SEQUENCE LISTING

<110> European Molecular Biology Laboratory (EMBL)

<120> FRAGMENTS OF THE PA SUBUNIT OF RNA DEPENDENT RNA POLYMERASE FROM PANDEMIC INFLUENZA VIRUS A 2009 H1N1, AND THEIR USE

<150> US 61/340,335
<151> 2010-03-16

<130> SG3380A

<160> 12

<170> PatentIn version 3.5

<210> 1
<211> 2151
<212> DNA
<213> Influenza A pandemic H1N1 virus (A/California/04/2009)

<220>
<221> CDS
<222> (1)..(2151)
<223> PA-subunit of the Influenza A pandemic H1N1 virus (A/California/04/2009) RNA-dependent RNA polymerase

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1               5                  10                  15

gcg gaa aag gca atg aaa gaa tat ggg gaa gat ccg aaa atc gaa act          96
Ala Glu Lys Ala Met Lys Glu Tyr Gly Glu Asp Pro Lys Ile Glu Thr
            20                  25                  30

aac aag ttt gct gca ata tgc aca cat ttg gaa gtt tgt ttc atg tat         144
Asn Lys Phe Ala Ala Ile Cys Thr His Leu Glu Val Cys Phe Met Tyr
        35                  40                  45

tcg gat ttc cat ttc atc gac gaa cgg ggt gaa tca ata att gta gaa         192
Ser Asp Phe His Phe Ile Asp Glu Arg Gly Glu Ser Ile Ile Val Glu
    50                  55                  60

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Ser Gly Asp Pro Asn Ala Leu Leu Lys His Arg Phe Glu Ile Ile Glu
65                  70                  75                  80

gga aga gac cga atc atg gcc tgg aca gtg gtg aac agt ata tgt aac         288
Gly Arg Asp Arg Ile Met Ala Trp Thr Val Val Asn Ser Ile Cys Asn
                85                  90                  95

aca aca ggg gta gag aag cct aaa ttt ctt cct gat ttg tat gat tac         336
Thr Thr Gly Val Glu Lys Pro Lys Phe Leu Pro Asp Leu Tyr Asp Tyr
            100                 105                 110

aaa gag aac cgg ttc att gaa att gga gta aca cgg agg gaa gtc cac         384
Lys Glu Asn Arg Phe Ile Glu Ile Gly Val Thr Arg Arg Glu Val His
        115                 120                 125

ata tat tac cta gag aaa gcc aac aaa ata aaa tct gag aag aca cac         432
Ile Tyr Tyr Leu Glu Lys Ala Asn Lys Ile Lys Ser Glu Lys Thr His
    130                 135                 140

att cac atc ttt tca ttc act gga gag gag atg gcc acc aaa gcg gac         480
Ile His Ile Phe Ser Phe Thr Gly Glu Glu Met Ala Thr Lys Ala Asp
145                 150                 155                 160
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tac acc ctt gac gaa gag agc agg gca aga atc aaa act agg ctt ttc          528
Tyr Thr Leu Asp Glu Glu Ser Arg Ala Arg Ile Lys Thr Arg Leu Phe
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act ata aga caa gaa atg gcc agt agg agt cta tgg gat tcc ttt cgt          576
Thr Ile Arg Gln Glu Met Ala Ser Arg Ser Leu Trp Asp Ser Phe Arg
            180                 185                 190

cag tcc gaa aga ggc gaa gag aca att gaa gaa aaa ttt gag att aca          624
Gln Ser Glu Arg Gly Glu Glu Thr Ile Glu Glu Lys Phe Glu Ile Thr
        195                 200                 205

gga act atg cgc aag ctt gcc gac caa agt ctc cca ccg aac ttc ccc          672
Gly Thr Met Arg Lys Leu Ala Asp Gln Ser Leu Pro Pro Asn Phe Pro
    210                 215                 220

agc ctt gaa aac ttt aga gcc tat gta gat gga ttc gag ccg aac ggc          720
Ser Leu Glu Asn Phe Arg Ala Tyr Val Asp Gly Phe Glu Pro Asn Gly
225                 230                 235                 240

tgc att gag ggc aag ctt tcc caa atg tca aaa gaa gtg aac gcc aaa          768
Cys Ile Glu Gly Lys Leu Ser Gln Met Ser Lys Glu Val Asn Ala Lys
                245                 250                 255

att gaa cca ttc ttg agg acg aca cca cgc ccc ctc aga ttg cct gat          816
Ile Glu Pro Phe Leu Arg Thr Thr Pro Arg Pro Leu Arg Leu Pro Asp
            260                 265                 270

