatg atggaagtaa taagttctac	180
ctagactccg tgcagggccg attcaccatc tccagagaca attccaagaa cacgctgtat	240
ctggaaatgg acagcctgag acttgaggac acggctgtct atttctgtgc gaaagtgggg	300
gacgggacag tggctggtac tattgactac tggggccagg gaacgctggt caccgtctcc	360
tcag	364

<210> 153
 <211> 334
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MGH2 VL nuc

<400> 153	
tatattgtga tgactcagtc tccactctcc ctgcccgtca cccttggaca gccggcctcc	60
atctcctgca ggtctagtca aagcctcgta tatagtgatg gaaacaccta cttgaattgg	120
tatcagcaga ggccaggcca atctccaagg cgcctaattt ataaggtttc taatcgggac	180
tctgggggtcc cagacagatt tagcggcagt gggtcaggca ctgatttcac actgaaaatc	240
agcaggggtgg aggctgagga tggtgggggtt tattactgca tgcaaggtag acactgggtg	300
acgttcggcc aagggaacaa ggtggaaatc aaac	334

<210> 154
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MGH3 CDRH1 aa

<400> 154

Gly	Phe	Thr	Phe	Ser	Ser	Tyr	Thr
1				5			

<210> 155
 <211> 8
 <212> PRT

<213> Artificial Sequence

<220>

<223> MGH3 CDRH2 aa

<400> 155

Ile Ser Ser Ser Gly Ser Tyr Ile
1 5

<210> 156

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> MGH3 CDRH3 aa

<400> 156

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

<210> 157

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> MGH3 CDRL1 aa

<400> 157

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

<210> 158

<400> 158

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<210> 159

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> MGH3 CDRL2 long aa

<400> 159

Leu Ile Tyr Leu Gly Ser Asn Arg Ala
1 5

<210> 160
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> MGH3 CDRL3 aa

<400> 160

Met Gln Ala Val Gln Thr Pro Leu Thr
1 5

<210> 161
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> MGH3 VH aa

<400> 161

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

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

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

Ser Ser Ile Ser Ser Ser Gly Ser Tyr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

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

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 162
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> MGH3 VL aa

<400> 162

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

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Tyr Ser
20 25 30

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

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

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

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

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

<210> 163
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> MGH3 CDRH1 nuc

<400> 163
ggattcacct tcagtagtta tacc 24

<210> 164
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> MGH3 CDRH2 nuc

<400> 164
attagtagta gtggtagtta cata 24

<210> 165
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> MGH3 CDRH3 nuc

<400> 165
gcaagaaatg tcttggacag tagtggttac cccacgtact ttgactat 48

<210> 166
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> MGH3 CDRL1 nuc

<400> 166
agagcctcct atatagtaat ggatacaact at 32

<210> 167

<400> 167
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<210> 168
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> MGH3 CDRL2 long nuc

<400> 168
ctgatctatt tgggttctaa tcgggcc 27

<210> 169
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> MGH3 CDRL3 nuc

<400> 169
atgcaagctg tacaaactcc cctcact 27

<210> 170
<211> 370
<212> DNA
<213> Artificial Sequence

<220>
<223> MGH3 VH nuc

<400> 170
gaggtgcagc tgggtggagtc tggggggaggc ctggtcaagc ctgggggggtc cctgagactc 60
tcctgtgcag cctctggatt caccttcagt agttatacca tgaactgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtctcatcc attagtagta gtggtagtta catatattac 180
gcagactcag tgaagggccg atgcaccatc tccagagaca acgccaagaa ctactggat 240
ctgcaaatga acagcctgag agccgaggac gcggctgtgt attactgtgc aagaaatgtc 300
ttggacagta gtggttaccc cacgtacttt gactattggg gccagggaac gctggtcacc 360
gtctcctcag 370

<210> 171
<211> 337
<212> DNA
<213> Artificial Sequence

<220>
<223> MGH3 VL nuc

<400> 171
gatattgtga tgactcagtc tccactctcc ctgcccgtca cccctggaga gccggcctcc 60
atctcctgca ggtctagtca gagcctccta tatagtaatg gatacaacta tctggattgg 120

tacgtgcaga agccagggca gtctccacgc ctcctgatct atttgggttc taatcgggcc	180
tccgggggtcc ctgacagggt cagtggcagt ggatcaggca cagattttac actgagaatc	240
agcagagtgg aggctgagga tgttgggttt tattactgca tgcaagctgt acaaactccc	300
ctcactttcg gcggaggac caaggtggag atcaaac	337

<210> 172
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MGU1 CDRH1 aa

<400> 172

Gly	Phe	Ala	Phe	Ser	Ser	Tyr	Gly
1				5			

<210> 173
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MGU1 CDRH2 aa

<400> 173

Ile	Trp	His	Asp	Gly	Thr	Asn	Lys
1				5			

<210> 174
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MGU1 CDRH3 aa

<400> 174

Ala	Ile	Trp	Tyr	Leu	Asp	Ser	Pro	Asp	His	Gly	Phe	Asp	Ile
1				5						10			

<210> 175

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

<220>
<223> MGU1 CDRL1 aa

<400> 175

Asn Gly His Ser Ser Asn Ala
1 5

<210> 176
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> MGU1 CDRL2 aa

<400> 176

Val Asn Ser Asp Gly Ser His
1 5

<210> 177
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> MGU1 CDRL3 aa

<400> 177

Gln Ala Trp Asp Ser Gly Ile Trp Val
1 5

<210> 178
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> MGU1 VH aa

<400> 178

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

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

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

Ala Val Ile Trp His Asp Gly Thr Asn Lys Tyr Tyr Arg Asp Ser Val
50 55 60

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

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

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

Arg Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 179
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> MGU1 VL aa

