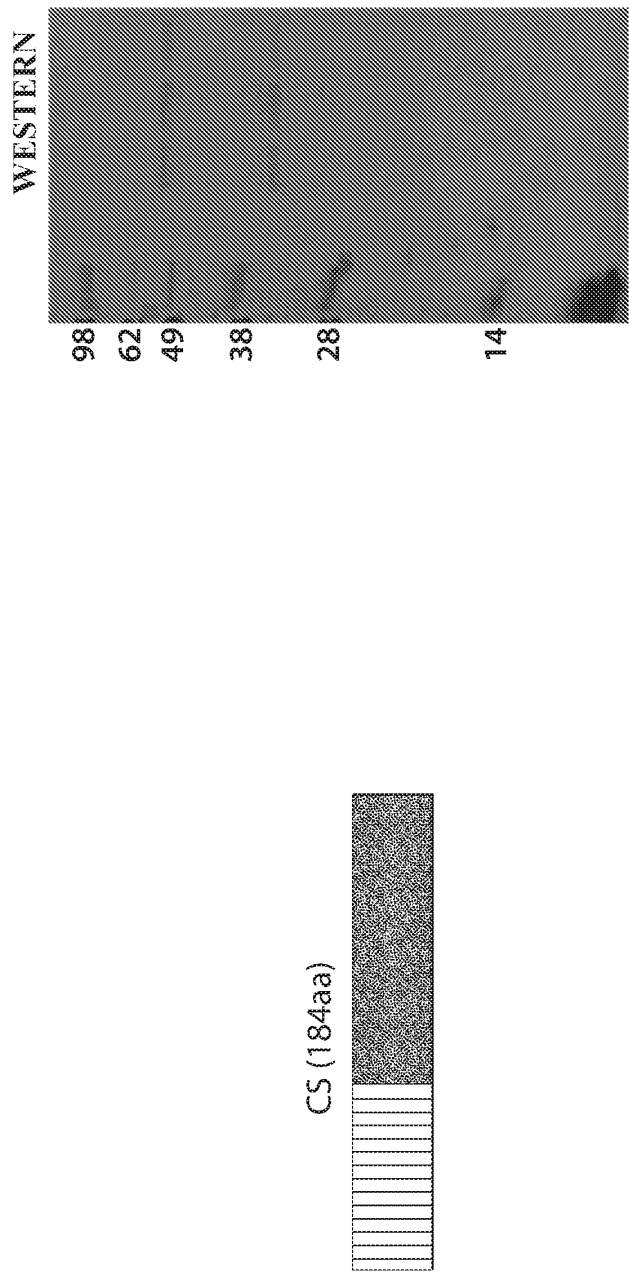
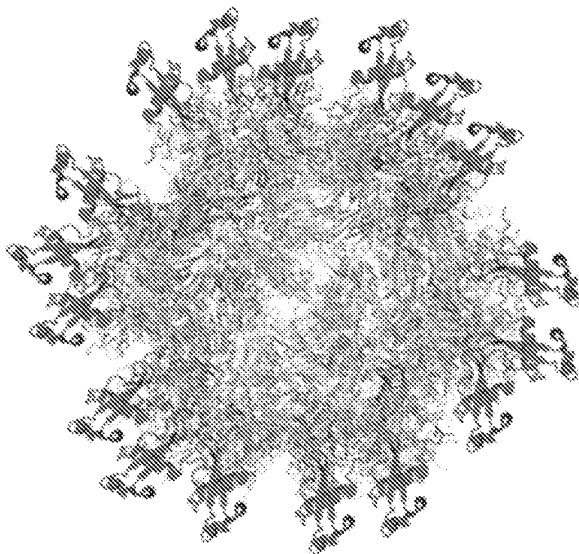




Construct Name	Description
pRTx-7062 CS-CTerm	184 C-Terminal residues of CS protein for 293 expression
pRTx-7063 CS-CTerm-CTC	184 C-Terminal residues of CS protein with additional C-Terminal Cysteine for conjugation

FIG. 1



Construct Name	Description
CS-Ring10-ORF1 Fusion	184 C-Terminal residues of CS protein fused into ORF1 replacing HVRs (251-383)

FIG. 2

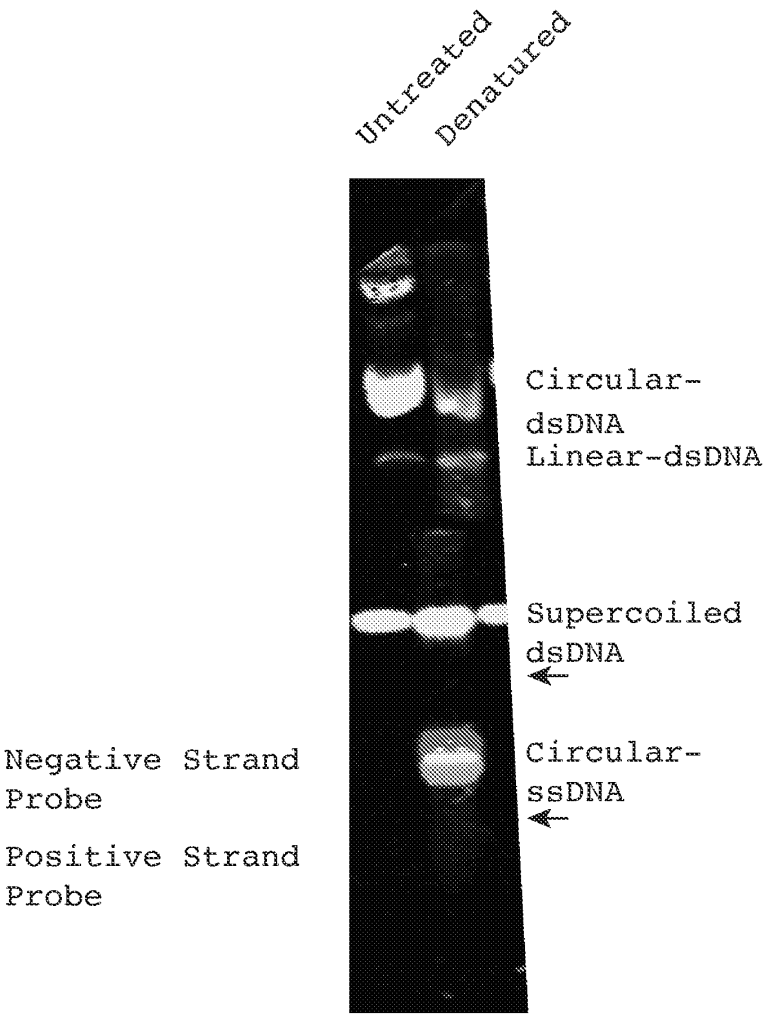


FIG. 3

Strain	Genus	Tissue of origin	Sf9 Expression	ORF1 (Da)	ORF1 (# residues)	Genome Size (bp)
Ring1	α	spleen	-	87961	743	3753
Ring2	β	lung	+++	78696	666	2975
Ring3	γ	CD8	+	80593	677	3264
Ring4	γ	CD8	++	78835	662	3174
Ring5	α	pan	+	87304	728	3696
Ring6	α	pan	+	90194	767	3828
Ring7	α	pan	-	90605	766	3815
Ring9	β	blood	+++	79700	673	2845
Ring10	β	lung	+++	81700	689	2912
Ring20	α	serum	-	90022	769	3853

FIG.4A

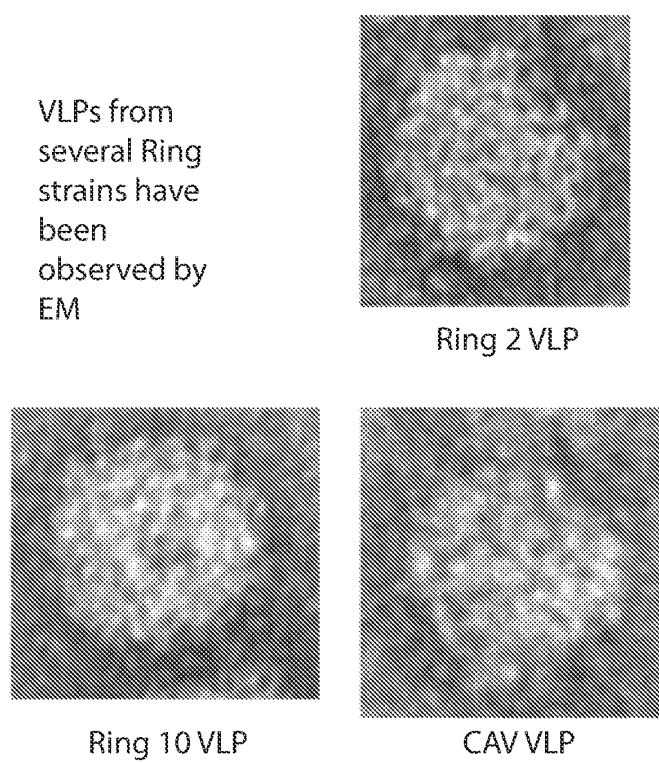


FIG. 4B

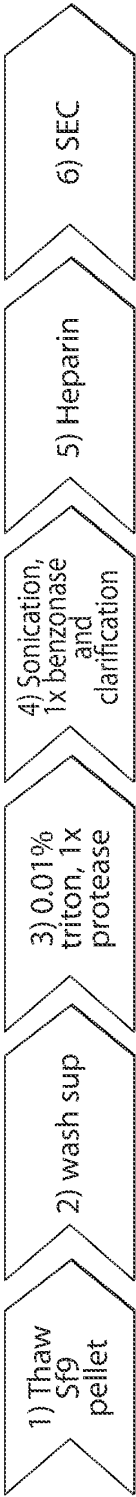
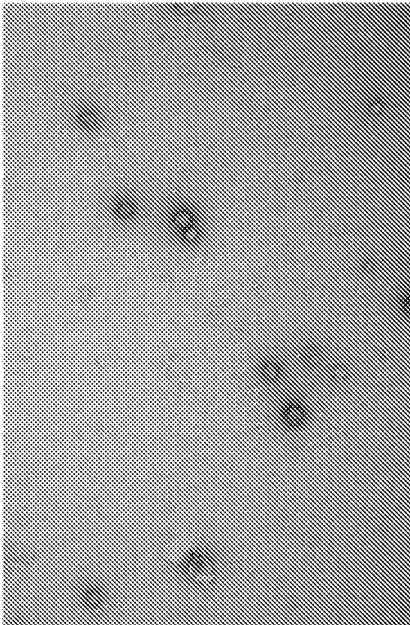


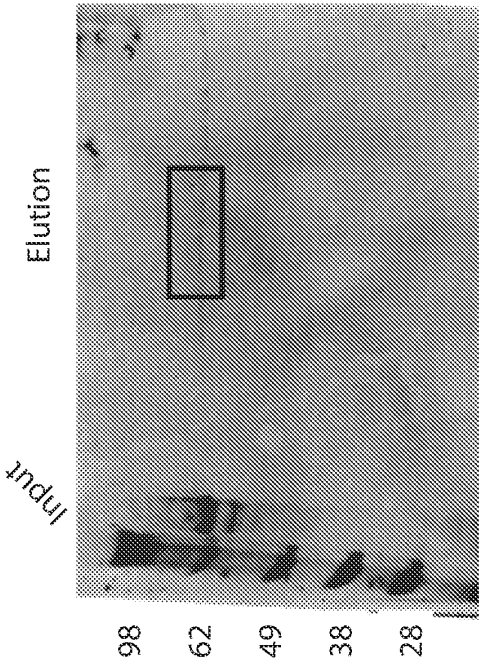
FIG. 5A

Numerous particles observed by EM



RingTx 040921018.tif
Dil ring2 heparin 3 sec d7 45b
Cal: 0.259 mm/pix
16:42 04/09/21
TEM Mode: imaging
100 nm
HV - 80.0kV
Direct Mag: 65000x
AMT Camera System

