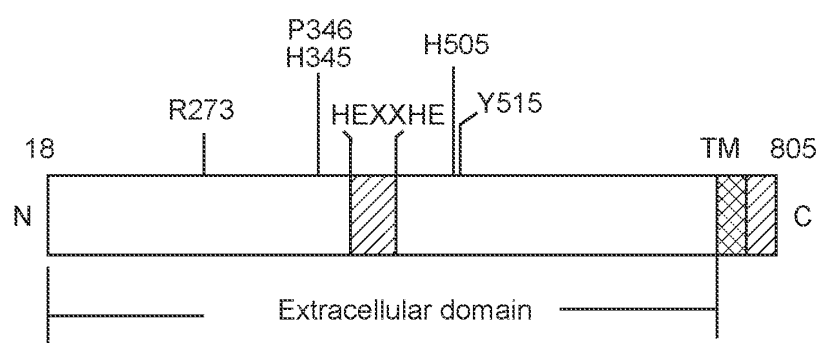




TM: transmembrane domain
Zinc-binding motif: H374E375XXH378...E402

FIG. 1

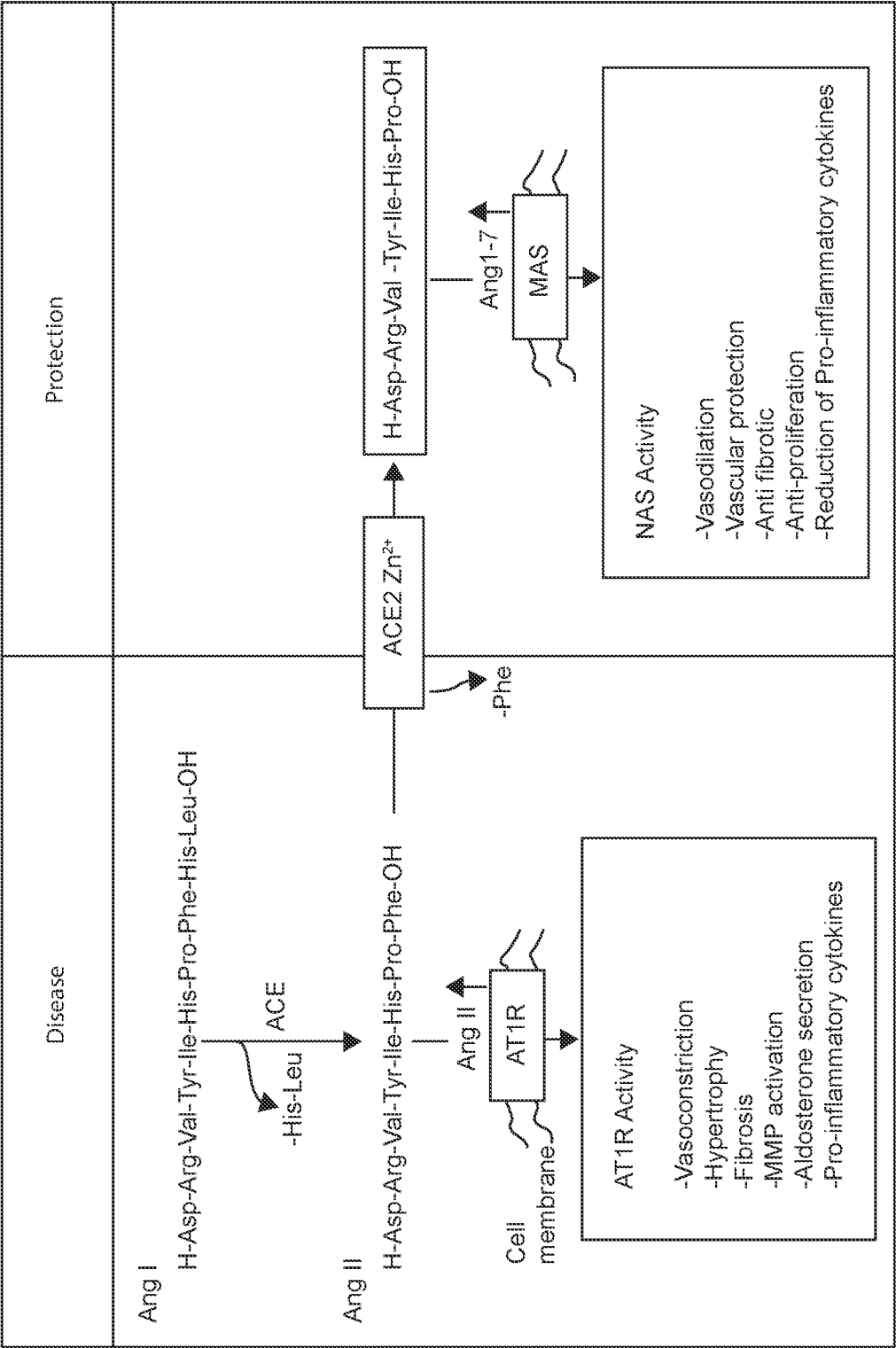


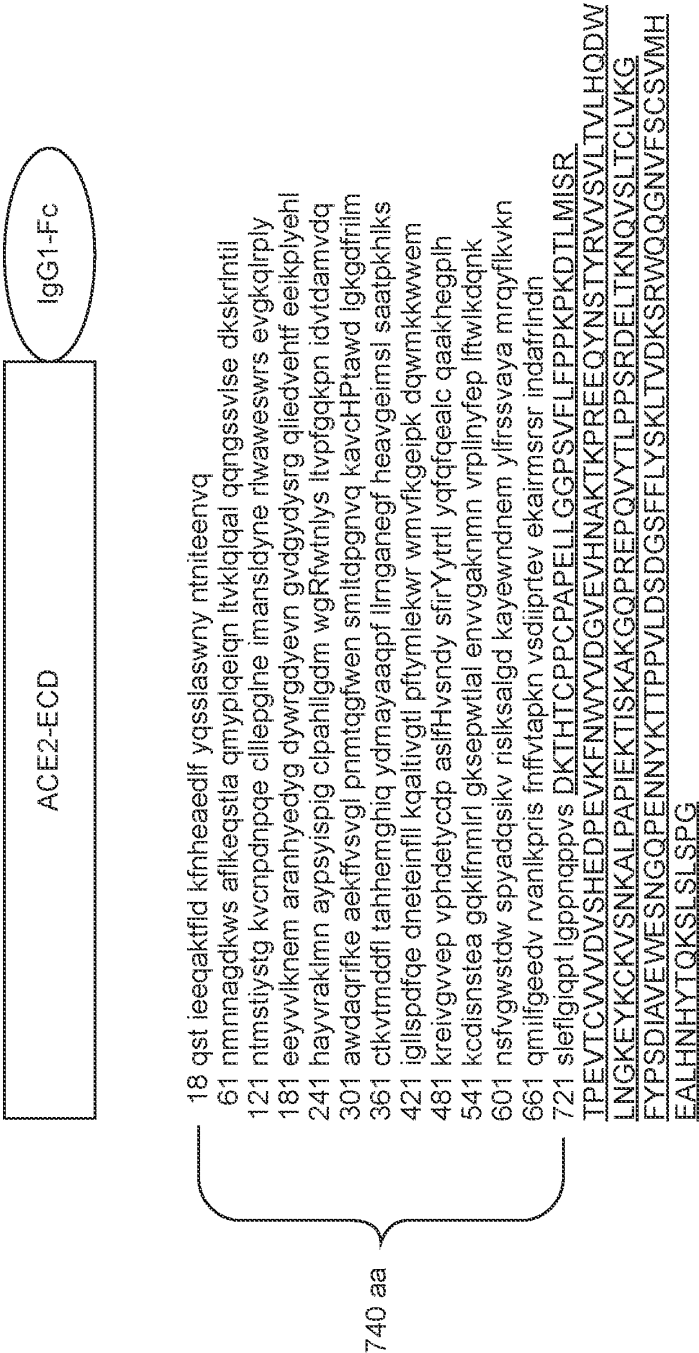
FIG. 2

Length		Whole Protein
► Molecular Weight		805 aa
► Extinction Coefficient (280 nm)		92,463.25 Da
► Absorbance (280 nm, 0.1%)		175,670 M ⁻¹ cm ⁻¹
Isoelectric Point (pI)		1.90
Charge at pH 7.0 ▼		5.21
		-21.44
Amino Acid		Number Percent
A Ala	Alanine	51 6.34
C Cys	Cysteine	8 0.99
D Asp	Aspartic Acid	43 5.34
E Glu	Glutamic Acid	56 0.90
F Phe	Phenylalanine	39 4.84
G Gly	Glycine	43 5.34
H His	Histidine	16 1.99
I Ile	Isoleucine	40 4.97
K Lys	Lysine	47 5.84
L Leu	Leucine	76 9.44
M Met	Methionine	27 3.35
N Asn	Asparagine	54 6.71
P Pro	Proline	37 4.60
Q Gln	Glutamine	38 4.72
R Arg	Arginine	31 3.85
S Ser	Serine	54 6.71
T Thr	Threonine	39 4.84
V Val	Valine	50 6.21
W Trp	Tryptophan	23 2.86
Y Tyr	Tyrosine	33 4.10

1 msssswlls lvavtaaqst ieeqaktfld kfnheaedlf yqsslaswny ntniteenvq
61 nmnnagdkws afikeqstla qmypyqeign ltvklqlqal qqngssvlse dkskrlntil
121 ntmtsiystg kvcpndnpqe cllepgline imansldyne rlwaweswrs evgqlrply
181 eeyvvlknem aranhyledyg dywrgdyevn gvdydyysrg ltvpgqkpn idvtdamvdq
241 hayvraklmn aypsyispig cipahllgdm wgrfwnliys ltvpgqkpn idvtdamvdq
301 awdaqrifke aekffvsvgl pnmtdqfwen smldpognvq kavchptawd lgkgdfrlm
361 ctkvtmddfl tahemghiq ydmayaaqpf lrrnganegf heavgeimsl saatpkhiks
421 igllspdfqe dneiteinfl kqaltivgtl pftymlekwr wmvfkgeipk dqwmkkwwem
481 kreivgvvep vphdetycdp aslfhvsndy sfirytrtl yqfqfqaic qaakhegplh
541 kcdisntea gqklfnmirl gksepwtlal envvgaknmn vrpilnyfep lftwlkdqnk
601 nsfvgwstdw spyadqsikv risksalgd kayewndnem ylfrrsvaya mrqyflkvkn
661 qmilfgeedv rvanikpris fnffvtapkn vsdiiprtv ekairmsr indafrindn
721 siefigiqpt lgppnqppvs iwlivgvvm gvivvgivil iftgirdrkk knkarsgenp
781 yasidiske nnpqfntdd vqtsf (805)

