

eolf-seql
SEQUENCE LISTING

<110> Bavarian Nordic A/S

<120> RECOMBINANT MODIFIED VACCINIA VIRUS ANKARA (MVA) RESPIRATORY
SYNCYTIAL VIRUS (RSV) VACCINE

<130> BNI14747PCT

<140> Not yet assigned

<141> 2013-03-15

<150> US 61/678,367

<151> 2012-08-01

<150> EP 12005594.2

<151> 2012-08-01

<160> 43

<170> PatentIn version 3.5

<210> 1

<211> 897

<212> DNA

<213> Human Respiratory Syncytial Virus (hRSV), strain A2

<400> 1

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cccagcaacc ccagcgagat caccagccag atcacaacca tcctggcctc caccaccct	360
ggcgtgaagt ccaccctgca gagcaccacc gtgaaaacca agaataccac caccacacag	420
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aagcctacca agaagcctac cctgaaaacc accaagaagg accccaagcc ccagaccacc	660
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accaacatca tcaccaccct gctgacctcc aacaccaccg gcaaccccga gctgacaagc 780
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<210> 2
 <211> 298
 <212> PRT
 <213> hRSV strain A2

<400> 2

Met Ser Lys Asn Lys Asp Gln Arg Thr Ala Lys Thr Leu Glu Arg Thr
 1 5 10 15

Trp Asp Thr Leu Asn His Leu Leu Phe Ile Ser Ser Cys Leu Tyr Lys
 20 25 30

Leu Asn Leu Lys Ser Val Ala Gln Ile Thr Leu Ser Ile Leu Ala Met
 35 40 45

Ile Ile Ser Thr Ser Leu Ile Ile Ala Ala Ile Ile Phe Ile Ala Ser
 50 55 60

Ala Asn His Lys Val Thr Pro Thr Thr Ala Ile Ile Gln Asp Ala Thr
 65 70 75 80

Ser Gln Ile Lys Asn Thr Thr Pro Thr Tyr Leu Thr Gln Asn Pro Gln
 85 90 95

Leu Gly Ile Ser Pro Ser Asn Pro Ser Glu Ile Thr Ser Gln Ile Thr
 100 105 110

Thr Ile Leu Ala Ser Thr Thr Pro Gly Val Lys Ser Thr Leu Gln Ser
 115 120 125

Thr Thr Val Lys Thr Lys Asn Thr Thr Thr Thr Gln Thr Gln Pro Ser
 130 135 140

Lys Pro Thr Thr Lys Gln Arg Gln Asn Lys Pro Pro Ser Lys Pro Asn

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145 150 155 160

Asn Asp Phe His Phe Glu Val Phe Asn Phe Val Pro Cys Ser Ile Cys
165 170 175

Ser Asn Asn Pro Thr Cys Trp Ala Ile Cys Lys Arg Ile Pro Asn Lys
180 185 190

Lys Pro Gly Lys Lys Thr Thr Thr Lys Pro Thr Lys Lys Pro Thr Leu
195 200 205

Lys Thr Thr Lys Lys Asp Pro Lys Pro Gln Thr Thr Lys Ser Lys Glu
210 215 220

Val	Pro	Thr	Thr	Lys	Pro	Thr	Glu	Glu	Pro	Thr	Ile	Asn	Thr	Thr	Lys
225					230					235					240

Thr Asn Ile Ile Thr Thr Leu Leu Thr Ser Asn Thr Thr Gly Asn Pro
245 250 255

Glu Leu Thr Ser Gln Met Glu Thr Phe His Ser Thr Ser Ser Glu Gly
260 265 270

Asn Pro Ser Pro Ser Gln Val Ser Thr Thr Ser Glu Tyr Pro Ser Gln
275 280 285

Pro Ser Ser Pro Pro Asn Thr Pro Arg Gln
290 295

 $\langle 210 \rangle$ 3

<211> 1725

<212> DNA

<213> hRSV strain A2

<400> 3

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agcaaggggct acctgagcgc cctgagaacc ggctggtaca cctccgtgat caccatcgag 180

ctgtccaaca tcaaagaaaa caagtgaac ggcaccgacg ccaaagtgaa gctgatcaag 240

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cctgccacca acaaccgggc cagaagagaa ctgccccggt ttatgaacta cacactgaac	360
aacgcaaaaa agaccaatgt cactctgagc aagaagcgga agcggcggtt cctgggcttt	420
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cagagcctgg ccttcatcag aaagagcgac gaactgctgc acaatgtgaa cgctggcaag	1560
agtaccacaa acatcatgat caccaccatc atcatcgtga tcattgtgat cctgctgagt	1620
ctgatcgccg tgggcctgct gctgtactgc aaggcccga gcaccctgt gaccctgtcc	1680
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<210> 4

<211> 574

<212> PRT

<213> hRSV strain A2

<400> 4

Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
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Ala Val Thr Phe Cys Phe Ala Ser Gly Gln Asn Ile Thr Glu Glu Phe
20 25 30

Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
35 40 45

Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
50 55 60

Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
65 70 75 80

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

Met Gln Ser Thr Pro Ala Thr Asn Asn Arg Ala Arg Arg Glu Leu Pro
100 105 110

Arg Phe Met Asn Tyr Thr Leu Asn Asn Ala Lys Lys Thr Asn Val Thr
115 120 125

Leu Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val
130 135 140

Gly Ser Ala Ile Ala Ser Gly Val Ala Val Ser Lys Val Leu His Leu
145 150 155 160

Glu Gly Glu Val Asn Lys Ile Lys Ser Ala Leu Leu Ser Thr Asn Lys
165 170 175

Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Ser Lys Val

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180

185

190

Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Val Asn
 195 200 205

Lys Gln Ser Cys Ser Ile Ser Asn Ile Glu Thr Val Ile Glu Phe Gln
 210 215 220

Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn
 225 230 235 240

Ala Gly Val Thr Thr Pro Val Ser Thr Tyr Met Leu Thr Asn Ser Glu
 245 250 255

Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys
 260 265 270

Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile
 275 280 285

Met Ser Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro
 290 295 300

Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
 305 310 315 320

Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg
 325 330 335

Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe
 340 345 350

Pro Gln Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp
 355 360 365

Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Val Asn Leu Cys Asn Val
 370 375 380

Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr

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<400> 5

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cctgccgcca acaaccgggc cagaagagaa ctgccccggt ttatgaacta cacactgaac	360
aacacaaaa agaccaatgt gaccctgagc aagaagcgga agcggcggtt cctgggcttt	420
ctgctgggcg tgggcagcgc cattgccagc ggcattgccg tgtccaaggt gctgcacctg	480
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cagagcctgg ccttcatcag aaagagcgac gaactgctgc acaatgtgaa cgctggcaag	1560

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agtaccacaa acatcatgat caccaccatc atcatcgtga tcattgtgat cctgctgagt 1620
 ctgatcgccg tgggcctgct gctgtactgc aaggcccgcga gcaccctgt gaccctgtcc 1680
 aaggatcagc tgtccggcat caacaatatc gccttctcca actga 1725

<210> 6
 <211> 574
 <212> PRT
 <213> hRSV strain A-Long

<400> 6

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Ala Val Thr Phe Cys Phe Ala Ser Ser Gln Asn Ile Thr Glu Glu Phe
 20 25 30

Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
 35 40 45

Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
 50 55 60

Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
 65 70 75 80

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

Met Gln Ser Thr Pro Ala Ala Asn Asn Arg Ala Arg Arg Glu Leu Pro
 100 105 110

Arg Phe Met Asn Tyr Thr Leu Asn Asn Thr Lys Lys Thr Asn Val Thr
 115 120 125

Leu Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val
 130 135 140

Gly Ser Ala Ile Ala Ser Gly Ile Ala Val Ser Lys Val Leu His Leu

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145		150		155		160									
Glu	Gly	Glu	Val	Asn	Lys	Ile	Lys	Ser	Ala	Leu	Leu	Ser	Thr	Asn	Lys
				165					170					175	
Ala	Val	Val	Ser	Leu	Ser	Asn	Gly	Val	Ser	Val	Leu	Thr	Ser	Lys	Val
			180					185					190		
Leu	Asp	Leu	Lys	Asn	Tyr	Ile	Asp	Lys	Gln	Leu	Leu	Pro	Ile	Val	Asn
		195					200					205			
Lys	Gln	Ser	Cys	Arg	Ile	Ser	Asn	Ile	Glu	Thr	Val	Ile	Glu	Phe	Gln
	210					215					220				
Gln	Lys	Asn	Asn	Arg	Leu	Leu	Glu	Ile	Thr	Arg	Glu	Phe	Ser	Val	Asn
225					230					235					240
Val	Gly	Val	Thr	Thr	Pro	Val	Ser	Thr	Tyr	Met	Leu	Thr	Asn	Ser	Glu
				245					250					255	
Leu	Leu	Ser	Leu	Ile	Asn	Asp	Met	Pro	Ile	Thr	Asn	Asp	Gln	Lys	Lys
			260					265					270		
Leu	Met	Ser	Asn	Asn	Val	Gln	Ile	Val	Arg	Gln	Gln	Ser	Tyr	Ser	Ile
		275					280					285			
Met	Ser	Ile	Ile	Lys	Glu	Glu	Val	Leu	Ala	Tyr	Val	Val	Gln	Leu	Pro
	290					295					300				
Leu	Tyr	Gly	Val	Ile	Asp	Thr	Pro	Cys	Trp	Lys	Leu	His	Thr	Ser	Pro
305					310					315					320
Leu	Cys	Thr	Thr	Asn	Thr	Lys	Glu	Gly	Ser	Asn	Ile	Cys	Leu	Thr	Arg
				325					330					335	
Thr	Asp	Arg	Gly	Trp	Tyr	Cys	Asp	Asn	Ala	Gly	Ser	Val	Ser	Phe	Phe
			340					345					350		
Pro	Gln	Ala	Glu	Thr	Cys	Lys	Val	Gln	Ser	Asn	Arg	Val	Phe	Cys	Asp

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355

360

365

Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Val Asn Leu Cys Asn Val
370 375 380

Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr
385 390 395 400

Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys
405 410 415

Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile
420 425 430

Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp
435 440 445

Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly
450 455 460

Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro
465 470 475 480

Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn
485 490 495

Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Lys Ser Asp Glu Leu
500 505 510

