SEQUENCE LISTING

<110> Novavax, Inc.

<120> Functional Influenza Virus Like Particles (VLPs)

<130> SP9403B

<150> US 60/727,513
<151> 2005-10-18

<150> US 60/780,847
<151> 2006-03-10

<150> US 60/800,006
<151> 2006-05-15

<150> US 60/831,196
<151> 2006-07-17

<150> US 60/832,116
<151> 2006-07-21

<150> US 60/845,495
<151> 2006-09-19

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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
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Pro Met Cys Asp Glu Phe Ile Asn Val Pro Glu Trp Ser Tyr Ile Val
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Ser Gly Val Ser Ser Ala Cys Pro Tyr Leu Gly Ser Pro Ser Phe Phe
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Arg Asn Val Val Trp Leu Ile Lys Lys Asn Ser Thr Tyr Pro Thr Ile
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Lys Lys Ser Tyr Asn Asn Thr Asn Gln Glu Asp Leu Leu Val Leu Trp
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Gly Ile His His Pro Asn Asp Ala Ala Glu Gln Thr Arg Leu Tyr Gln
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Val Lys Lys Gly Asp Ser Ala Ile Met Lys Ser Glu Leu Glu Tyr Gly
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Asn Cys Asn Thr Lys Cys Gln Thr Pro Met Gly Ala Ile Asn Ser Ser
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Tyr Val Lys Ser Asn Arg Leu Val Leu Ala Thr Gly Leu Arg Asn Ser
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Gly Phe Leu Asp Val Trp Thr Tyr Asn Ala Glu Leu Leu Val Leu Met
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Asn Gly Cys Phe Glu Phe Tyr His Lys Cys Asp Asn Glu Cys Met Glu
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Ser Ile Arg Asn Gly Thr Tyr Asn Tyr Pro Gln Tyr Ser Glu Glu Ala
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Arg Leu Lys Arg Glu Glu Ile Ser Gly Val Lys Leu Glu Ser Ile Gly
515 520 525

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

450 455 460

Val Lys Asn Leu Tyr Asp Lys Val Arg Leu Gln Leu Arg Asp Asn Ala
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Lys Glu Leu Gly Asn Gly Cys Phe Glu Phe Tyr His Lys Cys Asp Asn
485 490 495

Glu Cys Met Glu Ser Ile Arg Asn Gly Thr Tyr Asn Tyr Pro Gln Tyr
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Ser Glu Glu Ala Arg Leu Lys Arg Glu Glu Ile Ser Gly Val Lys Leu
515 520 525

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Met Glu Thr Ile Ser Leu Ile Thr Ile Leu Leu Val Val Thr Ala Ser
1 5 10 15

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

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

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

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

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

Ile Val Glu Lys Ala Asn Pro Thr Asn Asp Leu Cys Tyr Pro Gly Ser
100 105 110

Phe Asn Asp Tyr Glu Glu Leu Lys His Leu Leu Ser Arg Ile Asn His
115 120 125

Phe Glu Lys Ile Gln Ile Ile Pro Lys Ser Ser Trp Ser Asp His Glu
130 135 140

Ala Ser Ser Gly Val Ser Ser Ala Cys Pro Tyr Leu Gly Ser Pro Ser
145 150 155 160

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

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

Leu Trp Gly Ile His His Pro Asn Asp Ala Ala Glu Gln Thr Arg Leu
195 200 205

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

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

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

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

Lys Ile Val Lys Lys Gly Asp Ser Ala Ile Met Lys Ser Glu Leu Glu
275 280 285

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

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

Pro Lys Tyr Val Lys Ser Asn Arg Leu Val Leu Ala Thr Gly Leu Arg

325 330 335

Asn Ser Pro Gln Arg Glu Ser Arg Arg Lys Lys Arg Gly Leu Phe Gly
340 345 350

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

Trp Tyr Gly Tyr His His Ser Asn Glu Gln Gly Ser Gly Tyr Ala Ala
370 375 380

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

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

Glu Phe Asn Asn Leu Glu Arg Arg Ile Glu Asn Leu Asn Lys Lys Met
420 425 430

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

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

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

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

Met Glu Ser Ile Arg Asn Gly Thr Tyr Asn Tyr Pro Gln Tyr Ser Glu
500 505 510

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

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

Leu Ala Leu Ala Ile Met Met Ala Gly Leu Ser Leu Trp Met Cys Ser
545 550 555 560

Asn Gly Ser Leu Gln Cys Arg Ile Cys Ile
565 570

<210> 30
<211> 564
<212> PRT
<213> Unknown

<220>
<223> Vac2-hac-cs-opt

<400> 30

Met Glu Lys Ile Val Leu Leu Leu Ala Ile Val Ser Leu Val Lys Ser
1 5 10 15

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 Thr Asn Asp Leu Cys Tyr Pro Gly Ser Phe Asn
100 105 110

Asp Tyr Glu Glu Leu Lys His Leu Leu Ser Arg Ile Asn His Phe Glu
115 120 125

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 Leu Gly Ser Pro Ser Phe Phe
145 150 155 160

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

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

Gly Ile His His Pro Asn Asp Ala Ala Glu Gln Thr Arg Leu Tyr Gln

195 200 205

Asn Pro Thr Thr Tyr Ile Ser Ile 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 Glu 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 Met Lys Ser Glu Leu Glu Tyr Gly
275 280 285

Asn Cys Asn Thr Lys Cys Gln Thr Pro Met 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 Arg Leu Val Leu Ala Thr Gly Leu Arg Asn Ser
325 330 335

Pro Gln Arg Glu Ser Arg Gly Leu Phe Gly Ala Ile Ala Gly Phe Ile
340 345 350

Glu Gly Gly Trp Gln Gly Met Val Asp Gly Trp Tyr Gly Tyr His His
355 360 365

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

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

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

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

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

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

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

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

Gly Thr Tyr Asn Tyr Pro Gln Tyr Ser Glu Glu Ala Arg Leu Lys Arg
500 505 510

Glu Glu Ile Ser Gly Val Lys Leu Glu Ser Ile Gly Thr Tyr Gln Ile
515 520 525

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

Met Ala Gly Leu Ser Leu Trp Met Cys Ser Asn Gly Ser Leu Gln Cys
545 550 555 560

Arg Ile Cys Ile

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<211> 449
<212> PRT
<213> Unknown

