SEQUENCE LISTING

<110> Temasek Life Sciences Laboratory Limited

<120> Monoclonal Antibodies Targeting Neutralizing Epitopes On H5 Influenza Virus Of Clade 2.3

<130> FP5738

<160> 4

<170> PatentIn version 3.5

<210> 1
<211> 1704
<212> DNA
<213> Influenza A virus

<220>
<221> CDS
<222> (1)..(1704)

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1               5                  10                  15

gat cag att tgc att ggt tac cat gca aac aac tcg aca gag cag gtt        96
Asp Gln Ile Cys Ile Gly Tyr His Ala Asn Asn Ser Thr Glu Gln Val
            20                  25                  30

gac aca ata atg gaa aag aac gtt act gtt aca cat gcc caa gac ata       144
Asp Thr Ile Met Glu Lys Asn Val Thr Val Thr His Ala Gln Asp Ile
        35                  40                  45

ctg gaa aag aca cac aac ggg aag ctc tgc gat cta gat gga gtg aag       192
Leu Glu Lys Thr His Asn Gly Lys Leu Cys Asp Leu Asp Gly Val Lys
    50                  55                  60

cct ctg att tta aga gat tgt agt gta gct gga tgg ctc ctc gga aac       240
Pro Leu Ile Leu Arg Asp Cys Ser Val Ala Gly Trp Leu Leu Gly Asn
65                  70                  75                  80

cca atg tgt gac gaa ttc atc aat gtg ccg gaa tgg tct tac ata gtg       288
Pro Met Cys Asp Glu Phe Ile Asn Val Pro Glu Trp Ser Tyr Ile Val
                85                  90                  95

gag aag gcc aac cca gcc aat gac ctc tgt tac cca ggg aat ttc aac       336
Glu Lys Ala Asn Pro Ala Asn Asp Leu Cys Tyr Pro Gly Asn Phe Asn
            100                 105                 110

gac tat gaa gaa ctg aaa cac cta ttg agc aga ata aac cat ttt gag       384
Asp Tyr Glu Glu Leu Lys His Leu Leu Ser Arg Ile Asn His Phe Glu
        115                 120                 125

aaa att cag atc atc ccc aaa agt tct tgg tcc gat cat gaa gcc tca       432
Lys Ile Gln Ile Ile Pro Lys Ser Ser Trp Ser Asp His Glu Ala Ser
    130                 135                 140

tca ggg gtg agc tca gca tgt cca tac cag gga acg ccc tcc ttt ttc       480
Ser Gly Val Ser Ser Ala Cys Pro Tyr Gln Gly Thr Pro Ser Phe Phe
145                 150                 155                 160

aga aat gtg gta tgg ctt atc aaa aag aac aat aca tac cca aca ata       528
Arg Asn Val Val Trp Leu Ile Lys Lys Asn Asn Thr Tyr Pro Thr Ile
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aag aga agc tac aat aat acc aac cag gaa gat ctt ttg ata ctg tgg      576
Lys Arg Ser Tyr Asn Asn Thr Asn Gln Glu Asp Leu Leu Ile Leu Trp
            180                 185                 190

ggg att cat cat tct aat gat gcg gca gag cag aca aag ctc tat caa      624
Gly Ile His His Ser Asn Asp Ala Ala Glu Gln Thr Lys Leu Tyr Gln
        195                 200                 205

aac cca acc acc tat att tcc gtt ggg aca tca aca cta aac cag aga      672
Asn Pro Thr Thr Tyr Ile Ser Val Gly Thr Ser Thr Leu Asn Gln Arg
    210                 215                 220

ttg gta cca aaa ata gct act aga tcc aaa gta aac ggg caa agt gga      720
Leu Val Pro Lys Ile Ala Thr Arg Ser Lys Val Asn Gly Gln Ser Gly
225                 230                 235                 240

agg atg gat ttc ttc tgg aca att tta aaa ccg aat gat gca atc aac      768
Arg Met Asp Phe Phe Trp Thr Ile Leu Lys Pro Asn Asp Ala Ile Asn
                245                 250                 255

ttc gag agt aat gga aat ttc att gct cca gaa tat gca tac aaa att      816
Phe Glu Ser Asn Gly Asn Phe Ile Ala Pro Glu Tyr Ala Tyr Lys Ile
            260                 265                 270