FIG. 5C



Anti-ORF1 western blot

FIG. 5B

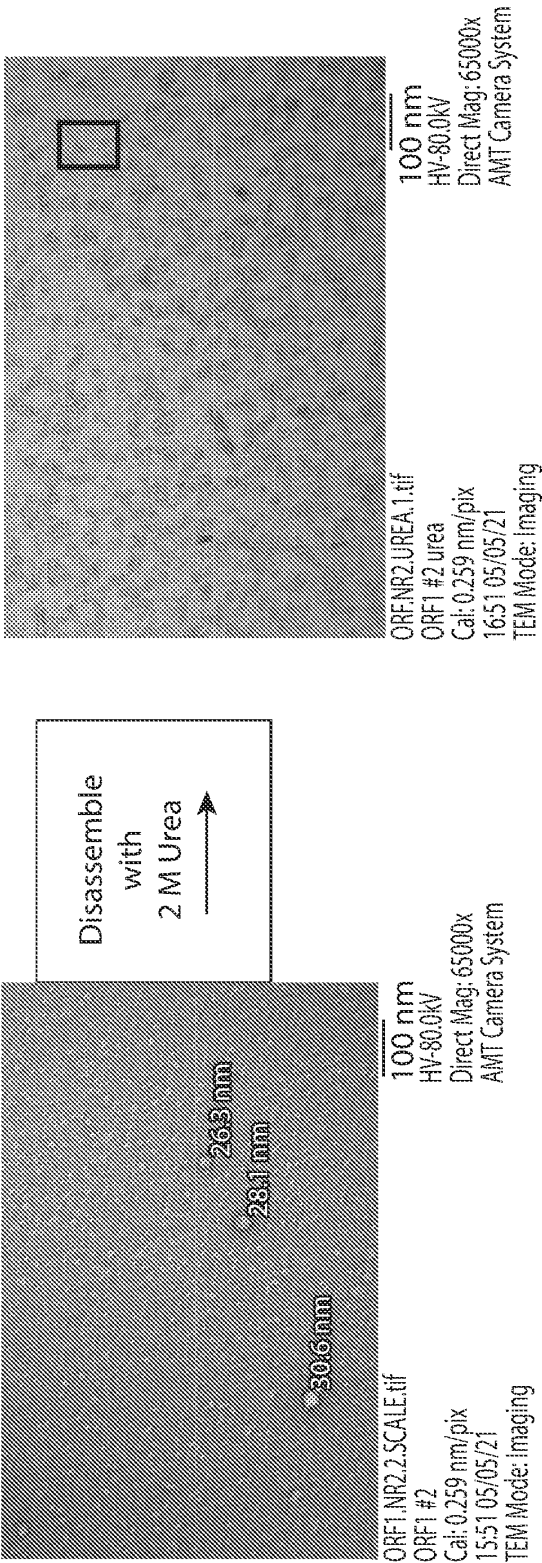


FIG. 6A

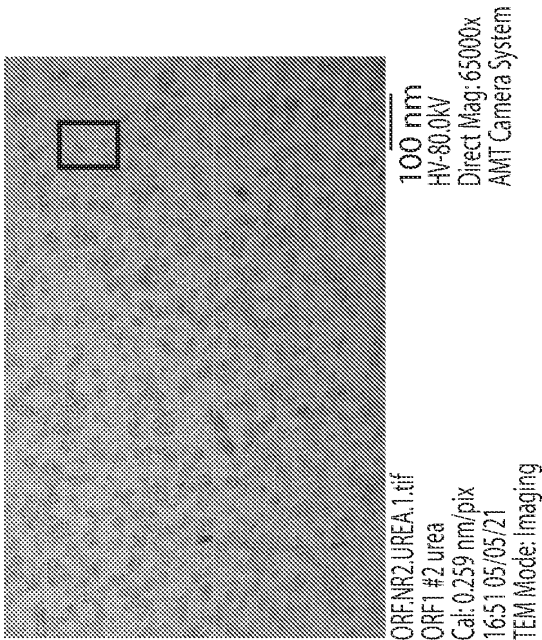


FIG. 6B

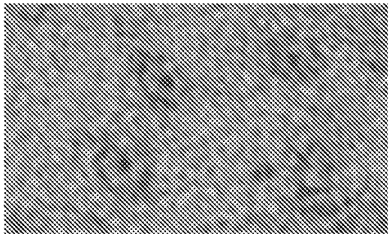


FIG. 6C

phenotype similar
to capsomer
decamers

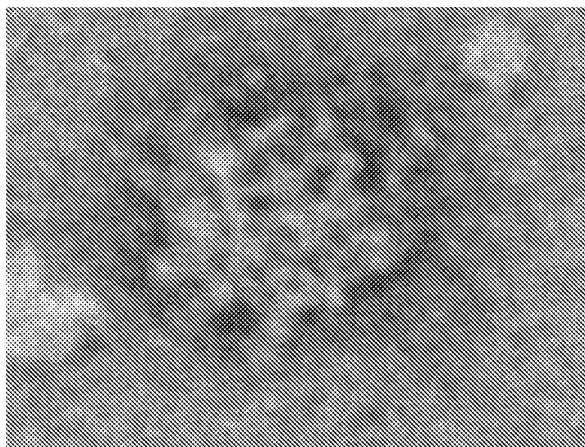


FIG. 7A

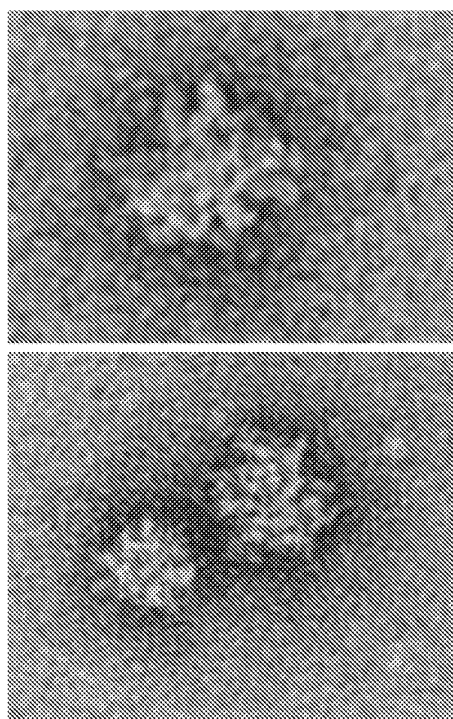


FIG. 7B

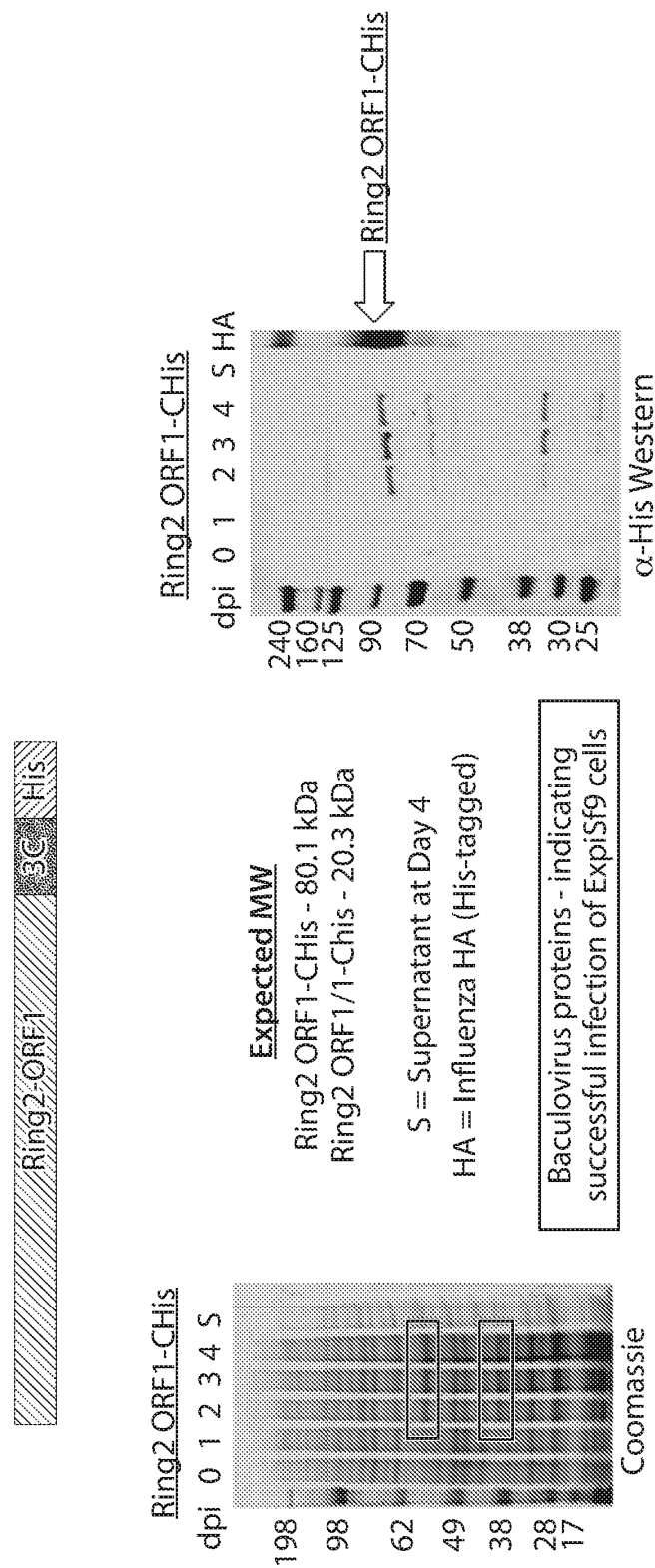


FIG. 8

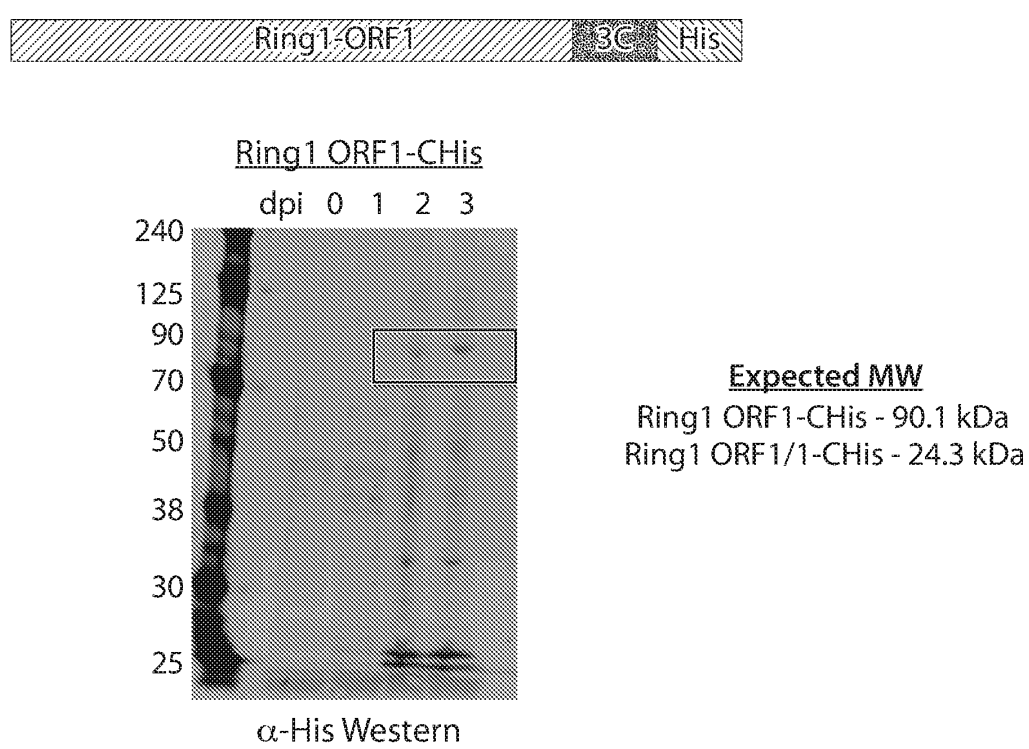


FIG. 9

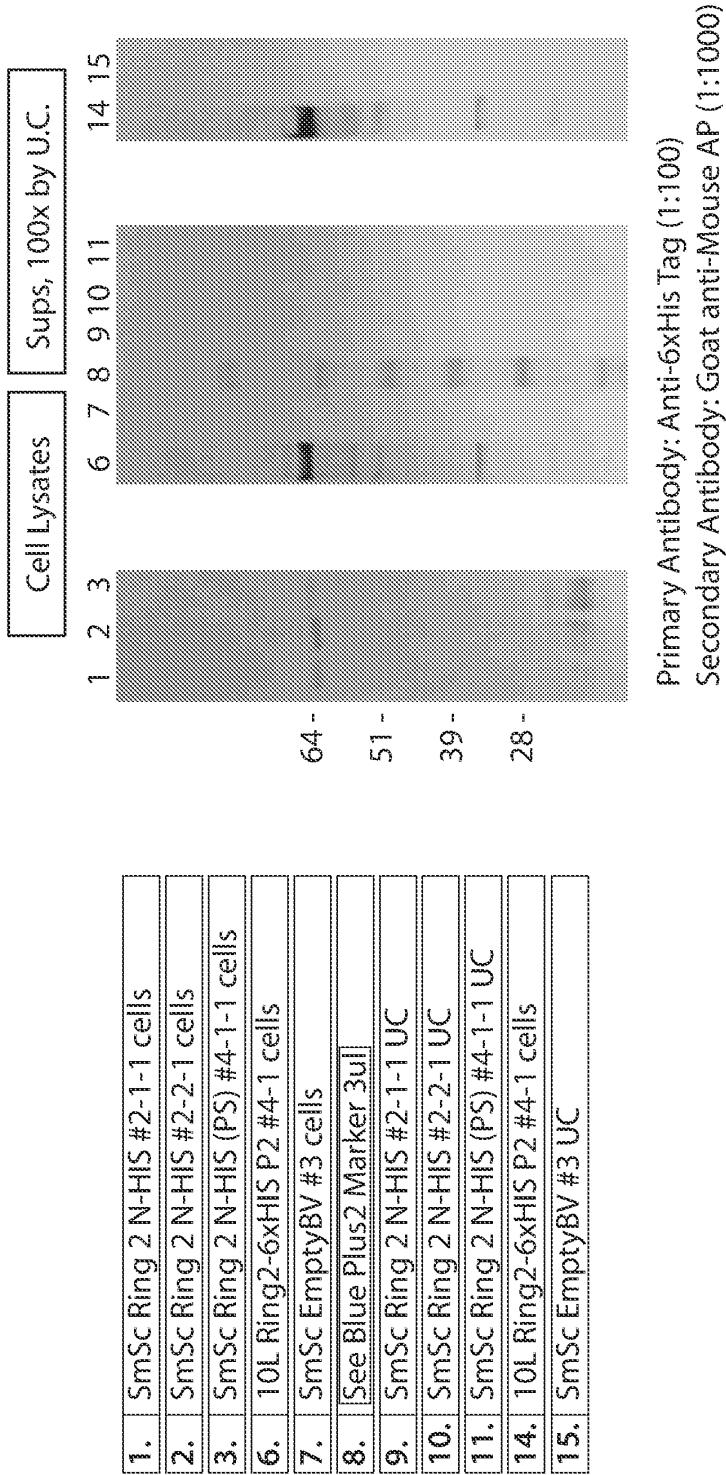


FIG. 10

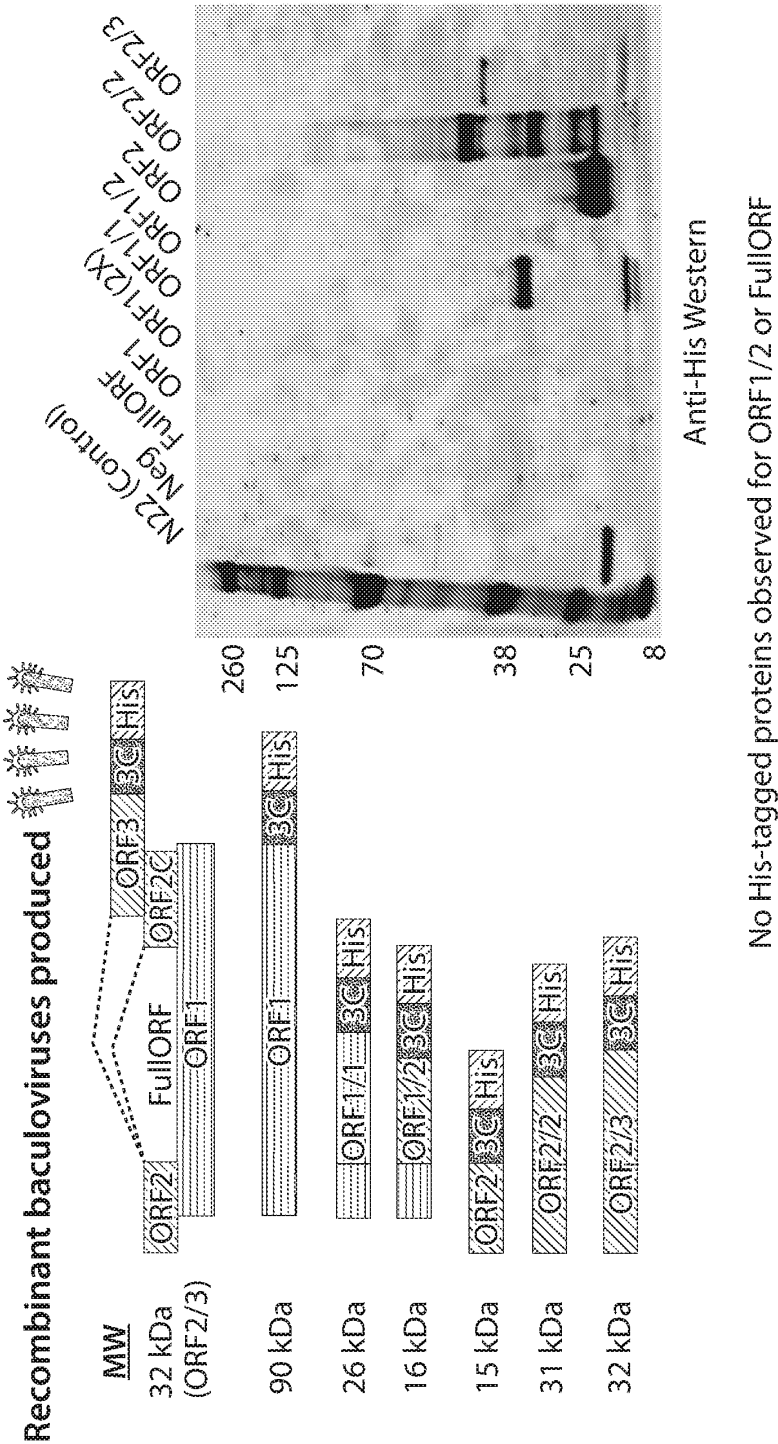


FIG. 11

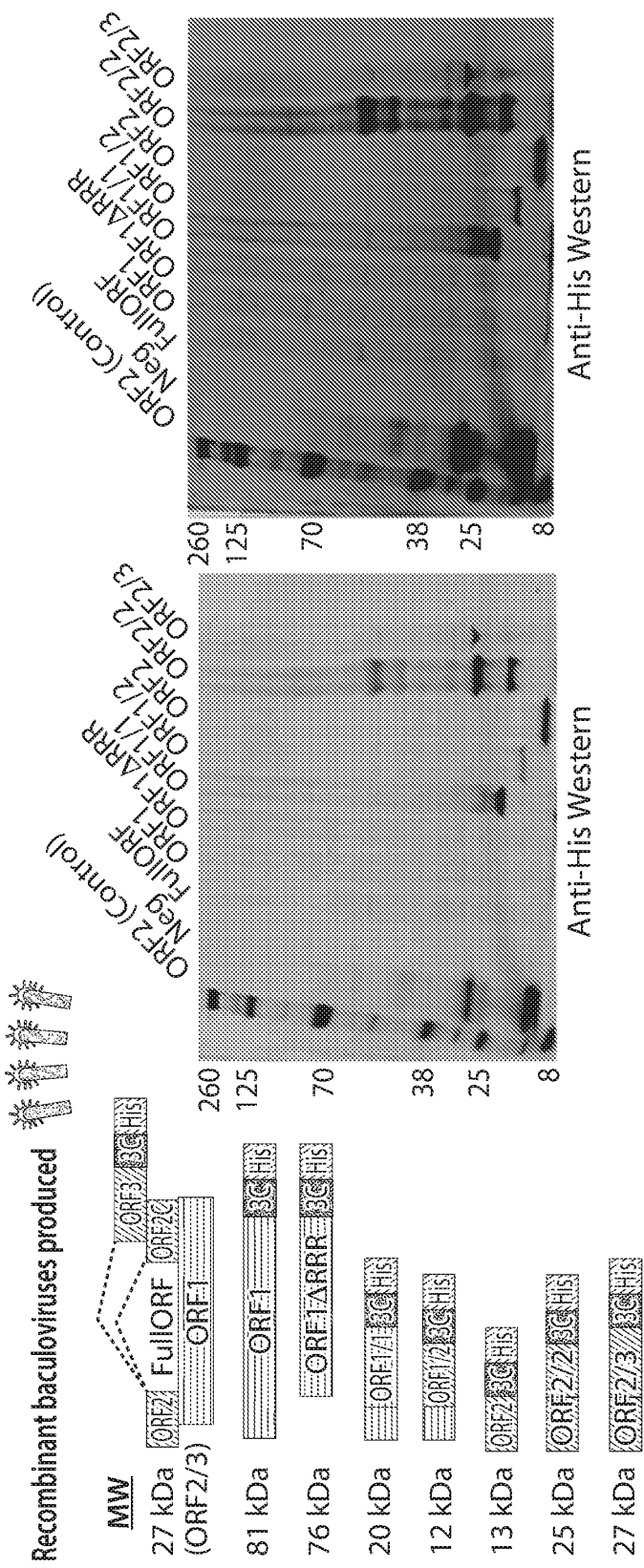


