FIGURE 1

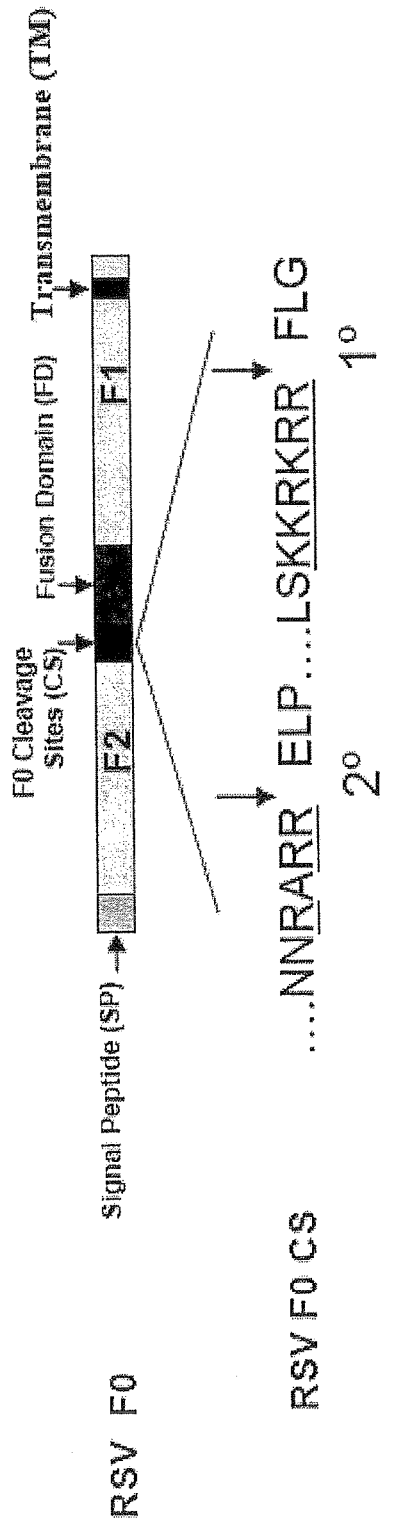

Transmembrane (TM)
Fusion Domain (FD)
F0 Cleavage Sites (CS)
F1
F2
Signal Peptide (SP)
RSV F0
RSV F0 CS
....NNRARR
ELP....LSKKRKRR
FLG
2°
1°

FIGURE 2

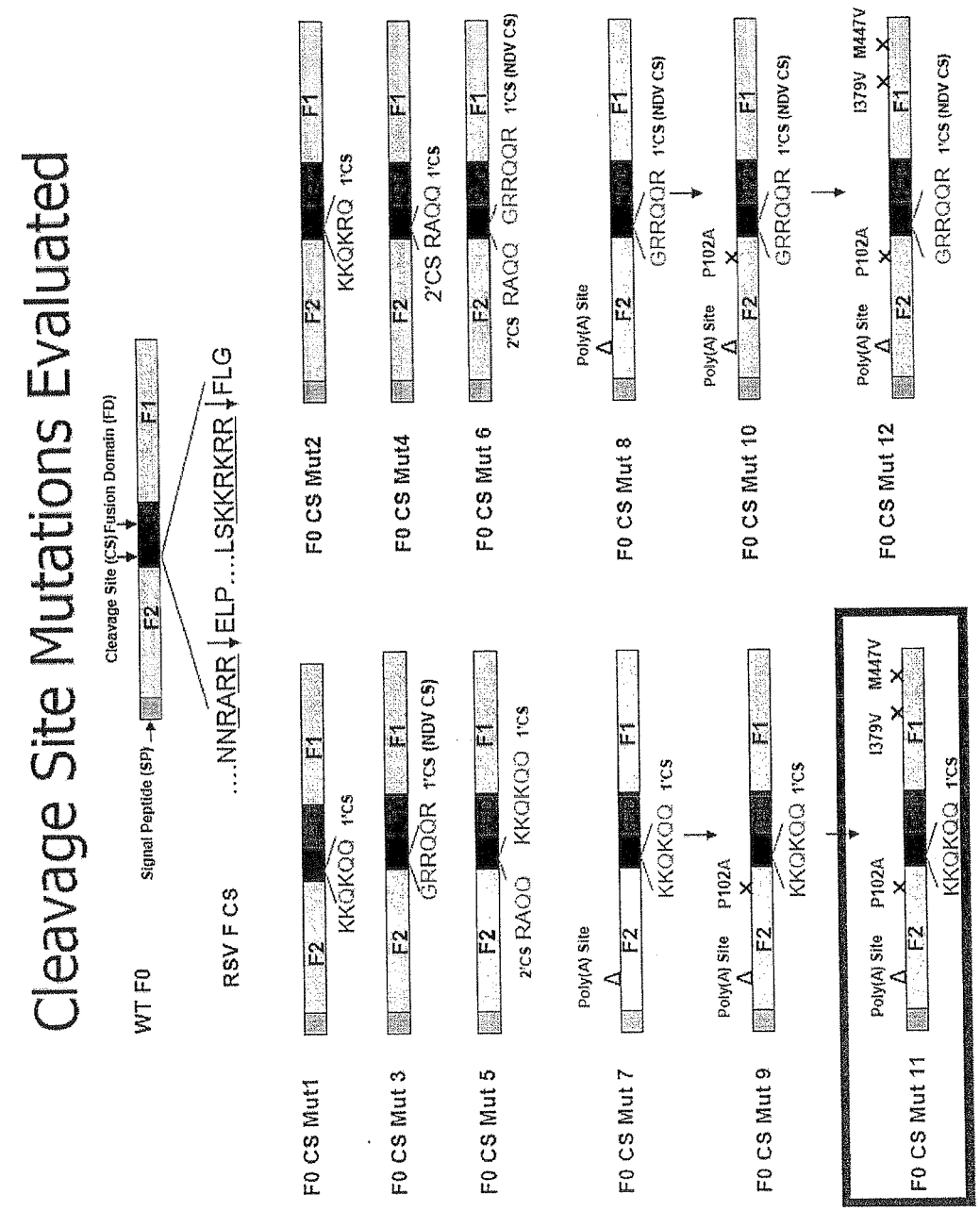
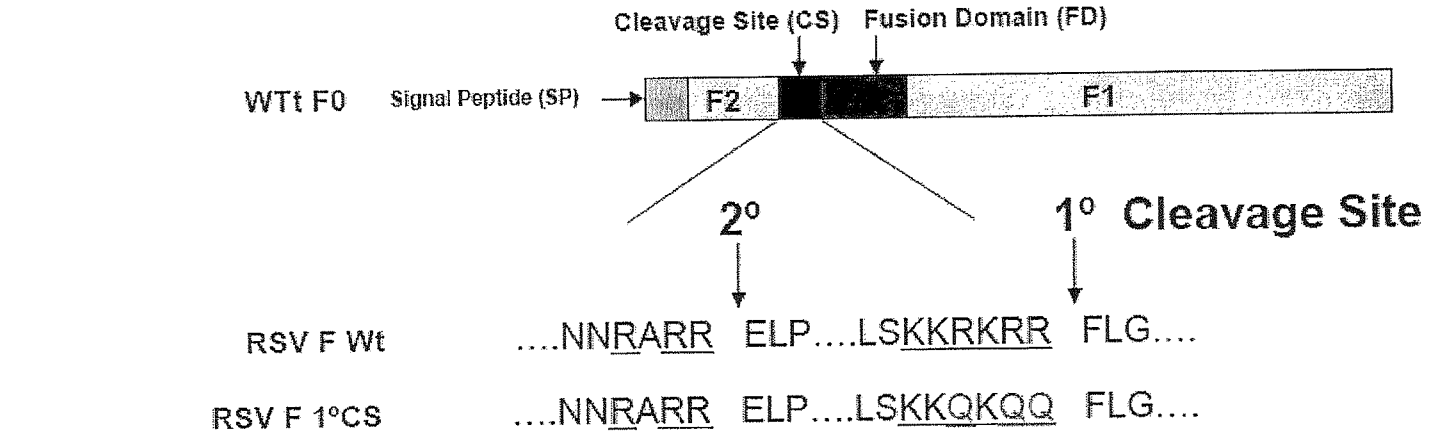
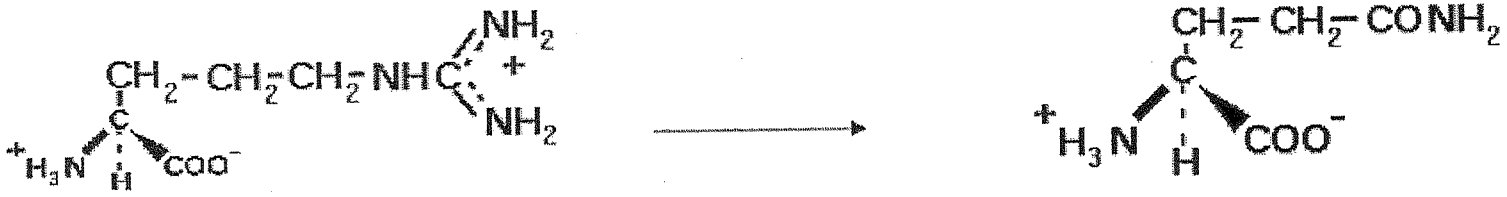

Cleavage Site Mutations Evaluated
Cleavage Site (CS)
Fusion Domain (FD)
WT F0
Signal Peptide (SP)
F2
F1
RSV F CS
....NNRARR↓ELP....LSKKRKRR↓FLG
F0 CS Mut1
KKQKQQ 1°CS
F0 CS Mut2
KKQKRQ 1°CS
F0 CS Mut 3
GRRQQR 1°CS (NDV CS)
F0 CS Mut4
2°CS RAQQ 1°CS
F0 CS Mut 5
2°CS RAQQ KKQKQQ 1°CS
F0 CS Mut 6
2°CS RAQQ GRRQQR 1°CS (NDV CS)
Poly(A) Site
F0 CS Mut 7
F0 CS Mut 8
F0 CS Mut 9
P102A
F0 CS Mut 10
I379V
M447V
F0 CS Mut 11
F0 CS Mut 12

FIGURE 3





Arginine (R)
polar - charged

- Preserve 3D structure
- Alter the charge
- Prevent cleavage
- Down regulate fusion

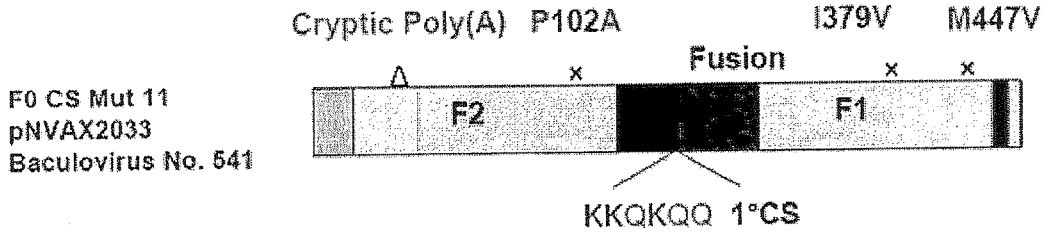
Glutamine (Q)
polar - neutral

FIGURE 4

Modified RSV F0 (GeneBank Assession AAB59858): pNVAX 2023 clone

MELLILKANA ITTILTAVTF CFASGQNITE EFYQSTCSAV SKGYLSALRT
GWYTSVITIE LSNIKENKCN GTDAKVKLIK QELDKYKNAV TELQLLMQST
PATNN[redacted]E LPRFMNYTLN NAKKTNVTLS KKKQKQGFLGF LLGVGSAIAS
GVAVSKVLHL EGEVNKIKSA LLSTNKAVVS LSNGVSVLTS KVLDLKNYID
KQLLPIVNKQ SCSISNIETV IEFQQKNNRL LEITREFSVN AGVTTPVSTY
MLTNSELLSL INDMPITNDQ KKLMSNNVQI VRQQSYSIMS IIKEEVLAYV
VQLPLYGVID TPCWKLHTSP LCTTNTKEGS NICLTRTDRG WYCDNAGSVS
FFPQAETCKV QSNRVFCDTM NSLTLPSEVN LCNVDIFNPK YDCKIMTSKT
DVSSSVITSL GAIVSCYGKT KCTASNKNRG IIKTFSNGCD YVSNKGVDTV
SVGNTLYYVN KQEGKSLYVK GEPIINFYDP LVFPSDEFDA SISQVNEKIN
QSLAFIRKSD ELLHNVNAGK STTNIMITTI IIVIIVILLS LIAVGLLLYC
KARSTPVTLS KDQLSGINNI AFSN

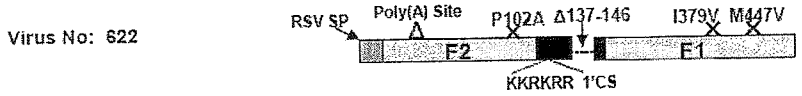
2° Cleavage Site 1° Cleavage Site Fusion domain