ggg cct ctt tgc cat cag cgg tca aag ttc ctg ctg atg gat gct ctg          864
Gly Pro Leu Cys His Gln Arg Ser Lys Phe Leu Leu Met Asp Ala Leu
        275                 280                 285

aaa tta agt att gaa gac ccg agt cac gag ggg gag gga ata cca cta          912
Lys Leu Ser Ile Glu Asp Pro Ser His Glu Gly Glu Gly Ile Pro Leu
    290                 295                 300

tat gat gca atc aaa tgc atg aag aca ttc ttt ggc tgg aaa gag cct          960
Tyr Asp Ala Ile Lys Cys Met Lys Thr Phe Phe Gly Trp Lys Glu Pro
305                 310                 315                 320

aac ata gtc aaa cca cat gag aaa ggc ata aat ccc aat tac ctc atg         1008
Asn Ile Val Lys Pro His Glu Lys Gly Ile Asn Pro Asn Tyr Leu Met
                325                 330                 335

gct tgg aag cag gtg cta gca gag cta cag gac att gaa aat gaa gag         1056
Ala Trp Lys Gln Val Leu Ala Glu Leu Gln Asp Ile Glu Asn Glu Glu
            340                 345                 350

aag atc cca agg aca aag aac atg aag aga aca agc caa ttg aag tgg         1104
Lys Ile Pro Arg Thr Lys Asn Met Lys Arg Thr Ser Gln Leu Lys Trp
        355                 360                 365

gca ctc ggt gaa aat atg gca cca gaa aaa gta gac ttt gat gac tgc         1152
Ala Leu Gly Glu Asn Met Ala Pro Glu Lys Val Asp Phe Asp Asp Cys
    370                 375                 380

aaa gat gtt gga gac ctt aaa cag tat gac agt gat gag cca gag ccc         1200
Lys Asp Val Gly Asp Leu Lys Gln Tyr Asp Ser Asp Glu Pro Glu Pro
385                 390                 395                 400

aga tct cta gca agc tgg gtc caa aat gaa ttc aat aag gca tgt gaa         1248
Arg Ser Leu Ala Ser Trp Val Gln Asn Glu Phe Asn Lys Ala Cys Glu
                405                 410                 415

ttg act gat tca agc tgg ata gaa ctt gat gaa ata gga gaa gat gtt         1296
Leu Thr Asp Ser Ser Trp Ile Glu Leu Asp Glu Ile Gly Glu Asp Val
            420                 425                 430
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gcc ccg att gaa cat atc gca agc atg agg agg aac tat ttt aca gca      1344
Ala Pro Ile Glu His Ile Ala Ser Met Arg Arg Asn Tyr Phe Thr Ala
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gaa gtg tcc cac tgc agg gct act gaa tac ata atg aag gga gtg tac      1392
Glu Val Ser His Cys Arg Ala Thr Glu Tyr Ile Met Lys Gly Val Tyr
    450                 455                 460

ata aat acg gcc ttg ctc aat gca tcc tgt gca gcc atg gat gac ttt      1440
Ile Asn Thr Ala Leu Leu Asn Ala Ser Cys Ala Ala Met Asp Asp Phe
465                 470                 475                 480

cag ctg atc cca atg ata agc aaa tgt agg acc aaa gaa gga aga cgg      1488
Gln Leu Ile Pro Met Ile Ser Lys Cys Arg Thr Lys Glu Gly Arg Arg
                485                 490                 495

aaa aca aac ctg tat ggg ttc att ata aaa gga agg tct cat ttg aga      1536
Lys Thr Asn Leu Tyr Gly Phe Ile Ile Lys Gly Arg Ser His Leu Arg
            500                 505                 510

aat gat act gat gtg gtg aac ttt gta agt atg gag ttc tca ctc act      1584
Asn Asp Thr Asp Val Val Asn Phe Val Ser Met Glu Phe Ser Leu Thr
        515                 520                 525

gac ccg aga ctg gag cca cac aaa tgg gaa aaa tac tgt gtt ctt gaa      1632
Asp Pro Arg Leu Glu Pro His Lys Trp Glu Lys Tyr Cys Val Leu Glu
    530                 535                 540

ata gga gac atg ctc ttg agg act gcg ata ggc caa gtg tcg agg ccc      1680
Ile Gly Asp Met Leu Leu Arg Thr Ala Ile Gly Gln Val Ser Arg Pro
545                 550                 555                 560

