SEQUENCE LISTING

<110> Berry, Jody
Saphire, Erica

<120> MARBURG MONOCLONAL ANTIBODIES

<130> EMER-045/01WO 309814-2733

<140> PCT/US2015/016708
<141> 2015-02-19

<150> US 62/016,419
<151> 2014-06-24

<150> US 61/941,807
<151> 2014-02-19

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<170> PatentIn version 3.5

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tacctgcaga agccaggcca gtctccaaac ctcctgatct acaaagtttc caaccgattt 180

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Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
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Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

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

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

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

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100 105 110

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atctcttgca gatctagt 78

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ccaggaaagg gtttggaatg ggttgctcgc ataagaatta aaagtggtaa ttatgcaaca 180

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

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

Ala Arg Ile Arg Ile Lys Ser Gly Asn Tyr Ala Thr Ser Tyr Ala Gly
50 55 60

Ser Val Thr Asp Arg Phe Thr Val Ser Arg Asp Asp Ser Gln Asn Leu
65 70 75 80

Phe Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Met Tyr
85 90 95

Tyr Cys Val Arg Glu Trp Glu Gly Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Ser Val Thr Val Ser Ser
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tcatgtgccg cctct 75

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ttgttacaga ggccaggcca gtctccaaag cgcctaatcc atctggtgtc taaactggac 180

tctggagtcc ctgacaggat cactggcagt ggatctggga cagatttcac actgaaaatc 240

aacagagtgg aggctgagga tttgggaatt tattattgct ggcaaggtac acattttccg 300

tggacgttcg gtggaggcac caagctggaa atcaaac 337

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Asp Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser Val Thr Ile Gly
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Gln Pro Ala Ser Ile Ser Cys Thr Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

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

Pro Lys Arg Leu Ile His Leu Val Ser Lys Leu Asp Ser Gly Val Pro
50 55 60

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

Asn Arg Val Glu Ala Glu Asp Leu Gly Ile Tyr Tyr Cys Trp Gln Gly
85 90 95

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

<210> 27
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<212> DNA
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Gln Ser Leu Leu Asn Ser Asp Gly Glu Thr Tyr
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Leu Val Ser
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Trp Gln Gly Thr His Phe Pro Trp Thr
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atctcttgca cgtcaagt 78

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ctgaaaatca acagagtgga ggctgaggat ttgggaattt attattgc 108

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cctggacatg gacttgaatg gattggagat atttaccctg gaggtgataa tacttactac 180

aatgagaagt tcaagggcaa agtcacgctg actgcagaca aatcctcgaa cacagcctat 240

atgcagttca gtagcctgac atctgaggac tctgctgtct atttctgttt tatgattctc 300

tatactttgg actactgggg tcaaggaacc tcagtcaccg tctcctcag 349

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20 25 30

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

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

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

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

Phe Met Ile Leu Tyr Thr Leu Asp Tyr Trp Gly Gln Gly Thr Ser Val
100 105 110

Thr Val Ser Ser
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<210> 43
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<212> PRT
<213> Mus sp.

<400> 43

Ile Tyr Pro Gly Gly Asp Asn Thr
1 5

<210> 44
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<400> 44

Phe Met Ile Leu Tyr Thr Leu Asp Tyr
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<212> DNA
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tcctgcaagg cttct 75

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<210> 47
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gcctatatgc agttcagtag cctgacatct gaggactctg ctgtctattt ctgt 114

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<210> 49
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tacctgcaga aaccaggcca gtctccaaag ctcctgatct acaaagtttc caaccgattt 180

tctggggtcc cagacaggtt cagtggcagt ggatcaggga cagatttcac actcaggatc 240

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tggacgttcg gtggaggcac caagctggaa atcaaac 337

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

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

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

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

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

<210> 51
<211> 33
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<210> 52
<211> 9
<212> DNA
<213> Mus sp.

<400> 52
aaagtttcc 9

<210> 53
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<212> DNA
<213> Mus sp.

<400> 53
tttcaaggtt cacattttcc gtggacg 27

<210> 54
<211> 11
<212> PRT
<213> Mus sp.

<400> 54

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<212> PRT
<213> Mus sp.

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<211> 9
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<400> 56

Phe Gln Gly Ser His Phe Pro Trp Thr
1 5

<210> 57
<211> 78
<212> DNA
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atctcttgca gatctagt 78

<210> 58
<211> 51
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<210> 59
<211> 108
<212> DNA
<213> Mus sp.

<400> 59
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ctcaggatca gcagagtgga ggctgaggat ctgggagttt attactgc 108

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tcctgtacag cctctggatt cactttcagt agctttggaa tgcactgggt tcgtcaggct 120

ccagagaagg ggctggagtg ggtcgcatac attagtagtg gcagtagtaa aatctactat 180

gcagacacgg tgaagggccg attcaccatc tccagagaca atcccaagaa caccctgttc 240

ctgcaaatga ccagtctaag gtctgaggac acggccatgt attactgtgc aagagggtgg 300

tacgaggggg cctggtttgc ttactggggc caagggactc tggtcactgt ctctgcag 358

<210> 62
<211> 119
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<213> Mus sp.

<400> 62

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

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

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

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

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

Ala Arg Gly Trp Tyr Glu Gly Ala Trp Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ala
115

<210> 63
<211> 24
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<210> 64
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<213> Mus sp.

<400> 64
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<210> 65
<211> 36
<212> DNA
<213> Mus sp.

<400> 65
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<210> 66
<211> 8
<212> PRT
<213> Mus sp.

<400> 66

Gly Phe Thr Phe Ser Ser Phe Gly
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<210> 67
<211> 8
<212> PRT
<213> Mus sp.

<400> 67

Ile Ser Ser Gly Ser Ser Lys Ile
1 5

<210> 68
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<212> PRT
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<400> 68

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1 5 10

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<211> 75
<212> DNA
<213> Mus sp.

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tcctgtacag cctct 75

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<210> 71
<211> 114
<212> DNA
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<400> 71
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ctgttcctgc aaatgaccag tctaaggtct gaggacacgg ccatgtatta ctgt 114

<210> 72
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<213> Mus sp.

<400> 72
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<210> 73
<211> 334
<212> DNA
<213> Mus sp.

<400> 73
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atctcctgca aggccagcca aagtgttgat catgatggtg atagttatat gaactggtac 120

caacagaaac caggacagcc acccaaactc ctcatctatg ctacatccaa tctagaatct 180

gggatcccag ccaggtttag tggcagtggg tctgggacag acttcaccct caacatccat 240

cctgtggagg aggaggatgc tgcaacctat tactgtcagc agagttatga ggttccgctc 300

acgttcggtg ctgggaccaa gctggagctg aaac 334

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<211> 111
<212> PRT
<213> Mus sp.

<400> 74

Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
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Gln Arg Ala Ser Ile Ser Cys Lys Ala Ser Gln Ser Val Asp His Asp
20 25 30

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

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

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

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

Glu Val Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105 110

<210> 75
<211> 30
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<210> 76
<211> 9
<212> DNA
<213> Mus sp.

<400> 76
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<210> 77
<211> 27
<212> DNA
<213> Mus sp.

<400> 77
cagcagagtt atgaggttcc gctcacg 27

<210> 78
<211> 10
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<213> Mus sp.

<400> 78

Gln Ser Val Asp His Asp Gly Asp Ser Tyr
1 5 10

<210> 79
<211> 3
<212> PRT
<213> Mus sp.

<400> 79

Ala Thr Ser
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<210> 80
<211> 9
<212> PRT
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<400> 80

Gln Gln Ser Tyr Glu Val Pro Leu Thr
1 5

<210> 81
<211> 78
<212> DNA
<213> Mus sp.

<400> 81
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atctcctgca aggccagc 78

<210> 82
<211> 51
<212> DNA
<213> Mus sp.

<400> 82
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<210> 83
<211> 108
<212> DNA
<213> Mus sp.

<400> 83
aatctagaat ctgggatccc agccaggttt agtggcagtg ggtctgggac agacttcacc 60

ctcaacatcc atcctgtgga ggaggaggat gctgcaacct attactgt 108

<210> 84
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<400> 84
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<210> 85
<211> 343
<212> DNA
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tcctgcagga cttctggata cacattcact gaatacacca ttcactgggt gaagcagagc 120

cgtggaaaga gccttgagtg gattggaggt attaatccta accatggtgg tactctctac 180

aaccagaagt tcaaggtcaa ggccacattg actgtagaca agtcctccag cacagcctac 240

atggagctcc gcagcctgac atctgaggat tctgcagtct attactgtgc aagatttact 300

tacgactact ggggccaagg caccactctc acagtctcct cag 343

<210> 86
<211> 114
<212> PRT
<213> Mus sp.

<400> 86

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

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

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

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

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

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

Ser Ser

<210> 87
<211> 24
<212> DNA
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<400> 87
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<210> 88
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<400> 88
attaatccta accatggtgg tact 24

<210> 89
<211> 21
<212> DNA
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<400> 89
gcaagattta cttacgacta c 21

<210> 90
<211> 8
<212> PRT
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<400> 90

Gly Tyr Thr Phe Thr Glu Tyr Thr
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<210> 91
<211> 8
<212> PRT
<213> Mus sp.

<400> 91

Ile Asn Pro Asn His Gly Gly Thr
1 5

<210> 92
<211> 7
<212> PRT
<213> Mus sp.

<400> 92

Ala Arg Phe Thr Tyr Asp Tyr
1 5

<210> 93
<211> 75
<212> DNA
<213> Mus sp.

<400> 93
gaggtccagc tgcaacagtc tggacctgag ctggtgaagc ctggggcttc agtgaagata 60

tcctgcagga cttct 75

<210> 94
<211> 51
<212> DNA
<213> Mus sp.

<400> 94
attcactggg tgaagcagag ccgtggaaag agccttgagt ggattggagg t 51

<210> 95
<211> 114
<212> DNA
<213> Mus sp.

<400> 95
ctctacaacc agaagttcaa ggtcaaggcc acattgactg tagacaagtc ctccagcaca 60

gcctacatgg agctccgcag cctgacatct gaggattctg cagtctatta ctgt 114

<210> 96
<211> 34
<212> DNA
<213> Mus sp.

<400> 96
tggggccaag gcaccactct cacagtctcc tcag 34

<210> 97
<211> 319
<212> DNA
<213> Mus sp.

<400> 97
gaaaatgttc tcacccagtc tccagcaatc atgtctgcat ctccagggga aaaggtcacc 60

atgacctgca gtgccagctc aagtgtaact tacatgcact ggtaccagca gaagtcaagc 120

acctccccca aactctggat ttatgacaca tccaaactgg cttctggagt cccaggtcgc 180

ttcagtggca gtgggtctgg aaactcttac tctctcacga tcagcagcat ggaggctgaa 240

gatgttgcca cttattactg ttttcagggg agtgggtacc cgtacacgtt cggaggggg 300

accaagctgg aaataaaac 319

<210> 98
<211> 106
<212> PRT

<213> Mus sp.

<400> 98

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

Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Thr Tyr Met
20 25 30

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

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

Gly Ser Gly Asn Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
65 70 75 80

Asp Val Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Tyr Thr
85 90 95

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

<210> 99
<211> 21
<212> DNA
<213> Mus sp.

<400> 99
gccagctcaa gtgtaactta c 21

<210> 100
<211> 9
<212> DNA
<213> Mus sp.

<400> 100
gacacatcc 9

<210> 101
<211> 27
<212> DNA
<213> Mus sp.

<400> 101
tttcagggga gtgggtaccc gtacacg 27

<210> 102
<211> 7
<212> PRT
<213> Mus sp.

<400> 102

Ala Ser Ser Ser Val Thr Tyr
1 5

<210> 103
<211> 3
<212> PRT
<213> Mus sp.

<400> 103

Asp Thr Ser
1

<210> 104
<211> 9
<212> PRT
<213> Mus sp.

<400> 104

Phe Gln Gly Ser Gly Tyr Pro Tyr Thr
1 5

<210> 105
<211> 72
<212> DNA
<213> Mus sp.

<400> 105
gaaaatgttc tcacccagtc tccagcaatc atgtctgcat ctccagggga aaaggtcacc 60

atgacctgca gt 72

<210> 106
<211> 51
<212> DNA
<213> Mus sp.

<400> 106
atgcactggt accagcagaa gtcaagcacc tcccccaaac tctggattta t 51

<210> 107
<211> 108
<212> DNA
<213> Mus sp.

<400> 107
aaactggctt ctggagtccc aggtcgcttc agtggcagtg ggtctggaaa ctcttactct 60

ctcacgatca gcagcatgga ggctgaagat gttgccactt attactgt 108

<210> 108
<211> 31
<212> DNA
<213> Mus sp.

<400> 108
ttcggagggg ggaccaagct ggaaataaaa c 31

<210> 109
<211> 349
<212> DNA
<213> Mus sp.

<400> 109
cagatccagt tggtgcagtc tggacctgag ctgaagaagc ctggagagac agtcaagatc 60

tcctgcaagg cttctgggta taccttcaca aactatggaa tgaactgggt gaagcaggct 120

ccaggaaagg gtttaaagtg gatgggctgg ataaacacct acactggaaa gccaacatat 180

gttgatgact tcaagggacg gtttgccttc tctttggaaa cctctgccaa cactgcctat 240

ttgcagatca acaacctcaa aaatgaggac acggctacat atttctgtga aagtggaggt 300

tacgacgagg actactgggg ccaaggcacc actctcacag tctcctcag 349

<210> 110
<211> 116
<212> PRT
<213> Mus sp.