F0 CS Mut 11
pNVAX2033
Baculovirus No. 541

FIGURE 5

Partial deletion (Δ137-146) of F fusion domain




```
Δ137-146    MELLILKANAITTILTAVTFCFASGQNITEEFYQSTCSAVSKGYLSALRTGWYTSVITIE 60
WT F0       MELLILKANAITTILTAVTFCFASGQNITEEFYQSTCSAVSKGYLSALRTGWYTSVITIE 60
            ************************************************************

Δ137-146    LSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQSTPATNNRARRELPRFMNYTLN 120
WT F0       LSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQSTPATNNRARRELPRFMNYTLN 120
            ************************************************************

Δ137-146    NAKKTNVTLSKKRKRR----------AIASGVAVSKVLHLEGEVNKIKSALLSTNKAVVS 170
WT F0       NAKKTNVTLSKKRKRRFLGFLLGVGSAIASGVAVSKVLHLEGEVNKIKSALLSTNKAVVS 180
            ****************            ********************************

Δ137-146    LSNGVSVLTSKVLDLKNHIDKQLLPIVNKQSCSISNIETVIEFQQKNNRLLEITREFSVN 230
WT F0       LSNGVSVLTSKVLDLKNYIDKQLLPIVNKQSCSISNIETVIEFQQKNNRLLEITREFSVN 240
            ****************;*************************************

Δ137-146    AGVTTPVSTYMLTNSELLSLINDMPITNDQKKLMSNNVQIVRQQSYSIMSIIKEEVLAYV 290
WT F0       AGVTTPVSTYMLTNSELLSLINDMPITNDQKKLMSNNVQIVRQQSYSIMSIIKEEVLAYV 300
            ************************************************************

Δ137-146    VQLPLYGVIDTPCWKLHTSPLCTINTKEGSNICLTRTDRGWYCDNAGSVSFFPQAETCKV 350
WT F0       VQLPLYGVIDTPCWKLHTSPLCTINTKEGSNICLTRTDRGWYCDNAGSVSFFPQAETCKV 360
            ************************************************************

Δ137-146    QSNRVFCDTMNSLTLPSEVNLCNVDIFNPKYDCKIMTSKTDVSSSVITSLGAIVSCYGKT 410
WT F0       QSNRVFCDTMNSLTLPSEVNLCNVDIFNPKYDCKIMTSKTDVSSSVITSLGAIVSCYGKT 420
            ************************************************************

Δ137-146    KCTASNKNRGIIKTFSNGCDYVSNKGVDTVSVGNTLYYVNKQEGKSLYVKGEPIINFYDP 470
WT F0       KCTASNKNRGIIKTFSNGCDYVSNKGVDTVSVGNTLYYVNKQEGKSLYVKGEPIINFYDP 480
            ************************************************************

Δ137-146    LVFPSDEFDASISQVNEKINQSLAFIRKSDELLHNVNAGKSTTNIMITTIIIVIIVILLS 530
WT F0       LVFPSDEFDASISQVNEKINQSLAFIRKSDELLHNVNAGKSTTNIMITTIIIVIIVILLS 540
            ************************************************************

Δ137-146    LIAVGLLLYCKARSTPVTLSKDQLSGINNIAFSN- 564
WT F0       LIAVGLLLYCKARSTPVTLSKDQLSGINNIAFSN- 574
            ********************************
```

FIGURE 6

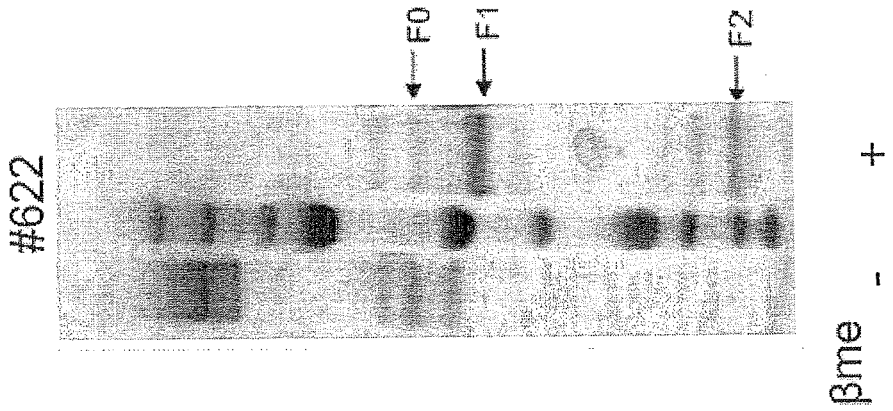
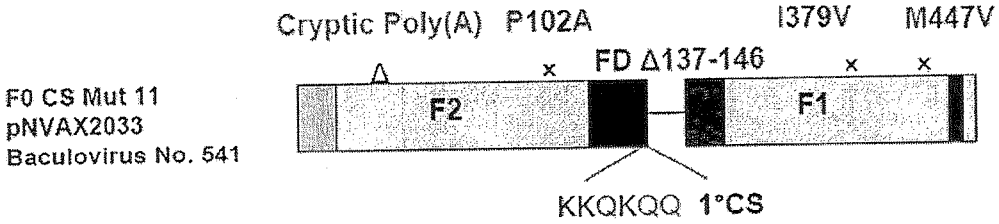


FIGURE 7

BV #683 Modified RSV F0



Codon optimized
1° cleavage site inactivation (3 conservative aa changes)
Cryptic poly(A) in F2 removed
3 aa corrections to GenBank sequence
Deletion of N-terminal half of the F1 fusion domain

FIGURE 8

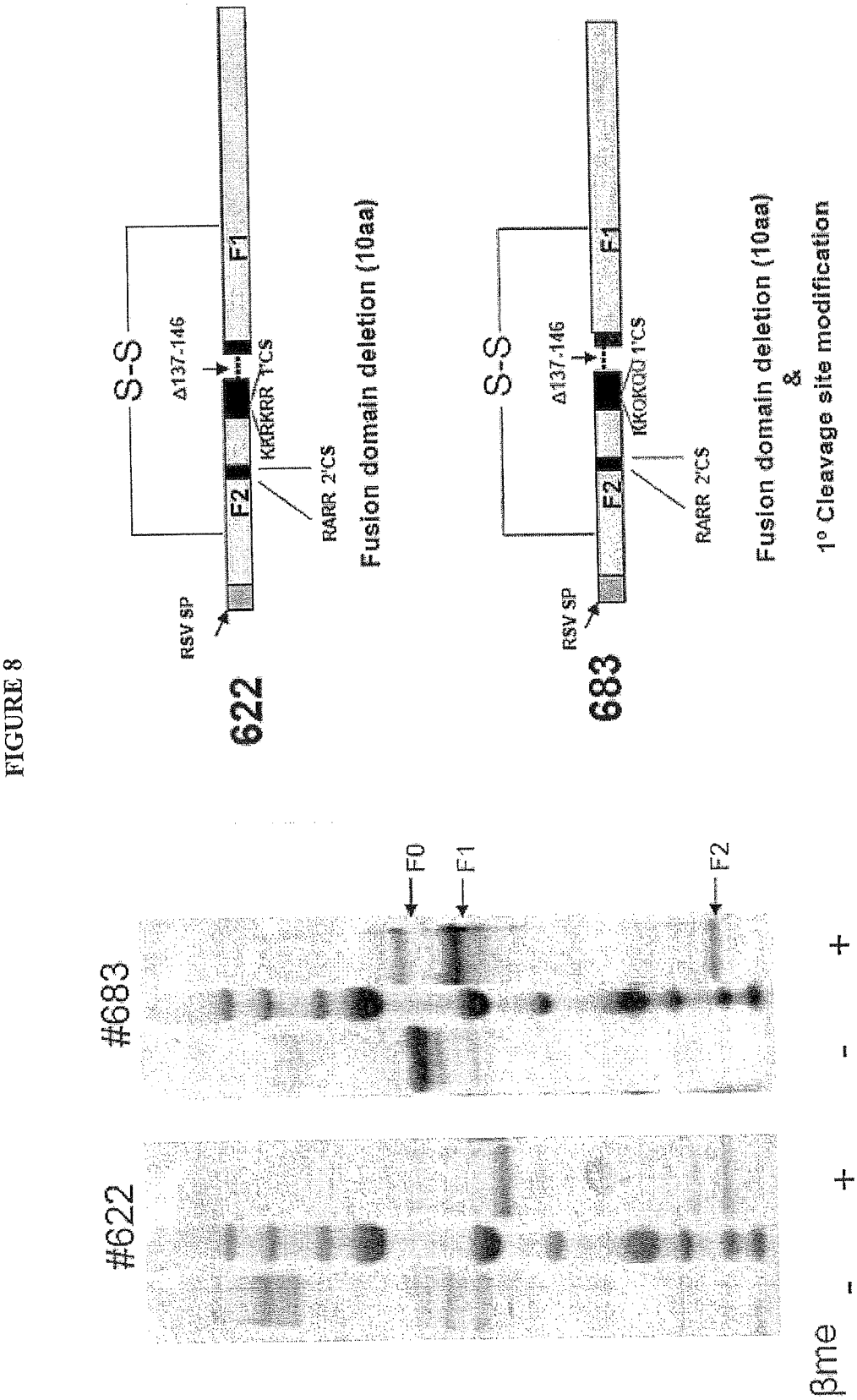

S-S
Δ137-146
F1
F2
KRRKRR 1°CS
RARR 2°CS
RSV SP
622
Fusion domain deletion (10aa)
S-S
Δ137-146
F1
F2
KKOKOO 1°CS
RARR 2°CS
RSV SP
683
Fusion domain deletion (10aa)
&
1° Cleavage site modification
F0
F1
F2
#683
#622
βme - + - +

FIGURE 9

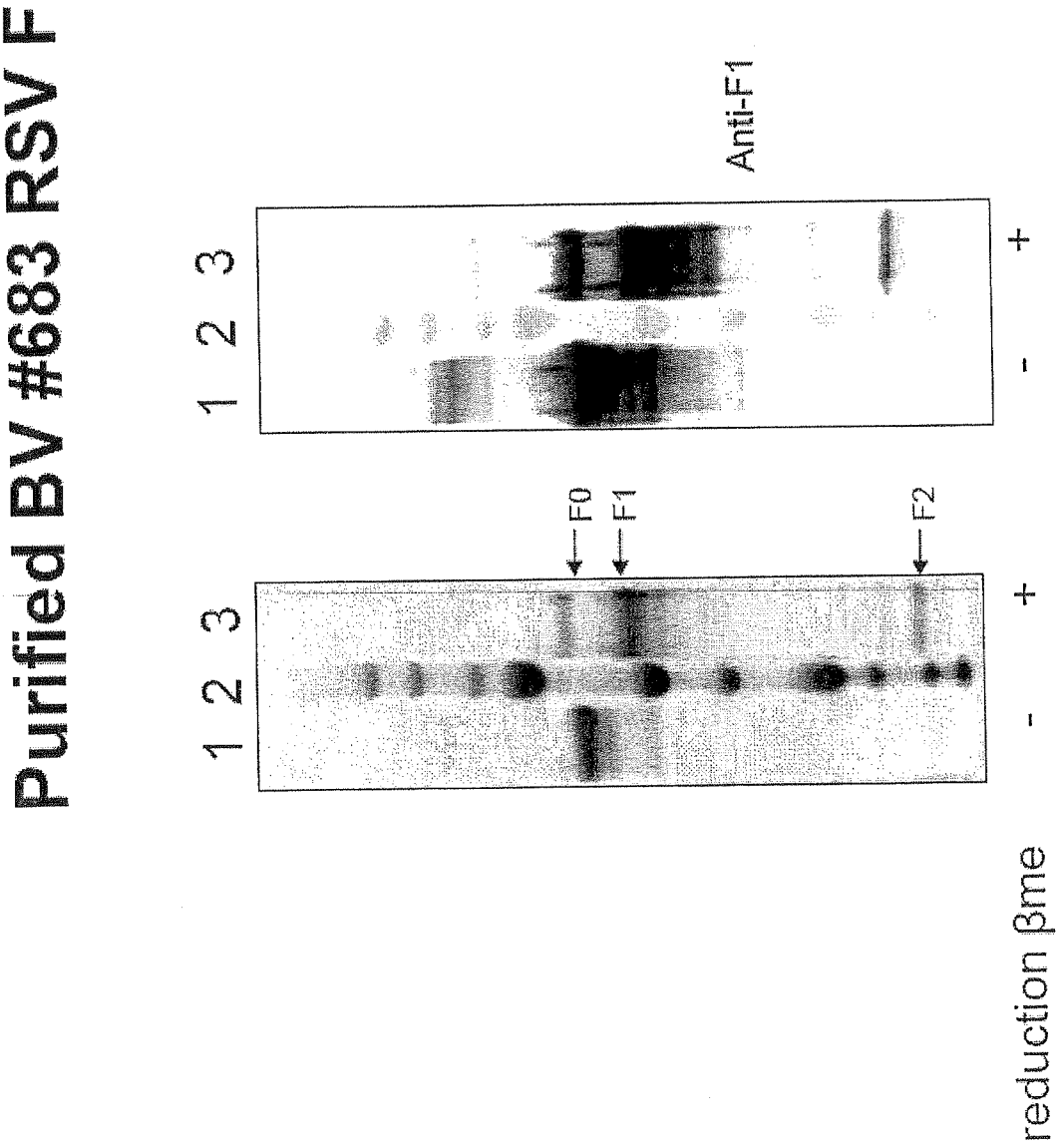
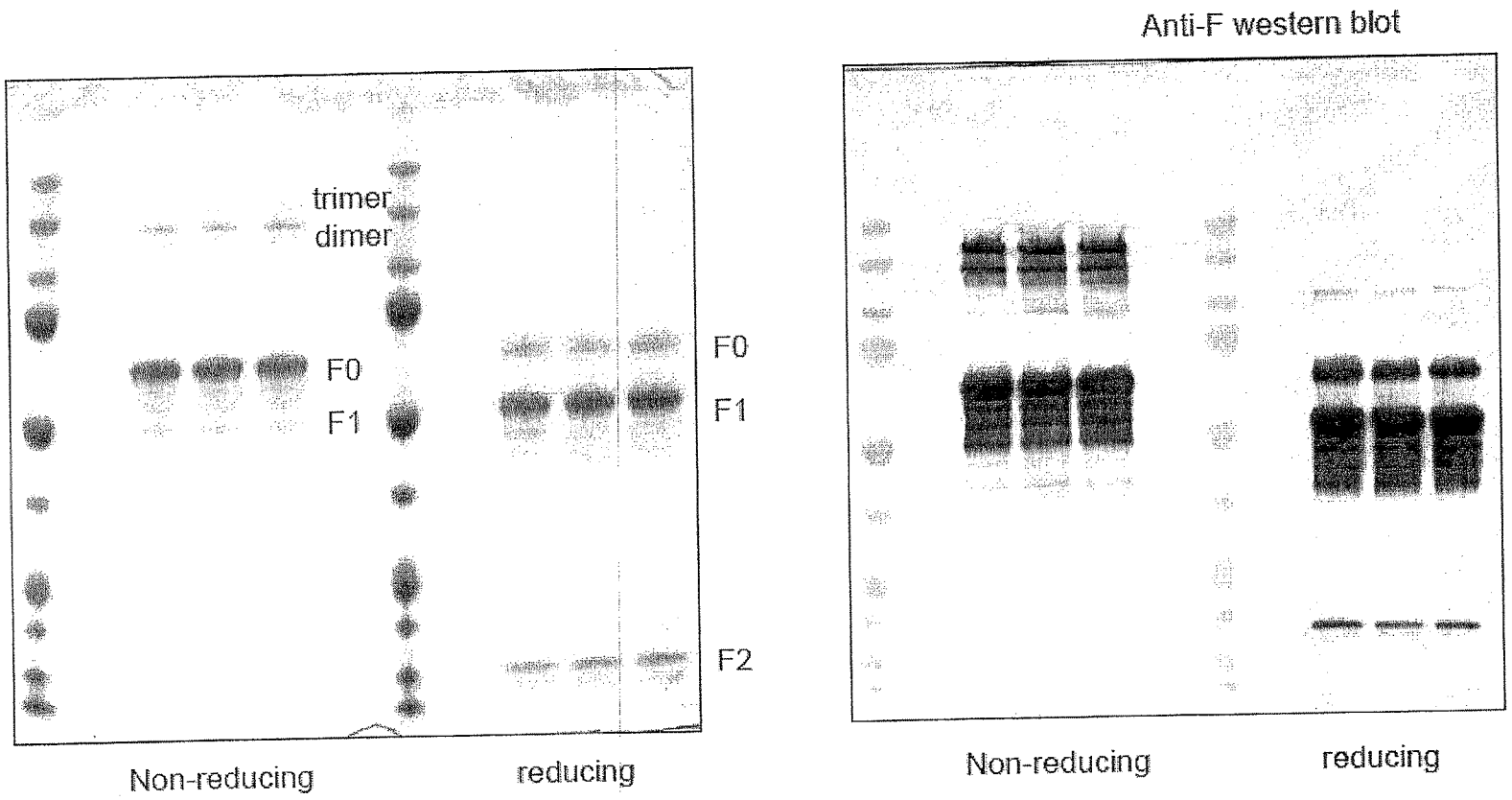