Leu His Asn Val Asn Ala Gly Lys Ser Thr Thr Asn Ile Met Ile Thr
515 520 525

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

Gly Leu Leu Leu Tyr Cys Lys Ala Arg Ser Thr Pro Val Thr Leu Ser
545 550 555 560

Lys Asp Gln Leu Ser Gly Ile Asn Asn Ile Ala Phe Ser Asn

<210> 7
<211> 738
<212> DNA
<213> hRSV strain B

<400> 7
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aaagtcaccc tcacaaccgt caccgtgcag accattaaaa accataccga gaagaatatt 120
tcaacatatc tgacacaggt ccccccgaa agagtgaact cttccaaaca gcccaaac 180
acctccccca ttcataccaa tagtgccaca atttctccca acacaaagtc tgaaacacac 240
cacactactg ctgagacaaa gggccgaatc accacctcta ctgagaccaa taagccatca 300
acaaaatccc gtcctaaaaa cccacctaaa aaacctaaag atgactatca tttcgaagtc 360
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accatcccct ctaacaagcc aaaaaagaaa cctactatta aaccaactaa taagcccacc 480
actaagacta ctaacaaacg cgatccaaaa acacccgcca aaatgcctaa aaaagagatc 540
attacaaacc cagccaagaa accaactctc aaaactaccg aacgggacac ctccatttct 600
cagtctaccg tgctcgatac catcactccc aaatacacta tccagcagca gtcactccac 660
tcaacaacct ccgagaacac cccctcctca acccagattc ctactgcttc cgaaccatcc 720
accctcaacc ccaattga 738

<210> 8
<211> 245
<212> PRT
<213> hRSV strain B

<400> 8
Met Ile Ile Ser Thr Ser Leu Ile Ile Ala Ala Ile Ile Phe Ile Ile
1 5 10 15
Ser Ala Asn His Lys Val Thr Leu Thr Thr Val Thr Val Gln Thr Ile
20 25 30
Lys Asn His Thr Glu Lys Asn Ile Ser Thr Tyr Leu Thr Gln Val Pro

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35

40

45

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

His Thr Asn Ser Ala Thr Ile Ser Pro Asn Thr Lys Ser Glu Thr His
65 70 75 80

His Thr Thr Ala Gln Thr Lys Gly Arg Ile Thr Thr Ser Thr Gln Thr
85 90 95

Asn Lys Pro Ser Thr Lys Ser Arg Ser Lys Asn Pro Pro Lys Lys Pro
100 105 110

Lys Asp Asp Tyr His Phe Glu Val Phe Asn Phe Val Pro Cys Ser Ile
115 120 125

Cys Gly Asn Asn Gln Leu Cys Lys Ser Ile Cys Lys Thr Ile Pro Ser
130 135 140

Asn Lys Pro Lys Lys Lys Pro Thr Ile Lys Pro Thr Asn Lys Pro Thr
145 150 155 160

Thr Lys Thr Thr Asn Lys Arg Asp Pro Lys Thr Pro Ala Lys Met Pro
165 170 175

Lys Lys Glu Ile Ile Thr Asn Pro Ala Lys Lys Pro Thr Leu Lys Thr
180 185 190

Thr Glu Arg Asp Thr Ser Ile Ser Gln Ser Thr Val Leu Asp Thr Ile
195 200 205

Thr Pro Lys Tyr Thr Ile Gln Gln Gln Ser Leu His Ser Thr Thr Ser
210 215 220

Glu Asn Thr Pro Ser Ser Thr Gln Ile Pro Thr Ala Ser Glu Pro Ser
225 230 235 240

Thr Leu Asn Pro Asn

<210> 9
 <211> 1176
 <212> DNA
 <213> hRSV strain A2

<400> 9
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 cagaagcaca tcaataagct gtgcggcatg ctgctgatca ccgaggacgc caaccacaag 180
 ttcaccggcc tgatcgggat gctgtacgcc atgagccggc tgggccggga ggacaccatc 240
 aagatcctgc gggacgccgg ctaccacgtg aaggccaacg gcgtggacgt gaccaccac 300
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 gaaatgggcg aggtggcccc cgagtacaga cacgacagcc ccgactgcgg catgatcatc 480
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 gccgtgatca gacgggcaa caacgtgctg aagaacgaga tgaagcggta caagggcctg 600
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<210> 10
 <211> 391

eolf-seql

<212> PRT

<213> hRSV strain A2

<400> 10

Met Ala Leu Ser Lys Val Lys Leu Asn Asp Thr Leu Asn Lys Asp Gln
1 5 10 15

Leu Leu Ser Ser Ser Lys Tyr Thr Ile Gln Arg Ser Thr Gly Asp Ser
20 25 30

Ile Asp Thr Pro Asn Tyr Asp Val Gln Lys His Ile Asn Lys Leu Cys
35 40 45

Gly Met Leu Leu Ile Thr Glu Asp Ala Asn His Lys Phe Thr Gly Leu
50 55 60

Ile Gly Met Leu Tyr Ala Met Ser Arg Leu Gly Arg Glu Asp Thr Ile
65 70 75 80

Lys Ile Leu Arg Asp Ala Gly Tyr His Val Lys Ala Asn Gly Val Asp
85 90 95

Val Thr Thr His Arg Gln Asp Ile Asn Gly Lys Glu Met Lys Phe Glu
100 105 110

Val Leu Thr Leu Ala Ser Leu Thr Thr Glu Ile Gln Ile Asn Ile Glu
115 120 125

Ile Glu Ser Arg Lys Ser Tyr Lys Lys Met Leu Lys Glu Met Gly Glu
130 135 140

Val Ala Pro Glu Tyr Arg His Asp Ser Pro Asp Cys Gly Met Ile Ile
145 150 155 160

Leu Cys Ile Ala Ala Leu Val Ile Thr Lys Leu Ala Ala Gly Asp Arg
165 170 175

Ser Gly Leu Thr Ala Val Ile Arg Arg Ala Asn Asn Val Leu Lys Asn
180 185 190

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Glu Met Lys Arg Tyr Lys Gly Leu Leu Pro Lys Asp Ile Ala Asn Ser
195 200 205