gtc aag aaa ggg gac tca gca att gtt aaa agt gaa gtg gaa tat ggt      864
Val Lys Lys Gly Asp Ser Ala Ile Val Lys Ser Glu Val Glu Tyr Gly
        275                 280                 285

aac tgc aac aca aag tgt caa act cca ata ggg gcg ata aac tct agt      912
Asn Cys Asn Thr Lys Cys Gln Thr Pro Ile Gly Ala Ile Asn Ser Ser
    290                 295                 300

atg cca ttc cac aac ata cac cct ctc acc atc ggg gaa tgc ccc aaa      960
Met Pro Phe His Asn Ile His Pro Leu Thr Ile Gly Glu Cys Pro Lys
305                 310                 315                 320

tat gtg aaa tca aac aaa tta gtc ctt gcg act ggg ctc aga aat agt     1008
Tyr Val Lys Ser Asn Lys Leu Val Leu Ala Thr Gly Leu Arg Asn Ser
                325                 330                 335

cct cta aga gaa aga aga aga aaa aga gga cta ttt gga gct ata gca     1056
Pro Leu Arg Glu Arg Arg Arg Lys Arg Gly Leu Phe Gly Ala Ile Ala
            340                 345                 350

ggg ttt ata gag gga gga tgg cag gga atg gta gat ggt tgg tat ggg     1104
Gly Phe Ile Glu Gly Gly Trp Gln Gly Met Val Asp Gly Trp Tyr Gly
        355                 360                 365

tac cac cat agc aat gag cag ggg agt ggg tac gct gca gac aaa gaa     1152
Tyr His His Ser Asn Glu Gln Gly Ser Gly Tyr Ala Ala Asp Lys Glu
    370                 375                 380

tcc act caa aag gca ata gat gga gtc acc aat aag gtc aac tcg atc     1200
Ser Thr Gln Lys Ala Ile Asp Gly Val Thr Asn Lys Val Asn Ser Ile
385                 390                 395                 400

att gac aaa atg aac act cag ttt gag gcc gtt gga agg gaa ttt aat     1248
Ile Asp Lys Met Asn Thr Gln Phe Glu Ala Val Gly Arg Glu Phe Asn
                405                 410                 415

aac tta gaa agg aga ata gag aat tta aac aag aaa atg gaa gac gga     1296
Asn Leu Glu Arg Arg Ile Glu Asn Leu Asn Lys Lys Met Glu Asp Gly
            420                 425                 430

ttc cta gat gtc tgg act tat aat gct gaa ctt ctg gtt ctc atg gaa     1344
Phe Leu Asp Val Trp Thr Tyr Asn Ala Glu Leu Leu Val Leu Met Glu
        435                 440                 445

aat gag aga act cta gac ttc cat gat tca aat gtc aag aac ctt tac     1392
Asn Glu Arg Thr Leu Asp Phe His Asp Ser Asn Val Lys Asn Leu Tyr
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    450                 455                 460

gac aag gtc cga cta cag ctt agg gat aat gca aag gag ctg ggt aac      1440
Asp Lys Val Arg Leu Gln Leu Arg Asp Asn Ala Lys Glu Leu Gly Asn
465                 470                 475                 480

ggt tgt ttc gag ttc tat cac aaa tgt gat aat gaa tgt atg gaa agt      1488
Gly Cys Phe Glu Phe Tyr His Lys Cys Asp Asn Glu Cys Met Glu Ser
                485                 490                 495

gta aga aac gga acg tat gac tac ccg cag tat tca gaa gaa gca aga      1536
Val Arg Asn Gly Thr Tyr Asp Tyr Pro Gln Tyr Ser Glu Glu Ala Arg
            500                 505                 510

tta aaa aga gag gaa ata agt gga gta aaa ttg gaa tca ata gga act      1584
Leu Lys Arg Glu Glu Ile Ser Gly Val Lys Leu Glu Ser Ile Gly Thr
        515                 520                 525

tac caa ata ctg tca att tat tca aca gtt gcg agt tct cta gca ctg      1632
Tyr Gln Ile Leu Ser Ile Tyr Ser Thr Val Ala Ser Ser Leu Ala Leu
    530                 535                 540

gca atc atg gtg gct ggt cta tct ttg tgg atg tgc tcc aat ggg tcg      1680
Ala Ile Met Val Ala Gly Leu Ser Leu Trp Met Cys Ser Asn Gly Ser
545                 550                 555                 560

tta caa tgc aga att tgc att taa                                     1704
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<210> 2
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<212> PRT
<213> Influenza A virus