Functional Regions of ACE2
1-17: Signal peptide
18..740 /region_name="Topological domain"
741..761 /region_name="Transmembrane region"
762..805 /region_name="Topological domain"

FIG. 3



The underlined region is human IgG1 Fc sequence

FIG. 4

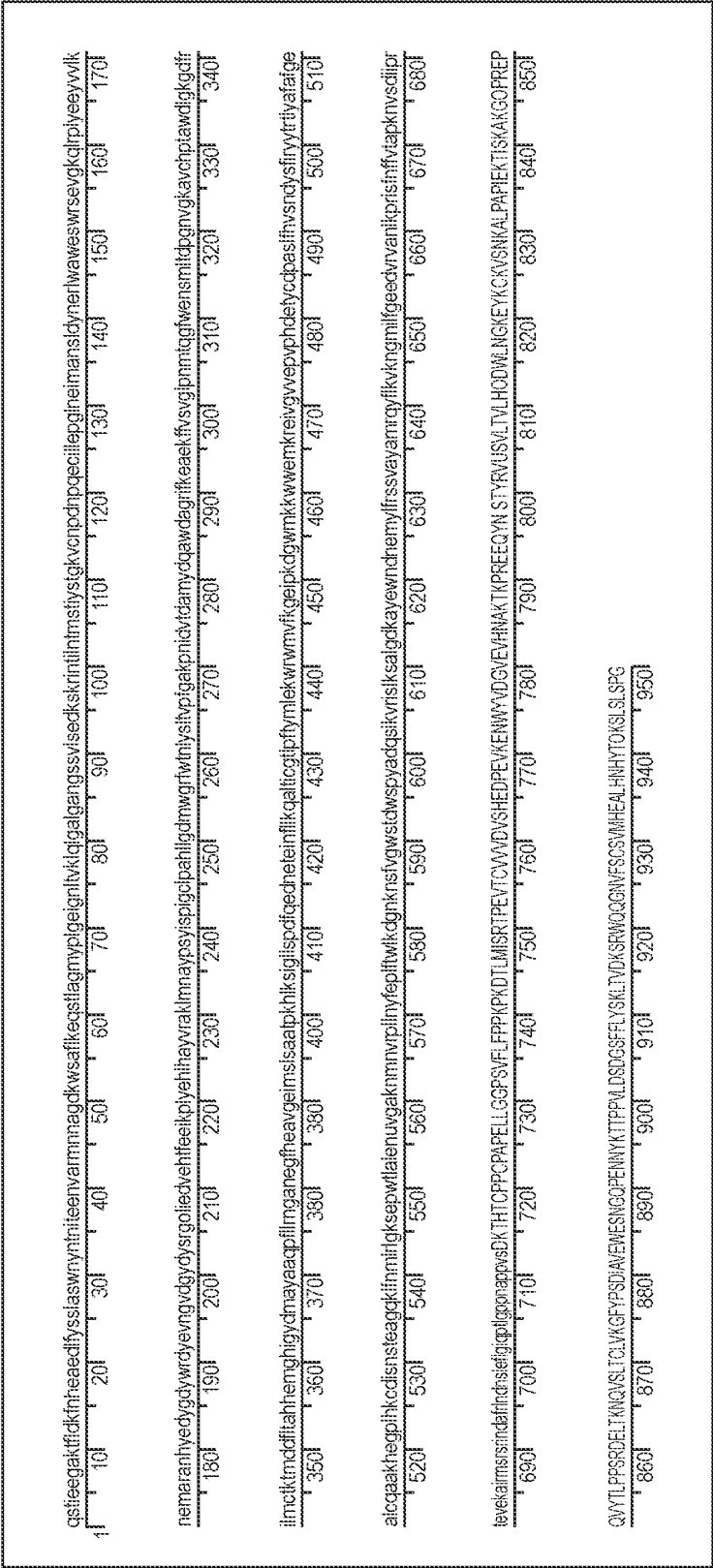
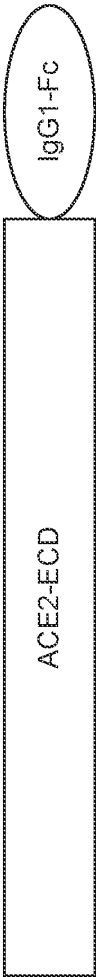


FIG. 5A

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Length			Whole Protein		Selection	
▶ Molecular Weight			950 codons			
▶ Extinction Coefficient (280 nm)			-			
▶ Absorbance (280 nm, 0.1%)			-			
Isoelectric Point (pI)			-			
Charge at pH 7.0			-			
Amino Acid			Number	Percent	Number	Percent
A	Ala	Alanine	53	5.58		
C	Cys	Cysteine	14	1.47		
D	Asp	Aspartic Acid	50	5.26		
E	Glu	Glutamic Acid	69	7.26		
F	Phe	Phenylalanine	42	4.42		
G	Gly	Glycine	46	4.84		
H	His	Histidine	23	2.42		
I	Ile	Isoleucine	35	3.68		
K	Lys	Lysine	61	6.42		
L	Leu	Leucine	88	9.26		
M	Met	Methionine	27	2.84		
N	Asn	Asparagine	60	6.32		
P	Pro	Proline	57	6.00		
Q	Gln	Glutamine	45	4.74		
R	Arg	Arginine	34	3.58		
S	Ser	Serine	65	6.84		
T	Thr	Threonine	51	5.37		
V	Val	Valine	63	6.63		
W	Trp	Tryptophan	25	2.63		
Y	Tyr	Tyrosine	41	4.32		
*	*	STOP	1	-		