<400> 179

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

Ser Val Thr Leu Thr Cys Thr Leu Asn Asn Gly His Ser Ser Asn Ala
20 25 30

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

Lys Val Asn Ser Asp Gly Ser His Asn Lys Gly Ala Ala Val Pro Asp

50

55

60

Arg Phe Ser Gly Ser Ser Ser Gly Thr Glu Arg His Leu Thr Ile Ser
65 70 75 80

Ser Leu Gln Ser Asp Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp
85 90 95

Ser Gly Ile Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 180
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> MGU1 CDRH1 nuc

<400> 180
ggattcgctt tcagtagtta tggc 24

<210> 181
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> MGU1 CDRH2 nuc

<400> 181
atttggcatg atggcaccaa taaa 24

<210> 182
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> MGU1 CDRH3 nuc

<400> 182
gccatttgggt atcttgatag tcctgatcat ggtttcgata tc 42

<210> 183
<211> 21

<212> DNA
<213> Artificial Sequence

<220>
<223> MGU1 CDRL1 nuc

<400> 183
aatggccaca gttccaatgc c 21

<210> 184
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> MGU1 CDRL2 nuc

<400> 184
gttaatagtg atggcagcca 20

<210> 185
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> MGU1 CDRL3 nuc

<400> 185
caggcctggg acagtggcat ttgggtt 27

<210> 186
<211> 364
<212> DNA
<213> Artificial Sequence

<220>
<223> MGU1 VH nuc

<400> 186
caggtgcagc tgggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcatgtgcag cctccggatt cgctttcagt agttatggca tgaactgggt ccgccaggct 120

ccaggcaagg gactggagtg ggtggcagtt atttggcatg atggcaccaa taaatactat 180

agagactccg tgaagggccg attcatcatc tccagagaca atgccaagaa caccttgtat 240

ctgcaaatgg acagcctgag cgctgaggac acggctatgt attactgtgc catttggtat 300

cttgatagtc ctgatcatgg tttcgatatc tggggccgag ggacaatggt caccgtctct 360
tcag 364

<210> 187
<211> 334
<212> DNA
<213> Artificial Sequence

<220>
<223> MGU1 VL nuc

<400> 187
cagcttgtcc tgactcaatc gccctctgcc tctgcctccc tgggagtctc ggtcaccctc 60
acctgtactc tgaacaatgg ccacagttcc aatgccatcg catggcatca acagcagcca 120
gggaagggcc ctcgttattt gatgaagggt aatagtgatg gcagccacaa taagggggcc 180
gctgtccctg atcgcttctc aggctctagt tctgggactg agcgccacct caccatctcc 240
agcctccagt ctgacgatga ggctgactat tattgtcagg cctgggacag tggcatttgg 300
gttttcggcg gagggaccaa gttgaccgtc ctag 334

<210> 188
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> MGU3 CDRH1 aa

<400> 188

Gly Phe Thr Phe Ser Asp Tyr Asn
1 5

<210> 189
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> MGU3 CDRH2 aa

<400> 189

Ile Ser His Ser Ser Ser Thr Thr
1 5

<210> 190
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> MGU3 CDRH3 aa

<400> 190

Ala	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Ser	Gly	Arg	Tyr	Arg	Asp	Tyr
1				5					10					15

<210> 191
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> MGU3 CDRL1 aa

<400> 191

Gln	Asp	Val	Ser	Asn	Tyr
1				5	

<210> 192

<400> 192
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<210> 193
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> MGU3 CDRL2 long aa

<400> 193

Leu	Ile	Tyr	Asp	Ala	Ser	Thr	Leu	Gln
1					5			

<210> 194
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> MGU3 CDRL3 aa

<400> 194

Gln Gln Tyr Asp Ser Leu Pro Leu Thr
1 5

<210> 195

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> MGU3 VH aa

<400> 195

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

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

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

Ser Tyr Ile Ser His Ser Ser Ser Thr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

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

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 196

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

<220>
<223> MGU3 VL aa

<400> 196

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

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

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

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

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

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

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

<210> 197
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> MGU3 CDRH1 nuc

<400> 197

ggattcacct tcagtgacta taac

24

<210> 198
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
 <223> MGU3 CDRH2 nuc

 <400> 198
 attagtcata gtagtagtac caca 24

<210> 199
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MGU3 CDRH3 nuc

 <400> 199
 gcgagacttc gtcccttatc gtatagtggc aggtaccgcg actac 45

<210> 200
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MGU3 CDRL1 nuc

 <400> 200
 caggacgtta gtaattat 18

<210> 201

 <400> 201
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<210> 202
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MGU3 CDRL2 long nuc

 <400> 202
 ctgatctacg atgcatccac tttgcaa 27

<210> 203
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MGU3 CDRL3 nuc

<400> 203
 cagcagtatg atagcctccc actcact 27

<210> 204
 <211> 367
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MGU3 VH nuc

<400> 204
 gaggtgctac tagtggagtc tgggggaggc ttggtacaac ctgggggggtc cctgagactc 60
 tcctgtgcag cctctggatt caccttcagt gactataaca tgcactgggt ccgccaggct 120
 ccagggaagg ggctggagtg gctttcatac attagtcata gtagtagtac cacatactac 180
 gcagactctg tgagggggccg attcaccatc tccagagaca atgccaagaa ctcactgtat 240
 ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagacttcgt 300
 cccttatcgt atagtggcag gtaccgcgac tactggggcc agggaacgct ggtcaccgtc 360
 tcctcag 367

<210> 205
 <211> 322
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MGU3 VL nuc

