

Selection Cycle	pmol aptamer pool	Target change	Target excess	pmol selection target	pmole counter target	Negative beads	Matrix	+ve incub time (min)	-ve incub time (min)	Washes
2	27.7	0.5	25.00	692.50		2	0%	45	15	2
3	27.7	0.5	12.50	346.25		2	0%	30	30	2
4	27.7	0.5	6.25	173.13	86.56	4	0%	15	30	2
5	27.7	0.5	3.125	86.563	86.563	4	0%	15	30	4
6	27.7	0.5	1.563	43.281	86.563	6	20%	15	30	4
7	27.7	0.5	0.781	21.641	43.281	6	40%	15	30	4
8	27.7	0.5	0.391	10.820	21.641	8	60%	15	30	4
9	27.7	0.5	0.195	5.410	10.820	8	40%	10	45	6
10	27.7	0.5	0.098	2.705	5.410	8	60%	10	45	6
11	27.7	0.5	0.049	1.353	2.705	8	40%	10	45	6
12	27.7	0.5	0.024	0.676	1.353	8	60%	10	45	6
13	27.7	0.5	0.012	0.338	0.676	8	60%	10	45	6

FIG. 1

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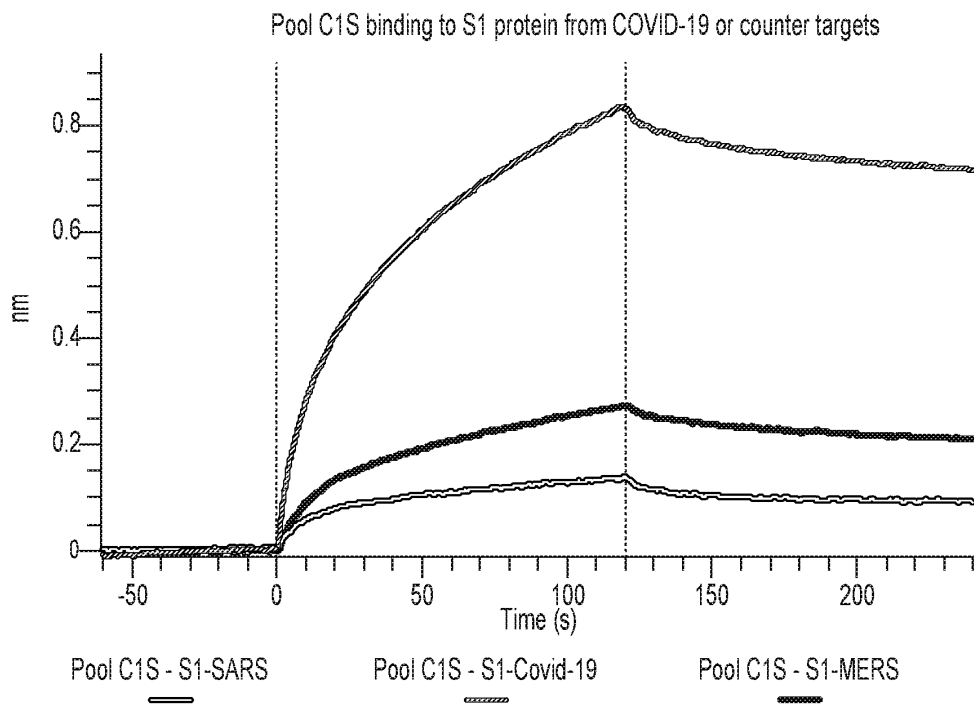