<400> 2

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Asp Gln Ile Cys Ile Gly Tyr His Ala Asn Asn Ser Thr Glu Gln Val
            20                  25                  30

Asp Thr Ile Met Glu Lys Asn Val Thr Val Thr His Ala Gln Asp Ile
        35                  40                  45

Leu Glu Lys Thr His Asn Gly Lys Leu Cys Asp Leu Asp Gly Val Lys
    50                  55                  60

Pro Leu Ile Leu Arg Asp Cys Ser Val Ala Gly Trp Leu Leu Gly Asn
65                  70                  75                  80

Pro Met Cys Asp Glu Phe Ile Asn Val Pro Glu Trp Ser Tyr Ile Val
                85                  90                  95

Glu Lys Ala Asn Pro Ala Asn Asp Leu Cys Tyr Pro Gly Asn Phe Asn
            100                 105                 110

Asp Tyr Glu Glu Leu Lys His Leu Leu Ser Arg Ile Asn His Phe Glu
        115                 120                 125
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Lys Ile Gln Ile Ile Pro Lys Ser Ser Trp Ser Asp His Glu Ala Ser
130 135 140

Ser Gly Val Ser Ser Ala Cys Pro Tyr Gln Gly Thr Pro Ser Phe Phe
145 150 155 160

Arg Asn Val Val Trp Leu Ile Lys Lys Asn Asn Thr Tyr Pro Thr Ile
165 170 175

Lys Arg Ser Tyr Asn Asn Thr Asn Gln Glu Asp Leu Leu Ile Leu Trp
180 185 190

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

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

Leu Val Pro Lys Ile Ala Thr Arg Ser Lys Val Asn Gly Gln Ser Gly
225 230 235 240

Arg Met Asp Phe Phe Trp Thr Ile Leu Lys Pro Asn Asp Ala Ile Asn
245 250 255

Phe Glu Ser Asn Gly Asn Phe Ile Ala Pro Glu Tyr Ala Tyr Lys Ile
260 265 270

Val Lys Lys Gly Asp Ser Ala Ile Val Lys Ser Glu Val Glu Tyr Gly
275 280 285

Asn Cys Asn Thr Lys Cys Gln Thr Pro Ile Gly Ala Ile Asn Ser Ser
290 295 300

Met Pro Phe His Asn Ile His Pro Leu Thr Ile Gly Glu Cys Pro Lys
305 310 315 320

Tyr Val Lys Ser Asn Lys Leu Val Leu Ala Thr Gly Leu Arg Asn Ser
325 330 335

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

Gly Phe Ile Glu Gly Gly Trp Gln Gly Met Val Asp Gly Trp Tyr Gly
355 360 365

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

Ser Thr Gln Lys Ala Ile Asp Gly Val Thr Asn Lys Val Asn Ser Ile
385 390 395 400

Ile Asp Lys Met Asn Thr Gln Phe Glu Ala Val Gly Arg Glu Phe Asn
405 410 415

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Asn Leu Glu Arg Arg Ile Glu Asn Leu Asn Lys Lys Met Glu Asp Gly
            420                 425                 430

Phe Leu Asp Val Trp Thr Tyr Asn Ala Glu Leu Leu Val Leu Met Glu
        435                 440                 445

Asn Glu Arg Thr Leu Asp Phe His Asp Ser Asn Val Lys Asn Leu Tyr
    450                 455                 460

Asp Lys Val Arg Leu Gln Leu Arg Asp Asn Ala Lys Glu Leu Gly Asn
465                 470                 475                 480

Gly Cys Phe Glu Phe Tyr His Lys Cys Asp Asn Glu Cys Met Glu Ser
                485                 490                 495

Val Arg Asn Gly Thr Tyr Asp Tyr Pro Gln Tyr Ser Glu Glu Ala Arg
            500                 505                 510

Leu Lys Arg Glu Glu Ile Ser Gly Val Lys Leu Glu Ser Ile Gly Thr
        515                 520                 525

Tyr Gln Ile Leu Ser Ile Tyr Ser Thr Val Ala Ser Ser Leu Ala Leu
    530                 535                 540