<400> 205
 gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
 atcacttgcc aggcgagtca ggacgttagt aattatgtaa attggtatca gcagaaacca 120
 gggaaagccc ctaaggtcct gatctacgat gcatccactt tgcaaacagg ggtcccatca 180
 aggttcagtg gaagtggatc ggggacagat tttactttca gcatcagcag cctgcagcct 240
 gaagatattg caacatatta ctgtcagcag tatgatagcc tcccactcac tttcggcgga 300
 gggaccaagg tggagatcaa ac 322

<210> 206
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> MGU5 CDRH1 aa

<400> 206

Gly Phe Ser Phe Ser Ser Tyr Gly
1 5

<210> 207
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> MGU5 CDRH2 aa

<400> 207

Ile Trp His Asp Gly Thr Asn Lys
1 5

<210> 208
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> MGU5 CDRH3 aa

<400> 208

Thr Lys Arg Ala Gly Trp Gly Asp Ala Leu Asp Ile
1 5 10

<210> 209
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> MGU5 CDRL1 aa

<400> 209

Gln Asp Ile Ser Asn Tyr
1 5

<210> 210

<400> 210
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<210> 211
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> MGU5 CDRL2 long aa

<400> 211

Leu Ile Tyr Asp Ala Ser Asn Leu Glu
1 5

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

<220>
<223> MGU5 CDRL3 aa

<400> 212

Gln Gln Gln Arg Ile
1 5

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

<220>
<223> MGU5 VH aa

<400> 213

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

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

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

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

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

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

Thr Lys Arg Ala Gly Trp Gly Asp Ala Leu Asp Ile Trp Gly Gln Gly
100 105 110

Thr Met Val Thr Val Ser Ser
115

<210> 214
<211> 103
<212> PRT
<213> Artificial Sequence

<220>
<223> MGU5 VL aa

<400> 214

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

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

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

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

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

65

70

75

80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Gln Arg Ile Phe Gly Gly
 85 90 95

Gly Thr Lys Val Glu Ile Lys
 100

<210> 215
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MGU5 CDRH1 nuc

<400> 215
 ggattcagct tcagtagtta tggc 24

<210> 216
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MGU5 CDRH2 nuc

<400> 216
 atatggcatg atggaactaa taaa 24

<210> 217
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MGU5 CDRH3 nuc

<400> 217
 acgaagcggg ctggctgggg tgatgctctt gatatc 36

<210> 218
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>

<223> MGU5 CDRL1 nuc

<400> 218
caggacatta gcaactat 18

<210> 219

<400> 219
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<210> 220
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> MGU5 CDRL2 long nuc

<400> 220
ctgatctacg atgcatccaa tttggaa 27

<210> 221
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> MGU5 CDRL3 nuc

<400> 221
caacaacaaa ggatt 15

<210> 222
<211> 358
<212> DNA
<213> Artificial Sequence

<220>
<223> MGU5 VH nuc

<400> 222
caggtgcagt tggaggagtc tgggggaggc gtgggtccagc ctgggaggtc cctgagactc 60
tcctgtgcag cctctggatt cagcttcagt agttatggca tgcactgggt ccgccaggct 120
ccaggcaagg ggctggattg ggtggctctt atatggcatg atggaactaa taaattttac 180
acagactccg tgaagggccg attcaccatc tccagagaca attccaagga cacactgttt 240
ctgcaaatga acagtctgag agttgaggac acggctgtgt attactgtac gaagcgggct 300

ggctgggggtg atgctcttga tatctggggc caagggacaa tggtcaccgt ctcttcag 358

<210> 223
<211> 310
<212> DNA
<213> Artificial Sequence

<220>
<223> MGU5 VL nuc

<400> 223
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc aggcgagtca ggacattagc aactatttaa attggtatca gcagaaacca 120
gggaaagccc ctaaactcct gatctacgat gcatccaatt tggaaacagg ggtcccatca 180
aggttcagtg gaagtggatc tgcgacagat ttactctca ccatcagcag cctgcagtct 240
gaagacattg caacatatta ctgtcaacaa caaaggattt tcggcggagg gaccaaggtg 300
gagatcaaac 310

<210> 224
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> MGU8 CDRH1 aa

<400> 224

Gly Phe Thr Phe Ser Asn Tyr Gly
1 5

<210> 225
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> MGU8 CDRH2 aa

<400> 225

Ile Trp His Asp Gly Thr Asn Lys
1 5

<210> 226
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> MGU8 CDRH3 aa

<400> 226

Thr Lys Arg Gly Gly Trp Gly Asp Gly Ser Asp Ile
1 5 10

<210> 227
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> MGU8 CDRL1 aa

<400> 227

Gln Asp Val Asp Asn Tyr
1 5

<210> 228

<400> 228
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<210> 229
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> MGU8 CDRL2 long aa

<400> 229

Leu Ile Tyr Asp Ala Ser Asn Leu Ala
1 5

<210> 230
<211> 5
<212> PRT
<213> Artificial Sequence

<220>

<223> MGU8 CDRL3 aa

<400> 230

Gln Gln Gln Arg Ile
1 5

<210> 231

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> MGU8 VH aa

<400> 231

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

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

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

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

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

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

Thr Lys Arg Gly Gly Trp Gly Asp Gly Ser Asp Ile Trp Gly Gln Gly
100 105 110

Thr Met Val Thr Val Ser Ser
115

<210> 232

<211> 103

<212> PRT
<213> Artificial Sequence

<220>
<223> MGU8 VL aa

<400> 232

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

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

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

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

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

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gln Arg Ile Phe Gly Gly
85 90 95

Gly Thr Arg Val Glu Ile Lys
100

<210> 233
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> MGU8 CDRH1 nuc

<400> 233
ggatttacct tcagtaacta tggc

24

<210> 234
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
 <223> MGU8 CDRH2 nuc