FIG. 5B

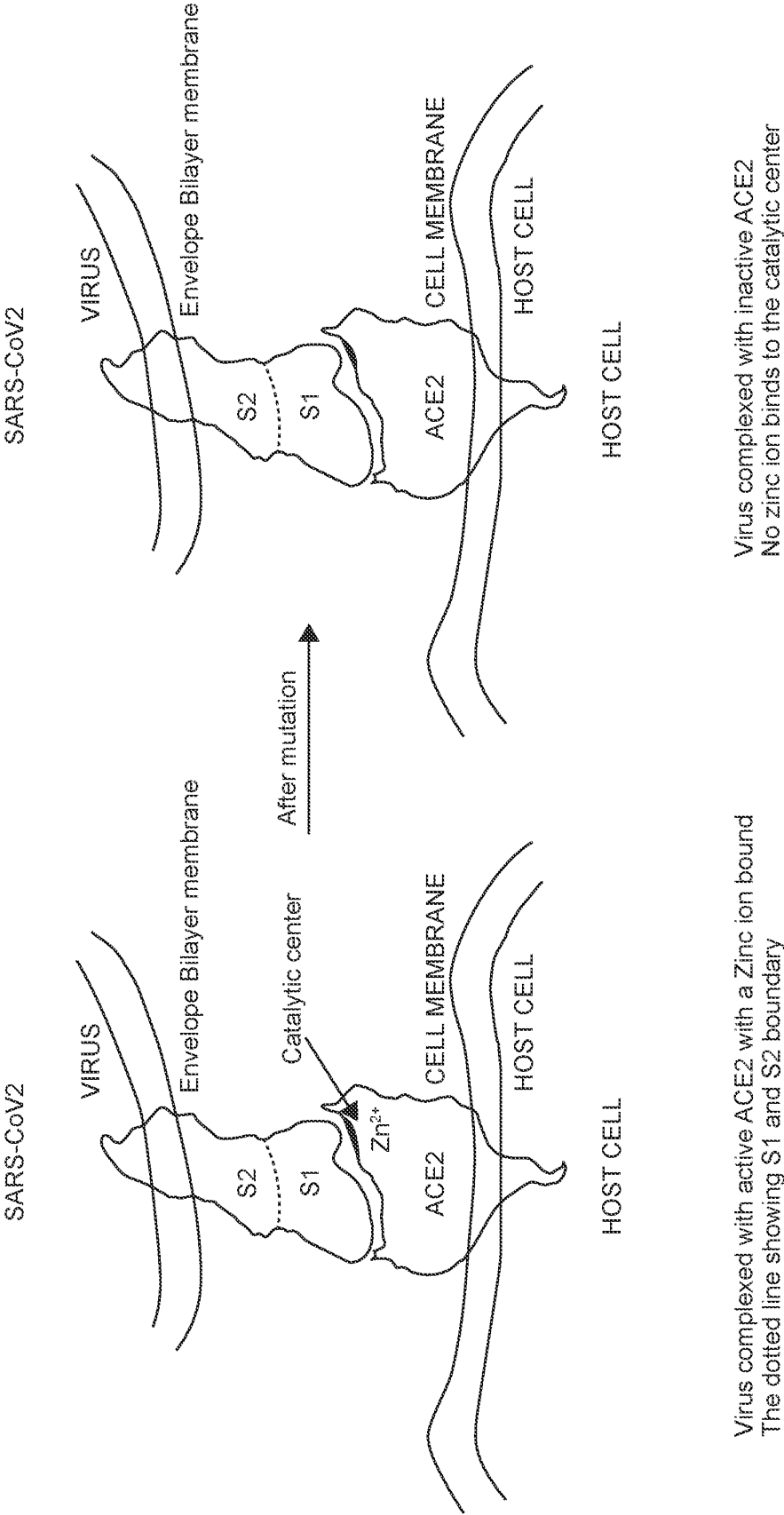


FIG. 6

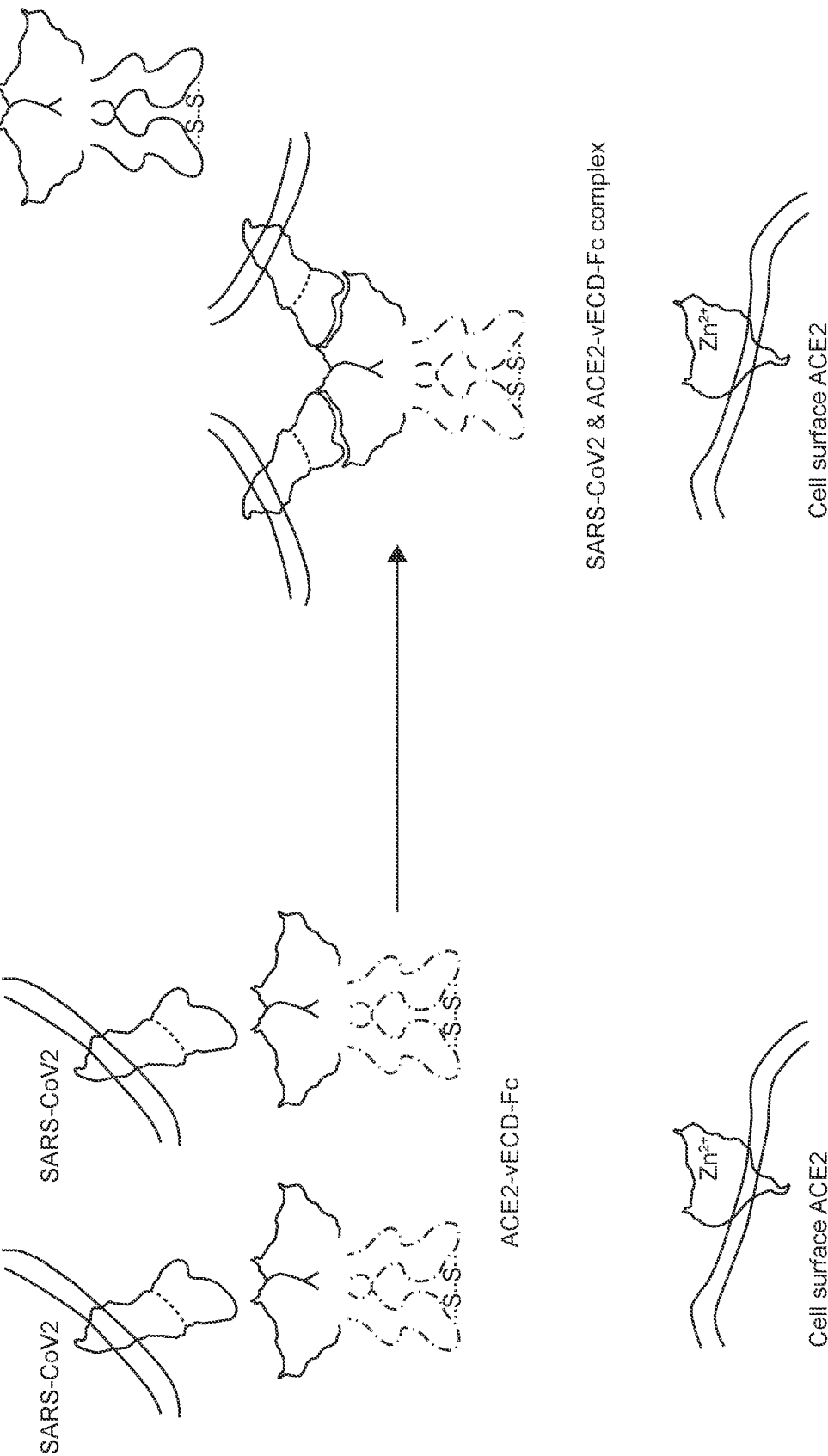


FIG. 7

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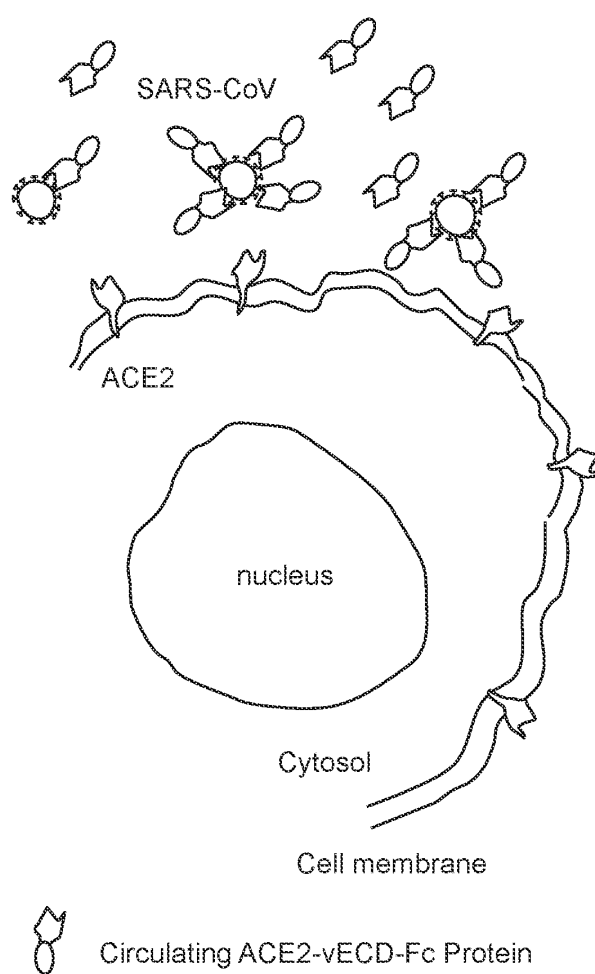


FIG. 8

Chain B, Angiotensin-converting enzyme 2 [Homo sapiens]
Sequence ID: 6M17_B Length: 814 Number of Matches: 1
[See 5 more title\(s\)](#) [Identical Proteins](#)

Range 1: 27 to 749		GenPept	Graphics	▼ Next Match ▲ Previous	
Score	Expect	Method	Identities	Positives	Gaps
1509 bit(3906)	0.0	Compositional matrix adjust.	719/723(99%)	721/723(99%)	0/723(0%)
Query 1		QSTIEEQAKTFLDKFNHEAEDLFYQSSSLASWNYNTNTEENVQNMNAGDKWSAFLKEQS	60		
Sbjct 27					
Query 61		TLAQMYPLQEIQNLTVKLQALQOQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDN	120		
Sbjct 87					
Query 121		PQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEYVVLKNEMARANIHYE	180		
Sbjct 147					
Query 181		DYGDYWRG DYEVNGVDGYDSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYIS	240		
Sbjct 207					
Query 241		PIGCLPAHLLGDMWGREWTNLYSLTVFFGQKPNIDVTDAMVDQAWDAQRIKFAEKFFVS	300		
Sbjct 267					
Query 301		VGLPNMTQGFWENSMLTDPGNVOKAVCHPTANDLGKGDFRILMCTKVTMDDFLTAHAQMG	360		
Sbjct 327					
Query 361		AIQYDMAYAAQPFLLRNGANEGFHQAVGEIMSLSAATPKHLKSGILLSPDFQEDNETEIN	420		
Sbjct 287		H E			
Query 421		FLLKQALTIVGTLPTFYMLEKWRWMVFKGEIPKDQWMKKWWMEMKREIVGWEPVPHDETY	480		
Sbjct 447					
Query 481		CDPASLFHVSNDYSFIRYYTRTLTYQFQFQEALCQAAKHEGPHKCDISNSTEAGQKLFNM	540		
Sbjct 507					
Query 541		LRLGKSEPWTLAENVVGAKNMNVRPLLNYFEPLFTWLDQNKNSFVGWSTDWSPYADQS	600		
Sbjct 567					
Query 601		IKVRISLKSALGDKAYEWDNDNEMYLFRSSVAYAMRQYFLVKVKNQMLFGEEDVRVANLKP	660		
Sbjct 627					
Query 661		RISFNFFVTAPKNVSDIIPRTEVEKAIMRSRINDAFRLNDNSLEFLGIQPTLGPPNQP	720		
Sbjct 687					
Query 721		PVS	723		
Sbjct 747			749		