FIG. 12

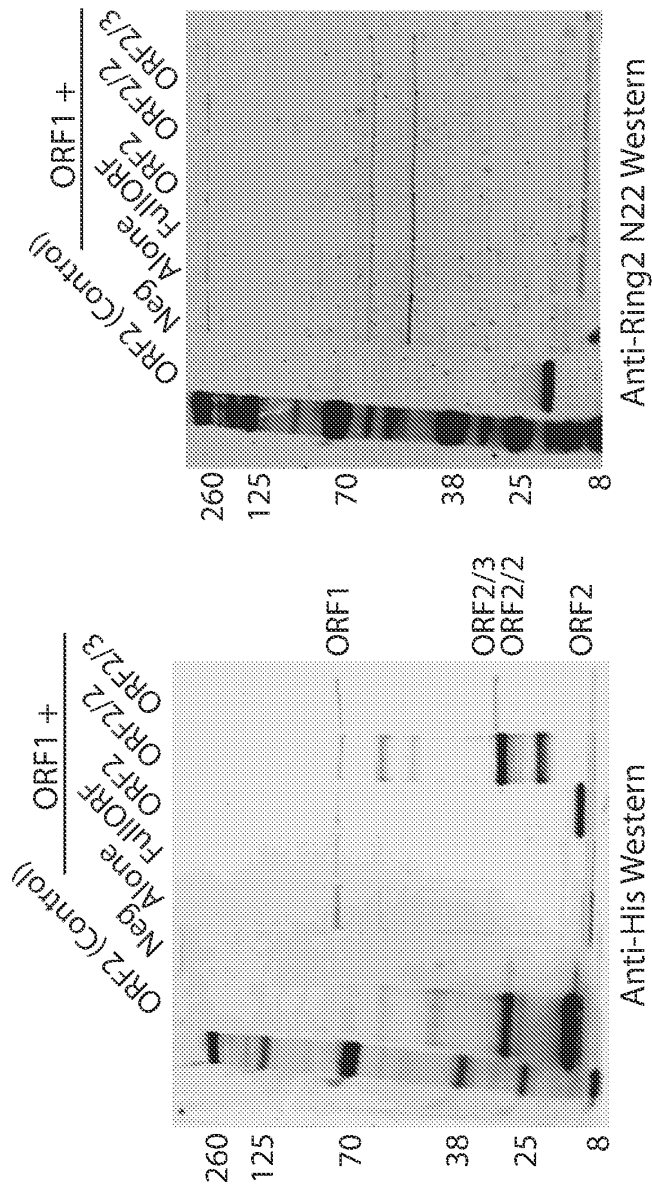


FIG. 13

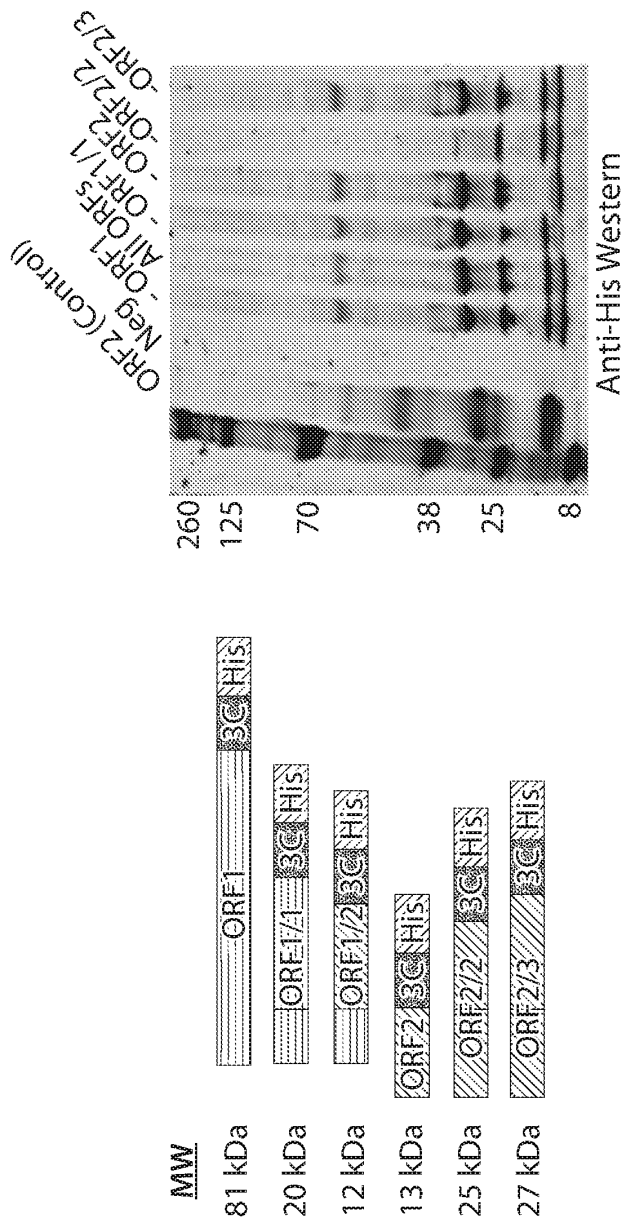


FIG. 14

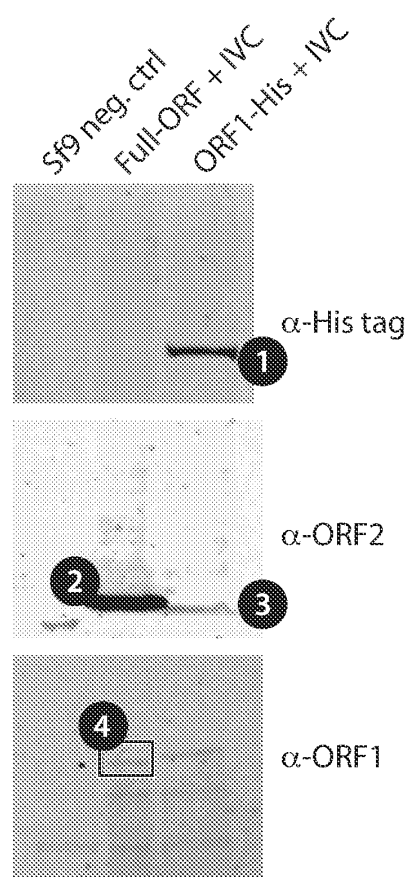


FIG. 15

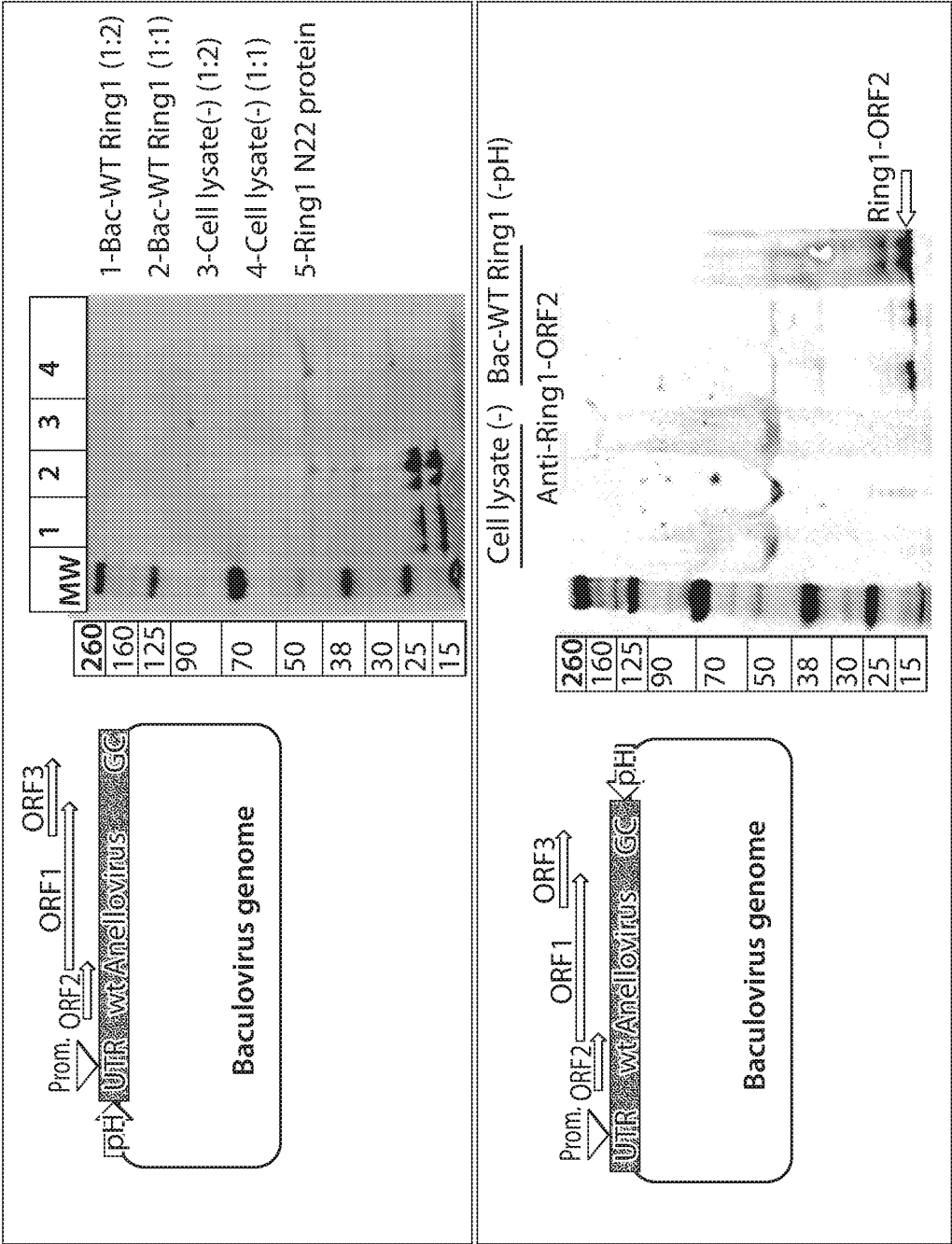


FIG. 16

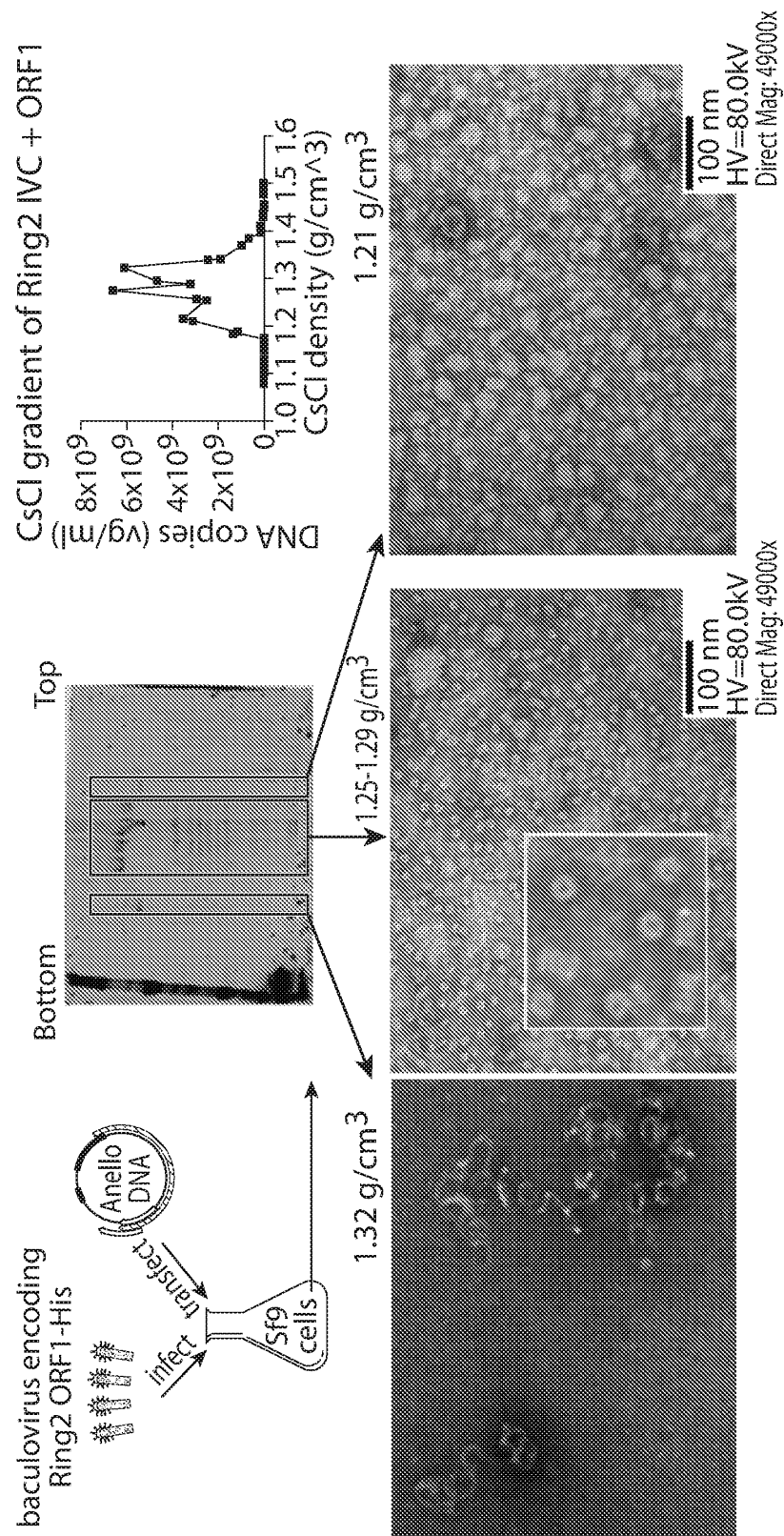


FIG. 17

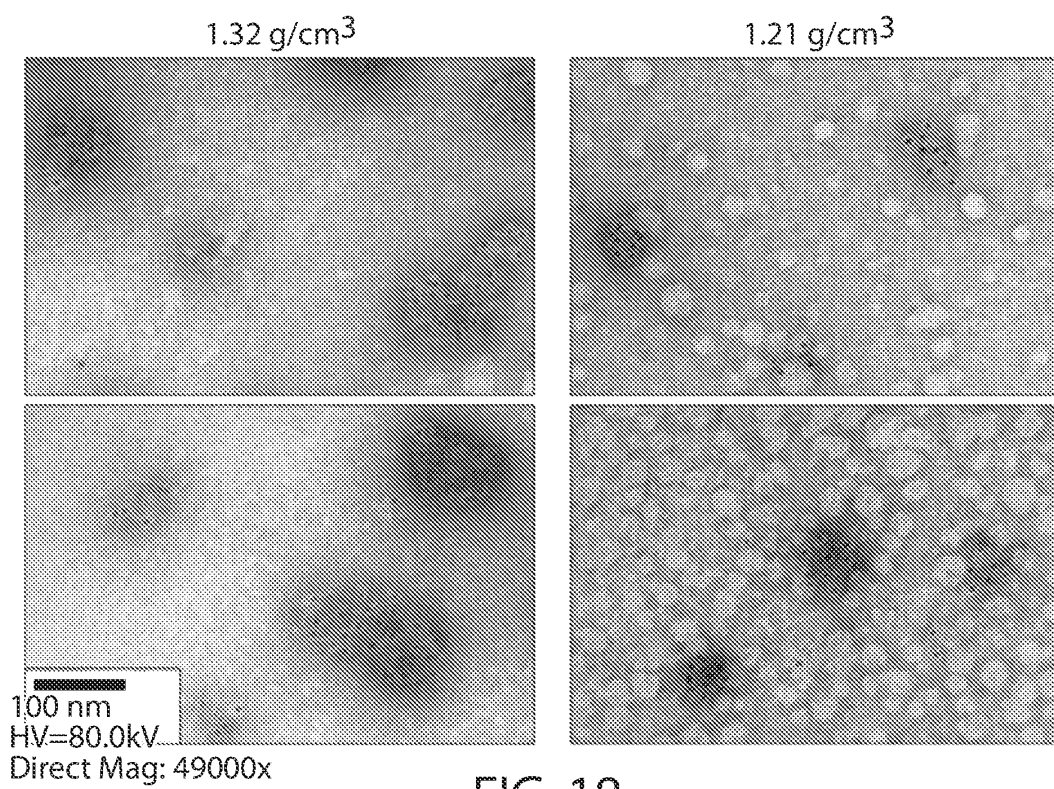


FIG. 18

Expression of several ORF1s in insect cells

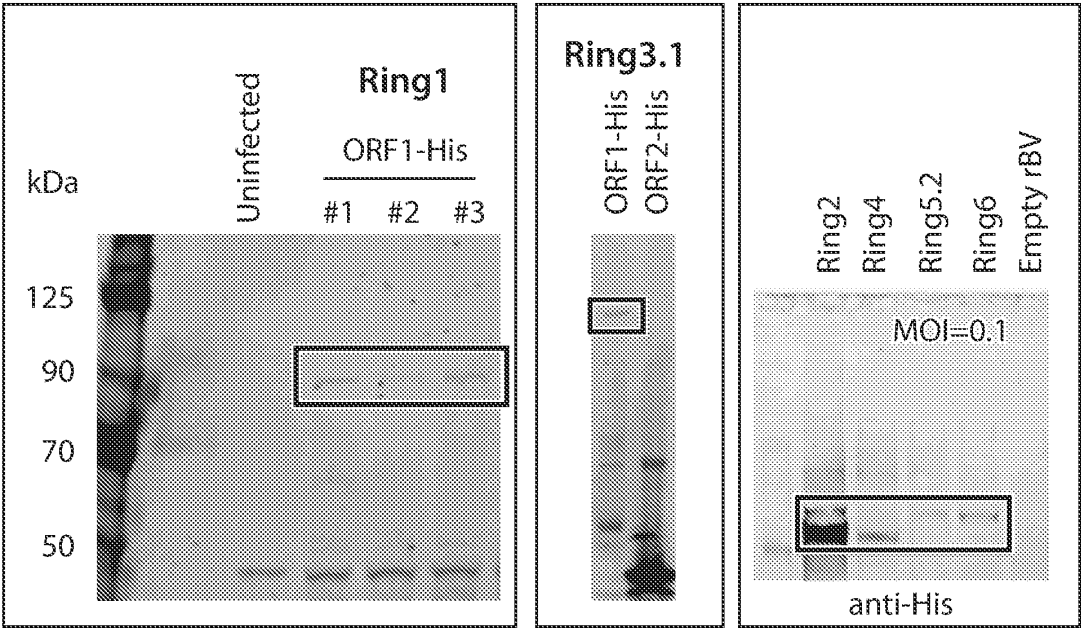


FIG. 19

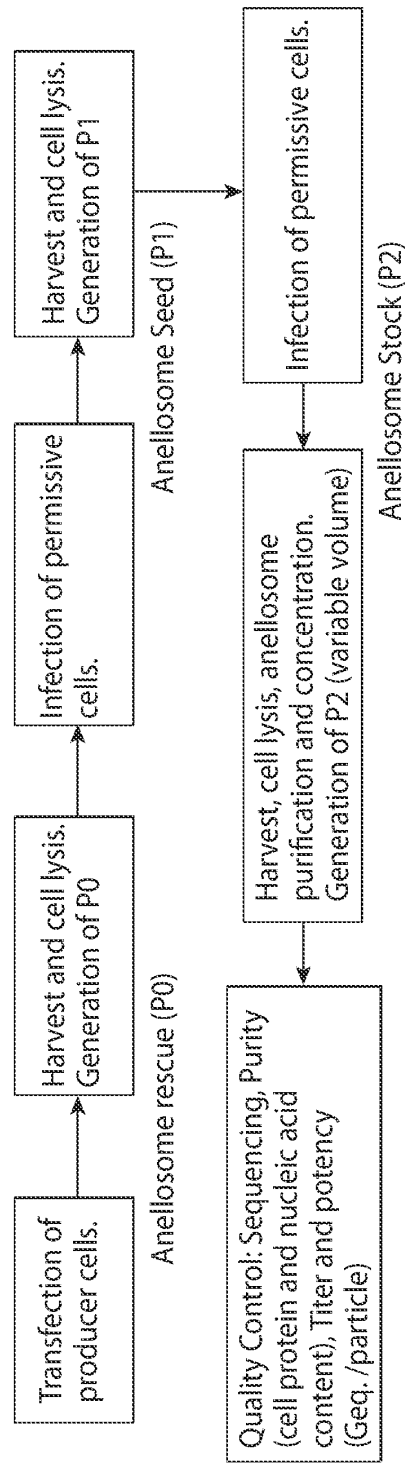


FIG. 20

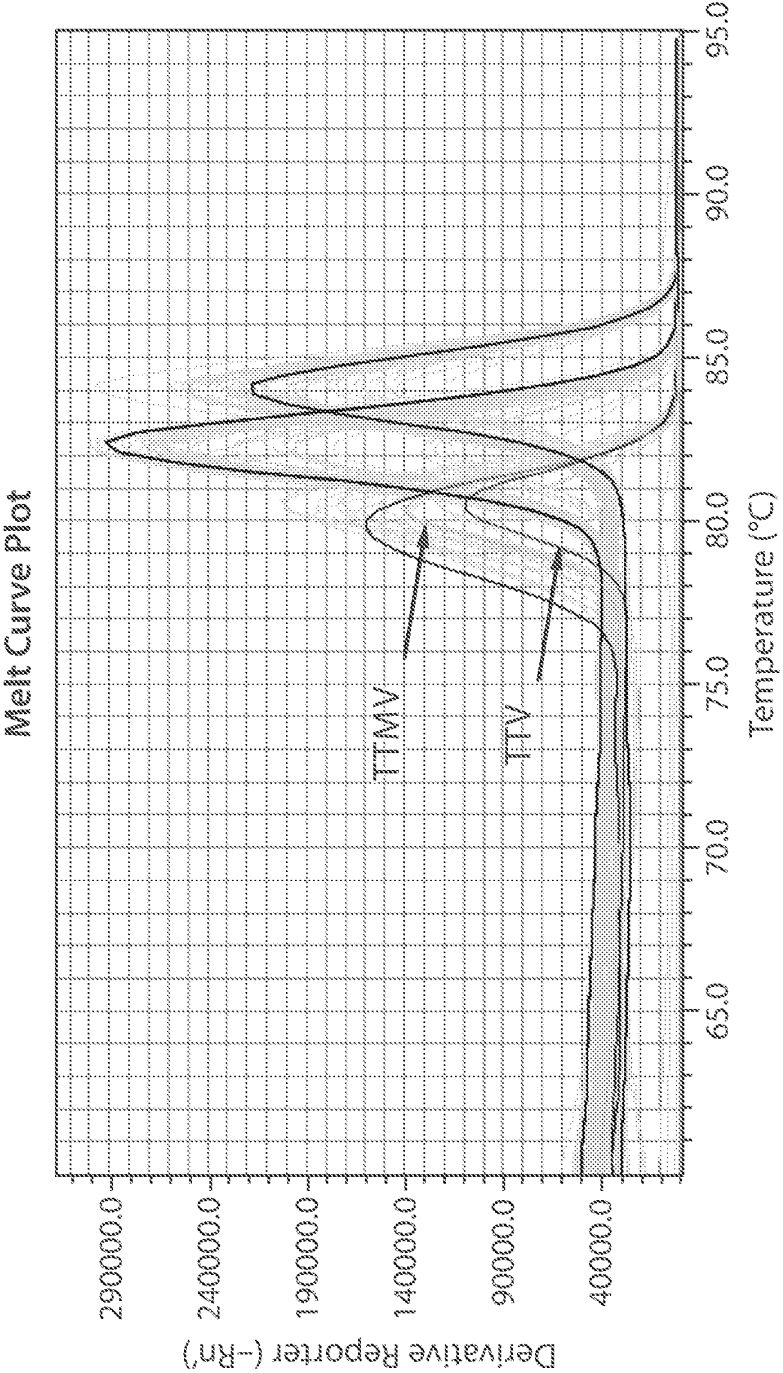
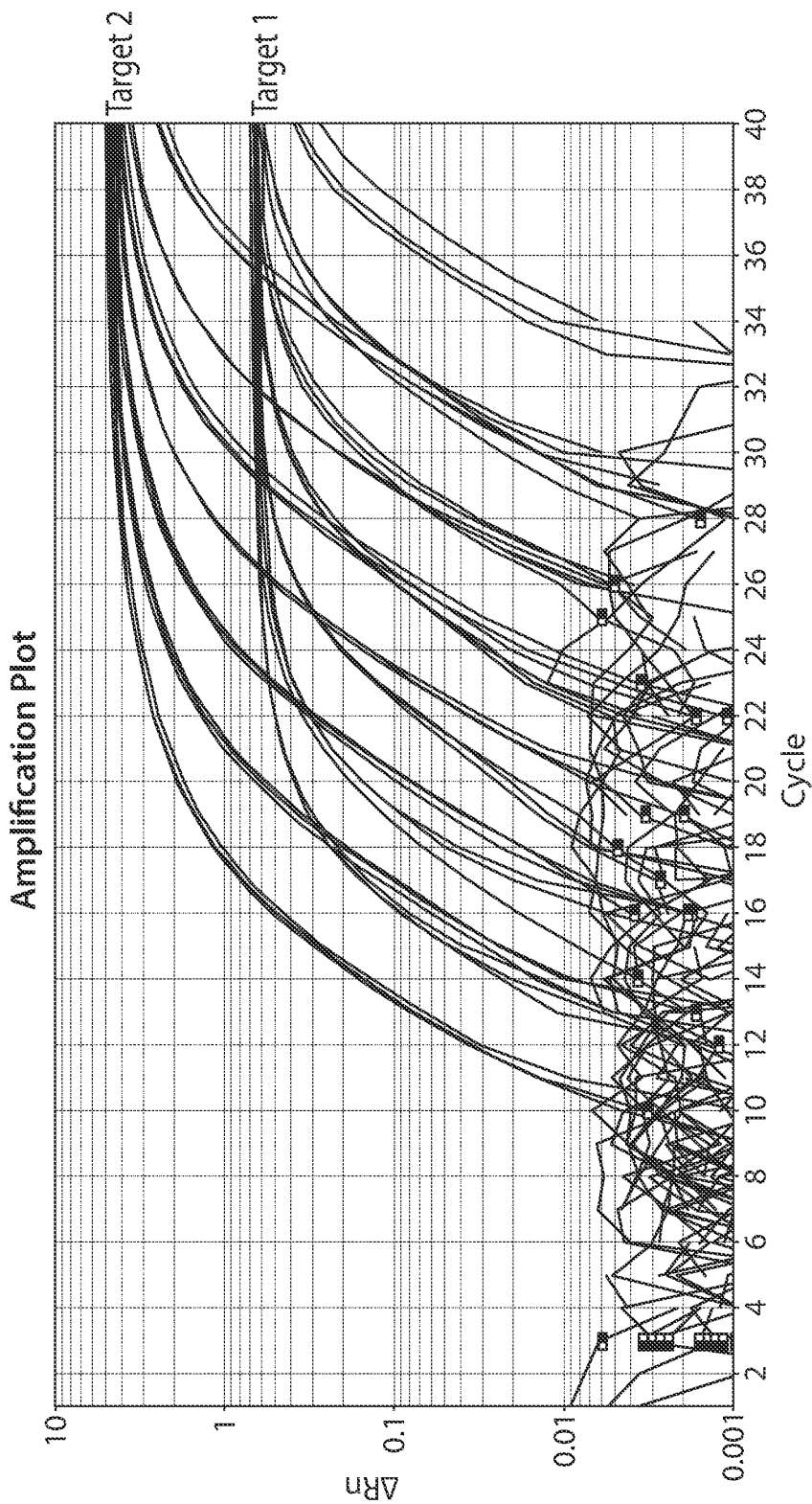


FIG. 21



Target 1 : TTMV. Target 2: TTV.