FIG. 2

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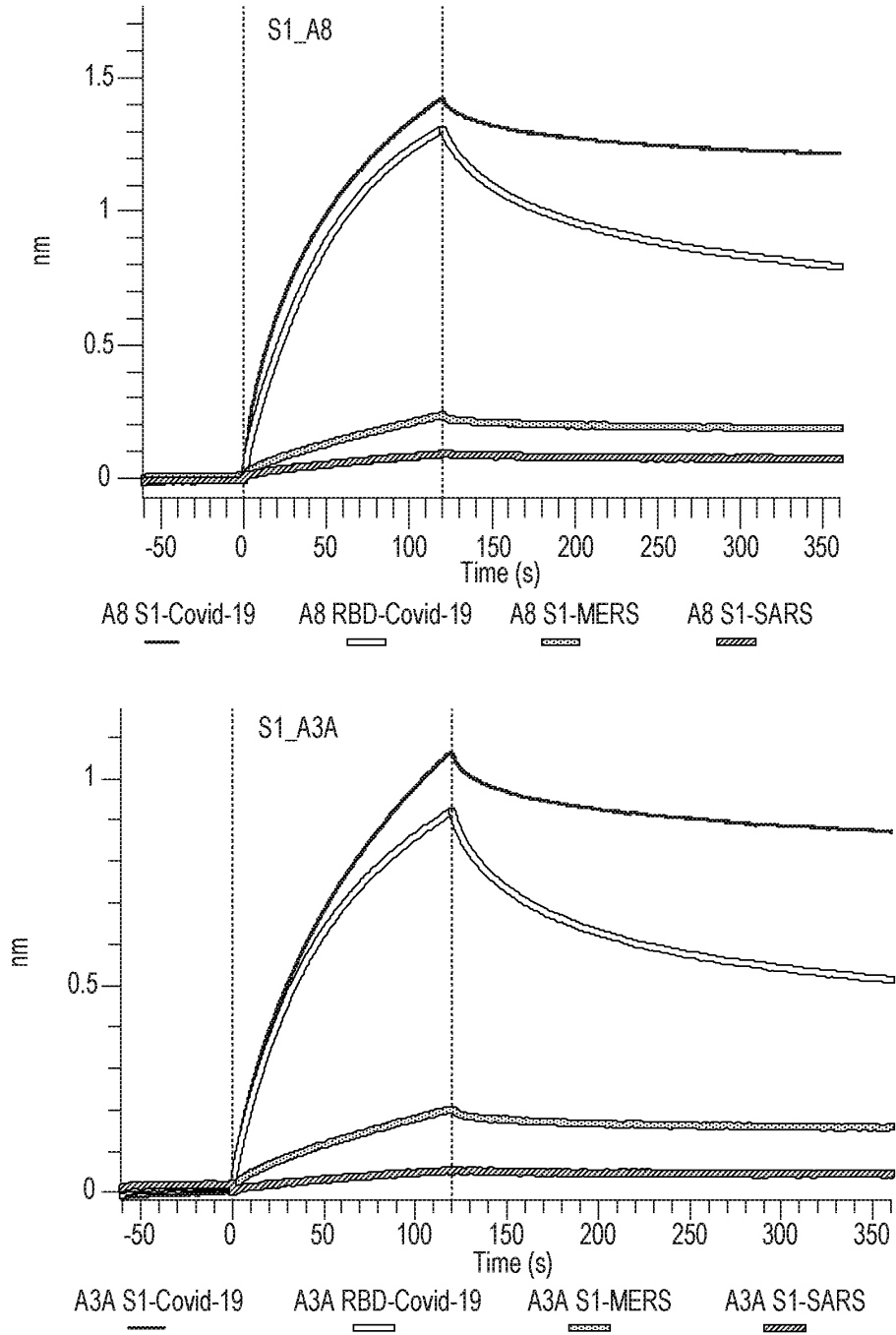


FIG. 3

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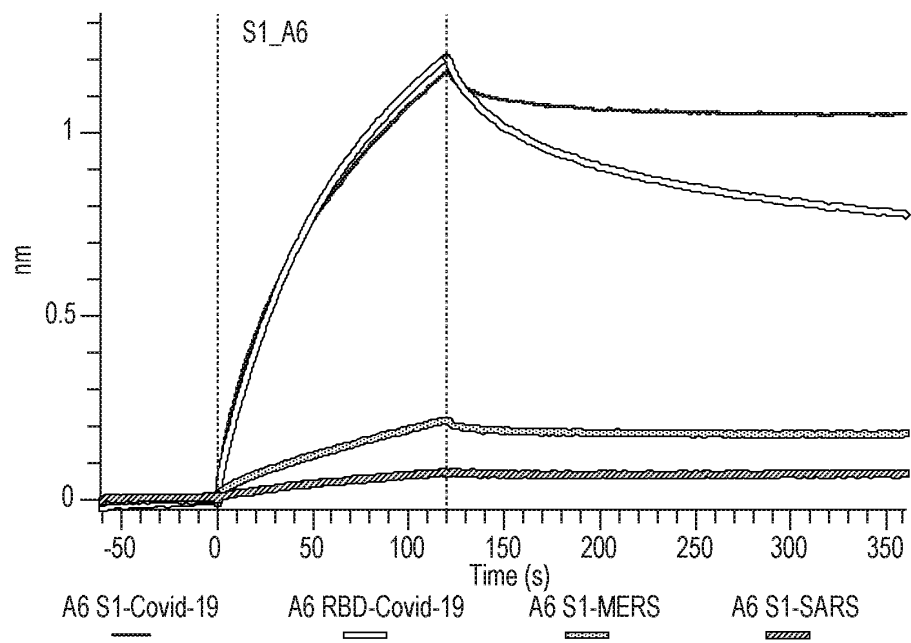