<400> 110

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

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

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

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

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

Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys
85 90 95

Glu Ser Gly Gly Tyr Asp Glu Asp Tyr Trp Gly Gln Gly Thr Thr Leu
100 105 110

Thr Val Ser Ser
115

<210> 111
<211> 24
<212> DNA
<213> Mus sp.

<400> 111
gggtatacct tcacaaacta tgga 24

<210> 112
<211> 24
<212> DNA
<213> Mus sp.

<400> 112
ataaacacct acactggaaa gcca 24

<210> 113
<211> 27
<212> DNA
<213> Mus sp.

<400> 113
gaaagtggag gttacgacga ggactac 27

<210> 114
<211> 8
<212> PRT
<213> Mus sp.

<400> 114

Gly Tyr Thr Phe Thr Asn Tyr Gly
1 5

<210> 115
<211> 8
<212> PRT
<213> Mus sp.

<400> 115

Ile Asn Thr Tyr Thr Gly Lys Pro
1 5

<210> 116
<211> 9
<212> PRT
<213> Mus sp.

<400> 116

Glu Ser Gly Gly Tyr Asp Glu Asp Tyr
1 5

<210> 117
<211> 75
<212> DNA
<213> Mus sp.

<400> 117
cagatccagt tggtgcagtc tggacctgag ctgaagaagc ctggagagac agtcaagatc 60

tcctgcaagg cttct 75

<210> 118
<211> 51
<212> DNA
<213> Mus sp.

<400> 118
atgaactggg tgaagcaggc tccaggaaag ggtttaaagt ggatgggctg g 51

<210> 119
<211> 114

<212> DNA
<213> Mus sp.

<400> 119
acatatgttg atgacttcaa gggacggttt gccttctctt tggaaacctc tgccaacact 60

gcctatttgc agatcaacaa cctcaaaaat gaggacacgg ctacatattt ctgt 114

<210> 120
<211> 34
<212> DNA
<213> Mus sp.

<400> 120
tggggccaag gcaccactct cacagtctcc tcag 34

<210> 121
<211> 337
<212> DNA
<213> Mus sp.

<400> 121
gatgttttga tgacccaaac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc 60

atctcttgca gatctagtca gaacattgta catagtaatg gaaacaccta tttagaatgg 120

tacctgcaga aatcaggcca gtctccaaag ctcctgatct acaaagtttc caaccgattt 180

tctggggtcc cagacaggtt cagtggcagt ggatcaggga cagatttcac actcaagatc 240

agcagagtgg aggctgagga tctgggagtt tattactgct ttcaaggttc acattttccg 300

tggacgttcg gtggaggcac caagctggaa atcaaac 337

<210> 122
<211> 112
<212> PRT
<213> Mus sp.

<400> 122

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

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

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

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

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

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

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

<210> 123
<211> 33
<212> DNA
<213> Mus sp.

<400> 123
cagaacattg tacatagtaa tggaaacacc tat 33

<210> 124
<211> 9
<212> DNA
<213> Mus sp.

<400> 124
aaagtttcc 9

<210> 125
<211> 27
<212> DNA
<213> Mus sp.

<400> 125
tttcaaggtt cacattttcc gtggacg 27

<210> 126
<211> 11
<212> PRT
<213> Mus sp.

<400> 126

Gln Asn Ile Val His Ser Asn Gly Asn Thr Tyr
1 5 10

<210> 127
<211> 3
<212> PRT
<213> Mus sp.

<400> 127

Lys Val Ser
1

<210> 128
<211> 9
<212> PRT
<213> Mus sp.

<400> 128

Phe Gln Gly Ser His Phe Pro Trp Thr
1 5

<210> 129
<211> 78
<212> DNA
<213> Mus sp.

<400> 129
gatgttttga tgacccaaac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc 60

atctcttgca gatctagt 78

<210> 130
<211> 51
<212> DNA
<213> Mus sp.

<400> 130
ttagaatggt acctgcagaa atcaggccag tctccaaagc tcctgatcta c 51

<210> 131
<211> 108
<212> DNA
<213> Mus sp.

<400> 131
aaccgatttt ctggggtccc agacaggttc agtggcagtg gatcagggac agatttcaca 60

ctcaagatca gcagagtgga ggctgaggat ctgggagttt attactgc 108

<210> 132
<211> 31
<212> DNA
<213> Mus sp.

<400> 132
ttcggtggag gcaccaagct ggaaatcaaa c 31

<210> 133
<211> 358
<212> DNA
<213> Mus sp.

<400> 133
caggtgcagc tgaaggagtc aggacctggc ctggtggcgc cctcacagag cctgtccatc 60

acatgcactg tctcagggtt ctccttaacc gactatggta taacctggat tcgccagcct 120

ccaggaaagg gtctggagtg gctgggagta atatggggtg gtggaagcgc atactataat 180

ttagttctca aatccagact gagcatcagc aaggacaact ccaagagtca agttttctta 240

aaaatgaaca gtctgcaaac tgatgacaca gccatgtact actgtgccaa acatcggact 300

ttgattacga ctgctatgga ctactggggt caaggaattt cagtcaccgt ctcctcag 358

<210> 134
<211> 119
<212> PRT
<213> Mus sp.

<400> 134

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

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

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

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

Ser Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu
65 70 75 80

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

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

Ile Ser Val Thr Val Ser Ser
115

<210> 135
<211> 24
<212> DNA
<213> Mus sp.

<400> 135
gggttctcct taaccgacta tggt 24

<210> 136
<211> 21
<212> DNA
<213> Mus sp.

<400> 136
atatggggtg gtggaagcgc a 21

<210> 137
<211> 39
<212> DNA
<213> Mus sp.

<400> 137
gccaaacatc ggactttgat tacgactgct atggactac 39

<210> 138
<211> 8
<212> PRT
<213> Mus sp.

<400> 138

Gly Phe Ser Leu Thr Asp Tyr Gly
1 5

<210> 139
<211> 7
<212> PRT
<213> Mus sp.

<400> 139

Ile Trp Gly Gly Gly Ser Ala
1 5

<210> 140
<211> 13
<212> PRT
<213> Mus sp.

<400> 140

Ala Lys His Arg Thr Leu Ile Thr Thr Ala Met Asp Tyr
1 5 10

<210> 141
<211> 75
<212> DNA
<213> Mus sp.

<400> 141
caggtgcagc tgaaggagtc aggacctggc ctggtggcgc cctcacagag cctgtccatc 60

acatgcactg tctca 75

<210> 142
<211> 51
<212> DNA
<213> Mus sp.

<400> 142
ataacctgga ttcgccagcc tccaggaaag ggtctggagt ggctgggagt a 51

<210> 143
<211> 114
<212> DNA
<213> Mus sp.

<400> 143
tactataatt tagttctcaa atccagactg agcatcagca aggacaactc caagagtcaa 60

gttttcttaa aaatgaacag tctgcaaact gatgacacag ccatgtacta ctgt 114

<210> 144
<211> 34
<212> DNA
<213> Mus sp.

<400> 144
tggggtcaag gaatttcagt caccgtctcc tcag 34

<210> 145
<211> 337
<212> DNA
<213> Mus sp.

<400> 145
gatgttttga tgacccaaac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc 60

atctcttgca gatctagtca gaacattgta catagtgatg gaaacaccta tttagaatgg 120

tacctgcaga aaccaggcca gtctccaaag ctcctgatct acaaattttc caaccgattt 180

tctggggtcc cagacaggtt cagtggcagt ggatcaggga cagatttcac actcaagatc 240

agcagagtgg aggctgagga tctgggagtt tattactgct ttcaaggttc acatgttcct 300

cccacgttcg gtgctgggac caagctggag ctgaaac 337

<210> 146
<211> 112
<212> PRT
<213> Mus sp.

<400> 146

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

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

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

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

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

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

Ser His Val Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105 110

<210> 147
<211> 33
<212> DNA
<213> Mus sp.

<400> 147
cagaacattg tacatagtga tggaaacacc tat 33

<210> 148
<211> 9
<212> DNA
<213> Mus sp.

<400> 148
aaattttcc 9

<210> 149
<211> 27
<212> DNA
<213> Mus sp.

<400> 149

tttcaaggtt cacatgttcc tcccacg 27

<210> 150
<211> 11
<212> PRT
<213> Mus sp.

<400> 150

Gln Asn Ile Val His Ser Asp Gly Asn Thr Tyr
1 5 10

<210> 151
<211> 3
<212> PRT
<213> Mus sp.

<400> 151

Lys Phe Ser
1

<210> 152
<211> 9
<212> PRT
<213> Mus sp.

<400> 152

Phe Gln Gly Ser His Val Pro Pro Thr
1 5

<210> 153
<211> 78
<212> DNA
<213> Mus sp.

<400> 153
gatgttttga tgacccaaac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc 60

atctcttgca gatctagt 78

<210> 154
<211> 51
<212> DNA
<213> Mus sp.

<400> 154
ttagaatggt acctgcagaa accaggccag tctccaaagc tcctgatcta c 51

<210> 155
<211> 108
<212> DNA
<213> Mus sp.

<400> 155
aaccgatttt ctggggtccc agacaggttc agtggcagtg gatcagggac agatttcaca 60

ctcaagatca gcagagtgga ggctgaggat ctgggagttt attactgc 108

<210> 156

<211> 31
<212> DNA
<213> Mus sp.

<400> 156
ttcggtgctg ggaccaagct ggagctgaaa c 31

<210> 157
<211> 364
<212> DNA
<213> Mus sp.

<400> 157
gaagtgaagc tggtggagtc tgggggaggc ttagtgaagt ctggagggtc cctgaaactc 60

tcctgtgcag tctctggatt cactttcagt acctatgcca tgtcttgggt tcgccagatt 120

ccggagaaga ggctggagtg ggtcgcaacc attagtaatg gtggtagtta tatctactat 180

tcagacagtg tgaagggtcg attcaccatc tccagagaca atgccaagaa caccctgtac 240

ctgcaaatga gcagtctgag gtctgaggac acggccatgt attactgtgc acgacatagg 300

gagtcctata ggtacgactg gtttgcttac tggggccaag ggactctggt cactgtctct 360

gcag 364

<210> 158
<211> 121
<212> PRT
<213> Mus sp.

<400> 158

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

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

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

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

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

Gln Gly Thr Leu Val Thr Val Ser Ala
115 120

<210> 159
<211> 24
<212> DNA
<213> Mus sp.

<400> 159
ggattcactt tcagtaccta tgcc 24

<210> 160
<211> 24
<212> DNA
<213> Mus sp.

<400> 160
attagtaatg gtggtagtta tatc 24

<210> 161
<211> 42
<212> DNA
<213> Mus sp.

<400> 161
gcacgacata gggagtccta taggtacgac tggtttgctt ac 42

<210> 162
<211> 8
<212> PRT
<213> Mus sp.

<400> 162

Gly Phe Thr Phe Ser Thr Tyr Ala
1 5

<210> 163
<211> 8
<212> PRT
<213> Mus sp.

<400> 163

Ile Ser Asn Gly Gly Ser Tyr Ile
1 5

<210> 164
<211> 14
<212> PRT
<213> Mus sp.

<400> 164

Ala Arg His Arg Glu Ser Tyr Arg Tyr Asp Trp Phe Ala Tyr
1 5 10

<210> 165
<211> 75
<212> DNA
<213> Mus sp.

<400> 165
gaagtgaagc tggtggagtc tgggggaggc ttagtgaagt ctggagggtc cctgaaactc 60

tcctgtgcag tctct 75

<210> 166
<211> 51
<212> DNA
<213> Mus sp.

<400> 166
atgtcttggg ttcgccagat tccggagaag aggctggagt gggtcgcaac c 51

<210> 167
<211> 114
<212> DNA
<213> Mus sp.

<400> 167
tactattcag acagtgtgaa gggtcgattc accatctcca gagacaatgc caagaacacc 60

ctgtacctgc aaatgagcag tctgaggtct gaggacacgg ccatgtatta ctgt 114

<210> 168
<211> 34
<212> DNA
<213> Mus sp.