atg ttc cta tat gtg aga acc aat gga acc tcc aag atc aag atg aaa      1728
Met Phe Leu Tyr Val Arg Thr Asn Gly Thr Ser Lys Ile Lys Met Lys
                565                 570                 575

tgg ggc atg gaa atg agg cgc tgc ctt ctt cag tct ctt cag cag att      1776
Trp Gly Met Glu Met Arg Arg Cys Leu Leu Gln Ser Leu Gln Gln Ile
            580                 585                 590

gag agc atg att gag gcc gag tct tct gtc aaa gag aaa gac atg acc      1824
Glu Ser Met Ile Glu Ala Glu Ser Ser Val Lys Glu Lys Asp Met Thr
        595                 600                 605

aag gaa ttc ttt gaa aac aaa tcg gaa aca tgg cca atc gga gag tca      1872
Lys Glu Phe Phe Glu Asn Lys Ser Glu Thr Trp Pro Ile Gly Glu Ser
    610                 615                 620

ccc agg gga gtg gag gaa ggc tct att ggg aaa gtg tgc agg acc tta      1920
Pro Arg Gly Val Glu Glu Gly Ser Ile Gly Lys Val Cys Arg Thr Leu
625                 630                 635                 640

ctg gca aaa tct gta ttc aac agt cta tat gcg tct cca caa ctt gag      1968
Leu Ala Lys Ser Val Phe Asn Ser Leu Tyr Ala Ser Pro Gln Leu Glu
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ggg ttt tcg gct gaa tct aga aaa ttg ctt ctc att gtt cag gca ctt      2016
Gly Phe Ser Ala Glu Ser Arg Lys Leu Leu Leu Ile Val Gln Ala Leu
            660                 665                 670

agg gac aac ctg gaa cct gga acc ttc gat ctt ggg ggg cta tat gaa      2064
Arg Asp Asn Leu Glu Pro Gly Thr Phe Asp Leu Gly Gly Leu Tyr Glu
        675                 680                 685

gca atc gag gag tgc ctg att aat gat ccc tgg gtt ttg ctt aat gca      2112
Ala Ile Glu Glu Cys Leu Ile Asn Asp Pro Trp Val Leu Leu Asn Ala
    690                 695                 700
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Asn Lys Phe Ala Ala Ile Cys Thr His Leu Glu Val Cys Phe Met Tyr
        35                  40                  45

Ser Asp Phe His Phe Ile Asp Glu Arg Gly Glu Ser Ile Ile Val Glu
    50                  55                  60

Ser Gly Asp Pro Asn Ala Leu Leu Lys His Arg Phe Glu Ile Ile Glu
65                  70                  75                  80

Gly Arg Asp Arg Ile Met Ala Trp Thr Val Val Asn Ser Ile Cys Asn
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Thr Thr Gly Val Glu Lys Pro Lys Phe Leu Pro Asp Leu Tyr Asp Tyr
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Lys Glu Asn Arg Phe Ile Glu Ile Gly Val Thr Arg Arg Glu Val His
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Ile Tyr Tyr Leu Glu Lys Ala Asn Lys Ile Lys Ser Glu Lys Thr His
    130                 135                 140

Ile His Ile Phe Ser Phe Thr Gly Glu Glu Met Ala Thr Lys Ala Asp
145                 150                 155                 160

Tyr Thr Leu Asp Glu Glu Ser Arg Ala Arg Ile Lys Thr Arg Leu Phe
                165                 170                 175

Thr Ile Arg Gln Glu Met Ala Ser Arg Ser Leu Trp Asp Ser Phe Arg
            180                 185                 190

Gln Ser Glu Arg Gly Glu Glu Thr Ile Glu Glu Lys Phe Glu Ile Thr
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Gly Thr Met Arg Lys Leu Ala Asp Gln Ser Leu Pro Pro Asn Phe Pro
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Cys Ile Glu Gly Lys Leu Ser Gln Met Ser Lys Glu Val Asn Ala Lys
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Ile Glu Pro Phe Leu Arg Thr Thr Pro Arg Pro Leu Arg Leu Pro Asp
            260                 265                 270

Gly Pro Leu Cys His Gln Arg Ser Lys Phe Leu Leu Met Asp Ala Leu
        275                 280                 285

Lys Leu Ser Ile Glu Asp Pro Ser His Glu Gly Glu Gly Ile Pro Leu
    290                 295                 300

Tyr Asp Ala Ile Lys Cys Met Lys Thr Phe Phe Gly Trp Lys Glu Pro
305                 310                 315                 320