FIG. 3 (continued)

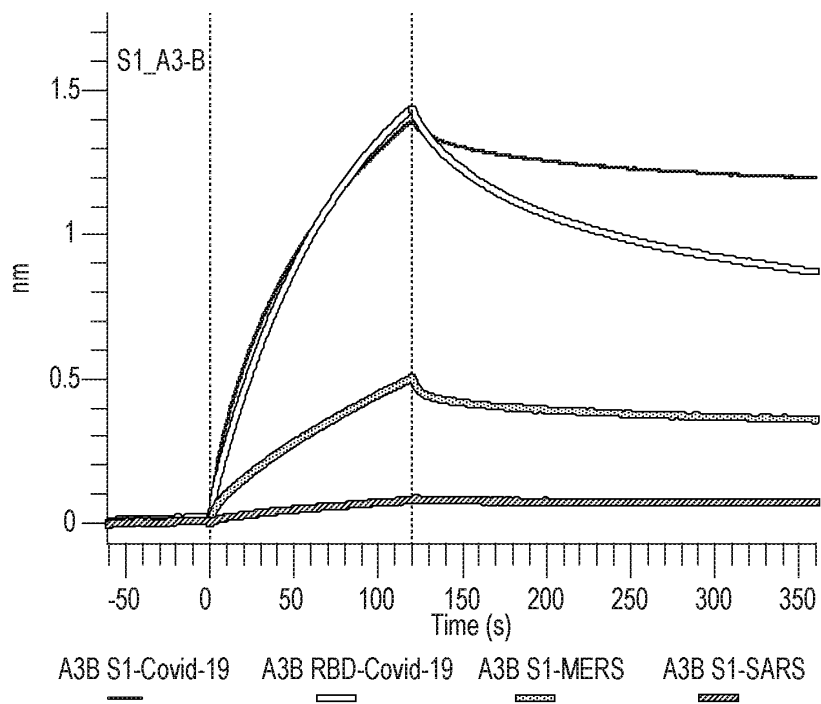


FIG. 4

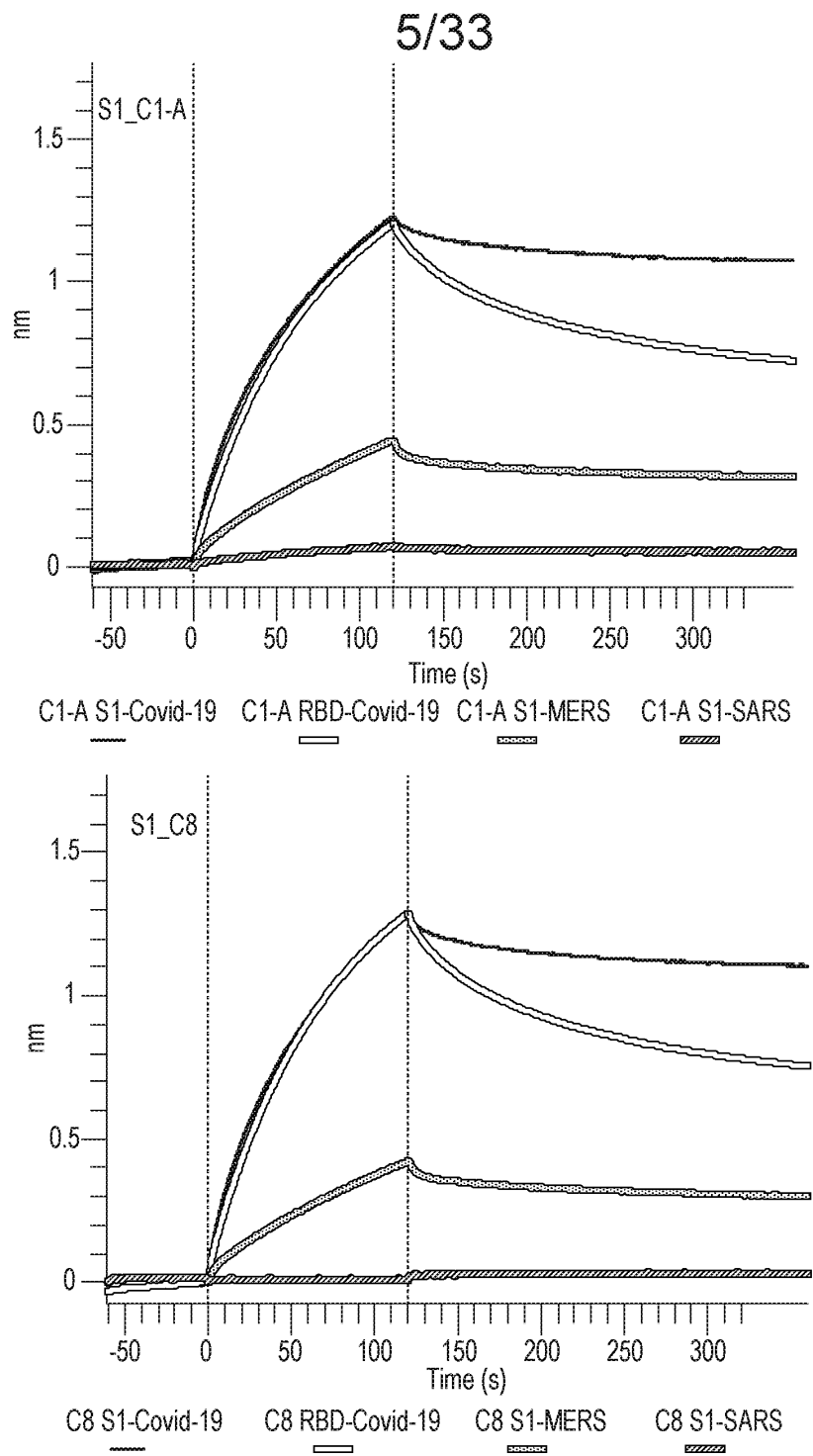


FIG. 4 (continued)