<400> 168
tggggccaag ggactctggt cactgtctct gcag 34

<210> 169
<211> 468
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Marburg virus Ravn GPe delta muc

<400> 169

Met Lys Thr Ile Tyr Phe Leu Ile Ser Leu Ile Leu Ile Gln Ser Ile
1 5 10 15

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

Val Asp Ser Val Cys Ser Gly Thr Leu Gln Lys Thr Glu Asp Val His
35 40 45

Leu Met Gly Phe Thr Leu Ser Gly Gln Lys Val Ala Asp Ser Pro Leu
50 55 60

Glu Ala Ser Lys Arg Trp Ala Phe Arg Thr Gly Val Pro Pro Lys Asn
65 70 75 80

Val Glu Tyr Thr Glu Gly Glu Glu Ala Lys Thr Cys Tyr Asn Ile Ser
85 90 95

Val Thr Asp Pro Ser Gly Lys Ser Leu Leu Leu Asp Pro Pro Ser Asn
100 105 110

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Ile Arg Asp Tyr Pro Lys Cys Lys Thr Val His His Ile Gln Gly Gln
        115                 120                 125

Asn Pro His Ala Gln Gly Ile Ala Leu His Leu Trp Gly Ala Phe Phe
    130                 135                 140

Leu Tyr Asp Arg Val Ala Ser Thr Thr Met Tyr Arg Gly Lys Val Phe
145                 150                 155                 160

Thr Glu Gly Asn Ile Ala Ala Met Ile Val Asn Lys Thr Val His Arg
                165                 170                 175

Met Ile Phe Ser Arg Gln Gly Gln Gly Tyr Arg His Met Asn Leu Thr
            180                 185                 190

Ser Thr Asn Lys Tyr Trp Thr Ser Ser Asn Glu Thr Gln Arg Asn Asp
        195                 200                 205

Thr Gly Cys Phe Gly Ile Leu Gln Glu Tyr Asn Ser Thr Asn Asn Gln
    210                 215                 220

Thr Cys Pro Pro Ser Leu Lys Pro Pro Ser Leu Pro Thr Val Thr Pro
225                 230                 235                 240

Ser Ile His Ser Thr Asn Thr Gln Ile Asn Thr Ala Lys Ser Gly Thr
                245                 250                 255

Met Arg Pro Pro Ile Tyr Phe Arg Lys Lys Arg Ser Ile Phe Trp Lys
            260                 265                 270

Glu Gly Asp Ile Phe Pro Phe Leu Asp Gly Leu Ile Asn Thr Glu Ile
        275                 280                 285

Asp Phe Asp Pro Ile Pro Asn Thr Glu Thr Ile Phe Asp Glu Ser Pro
    290                 295                 300

Ser Phe Asn Thr Ser Thr Asn Glu Glu Gln His Thr Pro Pro Asn Ile
305                 310                 315                 320

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

Ser Gly Glu Asn Glu Asn Asp Cys Asp Ala Glu Leu Arg Ile Trp Ser
            340                 345                 350

Val Gln Glu Asp Asp Leu Ala Ala Gly Leu Ser Trp Ile Pro Phe Phe
        355                 360                 365

Gly Pro Gly Ile Glu Gly Leu Tyr Thr Ala Gly Leu Ile Lys Asn Gln
    370                 375                 380
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Asn Asn Leu Val Cys Arg Leu Arg Arg Leu Ala Asn Gln Thr Ala Lys
385 390 395 400

Ser Leu Glu Leu Leu Leu Arg Val Thr Thr Glu Glu Arg Thr Phe Ser
405 410 415

Leu Ile Asn Arg His Ala Ile Asp Phe Leu Leu Thr Arg Trp Gly Gly
420 425 430

Thr Cys Lys Val Leu Gly Pro Asp Cys Cys Ile Gly Ile Glu Asp Leu
435 440 445

Ser Lys Asn Ile Ser Glu Gln Ile Asp Lys Ile Arg Lys Asp Glu Gln
450 455 460

Lys Glu Glu Thr
465

<210> 170
<211> 468
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Marburg virus Angola GPe delta muc

<400> 170

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

Lys Thr Leu Pro Ile Leu Glu Ile Ala Ser Asn Ile Gln Pro Gln Asn
20 25 30

Val Asp Ser Val Cys Ser Gly Thr Leu Gln Lys Thr Glu Asp Val His
35 40 45

Leu Met Gly Phe Thr Leu Ser Gly Gln Lys Val Ala Asp Ser Pro Leu
50 55 60

Glu Ala Ser Lys Arg Trp Ala Phe Arg Ala Gly Val Pro Pro Lys Asn
65 70 75 80

Val Glu Tyr Thr Glu Gly Glu Glu Ala Lys Thr Cys Tyr Asn Ile Ser
85 90 95

Val Thr Asp Pro Ser Gly Lys Ser Leu Leu Leu Asp Pro Pro Thr Asn
100 105 110

Ile Arg Asp Tyr Pro Lys Cys Lys Thr Ile His His Ile Gln Gly Gln
115 120 125

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Asn Pro His Ala Gln Gly Ile Ala Leu His Leu Trp Gly Ala Phe Phe
    130                 135                 140

Leu Tyr Asp Arg Ile Ala Ser Thr Thr Met Tyr Arg Gly Lys Val Phe
145                 150                 155                 160

Thr Glu Gly Asn Ile Ala Ala Met Ile Val Asn Lys Thr Val His Lys
                165                 170                 175

Met Ile Phe Ser Arg Gln Gly Gln Gly Tyr Arg His Met Asn Leu Thr
            180                 185                 190

Ser Thr Asn Lys Tyr Trp Thr Ser Ser Asn Gly Thr Gln Thr Asn Asp
        195                 200                 205

Thr Gly Cys Phe Gly Thr Leu Gln Glu Tyr Asn Ser Thr Lys Asn Gln
    210                 215                 220

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

Glu Val Lys Leu Thr Ser Thr Ser Thr Asp Ala Thr Lys Leu Asn Thr
                245                 250                 255

Thr Gln His Leu Val Tyr Phe Arg Arg Lys Arg Asn Ile Leu Trp Arg
            260                 265                 270

Glu Gly Asp Met Phe Pro Phe Leu Asp Gly Leu Ile Asn Ala Pro Ile
        275                 280                 285

Asp Phe Asp Pro Val Pro Asn Thr Lys Thr Ile Phe Asp Glu Ser Ser
    290                 295                 300

Ser Ser Gly Ala Ser Ala Glu Glu Asp Gln His Ala Ser Pro Asn Ile
305                 310                 315                 320

Ser Leu Thr Leu Ser Tyr Phe Pro Lys Val Asn Glu Asn Thr Ala His
                325                 330                 335

Ser Gly Glu Asn Glu Asn Asp Cys Asp Ala Glu Leu Arg Ile Trp Ser
            340                 345                 350

Val Gln Glu Asp Asp Leu Ala Ala Gly Leu Ser Trp Ile Pro Phe Phe
        355                 360                 365

Gly Pro Gly Ile Glu Gly Leu Tyr Thr Ala Gly Leu Ile Lys Asn Gln
    370                 375                 380

Asn Asn Leu Val Cys Arg Leu Arg Arg Leu Ala Asn Gln Thr Ala Lys
385                 390                 395                 400
```

Ser Leu Glu Leu Leu Leu Arg Val Thr Thr Glu Glu Arg Thr Phe Ser
405 410 415

Leu Ile Asn Arg His Ala Ile Asp Phe Leu Leu Ala Arg Trp Gly Gly
420 425 430

Thr Cys Lys Val Leu Gly Pro Asp Cys Cys Ile Gly Ile Glu Asp Leu
435 440 445

Ser Arg Asn Ile Ser Glu Gln Ile Asp Gln Ile Lys Lys Asp Glu Gln
450 455 460

Lys Glu Gly Thr
465

<210> 171
<211> 468
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Marburg virus Musoke GPe delta muc

<400> 171

Met Lys Thr Thr Cys Phe Leu Ile Ser Leu Ile Leu Ile Gln Gly Thr
1 5 10 15

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

Val Asp Ser Val Cys Ser Gly Thr Leu Gln Lys Thr Glu Asp Val His
35 40 45

Leu Met Gly Phe Thr Leu Ser Gly Gln Lys Val Ala Asp Ser Pro Leu
50 55 60

Glu Ala Ser Lys Arg Trp Ala Phe Arg Thr Gly Val Pro Pro Lys Asn
65 70 75 80

Val Glu Tyr Thr Glu Gly Glu Glu Ala Lys Thr Cys Tyr Asn Ile Ser
85 90 95

Val Thr Asp Pro Ser Gly Lys Ser Leu Leu Leu Asp Pro Pro Thr Asn
100 105 110

Ile Arg Asp Tyr Pro Lys Cys Lys Thr Ile His His Ile Gln Gly Gln
115 120 125

Asn Pro His Ala Gln Gly Ile Ala Leu His Leu Trp Gly Ala Phe Phe
130 135 140

Leu Tyr Asp Arg Ile Ala Ser Thr Thr Met Tyr Arg Gly Lys Val Phe
145 150 155 160

```
Thr Glu Gly Asn Ile Ala Ala Met Ile Val Asn Lys Thr Val His Lys
                165                 170                 175

Met Ile Phe Ser Arg Gln Gly Gln Gly Tyr Arg His Met Asn Leu Thr
            180                 185                 190

Ser Thr Asn Lys Tyr Trp Thr Ser Ser Asn Gly Thr Gln Thr Asn Asp
        195                 200                 205

Thr Gly Cys Phe Gly Ala Leu Gln Glu Tyr Asn Ser Thr Lys Asn Gln
    210                 215                 220

Thr Cys Ala Pro Ser Lys Ile Pro Pro Pro Leu Pro Thr Ala Arg Pro
225                 230                 235                 240

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

Thr Gln His Leu Val Tyr Phe Arg Arg Lys Arg Ser Ile Leu Trp Arg
            260                 265                 270

Glu Gly Asp Met Phe Pro Phe Leu Asp Gly Leu Ile Asn Ala Pro Ile
        275                 280                 285

Asp Phe Asp Pro Val Pro Asn Thr Lys Thr Ile Phe Asp Glu Ser Ser
    290                 295                 300

Ser Ser Gly Ala Ser Ala Glu Glu Asp Gln His Ala Ser Pro Asn Ile
305                 310                 315                 320

Ser Leu Thr Leu Ser Tyr Phe Pro Asn Ile Asn Glu Asn Thr Ala Tyr
                325                 330                 335

Ser Gly Glu Asn Glu Asn Asp Cys Asp Ala Glu Leu Arg Ile Trp Ser
            340                 345                 350

Val Gln Glu Asp Asp Leu Ala Ala Gly Leu Ser Trp Ile Pro Phe Phe
        355                 360                 365

Gly Pro Gly Ile Glu Gly Leu Tyr Thr Ala Val Leu Ile Lys Asn Gln
    370                 375                 380

Asn Asn Leu Val Cys Arg Leu Arg Arg Leu Ala Asn Gln Thr Ala Lys
385                 390                 395                 400

Ser Leu Glu Leu Leu Leu Arg Val Thr Thr Glu Glu Arg Thr Phe Ser
                405                 410                 415

