SEQUENCE LISTING

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<120> MONOCLONAL ANTIBODY NEUTRALIZING HUMAN RESPIRATORY SYNCYTIAL VIRUS

<130> 24158-US-PCT

<140> US62/247,841
<141> 2015-10-29

<140> US 62/367,359
<141> 2016-07-27

<160> 22

<170> PatentIn version 3.5

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Asp Ser Ala Met Ser
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Phe Ile Lys Ser Lys Thr Tyr Gly Gly Thr Lys Glu Tyr Ala Ala Ser
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Val Lys Gly

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Asp Ala Ser Ser Leu Glu Thr
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<210> 7
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<213> Artificial Sequence

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<223> RB1 heavy chain with amino acid substitution

<400> 7

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

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

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

Ser Phe Ile Lys Ser Lys Thr Tyr Gly Gly Thr Lys Glu Tyr Ala Ala
50 55 60

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

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

Tyr Cys Thr Arg Gly Ala Pro Tyr Gly Gly Asn Ser Asp Tyr Tyr Tyr
100 105 110

Gly Leu Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 8
<211> 109
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<213> Homo sapiens

<400> 8

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

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

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

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

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

Glu Asp Phe Ala Ala Tyr Tyr Cys Gln Gln Phe Leu Asp Phe Pro Phe
85 90 95

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

<210> 9
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<212> PRT
<213> Homo sapiens

<400> 9

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

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

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

Ser Phe Ile Lys Ser Lys Thr Tyr Gly Gly Thr Lys Glu Tyr Ala Ala
50 55 60

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

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

Tyr Cys Thr Arg Gly Ala Pro Tyr Gly Gly Asn Ser Asp Tyr Tyr Tyr

100 105 110

Gly Leu Asp Val Trp Gly Gln Gly Thr Thr Val Ile Val Ser Ser
115 120 125

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<213> Artificial Sequence

<220>
<223> Leader sequence

<400> 10

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser

<210> 11
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<213> Artificial Sequence

<220>
<223> RB1 VH amino acid substituted with leader

<400> 11

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Arg
20 25 30

Pro Gly Arg Ser Leu Arg Leu Ser Cys Thr Val Ser Gly Phe Ser Phe
35 40 45

Asp Asp Ser Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Ile Ser Phe Ile Lys Ser Lys Thr Tyr Gly Gly Thr Lys Glu
65 70 75 80

Tyr Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
85 90 95

Lys Asn Ile Ala Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Thr Arg Gly Ala Pro Tyr Gly Gly Asn Ser Asp
115 120 125

Tyr Tyr Tyr Gly Leu Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val

130 135 140

Ser Ser
145

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<223> RB1 VL and leader

<400> 12

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
20 25 30

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Gln Asp Val
35 40 45

Arg Gly Ala Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
50 55 60

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

Phe Ser Gly Ser Gly Ser Gly Thr Val Phe Thr Leu Thr Ile Ser Ser
85 90 95

Leu Gln Pro Glu Asp Phe Ala Ala Tyr Tyr Cys Gln Gln Phe Leu Asp
100 105 110

Phe Pro Phe Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr
115 120 125

<210> 13
<211> 330
<212> PRT
<213> Homo sapiens

<400> 13

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
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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

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65                  70                  75                  80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
            100                 105                 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
        115                 120                 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
    130                 135                 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145                 150                 155                 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
                165                 170                 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
            180                 185                 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
        195                 200                 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
    210                 215                 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225                 230                 235                 240

Leu 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
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Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 14
<211> 105
<212> PRT
<213> Homo sapiens

<400> 14

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

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

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

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

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

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

Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

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<212> DNA
<213> Artificial Sequence