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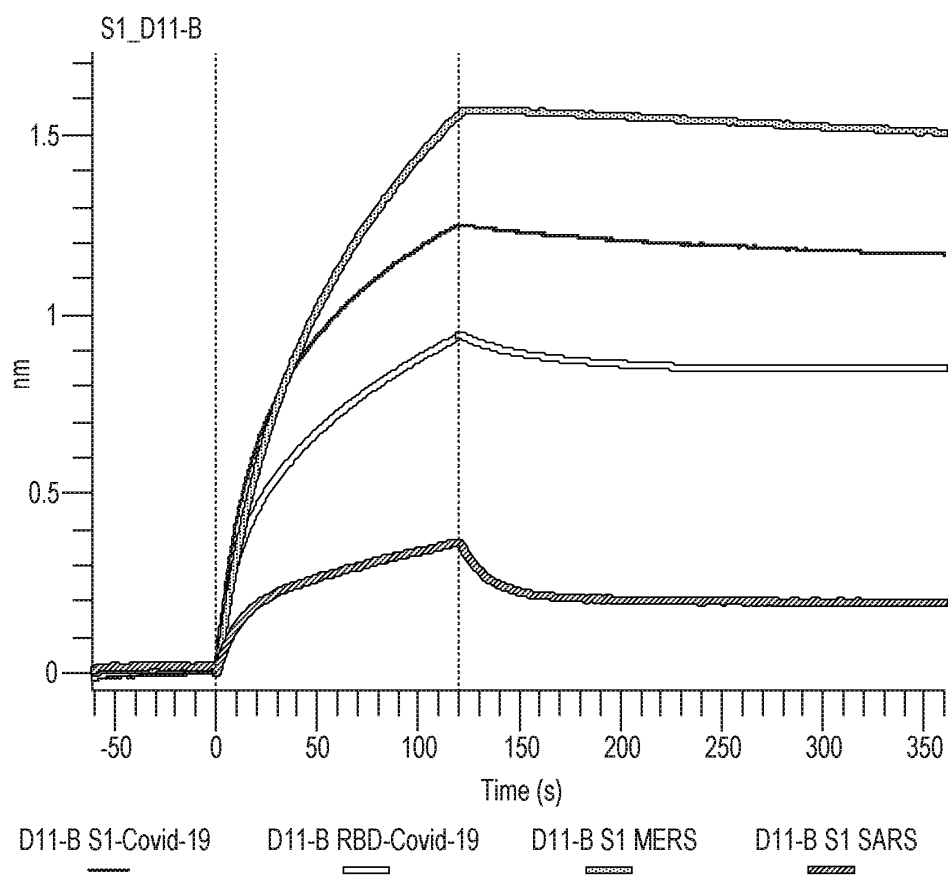
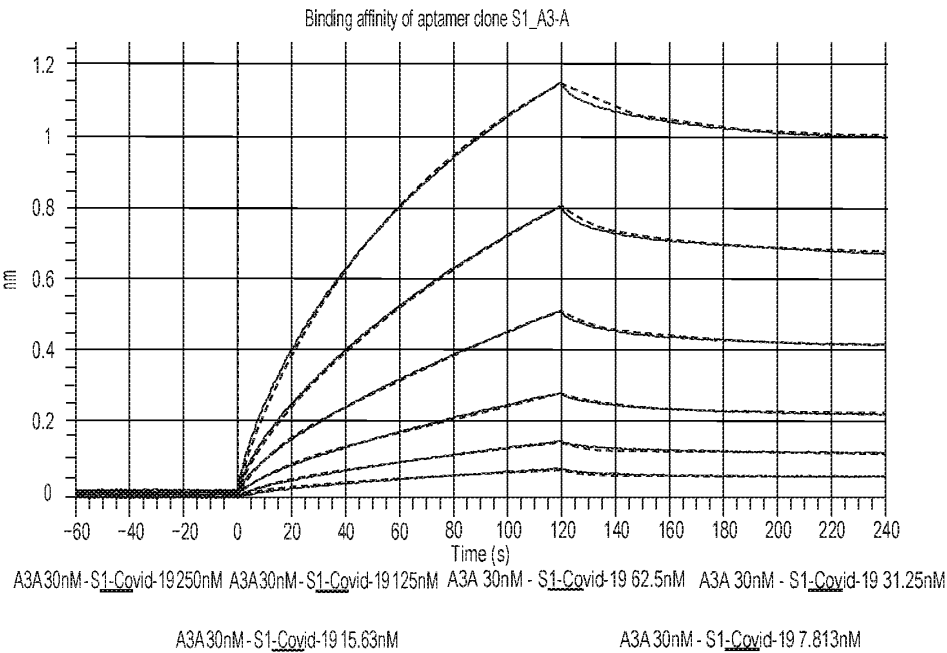


FIG. 5



Clone	KD 1 (M)	KD 2 (M)	ka 1 (1/Ms)	ka 2 (1/Ms)	kdis 1 (1/s)	kdis 2 (1/s)
S1_A3A	8.472E-09	7.15E-08	4.67E+04	8.21E+05	3.95E-04	5.87E-02
S1_A6	7.632E-12	3.588E-08	5.48E+04	1.04E+06	4.18E-07	3.72E-02