Asn Ile Val Lys Pro His Glu Lys Gly Ile Asn Pro Asn Tyr Leu Met
                325                 330                 335

Ala Trp Lys Gln Val Leu Ala Glu Leu Gln Asp Ile Glu Asn Glu Glu
            340                 345                 350

Lys Ile Pro Arg Thr Lys Asn Met Lys Arg Thr Ser Gln Leu Lys Trp
        355                 360                 365

Ala Leu Gly Glu Asn Met Ala Pro Glu Lys Val Asp Phe Asp Asp Cys
    370                 375                 380

Lys Asp Val Gly Asp Leu Lys Gln Tyr Asp Ser Asp Glu Pro Glu Pro
385                 390                 395                 400

Arg Ser Leu Ala Ser Trp Val Gln Asn Glu Phe Asn Lys Ala Cys Glu
                405                 410                 415

Leu Thr Asp Ser Ser Trp Ile Glu Leu Asp Glu Ile Gly Glu Asp Val
            420                 425                 430

Ala Pro Ile Glu His Ile Ala Ser Met Arg Arg Asn Tyr Phe Thr Ala
        435                 440                 445

Glu Val Ser His Cys Arg Ala Thr Glu Tyr Ile Met Lys Gly Val Tyr
    450                 455                 460

Ile Asn Thr Ala Leu Leu Asn Ala Ser Cys Ala Ala Met Asp Asp Phe
465                 470                 475                 480

Gln Leu Ile Pro Met Ile Ser Lys Cys Arg Thr Lys Glu Gly Arg Arg
                485                 490                 495
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Lys Thr Asn Leu Tyr Gly Phe Ile Ile Lys Gly Arg Ser His Leu Arg
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Asn Asp Thr Asp Val Val Asn Phe Val Ser Met Glu Phe Ser Leu Thr
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Asp Pro Arg Leu Glu Pro His Lys Trp Glu Lys Tyr Cys Val Leu Glu
    530                 535                 540

Ile Gly Asp Met Leu Leu Arg Thr Ala Ile Gly Gln Val Ser Arg Pro
545                 550                 555                 560

Met Phe Leu Tyr Val Arg Thr Asn Gly Thr Ser Lys Ile Lys Met Lys
                565                 570                 575

Trp Gly Met Glu Met Arg Arg Cys Leu Leu Gln Ser Leu Gln Gln Ile
            580                 585                 590

Glu Ser Met Ile Glu Ala Glu Ser Ser Val Lys Glu Lys Asp Met Thr
        595                 600                 605

Lys Glu Phe Phe Glu Asn Lys Ser Glu Thr Trp Pro Ile Gly Glu Ser
    610                 615                 620

Pro Arg Gly Val Glu Glu Gly Ser Ile Gly Lys Val Cys Arg Thr Leu
625                 630                 635                 640

Leu Ala Lys Ser Val Phe Asn Ser Leu Tyr Ala Ser Pro Gln Leu Glu
                645                 650                 655

Gly Phe Ser Ala Glu Ser Arg Lys Leu Leu Leu Ile Val Gln Ala Leu
            660                 665                 670

Arg Asp Asn Leu Glu Pro Gly Thr Phe Asp Leu Gly Gly Leu Tyr Glu
        675                 680                 685

Ala Ile Glu Glu Cys Leu Ile Asn Asp Pro Trp Val Leu Leu Asn Ala
    690                 695                 700

Ser Trp Phe Asn Ser Phe Leu Thr His Ala Leu Lys
705                 710                 715
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<210> 3
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<223> residues 80 to 90 of the PA-subunit of the Influenza A pandemic H1N1 virus (A/California/04/2009) RNA-dependent RNA polymerase

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<210> 8
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<220>
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<223> residues 100 to 110 of the PA-subunit of the Influenza A pandemic H1N1 virus (A/California/04/2009) RNA-dependent RNA polymerase

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Val Glu Lys Pro Lys Phe Leu Pro Asp Leu Tyr
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<210> 9
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<212> PRT
<213> Influenza A pandemic H1N1 virus (A/California/04/2009)

<220>
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<210> 10
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<212> PRT
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<212> PRT
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<223> residues 176 to 186 of the PA-subunit of the Influenza A pandemic H1N1 virus (A/California/04/2009) RNA-dependent RNA polymerase

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<210> 12
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<213> artificial

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<223> synthetic

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<222> (1)..(7)
<223> TEV protease recognition site

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