FIG. 9

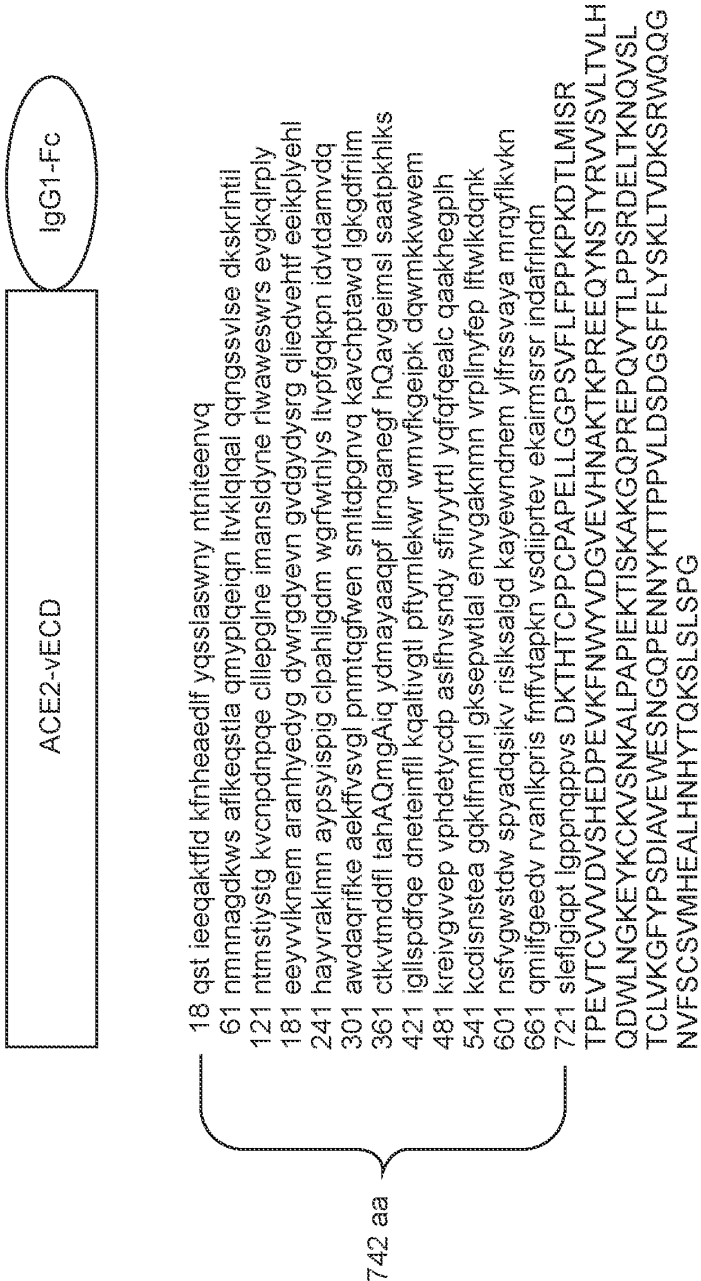


FIG. 10

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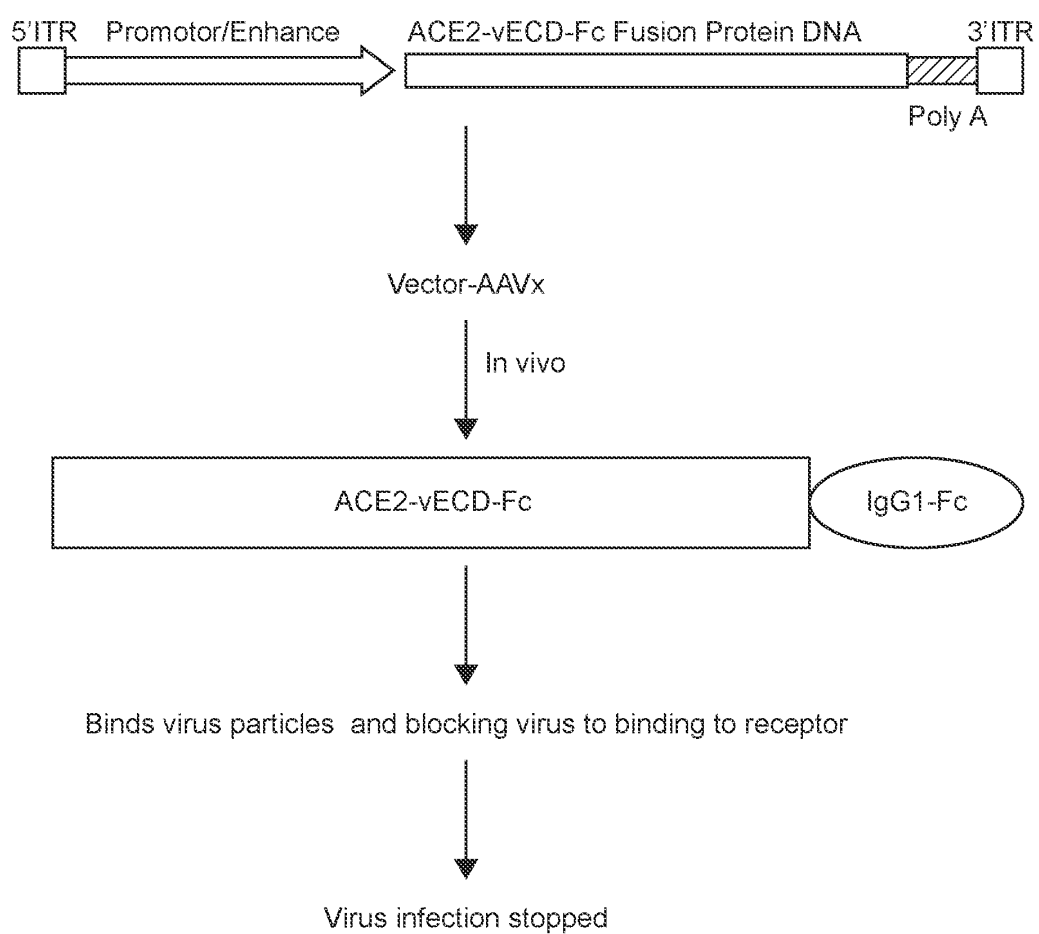
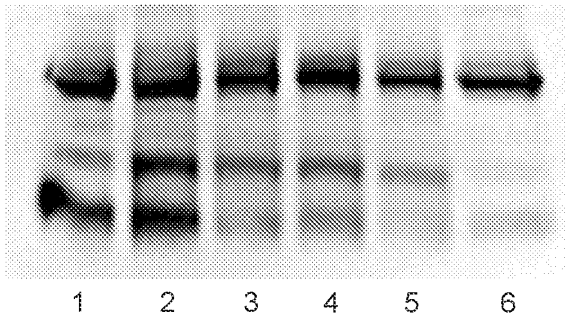


FIG. 11



Lane	ACE2-ECD Variant	ID
1	AMI 080	ACE2-ECD-Fc wt
2	AMI 090	ACE2-vECD-Fc (E402Q)
3	AMI 081	ACE2-vECD-Fc (E402Q,G466D)
4	AMI 082	ACE2-vECD-Fc (E374Q,402Q)
5	AMI 083	ACE2-vECD-Fc (E375Q,402Q)
6	AMI 084	ACE2-vECD-Fc (E375Q, E402Q,H374A)