FIGURE 10



Purity >98% scanning densitometry

FIGURE 11

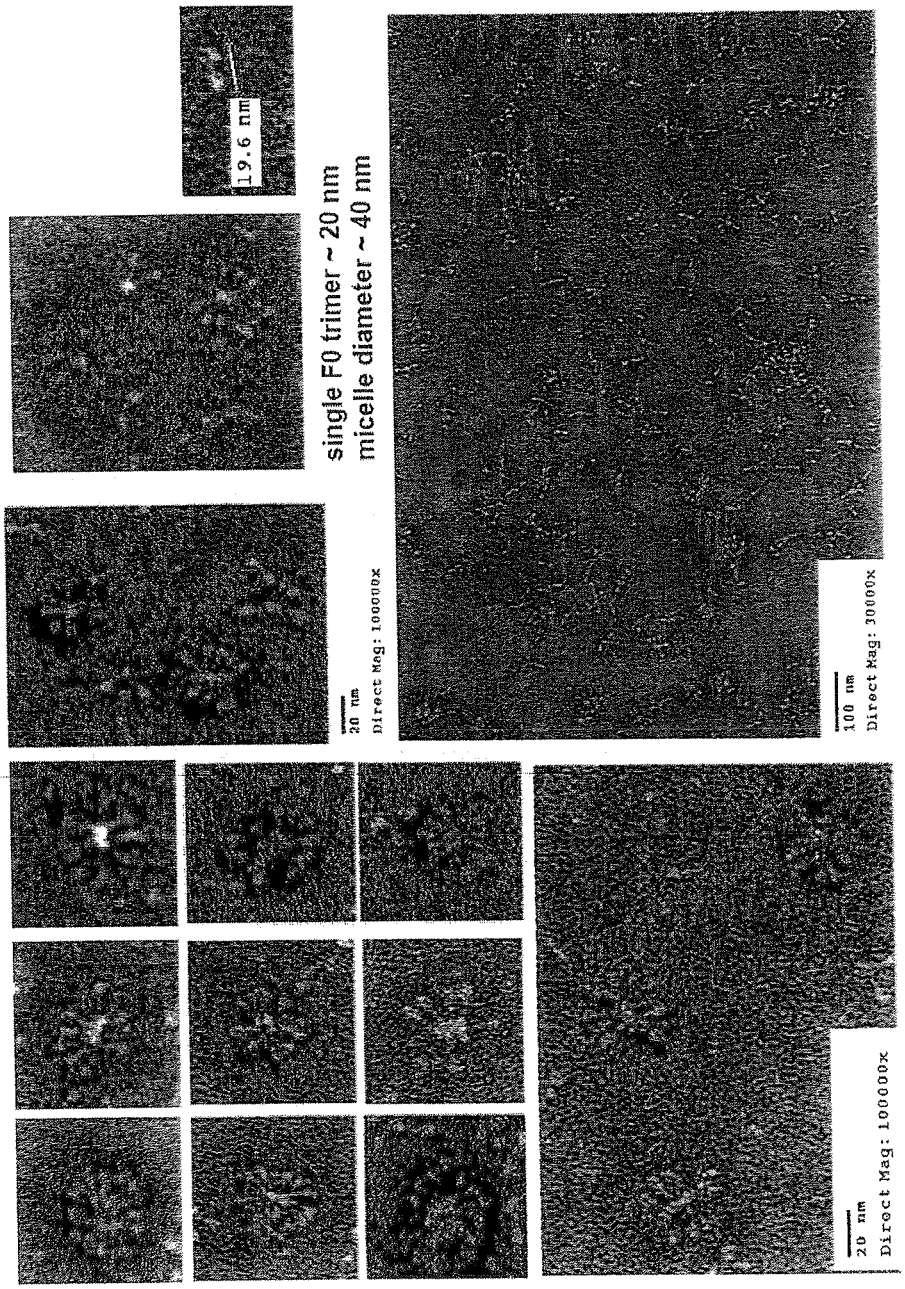

Purified RSV - F #683 micelles (rosettes)
19.6 nm
single F0 trimer ~ 20 nm
micelle diameter ~ 40 nm
20 nm
Direct Mag: 100000x
100 nm
Direct Mag: 30000x
20 nm
Direct Mag: 100000x

FIGURE 12

Particle size analysis shows RSV 683 F0 forms 40 nm particles

Results

Z-Average (d.nm):	40.2
PdI:	0.383
Intercept:	0.823

	Diam. (nm)	% Intensity	Width (nm)
Peak 1:	91.3	98.4	155
Peak 2:	4390	1.6	938
Peak 3:	0.00	0.0	0.00

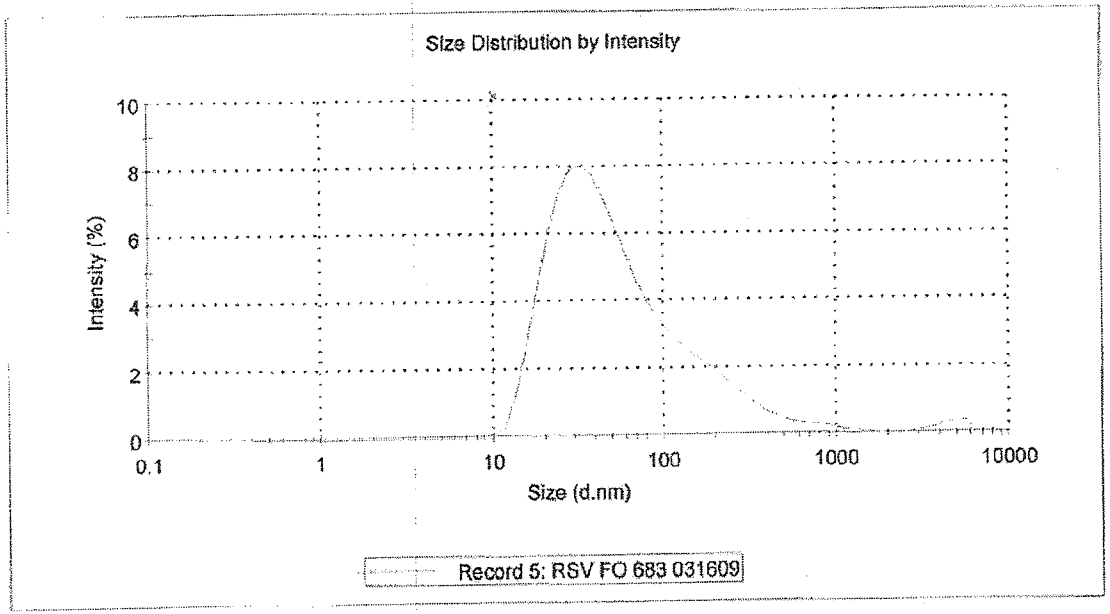
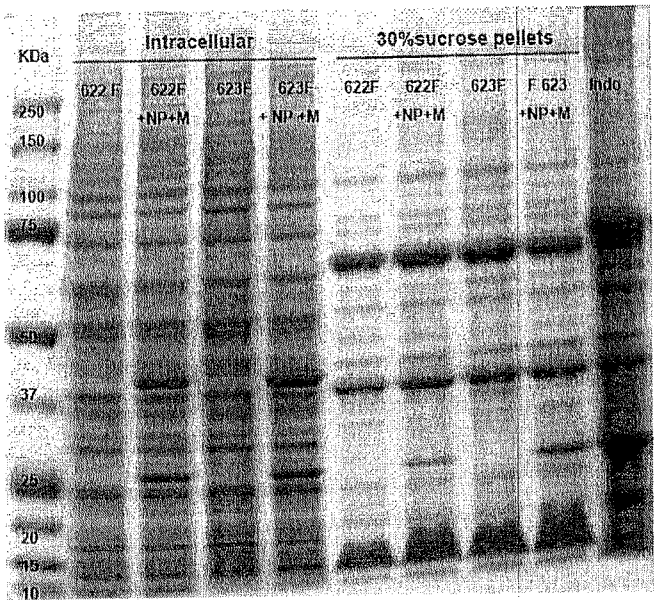
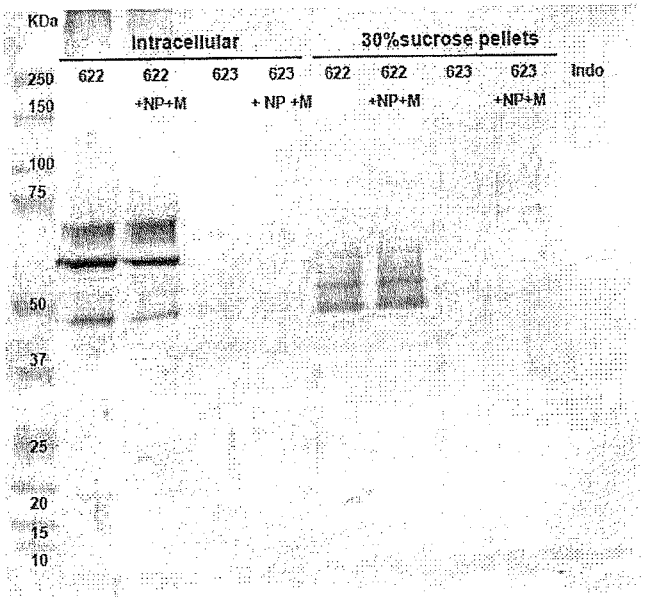


FIGURE 13

Modified RSF F: BV #622 and #623





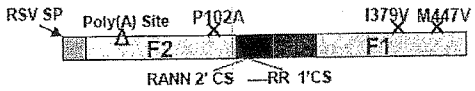
Anti-RSV F

Virus No: 622



Fusion domain partial deletion

Virus No: 623



Both cleavage site mutate.