<220>
<223> Vac2-naj-opt

<400> 31

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

Ile Gly Ile Val Ser Leu Met Leu Gln Ile Gly Asn Met Ile Ser Ile
20 25 30

Trp Val Ser His Ser Ile Gln Thr Gly Asn Gln His Gln Ala Glu Ser
35 40 45

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

Leu Ala Gly Asn Ser Ser Leu Cys Pro Ile Arg Gly Trp Ala Val His

65 70 75 80

Ser Lys Asp Asn Asn Ile Arg Ile Gly Ser Lys Gly Asp Val Phe Val
85 90 95

Ile Arg Glu Pro Phe Ile Ser Cys Ser His Leu Glu Cys Arg Thr Phe
100 105 110

Phe Leu Thr Gln Gly Ala Leu Leu Asn Asp Lys His Ser Asn Gly Thr
115 120 125

Val Lys Asp Arg Ser Pro His Arg Thr Leu Met Ser Cys Pro Val Gly
130 135 140

Glu Ala Pro Ser Pro Tyr Asn Ser Arg Phe Glu Ser Val Ala Trp Ser
145 150 155 160

Ala Ser Ala Cys His Asp Gly Thr Ser Trp Leu Thr Ile Gly Ile Ser
165 170 175

Gly Pro Asp Asn Glu Ala Val Ala Val Leu Lys Tyr Asn Gly Ile Ile
180 185 190

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

Ser Glu Cys Ala Cys Val Asn Gly Ser Cys Phe Thr Val Met Thr Asp
210 215 220

Gly Pro Ser Asp Gly Gln Ala Ser Tyr Lys Ile Phe Lys Met Glu Lys
225 230 235 240

Gly Lys Val Val Lys Ser Val Glu Leu Asp Ala Pro Asn Tyr His Tyr
245 250 255

Glu Glu Cys Ser Cys Tyr Pro Asp Ala Gly Glu Ile Thr Cys Val Cys
260 265 270

Arg Asp Asn Trp His Gly Ser Asn Arg Pro Trp Val Ser Phe Asn Gln
275 280 285

Asn Leu Glu Tyr Gln Ile Gly Tyr Ile Cys Ser Gly Val Phe Gly Asp
290 295 300

Asn Pro Arg Pro Asn Asp Gly Thr Gly Ser Cys Gly Pro Met Ser Pro
305 310 315 320

Asn Gly Ala Tyr Gly Val Lys Gly Phe Ser Phe Lys Tyr Gly Asn Gly
325 330 335

Val Trp Ile Gly Arg Thr Lys Ser Thr Asn Ser Arg Ser Gly Phe Glu
340 345 350

Met Ile Trp Asp Pro Asn Gly Trp Thr Gly Thr Asp Ser Ser Phe Ser
355 360 365

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

Ser Phe Val Gln His Pro Glu Leu Thr Gly Leu Asp Cys Ile Arg Pro
385 390 395 400

Cys Phe Trp Val Glu Leu Ile Arg Gly Arg Pro Lys Glu Ser Thr Ile
405 410 415

Trp Thr Ser Gly Ser Ser Ile Ser Phe Cys Gly Val Asn Ser Asp Thr
420 425 430

Val Ser Trp Ser Trp Pro Asp Gly Ala Glu Leu Pro Phe Thr Ile Asp
435 440 445

Lys

<210> 32
<211> 252
<212> PRT
<213> Unknown

<220>
<223> Vac2-mc-opt

<400> 32

Met Ser Leu Leu Thr Glu Val Glu Thr Tyr Val Leu Ser Ile Ile Pro
1 5 10 15

Ser Gly Pro Leu Lys Ala Glu Ile Ala Gln Lys Leu Glu Asp Val Phe
20 25 30

Ala Gly Lys Asn Thr Asp Leu Glu Ala Leu Met Glu Trp Leu Lys Thr
35 40 45

Arg Pro Ile Leu Ser Pro Leu Thr Lys Gly Ile Leu Gly Phe Val Phe

50 55 60

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

Gln Asn Ala Leu Asn Gly Asn Gly Asp Pro Asn Asn Met Asp Arg Ala
85 90 95

Val Lys Leu Tyr Lys Lys Leu Lys Arg Glu Ile Thr Phe His Gly Ala
100 105 110

Lys Glu Val Ser Leu Ser Tyr Ser Thr Gly Ala Leu Ala Ser Cys Met
115 120 125

Gly Leu Ile Tyr Asn Arg Met Gly Thr Val Thr Thr Glu Val Ala Phe
130 135 140

Gly Leu Val Cys Ala Thr Cys Glu Gln Ile Ala Asp Ser Gln His Arg
145 150 155 160

Ser His Arg Gln Met Ala Thr Ile Thr Asn Pro Leu Ile Arg His Glu
165 170 175

Asn Arg Met Val Leu Ala Ser Thr Thr Ala Lys Ala Met Glu Gln Met
180 185 190

Ala Gly Ser Ser Glu Gln Ala Ala Glu Ala Met Glu Val Ala Asn Gln
195 200 205

Ala Arg Gln Met Val Gln Ala Met Arg Thr Ile Gly Thr His Pro Asn
210 215 220

Ser Ser Ala Gly Leu Arg Asp Asn Leu Leu Glu Asn Leu Gln Ala Tyr
225 230 235 240

Gln Lys Arg Met Gly Val Gln Met Gln Arg Phe Lys
245 250

<210> 33
<211> 564
<212> PRT
<213> Unknown

<220>
<223> VN1203-ha-cs-opt

<400> 33

Met Glu Lys Ile Val Leu Leu Phe Ala Ile Val Ser Leu Val Lys Ser
1 5 10 15

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 Asp Phe Asn
100 105 110

Asp Tyr Glu Glu Leu Lys His Leu Leu Ser Arg Ile Asn His Phe Glu
115 120 125

Lys Ile Gln Ile Ile Pro Lys Asn Ser Trp Ser Ser His Glu Ala Ser
130 135 140

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

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

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

Gly Ile His His Pro Asn Asp Ala Ala Glu Gln Thr Arg 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 Asn Gly
225 230 235 240

Arg Met Glu 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 Met Lys Ser Glu Leu Glu Tyr Gly
275 280 285

Asn Cys Asn Thr Lys Cys Gln Thr Pro Met 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 Arg Leu Val Leu Ala Thr Gly Leu Arg Asn Ser
325 330 335

Pro Gln Arg Glu Thr Arg Gly Leu Phe Gly Ala Ile Ala Gly Phe Ile
340 345 350

Glu Gly Gly Trp Gln Gly Met Val Asp Gly Trp Tyr Gly Tyr His His
355 360 365

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

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

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

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

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

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

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

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

Gly Thr Tyr Asp Tyr Pro Gln Tyr Ser Glu Glu Ala Arg Leu Lys Arg
500 505 510

Glu Glu Ile Ser Gly Val Lys Leu Glu Ser Ile Gly Thr Tyr Gln Ile
515 520 525

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

Val Ala Gly Leu Ser Leu Trp Met Cys Ser Asn Gly Ser Leu Gln Cys
545 550 555 560

Arg Ile Cys Ile

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<211> 572
<212> PRT
<213> Unknown

<220>
<223> VN1203-ha-spc-opt

<400> 34

Met Pro Leu Tyr Lys Leu Leu Asn Val Leu Trp Leu Val Ala Val Ser
1 5 10 15

Asn Ala Ile Pro Asp Gln Ile Cys Ile Gly Tyr His Ala Asn Asn Ser
20 25 30

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

Ala Gln Asp Ile Leu Glu Lys Thr His Asn Gly Lys Leu Cys Asp Leu
50 55 60

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

Leu Leu Gly Asn Pro Met Cys Asp Glu Phe Ile Asn Val Pro Glu Trp
85 90 95

Ser Tyr Ile Val Glu Lys Ala Asn Pro Ala Asn Asp Leu Cys Tyr Pro
100 105 110

Gly Asp Phe Asn Asp Tyr Glu Glu Leu Lys His Leu Leu Ser Arg Ile

115 120 125

Asn His Phe Glu Lys Ile Gln Ile Ile Pro Lys Asn Ser Trp Ser Ser
130 135 140

His Glu Ala Ser Leu Gly Val Ser Ser Ala Cys Pro Tyr Gln Gly Lys
145 150 155 160

Ser Ser Phe Phe Arg Asn Val Val Trp Leu Ile Lys Lys Asn Asn Ala
165 170 175

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

Leu Val Leu Trp Gly Ile His His Pro Asn Asp Ala Ala Glu Gln Thr
195 200 205

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

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

Gly Gln Asn Gly Arg Met Glu Phe Phe Trp Thr Ile Leu Lys Pro Asn
245 250 255

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

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

Leu Glu Tyr Gly Asn Cys Asn Thr Lys Cys Gln Thr Pro Met Gly Ala
290 295 300

Ile Asn Ser Ser Met Pro Phe His Asn Ile His Pro Leu Thr Ile Gly
305 310 315 320

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

Leu Arg Asn Ser Pro Gln Arg Glu Arg Arg Arg Lys Lys Arg Gly Leu
340 345 350

Phe Gly Ala Ile Ala Gly Phe Ile Glu Gly Gly Trp Gln Gly Met Val
355 360 365

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Asp Gly Trp Tyr Gly Tyr His His Ser Asn Glu Gln Gly Ser Gly Tyr
    370                 375                 380

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

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

Gly Arg Glu Phe Asn Asn Leu Glu Arg Arg Ile Glu Asn Leu Asn Lys
            420                 425                 430

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

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

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

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

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

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

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

Ser Ser Leu Ala Leu Ala Ile Met Val Ala Gly Leu Ser Leu Trp Met
545                 550                 555                 560

Cys Ser Asn Gly Ser Leu Gln Cys Arg Ile Cys Ile
                565                 570
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<210> 35
<211> 570
<212> PRT
<213> Unknown

<220>
<223> VN1203-ha-sph9-opt

<400> 35

Met Glu Thr Ile Ser Leu Ile Thr Ile Leu Leu Val Val Thr Ala Ser
1 5 10 15

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

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

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

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

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

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

Phe Asn Asp Tyr Glu Glu Leu Lys His Leu Leu Ser Arg Ile Asn His
115 120 125

Phe Glu Lys Ile Gln Ile Ile Pro Lys Asn Ser Trp Ser Ser His Glu
130 135 140

Ala Ser Leu Gly Val Ser Ser Ala Cys Pro Tyr Gln Gly Lys Ser Ser
145 150 155 160

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

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

Leu Trp Gly Ile His His Pro Asn Asp Ala Ala Glu Gln Thr Arg Leu
195 200 205

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

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

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

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

Lys Ile Val Lys Lys Gly Asp Ser Ala Ile Met Lys Ser Glu Leu Glu
        275                 280                 285

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

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

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

Asn Ser Pro Gln Arg Glu Arg Arg Arg Lys Lys Arg Gly Leu Phe Gly
            340                 345                 350

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

Trp Tyr Gly Tyr His His Ser Asn Glu Gln Gly Ser Gly Tyr Ala Ala
    370                 375                 380

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

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

Glu Phe Asn Asn Leu Glu Arg Arg Ile Glu Asn Leu Asn Lys Lys Met
            420                 425                 430

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

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

Asn Leu Tyr Asp Lys Val Arg Leu Gln Leu Arg Asp Asn Ala Lys Glu
465                 470                 475                 480
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Leu Gly Asn Gly Cys Phe Glu Phe Tyr His Lys Cys Asp Asn Glu Cys
485 490 495