FIG. 6

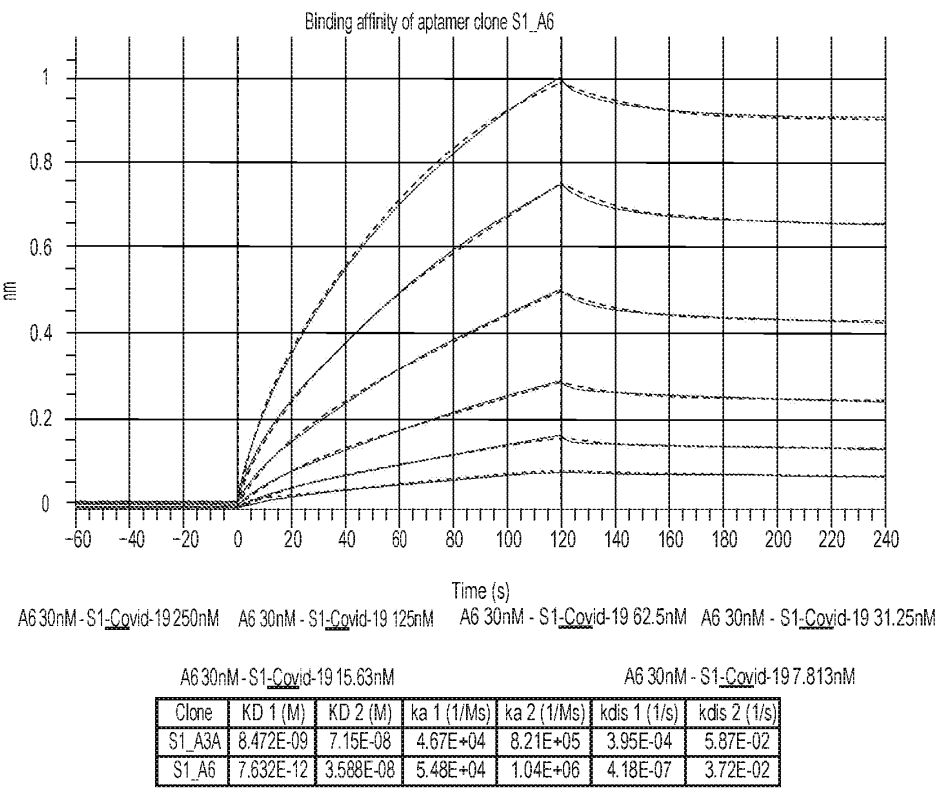


FIG. 6 (continued)

