SEQUENCE LISTING

<110> Temasek Life Sciences Laboratory Limited

<120> Monoclonal Antibodies Targeting Neutralizing Epitopes on H7 Influenza Viruses

<130> FP6643

<150> US 61/727,927
<151> 2012-12-19

<160> 2

<170> PatentIn version 3.5

<210> 1
<211> 1689
<212> DNA
<213> Influenza virus

<220>
<221> CDS
<222> (1)..(1689)

<400> 1

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1               5                   10                  15

aat gca gac aag atc tgc ctt ggg cat cat gcc gtg tca aac ggg act          96
Asn Ala Asp Lys Ile Cys Leu Gly His His Ala Val Ser Asn Gly Thr
            20                  25                  30

aaa gta aac aca tta act gag aga gga gtg gaa gtc gtt aat gca act         144
Lys Val Asn Thr Leu Thr Glu Arg Gly Val Glu Val Val Asn Ala Thr
        35                  40                  45

gaa acg gtg gaa cga aca aac gtt ccc agg atc tgc tca aaa ggg aaa         192
Glu Thr Val Glu Arg Thr Asn Val Pro Arg Ile Cys Ser Lys Gly Lys
    50                  55                  60

agg aca gtt gac ctc ggt caa tgt gga ctt ctg gga aca atc act ggg         240
Arg Thr Val Asp Leu Gly Gln Cys Gly Leu Leu Gly Thr Ile Thr Gly
65                  70                  75                  80

cca ccc caa tgt gac caa ttc cta gaa ttt tcg gcc gac tta att att         288
Pro Pro Gln Cys Asp Gln Phe Leu Glu Phe Ser Ala Asp Leu Ile Ile
                85                  90                  95

gag agg cga gaa gga agt gat gtc tgt tat cct ggg aaa ttc gtg aat         336
Glu Arg Arg Glu Gly Ser Asp Val Cys Tyr Pro Gly Lys Phe Val Asn
            100                 105                 110

gaa gaa gct ctg agg caa att ctc aga gag tca ggc gga att gac aag         384
Glu Glu Ala Leu Arg Gln Ile Leu Arg Glu Ser Gly Gly Ile Asp Lys
        115                 120                 125

gag aca atg gga ttc acc tac agc gga ata aga act aat gga aca acc         432
Glu Thr Met Gly Phe Thr Tyr Ser Gly Ile Arg Thr Asn Gly Thr Thr
    130                 135                 140

agt gca tgt agg aga tca gga tct tca ttc tat gca gag atg aaa tgg         480
Ser Ala Cys Arg Arg Ser Gly Ser Ser Phe Tyr Ala Glu Met Lys Trp
145                 150                 155                 160

ctc ctg tca aac aca gac aat gct gct ttc ccg caa atg act aag tca         528
Leu Leu Ser Asn Thr Asp Asn Ala Ala Phe Pro Gln Met Thr Lys Ser
                165                 170                 175
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tac aag aac aca agg aaa gac cca gct ctg ata ata tgg ggg atc cac        576
Tyr Lys Asn Thr Arg Lys Asp Pro Ala Leu Ile Ile Trp Gly Ile His
            180                 185                 190

cat tcc gga tca act aca gaa cag acc aag cta tat ggg agt gga aac        624
His Ser Gly Ser Thr Thr Glu Gln Thr Lys Leu Tyr Gly Ser Gly Asn
        195                 200                 205

aaa ctg ata aca gtt ggg agt tct aat tac caa cag tcc ttt gta ccg        672
Lys Leu Ile Thr Val Gly Ser Ser Asn Tyr Gln Gln Ser Phe Val Pro
    210                 215                 220

agt cca gga gcg aga cca caa gtg aat ggc caa tct gga aga att gac        720
Ser Pro Gly Ala Arg Pro Gln Val Asn Gly Gln Ser Gly Arg Ile Asp
225                 230                 235                 240

ttt cat tgg ctg ata cta aac cct aat gac acg gtc act ttc agt ttc        768
Phe His Trp Leu Ile Leu Asn Pro Asn Asp Thr Val Thr Phe Ser Phe
                245                 250                 255

aat ggg gcc ttc ata gct cca gac cgt gca agc ttt ctg aga ggg aag        816
Asn Gly Ala Phe Ile Ala Pro Asp Arg Ala Ser Phe Leu Arg Gly Lys
            260                 265                 270