FIG.22

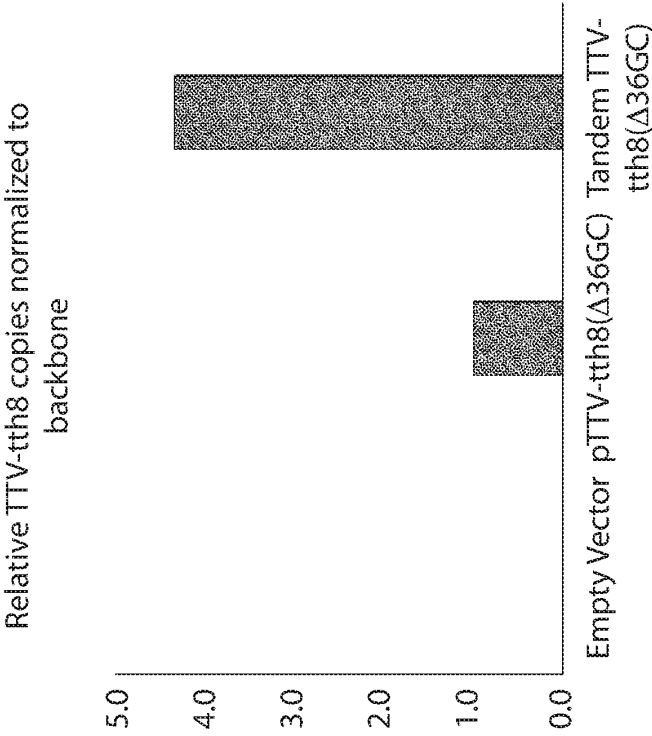


FIG. 23B

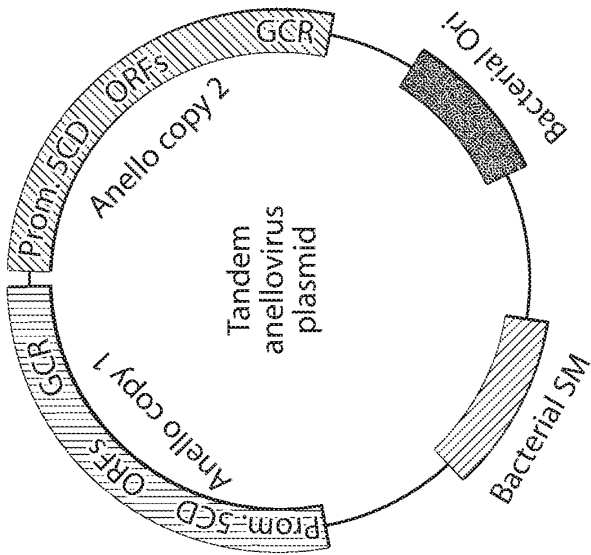


FIG. 23A



FIG. 23C

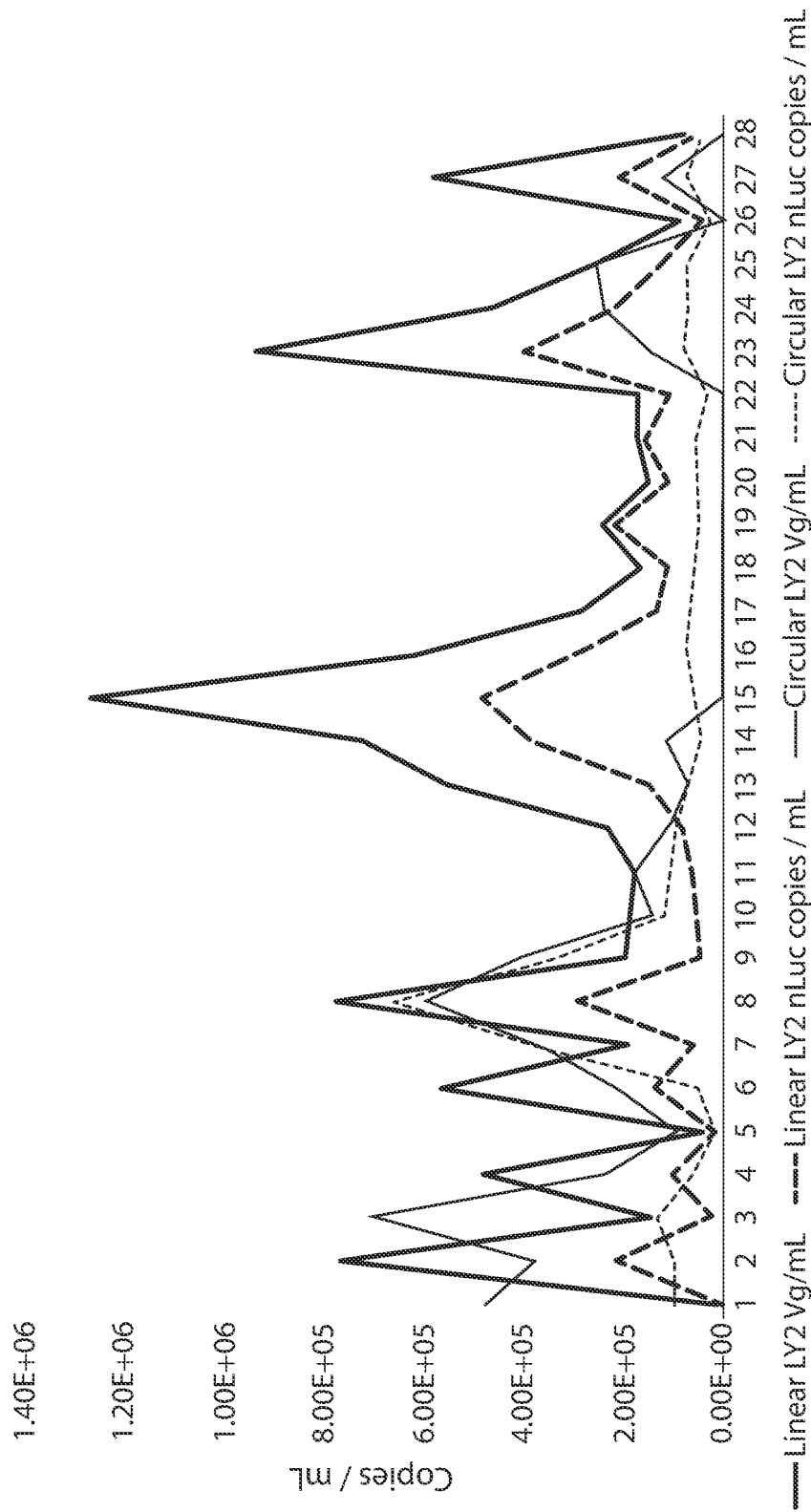


FIG. 23D

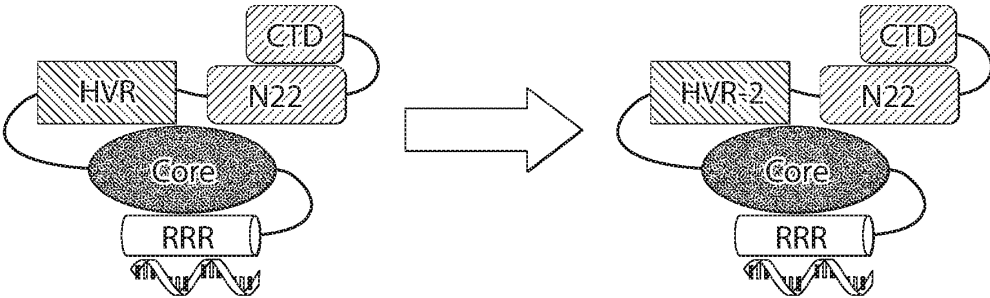


FIG. 24

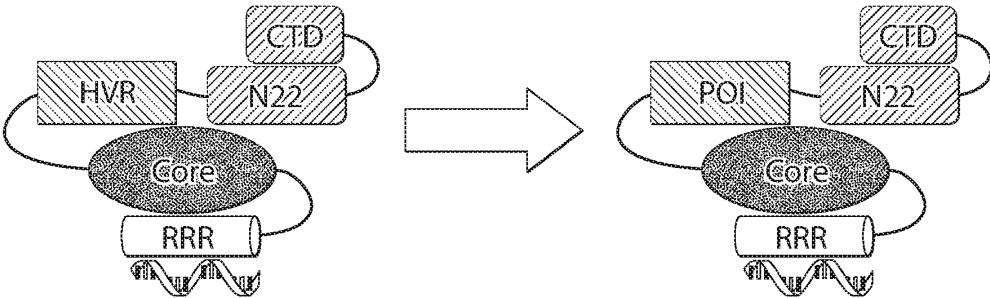


FIG. 25

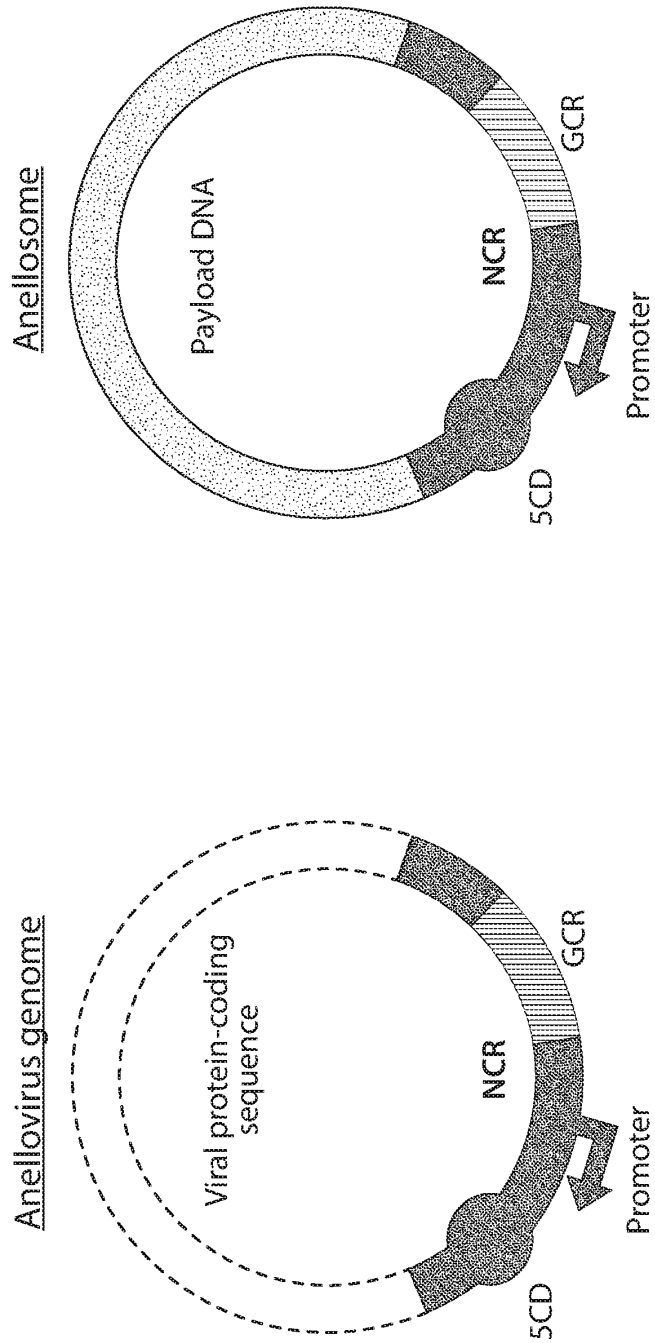
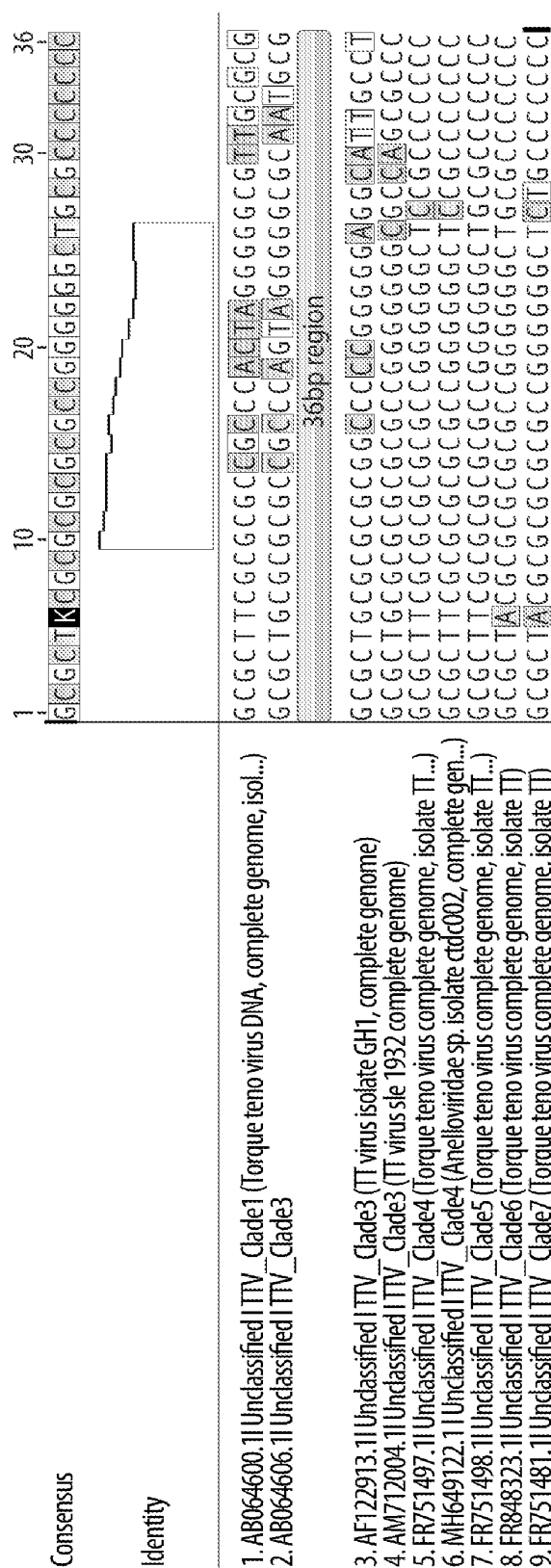