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

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

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

Leu Ala Leu Ala Ile Met Val Ala Gly Leu Ser Leu Trp Met Cys Ser
545 550 555 560

Asn Gly Ser Leu Gln Cys Arg Ile Cys Ile
565 570

<210> 36
<211> 1707
<212> DNA
<213> Influenza virus

<400> 36
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attggttacc atgcaaacaa ctcgacagag caggttgaca caataatgga aaagaacgtt 120

actgttacac atgcccaaga catactggaa aagaaacaca acgggaagct ctgcgatcta 180

gatggagtga agcctctaat tttgagagat tgtagcgtag ctggatggct cctcggaaac 240

ccaatgtgtg acgaattcat caatgtgccg gaatggtctt acatagtgga gaaggccaat 300

ccagtcaatg acctctgtta cccaggggat ttcaatgact atgaagaatt gaaacaccta 360

ttgagcagaa taaaccattt tgagaaaatt cagatcatcc ccaaaagttc ttggtccagt 420

catgaagcct cattaggggt gagctcagca tgtccatacc agggaaagtc ctccttttte 480

agaaatgtgg tatggcttat caaaaagaac agtacatacc caacaataaa gaggagctac 540

aataatacca accaagaaga tcttttggta ctgtgggggа ttcaccatcc taatgatgcg 600

gcagagcaga caaagctcta tcaaaaccca accacctata tttccgttgg gacatcaaca 660

ctaaaccaga gattggtacc aagaatagct actagatcca aagtaaacgg gcaaagtgga 720

aggatggagt tcttctggac aattttaaag ccgaatgatg caatcaactt cgagagtaat 780

ggaaatttca ttgctccaga atatgcatac aaaattgtca agaaagggga ctcaacaatt 840

atgaaaagtg aattggaata tggtaactgc aacaccaagt gtcaaactcc aatgggggcg 900

ataaactcta gcatgccatt ccacaatata caccctctca ccattgggga atgccccaaa 960

tatgtgaaat caaacagatt agtccttgcg actgggctca gaaatagccc tcaaagagag 1020

agaagaagaa aaaagagagg attatttgga gctatagcag gttttataga gggaggatgg 1080

cagggaatgg tagatggttg gtatgggtac caccatagca atgagcaggg gagtgggtac 1140

gctgcagaca aagaatccac tcaaaaggca atagatggag tcaccaataa ggtcaactcg 1200

atcattgaca aaatgaacac tcagtttgag gccgttggaa gggaatttaa caacttagaa 1260

aggagaatag agaatttaaa caagaagatg gaagacgggt tcctagatgt ctggacttat 1320

aatgctgaac ttctggttct catggaaaat gagagaactc tagactttca tgactcaaat 1380

gtcaagaacc tttacgacaa ggtccgacta cagcttaggg ataatgcaaa ggagctgggt 1440

aacggttgtt tcgagttcta tcataaatgt gataatgaat gtatggaaag tgtaagaaat 1500

ggaacgtatg actacccgca gtattcagaa gaagcgagac taaaaagaga ggaaataagt 1560

ggagtaaaat tggaatcaat aggaatttac caaatactgt caatttattc tacagtggcg 1620

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tcgttacaat gcagaatttg catttaa 1707