Leu Ile Asn Arg His Ala Ile Asp Phe Leu Leu Thr Arg Trp Gly Gly
            420                 425                 430
```

Thr Cys Lys Val Leu Gly Pro Asp Cys Cys Ile Gly Ile Glu Asp Leu
435 440 445

Ser Lys Asn Ile Ser Glu Gln Ile Asp Gln Ile Lys Lys Asp Glu Gln
450 455 460

Lys Glu Gly Thr
465

<210> 172
<211> 468
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Marburg virus Ci67 GPe delta muc

<400> 172

Met Lys Thr Thr Cys Leu Phe Ile Ser Leu Ile Leu Ile Gln Gly Ile
1 5 10 15

Lys Thr Leu Pro Ile Leu Glu Ile Ala Ser Asn Asn Gln Pro Gln Asn
20 25 30

Val Asp Ser Val Cys Ser Gly Thr Leu Gln Lys Thr Glu Asp Val His
35 40 45

Leu Met Gly Phe Thr Leu Ser Gly Gln Lys Val Ala Asp Ser Pro Leu
50 55 60

Glu Ala Ser Lys Arg Trp Ala Phe Arg Thr Gly Val Pro Pro Lys Asn
65 70 75 80

Val Glu Tyr Thr Glu Gly Glu Glu Ala Lys Thr Cys Tyr Asn Ile Ser
85 90 95

Val Thr Asp Pro Ser Gly Lys Ser Leu Leu Leu Asp Pro Pro Thr Asn
100 105 110

Ile Arg Asp Tyr Pro Lys Cys Lys Thr Ile His His Ile Gln Gly Gln
115 120 125

Asn Pro His Ala Gln Gly Ile Ala Leu His Leu Trp Gly Ala Phe Phe
130 135 140

Leu Tyr Asp Arg Ile Ala Ser Thr Thr Met Tyr Arg Gly Arg Val Phe
145 150 155 160

Thr Glu Gly Asn Ile Ala Ala Met Ile Val Asn Lys Thr Val His Lys
165 170 175

Met Ile Phe Ser Arg Gln Gly Gln Gly Tyr Arg His Met Asn Leu Thr
180 185 190

Ser Thr Asn Lys Tyr Trp Thr Ser Asn Asn Gly Thr Gln Thr Asn Asp
195 200 205

Thr Gly Cys Phe Gly Ala Leu Gln Glu Tyr Asn Ser Thr Lys Asn Gln
210 215 220

Thr Cys Ala Pro Ser Lys Ile Pro Ser Pro Leu Pro Thr Ala Arg Pro
225 230 235 240

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

Thr Gln His Leu Val Tyr Phe Arg Lys Lys Arg Ser Ile Leu Trp Arg
260 265 270

Glu Gly Asp Met Phe Pro Phe Leu Asp Gly Leu Ile Asn Ala Pro Ile
275 280 285

Asp Phe Asp Pro Val Pro Asn Thr Lys Thr Ile Phe Asp Glu Ser Ser
290 295 300

Ser Ser Gly Ala Ser Ala Glu Glu Asp Gln His Ala Ser Pro Asn Ile
305 310 315 320

Ser Leu Thr Leu Ser Tyr Phe Pro Asn Ile Asn Glu Asn Thr Ala Tyr
325 330 335

Ser Gly Glu Asn Glu Asn Asp Cys Asp Ala Glu Leu Arg Ile Trp Ser
340 345 350

Val Gln Glu Asp Asp Leu Ala Ala Gly Leu Ser Trp Ile Pro Phe Phe
355 360 365

Gly Pro Gly Ile Glu Gly Leu Tyr Thr Ala Gly Leu Ile Lys Asn Gln
370 375 380

Asn Asn Leu Val Cys Arg Leu Arg Arg Leu Ala Asn Gln Thr Ala Lys
385 390 395 400

Ser Leu Glu Leu Leu Leu Arg Val Thr Thr Glu Glu Arg Thr Phe Ser
405 410 415

Leu Ile Asn Arg His Ala Ile Asp Phe Leu Leu Thr Arg Trp Gly Gly
420 425 430

Thr Cys Lys Val Leu Gly Pro Asp Cys Cys Ile Gly Ile Glu Asp Leu
435 440 445

Ser Arg Asn Ile Ser Glu Gln Ile Asp Gln Ile Lys Lys Asp Glu Gln
450 455 460

Lys Glu Gly Thr
465

<210> 173
<211> 681
<212> PRT
<213> Ravn virus - Ravn, Kenya, 1987

<400> 173

Met Lys Thr Ile Tyr Phe Leu Ile Ser Leu Ile Leu Ile Gln Ser Ile
1 5 10 15

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

Val Asp Ser Val Cys Ser Gly Thr Leu Gln Lys Thr Glu Asp Val His
35 40 45

Leu Met Gly Phe Thr Leu Ser Gly Gln Lys Val Ala Asp Ser Pro Leu
50 55 60

Glu Ala Ser Lys Arg Trp Ala Phe Arg Thr Gly Val Pro Pro Lys Asn
65 70 75 80

Val Glu Tyr Thr Glu Gly Glu Glu Ala Lys Thr Cys Tyr Asn Ile Ser
85 90 95

Val Thr Asp Pro Ser Gly Lys Ser Leu Leu Leu Asp Pro Pro Ser Asn
100 105 110

Ile Arg Asp Tyr Pro Lys Cys Lys Thr Val His His Ile Gln Gly Gln
115 120 125

Asn Pro His Ala Gln Gly Ile Ala Leu His Leu Trp Gly Ala Phe Phe
130 135 140

Leu Tyr Asp Arg Val Ala Ser Thr Thr Met Tyr Arg Gly Lys Val Phe
145 150 155 160

Thr Glu Gly Asn Ile Ala Ala Met Ile Val Asn Lys Thr Val His Arg
165 170 175

Met Ile Phe Ser Arg Gln Gly Gln Gly Tyr Arg His Met Asn Leu Thr
180 185 190

Ser Thr Asn Lys Tyr Trp Thr Ser Ser Asn Glu Thr Gln Arg Asn Asp
195 200 205

Thr Gly Cys Phe Gly Ile Leu Gln Glu Tyr Asn Ser Thr Asn Asn Gln

210 215 220

Thr Cys Pro Pro Ser Leu Lys Pro Pro Ser Leu Pro Thr Val Thr Pro
225 230 235 240

Ser Ile His Ser Thr Asn Thr Gln Ile Asn Thr Ala Lys Ser Gly Thr
245 250 255

Met Asn Pro Ser Ser Asp Asp Glu Asp Leu Met Ile Ser Gly Ser Gly
260 265 270

Ser Gly Glu Gln Gly Pro His Thr Thr Leu Asn Val Val Thr Glu Gln
275 280 285

Lys Gln Ser Ser Thr Ile Leu Ser Thr Pro Ser Leu His Pro Ser Thr
290 295 300

Ser Gln His Glu Gln Asn Ser Thr Asn Pro Ser Arg His Ala Val Thr
305 310 315 320

Glu His Asn Gly Thr Asp Pro Thr Thr Gln Pro Ala Thr Leu Leu Asn
325 330 335

Asn Thr Asn Thr Thr Pro Thr Tyr Asn Thr Leu Lys Tyr Asn Leu Ser
340 345 350

Thr Pro Ser Pro Pro Thr Arg Asn Ile Thr Asn Asn Asp Thr Gln Arg
355 360 365

Glu Leu Ala Glu Ser Glu Gln Thr Asn Ala Gln Leu Asn Thr Thr Leu
370 375 380

Asp Pro Thr Glu Asn Pro Thr Thr Ala Gln Asp Thr Asn Ser Thr Thr
385 390 395 400

Asn Ile Ile Met Thr Thr Ser Asp Ile Thr Ser Lys His Pro Thr Asn
405 410 415

Ser Ser Pro Asp Ser Ser Pro Thr Thr Arg Pro Pro Ile Tyr Phe Arg
420 425 430

Lys Lys Arg Ser Ile Phe Trp Lys Glu Gly Asp Ile Phe Pro Phe Leu
435 440 445

Asp Gly Leu Ile Asn Thr Glu Ile Asp Phe Asp Pro Ile Pro Asn Thr
450 455 460

Glu Thr Ile Phe Asp Glu Ser Pro Ser Phe Asn Thr Ser Thr Asn Glu
465 470 475 480

Glu Gln His Thr Pro Pro Asn Ile Ser Leu Thr Phe Ser Tyr Phe Pro

485 490 495

Asp Lys Asn Gly Asp Thr Ala Tyr Ser Gly Glu Asn Glu Asn Asp Cys
500 505 510

Asp Ala Glu Leu Arg Ile Trp Ser Val Gln Glu Asp Asp Leu Ala Ala
515 520 525

Gly Leu Ser Trp Ile Pro Phe Phe Gly Pro Gly Ile Glu Gly Leu Tyr
530 535 540

Thr Ala Gly Leu Ile Lys Asn Gln Asn Asn Leu Val Cys Arg Leu Arg
545 550 555 560

Arg Leu Ala Asn Gln Thr Ala Lys Ser Leu Glu Leu Leu Leu Arg Val
565 570 575

Thr Thr Glu Glu Arg Thr Phe Ser Leu Ile Asn Arg His Ala Ile Asp
580 585 590

Phe Leu Leu Thr Arg Trp Gly Gly Thr Cys Lys Val Leu Gly Pro Asp
595 600 605

Cys Cys Ile Gly Ile Glu Asp Leu Ser Lys Asn Ile Ser Glu Gln Ile
610 615 620

Asp Lys Ile Arg Lys Asp Glu Gln Lys Glu Glu Thr Gly Trp Gly Leu
625 630 635 640

Gly Gly Lys Trp Trp Thr Ser Asp Trp Gly Val Leu Thr Asn Leu Gly
645 650 655

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

Cys Arg Ile Phe Thr Lys Tyr Ile Gly
675 680

<210> 174
<211> 681
<212> PRT
<213> Lake Victoria marburgvirus - Angola2005

<400> 174

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

Lys Thr Leu Pro Ile Leu Glu Ile Ala Ser Asn Ile Gln Pro Gln Asn
20 25 30

Val Asp Ser Val Cys Ser Gly Thr Leu Gln Lys Thr Glu Asp Val His
35 40 45

```
Leu Met Gly Phe Thr Leu Ser Gly Gln Lys Val Ala Asp Ser Pro Leu
    50                  55                  60

Glu Ala Ser Lys Arg Trp Ala Phe Arg Ala Gly Val Pro Pro Lys Asn
65                  70                  75                  80

Val Glu Tyr Thr Glu Gly Glu Glu Ala Lys Thr Cys Tyr Asn Ile Ser
                85                  90                  95

Val Thr Asp Pro Ser Gly Lys Ser Leu Leu Leu Asp Pro Pro Thr Asn
            100                 105                 110

Ile Arg Asp Tyr Pro Lys Cys Lys Thr Ile His His Ile Gln Gly Gln
        115                 120                 125

Asn Pro His Ala Gln Gly Ile Ala Leu His Leu Trp Gly Ala Phe Phe
    130                 135                 140

Leu Tyr Asp Arg Ile Ala Ser Thr Thr Met Tyr Arg Gly Lys Val Phe
145                 150                 155                 160

Thr Glu Gly Asn Ile Ala Ala Met Ile Val Asn Lys Thr Val His Lys
                165                 170                 175

Met Ile Phe Ser Arg Gln Gly Gln Gly Tyr Arg His Met Asn Leu Thr
            180                 185                 190

Ser Thr Asn Lys Tyr Trp Thr Ser Ser Asn Gly Thr Gln Thr Asn Asp
        195                 200                 205

Thr Gly Cys Phe Gly Thr Leu Gln Glu Tyr Asn Ser Thr Lys Asn Gln
    210                 215                 220

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

Glu Val Lys Leu Thr Ser Thr Ser Thr Asp Ala Thr Lys Leu Asn Thr
                245                 250                 255

Thr Asp Pro Asn Ser Asp Asp Glu Asp Leu Thr Thr Ser Gly Ser Gly
            260                 265                 270

Ser Gly Glu Gln Glu Pro Tyr Thr Thr Ser Asp Ala Ala Thr Lys Gln
        275                 280                 285

Gly Leu Ser Ser Thr Met Pro Pro Thr Pro Ser Pro Gln Pro Ser Thr
    290                 295                 300

Pro Gln Gln Gly Gly Asn Asn Thr Asn His Ser Gln Gly Val Val Thr
305                 310                 315                 320
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Glu Pro Gly Lys Thr Asn Thr Thr Ala Gln Pro Ser Met Pro Pro His
                325                 330                 335

Asn Thr Thr Thr Ile Ser Thr Asn Asn Thr Ser Lys His Asn Leu Ser
            340                 345                 350

Thr Pro Ser Val Pro Ile Gln Asn Ala Thr Asn Tyr Asn Thr Gln Ser
        355                 360                 365

Thr Ala Pro Glu Asn Glu Gln Thr Ser Ala Pro Ser Lys Thr Thr Leu
    370                 375                 380

Leu Pro Thr Glu Asn Pro Thr Thr Ala Lys Ser Thr Asn Ser Thr Lys
385                 390                 395                 400

Ser Pro Thr Thr Thr Val Pro Asn Thr Thr Asn Lys Tyr Ser Thr Ser
                405                 410                 415

Pro Ser Pro Thr Pro Asn Ser Thr Ala Gln His Leu Val Tyr Phe Arg
            420                 425                 430

Arg Lys Arg Asn Ile Leu Trp Arg Glu Gly Asp Met Phe Pro Phe Leu
        435                 440                 445

Asp Gly Leu Ile Asn Ala Pro Ile Asp Phe Asp Pro Val Pro Asn Thr
    450                 455                 460

Lys Thr Ile Phe Asp Glu Ser Ser Ser Ser Gly Ala Ser Ala Glu Glu
465                 470                 475                 480

Asp Gln His Ala Ser Pro Asn Ile Ser Leu Thr Leu Ser Tyr Phe Pro
                485                 490                 495

Lys Val Asn Glu Asn Thr Ala His Ser Gly Glu Asn Glu Asn Asp Cys
            500                 505                 510

Asp Ala Glu Leu Arg Ile Trp Ser Val Gln Glu Asp Asp Leu Ala Ala
        515                 520                 525

Gly Leu Ser Trp Ile Pro Phe Phe Gly Pro Gly Ile Glu Gly Leu Tyr
    530                 535                 540

Thr Ala Gly Leu Ile Lys Asn Gln Asn Asn Leu Val Cys Arg Leu Arg
545                 550                 555                 560

Arg Leu Ala Asn Gln Thr Ala Lys Ser Leu Glu Leu Leu Leu Arg Val
                565                 570                 575

Thr Thr Glu Glu Arg Thr Phe Ser Leu Ile Asn Arg His Ala Ile Asp
            580                 585                 590
```

Phe Leu Leu Ala Arg Trp Gly Gly Thr Cys Lys Val Leu Gly Pro Asp
595 600 605

Cys Cys Ile Gly Ile Glu Asp Leu Ser Arg Asn Ile Ser Glu Gln Ile
610 615 620

Asp Gln Ile Lys Lys Asp Glu Gln Lys Glu Gly Thr Gly Trp Gly Leu
625 630 635 640

Gly Gly Lys Trp Trp Thr Ser Asp Trp Gly Val Leu Thr Asn Leu Gly
645 650 655

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

Cys Arg Ile Phe Thr Lys Tyr Ile Gly
675 680

<210> 175
<211> 681
<212> PRT
<213> Marburg virus - Musoke, Kenya, 1980

<400> 175

Met Lys Thr Thr Cys Phe Leu Ile Ser Leu Ile Leu Ile Gln Gly Thr
1 5 10 15

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

Val Asp Ser Val Cys Ser Gly Thr Leu Gln Lys Thr Glu Asp Val His
35 40 45

Leu Met Gly Phe Thr Leu Ser Gly Gln Lys Val Ala Asp Ser Pro Leu
50 55 60

Glu Ala Ser Lys Arg Trp Ala Phe Arg Thr Gly Val Pro Pro Lys Asn
65 70 75 80

Val Glu Tyr Thr Glu Gly Glu Glu Ala Lys Thr Cys Tyr Asn Ile Ser
85 90 95

Val Thr Asp Pro Ser Gly Lys Ser Leu Leu Leu Asp Pro Pro Thr Asn
100 105 110

Ile Arg Asp Tyr Pro Lys Cys Lys Thr Ile His His Ile Gln Gly Gln
115 120 125

Asn Pro His Ala Gln Gly Ile Ala Leu His Leu Trp Gly Ala Phe Phe
130 135 140

```
Leu Tyr Asp Arg Ile Ala Ser Thr Thr Met Tyr Arg Gly Lys Val Phe
145                 150                 155                 160