Ala Ile Met Val Ala Gly Leu Ser Leu Trp Met Cys Ser Asn Gly Ser
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Leu Gln Cys Arg Ile Cys Ile
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<213> Influenza A virus

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<222> (1)..(1656)

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1               5                   10                  15

gac aca ata atg gaa aag aac gtt act gtt aca cat gcc caa gac ata          96
Asp Thr Ile Met Glu Lys Asn Val Thr Val Thr His Ala Gln Asp Ile
            20                  25                  30

ctg gaa aag aca cac aac ggg aag ctc tgc gat cta gat gga gtg aag         144
Leu Glu Lys Thr His Asn Gly Lys Leu Cys Asp Leu Asp Gly Val Lys
        35                  40                  45

cct ctg att tta aga gat tgt agt gta gct gga tgg ctc ctc gga aac         192
Pro Leu Ile Leu Arg Asp Cys Ser Val Ala Gly Trp Leu Leu Gly Asn
    50                  55                  60

cca atg tgt gac gaa ttc atc aat gtg ccg gaa tgg tct tac ata gtg         240
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Pro Met Cys Asp Glu Phe Ile Asn Val Pro Glu Trp Ser Tyr Ile Val
65                  70                  75                  80

gag aag gcc aac cca gcc aat gac ctc tgt tac cca ggg aat ttc aac      288
Glu Lys Ala Asn Pro Ala Asn Asp Leu Cys Tyr Pro Gly Asn Phe Asn
                85                  90                  95

gac tat gaa gaa ctg aaa cac cta ttg agc aga ata aac cat ttt gag      336
Asp Tyr Glu Glu Leu Lys His Leu Leu Ser Arg Ile Asn His Phe Glu
            100                 105                 110

aaa att cag atc atc ccc aaa agt tct tgg tcc gat cat gaa gcc tca      384
Lys Ile Gln Ile Ile Pro Lys Ser Ser Trp Ser Asp His Glu Ala Ser
        115                 120                 125

tca ggg gtg agc tca gca tgt cca tac cag gga acg ccc tcc ttt ttc      432
Ser Gly Val Ser Ser Ala Cys Pro Tyr Gln Gly Thr Pro Ser Phe Phe
    130                 135                 140

aga aat gtg gta tgg ctt atc aaa aag aac aat aca tac cca aca ata      480
Arg Asn Val Val Trp Leu Ile Lys Lys Asn Asn Thr Tyr Pro Thr Ile
145                 150                 155                 160

aag aga agc tac aat aat acc aac cag gaa gat ctt ttg ata ctg tgg      528
Lys Arg Ser Tyr Asn Asn Thr Asn Gln Glu Asp Leu Leu Ile Leu Trp
                165                 170                 175

ggg att cat cat tct aat gat gcg gca gag cag aca aag ctc tat caa      576
Gly Ile His His Ser Asn Asp Ala Ala Glu Gln Thr Lys Leu Tyr Gln
            180                 185                 190

aac cca acc acc tat att tcc gtt ggg aca tca aca cta aac cag aga      624
Asn Pro Thr Thr Tyr Ile Ser Val Gly Thr Ser Thr Leu Asn Gln Arg
        195                 200                 205

ttg gta cca aaa ata gct act aga tcc aaa gta aac ggg caa agt gga      672
Leu Val Pro Lys Ile Ala Thr Arg Ser Lys Val Asn Gly Gln Ser Gly
    210                 215                 220

agg atg gat ttc ttc tgg aca att tta aaa ccg aat gat gca atc aac      720
Arg Met Asp Phe Phe Trp Thr Ile Leu Lys Pro Asn Asp Ala Ile Asn
225                 230                 235                 240

ttc gag agt aat gga aat ttc att gct cca gaa tat gca tac aaa att      768
Phe Glu Ser Asn Gly Asn Phe Ile Ala Pro Glu Tyr Ala Tyr Lys Ile
                245                 250                 255

gtc aag aaa ggg gac tca gca att gtt aaa agt gaa gtg gaa tat ggt      816
Val Lys Lys Gly Asp Ser Ala Ile Val Lys Ser Glu Val Glu Tyr Gly
            260                 265                 270