Phe Tyr Glu Val Phe Glu Lys His Pro His Phe Ile Asp Val Phe Val
210 215 220

His Phe Gly Ile Ala Gln Ser Ser Thr Arg Gly Gly Ser Arg Val Glu
225 230 235 240

Gly Ile Phe Ala Gly Leu Phe Met Asn Ala Tyr Gly Ala Gly Gln Val
245 250 255

Met Leu Arg Trp Gly Val Leu Ala Lys Ser Val Lys Asn Ile Met Leu
260 265 270

Gly His Ala Ser Val Gln Ala Glu Met Glu Gln Val Val Glu Val Tyr
275 280 285

Glu Tyr Ala Gln Lys Leu Gly Gly Glu Ala Gly Phe Tyr His Ile Leu
290 295 300

Asn Asn Pro Lys Ala Ser Leu Leu Ser Leu Thr Gln Phe Pro His Phe
305 310 315 320

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

Tyr Arg Gly Thr Pro Arg Asn Gln Asp Leu Tyr Asp Ala Ala Lys Ala
340 345 350

Tyr Ala Glu Gln Leu Lys Glu Asn Gly Val Ile Asn Tyr Ser Val Leu
355 360 365

Asp Leu Thr Ala Glu Glu Leu Glu Ala Ile Lys His Gln Leu Asn Pro
370 375 380

Lys Asp Asn Asp Val Glu Leu
385 390

eolf-seql

<210> 11
 <211> 54
 <212> DNA
 <213> Foot and Mouth Disease Virus (FMDV)

<400> 11
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<210> 12
 <211> 18
 <212> PRT
 <213> FMDV

<400> 12

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 <212> DNA
 <213> hRSV strain A2

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 aacaacaagc agaccatcca tctgctgaag cggctgcccg ccgacgtgct gaaaaagacc 480
 atcaagaaca ccctggacat ccacaagtcc atcaccatca ataaccctaa agaaagcacc 540
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eolf-seql

<210> 14

<211> 194

<212> PRT

<213> hRSV strain A2

<400> 14

Met Ser Arg Arg Asn Pro Cys Lys Phe Glu Ile Arg Gly His Cys Leu
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Asn Gly Lys Arg Cys His Phe Ser His Asn Tyr Phe Glu Trp Pro Pro
20 25 30

His Ala Leu Leu Val Arg Gln Asn Phe Met Leu Asn Arg Ile Leu Lys
35 40 45

Ser Met Asp Lys Ser Ile Asp Thr Leu Ser Glu Ile Ser Gly Ala Ala
50 55 60

Glu Leu Asp Arg Thr Glu Glu Tyr Ala Leu Gly Val Val Gly Val Leu
65 70 75 80

Glu Ser Tyr Ile Gly Ser Ile Asn Asn Ile Thr Lys Gln Ser Ala Cys
85 90 95

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

Lys Leu Arg Asp Asn Glu Glu Leu Asn Ser Pro Lys Ile Arg Val Tyr
115 120 125

Asn Thr Val Ile Ser Tyr Ile Glu Ser Asn Arg Lys Asn Asn Lys Gln
130 135 140

Thr Ile His Leu Leu Lys Arg Leu Pro Ala Asp Val Leu Lys Lys Thr
145 150 155 160

Ile Lys Asn Thr Leu Asp Ile His Lys Ser Ile Thr Ile Asn Asn Pro
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Lys Glu Ser Thr Val Ser Asp Thr Asn Asp His Ala Lys Asn Asn Asp

Thr Thr

<210> 15

<211> 1575

<212> DNA

<213> hRSV strain A2

<400> 15

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eolf-seql

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<210> 16
 <211> 524
 <212> PRT
 <213> hRSV strain A2

<400> 16

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 1 5 10 15

Ala Val Thr Phe Cys Phe Ala Ser Ser Gln Asn Ile Thr Glu Glu Phe
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Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
 35 40 45

Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
 50 55 60

Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
 65 70 75 80

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

Met Gln Ser Thr Pro Ala Ala Asn Asn Arg Ala Arg Arg Glu Leu Pro
 100 105 110

Arg Phe Met Asn Tyr Thr Leu Asn Asn Thr Lys Lys Thr Asn Val Thr

eolf-seql

115

120

125

Leu Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val
130 135 140

Gly Ser Ala Ile Ala Ser Gly Ile Ala Val Ser Lys Val Leu His Leu
145 150 155 160

Glu Gly Glu Val Asn Lys Ile Lys Ser Ala Leu Leu Ser Thr Asn Lys
165 170 175

Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Ser Lys Val
180 185 190

Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Val Asn
195 200 205

Lys Gln Ser Cys Arg Ile Ser Asn Ile Glu Thr Val Ile Glu Phe Gln
210 215 220

Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn
225 230 235 240

Val Gly Val Thr Thr Pro Val Ser Thr Tyr Met Leu Thr Asn Ser Glu
245 250 255

Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys
260 265 270

Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile
275 280 285

Met Ser Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro
290 295 300

Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
305 310 315 320

Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg

eolf-seql

325

330

335

Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe
 340 345 350

Pro Gln Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp
 355 360 365

Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Val Asn Leu Cys Asn Val
 370 375 380

Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr
 385 390 395 400

Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys
 405 410 415

Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile
 420 425 430

Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp
 435 440 445

Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly
 450 455 460

Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro
 465 470 475 480

Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn
 485 490 495

Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Lys Ser Asp Glu Leu
 500 505 510

Leu His Asn Val Asn Ala Gly Lys Ser Thr Thr Asn
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<210> 17

eolf-seql

<211> 1809

<212> DNA

<213> Artificial

<220>

<223> cDNA encoding fusion protein comprising full-length N protein from hRSV strain A2 fused to the protease 2A fragment from FMDV fused to full-length M2 protein from hRSV strain A2.