Thr Glu Gly Asn Ile Ala Ala Met Ile Val Asn Lys Thr Val His Lys
                165                 170                 175

Met Ile Phe Ser Arg Gln Gly Gln Gly Tyr Arg His Met Asn Leu Thr
            180                 185                 190

Ser Thr Asn Lys Tyr Trp Thr Ser Ser Asn Gly Thr Gln Thr Asn Asp
        195                 200                 205

Thr Gly Cys Phe Gly Ala Leu Gln Glu Tyr Asn Ser Thr Lys Asn Gln
    210                 215                 220

Thr Cys Ala Pro Ser Lys Ile Pro Pro Pro Leu Pro Thr Ala Arg Pro
225                 230                 235                 240

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

Thr Asp Pro Ser Ser Asp Asp Glu Asp Leu Ala Thr Ser Gly Ser Gly
            260                 265                 270

Ser Gly Glu Arg Glu Pro His Thr Thr Ser Asp Ala Val Thr Lys Gln
        275                 280                 285

Gly Leu Ser Ser Thr Met Pro Pro Thr Pro Ser Pro Gln Pro Ser Thr
    290                 295                 300

Pro Gln Gln Gly Gly Asn Asn Thr Asn His Ser Gln Asp Ala Val Thr
305                 310                 315                 320

Glu Leu Asp Lys Asn Asn Thr Thr Ala Gln Pro Ser Met Pro Pro His
                325                 330                 335

Asn Thr Thr Thr Ile Ser Thr Asn Asn Thr Ser Lys His Asn Phe Ser
            340                 345                 350

Thr Leu Ser Ala Pro Leu Gln Asn Thr Thr Asn Asp Asn Thr Gln Ser
        355                 360                 365

Thr Ile Thr Glu Asn Glu Gln Thr Ser Ala Pro Ser Ile Thr Thr Leu
    370                 375                 380

Pro Pro Thr Gly Asn Pro Thr Thr Ala Lys Ser Thr Ser Ser Lys Lys
385                 390                 395                 400

Gly Pro Ala Thr Thr Ala Pro Asn Thr Thr Asn Glu His Phe Thr Ser
                405                 410                 415
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Pro Pro Pro Thr Pro Ser Ser Thr Ala Gln His Leu Val Tyr Phe Arg
            420                 425                 430

Arg Lys Arg Ser Ile Leu Trp Arg Glu Gly Asp Met Phe Pro Phe Leu
        435                 440                 445

Asp Gly Leu Ile Asn Ala Pro Ile Asp Phe Asp Pro Val Pro Asn Thr
    450                 455                 460

Lys Thr Ile Phe Asp Glu Ser Ser Ser Ser Gly Ala Ser Ala Glu Glu
465                 470                 475                 480

Asp Gln His Ala Ser Pro Asn Ile Ser Leu Thr Leu Ser Tyr Phe Pro
                485                 490                 495

Asn Ile Asn Glu Asn Thr Ala Tyr Ser Gly Glu Asn Glu Asn Asp Cys
            500                 505                 510

Asp Ala Glu Leu Arg Ile Trp Ser Val Gln Glu Asp Asp Leu Ala Ala
        515                 520                 525

Gly Leu Ser Trp Ile Pro Phe Phe Gly Pro Gly Ile Glu Gly Leu Tyr
    530                 535                 540

Thr Ala Val Leu Ile Lys Asn Gln Asn Asn Leu Val Cys Arg Leu Arg
545                 550                 555                 560

Arg Leu Ala Asn Gln Thr Ala Lys Ser Leu Glu Leu Leu Leu Arg Val
                565                 570                 575

Thr Thr Glu Glu Arg Thr Phe Ser Leu Ile Asn Arg His Ala Ile Asp
            580                 585                 590

Phe Leu Leu Thr Arg Trp Gly Gly Thr Cys Lys Val Leu Gly Pro Asp
        595                 600                 605

Cys Cys Ile Gly Ile Glu Asp Leu Ser Lys Asn Ile Ser Glu Gln Ile
    610                 615                 620

Asp Gln Ile Lys Lys Asp Glu Gln Lys Glu Gly Thr Gly Trp Gly Leu
625                 630                 635                 640

Gly Gly Lys Trp Trp Thr Ser Asp Trp Gly Val Leu Thr Asn Leu Gly
                645                 650                 655

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

Cys Arg Ile Phe Thr Lys Tyr Ile Gly
        675                 680
```

<210> 176
<211> 681
<212> PRT
<213> Lake Victoria marburgvirus - Ci67

<400> 176

```
Met Lys Thr Thr Cys Leu Phe Ile Ser Leu Ile Leu Ile Gln Gly Ile
1               5                  10                  15

Lys Thr Leu Pro Ile Leu Glu Ile Ala Ser Asn Asn Gln Pro Gln Asn
            20                  25                  30

Val Asp Ser Val Cys Ser Gly Thr Leu Gln Lys Thr Glu Asp Val His
        35                  40                  45

Leu Met Gly Phe Thr Leu Ser Gly Gln Lys Val Ala Asp Ser Pro Leu
    50                  55                  60

Glu Ala Ser Lys Arg Trp Ala Phe Arg Thr Gly Val Pro Pro Lys Asn
65                  70                  75                  80

Val Glu Tyr Thr Glu Gly Glu Glu Ala Lys Thr Cys Tyr Asn Ile Ser
                85                  90                  95

Val Thr Asp Pro Ser Gly Lys Ser Leu Leu Leu Asp Pro Pro Thr Asn
            100                 105                 110

Ile Arg Asp Tyr Pro Lys Cys Lys Thr Ile His His Ile Gln Gly Gln
        115                 120                 125

Asn Pro His Ala Gln Gly Ile Ala Leu His Leu Trp Gly Ala Phe Phe
    130                 135                 140

Leu Tyr Asp Arg Ile Ala Ser Thr Thr Met Tyr Arg Gly Arg Val Phe
145                 150                 155                 160

Thr Glu Gly Asn Ile Ala Ala Met Ile Val Asn Lys Thr Val His Lys
                165                 170                 175

Met Ile Phe Ser Arg Gln Gly Gln Gly Tyr Arg His Met Asn Leu Thr
            180                 185                 190

Ser Thr Asn Lys Tyr Trp Thr Ser Asn Asn Gly Thr Gln Thr Asn Asp
        195                 200                 205

Thr Gly Cys Phe Gly Ala Leu Gln Glu Tyr Asn Ser Thr Lys Asn Gln
    210                 215                 220

Thr Cys Ala Pro Ser Lys Ile Pro Ser Pro Leu Pro Thr Ala Arg Pro
225                 230                 235                 240
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```
Glu Ile Lys Pro Thr Ser Thr Pro Thr Asp Ala Thr Thr Leu Asn Thr
                245                 250                 255

Thr Asp Pro Asn Asn Asp Asp Glu Asp Leu Ile Thr Ser Gly Ser Gly
            260                 265                 270

Ser Gly Glu Gln Glu Pro Tyr Thr Thr Ser Asp Ala Val Thr Lys Gln
        275                 280                 285

Gly Leu Ser Ser Thr Met Pro Pro Thr Pro Ser Pro Gln Pro Ser Thr
    290                 295                 300

Pro Gln Gln Glu Gly Asn Asn Thr Asp His Ser Gln Gly Thr Val Thr
305                 310                 315                 320

Glu Pro Asn Lys Thr Asn Thr Thr Ala Gln Pro Ser Met Pro Pro His
                325                 330                 335

Asn Thr Thr Ala Ile Ser Thr Asn Asn Thr Ser Lys Asn Asn Phe Ser
            340                 345                 350

Thr Leu Ser Val Ser Leu Gln Asn Thr Thr Asn Tyr Asp Thr Gln Ser
        355                 360                 365

Thr Ala Thr Glu Asn Glu Gln Thr Ser Ala Pro Ser Lys Thr Thr Leu
    370                 375                 380

Pro Pro Thr Gly Asn Leu Thr Thr Ala Lys Ser Thr Asn Asn Thr Lys
385                 390                 395                 400

Gly Pro Thr Thr Thr Ala Pro Asn Met Thr Asn Gly His Leu Thr Ser
                405                 410                 415

Pro Ser Pro Thr Pro Asn Pro Thr Thr Gln His Leu Val Tyr Phe Arg
            420                 425                 430

Lys Lys Arg Ser Ile Leu Trp Arg Glu Gly Asp Met Phe Pro Phe Leu
        435                 440                 445

Asp Gly Leu Ile Asn Ala Pro Ile Asp Phe Asp Pro Val Pro Asn Thr
    450                 455                 460

Lys Thr Ile Phe Asp Glu Ser Ser Ser Ser Gly Ala Ser Ala Glu Glu
465                 470                 475                 480

Asp Gln His Ala Ser Pro Asn Ile Ser Leu Thr Leu Ser Tyr Phe Pro
                485                 490                 495

Asn Ile Asn Glu Asn Thr Ala Tyr Ser Gly Glu Asn Glu Asn Asp Cys
            500                 505                 510
```

Asp Ala Glu Leu Arg Ile Trp Ser Val Gln Glu Asp Asp Leu Ala Ala
515 520 525

Gly Leu Ser Trp Ile Pro Phe Phe Gly Pro Gly Ile Glu Gly Leu Tyr
530 535 540

Thr Ala Gly Leu Ile Lys Asn Gln Asn Asn Leu Val Cys Arg Leu Arg
545 550 555 560

Arg Leu Ala Asn Gln Thr Ala Lys Ser Leu Glu Leu Leu Leu Arg Val
565 570 575

Thr Thr Glu Glu Arg Thr Phe Ser Leu Ile Asn Arg His Ala Ile Asp
580 585 590

Phe Leu Leu Thr Arg Trp Gly Gly Thr Cys Lys Val Leu Gly Pro Asp
595 600 605

Cys Cys Ile Gly Ile Glu Asp Leu Ser Arg Asn Ile Ser Glu Gln Ile
610 615 620

Asp Gln Ile Lys Lys Asp Glu Gln Lys Glu Gly Thr Gly Trp Gly Leu
625 630 635 640

Gly Gly Lys Trp Trp Thr Ser Asp Trp Gly Val Leu Thr Asn Leu Gly
645 650 655

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

Cys Arg Ile Phe Thr Lys Tyr Ile Gly
675 680

<210> 177
<211> 676
<212> PRT
<213> Zaire ebolavirus

<400> 177

Met Gly Val Thr Gly Ile Leu Gln Leu Pro Arg Asp Arg Phe Lys Arg
1 5 10 15

Thr Ser Phe Phe Leu Trp Val Ile Ile Leu Phe Gln Arg Thr Phe Ser
20 25 30

Ile Pro Leu Gly Val Ile His Asn Ser Thr Leu Gln Val Ser Asp Val
35 40 45

Asp Lys Leu Val Cys Arg Asp Lys Leu Ser Ser Thr Asn Gln Leu Arg
50 55 60

Ser Val Gly Leu Asn Leu Glu Gly Asn Gly Val Ala Thr Asp Val Pro

65 70 75 80

Ser Ala Thr Lys Arg Trp Gly Phe Arg Ser Gly Val Pro Pro Lys Val
85 90 95

Val Asn Tyr Glu Ala Gly Glu Trp Ala Glu Asn Cys Tyr Asn Leu Glu
100 105 110

Ile Lys Lys Pro Asp Gly Ser Glu Cys Leu Pro Ala Ala Pro Asp Gly
115 120 125

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

Gly Pro Cys Ala Gly Asp Phe Ala Phe His Lys Glu Gly Ala Phe Phe
145 150 155 160

Leu Tyr Asp Arg Leu Ala Ser Thr Val Ile Tyr Arg Gly Thr Thr Phe
165 170 175

Ala Glu Gly Val Val Ala Phe Leu Ile Leu Pro Gln Ala Lys Lys Asp
180 185 190

Phe Phe Ser Ser His Pro Leu Arg Glu Pro Val Asn Ala Thr Glu Asp
195 200 205

Pro Ser Ser Gly Tyr Tyr Ser Thr Thr Ile Arg Tyr Gln Ala Thr Gly
210 215 220

Phe Gly Thr Asn Glu Thr Glu Tyr Leu Phe Glu Val Asp Asn Leu Thr
225 230 235 240

Tyr Val Gln Leu Glu Ser Arg Phe Thr Pro Gln Phe Leu Leu Gln Leu
245 250 255

Asn Glu Thr Ile Tyr Thr Ser Gly Lys Arg Ser Asn Thr Thr Gly Lys
260 265 270

Leu Ile Trp Lys Val Asn Pro Glu Ile Asp Thr Thr Ile Gly Glu Trp
275 280 285

Ala Phe Trp Glu Thr Lys Lys Asn Leu Thr Arg Lys Ile Arg Ser Glu
290 295 300

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

Gln Ser Pro Ala Arg Thr Ser Ser Asp Pro Gly Thr Asn Thr Thr Thr
325 330 335

Glu Asp His Lys Ile Met Ala Ser Glu Asn Ser Ser Ala Met Val Gln

340 345 350

Val His Ser Gln Gly Arg Glu Ala Ala Val Ser His Leu Thr Thr Leu
355 360 365

Ala Thr Ile Ser Thr Ser Pro Gln Ser Leu Thr Thr Lys Pro Gly Pro
370 375 380

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

Ala Thr Gln Val Glu Gln His His Arg Arg Thr Asp Asn Asp Ser Thr
405 410 415

Ala Ser Asp Thr Pro Ser Ala Thr Thr Ala Ala Gly Pro Pro Lys Ala
420 425 430

Glu Asn Thr Asn Thr Ser Lys Ser Thr Asp Phe Leu Asp Pro Ala Thr
435 440 445

Thr Thr Ser Pro Gln Asn His Ser Glu Thr Ala Gly Asn Asn Asn Thr
450 455 460

His His Gln Asp Thr Gly Glu Glu Ser Ala Ser Ser Gly Lys Leu Gly
465 470 475 480

Leu Ile Thr Asn Thr Ile Ala Gly Val Ala Gly Leu Ile Thr Gly Gly
485 490 495

Arg Arg Thr Arg Arg Glu Ala Ile Val Asn Ala Gln Pro Lys Cys Asn
500 505 510

Pro Asn Leu His Tyr Trp Thr Thr Gln Asp Glu Gly Ala Ala Ile Gly
515 520 525

Leu Ala Trp Ile Pro Tyr Phe Gly Pro Ala Ala Glu Gly Ile Tyr Ile
530 535 540

Glu Gly Leu Met His Asn Gln Asp Gly Leu Ile Cys Gly Leu Arg Gln
545 550 555 560

Leu Ala Asn Glu Thr Thr Gln Ala Leu Gln Leu Phe Leu Arg Ala Thr
565 570 575

Thr Glu Leu Arg Thr Phe Ser Ile Leu Asn Arg Lys Ala Ile Asp Phe
580 585 590

Leu Leu Gln Arg Trp Gly Gly Thr Cys His Ile Leu Gly Pro Asp Cys
595 600 605

Cys Ile Glu Pro His Asp Trp Thr Lys Asn Ile Thr Asp Lys Ile Asp

610 615 620

Gln Ile Ile His Asp Phe Val Asp Lys Thr Leu Pro Asp Gln Gly Asp
625 630 635 640

Asn Asp Asn Trp Trp Thr Gly Trp Arg Gln Trp Ile Pro Ala Gly Ile
645 650 655

Gly Val Thr Gly Val Ile Ile Ala Val Ile Ala Leu Phe Cys Ile Cys
660 665 670

Lys Phe Val Phe
675

<210> 178
<211> 676
<212> PRT
<213> Ebola virus - Zaire (1995)

<400> 178

Met Gly Val Thr Gly Ile Leu Gln Leu Pro Arg Asp Arg Phe Lys Arg
1 5 10 15

Thr Ser Phe Phe Leu Trp Val Ile Ile Leu Phe Gln Arg Thr Phe Ser
20 25 30

Ile Pro Leu Gly Val Ile His Asn Ser Thr Leu Gln Val Ser Asp Val
35 40 45

Asp Lys Leu Val Cys Arg Asp Lys Leu Ser Ser Thr Asn Gln Leu Arg
50 55 60

Ser Val Gly Leu Asn Leu Glu Gly Asn Gly Val Ala Thr Asp Val Pro
65 70 75 80

Ser Ala Thr Lys Arg Trp Gly Phe Arg Ser Gly Val Pro Pro Lys Val
85 90 95

Val Asn Tyr Glu Ala Gly Glu Trp Ala Glu Asn Cys Tyr Asn Leu Glu
100 105 110

Ile Lys Lys Pro Asp Gly Ser Glu Cys Leu Pro Ala Ala Pro Asp Gly
115 120 125

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

Gly Pro Cys Ala Gly Asp Phe Ala Phe His Lys Glu Gly Ala Phe Phe
145 150 155 160

Leu Tyr Asp Arg Leu Ala Ser Thr Val Ile Tyr Arg Gly Thr Thr Phe
165 170 175