tcc atg gga att cag agt gaa gta cag gtt gat gcc aat tgt gaa gga        864
Ser Met Gly Ile Gln Ser Glu Val Gln Val Asp Ala Asn Cys Glu Gly
        275                 280                 285

gat tgc tat cat agt gga ggg aca ata ata agt aat ttg ccc ttt cag        912
Asp Cys Tyr His Ser Gly Gly Thr Ile Ile Ser Asn Leu Pro Phe Gln
    290                 295                 300

aac ata aat agc agg gca gta gga aaa tgt ccg aga tat gtt aag caa        960
Asn Ile Asn Ser Arg Ala Val Gly Lys Cys Pro Arg Tyr Val Lys Gln
305                 310                 315                 320

gag agt ctg ctg ttg gca aca gga atg aag aat gtt ccc gaa atc cca       1008
Glu Ser Leu Leu Leu Ala Thr Gly Met Lys Asn Val Pro Glu Ile Pro
                325                 330                 335

aag agg agg agg aga ggc cta ttt ggt gct ata gcg ggt ttc att gaa       1056
Lys Arg Arg Arg Arg Gly Leu Phe Gly Ala Ile Ala Gly Phe Ile Glu
            340                 345                 350

aat gga tgg gaa ggt ttg att gat ggg tgg tat ggc ttc agg cat caa       1104
Asn Gly Trp Glu Gly Leu Ile Asp Gly Trp Tyr Gly Phe Arg His Gln
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aat gca caa ggg gag gga act gct gca gat tac aaa agc acc caa tca       1152
Asn Ala Gln Gly Glu Gly Thr Ala Ala Asp Tyr Lys Ser Thr Gln Ser
    370                 375                 380

gca att gat caa ata aca ggg aaa tta aat cgg ctt ata gaa aaa act       1200
Ala Ile Asp Gln Ile Thr Gly Lys Leu Asn Arg Leu Ile Glu Lys Thr
385                 390                 395                 400

aac caa cag ttt gag tta ata gac aac gaa ttc act gag gtt gaa agg       1248
Asn Gln Gln Phe Glu Leu Ile Asp Asn Glu Phe Thr Glu Val Glu Arg
                405                 410                 415

caa att ggc aat gtg ata aac tgg acc aga gat tcc atg aca gaa gtg       1296
Gln Ile Gly Asn Val Ile Asn Trp Thr Arg Asp Ser Met Thr Glu Val
            420                 425                 430

tgg tcc tat aac gct gaa ctc tta gta gca atg gag aat cag cac aca       1344
Trp Ser Tyr Asn Ala Glu Leu Leu Val Ala Met Glu Asn Gln His Thr
        435                 440                 445

att gat ctg gcc gac tca gaa atg aac aaa ctg tac gaa cga gtg aag       1392
Ile Asp Leu Ala Asp Ser Glu Met Asn Lys Leu Tyr Glu Arg Val Lys
    450                 455                 460
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aga caa ctg aga gag aat gcc gaa gaa gat ggc act ggt tgc ttc gaa       1440
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465                 470                 475                 480

ata ttt cac aag tgt gat gac gac tgc atg gcc agt att aga aac aac       1488
Ile Phe His Lys Cys Asp Asp Asp Cys Met Ala Ser Ile Arg Asn Asn
                485                 490                 495

acc tat gat cac agc aag tac agg gaa gaa gca ata caa aat aga ata       1536
Thr Tyr Asp His Ser Lys Tyr Arg Glu Glu Ala Ile Gln Asn Arg Ile
            500                 505                 510

cag att gac cca gtc aaa cta agc agc ggc tac aaa gat gtg ata ctt       1584
Gln Ile Asp Pro Val Lys Leu Ser Ser Gly Tyr Lys Asp Val Ile Leu
        515                 520                 525

tgg ttt agc ttc ggg gca tca tgt ttc ata ctt ctg gcc att gca atg       1632
Trp Phe Ser Phe Gly Ala Ser Cys Phe Ile Leu Leu Ala Ile Ala Met
    530                 535                 540

ggc ctt gtc ttc ata tgt gtg aag aat gga aac atg cgg tgc act att       1680
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tgt ata taa                                                          1689
Cys Ile
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Asn Ala Asp Lys Ile Cys Leu Gly His His Ala Val Ser Asn Gly Thr
            20                  25                  30

Lys Val Asn Thr Leu Thr Glu Arg Gly Val Glu Val Val Asn Ala Thr
        35                  40                  45