aac tgc aac aca aag tgt caa act cca ata ggg gcg ata aac tct agt      864
Asn Cys Asn Thr Lys Cys Gln Thr Pro Ile Gly Ala Ile Asn Ser Ser
        275                 280                 285

atg cca ttc cac aac ata cac cct ctc acc atc ggg gaa tgc ccc aaa      912
Met Pro Phe His Asn Ile His Pro Leu Thr Ile Gly Glu Cys Pro Lys
    290                 295                 300

tat gtg aaa tca aac aaa tta gtc ctt gcg act ggg ctc aga aat agt      960
Tyr Val Lys Ser Asn Lys Leu Val Leu Ala Thr Gly Leu Arg Asn Ser
305                 310                 315                 320

cct cta aga gaa aga aga aga aaa aga gga cta ttt gga gct ata gca     1008
Pro Leu Arg Glu Arg Arg Arg Lys Arg Gly Leu Phe Gly Ala Ile Ala
                325                 330                 335

ggg ttt ata gag gga gga tgg cag gga atg gta gat ggt tgg tat ggg     1056
Gly Phe Ile Glu Gly Gly Trp Gln Gly Met Val Asp Gly Trp Tyr Gly
            340                 345                 350
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Tyr His His Ser Asn Glu Gln Gly Ser Gly Tyr Ala Ala Asp Lys Glu
        355                 360                 365

tcc act caa aag gca ata gat gga gtc acc aat aag gtc aac tcg atc       1152
Ser Thr Gln Lys Ala Ile Asp Gly Val Thr Asn Lys Val Asn Ser Ile
    370                 375                 380

att gac aaa atg aac act cag ttt gag gcc gtt gga agg gaa ttt aat       1200
Ile Asp Lys Met Asn Thr Gln Phe Glu Ala Val Gly Arg Glu Phe Asn
385                 390                 395                 400

aac tta gaa agg aga ata gag aat tta aac aag aaa atg gaa gac gga       1248
Asn Leu Glu Arg Arg Ile Glu Asn Leu Asn Lys Lys Met Glu Asp Gly
                405                 410                 415

ttc cta gat gtc tgg act tat aat gct gaa ctt ctg gtt ctc atg gaa       1296
Phe Leu Asp Val Trp Thr Tyr Asn Ala Glu Leu Leu Val Leu Met Glu
            420                 425                 430

aat gag aga act cta gac ttc cat gat tca aat gtc aag aac ctt tac       1344
Asn Glu Arg Thr Leu Asp Phe His Asp Ser Asn Val Lys Asn Leu Tyr
        435                 440                 445

gac aag gtc cga cta cag ctt agg gat aat gca aag gag ctg ggt aac       1392
Asp Lys Val Arg Leu Gln Leu Arg Asp Asn Ala Lys Glu Leu Gly Asn
    450                 455                 460

ggt tgt ttc gag ttc tat cac aaa tgt gat aat gaa tgt atg gaa agt       1440
Gly Cys Phe Glu Phe Tyr His Lys Cys Asp Asn Glu Cys Met Glu Ser
465                 470                 475                 480

gta aga aac gga acg tat gac tac ccg cag tat tca gaa gaa gca aga       1488
Val Arg Asn Gly Thr Tyr Asp Tyr Pro Gln Tyr Ser Glu Glu Ala Arg
                485                 490                 495

tta aaa aga gag gaa ata agt gga gta aaa ttg gaa tca ata gga act       1536
Leu Lys Arg Glu Glu Ile Ser Gly Val Lys Leu Glu Ser Ile Gly Thr
            500                 505                 510

tac caa ata ctg tca att tat tca aca gtt gcg agt tct cta gca ctg       1584
Tyr Gln Ile Leu Ser Ile Tyr Ser Thr Val Ala Ser Ser Leu Ala Leu
        515                 520                 525

gca atc atg gtg gct ggt cta tct ttg tgg atg tgc tcc aat ggg tcg       1632
Ala Ile Met Val Ala Gly Leu Ser Leu Trp Met Cys Ser Asn Gly Ser
    530                 535                 540

tta caa tgc aga att tgc att taa                                      1656
Leu Gln Cys Arg Ile Cys Ile
545                 550
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<210> 4
<211> 551
<212> PRT
<213> Influenza A virus

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Asp Thr Ile Met Glu Lys Asn Val Thr Val Thr His Ala Gln Asp Ile
            20                  25                  30