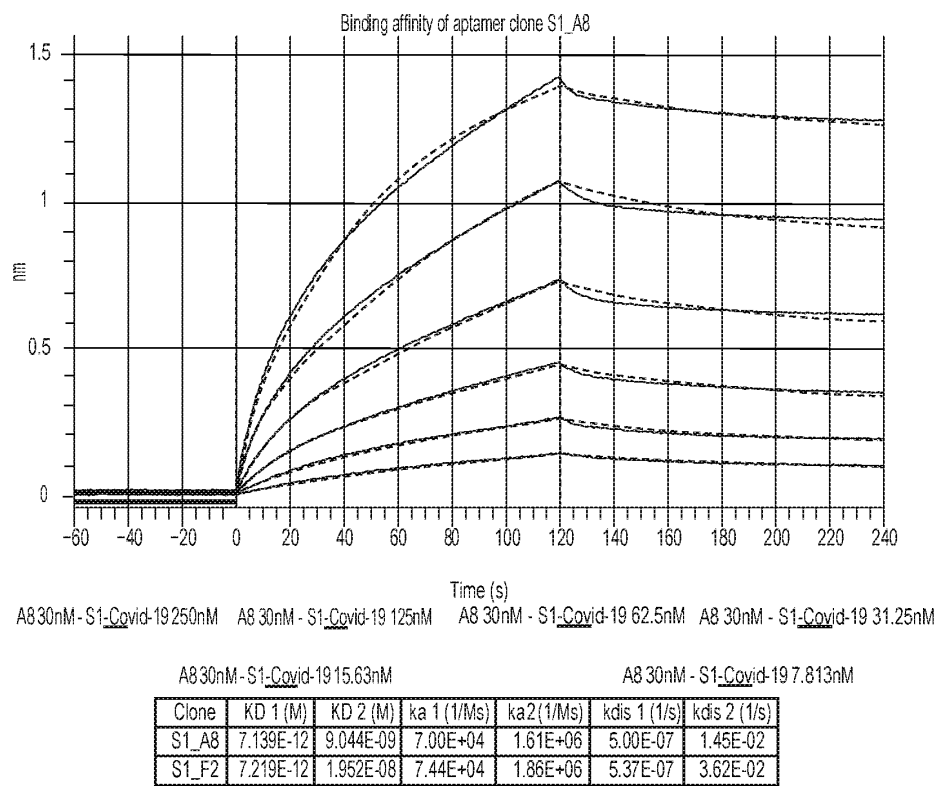


FIG. 7