Glu Thr Val Glu Arg Thr Asn Val Pro Arg Ile Cys Ser Lys Gly Lys
    50                  55                  60

Arg Thr Val Asp Leu Gly Gln Cys Gly Leu Leu Gly Thr Ile Thr Gly
65                  70                  75                  80

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

Glu Arg Arg Glu Gly Ser Asp Val Cys Tyr Pro Gly Lys Phe Val Asn
            100                 105                 110

Glu Glu Ala Leu Arg Gln Ile Leu Arg Glu Ser Gly Gly Ile Asp Lys
        115                 120                 125

Glu Thr Met Gly Phe Thr Tyr Ser Gly Ile Arg Thr Asn Gly Thr Thr
    130                 135                 140
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Ser Ala Cys Arg Arg Ser Gly Ser Ser Phe Tyr Ala Glu Met Lys Trp
145                 150                 155                 160

Leu Leu Ser Asn Thr Asp Asn Ala Ala Phe Pro Gln Met Thr Lys Ser
                165                 170                 175

Tyr Lys Asn Thr Arg Lys Asp Pro Ala Leu Ile Ile Trp Gly Ile His
            180                 185                 190

His Ser Gly Ser Thr Thr Glu Gln Thr Lys Leu Tyr Gly Ser Gly Asn
        195                 200                 205

Lys Leu Ile Thr Val Gly Ser Ser Asn Tyr Gln Gln Ser Phe Val Pro
    210                 215                 220

Ser Pro Gly Ala Arg Pro Gln Val Asn Gly Gln Ser Gly Arg Ile Asp
225                 230                 235                 240

Phe His Trp Leu Ile Leu Asn Pro Asn Asp Thr Val Thr Phe Ser Phe
                245                 250                 255

Asn Gly Ala Phe Ile Ala Pro Asp Arg Ala Ser Phe Leu Arg Gly Lys
            260                 265                 270

Ser Met Gly Ile Gln Ser Glu Val Gln Val Asp Ala Asn Cys Glu Gly
        275                 280                 285

Asp Cys Tyr His Ser Gly Gly Thr Ile Ile Ser Asn Leu Pro Phe Gln
    290                 295                 300

Asn Ile Asn Ser Arg Ala Val Gly Lys Cys Pro Arg Tyr Val Lys Gln
305                 310                 315                 320

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

Lys Arg Arg Arg Arg Gly Leu Phe Gly Ala Ile Ala Gly Phe Ile Glu
            340                 345                 350

Asn Gly Trp Glu Gly Leu Ile Asp Gly Trp Tyr Gly Phe Arg His Gln
        355                 360                 365

Asn Ala Gln Gly Glu Gly Thr Ala Ala Asp Tyr Lys Ser Thr Gln Ser
    370                 375                 380

Ala Ile Asp Gln Ile Thr Gly Lys Leu Asn Arg Leu Ile Glu Lys Thr
385                 390                 395                 400

Asn Gln Gln Phe Glu Leu Ile Asp Asn Glu Phe Thr Glu Val Glu Arg
                405                 410                 415

Gln Ile Gly Asn Val Ile Asn Trp Thr Arg Asp Ser Met Thr Glu Val
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            420                 425                 430

Trp Ser Tyr Asn Ala Glu Leu Leu Val Ala Met Glu Asn Gln His Thr
        435                 440                 445

Ile Asp Leu Ala Asp Ser Glu Met Asn Lys Leu Tyr Glu Arg Val Lys
    450                 455                 460

Arg Gln Leu Arg Glu Asn Ala Glu Glu Asp Gly Thr Gly Cys Phe Glu
465                 470                 475                 480

Ile Phe His Lys Cys Asp Asp Asp Cys Met Ala Ser Ile Arg Asn Asn
                485                 490                 495

Thr Tyr Asp His Ser Lys Tyr Arg Glu Glu Ala Ile Gln Asn Arg Ile
            500                 505                 510

Gln Ile Asp Pro Val Lys Leu Ser Ser Gly Tyr Lys Asp Val Ile Leu
        515                 520                 525

Trp Phe Ser Phe Gly Ala Ser Cys Phe Ile Leu Leu Ala Ile Ala Met
    530                 535                 540

Gly Leu Val Phe Ile Cys Val Lys Asn Gly Asn Met Arg Cys Thr Ile
545                 550                 555                 560

Cys Ile
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