<210> 37
<211> 1750
<212> DNA
<213> Influenza virus

<400> 37
agtgtgatgg atatctgcag aattcgccct taggcgcgcc atggagaaaa tagtgcttct 60

ttttgcaata gtcagtcttg ttaaaagtga tcagatttgc attggttacc atgcaaacaa 120

ctcgacagag caggttgaca caataatgga aaagaacgtt actgttacac atgcccaaga 180

catactggaa aagaaacaca acgggaagct ctgcgatcta gatggagtga agcctctaat 240

tttgagagat tgtagcgtag ctggatggct cctcggaaac ccaatgtgtg acgaattcat 300

caatgtgccg gaatggtctt acatagtgga gaaggccaat ccagtcaatg acctctgtta 360

cccaggggat ttcaatgact atgaagaatt gaaacaccta ttgagcagaa taaaccattt 420

tgagaaaatt cagatcatcc ccaaaagttc ttggtccagt catgaagcct cattaggggt 480

gagctcagca tgtccatacc agggaaagtc ctccttttttc agaaatgtgg tatggcttat 540

caaaaagaac agtacatacc caacaataaa gaggagctac aataatacca accaagaaga 600

tcttttggta ctgtgggggga ttcaccatcc taatgatgcg gcagagcaga caaagctcta 660

tcaaaaccca accacctata tttccgttgg gacatcaaca ctaaaccaga gattggtacc 720

aagaatagct actagatcca aagtaaacgg gcaaagtgga aggatggagt tcttctggac 780

aattttaaag ccgaatgatg caatcaactt cgagagtaat ggaaatttca ttgctccaga 840

atatgcatac aaaattgtca agaaagggga ctcaacaatt atgaaaagtg aattggaata 900

tggtaactgc aacaccaagt gtcaaactcc aatgggggcg ataaactcta gcatgccatt 960

ccacaatata caccctctca ccattgggga atgccccaaa tatgtgaaat caaacagatt 1020

agtccttgcg actgggctca gaaatagccc tcaaagagag agaagaagaa aaaagagagg 1080

attatttgga gctatagcag gttttataga gggaggatgg cagggaatgg tagatggttg 1140

gtatgggtac caccatagca atgagcaggg gagtgggtac gctgcagaca aagaatccac 1200

tcaaaaggca atagatggag tcaccaataa ggtcaactcg atcattgaca aaatgaacac 1260

tcagtttgag gccgttggaa gggaatttaa caacttagaa aggagaatag agaatttaaa 1320

caagaagatg gaagacgggt tcctagatgt ctggacttat aatgctgaac ttctggttct 1380

catggaaaat gagagaactc tagactttca tgactcaaat gtcaagaacc tttacgacaa 1440

ggtccgacta cagcttaggg ataatgcaaa ggagctgggt aacggttgtt tcgagttcta 1500

tcataaatgt gataatgaat gtatggaaag tgtaagaaat ggaacgtatg actacccgca 1560

gtattcagaa gaagcgagac taaaaagaga ggaaataagt ggagtaaaat tggaatcaat 1620

aggaatttac caaatactgt caatttattc tacagtggcg agttccctag cactggcaat 1680

catggtagct ggtctatcct tatggatgtg ctccaatggg tcgttacaat gcagaatttg 1740

catttaagcg 1750

<210> 38
<211> 1350
<212> DNA
<213> Influenza virus

<400> 38
atgaatccaa atcagaagat aataaccatc ggatcaatct gtatggtaac tggaatagtt 60

agcttaatgt tacaaattgg gaacatgatc tcaatatggg tcagtcattc aattcacaca 120

gggaatcaac accaatctga accaatcagc aatactaatt ttcttactga gaaagctgtg 180

gcttcagtaa aattagcggg caattcatct ctttgcccca ttaacggatg ggctgtatac 240

agtaaggaca acagtataag gatcggttcc aaggggatg tgtttgttat aagagagccg 300

ttcatctcat gctcccactt ggaatgcaga actttctttt tgactcaggg agccttgctg 360

aatgacaagc actccaatgg gactgtcaaa gacagaagcc ctcacagaac attaatgagt 420

tgtcctgtgg gtgaggctcc ctccccatat aactcaaggt ttgagtctgt tgcttggtca 480

gcaagtgctt gccatgatgg caccagttgg ttgacgattg gaatttctgg cccagacaat 540

ggggctgtgg ctgtattgaa atacaatggc ataataacag acactatcaa gagttggagg 600

aacaacatac tgagaactca agagtctgaa tgtgcatgtg taaatggctc ttgctttact 660

gtaatgactg acggaccaag taatggtcag gcatcacata agatcttcaa aatggaaaaa 720

gggaaagtgg ttaaatcagt cgaattggat gctcctaatt atcactatga ggaatgctcc 780

tgttatccta atgccggaga aatcacatgt gtgtgcaggg ataattggca tggctcaaat 840

cggccatggg tatctttcaa tcaaaatttg gagtatcaaa taggatatat atgcagtgga 900

gttttcggag acaatccacg ccccaatgat ggaacaggta gttgtggtcc ggtgtcctct 960

aacggggcat atggggtaaa agggttttca tttaaatacg gcaatggtgt ctggatcggg 1020

agaaccaaaa gcactaattc caggagcggc tttgaaatga tttgggatcc aaatgggtgg 1080

actgaaacgg acagtagctt ttcagtgaaa caagatatcg tagcaataac tgattggtca 1140

ggatatagcg ggagttttgt ccagcatcca gaactgacag gactagattg cataagacct 1200

tgtttctggg ttgagttgat cagagggcgg cccaaagaga gcacaatttg gactagtggg 1260

agcagcatat ctttttgtgg tgtaaatagt gacactgtgg gttggtcttg gccagacggt 1320

gccgagttgc cattcaccat tgacaagtag 1350

<210> 39
<211> 1400
<212> DNA
<213> Influenza virus

<400> 39
ccgggatgaa tccaaatcag aagataataa ccatcggatc aatctgtatg gtaactggaa 60

tagttagctt aatgttacaa attgggaaca tgatctcaat atgggtcagt cattcaattc 120

acacagggaa tcaacaccaa tctgaaccaa tcagcaatac taattttctt actgagaaag 180

ctgtggcttc agtaaaatta gcgggcaatt catctctttg ccccattaac ggatgggctg 240

tatacagtaa ggacaacagt ataaggatcg gttccaaggg ggatgtgttt gttataagag 300

agccgttcat ctcatgctcc cacttggaat gcagaacttt ctttttgact cagggagcct 360

cgctgaatga caagcactcc aatgggactg tcaaagacag aagccctcac agaacattaa 420

tgagttgtcc tgtgggtgag gctccctccc catataactc aaggtttgag tctgttgctt 480

ggtcagcaag tgcttgccat gatggcacca gttggttgac gattggaatt tctggcccag 540

acaatggggc tgtggctgta ttgaaataca atggcataat aacagacact atcaagagtt 600

ggaggaacaa catactgaga actcaagagt ctgaatgtgc atgtgtaaat ggctcttgct 660

ttactgtaat gactgacgga ccaagtaatg gtcaggcatc acataagatc ttcaaaatgg 720

aaaaagggaa agtggttaaa tcagtcgaat tggatgctcc taattatcac tatgaggaat 780

gctcctgtta tcctaatgcc ggagaaatca catgtgtgtg cagggataat tggcatggct 840

caaatcggcc atgggtatct ttcaatcaaa atttggagta tcaaatagga tatatatgca 900

gtggagtttt cggagacaat ccacgcccca atgatggaac aggtagttgt ggtccggtgt 960

cctctaacgg ggcatatggg gtaaaagggt tttcatttaa atacggcaat ggtgtctgga 1020

tcgggagaac caaaagcact aattccagga gcggctttga aatgatttgg gatccaaatg 1080

ggtggactga aacggacagt agcttttcag tgaaacaaga tatcgtagca ataactgatt 1140

ggtcaggata tagcgggagt tttgtccagc atccagaact gacaggacta gattgcataa 1200

gaccttgttt ctgggttgag ttgatcagag ggcggcccaa agagagcaca atttggacta 1260

gtgggagcag catatctttt tgtggtgtaa atagtgacac tgtgggttgg tcttggccag 1320

acggtgctga gttgccattc accattgaca agtaggggcc ctcgagtaag ggcgaattcc 1380

agcacactgg cggccgttac 1400

<210> 40
<211> 759
<212> DNA
<213> Influenza virus

<400> 40
atgagtcttc taaccgaggt cgaaacgtac gttctctcta tcatcccgtc aggcccctc 60

aaagccgaga tcgcacagaa acttgaagat gtctttgcag gaaagaacac cgatctcgag 120

gctctcatgg agtggctaaa gacaagacca atcctgtcac ctctgactaa agggattttg 180

ggatttgtat tcacgctcac cgtgcccagt gagcgaggac tgcagcgtag acgctttgtc 240

cagaatgccc taaatggaaa tggagatcca aataatatgg atagggcagt taagctatat 300

aagaagctga aaagagaaat aacattccat ggggctaagg aggtcgcact cagctactca 360

accggtgcac ttgccagttg catgggtctc atatacaaca ggatgggaac ggtgactacg 420

gaagtggctt ttggcctagt gtgtgccact tgtgagcaga ttgcagattc acagcatcgg 480

tctcacagac agatggcaac tatcaccaac ccactaatca gacatgagaa cagaatggtg 540

ctggccagca ctacagctaa ggctatggag cagatggcgg gatcaagtga gcaggcagcg 600

gaagccatgg agatcgctaa tcaggctagg cagatggtgc aggcaatgag gacaattggg 660

actcatccta actctagtgc tggtctgaga gataatcttc ttgaaaattt gcaggcctac 720

cagaaacgaa tgggagtgca gatgcagcga ttcaagtga 759

<210> 41
<211> 793
<212> DNA
<213> Influenza virus

<400> 41
atatctgcag aattcgccct tagaattcga cgtcatgagt cttctaaccg aggtcgaaac 60

gtacgttctc tctatcatcc cgtcaggccc cctcaaagcc gagatcgcac agaaacttga 120

agatgtcttt gcaggaaaga acaccgatct cgaggctctc atggagtggc taaagacaag 180

accaatcctg tcacctctga ctaaagggat tttgggattt gtattcacgc tcaccgtgcc 240

cagtgagcga ggactgcagc gtagacgctt tgtccagaat gccctaaatg gaaatggaga 300

tccaaataat atggataggg cagttaagct atataagaag ctgaaaagag aaataacatt 360

ccatggggct aaggaggtcg cactcagcta ctcaaccggt gcacttgcca gttgcatggg 420

tctcatatac aacaggatgg gaacggtgac tacggaagtg gcttttggcc tagtgtgtgc 480

cacttgtgag cagattgcag attcacagca tcggtctcac agacagatgg caactatcac 540

caacccacta atcagacatg agaacagaat ggtgctggcc agcactacag ctaaggctat 600

ggagcagatg gcgggatcaa gtgagcaggc agcggaagcc atggagatcg ctaatcaggc 660

taggcagatg gtgcaggcaa tgaggacaat tgggactcat cctaactcta gtgctggtct 720

gagagataat cttcttgaaa atttgcaggc ctaccagaaa cgaatgggag tgcagatgca 780

gcgattcaag tga 793

<210> 42
<211> 1740
<212> DNA
<213> Artificial sequence

<220>
<223> Influenza HA gene optimized for expression in insect cell expression system

<400> 42
ggtaccggat ccgccaccat ggagaagatc gtgctgctgc tggctatcgt gtccctggtg 60

aagtccgacc agatctgcat cggttaccac gctaacaact ccaccgagca ggtggacacc 120

atcatggaga agaacgtcac cgtgacccac gctcaggaca tcctcgaaaa gacccacaac 180

ggcaagctgt gcgacctgga cggtgtcaag ccctgatcc tgcgtgactg ctccgtggct 240

ggttggctgc tgggtaaccc catgtgcgac gagttcatca acgtgcccga gtggtcctac 300

atcgtggaga aggctaaccc caccaacgac ctgtgctacc ccggttcctt caacgactac 360

gaggagctga agcacctgct gtcccgtatc aaccacttcg agaagatcca gatcatcccc 420

aagtcctctt ggtccgacca cgaggcttcc tccggtgtct cctccgcttg ccctacctg 480

ggttcccct ccttcttccg taacgtggtg tggctgatca agaagaactc cacctacccc 540

accatcaaga agtcctacaa caacaccaac caggaggacc tgctggtcct gtggggtatc 600

caccacccca acgacgctgc cgagcagacc cgtctgtacc agaaccccac cacctacatc 660

tccatcggca cctccaccct gaaccagcgt ctggtgccca agatcgctac ccgttccaag 720

gtgaacggcc agtccggtcg tatggagttc ttctggacca tcctgaagcc taacgacgct 780

atcaacttcg agtccaacgg caacttcatc gctcccgagt acgcttacaa gatcgtgaag 840

aagggcgact ccgctatcat gaagtccgag ctggagtacg gtaactgcaa caccaagtgc 900

cagacccccа tgggtgctat caactcctcc atgcccttcc acaacatcca cccccctgacc 960

atcggcgagt gccccaagta cgtgaagtcc aaccgtctgg tgctggctac cggtctgcgt 1020

aactcccccc agcgcgagtc ccgtcgtaag aagcgtggtc tgttcggcgc tatcgctggt 1080

ttcatcgagg gcggttggca gggcatggtg gacggatggt acggttacca ccactctaac 1140

gagcagggtt ccggttacgc tgctgacaag gagtccaccc agaaggctat cgacggcgtc 1200

accaacaagg tgaactccat catcgacaag atgaacaccc agttcgaggc tgtgggtcgt 1260

gagttcaaca acctcgagcg tcgtatcgag aacctgaaca agaagatgga ggacggtttc 1320

ctggacgtgt ggacctacaa cgccgagctg ctggtgctga tggagaacga gcgtaccctg 1380

gacttccacg actccaacgt gaagaacctg tacgacaagg tccgcctgca gctgcgtgac 1440

aacgctaagg agctgggtaa cggttgcttc gagttctacc acaagtgcga caacgagtgc 1500

atggagtcca tccgtaacgg cacctacaac tacccccagt actccgagga ggctcgtctg 1560

aagcgtgagg agatctccgg cgtgaagctc gagtccatcg gaacctacca gatcctgtcc 1620

atctactcca ccgtggcttc ctccctggct ctggctatca tgatggctgg tctgtccctg 1680

tggatgtgct ccaacggttc cctgcagtgc cgtatctgca tctaatgaaa gcttgagctc 1740

<210> 43
<211> 568
<212> PRT
<213> Influenza virus

<400> 43

Met Glu Lys Ile Val Leu Leu Leu Ala Ile Val Ser Leu Val Lys Ser
1 5 10 15

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 Thr Asn Asp Leu Cys Tyr Pro Gly Ser Phe Asn
100 105 110