FIG. 12

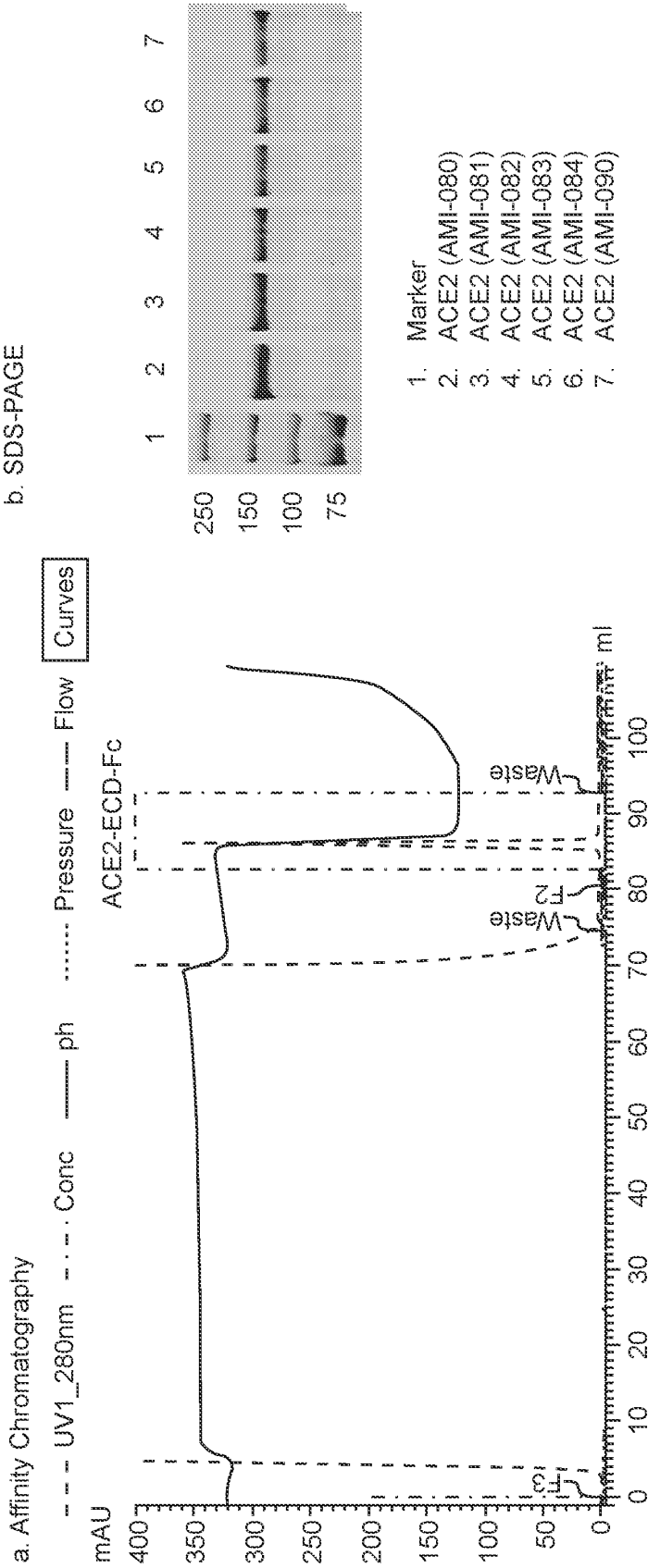


FIG. 13

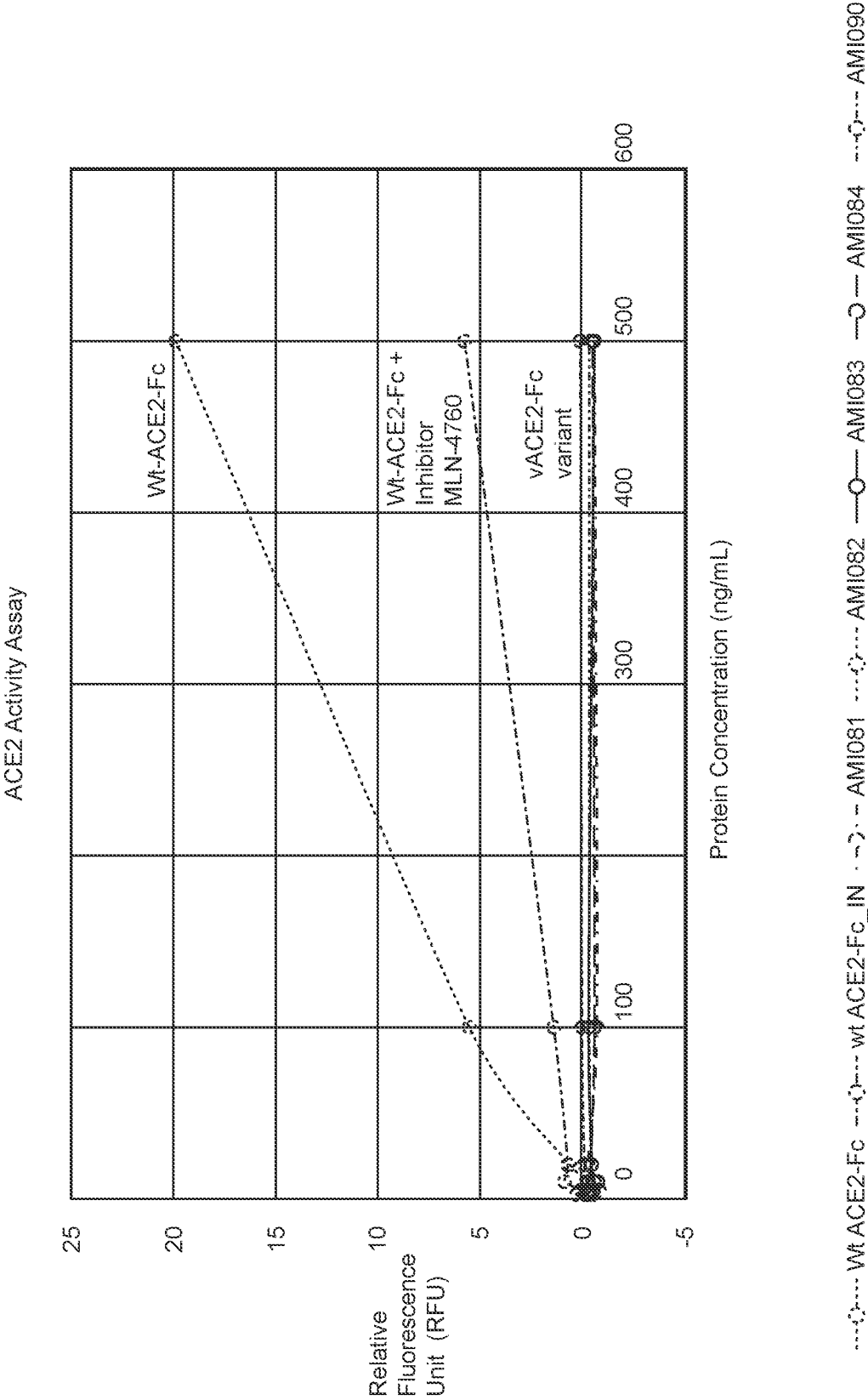


FIG. 14

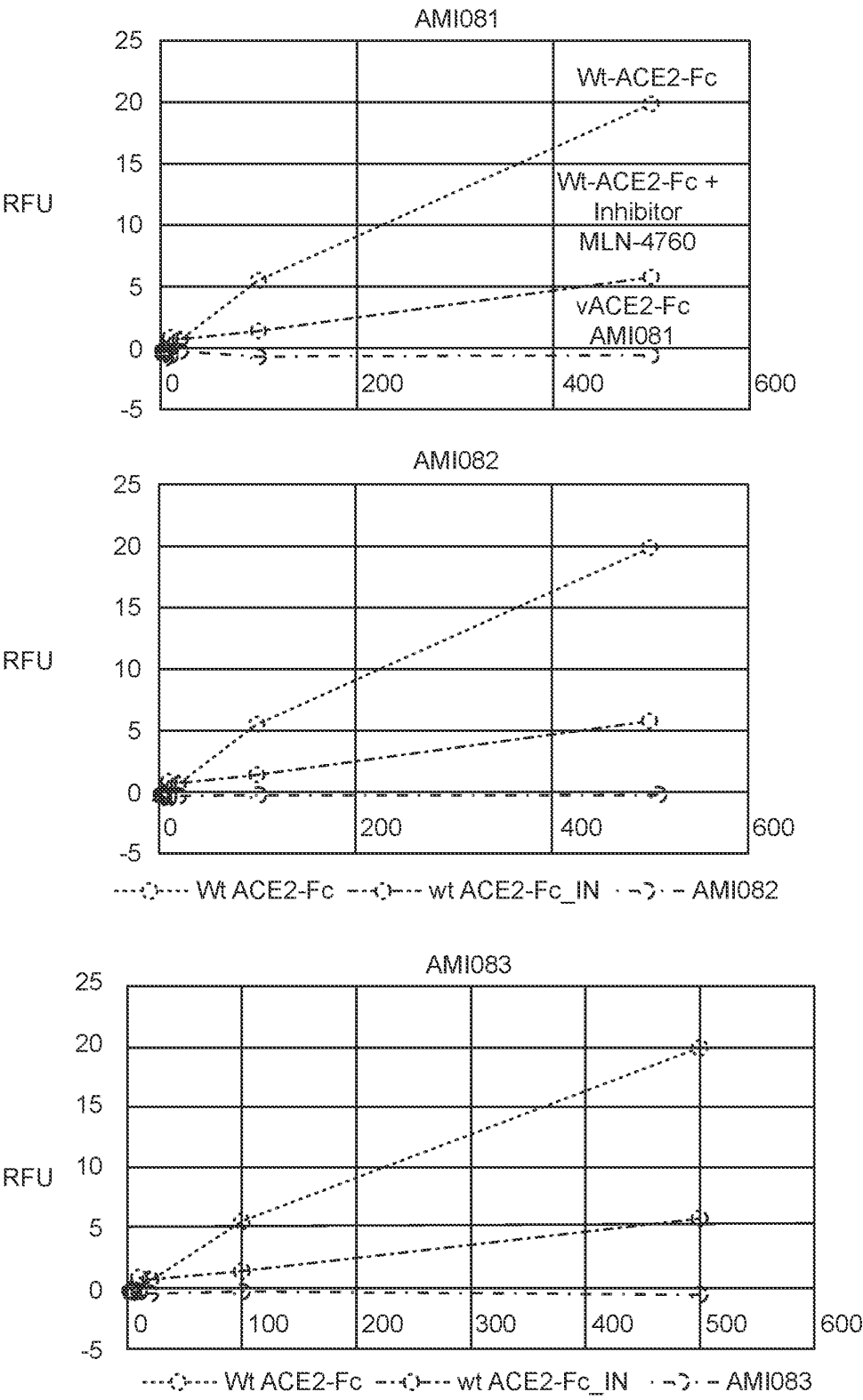


FIG. 15A

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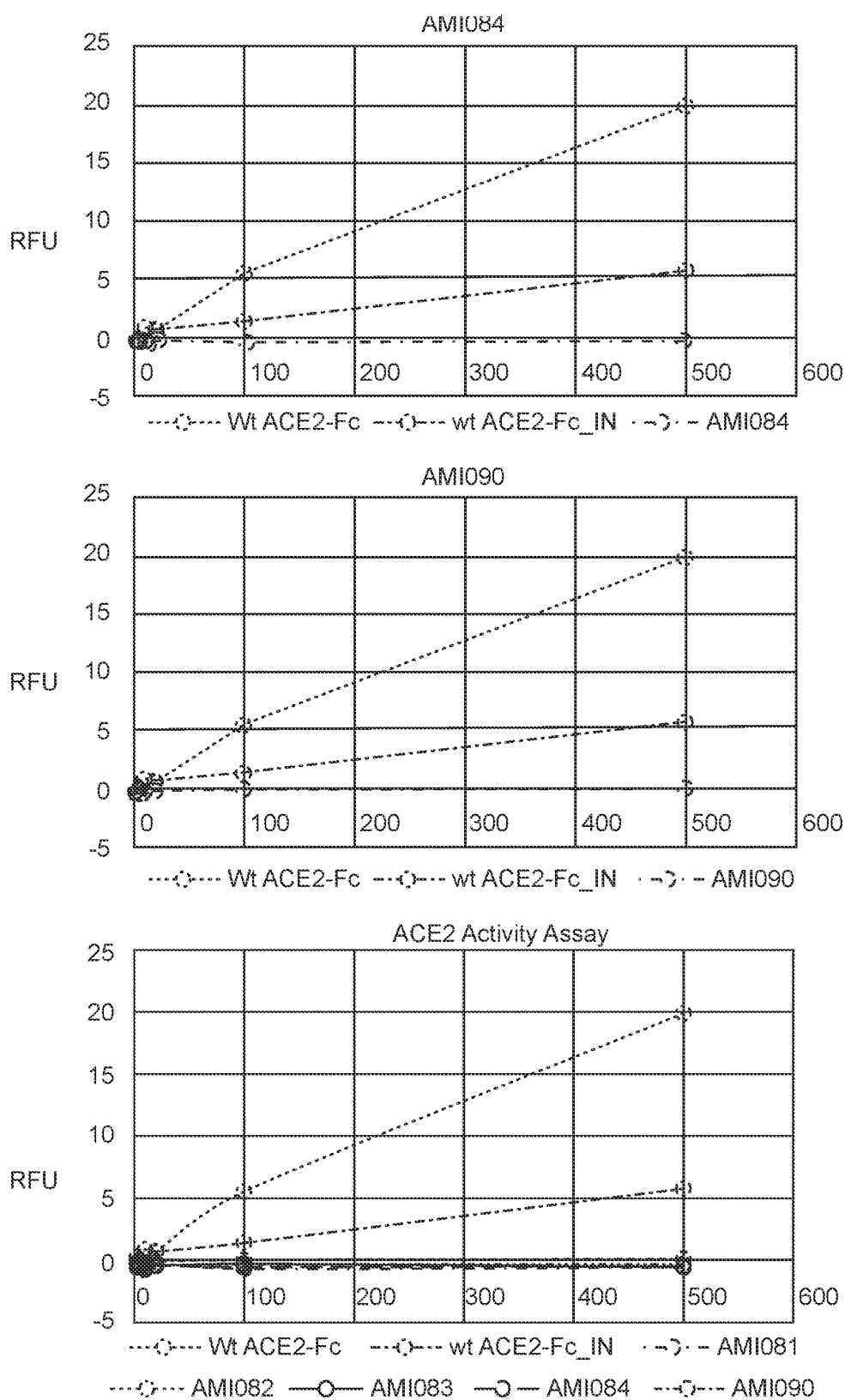