F0 : 70 KD
F1 : 48 KD
NP : 43.5 KD
M : 28 KD

FIGURE 14

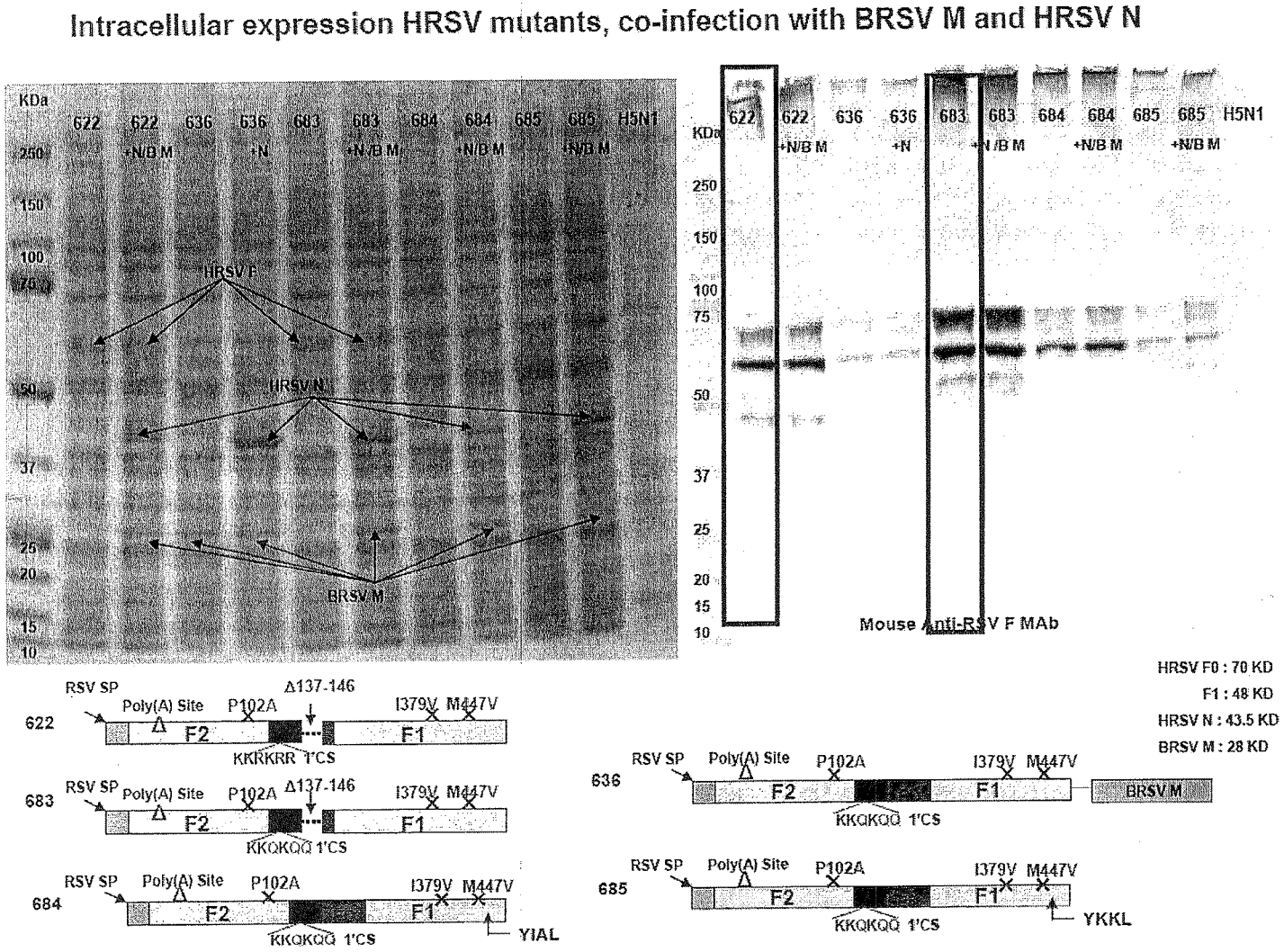
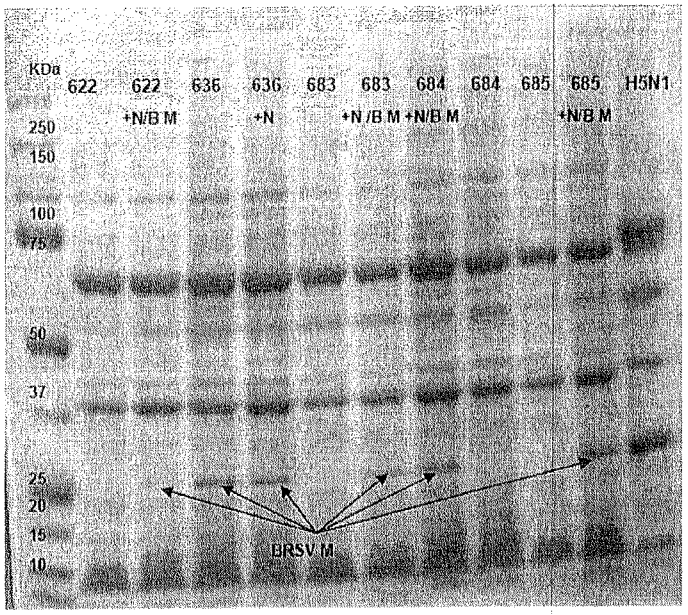
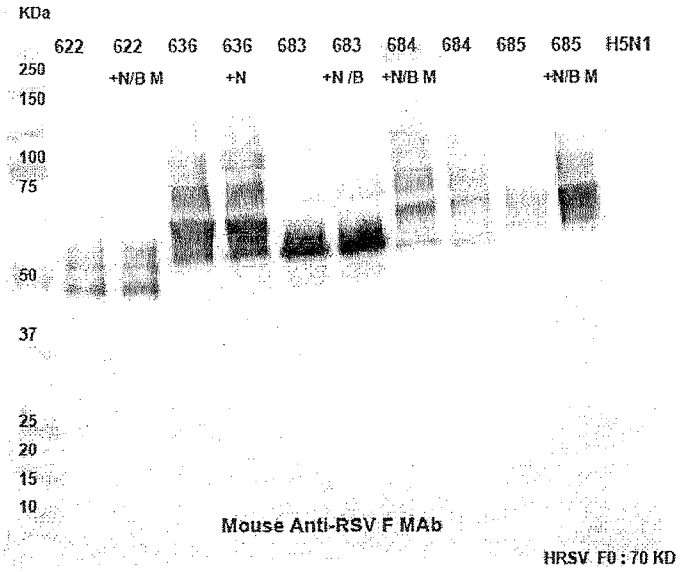
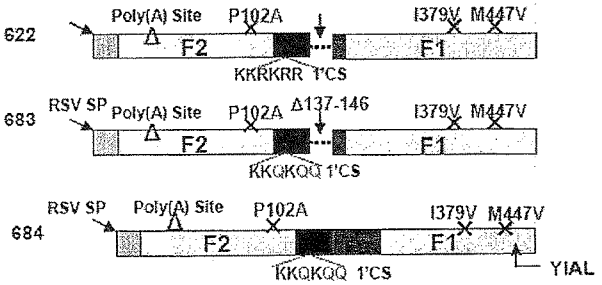

Intracellular expression HRSV mutants, co-infection with BRSV M and HRSV N
KDa
622
622 +N/B M
636
636 +N
683
683 +N/B M
684
684 +N/B M
685
685 +N/B M
H5N1
250
150
100
75
50
37
25
20
15
10
HRSV F
HRSV N
BRSV M
Mouse Anti-RSV F MAb
RSV SP
Poly(A) Site
P102A
Δ137-146
I379V
M447V
F2
F1
KKRKRR 1'CS
KKQKQQ 1'CS
BRSV M
YIAL
YKKL
HRSV F0 : 70 KD
F1 : 48 KD
HRSV N : 43.5 KD
BRSV M : 28 KD

FIGURE 15

30% sucrose VLPs HRSV mutants, co-infection with BRSV M and HRSV N







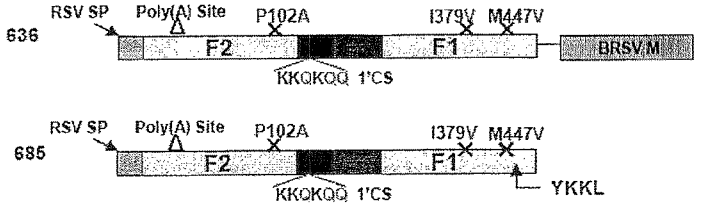
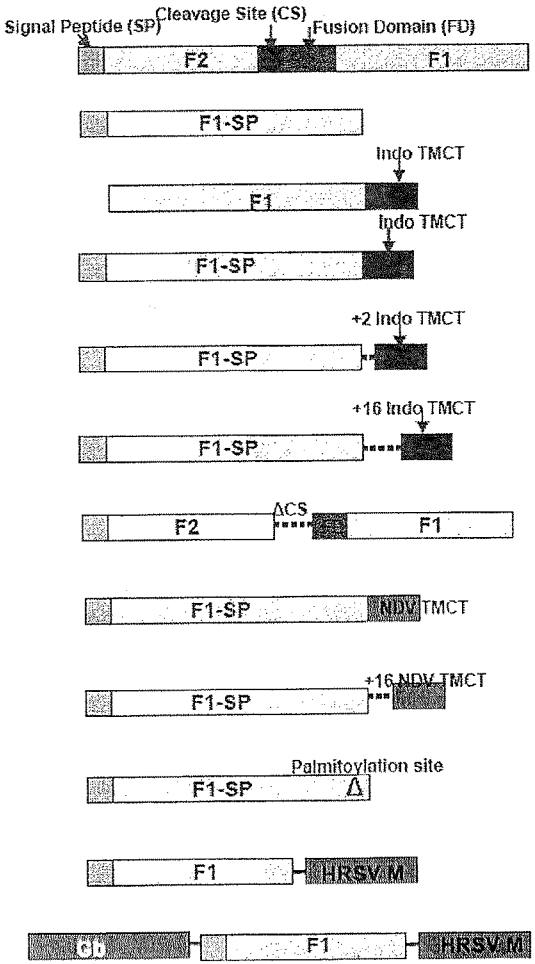
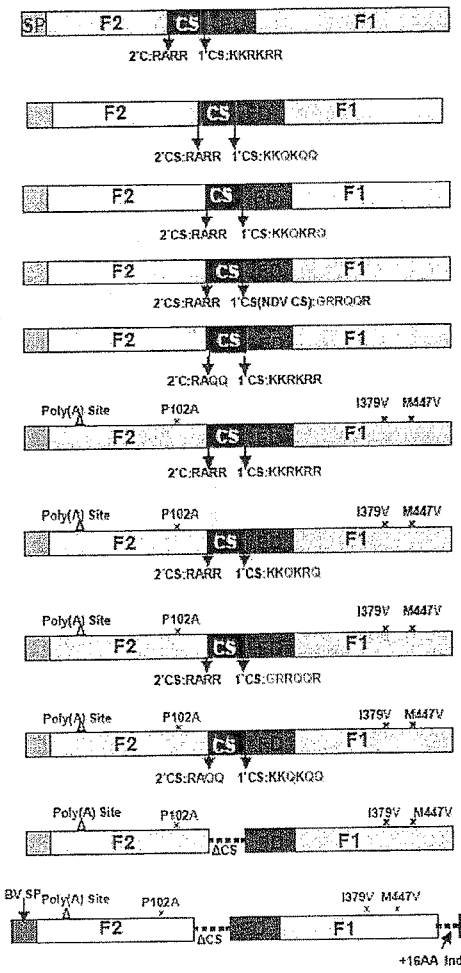


FIGURE 16a



Clone Name	Description	WB/Coomassie	Conclusion
WT HRSV F0	Genebank	+ / -	express really poor
F1-SP	ΔF2	++++ / ++++	express good but insoluble, might be misfolded
F1 w/ Indo TMCT	ΔF2, Chimeric F1 No SP	+++ / +++	express good but insoluble, might be misfolded
F1-SP w/ Indo TMCT	ΔF2,Chimeric F1 w Indo TMCT	+++ / +++	express good but insoluble, might be misfolded
F1-SP w/ Indo	ΔF2,Chimeric F1 with TMCT+2AA	+++ / +++	express good but insoluble, might be misfolded
F1-SP w/ Indo	Δ F2,Chimeric F1 with TMCT+16 AA	+++ / +++	express good but insoluble, might be misfolded
F0 Δ CS	CS(KKRKRR) replace with GASGAG	- / -	No protein express
F1-SP w/	Chimeric F1 with NDV HA NDV TMCT	+++ / +++	express good but doesn't assemble with NDV M well
F1-SP w/NDV TMCT+16AA	Chimeric F1 with NDV HA TMCT+ upstream 16AA	+++ / +++	express good but doesn't assemble with NDV M well
F1-SP ΔPalm site	Delete Palmitoylation site in F1, improve the solubility of F1	+++ / +++	express good but still insoluble
MF1 tandem	F1+ HRSV M	F1+++, M+++ / F1-, M+	both F1 and M express well in tandem, but VLP yield is poor. M expression inhibited when co-infection with F1
GbMF1 tandem	F1+ HRSV M+ Gb	F1++, M++/F1-, M+	both F1 and M express better in triple tandem than co-infection, but VLP yield is very poor.

FIGURE 16b



Clone Name	Description	WB/Coomassie	Conclusion
WT HRSV F0	Genebank, intact cleavage sites	+ / -	express really poor
HRSV F0 triple mutation	1' CS mutate to KKQKQQ	+ / -	1' CS mutation improve expression a little
HRSV F0 double mutation	1' CS mutate to KKQKRQ	+ / -	1' CS mutation doesn't improve expression
HRSV F0 with NDV CS	1' CS mutate to NDV CS (GRRQQR)	+ / -	1' CS mutation doesn't improve expression
HRSV F0 with 2' CS mutation	2'CS mutate to RAQQ	++ / -	2' CS mutation improve expression a little
HRSV F0(fixed) WT	Found errors in WT F0 derived from genebank, remove ploy(A)sitebut change P to A, I to V and M to V	++ / -	Error fixed F0 express better than genebank F0, but still doesn't express well, can't be detected by blue stained gel
HRSV F0 (fixed) WT with 1'CS mutation(541)	mutate 1'CS to KKQKQQ	+++ / -	1'CS mutate to KKQKQQ improve F0 expression, can assemble with BRSV M, HRSV N to form VLP, yield poor and rBV titerlow, need to improve
HRSV F0 (fixed) WT with 1'CS mutation	mutate 1'CS to NDV CS	+ / -	1'CS mutate to NDV CS doesn't improve F0 expression
HRSV F0 (fixed) with 1'CS and 2'CS mutation	mutate both 1'CS and 2'CS	- / -	No F0 expression
HRSV F0(fixed) ΔCS	delete entire CS	++ / -	doesn't express well
HRSV F0 (fixed) w/ ΔCS BV SP, Indo TMCT+16AA	delete CS, replace HRSV SP with BV SP, swap HRSV TMCT with Indo HA TMCT,+ upstream 16AA	++/-	VLP assemble efficient with Indo M1 poor

FIGURE 16c

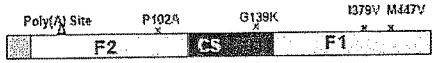
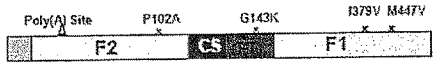
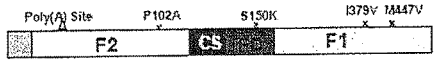
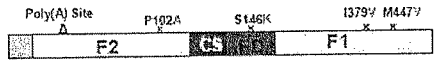
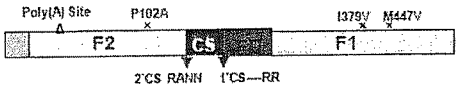
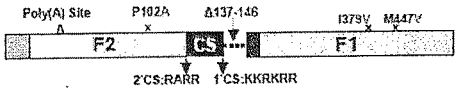
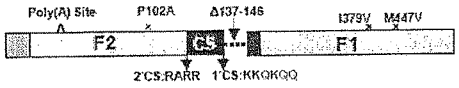
	Clone Name	Description	WB/Coomassie	Conclusion
	HRSV F0 (541) W/ BRSV F0 CT	HRSV F0 CT replaced by BRSV F0 CT	+++/-	Intracellular level is similar to 541, but inhibit BRSV M when co-infection. VLP yield is not as good as 541
	HRSV F0(541)+BRSV M	double genes tandem	F+++, M+++/ F-, M++	Both intracellular and VLP yield is better than 541 co-infection with BRSV M
	HRSV F0 (541) W/BRSV F0 CT+BRSV M	double genes tandem	F+++, M+++ F-, M++	Both intracellular and VLP yield is better than co-infection, inhibition of BRSV M solved
	HRSV F0 FD(G139K)	introduce G139K Point mutation (G139K) into Fusion domian	++/ -	FD(G139K) doesn't improve F0 expression
	HRSV F0 FD(G143K)	introduce G143K Point mutation (G139K) into Fusion domian	++/ -	FD(G143K) doesn't improve F0 expression
	HRSV F0 FD(S150K)	introduce S150K Point mutation (G139K) into Fusion domian	++/ -	FD(S150K) doesn't improve F0 expression
	HRSV F0 FD(S153K)	introduce S153K Point mutation (G139K) into Fusion domian	++/ -	FD(S153K) doesn't improve F0 expression
	HRSV F0 FD(S146K)	introduce S146K Point mutation (G139K) into Fusion domian	++/ -	FD(S146K) doesn't improve F0 expression
	HRSV F0 CS mut	delete 4AA in 1'CS, change 2'CS from RARR to RANN	++/ -	very poor F0 expression
	HRSV F0 CS mut (622)	F0 Fusion domain partial deletion(10AA) Intact Cleavage Site	++++/ +++	excellent F0 intracellular expression, strong band on coomassie gel
	HRSV F0 CS mut (683)	F0 Fusion domain partial deletion(10AA) Intact Cleavage Site	++++/ ++++	excellent F0 intracellular expression, strong band on coomassie gel