Asp Tyr Glu Glu Leu Lys His Leu Leu Ser Arg Ile Asn His Phe Glu
115 120 125

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 Leu Gly Ser Pro Ser Phe Phe
145 150 155 160

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

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

Gly Ile His His Pro Asn Asp Ala Ala Glu Gln Thr Arg Leu Tyr Gln
195 200 205

Asn Pro Thr Thr Tyr Ile Ser Ile 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 Glu 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 Met Lys Ser Glu Leu Glu Tyr Gly
275 280 285

Asn Cys Asn Thr Lys Cys Gln Thr Pro Met 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 Arg Leu Val Leu Ala Thr Gly Leu Arg Asn Ser
325 330 335

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

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

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

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

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

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

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

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

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

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

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

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

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

Leu Ala Ile Met Met Ala Gly Leu Ser Leu Trp Met Cys Ser Asn Gly
545 550 555 560

Ser Leu Gln Cys Arg Ile Cys Ile
565

<210> 44
<211> 1716
<212> DNA
<213> Artificial Sequence

<220>
<223> Influenza HA gene optimized for expression in insect cell expression system

<400> 44
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gaccagatct gcatcggtta ccacgctaac aactccaccg agcaggtgga caccatcatg 120

gagaagaacg tcaccgtgac ccacgctcag gacatcctcg aaaagaccca caacggcaag 180

ctgtgcgacc tggacggtgt caagcccctg atcctgcgtg actgctccgt ggctggttgg 240

ctgctgggta accccatgtg cgacgagttc atcaacgtgc ccgagtggtc ctacatcgtg 300

gagaaggcta accccaccaa cgacctgtgc taccccggtt ccttcaacga ctacgaggag 360

ctgaagcacc tgctgtcccg tatcaaccac ttcgagaaga tccagatcat ccccaagtcc 420

tcttggtccg accacgaggc ttcctccggt gtctcctccg cttgccccta cctgggttcc 480

ccctccttct tccgtaacgt ggtgtggctg atcaagaaga actccaccta ccccaccatc 540

aagaagtcct acaacaacac caaccaggag gacctgctgg tcctgtgggg tatccaccac 600

cccaacgacg ctgccgagca gaccccgtct gtaccagaacc ccaccaccta catctccatc 660

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ttcgagtcca acggcaactt catcgctccc gagtacgctt acaagatcgt gaagaagggc 840

gactccgcta tcatgaagtc cgagctggag tacggtaact gcaacaccaa gtgccagacc 900

cccatgggtg ctatcaactc ctccatgccc ttccacaaca tccaccccct gaccatcggc 960

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gtgaagaacc tgtacgacaa ggtccgcctg cagctgcgtg acaacgctaa ggagctgggt 1440

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ggcacctaca actaccccca gtactccgag gaggctcgtc tgaagcgtga ggagatctcc 1560

ggcgtgaagc tcgagtccat cggaacctac cagatcctgt ccatctactc caccgtggct 1620

tcctccctgg ctctggctat catgatggct ggtctgtccc tgtggatgtg ctccaacggt 1680

tccctgcagt gccgtatctg catctaatga aagctt 1716

<210> 45
<211> 564
<212> PRT
<213> Influenza virus

<400> 45

Met Glu Lys Ile Val Leu Leu Leu Ala Ile Val Ser Leu Val Lys Ser
1 5 10 15

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 Thr Asn Asp Leu Cys Tyr Pro Gly Ser Phe Asn
100 105 110

Asp Tyr Glu Glu Leu Lys His Leu Leu Ser Arg Ile Asn His Phe Glu
115 120 125

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 Leu Gly Ser Pro Ser Phe Phe
145 150 155 160

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

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

Gly Ile His His Pro Asn Asp Ala Ala Glu Gln Thr Arg Leu Tyr Gln
        195                 200                 205

Asn Pro Thr Thr Tyr Ile Ser Ile 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 Glu 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 Met Lys Ser Glu Leu Glu Tyr Gly
        275                 280                 285

Asn Cys Asn Thr Lys Cys Gln Thr Pro Met 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 Arg Leu Val Leu Ala Thr Gly Leu Arg Asn Ser
                325                 330                 335

Pro Gln Arg Glu Ser Arg Gly Leu Phe Gly Ala Ile Ala Gly Phe Ile
            340                 345                 350

Glu Gly Gly Trp Gln Gly Met Val Asp Gly Trp Tyr Gly Tyr His His
        355                 360                 365

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

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

Met Asn Thr Gln Phe Glu Ala Val Gly Arg Glu Phe Asn Asn Leu Glu
                405                 410                 415
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Arg Arg Ile Glu Asn Leu Asn Lys Lys Met Glu Asp Gly Phe Leu Asp
420 425 430

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

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

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

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

Gly Thr Tyr Asn Tyr Pro Gln Tyr Ser Glu Glu Ala Arg Leu Lys Arg
500 505 510

Glu Glu Ile Ser Gly Val Lys Leu Glu Ser Ile Gly Thr Tyr Gln Ile
515 520 525

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

Met Ala Gly Leu Ser Leu Trp Met Cys Ser Asn Gly Ser Leu Gln Cys
545 550 555 560

Arg Ile Cys Ile

<210> 46
<211> 1383
<212> DNA
<213> Artificial Sequence

<220>
<223> Influenza NA gene optimized for expression in insect cell expression system