 <400> 234
 atatggcatg atggaactaa taaa 24

 <210> 235
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> MGU8 CDRH3 nuc

 <400> 235
 acgaagcgag gtggctgggg tgatggttct gatatc 36

 <210> 236
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> MGU8 CDRL1 nuc

 <400> 236
 caggacgttg acaactat 18

 <210> 237

 <400> 237
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 <210> 238
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> MGU8 CDRL2 long nuc

 <400> 238
 ctgatctacg atgcatccaa tttggcg 27

 <210> 239
 <211> 15
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MGU8 CDRL3 nuc

<400> 239
 caacaacaaa ggatt 15

<210> 240
 <211> 358
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MGU8 VH nuc

<400> 240
 caggtgcagc tgggtggagtc tggggggaggc gtggtccagc ctgggaggtc cctaagactc 60
 tcctgtgcag ccggtggatt taccttcagt aactatggca tgcactgggt ccgccaggct 120
 ccaggcaagg ggctggagtg ggtggcactt atatggcatg atggaactaa taaattctat 180
 gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtct 240
 ctgcaaatgg acagcctgac aactgaggac acggctatat atttctgtac gaagcgaggt 300
 ggctggggtg atggttctga tatctggggc caagggacaa tggtcaccgt ctcttcag 358

<210> 241
 <211> 310
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MGU8 VL nuc

<400> 241
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
 atcacttgcc aggcgagtc ggacgttgac aactatttaa attggtatca gcataaacca 120
 gggaaagccc ctaagctcct gatctacgat gcatccaatt tggcgacagg ggtcccatca 180
 aggttcagtg gaagtggatc ttcgacagat tttactctca ccatcagcag cctgcagtct 240
 gatgactttg caacatatta ctgtcaacaa caaaggattt tcggcggagg gaccagggtg 300
 gaaatcaaac 310

<210> 242
 <211> 8

<212> PRT
<213> Artificial Sequence

<220>
<223> MGU10 CDRH1 aa

<400> 242

Gly Phe Ala Phe Ser Asn Tyr Gly
1 5

<210> 243
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> MGU10 CDRH2 aa

<400> 243

Ile Trp His Asp Gly Ser Leu Lys
1 5

<210> 244
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> MGU10 CDRH3 aa

<400> 244

Thr Val Trp Tyr Leu Glu Thr Pro Asp Asp Gly Phe Asp Ile
1 5 10

<210> 245
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> MGU10 CDRL1 aa

<400> 245

His Gly His Thr Ser Lys Ala
1 5

<210> 246
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> MGU10 CDRL2 aa

<400> 246

Val Asn Ser Asp Gly Ser His
1 5

<210> 247
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> MGU10 CDRL3 aa

<400> 247

Gln Ala Trp Asp Ser Gly Ile Trp Val
1 5

<210> 248
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> MGU10 VH aa

<400> 248

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

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

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

Ala Val Ile Trp His Asp Gly Ser Leu Lys Tyr Tyr Thr Gln Ser Val
50 55 60

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

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

Thr Val Trp Tyr Leu Glu Thr Pro Asp Asp Gly Phe Asp Ile Trp Gly
100 105 110

Arg Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 249
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> MGU10 VL aa

<400> 249

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

Ser Val Thr Leu Thr Cys Thr Leu Ser His Gly His Thr Ser Lys Ala
20 25 30

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

Lys Val Asn Ser Asp Gly Ser His Thr Lys Gly Ala Ala Val Pro Asp
50 55 60

Arg Phe Ser Gly Ser Thr Ser Gly Ala Glu Arg His Phe Thr Ile Ser
65 70 75 80

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

Ser Gly Ile Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu

100

105

110

<210> 250
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> MGU10 CDRH1 nuc

<400> 250
ggattcgctt tcagcaatta tggc

24

<210> 251
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> MGU10 CDRH2 nuc

<400> 251
atttggcatg acggcagtct taaa

24

<210> 252
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> MGU10 CDRH3 nuc

<400> 252
accgtttggt accttgaaac tcctgatgat ggtttcgata tt

42

<210> 253
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> MGU10 CDRL1 nuc

<400> 253
catggccaca cctccaaagc c

21

<210> 254
<211> 21

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> MGU10 CDRL2 nuc

 <400> 254
 gttaatagtg atggcagcca c 21

 <210> 255
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> MGU10 CDRL3 nuc

 <400> 255
 caggcctggg acagtggcat ttgggtt 27

 <210> 256
 <211> 364
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> MGU10 VH nuc

 <400> 256
 caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60
 tcatgtgcag cctccggatt cgctttcagc aattatggca tgaactgggt ccgccaggct 120
 ccaggcaagg gactggaatg ggtggcagtt atttggcatg acggcagtct taaatattat 180
 acacagtccg tgaagggccg attcaccatc tccagagaca atgccaagaa cacgttgttt 240
 ctccaaatgg acagcctgag cgctgacgac acggctatgt attattgtac cgtttggtac 300
 cttgaaactc ctgatgatgg tttcgatatt tggggccgag ggacaatggt caccgtctcg 360
 tcag 364

 <210> 257
 <211> 334
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> MGU10 VL nuc

<400> 257
 cagcttgtcc tgactcaacc gccctctgcc tctgcctccc tgggagtctc ggtcaccctc 60
 acctgtactc tgagtcattg ccacacctcc aaagccatcg cgtggcatca acagcagcca 120
 gggaagggcc ctctgtattt gatgaaagtt aatagtgatg gcagccacac taagggggcc 180
 gctgtccctg atcgcttctc aggctctact tctggggctg agcgccactt caccatctcc 240
 aacctccagt ctgacgatga ggctgattat tattgtcagg cctgggacag tggcatttgg 300
 gttttcggcg gagggaccaa gttgaccgtc ctag 334