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

Pro Leu Ile Leu Arg Asp Cys Ser Val Ala Gly Trp Leu Leu Gly Asn
50 55 60

Pro Met Cys Asp Glu Phe Ile Asn Val Pro Glu Trp Ser Tyr Ile Val
65 70 75 80

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

Asp Tyr Glu Glu Leu Lys His Leu Leu Ser Arg Ile Asn His Phe Glu
100 105 110

Lys Ile Gln Ile Ile Pro Lys Ser Ser Trp Ser Asp His Glu Ala Ser
115 120 125

Ser Gly Val Ser Ser Ala Cys Pro Tyr Gln Gly Thr Pro Ser Phe Phe
130 135 140

Arg Asn Val Val Trp Leu Ile Lys Lys Asn Asn Thr Tyr Pro Thr Ile
145 150 155 160

Lys Arg Ser Tyr Asn Asn Thr Asn Gln Glu Asp Leu Leu Ile Leu Trp
165 170 175

Gly Ile His His Ser Asn Asp Ala Ala Glu Gln Thr Lys Leu Tyr Gln
180 185 190

Asn Pro Thr Thr Tyr Ile Ser Val Gly Thr Ser Thr Leu Asn Gln Arg
195 200 205

Leu Val Pro Lys Ile Ala Thr Arg Ser Lys Val Asn Gly Gln Ser Gly
210 215 220

Arg Met Asp Phe Phe Trp Thr Ile Leu Lys Pro Asn Asp Ala Ile Asn
225 230 235 240

Phe Glu Ser Asn Gly Asn Phe Ile Ala Pro Glu Tyr Ala Tyr Lys Ile
245 250 255

Val Lys Lys Gly Asp Ser Ala Ile Val Lys Ser Glu Val Glu Tyr Gly
260 265 270

Asn Cys Asn Thr Lys Cys Gln Thr Pro Ile Gly Ala Ile Asn Ser Ser
275 280 285

Met Pro Phe His Asn Ile His Pro Leu Thr Ile Gly Glu Cys Pro Lys
290 295 300

Tyr Val Lys Ser Asn Lys Leu Val Leu Ala Thr Gly Leu Arg Asn Ser
305 310 315 320

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Pro Leu Arg Glu Arg Arg Arg Lys Arg Gly Leu Phe Gly Ala Ile Ala
                325                 330                 335

Gly Phe Ile Glu Gly Gly Trp Gln Gly Met Val Asp Gly Trp Tyr Gly
            340                 345                 350

Tyr His His Ser Asn Glu Gln Gly Ser Gly Tyr Ala Ala Asp Lys Glu
        355                 360                 365

Ser Thr Gln Lys Ala Ile Asp Gly Val Thr Asn Lys Val Asn Ser Ile
    370                 375                 380

Ile Asp Lys Met Asn Thr Gln Phe Glu Ala Val Gly Arg Glu Phe Asn
385                 390                 395                 400

Asn Leu Glu Arg Arg Ile Glu Asn Leu Asn Lys Lys Met Glu Asp Gly
                405                 410                 415

Phe Leu Asp Val Trp Thr Tyr Asn Ala Glu Leu Leu Val Leu Met Glu
            420                 425                 430

Asn Glu Arg Thr Leu Asp Phe His Asp Ser Asn Val Lys Asn Leu Tyr
        435                 440                 445

Asp Lys Val Arg Leu Gln Leu Arg Asp Asn Ala Lys Glu Leu Gly Asn
    450                 455                 460

Gly Cys Phe Glu Phe Tyr His Lys Cys Asp Asn Glu Cys Met Glu Ser
465                 470                 475                 480

Val Arg Asn Gly Thr Tyr Asp Tyr Pro Gln Tyr Ser Glu Glu Ala Arg
                485                 490                 495

Leu Lys Arg Glu Glu Ile Ser Gly Val Lys Leu Glu Ser Ile Gly Thr
            500                 505                 510

Tyr Gln Ile Leu Ser Ile Tyr Ser Thr Val Ala Ser Ser Leu Ala Leu
        515                 520                 525

Ala Ile Met Val Ala Gly Leu Ser Leu Trp Met Cys Ser Asn Gly Ser
    530                 535                 540

Leu Gln Cys Arg Ile Cys Ile
545                 550
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