FIG. 15B

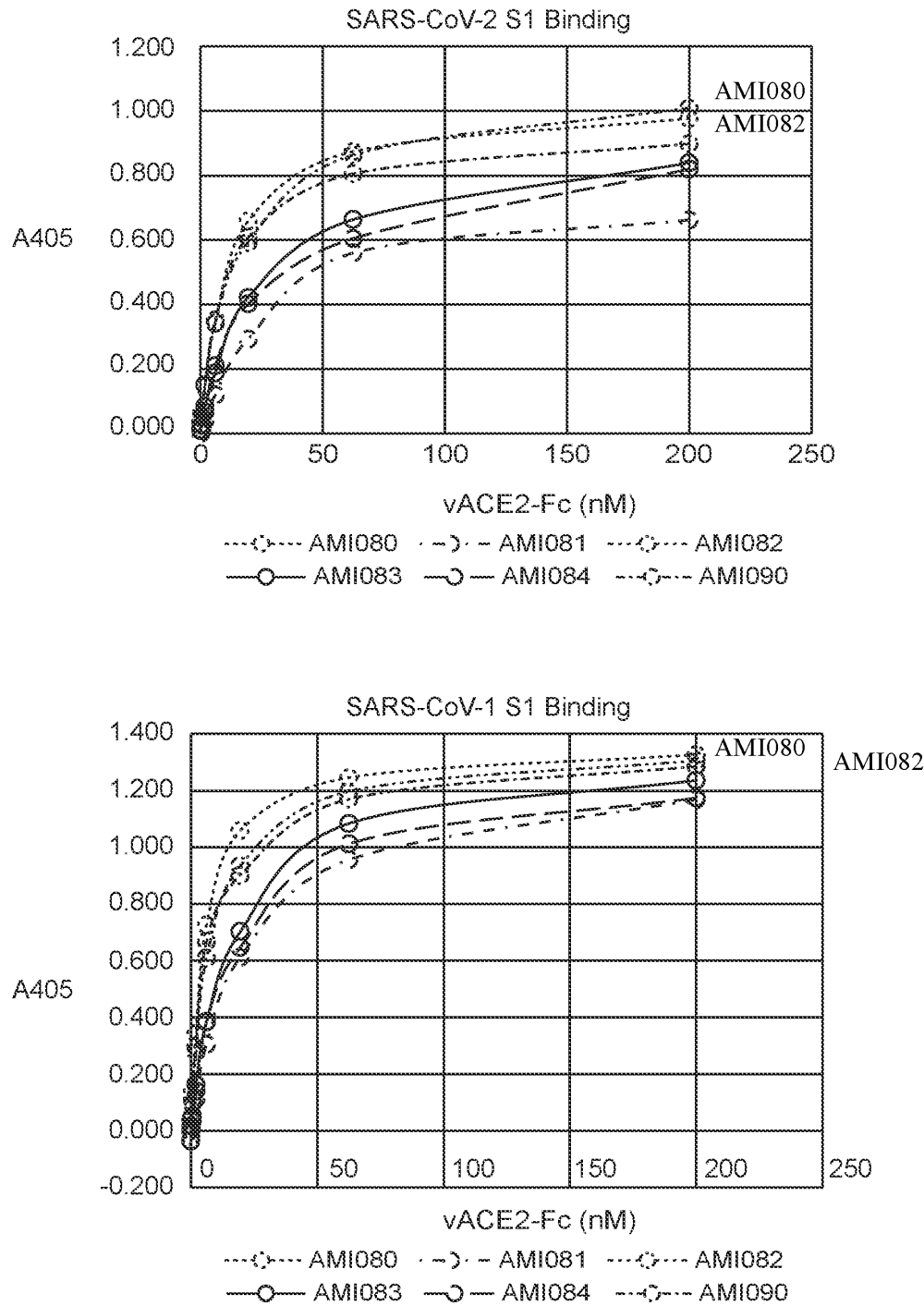


FIG. 16A

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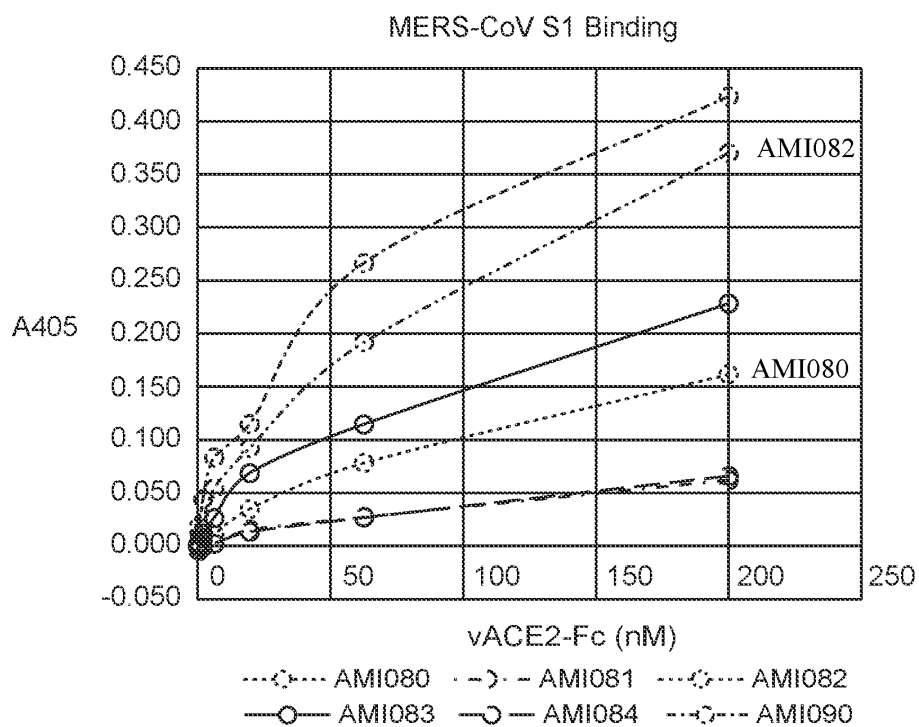


FIG. 16A (continued)

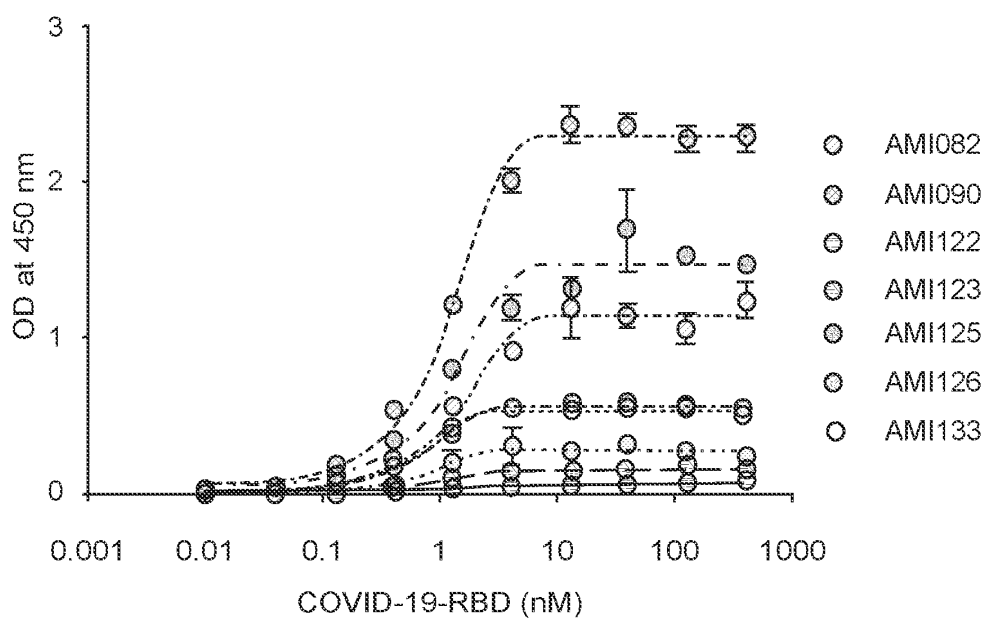


FIG. 16B

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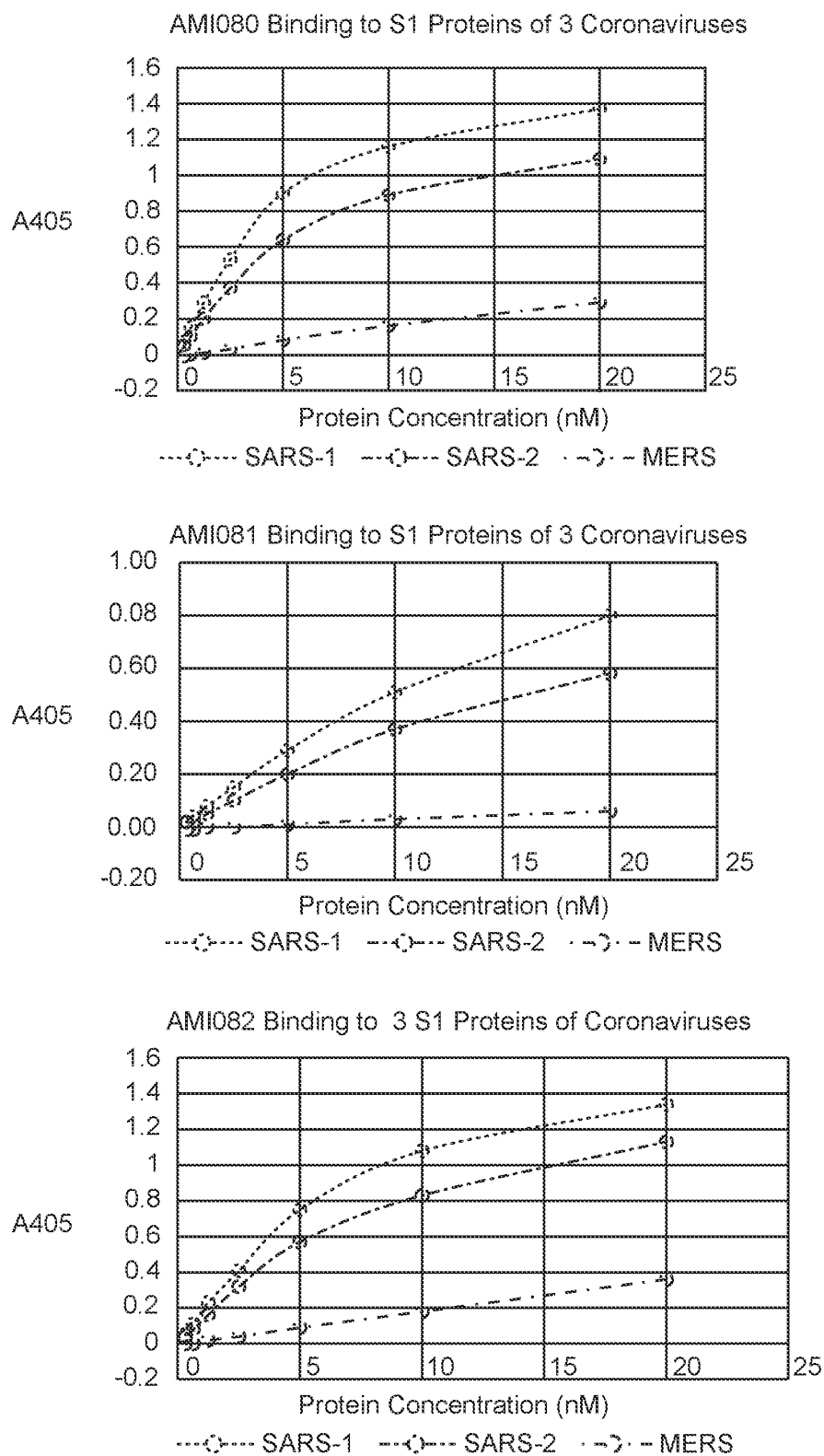