<210> 258
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MGU11 CDRH1 aa

<400> 258
 Gly Phe Ser Phe Ser Ser Tyr Gly
 1 5

<210> 259
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MGU11 CDRH2 aa

<400> 259
 Ile Trp Tyr Asp Gly Thr Asn Lys
 1 5

<210> 260
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MGU11 CDRH3 aa

<400> 260

Ala Asn Asp Ile Ala Gly Trp Gly Tyr Asp Gly Ser Asn Ala
1 5 10

<210> 261
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> MGU11 CDRL1 aa

<400> 261

Gln Ser Leu Val Tyr Ser Asp Gly Asn Thr Tyr
1 5 10

<210> 262

<400> 262
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<210> 263
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> MGU11 CDRL2 long aa

<400> 263

Leu Ile Tyr Lys Val Ser Asn Arg Asp
1 5

<210> 264
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> MGU11 CDRL3 aa

<400> 264

Met Gln Gly Thr Val Gly Phe Thr
1 5

<210> 265
<211> 121

<212> PRT
<213> Artificial Sequence

<220>
<223> MGU11 VH aa

<400> 265

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

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

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

Ala Val Ile Trp Tyr Asp Gly Thr Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

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

Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Asn Asp Ile Ala Gly Trp Gly Tyr Asp Gly Ser Asn Ala Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 266
<211> 103
<212> PRT
<213> Artificial Sequence

<220>
<223> MGU11 VL aa

<400> 266

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

Ser Ser Gln Ser Leu Val Tyr Ser Asp Gly Asn Thr Tyr Leu Asn Trp
20 25 30

Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr Lys Val
35 40 45

Ser Asn Arg Asp Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser
50 55 60

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

Gly Val Tyr Tyr Cys Met Gln Gly Thr Val Gly Phe Thr Phe Gly Pro
85 90 95

Gly Thr Thr Val Asp Ile Lys
100

<210> 267
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> MGU11 CDRH1 nuc

<400> 267
ggattcagct tcagtagcta tggc 24

<210> 268
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> MGU11 CDRH2 nuc

<400> 268
atatggtatg atggaaccaa taaa 24

<210> 269
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
 <223> MGU11 CDRH3 nuc

 <400> 269
 gcgaatgata ttgcggggtg gggctatgat ggtagtaatg cc 42

 <210> 270
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> MGU11 CDRL1 nuc

 <400> 270
 caaagcctcg tatatagtga tggaaacacc tac 33

 <210> 271

 <400> 271
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 <210> 272
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> MGU11 CDRL2 long nuc

 <400> 272
 ctaatttata aggtttctaa ccgggac 27

 <210> 273
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> MGU11 CDRL3 nuc

 <400> 273
 atgcaaggta cagtgggggtt cact 24

 <210> 274
 <211> 364
 <212> DNA
 <213> Artificial Sequence

<220>

<223> MGU11 VH nuc

<400> 274

caggtgcagc tggaggagtc tgggggaggc gtagtccagc ctgggaggtc cctgagactc	60
tcctgcgtag cctctggatt cagcttcagt agctatggca tgcactgggt ccgccaggct	120
ccaggcaagg ggctggagtg ggtggcagtt atatggtatg atggaaccaa taaatactat	180
gcagattccg tgaagggccg attcaccatc tccagagaca ataccaagaa cacgttgtac	240
ctgcaaatga acagcctgag agcggacgac acggctatgt attactgtgc gaatgatatt	300
gcgggggtggg gctatgatgg tagtaatgcc tggggccagg gaaccctggt caccgtctcc	360
tcag	364

<210> 275

<211> 310

<212> DNA

<213> Artificial Sequence

<220>

<223> MGU11 VL nuc

<400> 275

ctctccctgc ccgtcacccc tggacagccg gcctccatct cctgcaagtc tagtcaaagc	60
ctcgtatata gtgatggaaa cacctacttg aattggtttc agcagaggcc aggccaatct	120
ccaaggcgcc taatttataa ggtttctaac cgggactctg gggtcccaga cagattcagc	180
ggcagtgggt caggcactga ttccacactg aaaatcagca gggtggaggc tgaggatggt	240
ggggtttatt actgcatgca aggtacagtg gggttcactt tcggccctgg gaccacagtg	300
gatatcaaac	310

<210> 276

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> MGU12 CDRH1 aa

<400> 276

Gly Phe Ser Phe Ser Ser Tyr Gly

1 5

<210> 277
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> MGU12 CDRH2 aa

<400> 277

Ile Trp His Asp Gly Ser Tyr Ser
1 5

<210> 278
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> MGU12 CDRH3 aa

<400> 278

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

His Ile

<210> 279
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> MGU12 CDRL1 aa

<400> 279

Gln Thr Ile Asn Asn Trp
1 5

<210> 280

<400> 280
000

<210> 281
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> MGU12 CDRL2 long aa

<400> 281

Leu Ile Tyr Lys Ala Ser Ser Leu Glu
1 5

<210> 282
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> MGU12 CDRL3 aa

<400> 282

Gln Gln Tyr Ser Ser Tyr Trp Thr
1 5

<210> 283
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> MGU12 VH aa

<400> 283

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

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

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

Ala Val Ile Trp His Asp Gly Ser Tyr Ser Tyr Tyr Ala Asp Ser Val
50 55 60

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

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Gly Met Tyr His Cys
85 90 95

Val Lys Val Glu Asp Tyr Val Arg Gly Ser Ser His Gly Gly Ala Phe
100 105 110

His Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120 125

<210> 284
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> MGU12 VL aa

<400> 284

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

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

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

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

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

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

Phe Gly Gln Gly Thr Lys Val Asp Ile Lys

100

105

<210> 285
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MGU12 CDRH1 nuc

<400> 285
 ggattcagct tcagtagtta tggc

24

<210> 286
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MGU12 CDRH2 nuc

<400> 286
 atttggcatg atggaagtta cagt

24

<210> 287
 <211> 54
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MGU12 CDRH3 nuc