<400> 17

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ttcaccggcc tgatcgggat gctgtacgcc atgagccggc tgggccggga ggacaccatc	240
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cggcaggaca tcaacggcaa agaaatgaag ttcgaggtgc tgaccctggc cagcctgacc	360
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eolf-seql

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<210> 18
 <211> 602
 <212> PRT
 <213> Artificial

<220>
 <223> Fusion protein comprising full-length N protein from hRSV strain A2 fused to the protease 2A fragment from FMDV fused to full-length M2 protein from hRSV strain A2.

<400> 18

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1           5           10          15

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Leu Leu Ser Ser Ser Lys Tyr Thr Ile Gln Arg Ser Thr Gly Asp Ser
          20          25          30

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Ile Asp Thr Pro Asn Tyr Asp Val Gln Lys His Ile Asn Lys Leu Cys
          35          40          45

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Gly Met Leu Leu Ile Thr Glu Asp Ala Asn His Lys Phe Thr Gly Leu
          50          55          60

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Ile Gly Met Leu Tyr Ala Met Ser Arg Leu Gly Arg Glu Asp Thr Ile
65          70          75          80

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eolf-seql

Lys Ile Leu Arg Asp Ala Gly Tyr His Val Lys Ala Asn Gly Val Asp
85 90 95

Val Thr Thr His Arg Gln Asp Ile Asn Gly Lys Glu Met Lys Phe Glu
100 105 110

Val Leu Thr Leu Ala Ser Leu Thr Thr Glu Ile Gln Ile Asn Ile Glu
115 120 125

Ile Glu Ser Arg Lys Ser Tyr Lys Lys Met Leu Lys Glu Met Gly Glu
130 135 140

Val Ala Pro Glu Tyr Arg His Asp Ser Pro Asp Cys Gly Met Ile Ile
145 150 155 160

Leu Cys Ile Ala Ala Leu Val Ile Thr Lys Leu Ala Ala Gly Asp Arg
165 170 175

Ser Gly Leu Thr Ala Val Ile Arg Arg Ala Asn Asn Val Leu Lys Asn
180 185 190

Glu Met Lys Arg Tyr Lys Gly Leu Leu Pro Lys Asp Ile Ala Asn Ser
195 200 205

Phe Tyr Glu Val Phe Glu Lys His Pro His Phe Ile Asp Val Phe Val
210 215 220

His Phe Gly Ile Ala Gln Ser Ser Thr Arg Gly Gly Ser Arg Val Glu
225 230 235 240

Gly Ile Phe Ala Gly Leu Phe Met Asn Ala Tyr Gly Ala Gly Gln Val
245 250 255

Met Leu Arg Trp Gly Val Leu Ala Lys Ser Val Lys Asn Ile Met Leu
260 265 270

Gly His Ala Ser Val Gln Ala Glu Met Glu Gln Val Val Glu Val Tyr
275 280 285

eolf-seql

Glu Tyr Ala Gln Lys Leu Gly Gly Glu Ala Gly Phe Tyr His Ile Leu
290 295 300

Asn Asn Pro Lys Ala Ser Leu Leu Ser Leu Thr Gln Phe Pro His Phe
305 310 315 320

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

Tyr Arg Gly Thr Pro Arg Asn Gln Asp Leu Tyr Asp Ala Ala Lys Ala
340 345 350

Tyr Ala Glu Gln Leu Lys Glu Asn Gly Val Ile Asn Tyr Ser Val Leu
355 360 365

Asp Leu Thr Ala Glu Glu Leu Glu Ala Ile Lys His Gln Leu Asn Pro
370 375 380

Lys Asp Asn Asp Val Glu Leu Leu Asn Phe Asp Leu Leu Lys Leu Ala
385 390 395 400

Gly Asp Val Glu Ser Asn Pro Gly Pro Ser Arg Arg Asn Pro Cys Lys
405 410 415

Phe Glu Ile Arg Gly His Cys Leu Asn Gly Lys Arg Cys His Phe Ser
420 425 430

His Asn Tyr Phe Glu Trp Pro Pro His Ala Leu Leu Val Arg Gln Asn
435 440 445

Phe Met Leu Asn Arg Ile Leu Lys Ser Met Asp Lys Ser Ile Asp Thr
450 455 460

Leu Ser Glu Ile Ser Gly Ala Ala Glu Leu Asp Arg Thr Glu Glu Tyr
465 470 475 480

Ala Leu Gly Val Val Gly Val Leu Glu Ser Tyr Ile Gly Ser Ile Asn
485 490 495

eolf-seql

Asn Ile Thr Lys Gln Ser Ala Cys Val Ala Met Ser Lys Leu Leu Thr
 500 505 510

Glu Leu Asn Ser Asp Asp Ile Lys Lys Leu Arg Asp Asn Glu Glu Leu
 515 520 525

Asn Ser Pro Lys Ile Arg Val Tyr Asn Thr Val Ile Ser Tyr Ile Glu
 530 535 540

Ser Asn Arg Lys Asn Asn Lys Gln Thr Ile His Leu Leu Lys Arg Leu
 545 550 555 560

Pro Ala Asp Val Leu Lys Lys Thr Ile Lys Asn Thr Leu Asp Ile His
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Lys Ser Ile Thr Ile Asn Asn Pro Lys Glu Ser Thr Val Ser Asp Thr
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Asn Asp His Ala Lys Asn Asn Asp Thr Thr
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<220>
 <223> Synthetic peptide.