FIG. 26



729

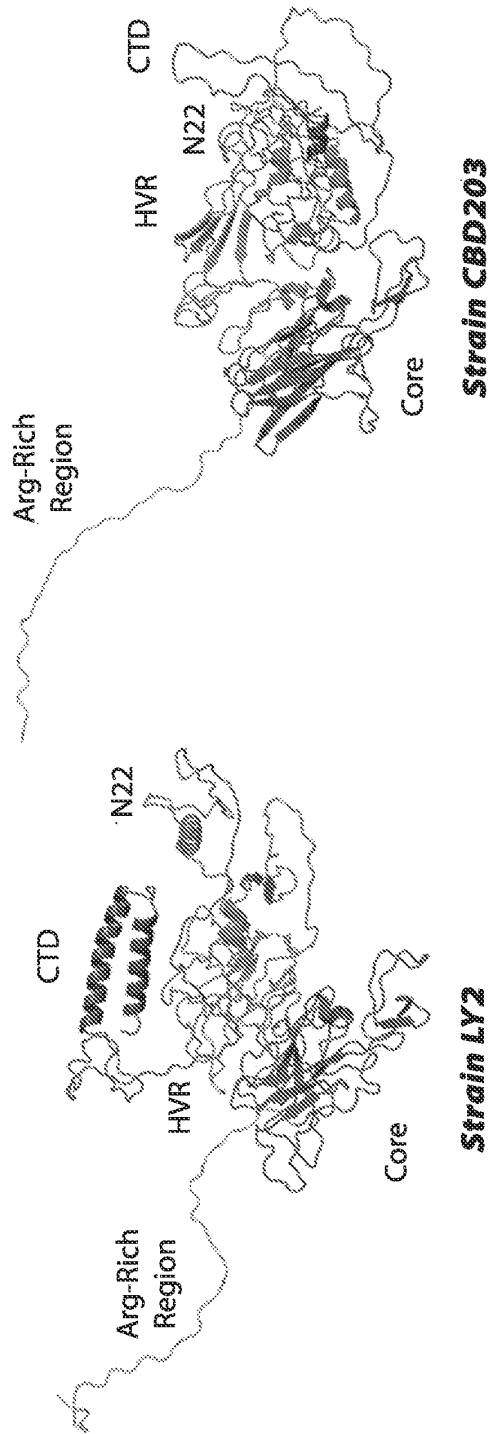


FIG. 28

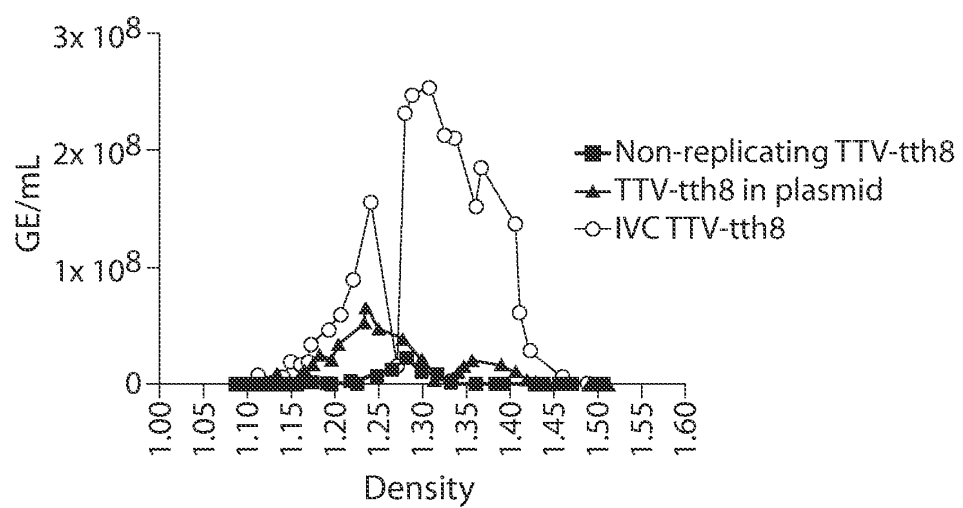


FIG. 29

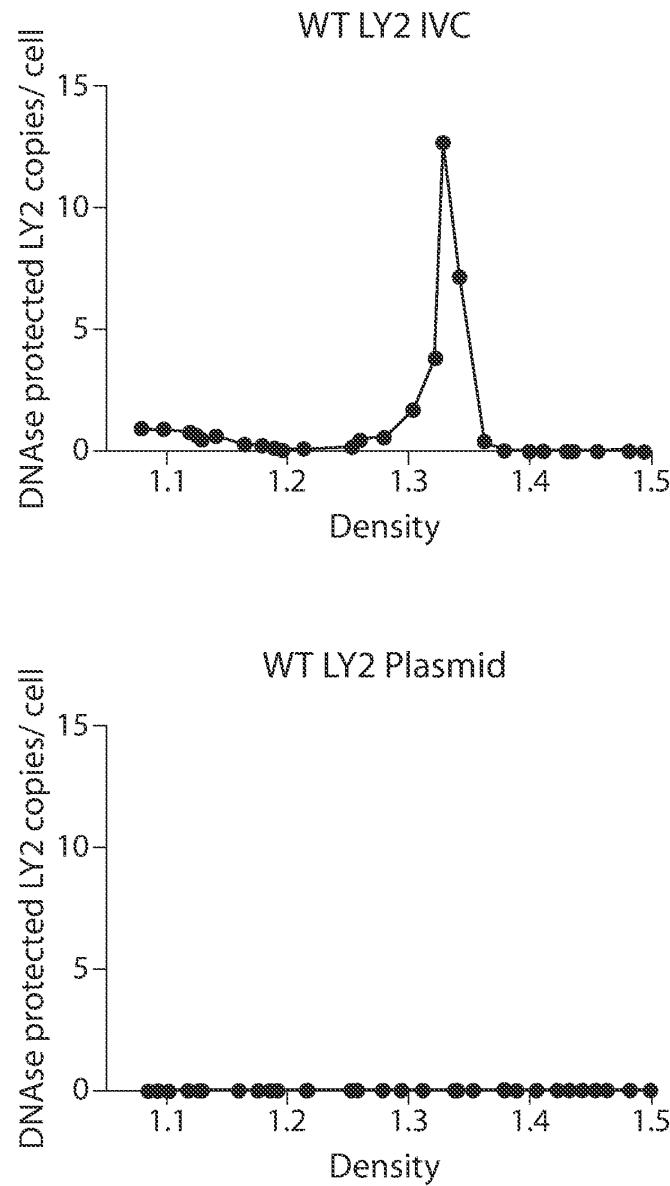


FIG. 30



FIG. 31A

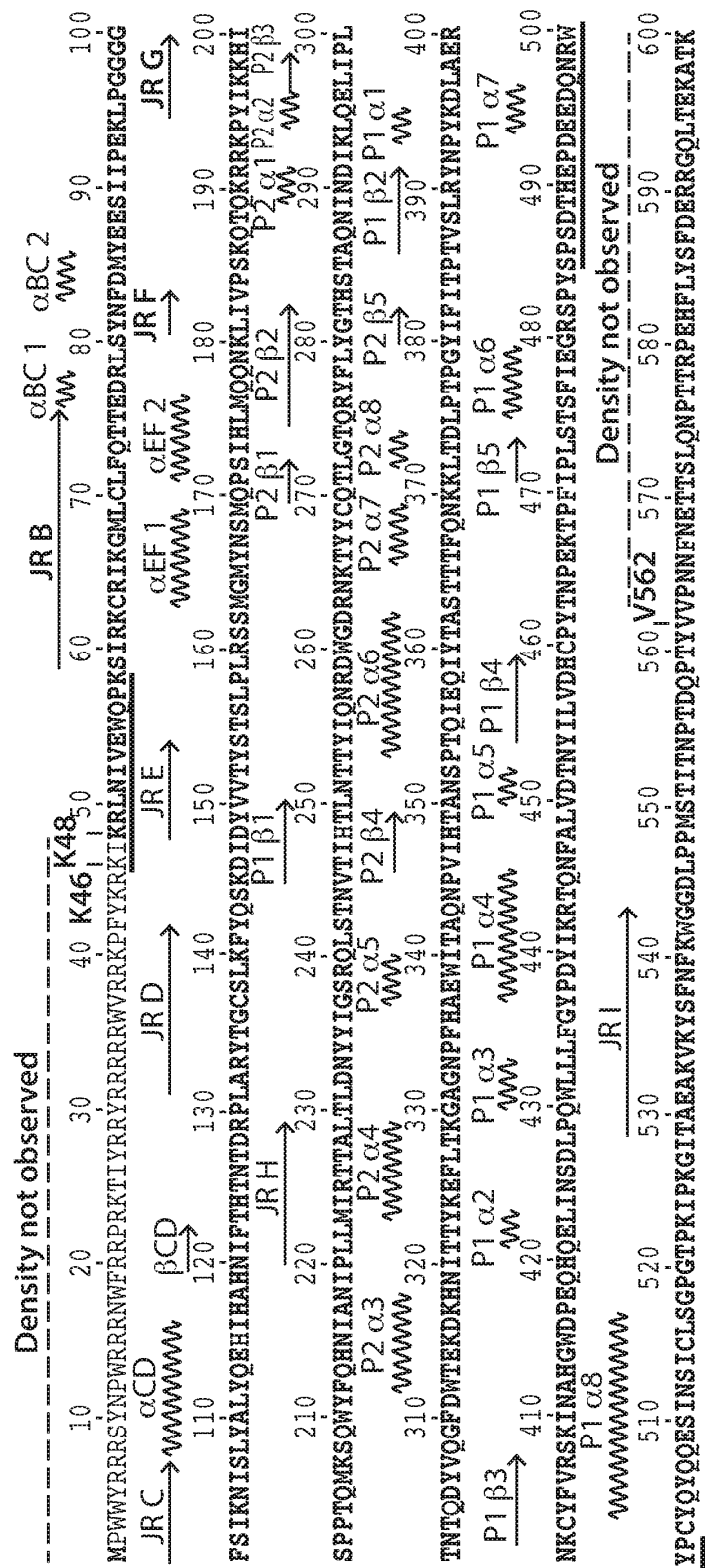


FIG. 31B

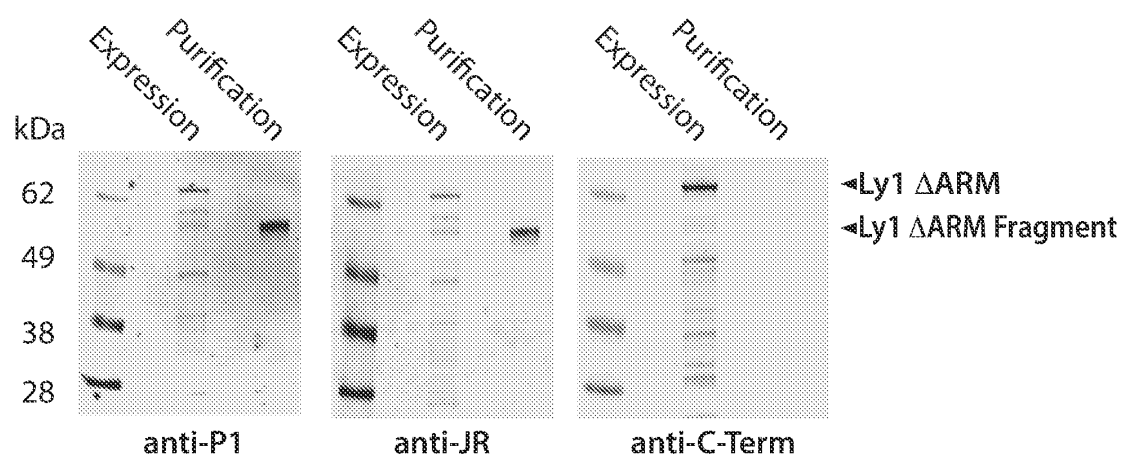


FIG. 31C

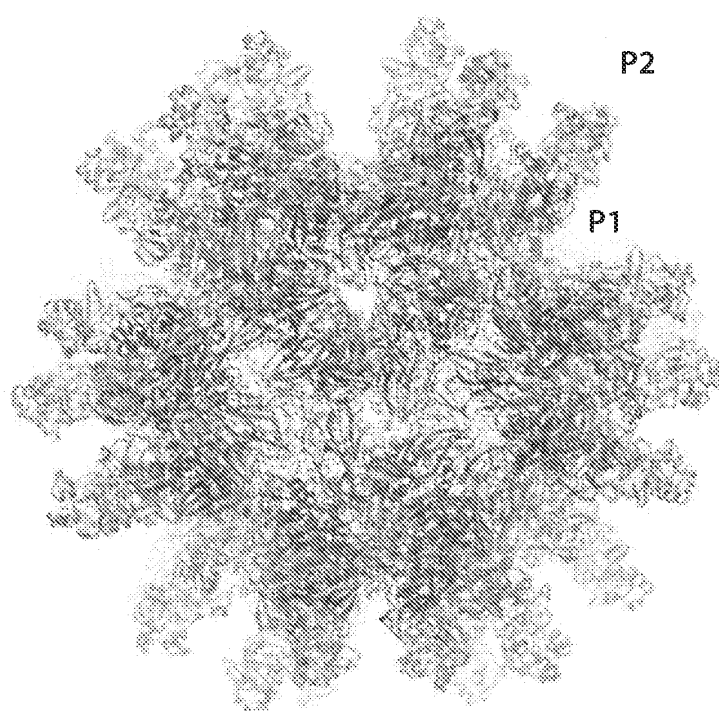


FIG. 31D

35/65

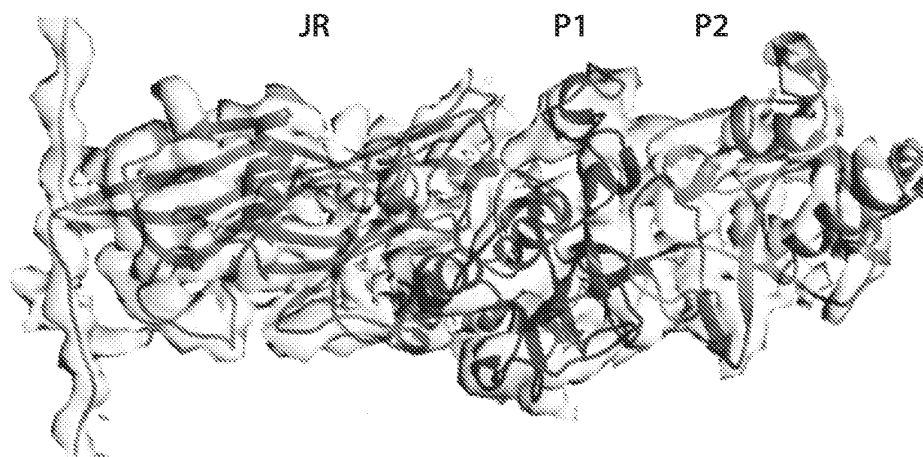


FIG. 31E

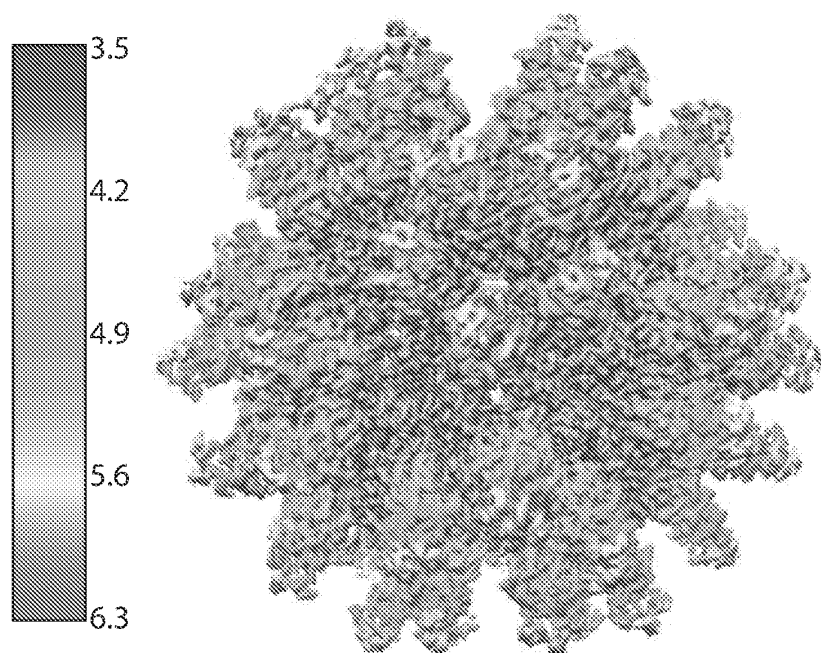


FIG. 31F

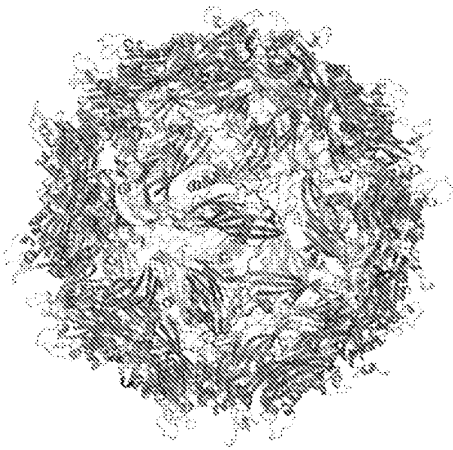


FIG. 32A

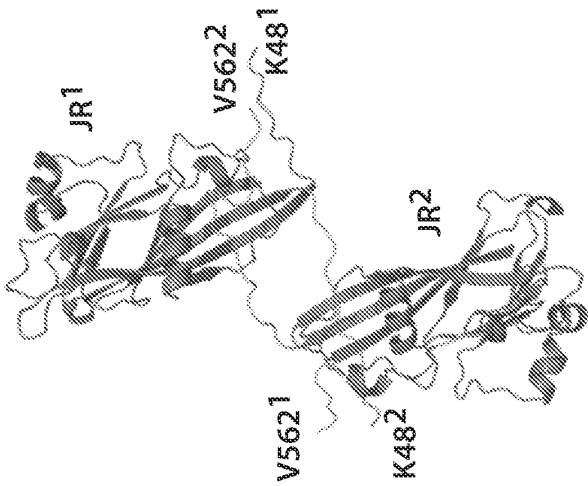


FIG. 32B

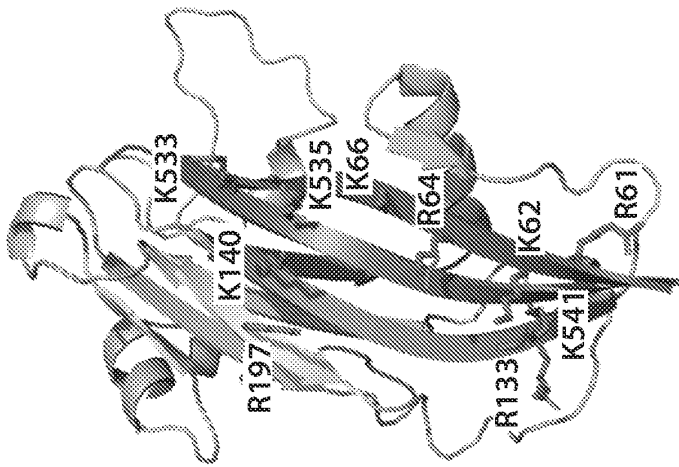
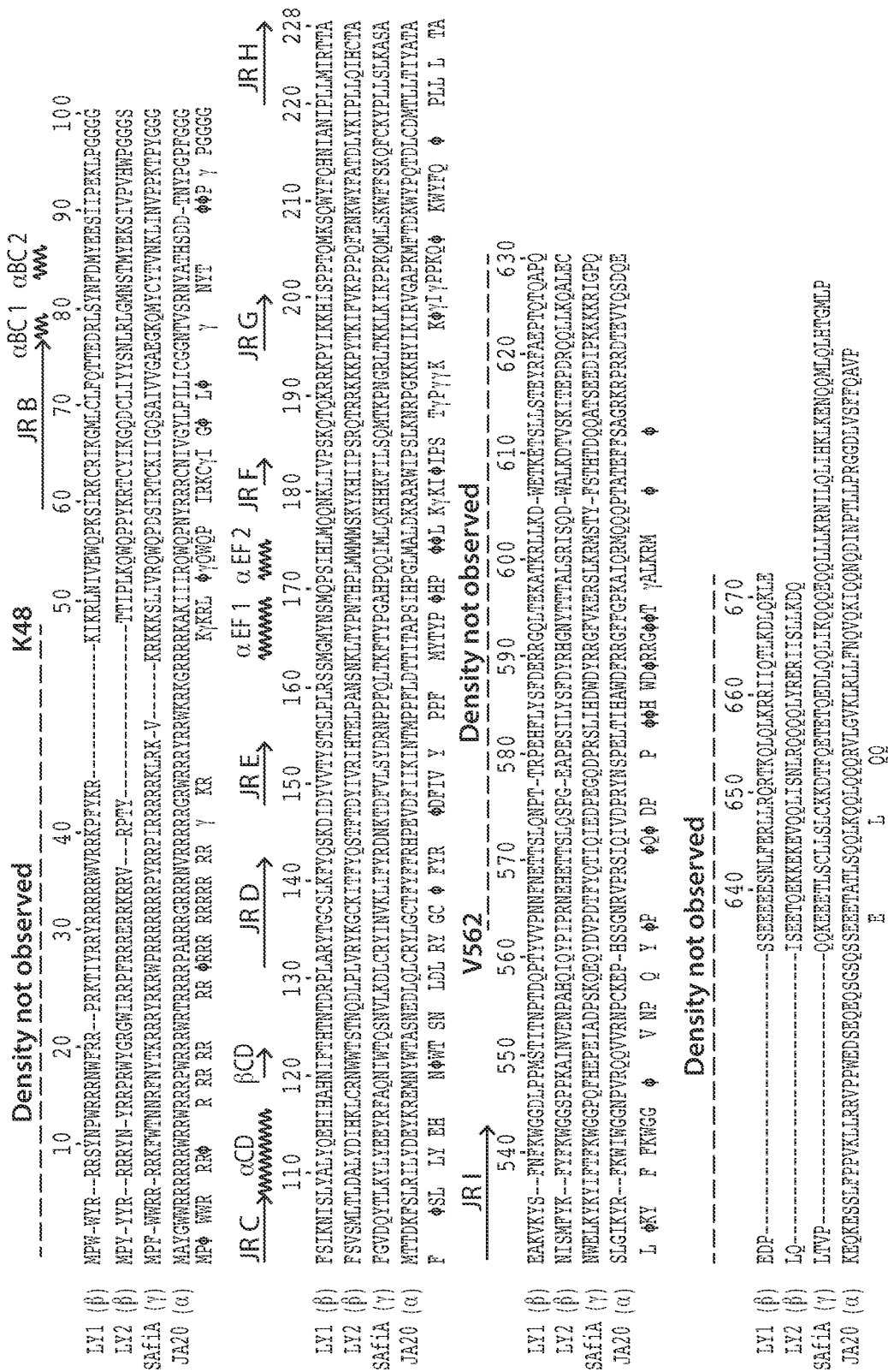