<400> 287
 gtgaaagttg aggattacgt tagggggagt tcacatgggg gtgcttttca tatc

54

<210> 288
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MGU12 CDRL1 nuc

<400> 288
 cagactatta ataactgg

18

<210> 289
 <211> 10

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> MGU12 CDRL2 nuc

 <400> 289
 taaggcgtct 10

 <210> 290
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> MGU12 CDRL2 long nuc

 <400> 290
 ctgatctata aggcgtctag tttagaa 27

 <210> 291
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> MGU12 CDRL3 nuc

 <400> 291
 caacagtata gtagttattg gacg 24

 <210> 292
 <211> 376
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> MGU12 VH nuc

 <400> 292
 cagggtacaac tgggtggaatc tgggggaggc gtgggtccagc ctgggaggtc cctgagactc 60
 tcctgtgcag cctccggatt cagcttcagt agttatggca tgcactgggt ccgccaggct 120
 ccaggcaagg ggccggagtg ggtggcagtg atttggcatg atggaagtta cagttactat 180
 gcagactccg tgagggggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgag acctgaggac acggggatgt atcactgtgt gaaagttgag 300

gattacgtta gggggagttc acatgggggt gcttttcata tctggggcca agggacaatg 360
 gtcaccgtct cttcag 376

<210> 293
 <211> 319
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MGU12 VL nuc

<400> 293
 gacatccaga tgaccagtc tccttcacc ctgtctgcat ctgtaggga cagagtcacc 60
 atcacttgcc gggccagtca gactattaat aactggttg cctggtatca gtggaaaccg 120
 gggaaagccc ctgagctcct gatctataag gcgtctagtt tagaaagtgg ggtcccatca 180
 aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240
 gatgattttg caacttatta ctgccaacag tatagtagtt attggacgtt cggccaaggg 300
 accaaggtgg acatcaaac 319

<210> 294
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MGV3 CDRH1 aa

<400> 294

Gly Phe Thr Val Ser Asp Ser Tyr
 1 5

<210> 295
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MGV3 CDRH2 aa

<400> 295

Ile Tyr Ser Gly Ser Ser Thr
 1 5

<210> 296
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> MG3 CDRH3 aa

<400> 296

Ala	Arg	Gly	Pro	Asn	Asp	Tyr	Arg	Asn	Arg	Lys	Tyr	Tyr	Tyr	Tyr	Met
1				5					10					15	

Asp Val

<210> 297
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> MG3 CDRL1 aa

<400> 297

Gln	Ser	Val	Asp	Ser	Pro	Tyr
1				5		

<210> 298

<400> 298
000

<210> 299
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> MG3 CDRL2 long aa

<400> 299

Leu	Ile	Phe	Gly	Ala	Ser	Ile	Arg	Ala
1				5				

<210> 300
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> MGV3 CDRL3 aa

<400> 300

His Gln Tyr Gly Asn Ala Pro Tyr Ile
1 5

<210> 301
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> MGV3 VH aa

<400> 301

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

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

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

Ser Val Ile Tyr Ser Gly Ser Ser Thr Tyr Tyr Ile Asp Ser Val Lys
50 55 60

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

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

Arg Gly Pro Asn Asp Tyr Arg Asn Arg Lys Tyr Tyr Tyr Tyr Met Asp
100 105 110

Val Trp Gly Lys Gly Thr Ala Val Thr Val Ser Ser

115

120

<210> 302
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MGV3 VL aa

<400> 302

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

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

Tyr Leu Ala Trp Tyr Gln Gln Arg Pro Gly Gln Thr Pro Arg Leu Leu
 35 40 45

Ile Phe Gly Ala Ser Ile Arg Ala Thr Asp Ile Pro Asp Arg Phe Ser
 50 55 60

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

Pro Glu Asp Ser Gly Val Tyr Tyr Cys His Gln Tyr Gly Asn Ala Pro
 85 90 95

Tyr Ile Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 303
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MGV3 CDRH1 nuc

<400> 303
 ggattcaccg tcagtgacag ctac

24

<210> 304
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> MG3 CDRH2 nuc

 <400> 304
 atctatagtg gtagtagtac a 21

<210> 305
 <211> 54
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> MG3 CDRH3 nuc

 <400> 305
 gcgagaggcc ctaatgacta cagaaatcgc aaatattact actacatgga cgtc 54

<210> 306
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> MG3 CDRL1 nuc

 <400> 306
 cagagtgttg acagtcctta c 21

<210> 307

 <400> 307
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<210> 308
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> MG3 CDRL2 long nuc

 <400> 308
 ctcatttttg gtcctctat tagggcc 27

<210> 309
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MG3 CDRL3 nuc

<400> 309
 caccagtatg gtaacgcacc ctacatt 27

<210> 310
 <211> 373
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MG3 VH nuc

<400> 310
 gaggtgcagg tgggtggagtc tggggggagac ttggtccagc cggggggggtc cctgagactc 60
 tcctgtgcag tctatggatt caccgtcagt gacagctaca tgagctgggt ccgccaggct 120
 ccggggaagg ggctggagtg ggtctcagtt atctatagtg gtagtagtac atactacata 180
 gactccgtga agggccgatt caccatctcc agagacaggt ccaagaacac cttgtatctt 240
 caaatgaaca ccctgagagt tgaggacacg gctctttatt actgcgcgag aggccctaata 300
 gactacagaa atcgcaaata ttactactac atggacgtct ggggcaaagg gaccgcggtc 360
 accgtctcct cag 373