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<210> 20
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<220>
 <223> Synthetic peptide.

<400> 20

eolf-seql

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<210> 21
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<213> Artificial

<220>
<223> Synthetic peptide.

<400> 21

Glu Leu Gln Leu Leu Met Gln Ser Thr Pro Ala Ala Asn Asn Arg
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<210> 22
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<213> Artificial

<220>
<223> Synthetic peptide.

<400> 22

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<210> 23
<211> 9
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<220>
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<400> 23

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<210> 24
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<212> PRT
<213> Artificial

eolf-seql

<220>

<223> Synthetic peptide.

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<210> 25

<211> 9

<212> PRT

<213> Artificial

<220>

<223> Synthetic peptide.

<400> 25

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<210> 26

<211> 9

<212> PRT

<213> Artificial

<220>

<223> Synthetic peptide.

<400> 26

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<210> 27

<211> 9

<212> PRT

<213> Artificial

<220>

<223> Synthetic peptide.

<400> 27

Ser Tyr Ile Gly Ser Ile Asn Asn Ile
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<210> 28

eolf-seql

<211> 1725

<212> DNA

<213> hRSV strain A2

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eolf-seql

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<210> 29
<211> 574
<212> PRT
<213> hRSV strain A2

<400> 29

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20 25 30

Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
35 40 45

Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
50 55 60

Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
65 70 75 80

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

Met Gln Ser Thr Pro Pro Thr Asn Asn Arg Ala Arg Arg Glu Leu Pro
100 105 110

Arg Phe Met Asn Tyr Thr Leu Asn Asn Ala Lys Lys Thr Asn Val Thr
115 120 125

Leu Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val

eolf-seql

130

135

140

Gly Ser Ala Ile Ala Ser Gly Val Ala Val Ser Lys Val Leu His Leu
 145 150 155 160

Glu Gly Glu Val Asn Lys Ile Lys Ser Ala Leu Leu Ser Thr Asn Lys
 165 170 175

Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Ser Lys Val
 180 185 190

Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Val Asn
 195 200 205

Lys Gln Ser Cys Ser Ile Ser Asn Ile Glu Thr Val Ile Glu Phe Gln
 210 215 220

Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn
 225 230 235 240

Ala Gly Val Thr Thr Pro Val Ser Thr Tyr Met Leu Thr Asn Ser Glu
 245 250 255

Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys
 260 265 270

Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile
 275 280 285

Met Ser Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro
 290 295 300

Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
 305 310 315 320

Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg
 325 330 335

Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe

eolf-seql

340

345

350

Pro Gln Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp
 355 360 365

Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Ile Asn Leu Cys Asn Val
 370 375 380

Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr
 385 390 395 400

Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys
 405 410 415

Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile
 420 425 430

Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Met Asp
 435 440 445

Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly
 450 455 460

Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro
 465 470 475 480

Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn
 485 490 495

Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Lys Ser Asp Glu Leu
 500 505 510

Leu His Asn Val Asn Ala Gly Lys Ser Thr Thr Asn Ile Met Ile Thr
 515 520 525

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

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

eolf-seql

545 550 555 560

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eolf-seql

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Trp	Asp	Thr	Leu
	20	Asn	His
		Leu	Leu
		Phe	Ile
		25	Ser
		Ser	Ser
		Cys	Leu
		30	Tyr
			Lys
Leu	Asn	Leu	Lys
	35	Ser	Val
		Ala	Gln
		40	Ile
		Thr	Leu
		Ser	Ile
		45	Leu
			Ala
			Met
Ile	Ile	Ser	Thr
	50	Ser	Leu
		Ile	Ile
		55	Ala
		Ala	Ile
		Ile	Ile
		60	Phe
			Ile
			Ala
			Ser
Ala	Asn	His	Lys
	65	Val	Thr
		70	Pro
		Thr	Thr
		Thr	Ala
		Ile	Ile
		75	Gln
			Asp
			Ala
			Thr
			80
Ser	Gln	Ile	Lys
	85	Asn	Thr
		Thr	Pro
		Thr	Thr
		Tyr	Leu
		90	Thr
		Gln	Asn
		95	Pro
			Gln
Leu	Gly	Ile	Ser
	100	Pro	Ser
		Asn	Pro
		Ser	Glu
		105	Ile
		Thr	Ser
		Gln	Ile
		110	Thr
Thr	Ile	Leu	Ala
	115	Ser	Thr
		Thr	Pro
		Gly	Val
		Lys	Ser
		120	Thr
		Leu	Gln
		125	Ser
Thr	Thr	Val	Lys
	130	Thr	Lys
		Asn	Thr
		135	Thr
		Thr	Thr
		Thr	Thr
		Gln	Thr
		140	Gln
		Pro	Ser
Lys	Pro	Thr	Thr
	145	Lys	Gln
		Arg	Gln
		Asn	Lys
		150	Pro
		Pro	Pro
		155	Ser
		Lys	Pro
		160	Asn
Asn	Asp	Phe	His
	165	Phe	Glu
		Val	Phe
		Asn	Phe
		170	Val
		Pro	Cys
		Ser	Ile
		175	Cys
Ser	Asn	Asn	Pro
	180	Thr	Cys
		Trp	Ala
		Ile	Cys
		185	Lys
		Arg	Ile
		190	Pro
		Asn	Lys
Lys	Pro	Gly	Lys
	195	Lys	Thr
		Thr	Thr
		200	Thr
		Lys	Pro
		Thr	Lys
		Lys	Lys
		205	Pro
		Thr	Leu
Lys	Thr	Thr	Lys
	Lys	Lys	Asp
		Pro	Lys
		Pro	Gln
		Thr	Thr
		Lys	Ser
		Lys	Glu