<400> 46
ggtaccggat ccgccaccat gaaccccaac cagaagatca tcaccatcgg ctccatctgc 60

atggtgatcg gtatcgtgtc cctgatgctg cagatcggta acatgatctc catctgggtg 120

tcccactcca tccagaccgg taaccagcac caggctgagt ccatctccaa caccaacccc 180

ctgaccgaga aggctgtggc ttccgtgacc ctggctggta actcctcccc gtgccccatc 240

cgtggttggg ctgtgcactc caaggacaac aacatccgca tcggttccaa gggtgacgtg 300

ttcgtgatcc gtgagccctt catctcctgc tcccacctcg agtgccgtac cttcttcctg 360

acccaaggtg ctctgctgaa cgacaagcac tccaacggca ccgtgaagga ccgttccccc 420

caccgtaccc tgatgtcctg ccccgtgggc gaggctccct ccccctacaa ctcccgtttc 480

gagtccgtgg cttggtccgc ttccgcttgc cacgacggca cctcttggct gaccatcggt 540

atctccggtc ccgacaacga ggctgtcgct gtgctgaagt acaacggcat catcaccgac 600

accatcaagt cctggcgtaa caacatcctg cgtacccagg agtccgagtg cgcttgcgtg 660

aacggttcct gcttcaccgt gatgaccgac ggtccctccg acggccaggc ttcctacaag 720

atcttcaaga tggagaaggg caaggtggtg aagtccgtgg agctggacgc tcccaactac 780

cactacgagg agtgctcttg ctaccccgac gctggcgaga tcacctgcgt gtgccgtgac 840

aactggcacg gttccaaccg tccctgggtg tccttcaacc agaacctcga gtaccagatc 900

ggttacatct gctccggcgt gttcggtgac aaccccccgtc ccaacgacgg aaccggttcc 960

tgcggtccca tgtcccccaa cggtgcttac ggtgtcaagg gcttctcctt caagtacggt 1020

aacggtgtct ggatcggtcg taccaagtcc accaactccc gctccggttt cgagatgatc 1080

tgggacccca acggttggac cggcaccgac tcttccttct ccgtgaagca ggacatcgtg 1140

gctatcaccg actggtccgg ttactccggt tccttcgtgc agcaccccga gctgaccggt 1200

ctggactgca ttcgtccctg cttctgggtg gagctgatcc gtggtcgtcc caaggagtcc 1260

accatctgga cctccggctc ctccatctct ttctgcggtg tgaactccga caccgtgtcc 1320

tggtcctggc ccgacggtgc cgagctgccc ttcaccatcg acaagtaatg aaagcttgag 1380

ctc 1383

<210> 47
<211> 449
<212> PRT
<213> Influenza virus

<400> 47

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

Ile Gly Ile Val Ser Leu Met Leu Gln Ile Gly Asn Met Ile Ser Ile
20 25 30

Trp Val Ser His Ser Ile Gln Thr Gly Asn Gln His Gln Ala Glu Ser
35 40 45

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

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

Ser Lys Asp Asn Asn Ile Arg Ile Gly Ser Lys Gly Asp Val Phe Val
85 90 95

Ile Arg Glu Pro Phe Ile Ser Cys Ser His Leu Glu Cys Arg Thr Phe
100 105 110

Phe Leu Thr Gln Gly Ala Leu Leu Asn Asp Lys His Ser Asn Gly Thr
115 120 125

Val Lys Asp Arg Ser Pro His Arg Thr Leu Met Ser Cys Pro Val Gly
130 135 140

Glu Ala Pro Ser Pro Tyr Asn Ser Arg Phe Glu Ser Val Ala Trp Ser
145 150 155 160

Ala Ser Ala Cys His Asp Gly Thr Ser Trp Leu Thr Ile Gly Ile Ser
165 170 175

Gly Pro Asp Asn Glu Ala Val Ala Val Leu Lys Tyr Asn Gly Ile Ile
180 185 190

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

Ser Glu Cys Ala Cys Val Asn Gly Ser Cys Phe Thr Val Met Thr Asp
210 215 220

Gly Pro Ser Asp Gly Gln Ala Ser Tyr Lys Ile Phe Lys Met Glu Lys
225 230 235 240

Gly Lys Val Val Lys Ser Val Glu Leu Asp Ala Pro Asn Tyr His Tyr
245 250 255

Glu Glu Cys Ser Cys Tyr Pro Asp Ala Gly Glu Ile Thr Cys Val Cys
260 265 270

Arg Asp Asn Trp His Gly Ser Asn Arg Pro Trp Val Ser Phe Asn Gln
275 280 285

Asn Leu Glu Tyr Gln Ile Gly Tyr Ile Cys Ser Gly Val Phe Gly Asp
290 295 300

Asn Pro Arg Pro Asn Asp Gly Thr Gly Ser Cys Gly Pro Met Ser Pro
305 310 315 320

Asn Gly Ala Tyr Gly Val Lys Gly Phe Ser Phe Lys Tyr Gly Asn Gly
325 330 335

Val Trp Ile Gly Arg Thr Lys Ser Thr Asn Ser Arg Ser Gly Phe Glu
340 345 350

Met Ile Trp Asp Pro Asn Gly Trp Thr Gly Thr Asp Ser Ser Phe Ser
355 360 365

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

Ser Phe Val Gln His Pro Glu Leu Thr Gly Leu Asp Cys Ile Arg Pro
385 390 395 400

Cys Phe Trp Val Glu Leu Ile Arg Gly Arg Pro Lys Glu Ser Thr Ile
405 410 415

Trp Thr Ser Gly Ser Ser Ile Ser Phe Cys Gly Val Asn Ser Asp Thr
420 425 430

Val Ser Trp Ser Trp Pro Asp Gly Ala Glu Leu Pro Phe Thr Ile Asp
435 440 445

Lys

<210> 48
<211> 792
<212> DNA
<213> Artificial Sequence

<220>
<223> Influenza M1 gene optimized for expression in insect cell expression system

<400> 48
ggtaccggat ccgccaccat gtccctgctg accgaggtgg agacctacgt gctgtccatc 60

atcccctccg gtcctctgaa ggctgagatc gctcagaagc tcgaggacgt tttcgctggc 120

aagaacaccg acctcgaggc tctgatggag tggctcaaga cccgtcccat cctgtccccc 180

ctgaccaagg gtatcctggg tttcgtgttc accctgaccg tgccctccga gcgtggtctg 240

cagcgtcgtc gtttcgtgca gaacgctctg aacggtaacg gtgaccccaa caacatggac 300

cgtgctgtga agctgtacaa gaagctgaag cgcgagatca ccttccacgg tgctaaggag 360

gtgtccctgt cctactccac cggtgctctg gctagctgca tgggcctgat ctacaaccgt 420

atgggcaccg tgaccaccga ggtggccttc ggtctggtct gcgctacctg cgagcagatc 480

gctgactccc agcaccgttc ccaccgtcag atggctacca tcaccaaccc cctgatccgt 540

cacgagaacc gtatggtgct ggcttccacc accgctaagg ctatggagca gatggctggt 600

tcctccgagc aggctgctga ggccatggag gtggccaacc aggctcgtca gatggtgcag 660

gctatgcgta ccatcggcac ccaccccaac tcctccgctg gtctgcgtga caacctgctc 720

gagaacctgc aggcttacca gaagcgtatg ggagtccaga tgcagcgctt caagtaatga 780

aagcttgagc tc 792

<210> 49
<211> 252
<212> PRT
<213> Influenza virus

<400> 49

Met Ser Leu Leu Thr Glu Val Glu Thr Tyr Val Leu Ser Ile Ile Pro
1 5 10 15

Ser Gly Pro Leu Lys Ala Glu Ile Ala Gln Lys Leu Glu Asp Val Phe
20 25 30

Ala Gly Lys Asn Thr Asp Leu Glu Ala Leu Met Glu Trp Leu Lys Thr
35 40 45

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

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

Gln Asn Ala Leu Asn Gly Asn Gly Asp Pro Asn Asn Met Asp Arg Ala
85 90 95

Val Lys Leu Tyr Lys Lys Leu Lys Arg Glu Ile Thr Phe His Gly Ala
100 105 110

Lys Glu Val Ser Leu Ser Tyr Ser Thr Gly Ala Leu Ala Ser Cys Met
115 120 125

Gly Leu Ile Tyr Asn Arg Met Gly Thr Val Thr Thr Glu Val Ala Phe
130 135 140

Gly Leu Val Cys Ala Thr Cys Glu Gln Ile Ala Asp Ser Gln His Arg
145 150 155 160

Ser His Arg Gln Met Ala Thr Ile Thr Asn Pro Leu Ile Arg His Glu
165 170 175

Asn Arg Met Val Leu Ala Ser Thr Thr Ala Lys Ala Met Glu Gln Met
180 185 190

Ala Gly Ser Ser Glu Gln Ala Ala Glu Ala Met Glu Val Ala Asn Gln
195 200 205

Ala Arg Gln Met Val Gln Ala Met Arg Thr Ile Gly Thr His Pro Asn
210 215 220

Ser Ser Ala Gly Leu Arg Asp Asn Leu Leu Glu Asn Leu Gln Ala Tyr
225 230 235 240

Gln Lys Arg Met Gly Val Gln Met Gln Arg Phe Lys
245 250

<210> 50
<211> 1736
<212> DNA
<213> Artificial Sequence

<220>
<223> Influenza HA gene optimized for expression in insect cell expression system

<400> 50
ggtaccggat ccctcgagat ggagaagatc gtgctgctgc tggctatcgt gtccctggtg 60

aagtccgacc agatctgcat cggttaccac gctaacaact ccaccgagca ggtggacacc 120

atcatggaga agaacgtcac cgtgacccac gctcaggaca tcctggaaaa gacccacaac 180

ggcaagctgt gcgacctgga cggtgtcaag ccctgatcc tgcgtgactg ctccgtggct 240

ggttggctgc tgggtaaccc catgtgcgac gagttcatca acgtgcccga gtggtcctac 300

atcgtggaga aggctaaccc cgctaacgac ctgtgctacc ccggtaactt caacgactac 360

gaggagctga agcacctgct gtcccgtatc aaccacttcg agaagatcca gatcatcccc 420

aagtcctctt ggtccgacca cgaggcttcc tccggtgtct cctccgcttg cccataccag 480

ggcaccccat ctttcttccg taacgtggtg tggctgatca agaagaacaa cacctacccc 540

accatcaagc gttcctacaa caacaccaac caggaggacc tgctgatcct gtggggtatc 600

caccactcca acgacgctgc cgagcagacc aagctgtacc agaaccccac cacctacatc 660

tccgtgggca cctccaccct gaaccagcgt ctggtgccca agatcgctac ccgttccaag 720

gtgaacggcc agtccggtcg tatggacttc ttctggacca tcctgaagcc taacgacgct 780

atcaacttcg agtccaacgg caacttcatc gctcccgagt acgcttacaa gatcgtgaag 840

aagggcgact ccgctatcgt caagtccgag gtggagtacg gtaactgcaa caccaagtgc 900

cagaccccca tcggtgctat caactcctcc atgcccttcc acaacatcca ccccctgacc 960

atcggcgagt gccccaagta cgtgaagtcc aacaagctgg tgctggctac cggtctgcgt 1020

aactcccccc tgcgtgagcg tggtctgttc ggcgctatcg ctggtttcat cgagggcggt 1080

tggcagggca tggtggacgg ttggtacggt taccaccaca gcaacgagca gggttccggt 1140

tacgctgctg acaaggagtc cacccagaag gctatcgacg gcgtcaccaa caaggtgaac 1200

tccatcatcg acaagatgaa cacccagttc gaggctgtgg gtcgtgagtt caacaacctg 1260

gagcgtcgta tcgagaacct gaacaagaag atggaggacg gtttcctgga cgtgtggacc 1320

tacaacgccg agctgctggt gctgatggag aacgagcgta ccctggactt ccacgactct 1380

aacgtgaaga acctgtacga caaggtccgc ctgcagctgc gtgacaacgc taaggagctg 1440

ggtaacggtt gcttcgagtt ctaccacaag tgcgacaacg agtgcatgga gtccgtgcgt 1500

aacggcacct acgactaccc ccagtactcc gaggaggctc gtctgaagcg tgaggagatc 1560

tccggcgtga agctggagtc catcggcacc taccagatcc tgtccatcta ctccaccgtg 1620

gcttcctccc tggctctggc tatcatggtg gctggtctgt ccctgtggat gtgctccaac 1680

ggttccctgc agtgccgtat ctgcatctaa taatgaggcg cgccaagctt gagctc 1736

<210> 51
<211> 563
<212> PRT
<213> Influenza virus

<400> 51

Met Glu Lys Ile Val Leu Leu Leu Ala Ile Val Ser Leu Val Lys Ser
1 5 10 15

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

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

Gly Gly Trp Gln Gly Met Val Asp Gly Trp Tyr Gly Tyr His His Ser
        355                 360                 365