<210> 311
 <211> 325
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MG3 VL nuc

<400> 311
 gaaattgtgt tgacacagtc tccagacacc ctgtccttgt ctgcagggga aagagtcacc 60
 ctctcttgca gggccagtca gagggttgac agtccctact tagcctggta tcagcaaaga 120
 cctggccaga ctcccaggct cctcattttt ggtgcctcta ttagggccac tgacatccca 180
 gacaggttca gtggcggtgg gtctgggaca gacttcactc tcaccatcag cagactggaa 240

cctgaagatt ctggagtgtg ttactgtcac cagtatggta acgcacccta catttttggc 300
caggggacca agctggagat caaac 325

<210> 312
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> CSP C-terminal peptide 282 - 383

<400> 312

Lys Asn Asn Gln Gly Asn Gly Gln Gly His Asn Met Pro Asn Asp Pro
1 5 10 15

Asn Arg Asn Val Asp Glu Asn Ala Asn Ala Asn Ser Ala Val Lys Asn
20 25 30

Asn Asn Asn Glu Glu Pro Ser Asp Lys His Ile Lys Glu Tyr Leu Asn
35 40 45

Lys Ile Gln Asn Ser Leu Ser Thr Glu Trp Ser Pro Cys Ser Val Thr
50 55 60

Cys Gly Asn Gly Ile Gln Val Arg Ile Lys Pro Gly Ser Ala Asn Lys
65 70 75 80

Pro Lys Asp Glu Leu Asp Tyr Ala Asn Asp Ile Glu Lys Lys Ile Cys
85 90 95

Lys Met Glu Lys Cys Ser
100

<210> 313
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG1 CH1-CH2-CH3 aa

<400> 313

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

Arg 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> 314
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG CK aa

<400> 314

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1 5 10 15

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

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
35 40 45

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
50 55 60

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

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
85 90 95

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 315
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG CL aa

<400> 315

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

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

Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro
35 40 45

Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn
50 55 60

Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
65 70 75 80

Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val
85 90 95

Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
100 105

<210> 316
 <211> 990
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IgG1 CH1-CH2-CH3 nuc

<400> 316
 gcgtcgacca agggcccatc ggtcttcccc ctggcacctt cctccaagag cacctctggg 60
 ggacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaacctgt gacggctctg 120
 tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 180
 ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc 240
 tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagag agttgagccc 300
 aaatcttggt acaaaactca cacatgcccc ccgtgcccag cacctgaact cctgggggga 360
 ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt 420
 gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 480
 tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 540
 agcacgtacc gtgtgggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 600
 gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 660
 aaagccaaag ggagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag 720
 atgaccaaga accagggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc 780
 gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 840
 ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg 900
 cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 960
 cagaagagcc tctccctgtc cccgggtaaa 990

<210> 317
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IgG CK nuc

<400> 317
 cgtacggtgg ctgcaccatc tgtcttcatc ttcccgccat ctgatgagca gttgaaatct 60
 ggaactgcct ctgttgtgtg cctgctgaat aacttctatc ccagagaggc caaagtacag 120
 tggaaggtgg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac 180
 agcaaggaca gcacctacag cctcagcagc accctgacgc tgagcaaagc agactacgag 240
 aaacacaaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaaag 300
 agcttcaaca ggggagagtg t 321

<210> 318
 <211> 318
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IgG CL nuc

<400> 318
 ggtcagccca aggctgcccc ctcggtcact ctgttccgc cctcctctga ggagcttcaa 60
 gccaacaagg ccacactggt gtgtctcata agtgacttct acccgggagc cgtgacagtg 120
 gcttggaaag cagatagcag ccccgtaag gcgggagtgg agaccaccac accctccaaa 180
 caaagcaaca acaagtacgc ggccagcagc tatctgagcc tgacgcctga gcagtgaag 240
 tcccacagaa gctacagctg ccaggtcacg catgaaggga gcaccgtgga gaagacagtg 300
 gcccctacag aatgttca 318

<210> 319
 <211> 226
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HBsAg S domain

<400> 319

Met Glu Asn Ile Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln
 1 5 10 15

Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu
 20 25 30

Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Thr Thr Val Cys
35 40 45

Leu Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser
50 55 60

Cys Pro Pro Thr Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe
65 70 75 80

Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val
85 90 95

Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Ile Pro Gly
100 105 110

Ser Ser Thr Thr Ser Thr Gly Pro Cys Arg Thr Cys Met Thr Thr Ala
115 120 125

Gln Gly Thr Ser Met Tyr Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp
130 135 140

Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Gly Lys
145 150 155 160

Phe Leu Trp Glu Trp Ala Ser Ala Arg Phe Ser Trp Leu Ser Leu Leu
165 170 175

Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu
180 185 190

Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Ser Ile
195 200 205

Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val
210 215 220

Tyr Ile
225

<210> 320
<211> 104
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminus of CSP