FIGURE 16d

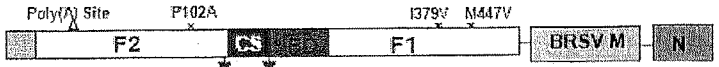
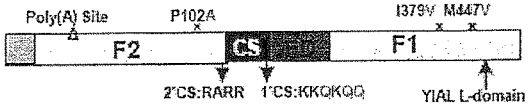
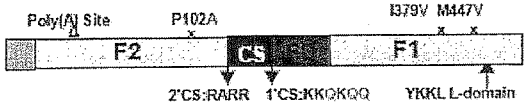
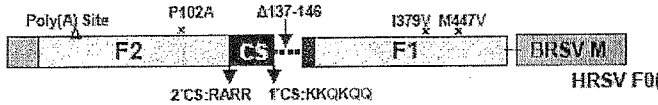
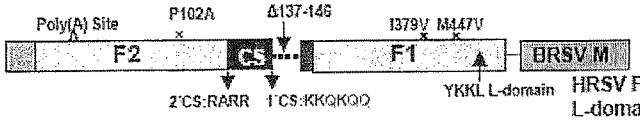
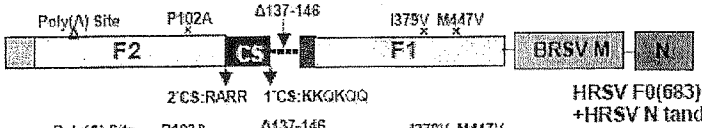
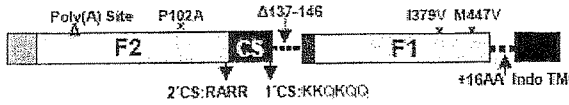
	Clone Name	Description	WB/Coomassie	Conclusion
	HRSV F0(541)+BRSV M +HRSV N tandem	triple genes tandem	F+++, M+++/ F-, M++	rBV with triple genes has much better titer than double tandem and 541. VLP yield is better than double tandem co-infection N or 541 co-infection BRSV M, N
	541 W/ YIAL L-domain	Introduce YIAL L-domain into 541 TM	+++ / -	Introduced YIAL L-domain doesn't affect the intracellular expression of 541, doesn't improve the secretion of VLP when co-infection BRSV M, N
	541 W/ YKKL L-domain	Introduce YKKL L-domain into 541 TM	+++ / -	Introduced YKKL L-domain doesn't affect the intracellular expression of 541, but enhance the secretion of VLP 2~3 folds when co-infection BRSV M, N
	HRSV F0(683)+BRSV M tandem	double genes tandem	ongoing	ongoing
	HRSV F0(683) w YKKL L-domain +BRSV M tandem	double genes tandem	ongoing	ongoing
	HRSV F0(683)+BRSV M +HRSV N tandem	triple genes tandem	ongoing	ongoing
	HRSV F0(683) w/Indo TMCT +16AA	chimeric HRSV F0(683) with Indo HA TMCT+ upstream 16AA	ongoing	ongoing

FIGURE 17

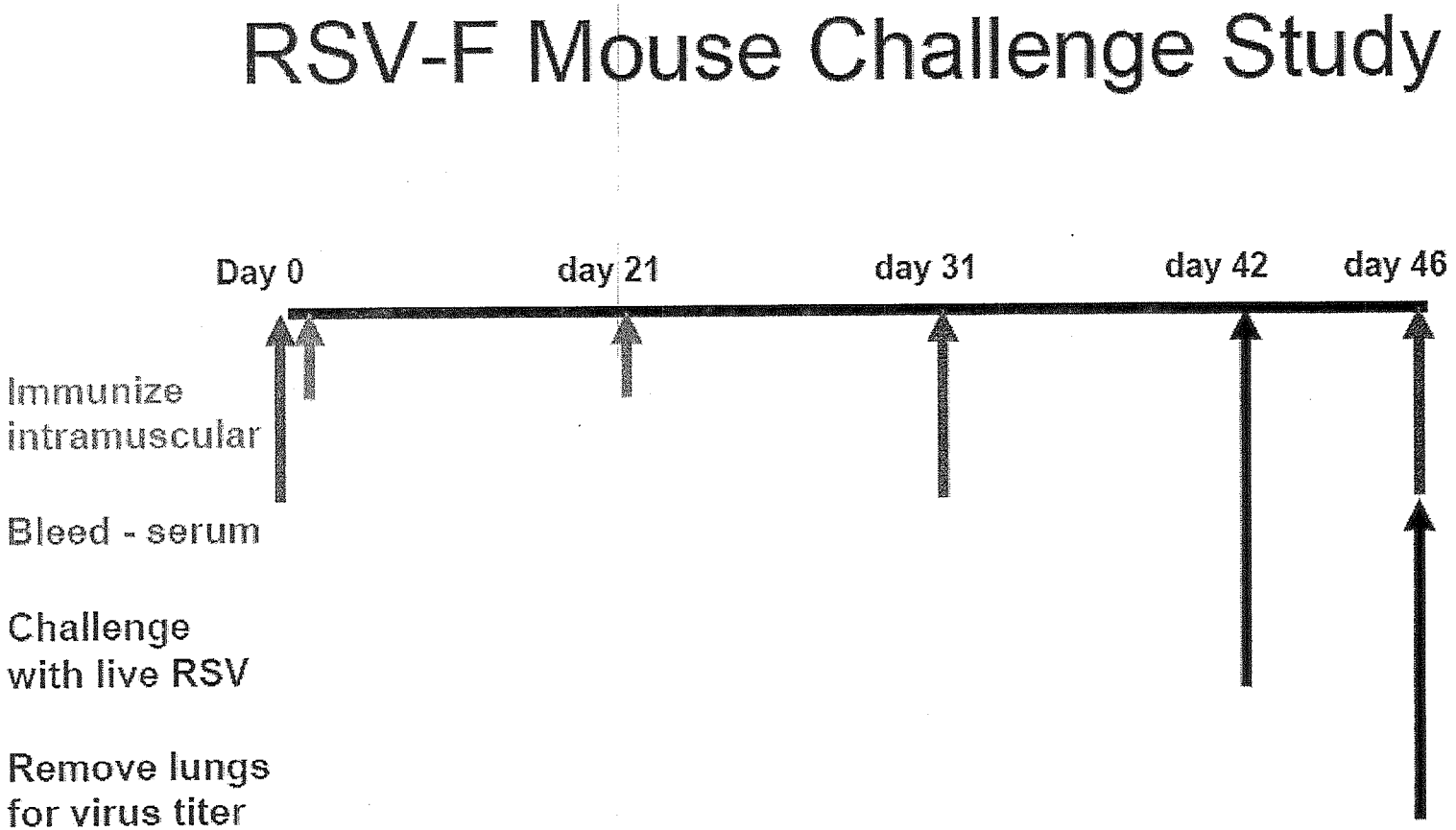

RSV-F Mouse Challenge Study
Day 0
day 21
day 31
day 42
day 46
Immunize
intramuscular
Bleed - serum
Challenge
with live RSV
Remove lungs
for virus titer

FIGURE 18

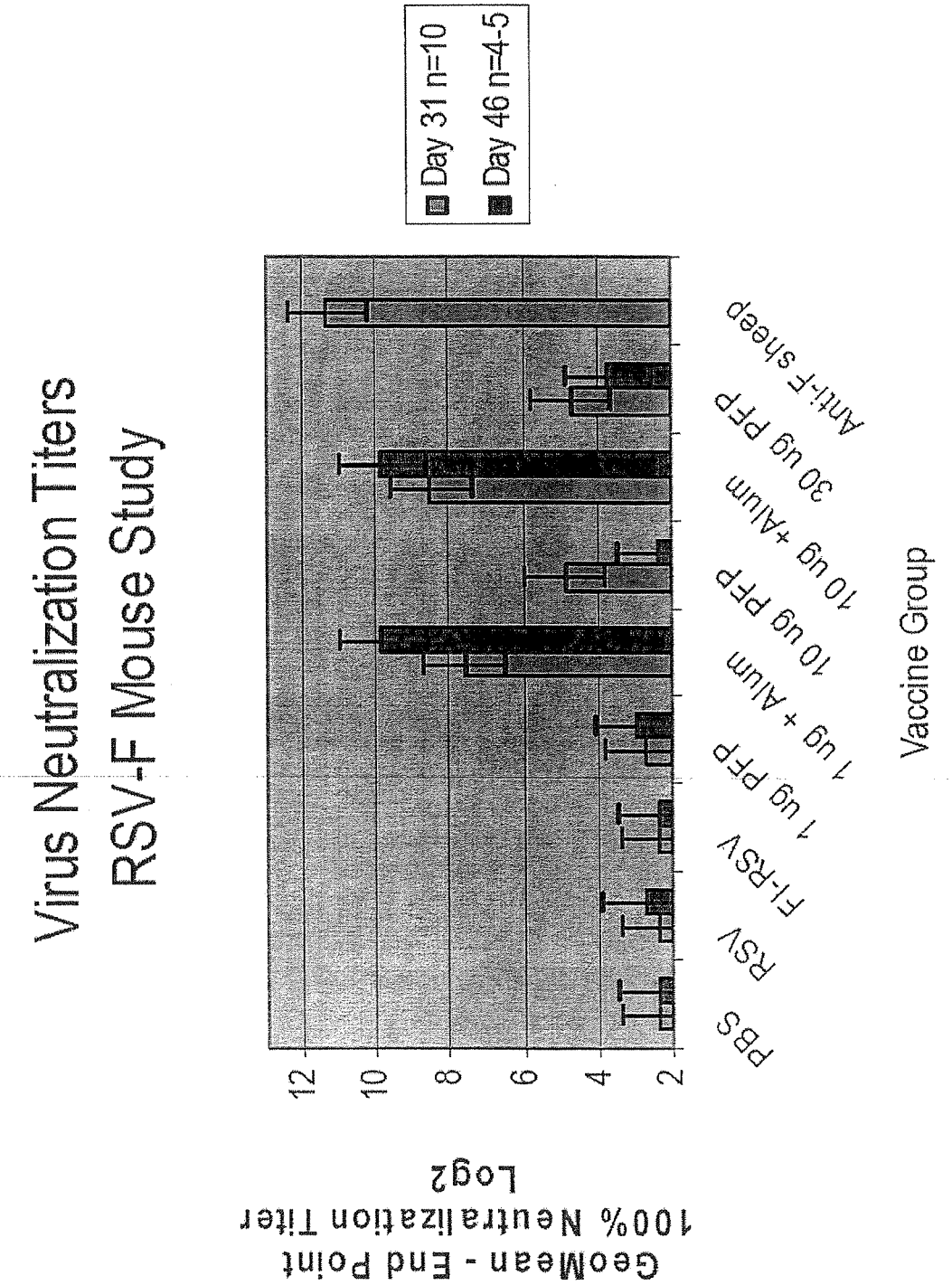

Virus Neutralization Titers
RSV-F Mouse Study
Day 31 n=10
Day 46 n=4-5
GeoMean - End Point
100% Neutralization Titer
Log2
12
10
8
6
4
2
PBS
RSV
F1-RSV
1 ug PFP
1 ug + Alum
10 ug PFP
10 ug +Alum
30 ug PFP
Anti-F sheep
Vaccine Group

FIGURE 19

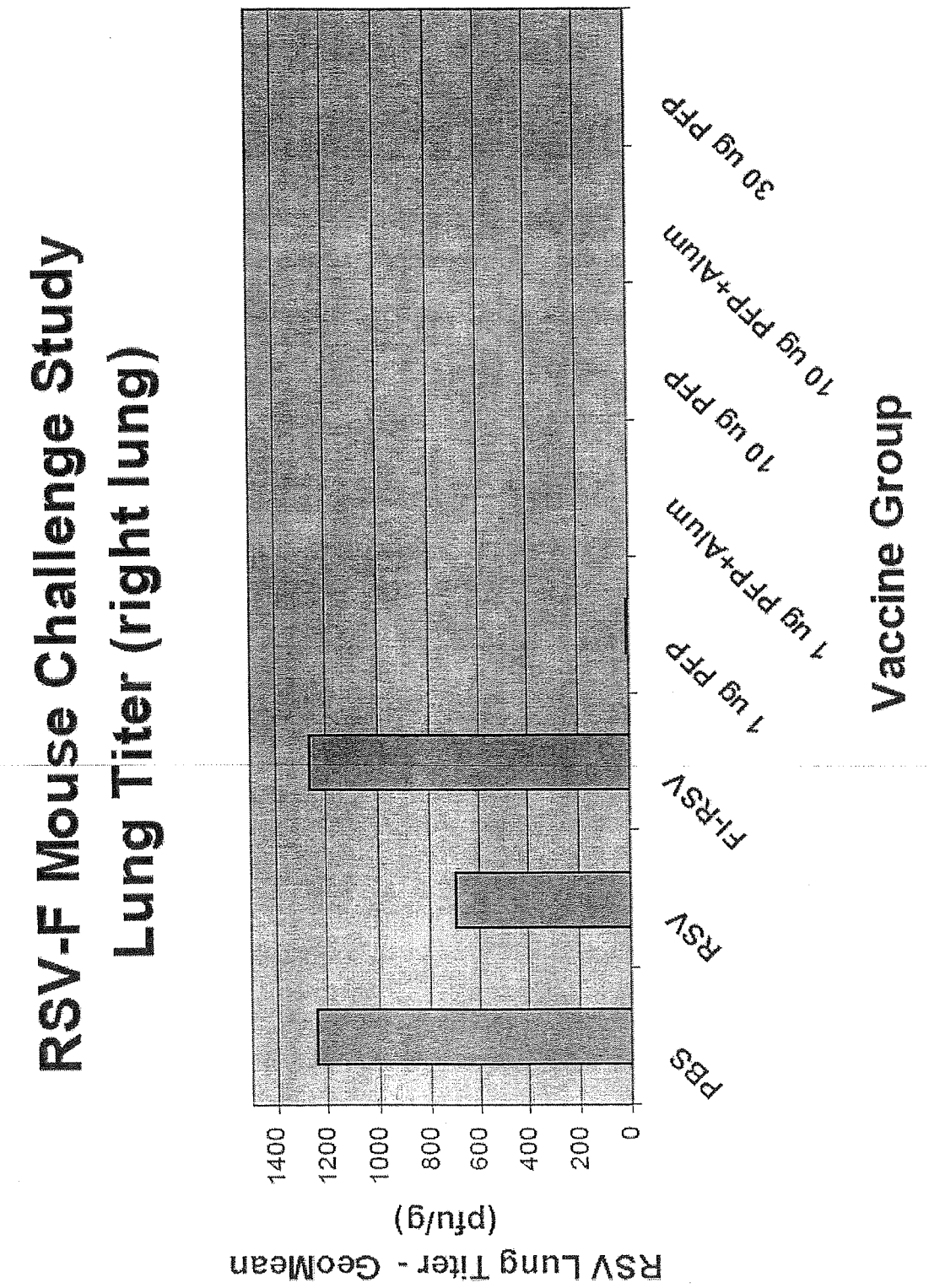

RSV-F Mouse Challenge Study
Lung Titer (right lung)
RSV Lung Titer - GeoMean
(pfu/g)
1400
1200
1000
800
600
400
200
0
PBS
RSV
F-RSV
1 ug PFP
1 ug PFP+Alum
10 ug PFP
10 ug PFP+Alum
30 ug PFP
Vaccine Group