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

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

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

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

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

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

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

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

Thr Tyr Asp Tyr Pro Gln Tyr Ser Glu Glu Ala Arg Leu Lys Arg Glu
            500                 505                 510

Glu Ile Ser Gly Val Lys Leu Glu Ser Ile Gly Thr Tyr Gln Ile Leu
        515                 520                 525

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

Ala Gly Leu Ser Leu Trp Met Cys Ser Asn Gly Ser Leu Gln Cys Arg
545                 550                 555                 560
```

Ile Cys Ile

<210> 52
<211> 1738
<212> DNA
<213> Artificial Sequence

<220>
<223> Influenza HA gene optimized for expression in insect cell expression system

<400> 52
cgggcgcgga gcggccgcat ggagaagatc gtgctgctgc tggctatcgt gtctctggtc 60

aagtccgacc agatctgcat cggttaccac gctaacaact ccaccgagca ggtggacacc 120

atcatggaga agaacgtcac cgtgacccac gctcaggaca tcctcgaaaa gacccacaac 180

ggcaagctgt gcgacctgga cggcgtgaag ccctgatcc tgcgtgactg ctccgtggct 240

ggttggctgc tgggtaaccc catgtgcgac gagttcctca acgtgcccga gtggtcctac 300

atcgtggaga agatcaaccc cgctaacgac ctgtgctacc ccggtaactt caacgactac 360

gaggagctga agcacctgct gtcccgtatc aaccacttcg agaagatcca gatcatcccc 420

aagtcctctt ggtccgacca cgaggcttcc tccggtgtct cctccgcttg cccataccag 480

ggccgttctt ccttcttccg caacgtggtg tggctgatca agaagaacaa cgcctacccc 540

accatcaagc gttcctacaa caacaccaac caggaggacc tgctggtcct gtggggtatc 600

caccacccca acgacgctgc cgagcagacc cgtctgtacc agaaccccac cacctacatc 660

tccgtgggca cctctaccct gaaccagcgt ctggtgccca agatcgctac ccgttccaag 720

gtgaacggcc agtccggtcg tatggagttc ttctggacca tcctgaagcc taacgacgct 780

atcaacttcg agtccaacgg caacttcatc gctcccgaga acgcttacaa gatcgtgaag 840

aagggcgact ccaccatcat gaagtccgag ctggagtacg gcaactgcaa cactaagtgc 900

cagaccccca tcggtgctat caactcctcc atgcccttcc acaacatcca cccctgact 960

atcggcgagt gccccaagta cgtgaagtcc aaccgtctgg tgctggctac cggtctgcgt 1020

aactcccccc agatcgagac tcgtggtctg ttcggcgcta tcgctggttt catcgagggc 1080

ggttggcagg gcatggtgga cggttggtac ggttaccacc actctaacga gcagggttcc 1140

ggttacgctg ctgacaagga gtctacccag aaggctatcg acggcgtcac caacaaggtg 1200

aactccatca tcgacaagat gaacacccag ttcgaggctg tgggtcgtga gttcaacaac 1260

ctcgaacgtc gtatcgagaa cctgaacaag aagatggagg acggtttcct ggacgtgtgg 1320

acctacaacg ccgagctgct ggtgctgatg gagaacgagc gtaccctgga cttccacgac 1380

tccaacgtga agaacctgta cgacaaggtc cgcctgcagc tgcgtgacaa cgctaaggag 1440

ctgggtaacg gttgcttcga gttctaccac cgttgcgaca acgagtgcat ggagtccgtg 1500

cgtaacggca cctacgacta cccccagtac tccgaggagg ctcgtctgaa gcgtgaggag 1560

atctccggtg tcaagctcga atccatcgga acctaccaga tcctgtccat ctactccacc 1620

gtggcttcct ccctggctct ggctatcatg gtggctggtc tgtccctgtg gatgtgctcc 1680

aacggttccc tgcagtgccg tatctgcatc taataatgag gcgcgccaag cttgtcga 1738

<210> 53
<211> 564
<212> PRT
<213> Influenza virus

<400> 53

Met Glu Lys Ile Val Leu Leu Leu Ala Ile Val Ser Leu Val Lys Ser
1 5 10 15

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 Leu Asn Val Pro Glu Trp Ser Tyr Ile Val
85 90 95

Glu Lys Ile 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

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 Arg Ser Ser Phe Phe
145 150 155 160

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

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

Gly Ile His His Pro Asn Asp Ala Ala Glu Gln Thr Arg 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 Glu 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 Asn Ala Tyr Lys Ile
260 265 270

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

Pro Gln Ile Glu Thr Arg Gly Leu Phe Gly Ala Ile Ala Gly Phe Ile
340 345 350

Glu Gly Gly Trp Gln Gly Met Val Asp Gly Trp Tyr Gly Tyr His His
355 360 365

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

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

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

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

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

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

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

Glu Phe Tyr His Arg Cys Asp Asn Glu Cys Met Glu Ser Val Arg Asn
485 490 495

Gly Thr Tyr Asp Tyr Pro Gln Tyr Ser Glu Glu Ala Arg Leu Lys Arg
500 505 510

Glu Glu Ile Ser Gly Val Lys Leu Glu Ser Ile Gly Thr Tyr Gln Ile
515 520 525

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

Val Ala Gly Leu Ser Leu Trp Met Cys Ser Asn Gly Ser Leu Gln Cys
545 550 555 560

Arg Ile Cys Ile

<210> 54
<211> 1422
<212> DNA
<213> Artificial Sequence

<220>
<223> Influenza NA gene optimized for expression in insect cell expression system

<400> 54
accgtcccac catcgggcgc ggatccctcg agatgaaccc caaccagaag atcatcacca 60

tcggctccat ctgcatggtg atcggtatcg tgtccctgat gctgcagatc ggtaacatga 120

tctccatctg ggtgtcccac tccatccaga ccggtaacca gcgtcaggcc gagcccatct 180

ccaacaccaa gttcctcacc gagaaggctg tggcttccgt gaccctggct ggtaactcct 240

ccctgtgccc catctccggt tgggctgtgt actccaagga caactccatc cgtatcggtt 300

cccgtggtga cgtgttcgtg atccgtgagc ccttcatctc ctgctcccac ctcgaatgcc 360

gtaccttctt cctgacccag ggtgctctgc tgaacgacaa gcactccaac ggcaccgtga 420

aggaccgttc cccccaccgt accctgatgt cctgccccgt gggcgaggct ccctcccct 480

acaactcccg tttcgagtcc gtggcttggt ccgcttccgc ttgccacgac ggcacctctt 540

ggctgaccat cggtatctcc ggtcccgaca acggtgctgt ggctgtgctg aagtacaacg 600

gcatcatcac cgacaccatc aagtcctggc gtaacaacat cctgcgtacc caagagtccg 660

agtgcgcttg cgtgaacggt tcctgcttca ccgtgatgac cgacggtccc tccaacggcc 720

aggcttccta caagatcttc aagatggaga agggcaaggt ggtgaagtcc gtggagctgg 780

acgctcccaa ctaccactac gaggagtgct cttgctaccc cgacgctggc gagatcacct 840

gcgtgtgccg tgacaactgg cacggttcca accgtccctg ggtgtccttc aaccagaacc 900

tcgaatacca gatcggttac atctgctccg gcgtgttcgg tgacaacccc cgtcccaacg 960

acggaaccgg ttcctgcggt cccgtgtccc ccaacggtgc ttacggtgtc aagggcttct 1020

ccttcaagta cggtaacggt gtctggatcg gtcgtaccaa gtccaccaac tcccgctccg 1080

gtttcgagat gatctgggac cccaacggtt ggaccggcac cgactcttcc ttctccgtga 1140

agcaggacat cgtggctatc accgactggt ccggttactc cggttccttc gtgcagcacc 1200

ccgagctgac cggtctggac tgtatccgtc cctgcttctg ggtggagctg atccgtggtc 1260

gtcccaagga gtccaccatc tggacctccg gctcctccat ctctttctgc ggtgtgaact 1320

ccgacaccgt gtcctggtcc tggcccgacg gtgccgagct gcccttcacc atcgacaagt 1380

aataatgaat cgatttgtcg agaagtacta gaggatcata at 1422

<210> 55
<211> 449
<212> PRT
<213> Influenza virus

<400> 55

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

Ile Gly Ile Val Ser Leu Met Leu Gln Ile Gly Asn Met Ile Ser Ile
20 25 30

Trp Val Ser His Ser Ile Gln Thr Gly Asn Gln Arg Gln Ala Glu Pro
35 40 45

Ile Ser Asn Thr Lys Phe Leu Thr Glu Lys Ala Val Ala Ser Val Thr
50 55 60