<400> 320

Met Met Arg Lys Leu Ala Ile Leu Ser Val Ser Ser Phe Leu Phe Val
1 5 10 15

Glu Ala Leu Phe Gln Glu Tyr Gln Cys Tyr Gly Ser Ser Ser Asn Thr
20 25 30

Arg Val Leu Asn Glu Leu Asn Tyr Asp Asn Ala Gly Thr Asn Leu Tyr
35 40 45

Asn Glu Leu Glu Met Asn Tyr Tyr Gly Lys Gln Glu Asn Trp Tyr Ser
50 55 60

Leu Lys Lys Asn Ser Arg Ser Leu Gly Glu Asn Asp Asp Gly Asn Asn
65 70 75 80

Glu Asp Asn Glu Lys Leu Arg Lys Pro Lys His Lys Lys Leu Lys Gln
85 90 95

Pro Ala Asp Gly Asn Pro Asp Pro
100

<210> 321
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal region of CSP

<400> 321

Lys Lys Leu Lys Gln Pro Ala
1 5

<210> 322

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

<220>
<223> N-terminal region of CSP

<400> 322

His Lys Lys Leu Lys Gln Pro Ala Asp
1 5

<210> 323
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal region of CSP

<400> 323

Lys His Lys Lys Leu Lys Gln Pro Ala Asp Gly
1 5 10

<210> 324
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal region of CSP

<400> 324

Lys His Lys Lys Leu Lys Gln Pro
1 5

<210> 325
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal region of CSP

<400> 325

Arg Lys Pro Lys His Lys Lys Leu Lys Gln Pro
1 5 10

<210> 326
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal region of CSP

<400> 326

Pro Lys His Lys Lys Leu Lys Gln Pro Ala Asp Gly Asn
1 5 10

<210> 327
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal region of CSP

<400> 327

Lys Pro Lys His Lys Lys Leu Lys Gln Pro Ala Asp Gly Asn Pro
1 5 10 15

<210> 328
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal region of CSP

<400> 328

Arg Lys Pro Lys His Lys Lys Leu Lys Gln Pro Ala Asp Gly Asn Pro
1 5 10 15

Asp

<210> 329
<211> 15
<212> PRT
<213> Artificial Sequence

<220>

<223> N-terminal region of CSP

<400> 329

Asn	Glu	Lys	Leu	Arg	Lys	Pro	Lys	His	Lys	Lys	Leu	Lys	Gln	Pro
1				5					10					15

<210> 330

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> N-terminal region of CSP

<400> 330

Asn	Glu	Lys	Leu	Arg	Lys	Pro	Lys	His	Lys	Lys	Leu	Lys	Gln	Pro	Ala
1				5					10					15	

Asp Gly

<210> 331

<211> 167

<212> PRT

<213> Artificial Sequence

<220>

<223> ferritin polypeptide

<400> 331

Met	Leu	Ser	Lys	Asp	Ile	Ile	Lys	Leu	Leu	Asn	Glu	Gln	Val	Asn	Lys
1				5					10					15	

Glu	Met	Asn	Ser	Ser	Asn	Leu	Tyr	Met	Ser	Met	Ser	Ser	Trp	Cys	Tyr
			20					25					30		

Thr	His	Ser	Leu	Asp	Gly	Ala	Gly	Leu	Phe	Leu	Phe	Asp	His	Ala	Ala
		35					40					45			

Glu	Glu	Tyr	Glu	His	Ala	Lys	Lys	Leu	Ile	Val	Phe	Leu	Asn	Glu	Asn
	50					55					60				

Asn Val Pro Val Gln Leu Thr Ser Ile Ser Ala Pro Glu His Lys Phe
65 70 75 80

Glu Gly Leu Thr Gln Ile Phe Gln Lys Ala Tyr Glu His Glu Gln His
85 90 95

Ile Ser Glu Ser Ile Asn Asn Ile Val Asp His Ala Ile Lys Gly Lys
100 105 110

Asp His Ala Thr Phe Asn Phe Leu Gln Trp Tyr Val Ala Glu Gln His
115 120 125

Glu Glu Glu Val Leu Phe Lys Asp Ile Leu Asp Lys Ile Glu Leu Ile
130 135 140

Gly Asn Glu Asn His Gly Leu Tyr Leu Ala Asp Gln Tyr Val Lys Gly
145 150 155 160

Ile Ala Lys Ser Arg Lys Ser
165

<210> 332

<211> 265

<212> PRT

<213> Artificial Sequence

<220>

<223> encapsulin polypeptide

<400> 332

Met Glu Phe Leu Lys Arg Ser Phe Ala Pro Leu Thr Glu Lys Gln Trp
1 5 10 15

Gln Glu Ile Asp Asn Arg Ala Arg Glu Ile Phe Lys Thr Gln Leu Tyr
20 25 30

Gly Arg Lys Phe Val Asp Val Glu Gly Pro Tyr Gly Trp Glu Tyr Ala
35 40 45

Ala His Pro Leu Gly Glu Val Glu Val Leu Ser Asp Glu Asn Glu Val
50 55 60

Val Lys Trp Gly Leu Arg Lys Ser Leu Pro Leu Ile Glu Leu Arg Ala
65 70 75 80

Thr Phe Thr Leu Asp Leu Trp Glu Leu Asp Asn Leu Glu Arg Gly Lys
85 90 95

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

Glu Phe Glu Asp Glu Val Ile Phe Arg Gly Cys Glu Lys Ser Gly Val
115 120 125

Lys Gly Leu Leu Ser Phe Glu Glu Arg Lys Ile Glu Cys Gly Ser Thr
130 135 140

Pro Lys Asp Leu Leu Glu Ala Ile Val Arg Ala Leu Ser Ile Phe Ser
145 150 155 160

Lys Asp Gly Ile Glu Gly Pro Tyr Thr Leu Val Ile Asn Thr Asp Arg
165 170 175

Trp Ile Asn Phe Leu Lys Glu Glu Ala Gly His Tyr Pro Leu Glu Lys
180 185 190

Arg Val Glu Glu Cys Leu Arg Gly Gly Lys Ile Ile Thr Thr Pro Arg
195 200 205

Ile Glu Asp Ala Leu Val Val Ser Glu Arg Gly Gly Asp Phe Lys Leu
210 215 220

Ile Leu Gly Gln Asp Leu Ser Ile Gly Tyr Glu Asp Arg Glu Lys Asp
225 230 235 240

Ala Val Arg Leu Phe Ile Thr Glu Thr Phe Thr Phe Gln Val Val Asn
245 250 255

Pro Glu Ala Leu Ile Leu Leu Lys Phe
260 265