FIG. 32C



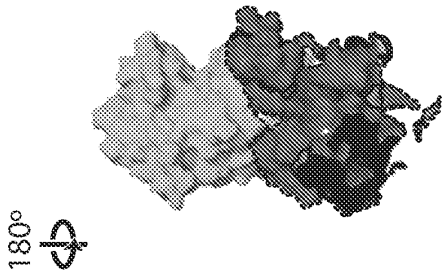


FIG. 33C

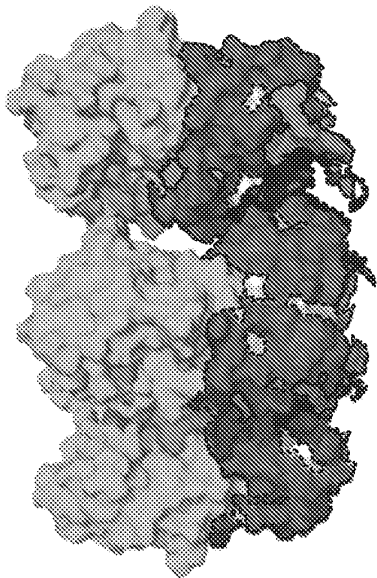


FIG. 33B

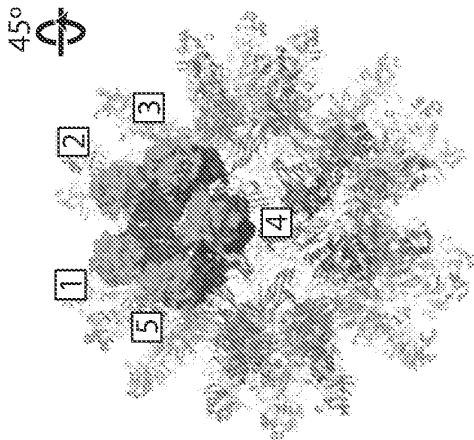


FIG. 33A

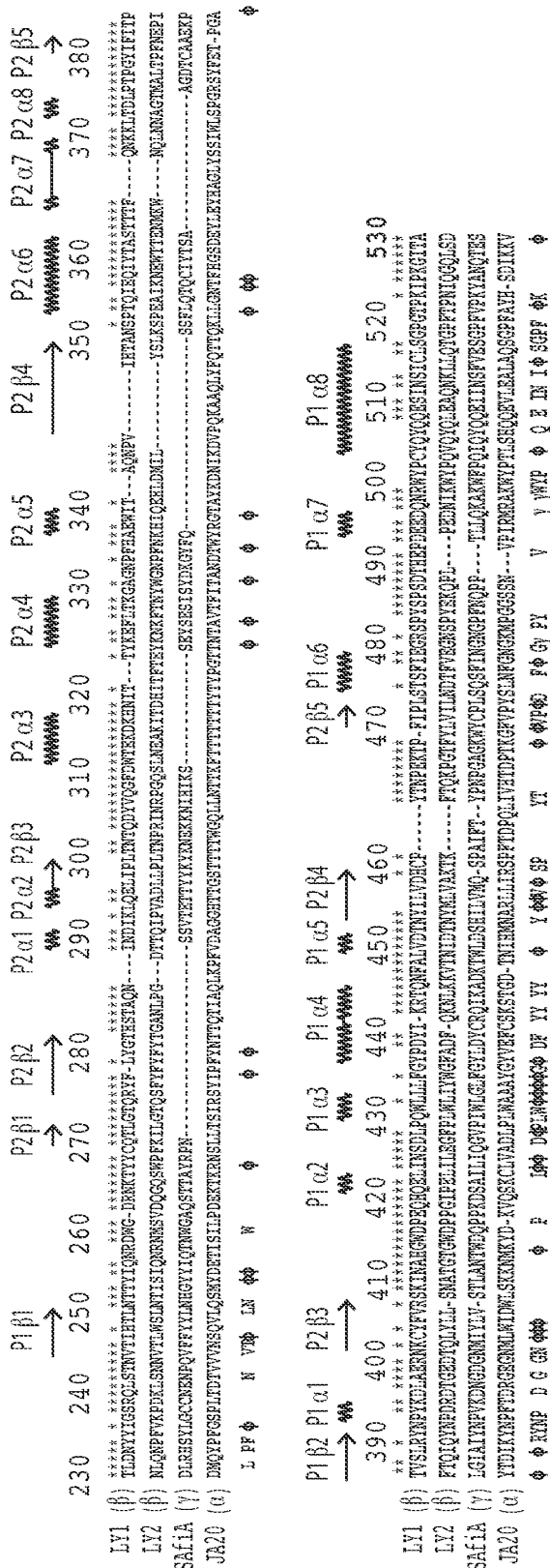


FIG. 33D

Ly1 Full-Length

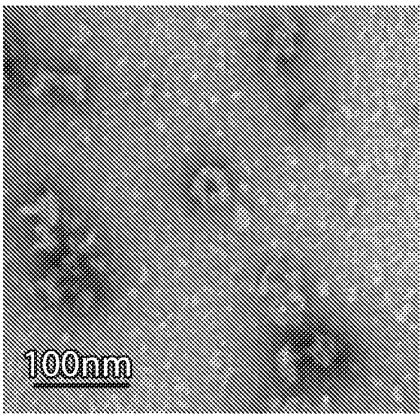
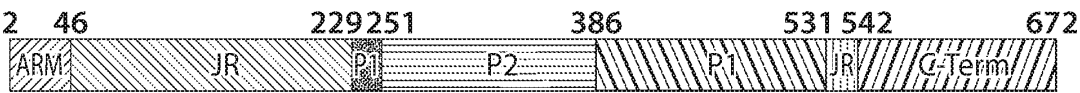


FIG. 34A

Ly1 ΔARM

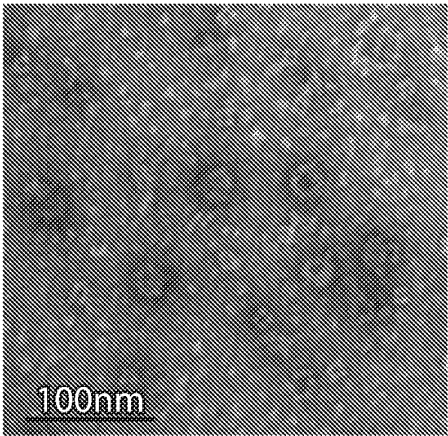
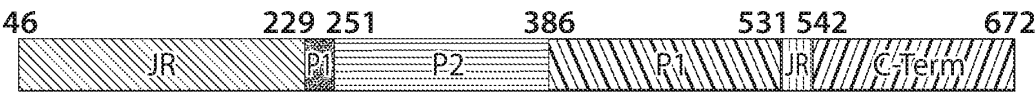


FIG. 34B

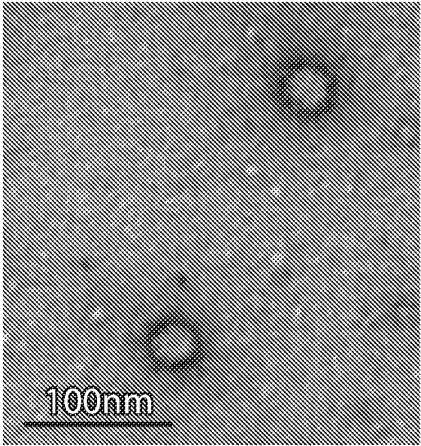
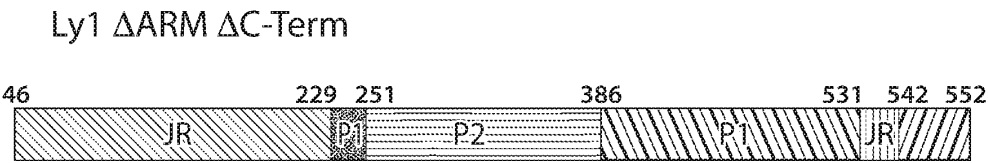


FIG. 34C

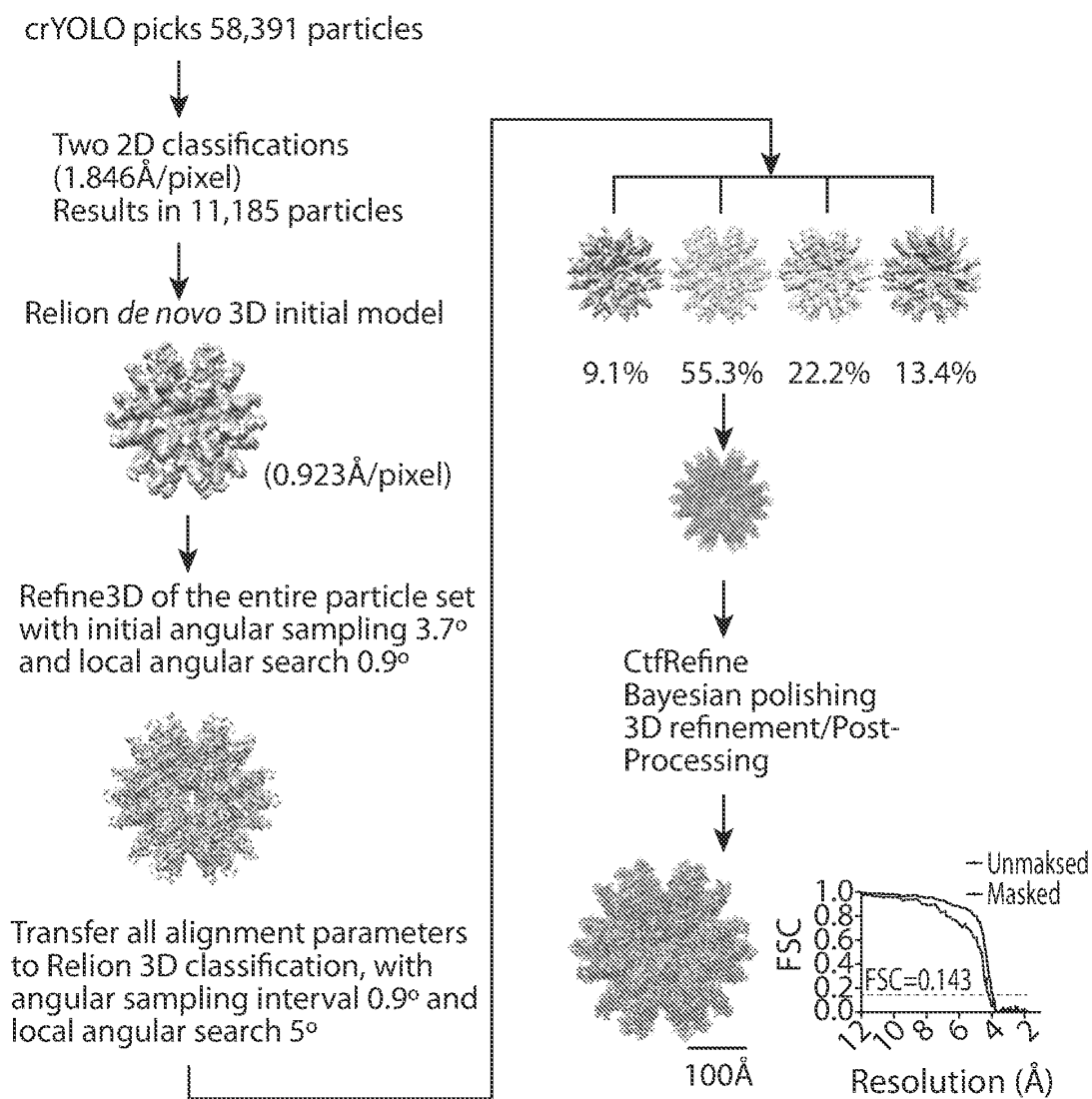


FIG. 35

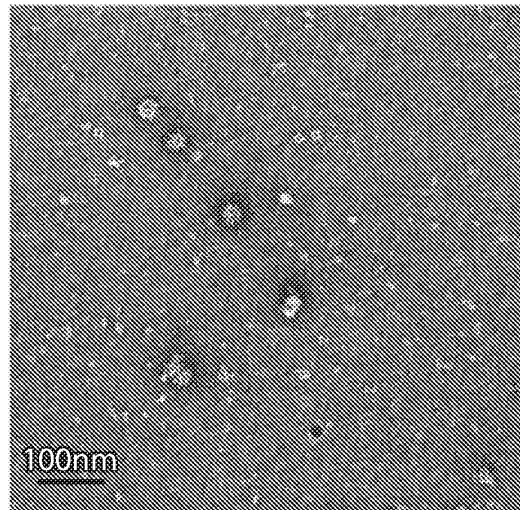


FIG. 36A

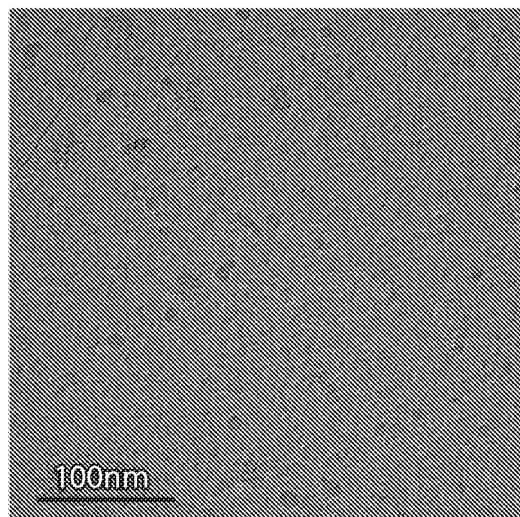


FIG. 36B

	α -helix	β -sheet	Turns	Unordered
SELCON	60.1%	4.4%	14.6%	21.6%
CONTILL	70.2%	2.2%	7.9%	19.8%
CDSSTR	87.7%	2.2%	3.8%	5.5%
average	72.7%	2.8%	8.8%	15.6%

FIG. 37A

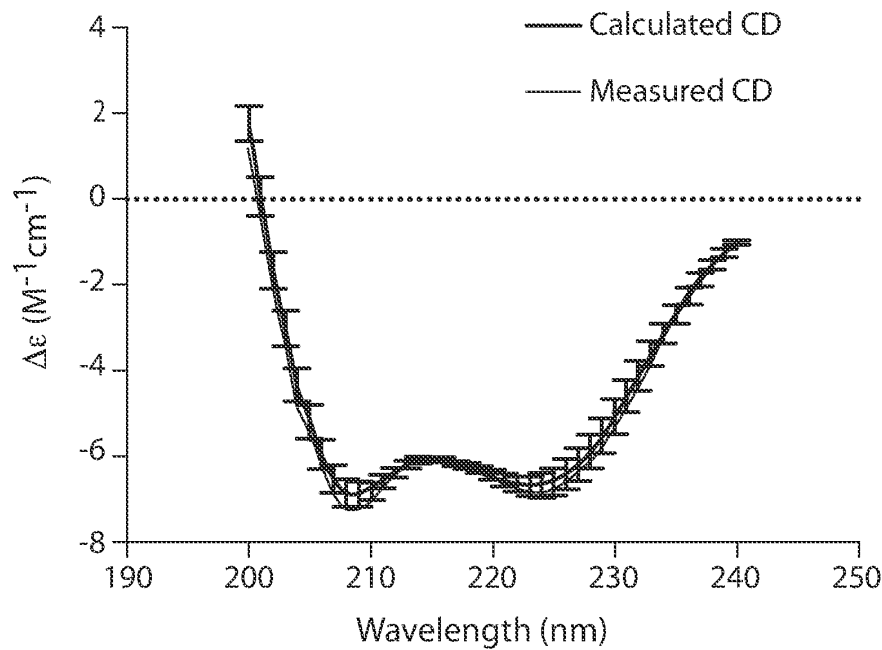
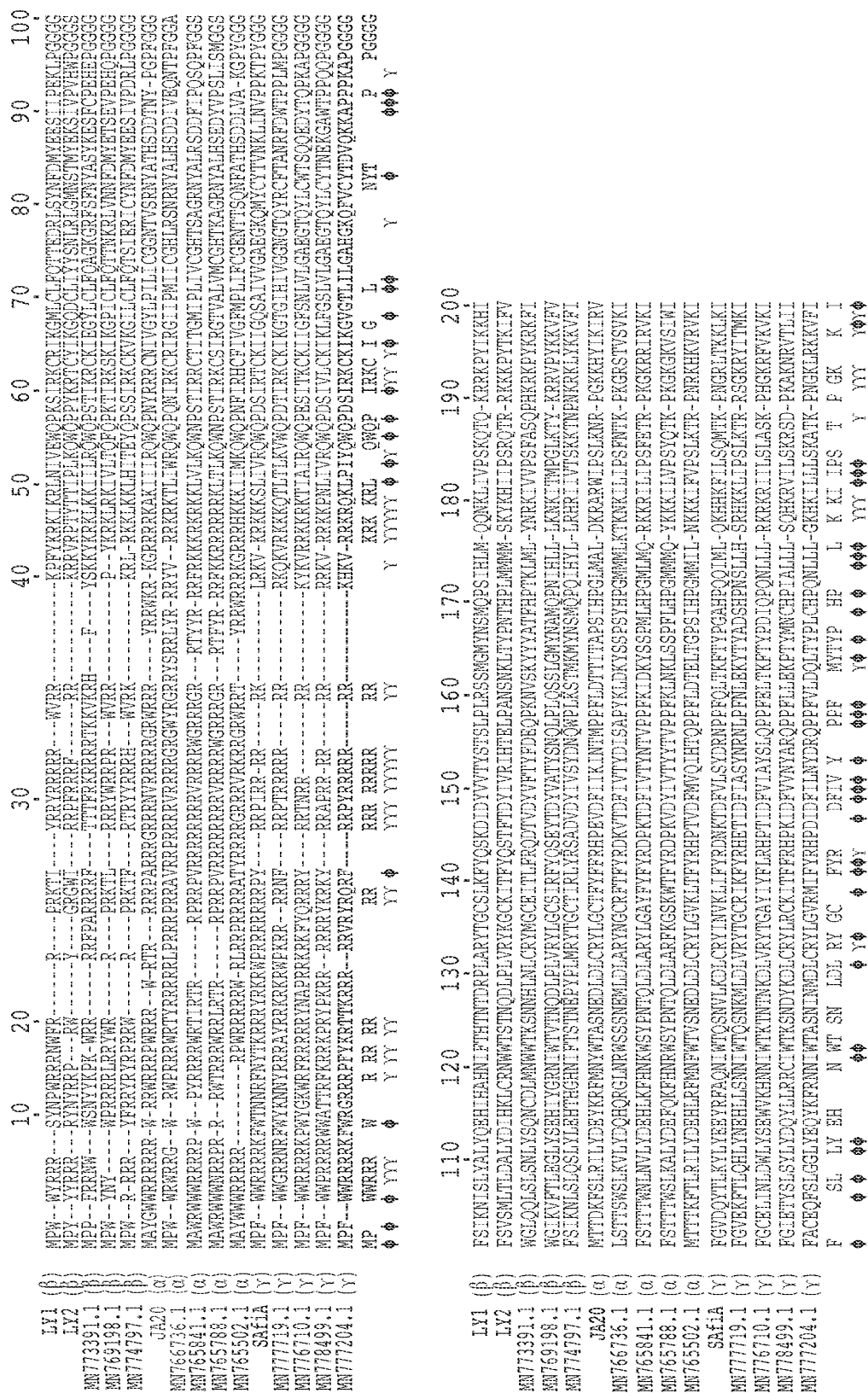
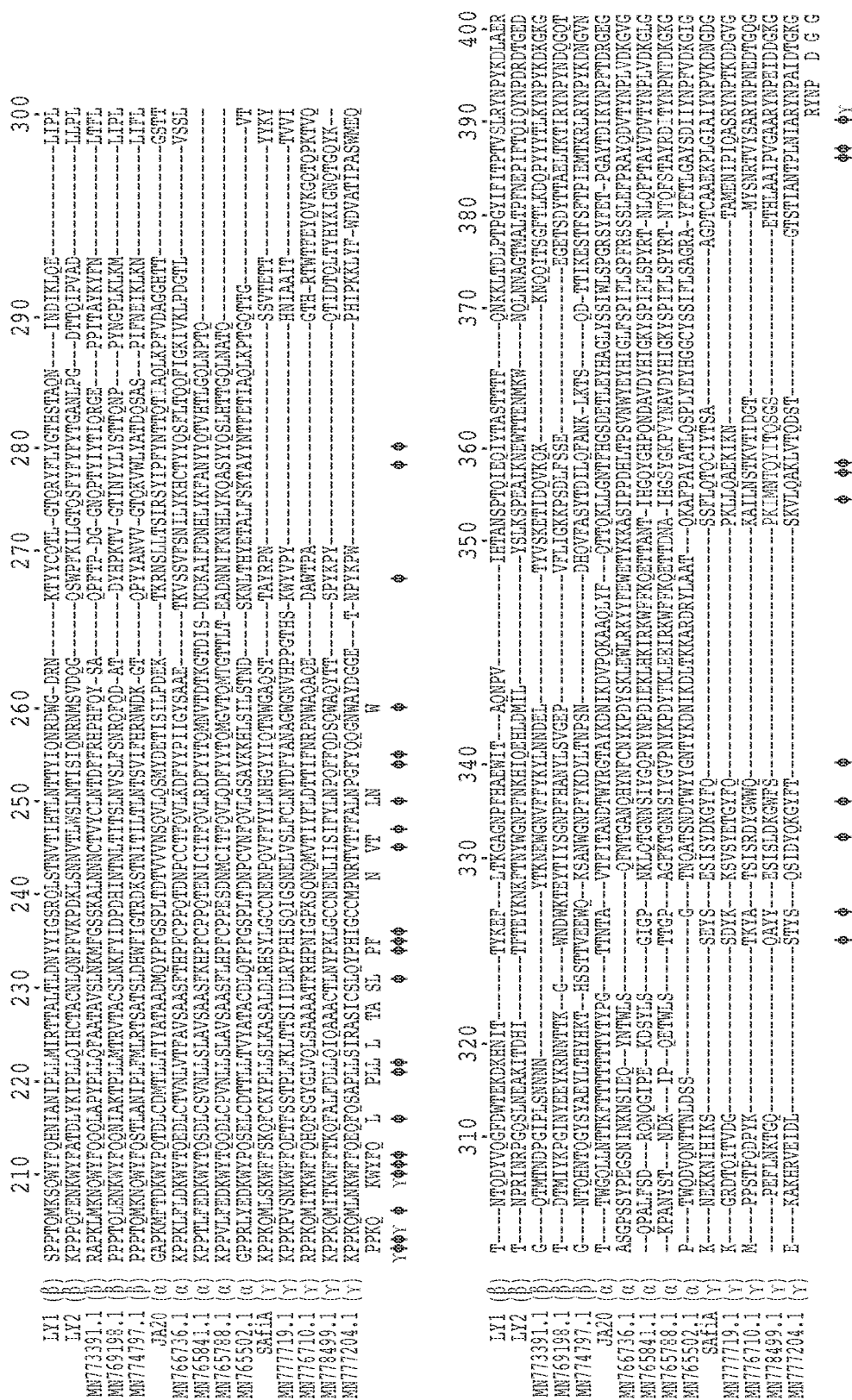
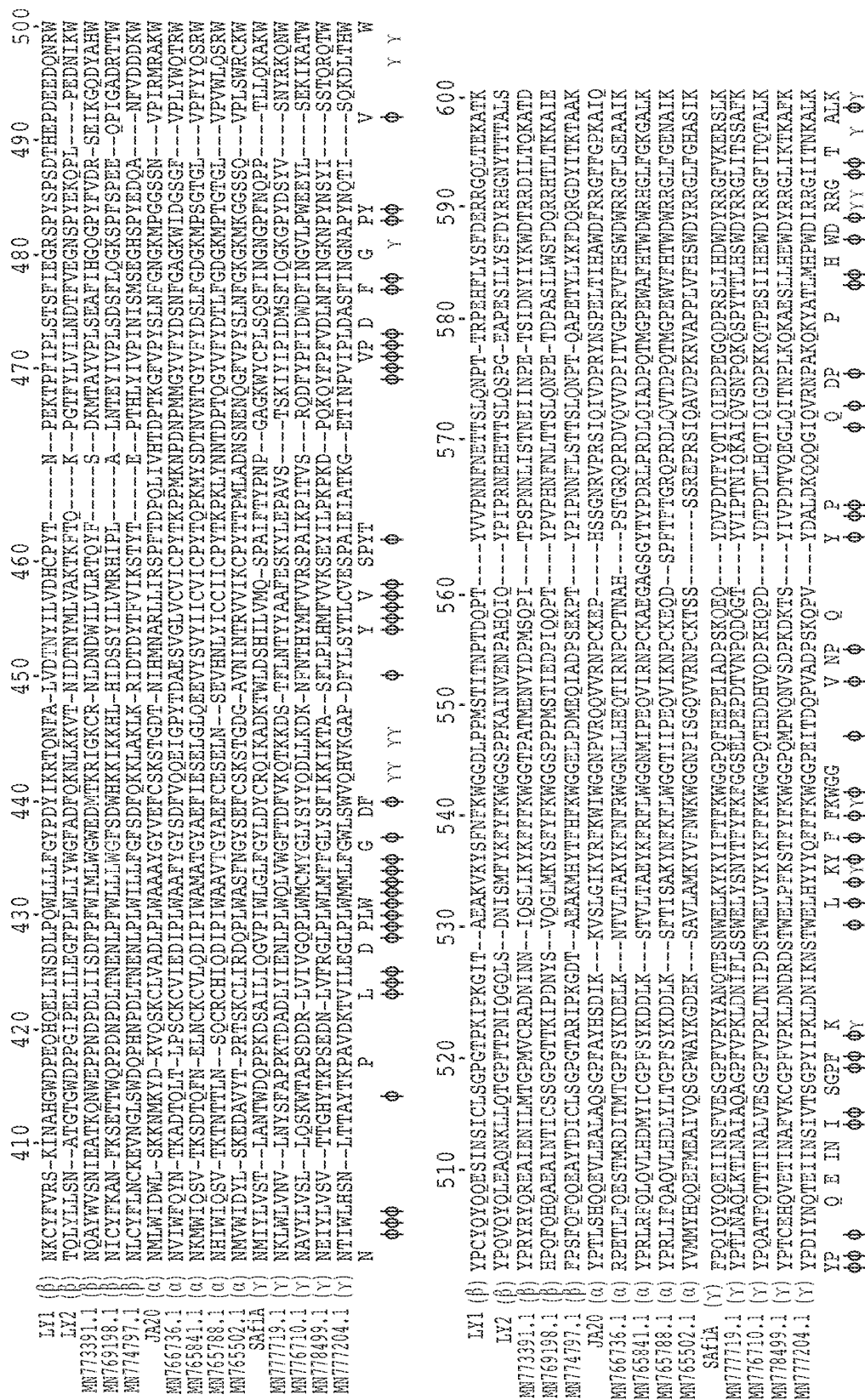