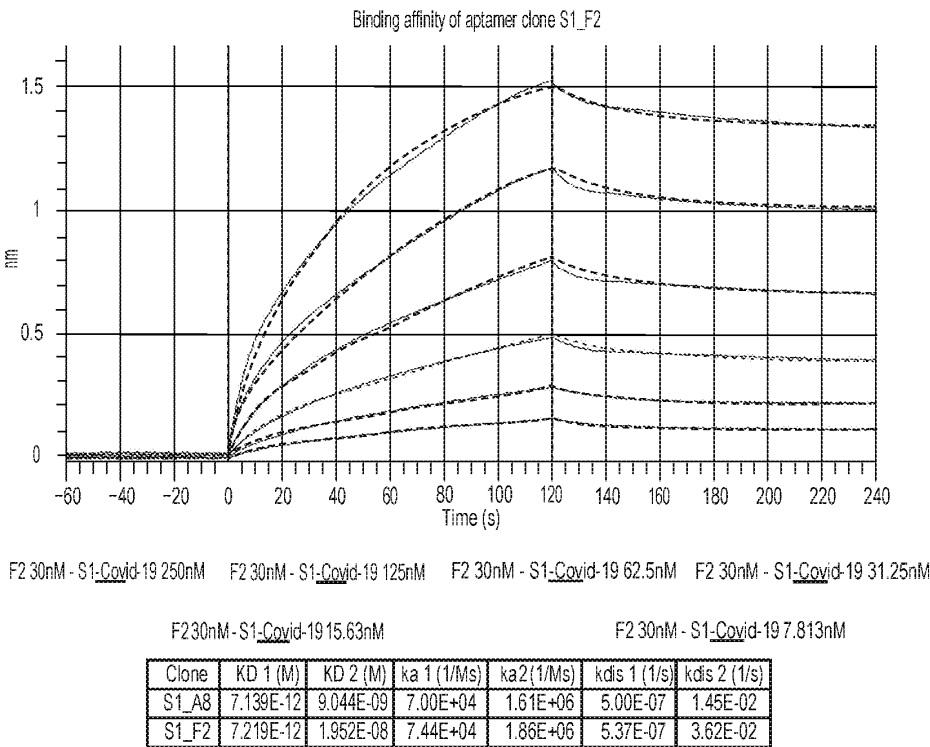
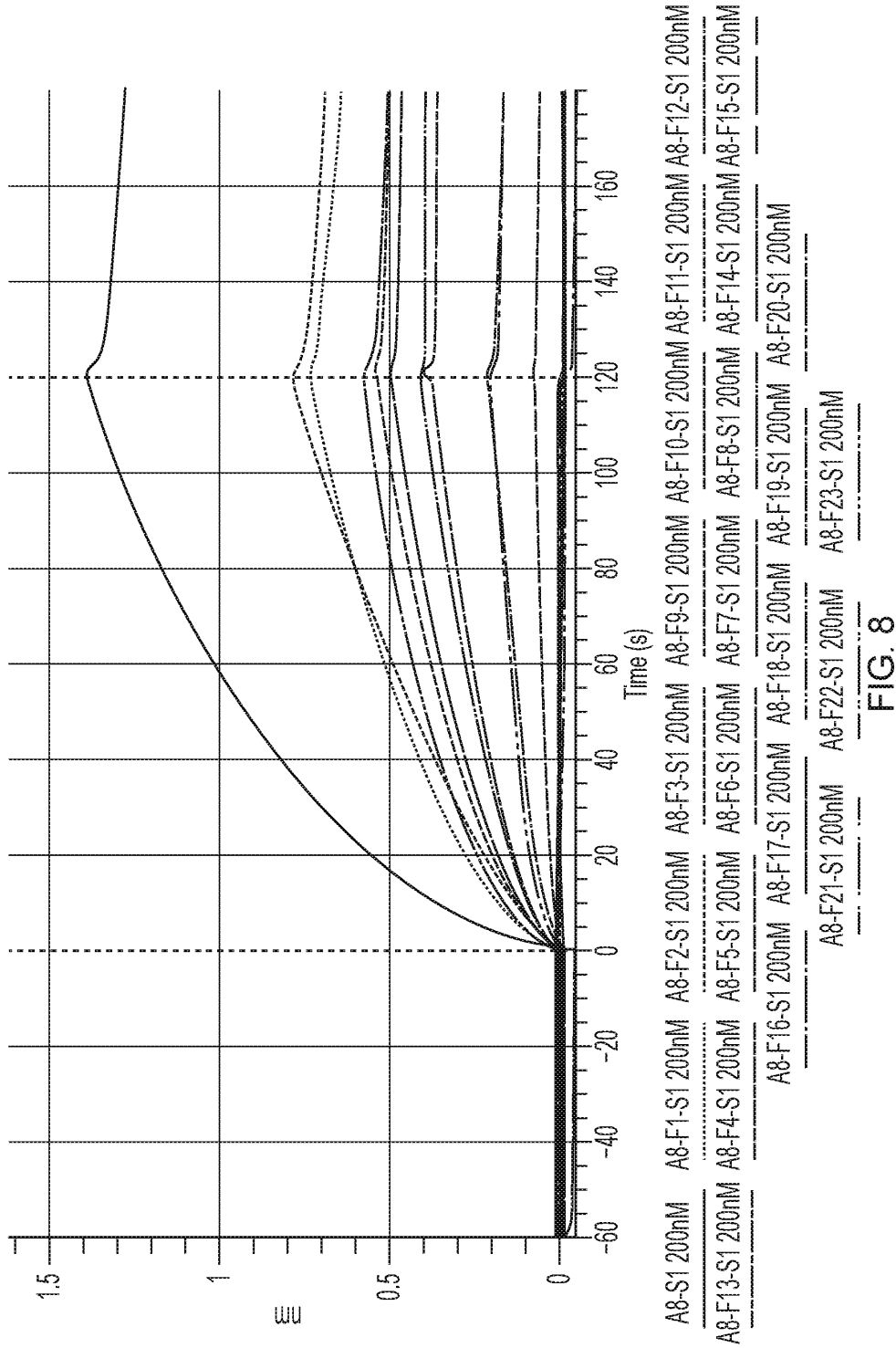