```
Ala Glu Gly Val Val Ala Phe Leu Ile Leu Pro Gln Ala Lys Lys Asp
            180                 185                 190

Phe Phe Ser Ser His Pro Leu Arg Glu Pro Val Asn Ala Thr Glu Asp
        195                 200                 205

Pro Ser Ser Gly Tyr Tyr Ser Thr Thr Ile Arg Tyr Gln Ala Thr Gly
    210                 215                 220

Phe Gly Thr Asn Glu Thr Glu Tyr Leu Phe Glu Val Asp Asn Leu Thr
225                 230                 235                 240

Tyr Val Gln Leu Glu Ser Arg Phe Thr Pro Gln Phe Leu Leu Gln Leu
                245                 250                 255

Asn Glu Thr Ile Tyr Thr Ser Gly Lys Arg Ser Asn Thr Thr Gly Lys
            260                 265                 270

Leu Ile Trp Lys Val Asn Pro Glu Ile Asp Thr Thr Ile Gly Glu Trp
        275                 280                 285

Ala Phe Trp Glu Thr Lys Lys Asn Leu Thr Arg Lys Ile Arg Ser Glu
    290                 295                 300

Glu Leu Ser Phe Thr Ala Val Ser Asn Arg Ala Lys Asn Ile Ser Gly
305                 310                 315                 320

Gln Ser Pro Ala Arg Thr Ser Ser Asp Pro Gly Thr Asn Thr Thr Thr
                325                 330                 335

Glu Asp His Lys Ile Met Ala Ser Glu Asn Ser Ser Ala Met Val Gln
            340                 345                 350

Val His Ser Gln Gly Arg Glu Ala Ala Val Ser His Leu Thr Thr Leu
        355                 360                 365

Ala Thr Ile Ser Thr Ser Pro Gln Pro Pro Thr Thr Lys Pro Gly Pro
    370                 375                 380

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

Ala Thr Gln Val Glu Gln His His Arg Arg Thr Asp Asn Asp Ser Thr
                405                 410                 415

Ala Ser Asp Thr Pro Pro Ala Thr Thr Ala Ala Gly Pro Leu Lys Ala
            420                 425                 430

Glu Asn Thr Asn Thr Ser Lys Gly Thr Asp Leu Leu Asp Pro Ala Thr
        435                 440                 445
```

```
Thr Thr Ser Pro Gln Asn His Ser Glu Thr Ala Gly Asn Asn Asn Thr
    450                 455                 460

His His Gln Asp Thr Gly Glu Glu Ser Ala Ser Ser Gly Lys Leu Gly
465                 470                 475                 480

Leu Ile Thr Asn Thr Ile Ala Gly Val Ala Gly Leu Ile Thr Gly Gly
                485                 490                 495

Arg Arg Ala Arg Arg Glu Ala Ile Val Asn Ala Gln Pro Lys Cys Asn
            500                 505                 510

Pro Asn Leu His Tyr Trp Thr Thr Gln Asp Glu Gly Ala Ala Ile Gly
        515                 520                 525

Leu Ala Trp Ile Pro Tyr Phe Gly Pro Ala Ala Glu Gly Ile Tyr Thr
    530                 535                 540

Glu Gly Leu Met His Asn Gln Asp Gly Leu Ile Cys Gly Leu Arg Gln
545                 550                 555                 560

Leu Ala Asn Glu Thr Thr Gln Ala Leu Gln Leu Phe Leu Arg Ala Thr
                565                 570                 575

Thr Glu Leu Arg Thr Phe Ser Ile Leu Asn Arg Lys Ala Ile Asp Phe
            580                 585                 590

Leu Leu Gln Arg Trp Gly Gly Thr Cys His Ile Leu Gly Pro Asp Cys
        595                 600                 605

Cys Ile Glu Pro His Asp Trp Thr Lys Asn Ile Thr Asp Lys Ile Asp
    610                 615                 620

Gln Ile Ile His Asp Phe Val Asp Lys Thr Leu Pro Asp Gln Gly Asp
625                 630                 635                 640

Asn Asp Asn Trp Trp Thr Gly Trp Arg Gln Trp Ile Pro Ala Gly Ile
                645                 650                 655

Gly Val Thr Gly Val Ile Ile Ala Val Ile Ala Leu Phe Cys Ile Cys
            660                 665                 670

Lys Phe Val Phe
        675
```

<210> 179
<211> 676
<212> PRT
<213> Sudan ebolavirus

<400> 179

```
Met Glu Gly Leu Ser Leu Leu Gln Leu Pro Arg Asp Lys Phe Arg Lys
1               5                  10                  15

Ser Ser Phe Phe Val Trp Val Ile Ile Leu Phe Gln Lys Ala Phe Ser
            20                  25                  30

Met Pro Leu Gly Val Val Thr Asn Ser Thr Leu Glu Val Thr Glu Ile
        35                  40                  45

Asp Gln Leu Val Cys Lys Asp His Leu Ala Ser Thr Asp Gln Leu Lys
    50                  55                  60

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

Ser Ala Thr Lys Arg Trp Gly Phe Arg Ser Gly Val Pro Pro Gln Val
                85                  90                  95

Val Ser Tyr Glu Ala Gly Glu Trp Ala Glu Asn Cys Tyr Asn Leu Glu
            100                 105                 110

Ile Lys Lys Pro Asp Gly Ser Glu Cys Leu Pro Pro Pro Pro Asp Gly
        115                 120                 125

Val Arg Gly Phe Pro Arg Cys Arg Tyr Val His Lys Ala Gln Gly Thr
    130                 135                 140

Gly Pro Cys Pro Gly Asp Tyr Ala Phe His Lys Asp Gly Ala Phe Phe
145                 150                 155                 160

Leu Tyr Asp Arg Leu Ala Ser Thr Val Ile Tyr Arg Gly Val Asn Phe
                165                 170                 175

Ala Glu Gly Val Ile Ala Phe Leu Ile Leu Ala Lys Pro Lys Glu Thr
            180                 185                 190

Phe Leu Gln Ser Pro Pro Ile Arg Glu Ala Ala Asn Tyr Thr Glu Asn
        195                 200                 205

Thr Ser Ser Tyr Tyr Ala Thr Ser Tyr Leu Glu Tyr Glu Ile Glu Asn
    210                 215                 220

Phe Gly Ala Gln His Ser Thr Thr Leu Phe Lys Ile Asn Asn Asn Thr
225                 230                 235                 240

Phe Val Leu Leu Asp Arg Pro His Thr Pro Gln Phe Leu Phe Gln Leu
                245                 250                 255

Asn Asp Thr Ile Gln Leu His Gln Gln Leu Ser Asn Thr Thr Gly Lys
            260                 265                 270
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```
Leu Ile Trp Thr Leu Asp Ala Asn Ile Asn Ala Asp Ile Gly Glu Trp
        275                 280                 285

Ala Phe Trp Glu Asn Lys Lys Asn Leu Ser Glu Gln Leu Arg Gly Glu
    290                 295                 300

Glu Leu Ser Phe Glu Thr Leu Ser Leu Asn Glu Thr Glu Asp Asp Asp
305                 310                 315                 320

Ala Thr Ser Ser Arg Thr Thr Lys Gly Arg Ile Ser Asp Arg Ala Thr
                325                 330                 335

Arg Lys Tyr Ser Asp Leu Val Pro Lys Asp Ser Pro Gly Met Val Ser
            340                 345                 350

Leu His Val Pro Glu Gly Glu Thr Thr Leu Pro Ser Gln Asn Ser Thr
        355                 360                 365

Glu Gly Arg Arg Val Asp Val Asn Thr Gln Glu Thr Ile Thr Glu Thr
    370                 375                 380

Thr Ala Thr Ile Ile Gly Thr Asn Gly Asn Asn Met Gln Ile Ser Thr
385                 390                 395                 400

Ile Gly Thr Gly Leu Ser Ser Ser Gln Ile Leu Ser Ser Ser Pro Thr
                405                 410                 415

Met Ala Pro Ser Pro Glu Thr Gln Thr Ser Thr Thr Tyr Thr Pro Lys
            420                 425                 430

Leu Pro Val Met Thr Thr Glu Glu Pro Thr Thr Pro Pro Arg Asn Ser
        435                 440                 445

Pro Gly Ser Thr Thr Glu Ala Pro Thr Leu Thr Thr Pro Glu Asn Ile
    450                 455                 460

Thr Thr Ala Val Lys Thr Val Trp Ala Gln Glu Ser Thr Ser Asn Gly
465                 470                 475                 480

Leu Ile Thr Ser Thr Val Thr Gly Ile Leu Gly Ser Leu Gly Leu Arg
                485                 490                 495

Lys Arg Ser Arg Arg Gln Val Asn Thr Arg Ala Thr Gly Lys Cys Asn
            500                 505                 510

Pro Asn Leu His Tyr Trp Thr Ala Gln Glu Gln His Asn Ala Ala Gly
        515                 520                 525