FIG. 37B



॥





333
G
4

	610	620	630	640	650	660	670
LY1 (b)	RLKD-WETKESL-LSTEYRAETPTQAP--CEDP-----						
LY2 (b)	RISQD-WALKDVS-KITEPDRQQLKQALE--CLO-----						
MN773391.1 (b)	RITKS-STYDSNVF-TDGETSTDIPLFTMT--CKA-----						
MN769188.1 (b)	RLXQD-TGKKTIV-TGGSHFTPTTISQEF--T-----						
MN774797.1 (b)	RIRKD-WSTKDSL-SITAPRAEAAQFQDF--S-----						
J420 (a)	RMQOQPTATEFFSA-GRKRPDRDTEVQSDQ--EKEOKESSLFPVKALLRRVPPWEDSEOFQSGSOSSEETATLSQOLKQOLQOQVRVGLKRLLFNOVKIQCNODINPTLPRGGDIAVSFTQAVP						
MN766736.1 (a)	RIRDQPLDYEAISF-MPKRPRTFPP-TTGGQPLPGEQVESSSS-----						
MN765841.1 (a)	RVSEKPDYDADYV-LPKKPRFTFP-TDGSQGOEKQSDLOEISLPP-----						
MN765788.1 (a)	RVSDQSHDADYVA-PKKPRFLFP-TDLGQDES-AFDFTFQELKI-----						
MN765502.1 (a)	RMSEESATPLFTGCPAGKRPDRDTS-VQQAEE-DQ-QKESSS--FVQRQIQFWIHSSQFTQSSQEMQAQTVQEQLIQQLGQFARLKQLETLASQVLYQVQAGQHHPILSSQA						
Saf1A (v)	RMSTY-FSTHTDQQ-ATSEEDIPKKKK--IGPQ-LIVP-----						
MN777719.1 (v)	RMCEH-OTTDITEFE-EDTTC-TIPAKKKKIQGNQ-LORA-----						
MN776710.1 (v)	RMSEN-IQTDTDFQ-SDDS-ASPRKKK--VTKK-WFIT-----						
MN778499.1 (v)	RMLEN-LSIESDVI-PSA--ETPRKROR--VENS-LHYQ-----						
MN777204.1 (v)	RMQON-LSIDSTFE-AGS--TPAKXPRI--TGPC-FTAL-----						
RM							
Y	Φ	Φ	Φ	Φ	Φ	Φ	Φ
				E	L	QQ	

FIG. 38-4

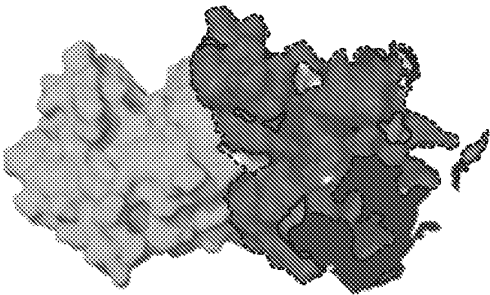


FIG. 39A

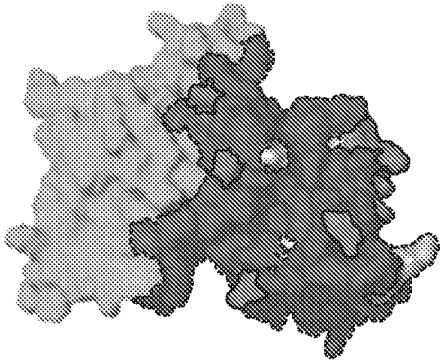


FIG. 39B

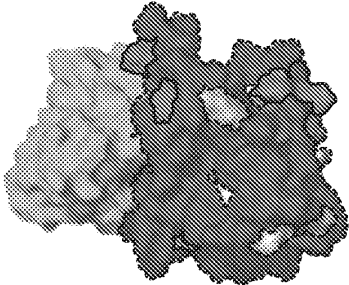


FIG. 39C

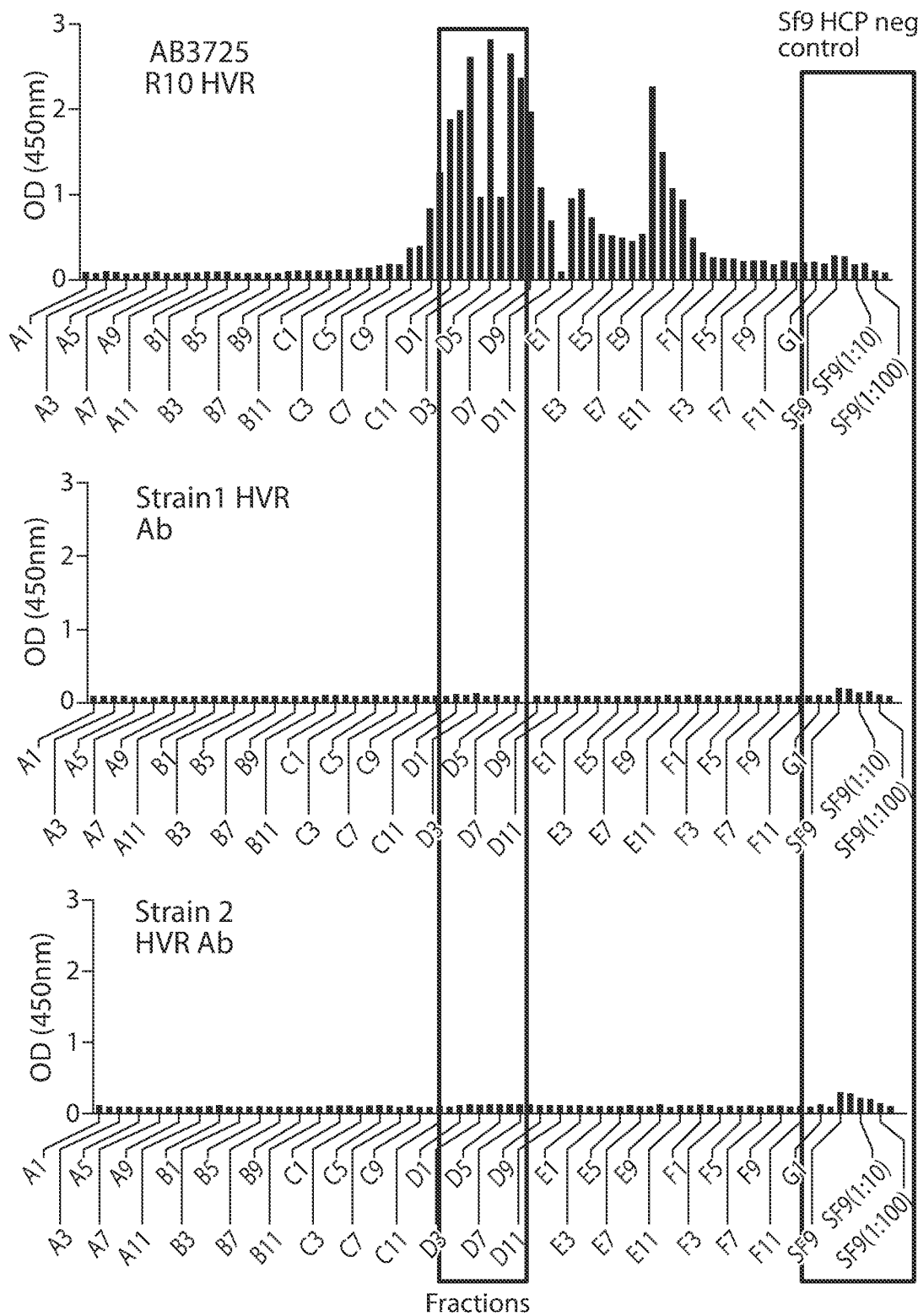


FIG. 40

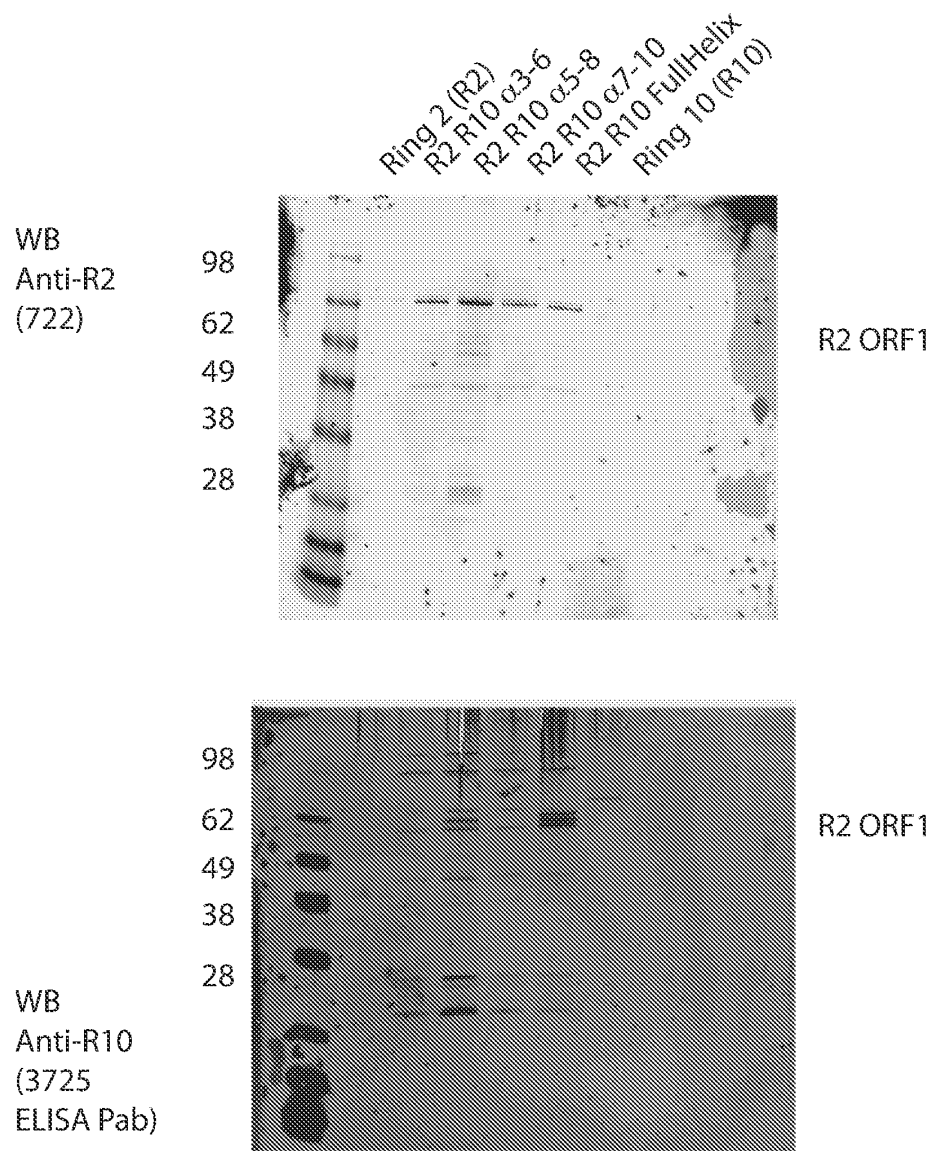


FIG. 41A

		ELISA α
Ring 2	WT	SLKSPEAIKNEW 360
Ring2.10	α 1-4	SLKSPTQIKNEW 360
Ring2.10	α 3-6	SLKSPTQIENEW 360
Ring2.10	α 5-8	SLKSPEAIEQIW 360
Ring2.10	α 7-10	SLKSPEAIKQIY 360
Ring2.10	Full Helix	SLKSPTQIEQIY 360
		***** *:: :

Ring 2 point mutations K357E, N358Q and E359I
Permit western blot recognition by AB3725