FIGURE 20

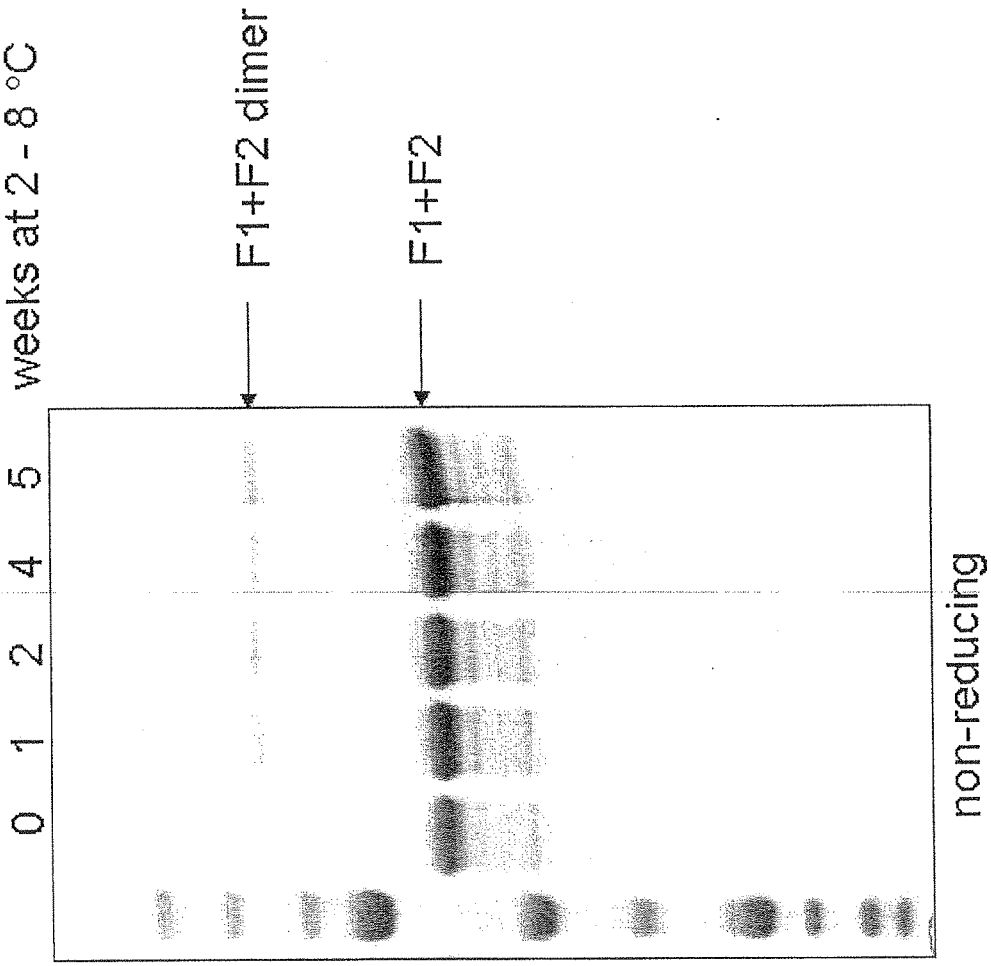
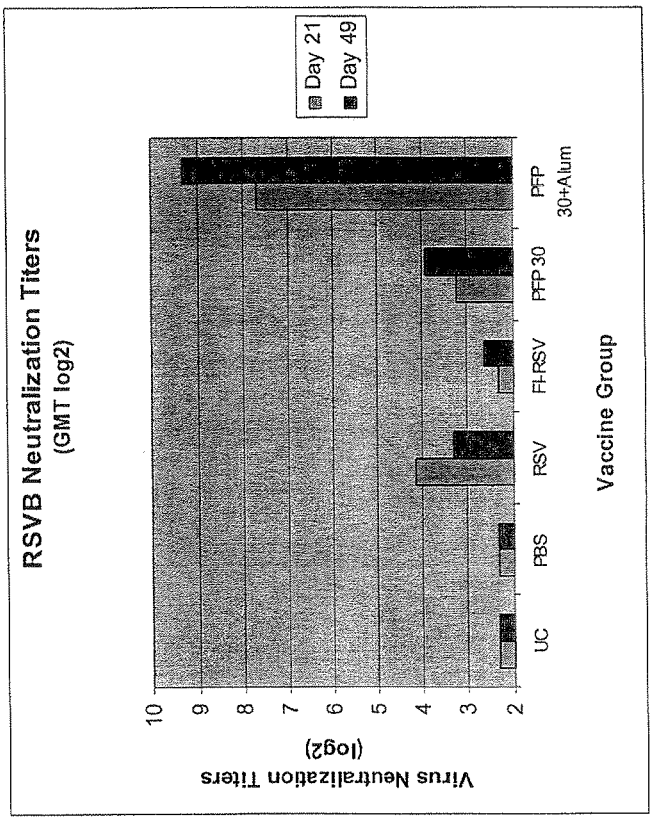


FIGURE 21


RSVB Neutralization Titers
(GMT log2)
Day 21
Day 49
Virus Neutralization Titers
(log2)
10
9
8
7
6
5
4
3
2
UC
PBS
RSV
FI-RSV
PFP 30
PFP 30+Alum
Vaccine Group

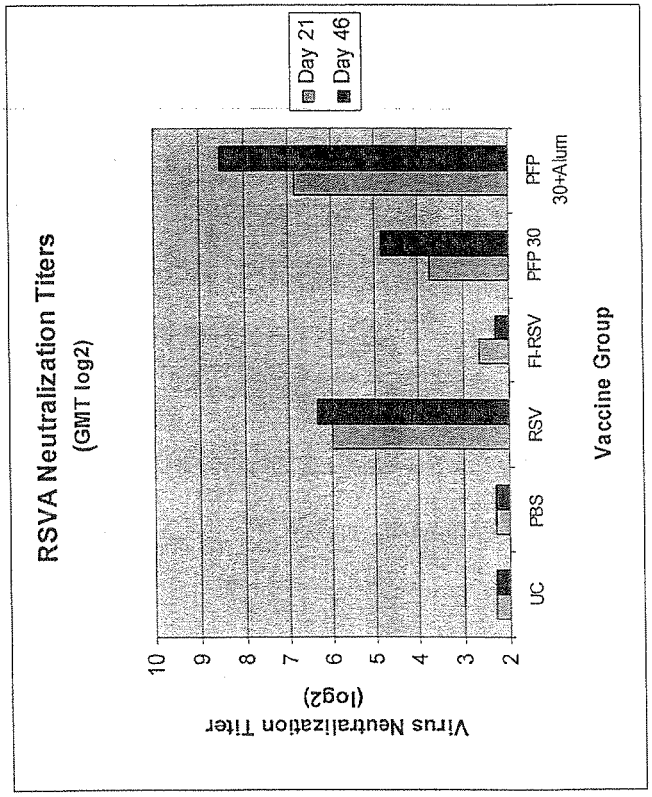
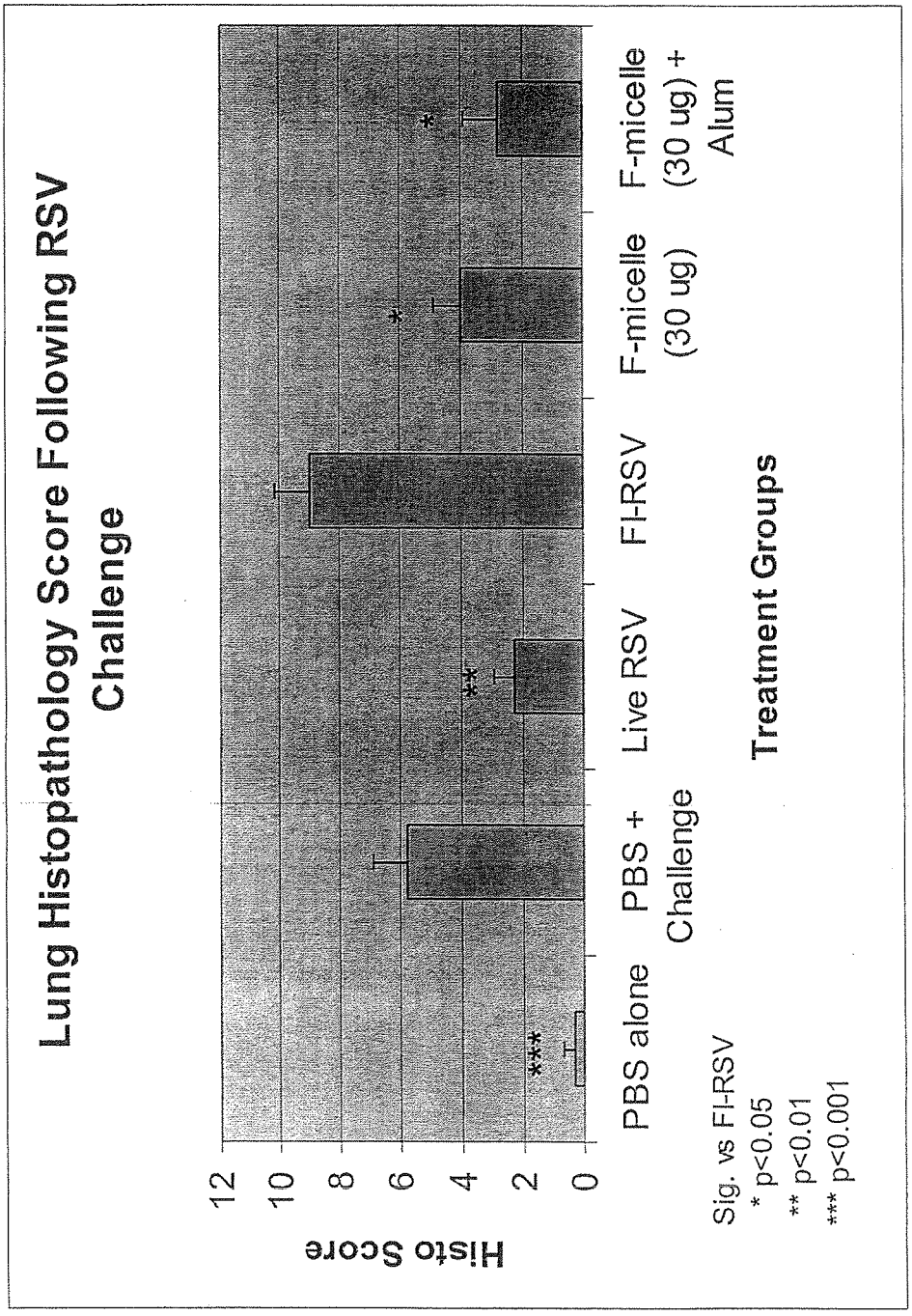

RSVA Neutralization Titers
(GMT log2)
Day 21
Day 46
Virus Neutralization Titer
(log2)
10
9
8
7
6
5
4
3
2
UC
PBS
RSV
FI-RSV
PFP 30
PFP 30+Alum
Vaccine Group

FIGURE 22


Lung Histopathology Score Following RSV Challenge
Histo Score
0
2
4
6
8
10
12
PBS alone
PBS + Challenge
Live RSV
FI-RSV
F-micelle (30 ug)
F-micelle (30 ug) + Alum
Treatment Groups
Sig. vs FI-RSV
* p<0.05
** p<0.01
*** p<0.001

SEQUENCE LISTING

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<151> 2009-04-14

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ccaccaacaa acaatcgagc cagaagagaa ctaccaaggt ttatgaatta tacactcaac 360

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ttatcaaatg gagttagtgt cttaaccagc aaagtgttag acctcaaaaa ctatatagat 600

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atagagttcc aacaaaagaa caacagacta ctagagatta ccagggaatt tagtgttaat 720

gcaggtgtaa ctacacctgt aagcacttac atgttaacta atagtgaatt attgtcatta 780

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gtacaattac cactatatgg tgttatagat acaccctgtt ggaaactaca cacatcccct 960

ctatgtacaa ccaacacaaa agaagggtcc aacatctgtt taacaagaac tgacagagga 1020

tggtactgtg acaatgcagg atcagtatct ttcttcccac aagctgaaac atgtaaagtt 1080

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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 Pro Thr Asn Asn Arg Ala Arg Arg Glu Leu Pro
100 105 110

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115 120 125

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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

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260 265 270

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

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340 345 350

Pro Gln Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp
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Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Lys Ser Asp Glu Leu
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agtacgacaa acattatgat cactaccatc attatcgtca ttatcgtgat ccttttgtca 1620

ctcattgctg taggtctgct tttgtactgt aaagcgaggt ctacgcccgt tacactcagc 1680

aaggatcaac tgtccggcat caataacatt gccttctcga attaa 1725

<210> 6
<211> 574
<212> PRT
<213> Artificial Sequence

<220>
<223> F protein 541

<400> 6

Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
1 5 10 15

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 Gln Lys Gln Gln 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
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
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
565 570