FIG. 17A

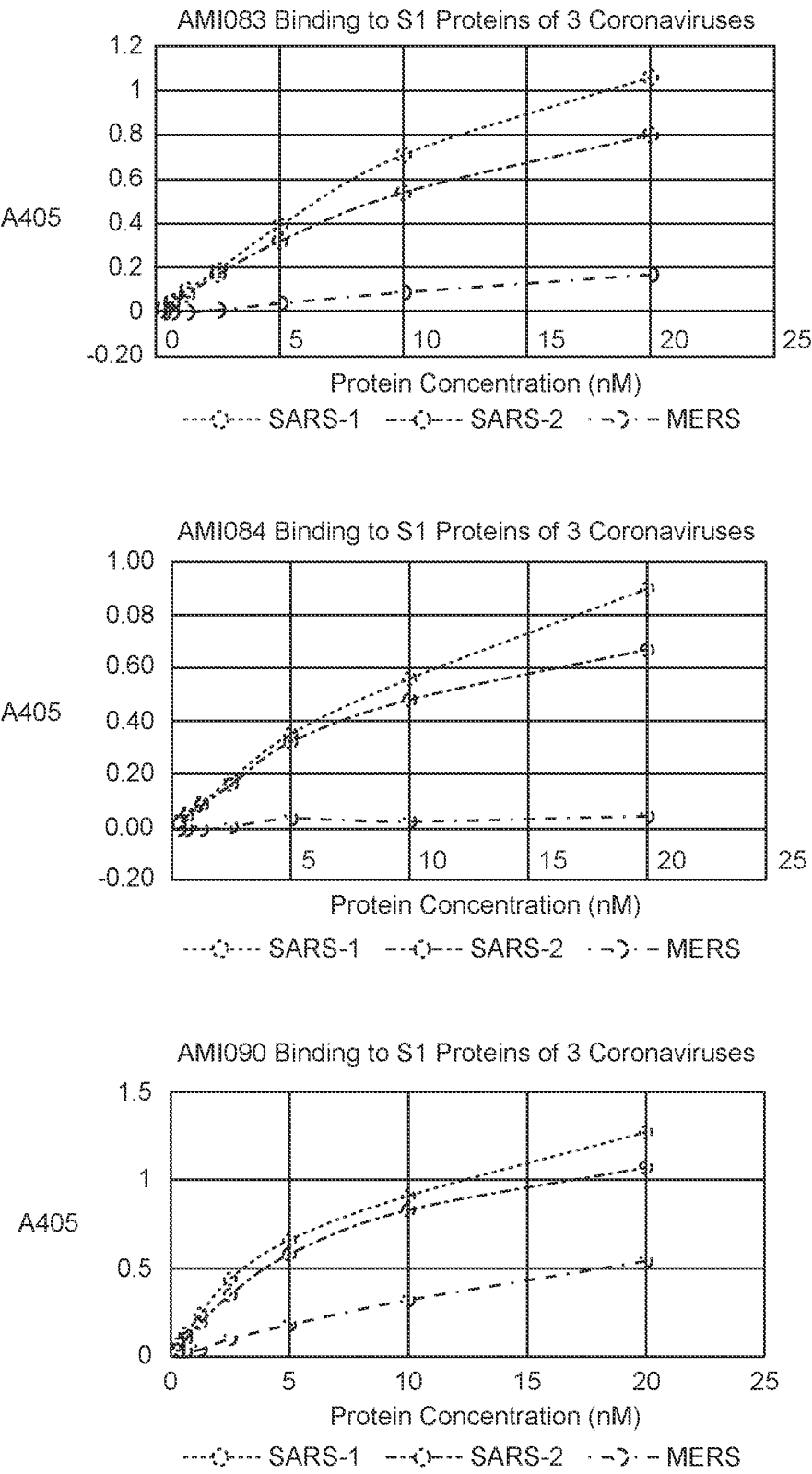
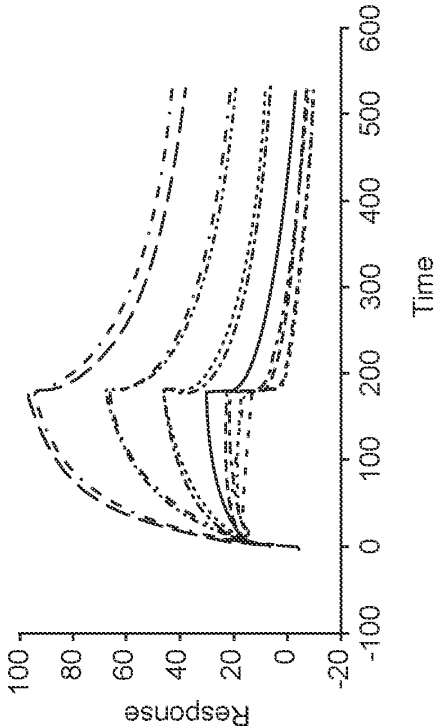


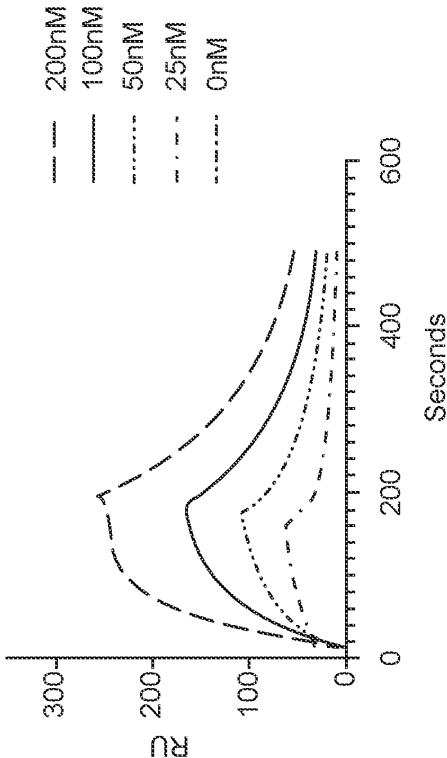
FIG. 17B

	Ka(1/Ms)	Kd(1/s)	Ka(1/M)	KD(M)
AMI-090	4.80E+04	2.40E-05	2.10E+09	4.90E-10

SARS-COV-2 S1 protein binds wt ACE2-Fc KD=16.81 nM



SARS-COV2-S1 binding to ACE2-vECD(AMI-090)