Ile Ala Trp Ile Pro Tyr Phe Gly Pro Gly Ala Glu Gly Ile Tyr Thr
    530                 535                 540
```

Glu Gly Leu Met His Asn Gln Asn Ala Leu Val Cys Gly Leu Arg Gln
545 550 555 560

Leu Ala Asn Glu Thr Thr Gln Ala Leu Gln Leu Phe Leu Arg Ala Thr
565 570 575

Thr Glu Leu Arg Thr Tyr Thr Ile Leu Asn Arg Lys Ala Ile Asp Phe
580 585 590

Leu Leu Arg Arg Trp Gly Gly Thr Cys Arg Ile Leu Gly Pro Asp Cys
595 600 605

Cys Ile Glu Pro His Asp Trp Thr Lys Asn Ile Thr Asp Lys Ile Asn
610 615 620

Gln Ile Ile His Asp Phe Ile Asp Asn Pro Leu Pro Asn Gln Asp Asn
625 630 635 640

Asp Asp Asn Trp Trp Thr Gly Trp Arg Gln Trp Ile Pro Ala Gly Ile
645 650 655

Gly Ile Thr Gly Ile Ile Ile Ala Ile Ile Ala Leu Leu Cys Val Cys
660 665 670

Lys Leu Leu Cys
675

<210> 180
<211> 676
<212> PRT
<213> Zaire ebolavirus

<400> 180

Met Gly Val Thr Gly Ile Leu Gln Leu Pro Arg Asp Arg Phe Lys Arg
1 5 10 15

Thr Ser Phe Phe Leu Trp Val Ile Ile Leu Phe Gln Arg Thr Phe Ser
20 25 30

Ile Pro Leu Gly Val Ile His Asn Ser Thr Leu Gln Val Ser Asp Val
35 40 45

Asp Lys Leu Val Cys Arg Asp Lys Leu Ser Ser Thr Asn Gln Leu Arg
50 55 60

Ser Val Gly Leu Asn Leu Glu Gly Asn Gly Val Ala Thr Asp Val Pro
65 70 75 80

Ser Val Thr Lys Arg Trp Gly Phe Arg Ser Gly Val Pro Pro Lys Val
85 90 95

```
Val Asn Tyr Glu Ala Gly Glu Trp Ala Glu Asn Cys Tyr Asn Leu Glu
            100                 105                 110

Ile Lys Lys Pro Asp Gly Ser Glu Cys Leu Pro Ala Ala Pro Asp Gly
        115                 120                 125

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

Gly Pro Cys Ala Gly Asp Phe Ala Phe His Lys Glu Gly Ala Phe Phe
145                 150                 155                 160

Leu Tyr Asp Arg Leu Ala Ser Thr Val Ile Tyr Arg Gly Thr Thr Phe
                165                 170                 175

Ala Glu Gly Val Val Ala Phe Leu Ile Leu Pro Gln Ala Lys Lys Asp
            180                 185                 190

Phe Phe Ser Ser His Pro Leu Arg Glu Pro Val Asn Ala Thr Glu Asp
        195                 200                 205

Pro Ser Ser Gly Tyr Tyr Ser Thr Thr Ile Arg Tyr Gln Ala Thr Gly
    210                 215                 220

Phe Gly Thr Asn Glu Thr Glu Tyr Leu Phe Glu Val Asp Asn Leu Thr
225                 230                 235                 240

Tyr Val Gln Leu Glu Ser Arg Phe Thr Pro Gln Phe Leu Leu Gln Leu
                245                 250                 255

Asn Glu Thr Ile Tyr Ala Ser Gly Lys Arg Ser Asn Thr Thr Gly Lys
            260                 265                 270

Leu Ile Trp Lys Val Asn Pro Glu Ile Asp Thr Thr Ile Gly Glu Trp
        275                 280                 285

Ala Phe Trp Glu Thr Lys Lys Asn Leu Thr Arg Lys Ile Arg Ser Glu
    290                 295                 300

Glu Leu Ser Phe Thr Ala Val Ser Asn Gly Pro Lys Asn Ile Ser Gly
305                 310                 315                 320

Gln Ser Pro Ala Arg Thr Ser Ser Asp Pro Glu Thr Asn Thr Thr Asn
                325                 330                 335

Glu Asp His Lys Ile Met Ala Ser Glu Asn Ser Ser Ala Met Val Gln
            340                 345                 350

Val His Ser Gln Gly Arg Lys Ala Ala Val Ser His Leu Thr Thr Leu
        355                 360                 365
```

```
Ala Thr Ile Ser Thr Ser Pro Gln Pro Pro Thr Thr Lys Thr Gly Pro
    370                 375                 380

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

Ala Thr Gln Val Gly Gln His His Arg Arg Ala Asp Asn Asp Ser Thr
                405                 410                 415

Ala Ser Asp Thr Pro Pro Ala Thr Thr Ala Ala Gly Pro Leu Lys Ala
            420                 425                 430

Glu Asn Thr Asn Thr Ser Lys Ser Ala Asp Ser Leu Asp Leu Ala Thr
        435                 440                 445

Thr Thr Ser Pro Gln Asn Tyr Ser Glu Thr Ala Gly Asn Asn Asn Thr
    450                 455                 460

His His Gln Asp Thr Gly Glu Glu Ser Ala Ser Ser Gly Lys Leu Gly
465                 470                 475                 480

Leu Ile Thr Asn Thr Ile Ala Gly Val Ala Gly Leu Ile Thr Gly Gly
                485                 490                 495

Arg Arg Thr Arg Arg Glu Val Ile Val Asn Ala Gln Pro Lys Cys Asn
            500                 505                 510

Pro Asn Leu His Tyr Trp Thr Thr Gln Asp Glu Gly Ala Ala Ile Gly
        515                 520                 525

Leu Ala Trp Ile Pro Tyr Phe Gly Pro Ala Ala Glu Gly Ile Tyr Thr
    530                 535                 540

Glu Gly Leu Met His Asn Gln Asp Gly Leu Ile Cys Gly Leu Arg Gln
545                 550                 555                 560

Leu Ala Asn Glu Thr Thr Gln Ala Leu Gln Leu Phe Leu Arg Ala Thr
                565                 570                 575

Thr Glu Leu Arg Thr Phe Ser Ile Leu Asn Arg Lys Ala Ile Asp Phe
            580                 585                 590

Leu Leu Gln Arg Trp Gly Gly Thr Cys His Ile Leu Gly Pro Asp Cys
        595                 600                 605

Cys Ile Glu Pro His Asp Trp Thr Lys Asn Ile Thr Asp Lys Ile Asp
    610                 615                 620

Gln Ile Ile His Asp Phe Val Asp Lys Thr Leu Pro Asp Gln Gly Asp
625                 630                 635                 640
```

Asn Asp Asn Trp Trp Thr Gly Trp Arg Gln Trp Ile Pro Ala Gly Ile
645 650 655

Gly Val Thr Gly Val Ile Ile Ala Val Ile Ala Leu Phe Cys Ile Cys
660 665 670

Lys Phe Val Phe
675

<210> 181
<211> 487
<212> PRT
<213> Zaire ebolavirus

<400> 181

Met Gly Val Thr Gly Ile Leu Gln Leu Pro Arg Asp Arg Phe Lys Arg
1 5 10 15

Thr Ser Phe Phe Leu Trp Val Ile Ile Leu Phe Gln Arg Thr Phe Ser
20 25 30

Ile Pro Leu Gly Val Ile His Asn Ser Thr Leu Gln Val Ser Asp Val
35 40 45

Asp Lys Leu Val Cys Arg Asp Lys Leu Ser Ser Thr Asn Gln Leu Arg
50 55 60

Pro Val Gly Leu Asn Leu Glu Gly Asn Gly Val Ala Thr Asp Val Pro
65 70 75 80

Ser Ala Thr Lys Arg Trp Gly Phe Arg Ser Gly Val Pro Pro Lys Val
85 90 95

Val Asn Tyr Glu Ala Gly Glu Trp Ala Glu Asn Cys Tyr Asn Leu Glu
100 105 110

Ile Lys Lys Pro Asp Gly Ser Glu Cys Leu Pro Ala Ala Pro Asp Gly
115 120 125

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

Gly Pro Cys Ala Gly Asp Phe Ala Phe His Lys Glu Gly Ala Phe Phe
145 150 155 160

Leu Tyr Asp Arg Leu Ala Ser Thr Val Ile Tyr Arg Gly Thr Thr Phe
165 170 175

Ala Glu Gly Val Val Ala Phe Leu Ile Leu Pro Gln Ala Lys Lys Asp
180 185 190

Phe Phe Ser Ser His Pro Leu Arg Glu Pro Val Asn Ala Thr Glu Asp

195 200 205

Pro Ser Ser Gly Tyr Tyr Ser Thr Thr Ile Arg Tyr Gln Ala Thr Gly
210 215 220

Phe Gly Thr Asn Glu Thr Glu Tyr Leu Phe Glu Val Asp Asn Leu Thr
225 230 235 240

Tyr Val Gln Leu Glu Pro Arg Phe Thr Pro Gln Phe Leu Leu Gln Leu
245 250 255

Asn Glu Thr Ile Tyr Thr Ser Gly Lys Arg Ser Asn Thr Thr Gly Lys
260 265 270

Leu Ile Trp Lys Val Asn Pro Glu Ile Asp Thr Thr Ile Gly Glu Trp
275 280 285

Ala Phe Trp Glu Thr Lys Lys Asn Leu Thr Arg Lys Ile Arg Ser Glu
290 295 300

Glu Leu Ser Phe Thr Val Val Ser Asn Thr His His Gln Asp Thr Gly
305 310 315 320

Glu Glu Ser Ala Ser Ser Gly Lys Leu Gly Leu Ile Thr Asn Thr Ile
325 330 335

Ala Gly Val Ala Gly Leu Ile Thr Gly Gly Arg Arg Thr Arg Arg Glu
340 345 350

Ala Ile Val Asn Ala Gln Pro Lys Cys Asn Pro Asn Leu His Tyr Trp
355 360 365

Thr Thr Gln Asp Glu Gly Ala Ala Ile Gly Leu Ala Trp Ile Pro Tyr
370 375 380

Phe Gly Pro Ala Ala Glu Gly Ile Tyr Thr Glu Gly Leu Met His Asn
385 390 395 400

Gln Asp Gly Leu Ile Cys Gly Leu Arg Gln Leu Ala Asn Glu Thr Thr
405 410 415

Gln Ala Leu Gln Leu Phe Leu Arg Ala Thr Thr Glu Leu Arg Thr Phe
420 425 430

Ser Ile Leu Asn Arg Lys Ala Ile Asp Phe Leu Leu Gln Arg Trp Gly
435 440 445

Gly Thr Cys His Ile Leu Gly Pro Asp Cys Cys Ile Glu Pro His Asp
450 455 460

Trp Thr Lys Asn Ile Thr Asp Lys Ile Asp Gln Ile Ile His Asp Phe

465 470 475 480

Val Asp Lys Thr Leu Pro Asp
485

<210> 182
<211> 487
<212> PRT
<213> Zaire ebolavirus

<400> 182

Met Gly Val Thr Gly Ile Leu Gln Leu Pro Arg Asp Arg Phe Lys Arg
1 5 10 15

Thr Ser Phe Phe Leu Trp Val Ile Ile Leu Phe Gln Arg Thr Phe Ser
20 25 30

Ile Pro Leu Gly Val Ile His Asn Ser Thr Leu Gln Val Ser Glu Val
35 40 45

Asp Lys Leu Val Cys Arg Asp Lys Leu Ser Ser Thr Asn Gln Leu Arg
50 55 60

Ser Val Gly Leu Asn Leu Glu Gly Asn Gly Val Ala Thr Asp Val Pro
65 70 75 80

Ser Ala Thr Lys Arg Trp Gly Phe Arg Ser Gly Val Pro Pro Lys Val
85 90 95

Val Asn Tyr Glu Ala Gly Glu Trp Ala Glu Asn Cys Tyr Asn Leu Glu
100 105 110

Ile Lys Lys Pro Asp Gly Ser Glu Cys Leu Pro Ala Ala Pro Asp Gly
115 120 125

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

Gly Pro Cys Ala Gly Asp Phe Ala Phe His Lys Glu Gly Ala Phe Phe
145 150 155 160

Leu Tyr Asp Arg Leu Ala Ser Thr Val Ile Tyr Arg Gly Thr Thr Phe
165 170 175

Ala Glu Gly Val Val Ala Phe Leu Ile Leu Pro Gln Ala Lys Lys Asp
180 185 190

Phe Phe Ser Ser His Pro Leu Arg Glu Pro Val Asn Ala Thr Glu Asp
195 200 205

Pro Ser Ser Gly Tyr Tyr Ser Thr Thr Ile Arg Tyr Gln Ala Thr Gly
210 215 220

```
Phe Gly Thr Asn Glu Thr Glu Tyr Leu Phe Glu Val Asp Asn Leu Thr
225                 230                 235                 240

Tyr Val Gln Leu Glu Ser Arg Phe Thr Pro Gln Phe Leu Leu Gln Leu
                245                 250                 255

Asn Glu Thr Ile Tyr Thr Ser Gly Lys Arg Ser Asn Thr Thr Gly Lys
            260                 265                 270

Leu Ile Trp Lys Val Asn Pro Glu Ile Asp Thr Thr Ile Gly Glu Trp
        275                 280                 285

Ala Phe Trp Glu Thr Lys Lys Asn Leu Thr Arg Lys Ile Arg Ser Glu
    290                 295                 300

Glu Leu Ser Phe Thr Ala Val Ser Asn Thr His His Gln Asp Thr Gly
305                 310                 315                 320

Glu Glu Ser Ala Ser Ser Gly Lys Leu Gly Leu Ile Thr Asn Thr Ile
                325                 330                 335

Ala Gly Val Ala Gly Leu Ile Thr Gly Gly Arg Arg Ala Arg Arg Glu
            340                 345                 350

Ala Ile Val Asn Ala Gln Pro Lys Cys Asn Pro Asn Leu His Tyr Trp
        355                 360                 365

Thr Thr Gln Asp Glu Gly Ala Ala Ile Gly Leu Ala Trp Ile Pro Tyr
    370                 375                 380

Phe Gly Pro Ala Ala Glu Gly Ile Tyr Thr Glu Gly Leu Met His Asn
385                 390                 395                 400