<210> 7
<211> 1695
<212> DNA
<213> Artificial Sequence

<220>
<223> F Protein 683

<400> 7
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tgctttgcat ccggtcagaa tattaccgaa gagttctacc aatctacttg tagcgctgtc 120

tcaaaaggct atctgtcggc cctccgtaca ggatggtaca cgagtgttat caccatcgaa 180

ttgtccaaca ttaaggagaa caagtgcaac ggtactgacg cgaaggtaaa gcttatcaaa 240

caggaactgg ataagtacaa gaacgcagtg acagagctcc aattgctgat gcagtctacc 300

cccgctacga ataaccgcgc taggagagaa cttccacgat tcatgaacta tactctcaat 360

aacgccaaaa agaccaacgt cacattgagc aaaaagcaga agcaacaggc tattgcgtcg 420

ggcgtagccg tgagtaaagt ccttcacttg gagggagaag ttaataagat caagtccgca 480

ctcctgtcta ctaacaaagc tgtggtcagc ttgtcaaacg gtgtatccgt gctgacctcg 540

aaggttcttg acctcaaaaa ttacatcgat aagcaattgc tgccgattgt caacaagcag 600

agttgttcta tcagcaatat tgagacggtg atcgagttcc aacagaaaaa caacagactc 660

ctggaaatca cacgtgagtt ttcagtaaat gccggcgtta ctacccccgt ctccacgtac 720

atgcttacaa actcggaatt gctcagtctg attaacgaca tgcctatcac taatgatcag 780

aagaagctta tgtctaacaa cgtgcaaatt gtccgccagc aaagctattc catcatgtca 840

atcattaaag aggaagtgtt ggcgtacgta gttcagctcc cactgtacgg agtcatcgac 900

accccgtgct ggaagcttca tacctcgccc ttgtgtacga caaatactaa agagggttct 960

aacatttgcc tcaccaggac ggatcgaggc tggtattgcg ataacgctgg aagtgtgagc 1020

ttcttccctc aagcagaaac atgtaaggta cagtccaata gagtttttg cgacactatg 1080

aactcactga cccttccatc tgaggtcaat ttgtgtaacg tcgatatctt caacccgaag 1140

tacgactgca aaattatgac gtccaagaca gatgtgtcga gtagcgtaat cacttcactc 1200

ggtgccatcg tttcttgcta cggcaagacc aaatgtacgg cttccaataa gaaccgtgga 1260

attatcaaaa cattctcgaa cggttgcgac tatgtcagca ataagggcgt ggacactgtg 1320

agtgtaggaa acaccctgta ctacgttaac aagcaagaag gtaaatcact gtatgtcaag 1380

ggcgagccca ttatcaattt ttacgatcct cttgtgttcc catccgacga gttcgatgcg 1440

tctatcagcc aggtaaacga aaagattaac cagtccttgg catttatccg caaatcggac 1500

gagctcctgc acaatgttaa cgccggaaag agtacgacaa acattatgat cactaccatc 1560

attatcgtca ttatcgtgat ccttttgtca ctcattgctg taggtctgct tttgtactgt 1620

aaagcgaggt ctacgcccgt tacactcagc aaggatcaac tgtccggcat caataacatt 1680

gccttctcga attaa 1695

<210> 8
<211> 564
<212> PRT
<213> Artificial Sequence

<220>
<223> F protein 683

<400> 8

Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
1 5 10 15

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 Gln Lys Gln Gln Ala Ile Ala Ser Gly Val Ala Val
130 135 140

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

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

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

Leu Leu Pro Ile Val Asn Lys Gln Ser Cys Ser Ile Ser Asn Ile Glu
195 200 205

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

Arg Glu Phe Ser Val Asn Ala Gly Val Thr Thr Pro Val Ser Thr Tyr

225 230 235 240

Met Leu Thr Asn Ser Glu Leu Leu Ser Leu Ile Asn Asp Met Pro Ile
245 250 255

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

Gln Gln Ser Tyr Ser Ile Met Ser Ile Ile Lys Glu Glu Val Leu Ala
275 280 285

Tyr Val Val Gln Leu Pro Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp
290 295 300

Lys Leu His Thr Ser Pro Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser
305 310 315 320

Asn Ile Cys Leu Thr Arg Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala
325 330 335

Gly Ser Val Ser Phe Phe Pro Gln Ala Glu Thr Cys Lys Val Gln Ser
340 345 350

Asn Arg Val Phe Cys Asp Thr Met Asn Ser Leu Thr Leu Pro Ser Glu
355 360 365

Val Asn Leu Cys Asn Val Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys
370 375 380

Ile Met Thr Ser Lys Thr Asp Val Ser Ser Ser Val Ile Thr Ser Leu
385 390 395 400

Gly Ala Ile Val Ser Cys Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn
405 410 415

Lys Asn Arg Gly Ile Ile Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val
420 425 430

Ser Asn Lys Gly Val Asp Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr
435 440 445

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

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

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

Arg Lys Ser Asp Glu Leu Leu His Asn Val Asn Ala Gly Lys Ser Thr

500 505 510

Thr Asn Ile Met Ile Thr Thr Ile Ile Ile Val Ile Ile Val Ile Leu
515 520 525

Leu Ser Leu Ile Ala Val Gly Leu Leu Leu Tyr Cys Lys Ala Arg Ser
530 535 540

Thr Pro Val Thr Leu Ser Lys Asp Gln Leu Ser Gly Ile Asn Asn Ile
545 550 555 560

Ala Phe Ser Asn

<210> 9
<211> 1695
<212> DNA
<213> Artificial Sequence

<220>
<223> F protein 622

<400> 9
atggagctgc tcatcttgaa ggctaacgcc attaccacta tccttacagc ggtgacgttc 60

tgctttgcat ccggtcagaa tattaccgaa gagttctacc aatctacttg tagcgctgtc 120

tcaaaaggct atctgtcggc cctccgtaca ggatggtaca cgagtgttat caccatcgaa 180

ttgtccaaca ttaaggagaa caagtgcaac ggtactgacg cgaaggtaaa gcttatcaaa 240

caggaactgg ataagtacaa gaacgcagtg acagagctcc aattgctgat gcagtctacc 300

cccgctacga ataaccgcgc taggagagaa cttccacgat tcatgaacta tactctcaat 360

aacgccaaaa agaccaacgt cacattgagc aaaaagcgta agcgcagggc tattgcgtcg 420

ggcgtagccg tgagtaaagt ccttcacttg gagggagaag ttaataagat caagtccgca 480

ctcctgtcta ctaacaaagc tgtggtcagc ttgtcaaacg gtgtatccgt gctgacctcg 540

aaggttcttg acctcaaaaa tcacatcgat aagcaattgc tgccgattgt caacaagcag 600

agttgttcta tcagcaatat tgagacggtg atcgagttcc aacagaaaaa caacagactc 660

ctggaaatca cacgtgagtt ttcagtaaat gccggcgtta ctacccccgt ctccacgtac 720

atgcttacaa actcggaatt gctcagtctg attaacgaca tgcctatcac taatgatcag 780

aagaagctta tgtctaacaa cgtgcaaatt gtccgccagc aaagctattc catcatgtca 840

atcattaaag aggaagtgtt ggcgtacgta gttcagctcc cactgtacgg agtcatcgac 900

accccgtgct ggaagcttca tacctcgccc ttgtgtacga caaatactaa agagggttct 960

aacatttgcc tcaccaggac ggatcgaggc tggtattgcg ataacgctgg aagtgtgagc 1020

ttcttccctc aagcagaaac atgtaaggta cagtccaata gagtttttg cgacactatg 1080

aactcactga cccttccatc tgaggtcaat ttgtgtaacg tcgatatctt caacccgaag 1140

tacgactgca aaattatgac gtccaagaca gatgtgtcga gtagcgtaat cacttcactc 1200

ggtgccatcg tttcttgcta cggcaagacc aaatgtacgg cttccaataa gaaccgtgga 1260

attatcaaaa cattctcgaa cggttgcgac tatgtcagca ataagggcgt ggacactgtg 1320

agtgtaggaa acaccctgta ctacgttaac aagcaagaag gtaaatcact gtatgtcaag 1380

ggcgagccca ttatcaattt ttacgatcct cttgtgttcc catccgacga gttcgatgcg 1440

tctatcagcc aggtaaacga aaagattaac cagtccttgg catttatccg caaatcggac 1500

gagctcctgc acaatgttaa cgccggaaag agtacgacaa acattatgat cactaccatc 1560

attatcgtca ttatcgtgat ccttttgtca ctcattgctg taggtctgct tttgtactgt 1620

aaagcgaggt ctacgcccgt tacactcagc aaggatcaac tgtccggcat caataacatt 1680

gccttctcga attaa 1695

<210> 10
<211> 564
<212> PRT
<213> Artificial Sequence

<220>
<223> F protein 622

<400> 10

Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
1 5 10 15

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 Ala Ile Ala Ser Gly Val Ala Val
130 135 140

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

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

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

Leu Leu Pro Ile Val Asn Lys Gln Ser Cys Ser Ile Ser Asn Ile Glu
195 200 205

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

Arg Glu Phe Ser Val Asn Ala Gly Val Thr Thr Pro Val Ser Thr Tyr
225 230 235 240

Met Leu Thr Asn Ser Glu Leu Leu Ser Leu Ile Asn Asp Met Pro Ile
245 250 255

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

Gln Gln Ser Tyr Ser Ile Met Ser Ile Ile Lys Glu Glu Val Leu Ala
275 280 285

Tyr Val Val Gln Leu Pro Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp
290 295 300

Lys Leu His Thr Ser Pro Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser
305 310 315 320

Asn Ile Cys Leu Thr Arg Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala
325 330 335

Gly Ser Val Ser Phe Phe Pro Gln Ala Glu Thr Cys Lys Val Gln Ser
340 345 350

Asn Arg Val Phe Cys Asp Thr Met Asn Ser Leu Thr Leu Pro Ser Glu
355 360 365

Val Asn Leu Cys Asn Val Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys
370 375 380

Ile Met Thr Ser Lys Thr Asp Val Ser Ser Ser Val Ile Thr Ser Leu
385 390 395 400

Gly Ala Ile Val Ser Cys Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn
405 410 415

Lys Asn Arg Gly Ile Ile Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val
420 425 430

Ser Asn Lys Gly Val Asp Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr
435 440 445

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

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

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

Arg Lys Ser Asp Glu Leu Leu His Asn Val Asn Ala Gly Lys Ser Thr
500 505 510

Thr Asn Ile Met Ile Thr Thr Ile Ile Ile Val Ile Ile Val Ile Leu
515 520 525

Leu Ser Leu Ile Ala Val Gly Leu Leu Leu Tyr Cys Lys Ala Arg Ser
530 535 540

Thr Pro Val Thr Leu Ser Lys Asp Gln Leu Ser Gly Ile Asn Asn Ile
545 550 555 560

Ala Phe Ser Asn

<210> 11
<211> 771
<212> DNA
<213> Bovine respiratory syncytial virus

<400> 11
atggagacat acgtgaacaa actccatgaa ggatcaactt acacagctgc tgttcagtac 60

aatgtcatag aaaaagatga tgatcctgca tctctcacaa tatgggttcc tatgttccaa 120

tcatccatct ctgctgattt gcttataaaa gaactaatca atgtgaacat attagttcga 180

caaatttcta ctctgaaagg tccttcattg aagattatga taaactcaag aagtgctgta 240

ctagcccaaa tgcccagcaa atttaccata agtgcaaatg tatcattgga tgaacgaagc 300

aaattagcat atgacataac tactccttgt gaaattaagg cttgtagttt aacatgttta 360

aaggtgaaaa atatgctcac aactgtgaaa gatctcacca tgaaaacatt caatcctacc 420

catgagatca ttgcactgtg tgaatttgaa aatatcatga catccaaaag agttgttata 480

ccaactttct taaggtcaat caatgtaaaa gcaaaggatt tggactcact agagaatata 540

gctaccacag agttcaaaaa tgccatcact aatgctaaaa ttatacctta tgctgggttg 600

gtattagtta tcactgtaac tgacaataaa ggggcattca agtacattaa accacaaagt 660

caatttatag tagatcttgg tgcatatcta gagaaagaga gcatatatta tgtaactaca 720

aattggaaac acacggccac taaattctcc attaagccta tagaggactg a 771

<210> 12
<211> 256
<212> PRT
<213> Bovine respiratory syncytial virus

<400> 12

Met Glu Thr Tyr Val Asn Lys Leu His Glu Gly Ser Thr Tyr Thr Ala
1 5 10 15

Ala Val Gln Tyr Asn Val Ile Glu Lys Asp Asp Asp Pro Ala Ser Leu
20 25 30

Thr Ile Trp Val Pro Met Phe Gln Ser Ser Ile Ser Ala Asp Leu Leu
35 40 45

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

Leu Lys Gly Pro Ser Leu Lys Ile Met Ile Asn Ser Arg Ser Ala Val
65 70 75 80

Leu Ala Gln Met Pro Ser Lys Phe Thr Ile Ser Ala Asn Val Ser Leu
85 90 95

Asp Glu Arg Ser Lys Leu Ala Tyr Asp Ile Thr Thr Pro Cys Glu Ile
100 105 110

Lys Ala Cys Ser Leu Thr Cys Leu Lys Val Lys Asn Met Leu Thr Thr
115 120 125

Val Lys Asp Leu Thr Met Lys Thr Phe Asn Pro Thr His Glu Ile Ile
130 135 140

Ala Leu Cys Glu Phe Glu Asn Ile Met Thr Ser Lys Arg Val Val Ile
145 150 155 160

Pro Thr Phe Leu Arg Ser Ile Asn Val Lys Ala Lys Asp Leu Asp Ser
165 170 175

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

Lys Ile Ile Pro Tyr Ala Gly Leu Val Leu Val Ile Thr Val Thr Asp
195 200 205

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

Asp Leu Gly Ala Tyr Leu Glu Lys Glu Ser Ile Tyr Tyr Val Thr Thr
225 230 235 240

Asn Trp Lys His Thr Ala Thr Lys Phe Ser Ile Lys Pro Ile Glu Asp
245 250 255

<210> 13
<211> 771
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon Optimized Bovine RSV M