eolf-seql

210

215

220

Val Pro Thr Thr Lys Pro Thr Glu Glu Pro Thr Ile Asn Thr Thr Lys
225 230 235 240

Thr Asn Ile Ile Thr Thr Leu Leu Thr Ser Asn Thr Thr Gly Asn Pro
245 250 255

Glu Leu Thr Ser Gln Met Glu Thr Phe His Ser Thr Ser Ser Glu Gly
260 265 270

Asn Pro Ser Pro Ser Gln Val Ser Thr Thr Ser Glu Tyr Pro Ser Gln
275 280 285

Pro Ser Ser Pro Pro Asn Thr Pro Arg Gln
290 295

<210> 32
<211> 585
<212> DNA
<213> hRSV strain A2

<400> 32
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tgtcatttta gtcataatta ttttgaatgg ccaccccatg cactgcttgt aagacaaaac 120
tttatgttaa acagaatact taagtctatg gataaaagta tagatacctt atcagaaata 180
agtggagctg cagagttgga cagaacagaa gagtatgctc ttggtgtagt tggagtgcta 240
gagagttata taggatcaat aaacaatata actaaacaat cagcatgtgt tgccatgagc 300
aaactcctca ctgaactcaa tagtgatgat atcaaaaagc tgagggacaa tgaagagcta 360
aattcaccca agataagagt gtacaatact gtcatatcat atattgaaag caacaggaaa 420
aacaataaac aaactatcca tctgttaaaa agattgccag cagacgtatt gaagaaaacc 480
atcaaaaaca cattggatat ccataagagc ataaccatca acaacccaaa agaatcaact 540
gttagtgata caaatgacca tgccaaaaat aatgatacta cctga 585

<210> 33
<211> 194

eolf-seql

<212> PRT

<213> hRSV strain A2

<400> 33

Met Ser Arg Arg Asn Pro Cys Lys Phe Glu Ile Arg Gly His Cys Leu
 1 5 10 15

Asn Gly Lys Arg Cys His Phe Ser His Asn Tyr Phe Glu Trp Pro Pro
 20 25 30

His Ala Leu Leu Val Arg Gln Asn Phe Met Leu Asn Arg Ile Leu Lys
 35 40 45

Ser Met Asp Lys Ser Ile Asp Thr Leu Ser Glu Ile Ser Gly Ala Ala
 50 55 60

Glu Leu Asp Arg Thr Glu Glu Tyr Ala Leu Gly Val Val Gly Val Leu
 65 70 75 80

Glu Ser Tyr Ile Gly Ser Ile Asn Asn Ile Thr Lys Gln Ser Ala Cys
 85 90 95

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

Lys Leu Arg Asp Asn Glu Glu Leu Asn Ser Pro Lys Ile Arg Val Tyr
 115 120 125

Asn Thr Val Ile Ser Tyr Ile Glu Ser Asn Arg Lys Asn Asn Lys Gln
 130 135 140

Thr Ile His Leu Leu Lys Arg Leu Pro Ala Asp Val Leu Lys Lys Thr
 145 150 155 160

Ile Lys Asn Thr Leu Asp Ile His Lys Ser Ile Thr Ile Asn Asn Pro
 165 170 175

Lys Glu Ser Thr Val Ser Asp Thr Asn Asp His Ala Lys Asn Asn Asp
 180 185 190

eolf-seql

Thr Thr

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<210> 34
<211> 1176
<212> DNA
<213> hRSV strain A2

<400> 34
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cagaaacaca tcaataagtt atgtggcatg ttattaatca cagaagatgc taatcataaa      180
ttcactgggt taataggtat gttatatgcg atgtctaggt taggaagaga agacaccata      240
aaaatactca gagatgcggg atatcatgta aaagcaaatg gagtagatgt aacaacacat      300
cgtcaagaca ttaatggaaa agaaatgaaa tttgaagtgt taacattggc aagcttaaca      360
actgaaattc aaatcaacat tgagatagaa tctagaaaat cctacaaaaa aatgctaaaa      420
gaaatgggag aggtagctcc agaatacagg catgactctc ctgattgtgg gatgataata      480
ttatgtatag cagcattagt aataactaaa ttagcagcag gggacagatc tggtcttaca      540
gccgtgatta ggagagctaa taatgtccta aaaaatgaaa tgaaacgtta caaaggctta      600
ctaccaaggg acatagccaa cagcttctat gaagtgtttg aaaaacatcc ccactttata      660
gatgtttttg ttcattttgg tatagcacia tcttctacca gaggtggcag tagagttgaa      720
gggatttttg caggattgtt tatgaatgcc tatggtgcag ggcaagtgat gttacggtgg      780
ggagtcttag caaaatcagt taaaaatatt atgttaggac atgctagtgt gcaagcagaa      840
atggaacaag ttgttgaggt ttatgaatat gcccaaaaat tgggtggtga agcaggattc      900
taccatatat tgaacaaccc aaaagcatca ttattatctt tgactcaatt tcctcacttc      960
tccagtgtag tattaggcaa tgctgctggc ctaggcataa tgggagagta cagaggtaca     1020
ccgaggaatc aagatctata tgatgcagca aaggcatatg ctgaacaact caaagaaaat     1080
ggtgtgatta actacagtgt actagacttg acagcagaag aactagaggc tatcaaacat     1140
cagcttaatc caaaagataa tgatgtagag ctttga                                1176