```
Leu Ala Gly Asn Ser Ser Leu Cys Pro Ile Ser Gly Trp Ala Val Tyr
65                  70                  75                  80

Ser Lys Asp Asn Ser Ile Arg Ile Gly Ser Arg Gly Asp Val Phe Val
                85                  90                  95

Ile Arg Glu Pro Phe Ile Ser Cys Ser His Leu Glu Cys Arg Thr Phe
            100                 105                 110

Phe Leu Thr Gln Gly Ala Leu Leu Asn Asp Lys His Ser Asn Gly Thr
        115                 120                 125

Val Lys Asp Arg Ser Pro His Arg Thr Leu Met Ser Cys Pro Val Gly
    130                 135                 140

Glu Ala Pro Ser Pro Tyr Asn Ser Arg Phe Glu Ser Val Ala Trp Ser
145                 150                 155                 160

Ala Ser Ala Cys His Asp Gly Thr Ser Trp Leu Thr Ile Gly Ile Ser
                165                 170                 175

Gly Pro Asp Asn Gly Ala Val Ala Val Leu Lys Tyr Asn Gly Ile Ile
            180                 185                 190

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

Ser Glu Cys Ala Cys Val Asn Gly Ser Cys Phe Thr Val Met Thr Asp
    210                 215                 220

Gly Pro Ser Asn Gly Gln Ala Ser Tyr Lys Ile Phe Lys Met Glu Lys
225                 230                 235                 240

Gly Lys Val Val Lys Ser Val Glu Leu Asp Ala Pro Asn Tyr His Tyr
                245                 250                 255

Glu Glu Cys Ser Cys Tyr Pro Asp Ala Gly Glu Ile Thr Cys Val Cys
            260                 265                 270

Arg Asp Asn Trp His Gly Ser Asn Arg Pro Trp Val Ser Phe Asn Gln
        275                 280                 285

Asn Leu Glu Tyr Gln Ile Gly Tyr Ile Cys Ser Gly Val Phe Gly Asp
    290                 295                 300
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Asn Pro Arg Pro Asn Asp Gly Thr Gly Ser Cys Gly Pro Val Ser Pro
305 310 315 320

Asn Gly Ala Tyr Gly Val Lys Gly Phe Ser Phe Lys Tyr Gly Asn Gly
325 330 335

Val Trp Ile Gly Arg Thr Lys Ser Thr Asn Ser Arg Ser Gly Phe Glu
340 345 350

Met Ile Trp Asp Pro Asn Gly Trp Thr Gly Thr Asp Ser Ser Phe Ser
355 360 365

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

Ser Phe Val Gln His Pro Glu Leu Thr Gly Leu Asp Cys Ile Arg Pro
385 390 395 400

Cys Phe Trp Val Glu Leu Ile Arg Gly Arg Pro Lys Glu Ser Thr Ile
405 410 415

Trp Thr Ser Gly Ser Ser Ile Ser Phe Cys Gly Val Asn Ser Asp Thr
420 425 430

Val Ser Trp Ser Trp Pro Asp Gly Ala Glu Leu Pro Phe Thr Ile Asp
435 440 445

Lys

<210> 56
<211> 1750
<212> DNA
<213> Influenza virus

<400> 56
attcgccctt aacggtccga tggagaaaat agtgcttctt cttgcaatag tcagtcttgt 60

taaaagtgat cagatttgca ttggttacca tgcaaacaat tcaacagagc aggttgacac 120

aatcatggaa aagaacgtta ctgttacaca tgcccaagac atactggaaa agacacacaa 180

cgggaagctc tgcgatctag atggagtgaa gcctctaatt ttaagagatt gtagtgtagc 240

tggatggctc ctcgggaacc caatgtgtga cgaattcatc aatgtaccgg aatggtctta 300

catagtggag aaggccaatc caaccaatga cctctgttac ccagggagtt tcaacgacta 360

tgaagaactg aaacacctat tgagcagaat aaaccatttt gagaaaattc aaatcatccc 420

caaaagttct tggtccgatc atgaagcctc atcaggagtg agctcagcat gtccatacct 480

gggaagtccc tcctttttta gaaatgtggt atggcttatc aaaaagaaca gtacataccc 540

aacaataaag aaaagctaca ataataccaa ccaagaagat cttttggtac tgtggggaat 600

tcaccatcct aatgatgcgg cagagcagac aaggctatat caaaacccaa ccacctatat 660

ttccattggg acatcaacac taaaccagag attggtacca aaaatagcta ctagatccaa 720

agtaaacggg caaagtggaa ggatggagtt cttctggaca attttaaaac ctaatgatgc 780

aatcaacttc gagagtaatg gaaatttcat tgctccagaa tatgcataca aaattgtcaa 840

gaaaggggac tcagcaatta tgaaaagtga attggaatat ggtaactgca acaccaagtg 900

tcaaactcca atgggggcga taaactctag tatgccattc cacaacatac accctctcac 960

catcggggaa tgccccaaat atgtgaaatc aaacagatta gtccttgcaa cagggctcag 1020

aaatagccct caaagagaga gcagaagaaa aaagagagga ctatttggag ctatagcagg 1080

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tgagcagggg agtgggtacg ctgcagacaa agaatccact caaaaggcaa tggatggagt 1200

caccaataag gtcaactcaa tcattgacaa aatgaacact cagtttgagg ccgttggaag 1260

ggaatttaat aacttagaaa ggagaataga gaatttaaac aagaagatgg aagacgggtt 1320

tctagatgtc tggacttata atgccgaact tctggttctc atggaaaatg agagaactct 1380

agactttcat gactcaaatg ttaagaacct ctacgacaag gtccgactac agcttaggga 1440

taatgcaaag gagctgggta acggttgttt cgagttctat cacaaatgtg ataatgaatg 1500

tatggaaagt ataagaaacg gaacgtgcaa ctatccgcag tattcagaag aagcaagatt 1560

aaaaagagag gaaataagtg gggtaaaatt ggaatcaata ggaacttacc aaatactgtc 1620

aatttattca acagtggcga gttccctagc actggcaatc atgatggctg gtctatcttt 1680

atggatgtgc tccaatggat cgttacaatg cagaatttgc atttaaaagc tttaagggcg 1740

aattccagca 1750

<210> 57
<211> 568
<212> PRT
<213> Influenza virus

<400> 57

Met Glu Lys Ile Val Leu Leu Leu Ala Ile Val Ser Leu Val Lys Ser
1 5 10 15

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 Thr Asn Asp Leu Cys Tyr Pro Gly Ser Phe Asn
100 105 110

Asp Tyr Glu Glu Leu Lys His Leu Leu Ser Arg Ile Asn His Phe Glu
115 120 125

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 Leu Gly Ser Pro Ser Phe Phe
145 150 155 160

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

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

Gly Ile His His Pro Asn Asp Ala Ala Glu Gln Thr Arg Leu Tyr Gln
195 200 205

Asn Pro Thr Thr Tyr Ile Ser Ile 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 Glu 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 Met Lys Ser Glu Leu Glu Tyr Gly

275 280 285

Asn Cys Asn Thr Lys Cys Gln Thr Pro Met 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 Arg Leu Val Leu Ala Thr Gly Leu Arg Asn Ser
325 330 335

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

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

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

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

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

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

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

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

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

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

Ser Ile Arg Asn Gly Thr Cys Asn Tyr Pro Gln Tyr Ser Glu Glu Ala
500 505 510

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

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

Leu Ala Ile Met Met Ala Gly Leu Ser Leu Trp Met Cys Ser Asn Gly
545 550 555 560

Ser Leu Gln Cys Arg Ile Cys Ile
565

<210> 58
<211> 568
<212> PRT
<213> Influenza virus

<400> 58

Met Glu Lys Ile Val Leu Leu Leu Ala Ile Val Ser Leu Val Lys Ser
1 5 10 15

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 Thr Asn Asp Leu Cys Tyr Pro Gly Ser Phe Asn
100 105 110

Asp Tyr Glu Glu Leu Lys His Leu Leu Ser Arg Ile Asn His Phe Glu
115 120 125

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 Leu Gly Ser Pro Ser Phe Phe
145 150 155 160

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

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

Gly Ile His His Pro Asn Asp Ala Ala Glu Gln Thr Arg Leu Tyr Gln
195 200 205

Asn Pro Thr Thr Tyr Ile Ser Ile 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 Glu 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 Met Lys Ser Glu Leu Glu Tyr Gly
275 280 285

Asn Cys Asn Thr Lys Cys Gln Thr Pro Met 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 Arg Leu Val Leu Ala Thr Gly Leu Arg Asn Ser
325 330 335

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

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

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

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

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

405 410 415

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

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

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

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

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

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

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

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

Leu Ala Ile Met Met Ala Gly Leu Ser Leu Trp Met Cys Ser Asn Gly
545 550 555 560

Ser Leu Gln Cys Arg Ile Cys Ile
565