<400> 13
atggagactt acgtgaacaa gctgcacgag ggttccacct acaccgctgc tgtgcagtac 60

aacgtgatcg agaaggacga cgaccccgct tccctgacca tctgggtgcc catgttccag 120

tcctccatct ccgctgacct gctgatcaag gagctgatca acgtcaacat cctcgtgcgt 180

cagatctcca ccctgaaggg tcccagcctg aagatcatga tcaactcccg ttccgctgtg 240

ctggctcaga tgccctccaa gttcaccatc tccgccaacg tgtccctgga cgagcgttcc 300

aagctggctt acgacatcac cacccctgc gagatcaagg cttgctccct gacctgcctg 360

aaggtcaaga acatgctgac caccgtgaag gacctgacca tgaagacctt caaccccacc 420

cacgagatca tcgctctgtg cgagttcgag aacatcatga cctccaagcg tgtggtcatc 480

cccaccttcc tccgctccat caacgtgaag gctaaggacc tggactccct cgagaacatc 540

gctaccaccg agttcaagaa cgctatcacc aacgctaaga tcatccctta cgctggcctg 600

gtgctggtca tcaccgtgac cgacaacaag ggcgctttca agtacatcaa gccccagtcc 660

cagttcatcg tggacctggg cgcttacctc gagaaggagt ccatctacta cgtcaccacc 720

aactggaagc acaccgctac caagttctcc atcaagccca tcgaggacta a 771

<210> 14
<211> 256
<212> PRT
<213> Artificial Sequence

<220>
<223> Codon Optimized Bovine RSV M

<400> 14

Met Glu Thr Tyr Val Asn Lys Leu His Glu Gly Ser Thr Tyr Thr Ala
1 5 10 15

Ala Val Gln Tyr Asn Val Ile Glu Lys Asp Asp Asp Pro Ala Ser Leu
20 25 30

Thr Ile Trp Val Pro Met Phe Gln Ser Ser Ile Ser Ala Asp Leu Leu
35 40 45

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

Leu Lys Gly Pro Ser Leu Lys Ile Met Ile Asn Ser Arg Ser Ala Val

65 70 75 80

Leu Ala Gln Met Pro Ser Lys Phe Thr Ile Ser Ala Asn Val Ser Leu
85 90 95

Asp Glu Arg Ser Lys Leu Ala Tyr Asp Ile Thr Thr Pro Cys Glu Ile
100 105 110

Lys Ala Cys Ser Leu Thr Cys Leu Lys Val Lys Asn Met Leu Thr Thr
115 120 125

Val Lys Asp Leu Thr Met Lys Thr Phe Asn Pro Thr His Glu Ile Ile
130 135 140

Ala Leu Cys Glu Phe Glu Asn Ile Met Thr Ser Lys Arg Val Val Ile
145 150 155 160

Pro Thr Phe Leu Arg Ser Ile Asn Val Lys Ala Lys Asp Leu Asp Ser
165 170 175

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

Lys Ile Ile Pro Tyr Ala Gly Leu Val Leu Val Ile Thr Val Thr Asp
195 200 205

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

Asp Leu Gly Ala Tyr Leu Glu Lys Glu Ser Ile Tyr Tyr Val Thr Thr
225 230 235 240

Asn Trp Lys His Thr Ala Thr Lys Phe Ser Ile Lys Pro Ile Glu Asp
245 250 255

<210> 15
<211> 1176
<212> DNA
<213> respiratory syncytial virus

<400> 15
atggctctta gcaaagtcaa gttgaatgat acactcaaca aagatcaact tctgtcatcc 60

agcaaataca ccatccaacg gagcacagga gatagtattg atactcctaa ttatgatgtg 120

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

ctacccaagg acatagccaa cagcttctat gaagtgtttg aaaaacatcc ccactttata 660

gatgtttttg ttcattttgg tatagcacaa 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

<210> 16
<211> 391
<212> PRT
<213> respiratory syncytial virus

<400> 16

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

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> 17
<211> 1176
<212> DNA

<213> Artificial Sequence

<220>
<223> Codon Optimized RSV N

<400> 17
atggctctgt ccaaggtcaa gctgaacgac accctgaaca aggaccagct gctgtcctcc 60

tccaagtaca ccatccagcg ttccaccggt gactccatcg acacccccaa ctacgacgtg 120

cagaagcaca tcaacaagct gtgcggcatg ctgctgatca ccgaggacgc taaccacaag 180

ttcaccggtc tgatcggcat gctgtacgct atgtcccgtc tgggtcgtga ggacaccatc 240

aagatcctgc gtgacgctgg ttaccacgtg aaggctaacg gtgtcgacgt gaccacccac 300

cgtcaggaca tcaacggcaa ggagatgaag ttcgaggtcc tgaccctggc ttccctgacc 360

accgagatcc agatcaacat cgagatcgag tcccgtaagt cctacaagaa gatgctgaag 420

gagatgggcg aggtcgcccc cgagtaccgt cacgactccc ccgactgcgg catgatcatc 480

ctgtgcatcg ctgctctcgt catcaccaag ctggctgctg gtgaccgttc cggtctgacc 540

gctgtgatcc gtcgtgctaa caacgtgctg aagaacgaga tgaagcgcta caagggtctg 600

ctgcccaagg acatcgctaa cagcttctac gaggtgttcg agaagcaccc ccacttcatc 660

gacgtgttcg tgcacttcgg tatcgctcag tcctccaccc gtggtggttc ccgtgtggag 720

ggcatcttcg ctggtctgtt catgaacgct tacggtgctg gccaggtcat gctgcgttgg 780

ggtgtgctgg ctaagtccgt gaagaacatc atgctgggtc acgcttccgt gcaggctgag 840

atggagcagg tggtggaggt gtacgagtac gctcagaagc tgggcggcga ggctggtttc 900

taccacatcc tgaacaaccc caaggcttcc ctgctgtccc tgacccagtt cccccacttc 960

tcctccgtgg tgctgggtaa cgctgctggt ctgggtatca tgggcgagta ccgtggcacc 1020

ccccgtaacc aggacctgta cgacgctgct aaggcttacg ccgagcagct caaggagaac 1080

ggcgtcatca actactccgt gctggacctg accgctgagg agctggaggc tatcaagcac 1140

cagctgaacc ccaaggacaa cgacgtggag ctgtaa 1176

<210> 18
<211> 391
<212> PRT
<213> Artificial Sequence

<220>
<223> Codon Optimized RSV N

<400> 18

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

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> 19
<211> 1725
<212> DNA
<213> Artificial Sequence

<220>
<223> F protein 368

<400> 19
atggagctgc tcatcttgaa ggctaacgcc attaccacta tccttacagc ggtgacgttc 60

tgctttgcat ccggtcagaa tattaccgaa gagttctacc aatctacttg tagcgctgtc 120

tcaaaaggct atctatcggc cttacgtaca ggatggtaca cgagtgttat caccatcgaa 180

ctgtccaaca ttaaggagaa taaatgcaac ggtactgacg cgaaggtaaa gctcatcaaa 240

caggaattgg ataagtacaa gaacgcagtg acagagcttc aactgctaat gcagtctacc 300

ccccctacga ataaccgcgc taggagagaa ctcccacgat tcatgaacta tactttaaat 360

aacgccaaaa agaccaacgt cacattgagc aaaaagcgta agcgcaggtt tctgggcttc 420

cttctcggag ttggttcagc tattgcgtcg ggcgtagccg tgagtaaagt cttgcacctg 480

gagggagaag ttaataagat caagtccgca ctcctgtcta ctaacaaagc tgtggtcagc 540

ctatcaaacg gtgtatccgt gttaacctcg aaggttcttg acttgaaaaa ttacatcgat 600

aagcaactcc tgccgattgt caacaagcag agttgttcta tcagcaatat tgagacggtg 660

atcgagttcc aacagaaaaa caacagattg ctggaaatca cacgtgagtt ttcagtaaat 720

gccggcgtta ctacccccgt ctccacgtac atgctaacaa actcggaatt acttagtctc 780

attaacgaca tgcctatcac taatgatcag aagaagttga tgtctaacaa cgtgcaaatt 840

gtccgccagc aaagctattc catcatgtca atcattaaag aggaagtgct ggcgtacgta 900

gttcagctcc cactgtacgg agtcatcgac accccgtgct ggaagctaca tacctcgccc 960

ttatgtacga caaatactaa agagggttct aacatttgcc ttaccaggac ggatcgaggc 1020

tggtattgcg ataacgctgg aagtgtgagc ttcttccctc aagcagaaac atgtaaggta 1080

cagtccaata gagtttttg cgacactatg aactcattga ccctcccatc tgagatcaat 1140

ctgtgtaacg tcgatatctt caacccgaag tacgactgca aaattatgac gtccaagaca 1200

gatgtgtcga gtagcgtaat cacttcacta ggtgccatcg tttcttgcta cggcaagacc 1260

aaatgtacgg cttccaataa gaaccgtgga attatcaaaa cattctcgaa cggttgcgac 1320

tatgtcagca ataagggcat ggacactgtg agtgtaggaa acaccttata ctacgttaac 1380

aagcaagaag gtaaatcact ttatgtcaag ggcgagccca ttatcaattt ttacgatcct 1440

ttggtgttcc catccgacga gttcgatgcg tctatcagcc aggtaaacga aaagattaac 1500

cagtccctcg catttatccg caaatcggac gagctgctac acaatgttaa cgccggaaag 1560

agtacgacaa acattatgat cactaccatc attatcgtca ttatcgtgat ccttttgtca 1620

ctcattgctg taggtctgtt actatactgt aaagcgaggt ctacgcccgt tacacttagc 1680

aaggatcaat tgtccggcat caataacatt gccttctcga attaa 1725

<210> 20
<211> 574
<212> PRT
<213> Artificial Sequence

<220>
<223> F protein 368

<400> 20

Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
1 5 10 15

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 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
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
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
545 550 555 560

Lys Asp Gln Leu Ser Gly Ile Asn Asn Ile Ala Phe Ser Asn
565 570

<210> 21
<211> 560
<212> PRT
<213> Artificial Sequence

<220>
<223> F protein 623

<400> 21

Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
1 5 10 15

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 Asn Asn 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 Arg Arg Ala Ile Ala Ser Gly Val Ala Val Ser Lys Val Leu
    130                 135                 140

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

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

Lys Val Leu Asp Leu Lys Asn His Ile Asp Lys Gln Leu Leu Pro Ile
            180                 185                 190

Val Asn Lys Gln Ser Cys Ser Ile Ser Asn Ile Glu Thr Val Ile Glu
        195                 200                 205

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

Val Asn Ala Gly Val Thr Thr Pro Val Ser Thr Tyr Met Leu Thr Asn
225                 230                 235                 240

Ser Glu Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln
                245                 250                 255

Lys Lys Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr
            260                 265                 270

Ser Ile Met Ser Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln
        275                 280                 285

Leu Pro Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr
    290                 295                 300

Ser Pro Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu
305                 310                 315                 320

Thr Arg Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser
                325                 330                 335

Phe Phe Pro Gln Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe
            340                 345                 350
```

Cys Asp Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Val Asn Leu Cys
355 360 365

Asn Val Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser
370 375 380

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

Ser Cys Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly
405 410 415

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

Val Asp Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln
435 440 445

Glu Gly Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr
450 455 460

Asp Pro Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln
465 470 475 480

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

Glu Leu Leu His Asn Val Asn Ala Gly Lys Ser Thr Thr Asn Ile Met
500 505 510

Ile Thr Thr Ile Ile Ile Val Ile Ile Val Ile Leu Leu Ser Leu Ile
515 520 525

Ala Val Gly Leu Leu Leu Tyr Cys Lys Ala Arg Ser Thr Pro Val Thr
530 535 540

Leu Ser Lys Asp Gln Leu Ser Gly Ile Asn Asn Ile Ala Phe Ser Asn
545 550 555 560

<210> 22
<211> 252
<212> PRT
<213> Avian influenza virus

<400> 22

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
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<210> 23
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Secondary Cleavage Site

<400> 23

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Arg Ala Arg Arg
1
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<210> 24
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Primary Cleavage Site

<400> 24

Lys Lys Arg Lys Arg Arg
1 5

<210> 25
<211> 897
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon Optimized RSV G

<400> 25
atgtccaaga acaaagacca gcgtaccgct aagactctgg agcgcacatg ggatacgctc 60

aatcacttgc ttttcatctc tagctgcctg tacaaactca acttgaagtc agtggcccaa 120

attacccttt cgatcctggc gatgattatc agtacttccc tcatcattgc agctatcatt 180

tttatcgcct ctgcgaatca taaggtcaca cccacgaccg caatcattca ggacgctact 240

agccaaatca aaaacacaac ccctacgtat ttgactcaga acccacaact gggtatttca 300

ccgtcgaatc ccagtgaaat cacctcccag atcacaacta ttcttgcctc taccacgcct 360

ggcgttaaga gcacactcca atcaactacc gtaaagacga aaaacacaac taccacccag 420

acgcagccat ccaagccgac aactaaacaa aggcagaaca agccccttc gaagccaaat 480

aacgatttcc acttcgaggt gtttaacttc gtcccgtgta gtatctgctc taataacccc 540

acctgttggg ctatttgcaa aagaatccct aacaagaagc caggaaaaaa gacgacaact 600

aaacccacca agaagcctac gttgaaaaca actaagaagg acccgaaacc acaaaccacg 660

aagagcaaag aagttcccac aactaagcct accgaggaac cgacgatcaa tacaactaag 720

accaacatta tcacgacact gctcacttca aataccactg gtaacccaga gctgacctcc 780

cagatggaaa ccttccattc gacgagttct gagggcaacc ccagcccttc ccaagtatca 840

acaacttcgg aatacccatc tcagcccagt agccctccga ataccccacg acaataa 897

<210> 26
<211> 298
<212> PRT
<213> Artificial Sequence

<220>
<223> Codon Optimized RSV G

<400> 26

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
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

<210> 27
<211> 65
<212> PRT
<213> respiratory syncytial virus

<400> 27

Met Gly Asn Thr Ser Ile Thr Ile Glu Phe Thr Ser Lys Phe Trp Pro
1 5 10 15

Tyr Phe Thr Leu Ile His Met Ile Leu Thr Leu Ile Ser Leu Leu Ile
20 25 30

Ile Ile Thr Ile Met Ile Ala Ile Leu Asn Lys Leu Ser Glu His Lys
35 40 45

Thr Phe Cys Asn Asn Thr Leu Glu Leu Gly Gln Met His Gln Ile Asn
50 55 60

Thr
65

<210> 28
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Furin Recognition Site Mutation

<400> 28

Lys Lys Gln Lys Gln Gln
1 5

<210> 29
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Furin Recognition Site Mutation

<400> 29

Gly Arg Arg Gln Gln Arg
1 5