FIG. 41B

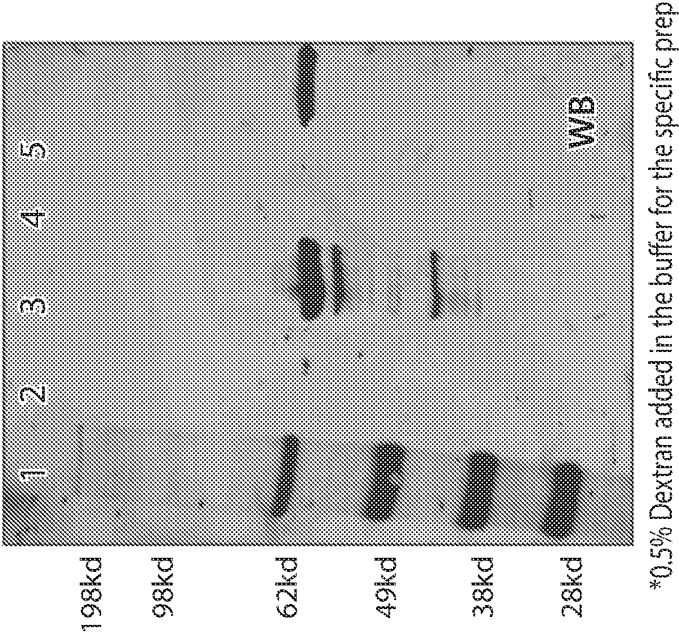


FIG. 42B

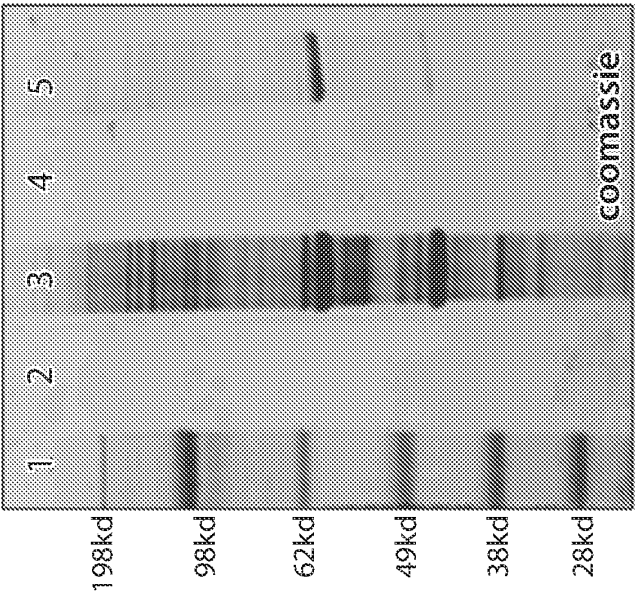


FIG. 42A

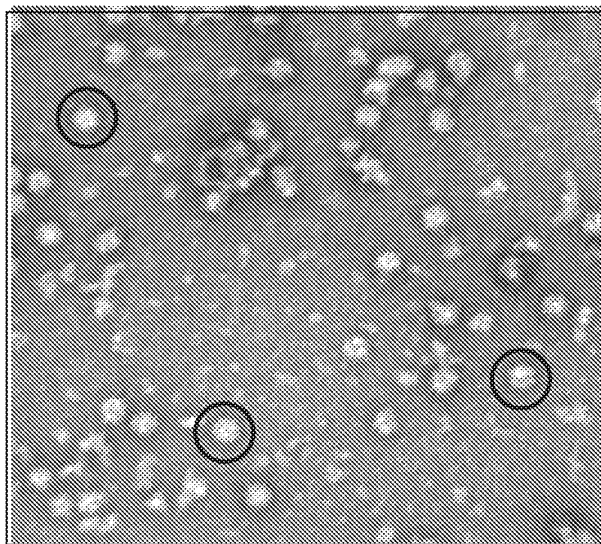


FIG. 43

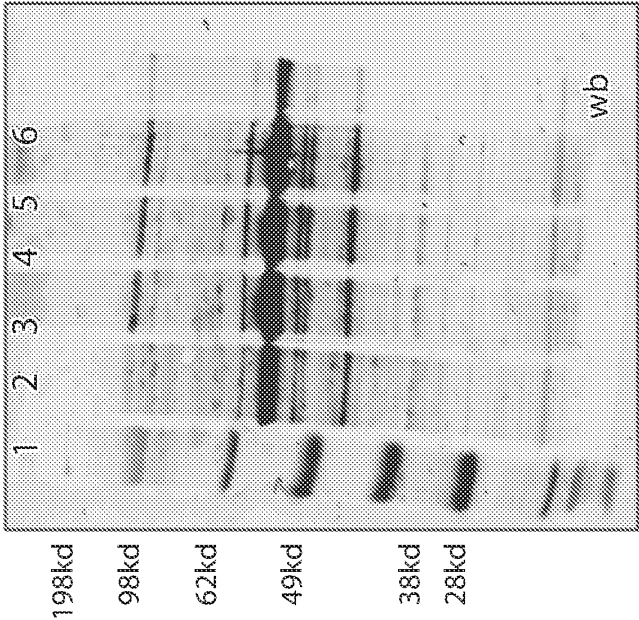


FIG. 44B

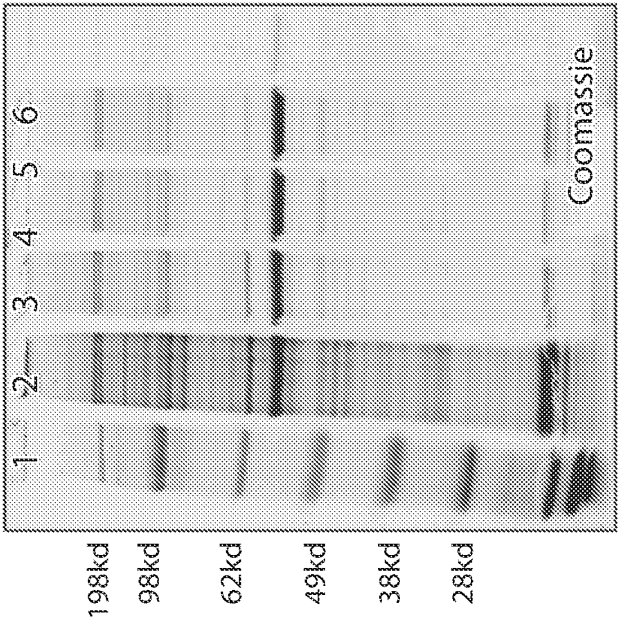


FIG. 44A

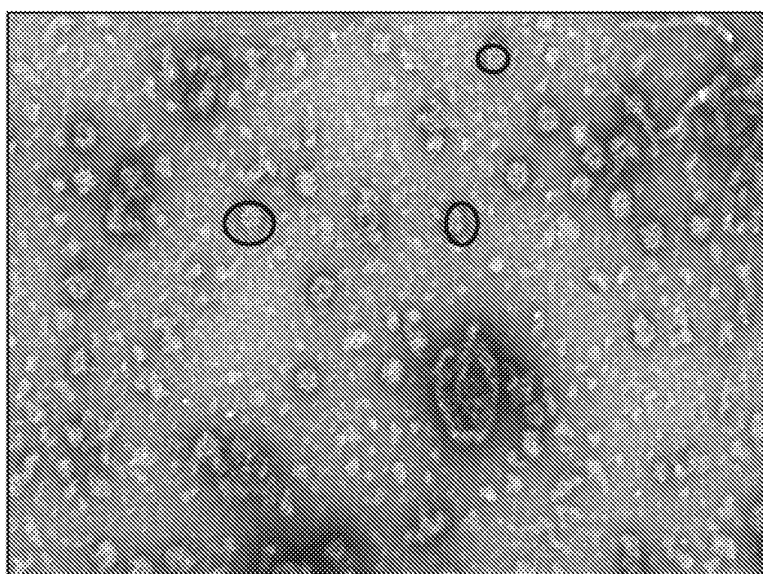


FIG. 45

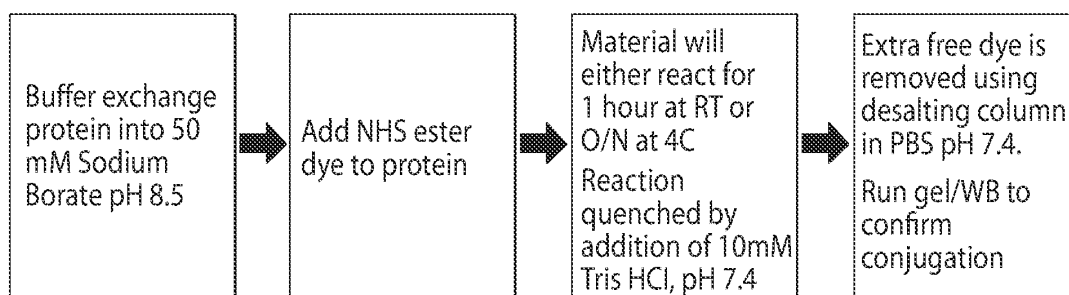


FIG. 46

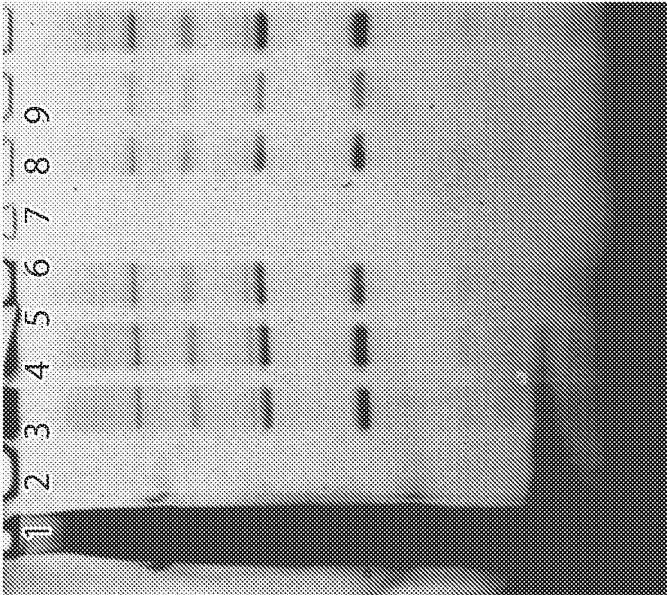


FIG. 47B

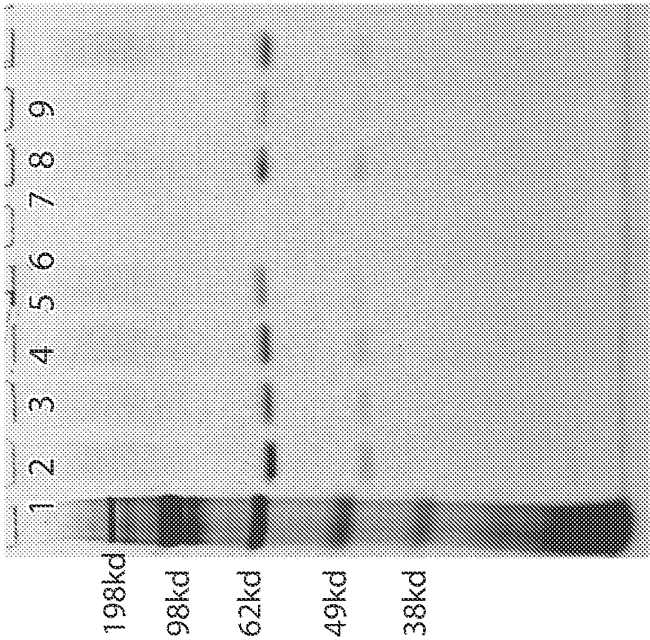


FIG. 47A

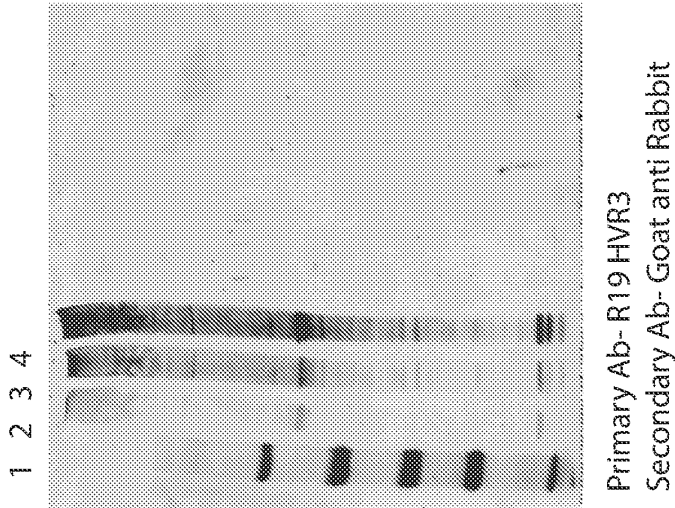


FIG. 48B

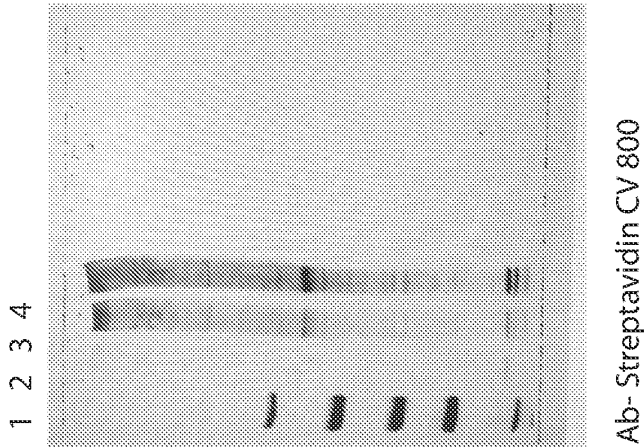


FIG. 48A

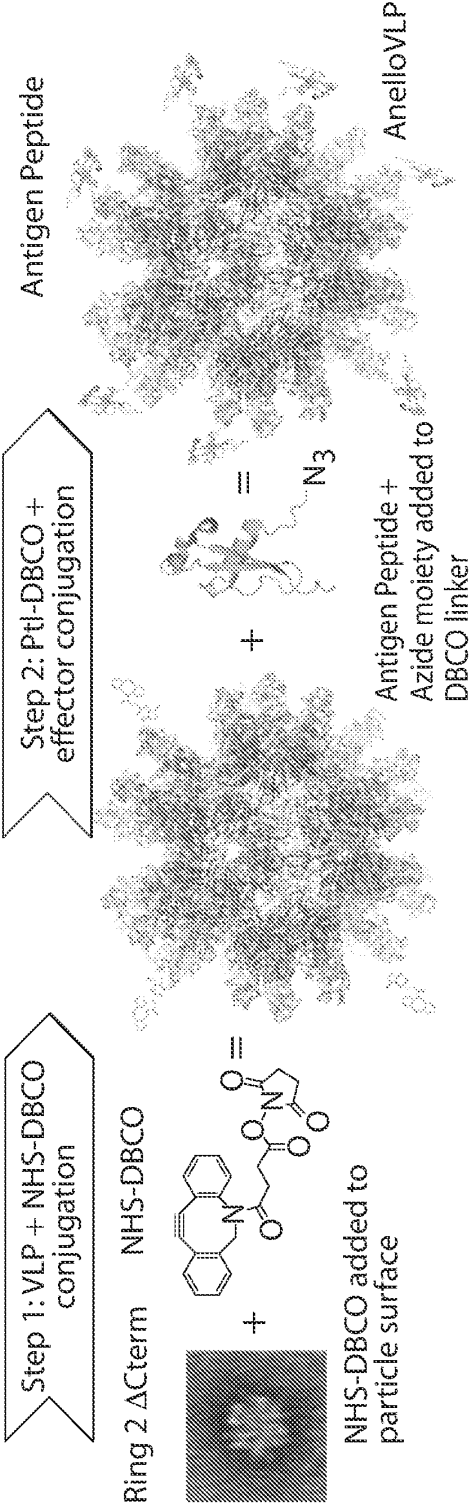


FIG. 49

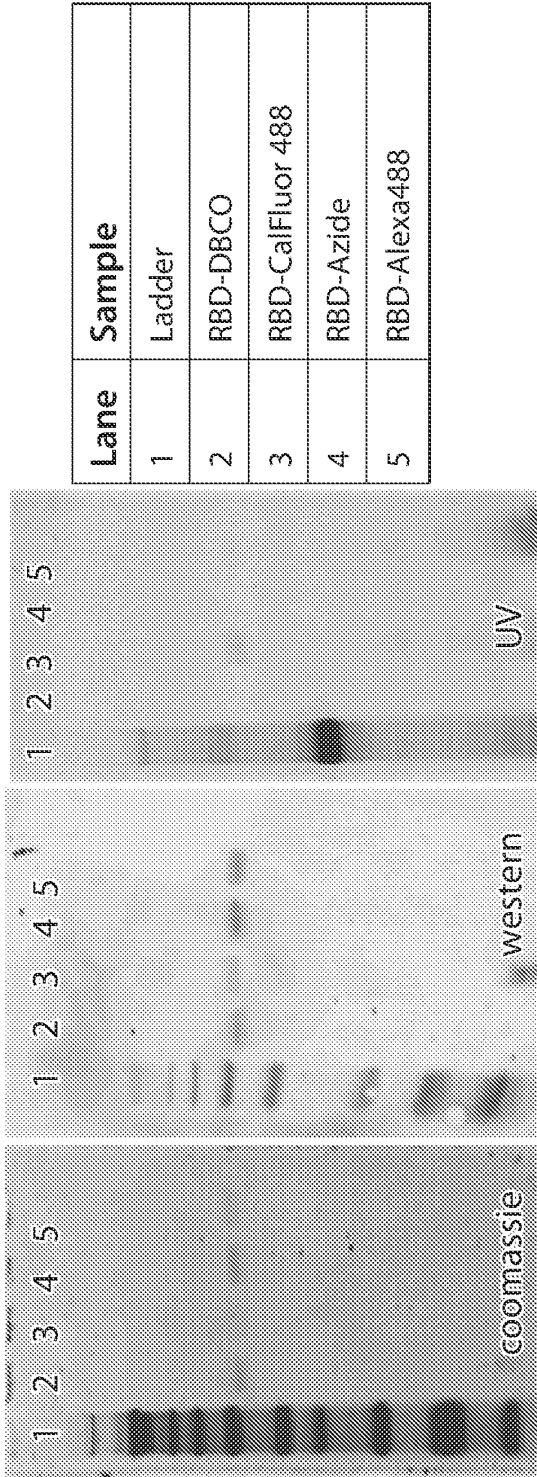


FIG. 50

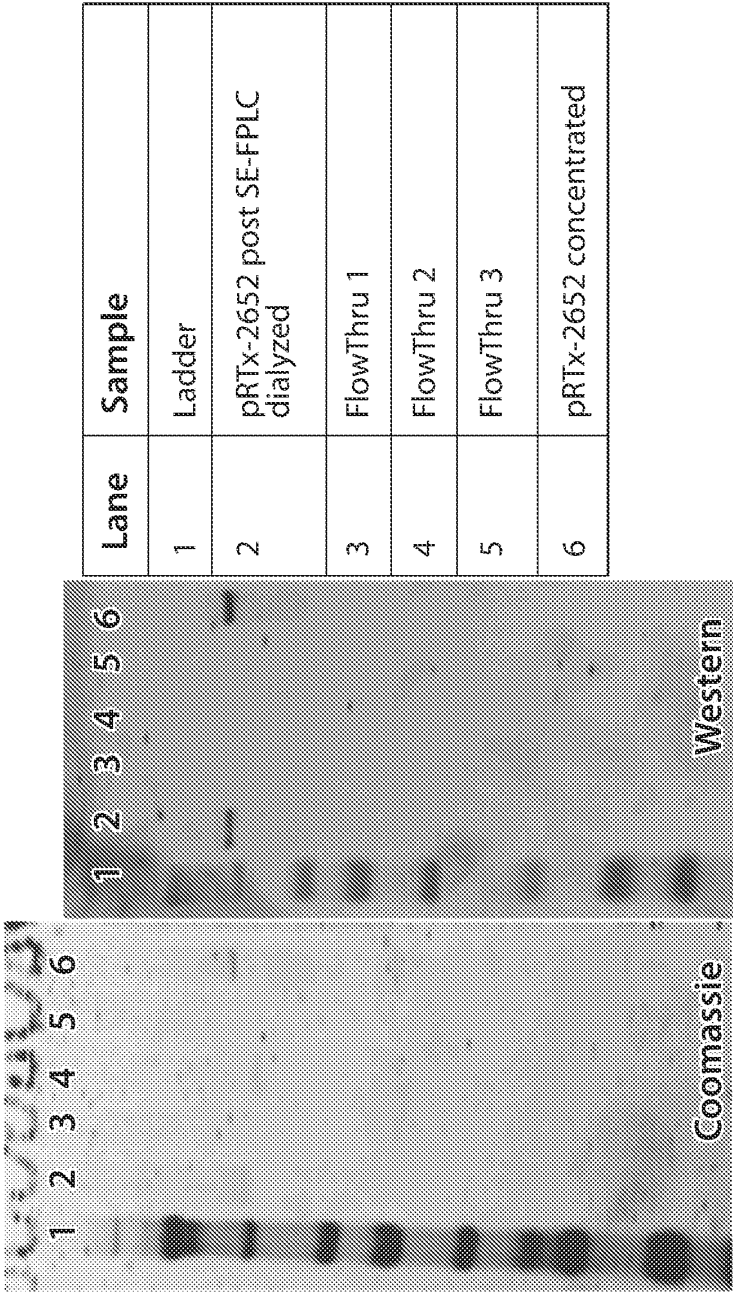


FIG. 51

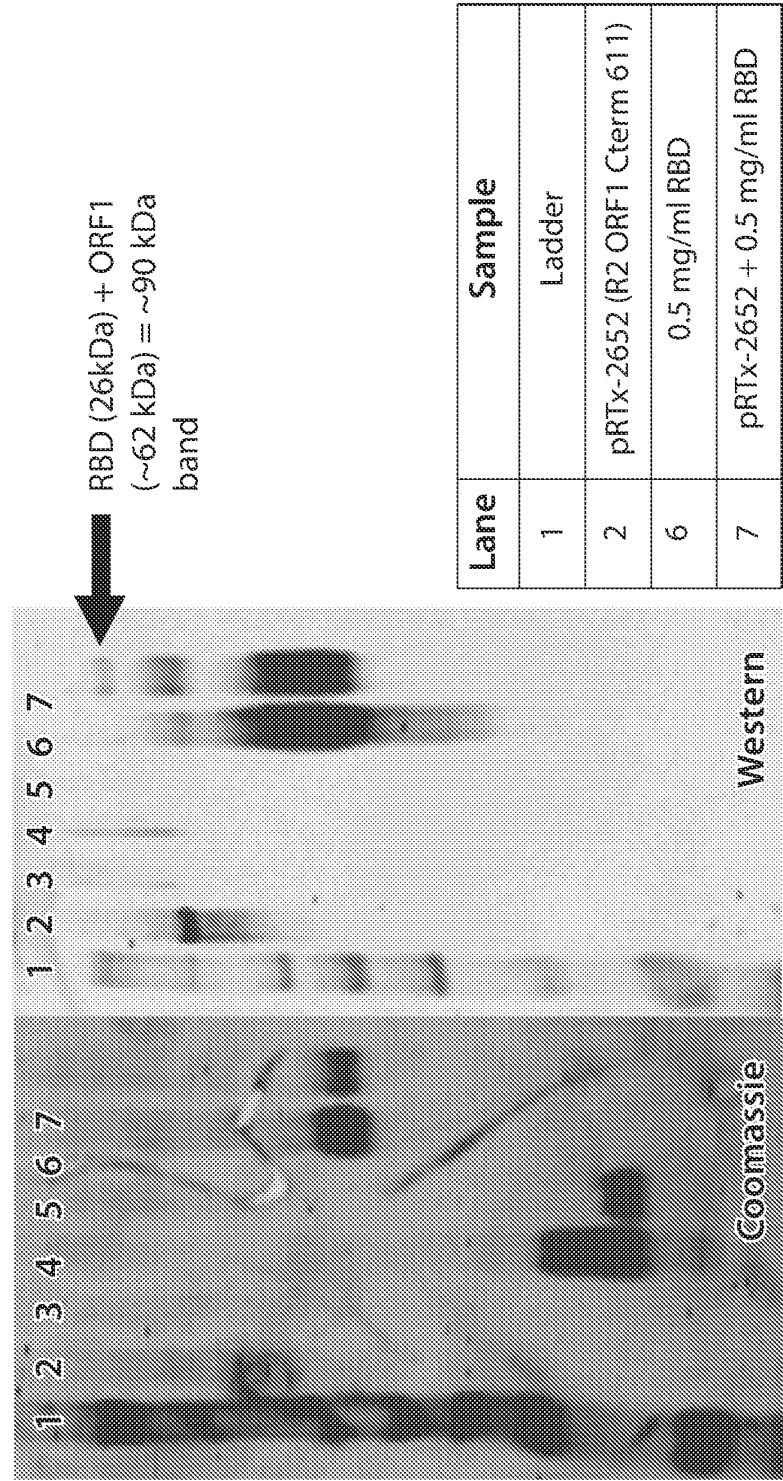


FIG. 52