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<400> 15
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tcctgcacag tttctggatt cagctttgac gactctgcta tgagctgggt ccgccaggct 120

ccagggaagg ggctggaatg gataagtttc attaaaagta aaacttatgg tgggacaaaa 180

gaatacgccg cgtctgtgaa aggcaggttc accatctcaa gagatgattc caaaaacatc 240

gcctatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtatta ttgtactaga 300

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accacggtca ctgtctcctc a 381

<210> 16
<211> 327
<212> DNA
<213> Homo sapiens

<400> 16
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc ggacaagtca ggacgttaga ggtgctttag cctggtatca acagaaacca 120

gggaaagctc ctaaactcct gatctttgat gcctccagtt tggagactgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagtt ttcactctca ccatcagcag cctgcagcct 240

gaagattttg cagcttatta ctgtcagcag tttcttgatt tccctttcac cttcggccag 300

gggacacgac tggaaatcaa acgtacg 327

<210> 17
<211> 381
<212> DNA
<213> Artificial Sequence

<220>
<223> RB1 VH codon optimized

<400> 17
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agctgcaccg tgagcggctt ctcctttgac gattctgcca tgagctgggt gcggcaggct 120

ccaggcaagg gactggagtg gatctccttc atcaagtcta agacctacgg cggcacaaag 180

gagtacgccg cttccgtgaa gggccggttt accatcagca gggacgattc caagaacatc 240

gcctatctgc agatgaacag cctgaagacc gaggacacag ccgtgtacta ttgcacaaga 300

ggagctcctt acggaggcaa cagcgactac tattacggac tggacgtgtg gggacaggga 360

accacagtga ccgtgagctc c 381

<210> 18
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> RB1 VL codon optimized

<400> 18
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atcacatgcc ggaccagcca ggatgtgcgg ggcgccctgg cttggtacca gcagaagcca 120

ggcaaggccc ccaagctgct gatctttgac gctagctccc tggagaccgg cgtgccctcc 180

aggttttctg gcagcggctc cggcacagtg ttcaccctga caatctctag cctgcagcct 240

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ggcacacggc tggagatcaa gaggacc 327

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<223> Leader sequence heavy chain

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<210> 20
<211> 57
<212> DNA
<213> Artificial Sequence

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<223> Leader sequence light chain

<400> 20
atgggctggt cctgtattat cctgttcctg gtggcaaccg caactggtgt gcatagc 57

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<211> 990
<212> DNA
<213> Homo sapiens

<400> 21
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tggaactctg gcgccctgac cagcggagtg cacacatttc cagctgtgct gcagtcctct 180

ggcctgtatt ccctgagctc cgtggtgacc gtgccctcta gctccctggg cacccagaca 240

tacatctgta acgtgaatca caagccaagc aatacaaagg tggacaagaa ggtcgagccc 300

aagtcctgtg ataagaccca cacatgcccc ccttgtcctg ctccagagct gctgggagga 360

cctagcgtgt tcctgtttcc acccaagcct aaggacaccc tgatgatctc taggaccccc 420

gaggtgacat gcgtggtggt ggacgtgagc cacgaggatc ctgaggtgaa gtttaactgg 480

tacgtcgatg gcgtggaggt gcacaatgcc aagacaaagc ccagagagga gcagtataac 540

tccacctacc gggtggtgtc tgtgctgaca gtgctgcacc aggactggct gaacggcaag 600

gagtacaagt gcaaggtgtc caataaggcc ctgcccgctc ctatcgagaa gaccatctct 660

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cagaagagcc tgtccctgtc acctggtaaa 990

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<211> 315
<212> DNA
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<400> 22
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gctagcgtgg tgtgcctgct gaacaatttc taccctcggg aggccaaggt gcagtggaag 120

gtggataacg ctctgcagtc tggcaatagc caggagtccg tgaccgagca ggactctaag 180

gatagcacat attccctgtc ctctaccctg acactgtcta aggccgatta cgagaagcac 240

aaggtgtatg cttgtgaagt cacccaccag gggctgagtt caccagtcac caagtcattc 300

aatcggggcg agtgc 315