200, 100, 50, 25, 12.5, 6.25, 3.25 & 1.65 nM SARS-CoV-2 S1 Protein

FIG. 18

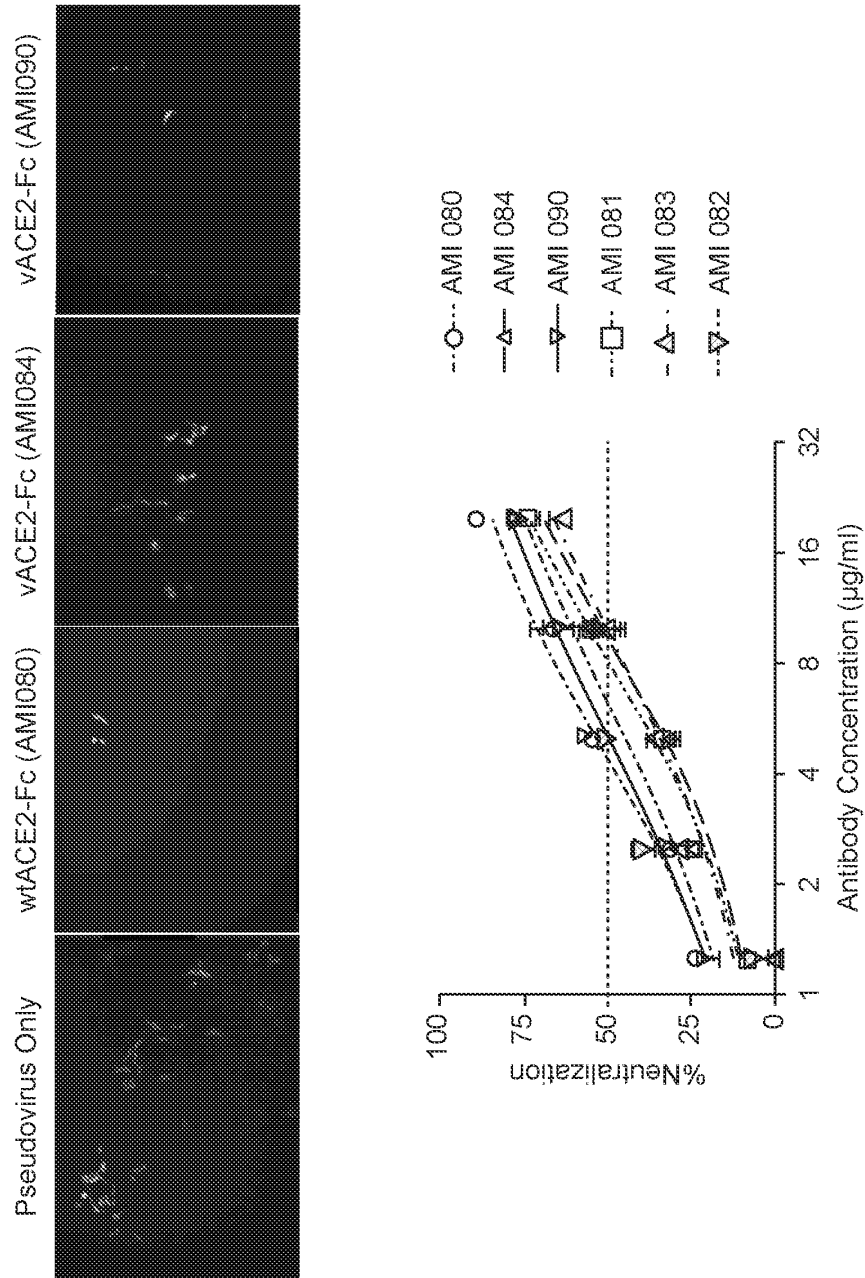


FIG. 19

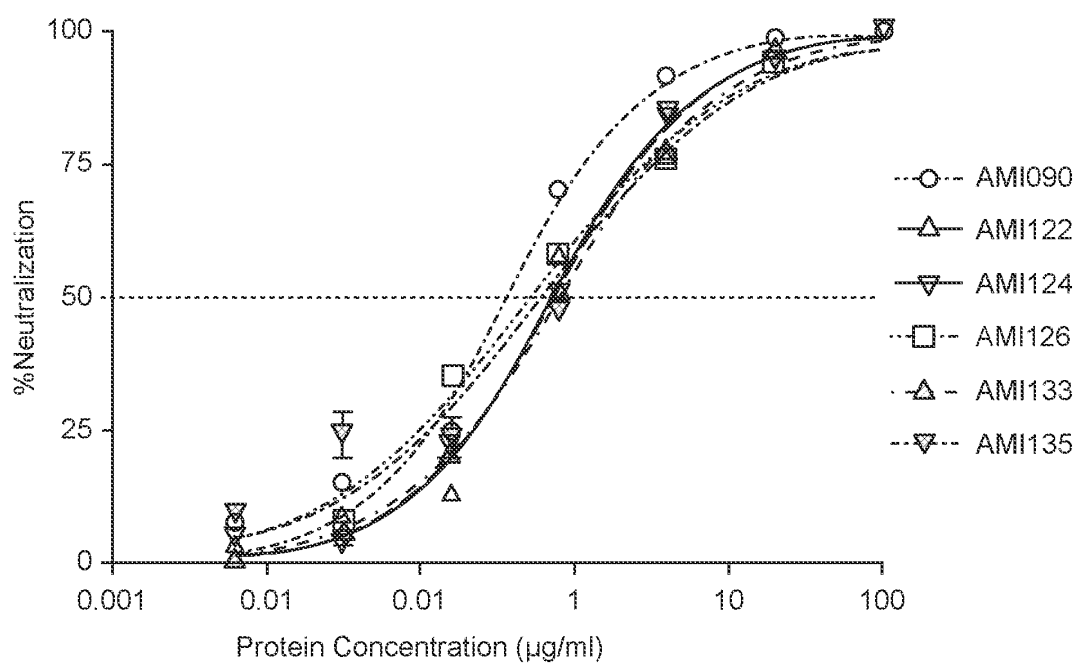


FIG. 20

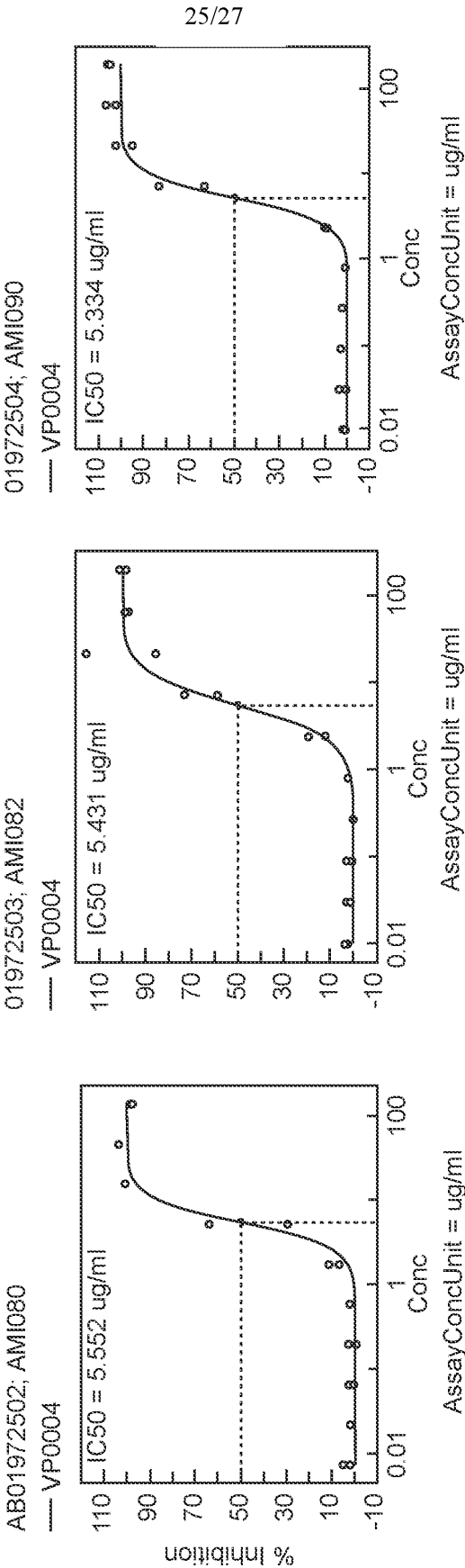


FIG. 21

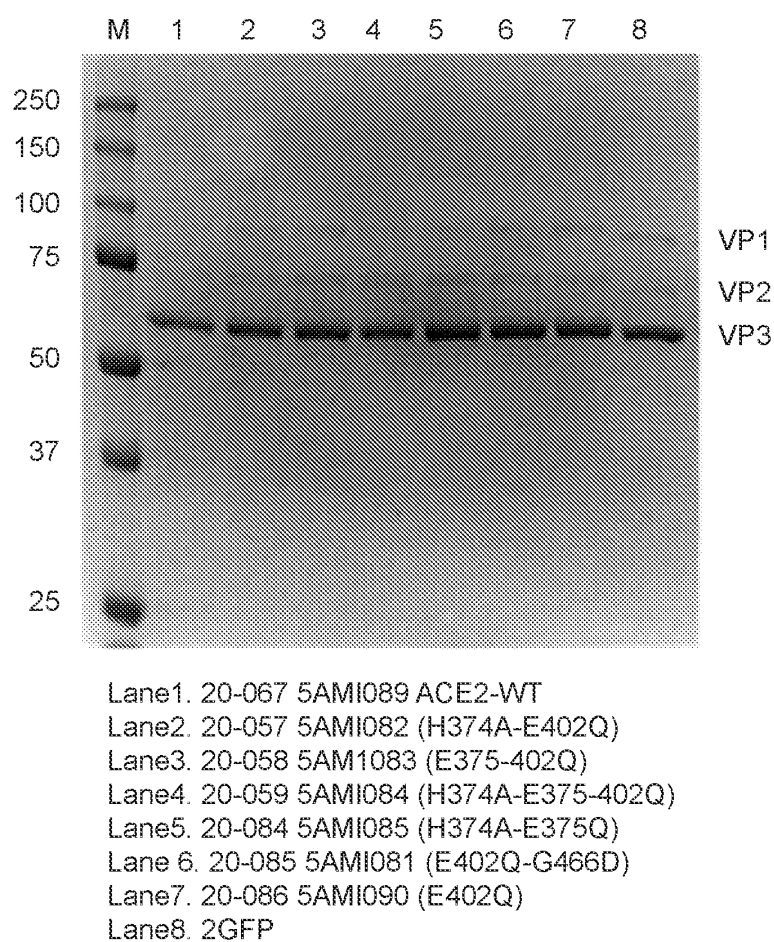


FIG. 22

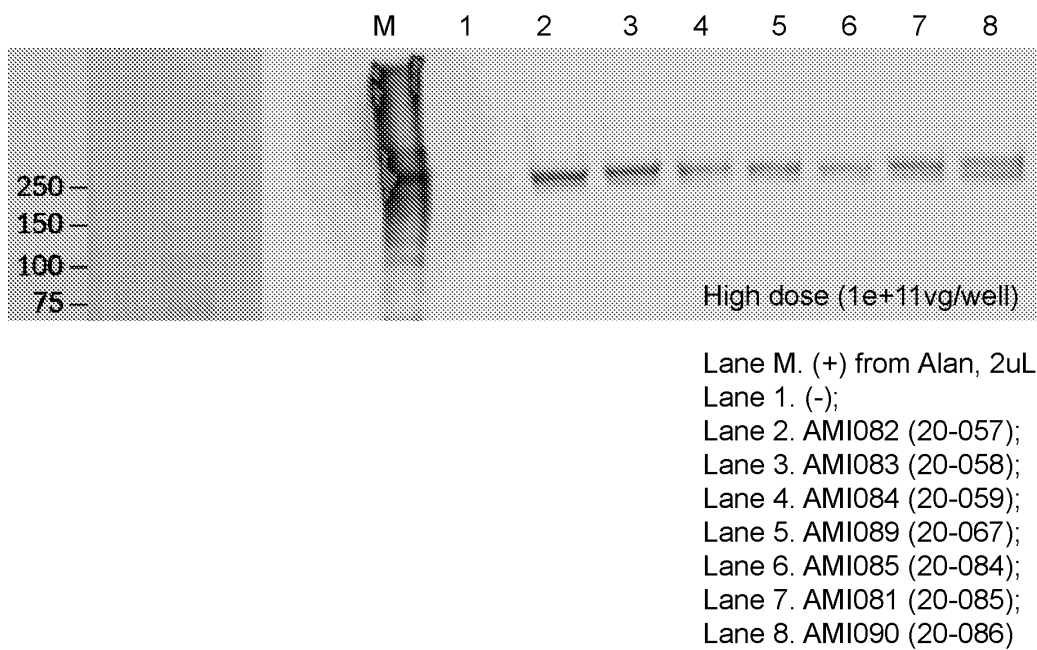


FIG. 23