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eolf-seql

<210> 35

<211> 391

<212> PRT

<213> hRSV strain A2

<400> 35

Met Ala Leu Ser Lys Val Lys Leu Asn Asp Thr Leu Asn Lys Asp Gln
1 5 10 15

Leu Leu Ser Ser Ser Lys Tyr Thr Ile Gln Arg Ser Thr Gly Asp Ser
20 25 30

Ile Asp Thr Pro Asn Tyr Asp Val Gln Lys His Ile Asn Lys Leu Cys
35 40 45

Gly Met Leu Leu Ile Thr Glu Asp Ala Asn His Lys Phe Thr Gly Leu
50 55 60

Ile Gly Met Leu Tyr Ala Met Ser Arg Leu Gly Arg Glu Asp Thr Ile
65 70 75 80

Lys Ile Leu Arg Asp Ala Gly Tyr His Val Lys Ala Asn Gly Val Asp
85 90 95

Val Thr Thr His Arg Gln Asp Ile Asn Gly Lys Glu Met Lys Phe Glu
100 105 110

Val Leu Thr Leu Ala Ser Leu Thr Thr Glu Ile Gln Ile Asn Ile Glu
115 120 125

Ile Glu Ser Arg Lys Ser Tyr Lys Lys Met Leu Lys Glu Met Gly Glu
130 135 140

Val Ala Pro Glu Tyr Arg His Asp Ser Pro Asp Cys Gly Met Ile Ile
145 150 155 160

Leu Cys Ile Ala Ala Leu Val Ile Thr Lys Leu Ala Ala Gly Asp Arg
165 170 175

Ser Gly Leu Thr Ala Val Ile Arg Arg Ala Asn Asn Val Leu Lys Asn

eolf-seql

180

185

190

Glu Met Lys Arg Tyr Lys Gly Leu Leu Pro Lys Asp Ile Ala Asn Ser
 195 200 205

Phe Tyr Glu Val Phe Glu Lys His Pro His Phe Ile Asp Val Phe Val
 210 215 220

His Phe Gly Ile Ala Gln Ser Ser Thr Arg Gly Gly Ser Arg Val Glu
 225 230 235 240

Gly Ile Phe Ala Gly Leu Phe Met Asn Ala Tyr Gly Ala Gly Gln Val
 245 250 255

Met Leu Arg Trp Gly Val Leu Ala Lys Ser Val Lys Asn Ile Met Leu
 260 265 270

Gly His Ala Ser Val Gln Ala Glu Met Glu Gln Val Val Glu Val Tyr
 275 280 285

Glu Tyr Ala Gln Lys Leu Gly Gly Glu Ala Gly Phe Tyr His Ile Leu
 290 295 300

Asn Asn Pro Lys Ala Ser Leu Leu Ser Leu Thr Gln Phe Pro His Phe
 305 310 315 320

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

Tyr Arg Gly Thr Pro Arg Asn Gln Asp Leu Tyr Asp Ala Ala Lys Ala
 340 345 350

Tyr Ala Glu Gln Leu Lys Glu Asn Gly Val Ile Asn Tyr Ser Val Leu
 355 360 365

Asp Leu Thr Ala Glu Glu Leu Glu Ala Ile Lys His Gln Leu Asn Pro
 370 375 380

Lys Asp Asn Asp Val Glu Leu

385

390

<210> 36

<211> 27

<212> DNA

<213> Artificial

<220>

<223> RT-PCR primer.

<400> 36

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27

<210> 37

<211> 25

<212> DNA

<213> Artificial

<220>

<223> RT-PCR primer.

<400> 37

ttcagctatc attttctctg ccaat

25

<210> 38

<211> 27

<212> DNA

<213> Artificial

<220>

<223> RT-PCR probe.

<400> 38

tttgaacctg tctgaacatt cccggtt

27

<210> 39

<211> 40

<212> DNA

<213> Artificial

<220>

<223> Synthetic promoter.

<400> 39

aaaaattgaa attttat ttttttttgg aatataaata

40

<210> 40

eolf-seql

<211> 104
 <212> DNA
 <213> Artificial

<220>
 <223> Synthetic promoter.

<400> 40
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 aatttctcgt aaaagtagaa aatatattct aatttattgc acgg 104

<210> 41
 <211> 73
 <212> DNA
 <213> Artificial

<220>
 <223> Synthetic promoter.

<400> 41
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 ataaataata aat 73

<210> 42
 <211> 227
 <212> DNA
 <213> Artificial

<220>
 <223> Synthetic promoter.

<400> 42
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 gaaaaactat tctaatttat tgcacggtcc ggtaaaaatt gaaaaactat tctaatttat 180
 tgcacggtcc ggtaaaaatt gaaaaactat tctaatttat tgcacgg 227

<210> 43
 <211> 112
 <212> DNA
 <213> Artificial

<220>
 <223> Synthetic promoter.

eolf-seql

<400> 43

tacttaaaaa ttgaaaataa atacaaaggt tcttgagggt tgtgttaaataa tgaaagcgag 60

aaataatcat aaataatttc attatcgcga tatccgttaa gtttgtatcg ta 112