Gln Asp Gly Leu Ile Cys Gly Leu Arg Gln Leu Ala Asn Glu Thr Thr
                405                 410                 415

Gln Ala Leu Gln Leu Phe Leu Arg Ala Thr Thr Glu Leu Arg Thr Phe
            420                 425                 430

Ser Ile Leu Asn Arg Lys Ala Ile Asp Phe Leu Leu Gln Arg Trp Gly
        435                 440                 445

Gly Thr Cys His Ile Leu Gly Pro Asp Cys Cys Ile Glu Pro His Asp
    450                 455                 460

Trp Thr Lys Asn Ile Thr Asp Lys Ile Asp Gln Ile Ile His Asp Phe
465                 470                 475                 480

Val Asp Lys Thr Leu Pro Asp
                485
```

<210> 183
<211> 487
<212> PRT
<213> Sudan ebolavirus

<400> 183

```
Met Gly Gly Leu Ser Leu Leu Gln Leu Pro Arg Asp Lys Phe Arg Lys
1               5                   10                  15

Ser Ser Phe Phe Val Trp Val Ile Ile Leu Phe Gln Lys Ala Phe Ser
            20                  25                  30

Met Pro Leu Gly Val Val Thr Asn Ser Thr Leu Glu Val Thr Glu Ile
        35                  40                  45

Asp Gln Leu Val Cys Lys Asp His Leu Ala Ser Thr Asp Gln Leu Lys
    50                  55                  60

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

Ser Ala Thr Lys Arg Trp Gly Phe Arg Ser Gly Val Pro Pro Lys Val
                85                  90                  95

Val Ser Tyr Glu Ala Gly Glu Trp Ala Glu Asn Cys Tyr Asn Leu Glu
            100                 105                 110

Ile Lys Lys Pro Asp Gly Ser Glu Cys Leu Pro Pro Pro Pro Asp Gly
        115                 120                 125

Val Arg Gly Phe Pro Arg Cys Arg Tyr Val His Lys Ala Gln Gly Thr
    130                 135                 140

Gly Pro Cys Pro Gly Asp Tyr Ala Phe His Lys Asp Gly Ala Phe Phe
145                 150                 155                 160

Leu Tyr Asp Arg Leu Ala Ser Thr Val Ile Tyr Arg Gly Val Asn Phe
                165                 170                 175

Ala Glu Gly Val Ile Ala Phe Leu Ile Leu Ala Lys Pro Lys Glu Thr
            180                 185                 190

Phe Leu Gln Ser Pro Pro Ile Arg Glu Ala Val Asn Tyr Thr Glu Asn
        195                 200                 205

Thr Ser Ser Tyr Tyr Ala Thr Ser Tyr Leu Glu Tyr Glu Ile Glu Asn
    210                 215                 220

Phe Gly Ala Gln His Ser Thr Thr Leu Phe Lys Ile Asp Asn Asn Thr
225                 230                 235                 240
```

```
Phe Val Arg Leu Asp Arg Pro His Thr Pro Gln Phe Leu Phe Gln Leu
                245                 250                 255

Asn Asp Thr Ile His Leu His Gln Gln Leu Ser Asn Thr Thr Gly Arg
            260                 265                 270

Leu Ile Trp Thr Leu Asp Ala Asn Ile Asn Ala Asp Ile Gly Glu Trp
        275                 280                 285

Ala Phe Trp Glu Asn Lys Lys Asn Leu Ser Glu Gln Leu Arg Gly Glu
    290                 295                 300

Glu Leu Ser Phe Glu Ala Leu Ser Asn Ile Thr Thr Ala Val Lys Thr
305                 310                 315                 320

Val Leu Pro Gln Glu Ser Thr Ser Asn Gly Leu Ile Thr Ser Thr Val
                325                 330                 335

Thr Gly Ile Leu Gly Ser Leu Gly Leu Arg Lys Arg Ser Arg Arg Gln
            340                 345                 350

Thr Asn Thr Lys Ala Thr Gly Lys Cys Asn Pro Asn Leu His Tyr Trp
        355                 360                 365

Thr Ala Gln Glu Gln His Asn Ala Ala Gly Ile Ala Trp Ile Pro Tyr
    370                 375                 380

Phe Gly Pro Gly Ala Glu Gly Ile Tyr Thr Glu Gly Leu Met His Asn
385                 390                 395                 400

Gln Asn Ala Leu Val Cys Gly Leu Arg Gln Leu Ala Asn Glu Thr Thr
                405                 410                 415

Gln Ala Leu Gln Leu Phe Leu Arg Ala Thr Thr Glu Leu Arg Thr Tyr
            420                 425                 430

Thr Ile Leu Asn Arg Lys Ala Ile Asp Phe Leu Leu Arg Arg Trp Gly
        435                 440                 445

Gly Thr Cys Arg Ile Leu Gly Pro Asp Cys Cys Ile Glu Pro His Asp
    450                 455                 460

Trp Thr Lys Asn Ile Thr Asp Lys Ile Asn Gln Ile Ile His Asp Phe
465                 470                 475                 480

Ile Asp Asn Pro Leu Pro Asn
                485
```

<210> 184
<211> 15
<212> PRT

<213> Ravn virus - Ravn, Kenya, 1987

<400> 184

Leu Ile Asn Thr Glu Ile Asp Phe Asp Pro Ile Pro Asn Thr Glu
1 5 10 15

<210> 185
<211> 15
<212> PRT
<213> Ravn virus - Ravn, Kenya, 1987

<400> 185

Ile Asp Phe Asp Pro Ile Pro Asn Thr Glu Thr Ile Phe Asp Glu
1 5 10 15

<210> 186
<211> 15
<212> PRT
<213> Ravn virus - Ravn, Kenya, 1987

<400> 186

Ile Asp Phe Asp Pro Ile Pro Asn Thr Glu Thr Ile Phe Asp Glu
1 5 10 15

<210> 187
<211> 15
<212> PRT
<213> Ravn virus - Ravn, Kenya, 1987

<400> 187

Ile Pro Asn Thr Glu Thr Ile Phe Asp Glu Ser Pro Ser Phe Asn
1 5 10 15

<210> 188
<211> 15
<212> PRT
<213> Ravn virus - Ravn, Kenya, 1987

<400> 188

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

<210> 189
<211> 15
<212> PRT
<213> Ravn virus - Ravn, Kenya, 1987

<400> 189

Leu Ile Asn Thr Glu Ile Asp Phe Asp Pro Ile Pro Asn Thr Glu
1 5 10 15

<210> 190
<211> 15
<212> PRT
<213> Ravn virus - Ravn, Kenya, 1987

<400> 190

Ile Asp Phe Asp Pro Ile Pro Asn Thr Glu Thr Ile Phe Asp Glu
1 5 10 15

<210> 191
<211> 15
<212> PRT
<213> Ravn virus - Ravn, Kenya, 1987

<400> 191

Leu Ile Asn Thr Glu Ile Asp Phe Asp Pro Ile Pro Asn Thr Glu
1 5 10 15

<210> 192
<211> 15
<212> PRT
<213> Ravn virus - Ravn, Kenya, 1987

<400> 192

Ile Asp Phe Asp Pro Ile Pro Asn Thr Glu Thr Ile Phe Asp Glu
1 5 10 15

<210> 193
<211> 15
<212> PRT
<213> Ravn virus - Ravn, Kenya, 1987

<400> 193

Ile Pro Asn Thr Glu Thr Ile Phe Asp Glu Ser Pro Ser Glu Asn
1 5 10 15

<210> 194
<211> 15
<212> PRT
<213> Ravn virus - Ravn, Kenya, 1987

<400> 194

Leu Ile Asn Thr Glu Ile Asp Phe Asp Pro Ile Pro Asn Thr Glu
1 5 10 15

<210> 195
<211> 15
<212> PRT
<213> Ravn virus - Ravn, Kenya, 1987

<400> 195

Ile Asp Phe Asp Pro Ile Pro Asn Thr Glu Thr Ile Phe Asp Glu
1 5 10 15

<210> 196
<211> 15
<212> PRT
<213> Ravn virus - Ravn, Kenya, 1987

<400> 196

Leu Ile Asn Thr Glu Ile Asp Phe Asp Pro Ile Pro Asn Thr Glu
1 5 10 15

<210> 197
<211> 15
<212> PRT
<213> Ravn virus - Ravn, Kenya, 1987

<400> 197

Ile Asp Phe Asp Pro Ile Pro Asn Thr Glu Thr Ile Phe Asp Glu
1 5 10 15

<210> 198
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Marburg virus Ravn GPe delta muc

<400> 198

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

Glu Thr Ile Phe Asp Glu Ser
20

<210> 199
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Marburg virus Ci67 GPe delta muc

<400> 199

Asp Gly Leu Ile Asn Ala Pro Ile Asp Phe Asp Pro Val Pro Asn Thr
1 5 10 15

Lys Thr Ile Phe Asp Glu Ser
20

<210> 200
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Marburg virus Musoke GPe delta muc

<400> 200

Asp Gly Leu Ile Asn Ala Pro Ile Asp Phe Asp Pro Val Pro Asn Thr
1 5 10 15

Lys Thr Ile Phe Asp Glu Ser
20

<210> 201
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Marburg virus Angola GPe delta muc

<400> 201

Asp Gly Leu Ile Asn Ala Pro Ile Asp Phe Asp Pro Val Pro Asn Thr
1 5 10 15

Lys Thr Ile Phe Asp Glu Ser
20

<210> 202
<211> 337
<212> DNA
<213> Mus sp.

<400> 202
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atctcttgca gatctagtca gagccttgta cacagtaatg gaaacaccta tttacattgg 120

tacctgcaga agccaggcca gtctccaaac ctcctgatct acaaagtttc caaccgattt 180

tctggggtcc cagacaggtt cagtggcagt ggatcaggga cagatttcac actcaagatc 240

agcagagtgg aggctgagga tctgggagtt tatttctgct ctcaaagtac acatgttccg 300

tggacgttcg gtggaggcac caagctggaa atcaaac 337

<210> 203
<211> 358
<212> DNA
<213> Mus sp.

<400> 203
gaggtgcagc ttgttgagtc tggtggagga ttggtgcagc ctaaaggatc attgaaactc 60

tcatgtgccg cctctggttt cgccttcaat tcctatgcca tgcactgggt ctgccaggct 120

ccaggaaagg gtttggaatg ggttgctcgc ataagaatta aaagtggtaa ttatgcaaca 180

tcttatgccg gttcagtgac agacagattc accgtctcca gagatgattc acaaaacttg 240

ttctatctgc aaatgaacaa cctgaaaact gaggacacag ccatgtatta ctgtgtgaga 300

gagtgggaag gggctatgga ctactggggt caaggaacct cagtcaccgt ctcctcag 358

<210> 204
<211> 334
<212> DNA
<213> Mus sp.

<400> 204
gacattgtgc tgacccaatc tccagcttct ttggctgtgt ctctagggca gagggcctcc 60

atctcctgca aggccagcca aagtgttgat catgatggtg atagttatat gaactggtac 120

caacagaaac caggacagcc acccaaactc ctcatctatg ctacatccaa tctagaatct 180

gggatcccag ccaggtttag tggcagtggg tctgggacag acttcaccct caacatccat 240

cctgtggagg aggaggatgc tgcaacctat tactgtcagc aaagttatga ggttccgctc 300

acgttcggtg ctgggaccaa gctggagctg aaac 334

<210> 205
<211> 343
<212> DNA
<213> Mus sp.

<400> 205
gaggtccagc tgcaacagtc tggacctgag ctggtgaagc ctggggcttc agtgaagata 60

tcctgcagga cttctggata cacattcact gaatacacca ttcactgggt gaagcagagc 120

cgtggaaaga gccttgagtg gattggaggt attaatccta accatggtgg tactctctac 180

aaccagaagt tcaaggtcaa ggccacattg actgtagaca agtcctccag cacagcctac 240

atggagctcc gcagcctgac atctgaggat tctgcagtct attactgtgc aagatttact 300

tacgactact ggggccaagg caccactctc acagtctcct cag 343

<210> 206
<211> 337
<212> DNA
<213> Mus sp.

<400> 206
gatgttgtga tgacccagac tcccctcact ttgtcggtta ccattggaca gccagcctcc 60

atctcttgca cgtcaagtca gagcctctta aatagtgatg gggagacata tttgaattgg 120

ttgttacaga ggccaggcca gtctccaaag cgcctaatcc atctggtgtc taaactggac 180

tctggagtcc ctgacaggat cactggcagt ggatctggga cagatttcac actgaaaatc 240

aacagagtgg aggctgagga tttgggaatt tattattgct ggcaaggtac acattttccg 300

tggacgttcg gtggaggcac caagctggaa atcaaac 337

<210> 207
<211> 349
<212> DNA
<213> Mus sp.

<400> 207
caggtccagt tgcagcagtc tggaactgag ctggtaaggc ctgggacttc agtgaagata 60

tcctgcaagg cttctggata cgacttcact aacttttggc taggttggat aaagcagagg 120

cctggacatg gacttgaatg gattggagat atttaccctg gaggtgataa tacttactac 180

aatgagaagt tcaagggcaa agtcacgctg actgcagaca aatcctcgaa cacagcctat 240

atgcagttca gtagcctgac atctgaggac tctgctgtct atttctgttt tatgattctc 300

tatactttgg actactgggg tcaaggaacc tcagtcaccg tctcctcag 349