FIG. 7 (continued)

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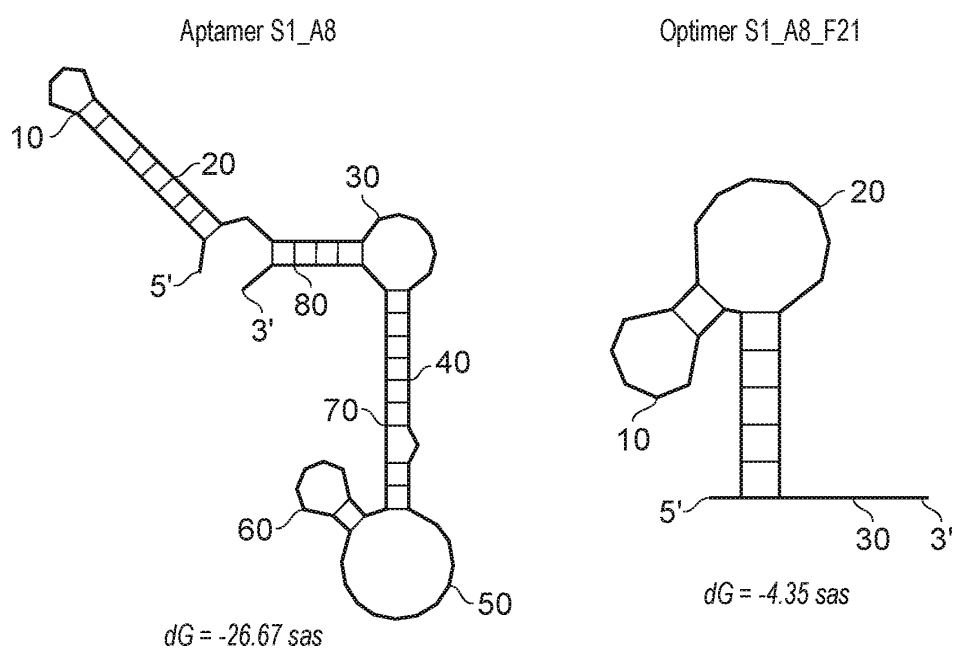


FIG. 8 (continued)

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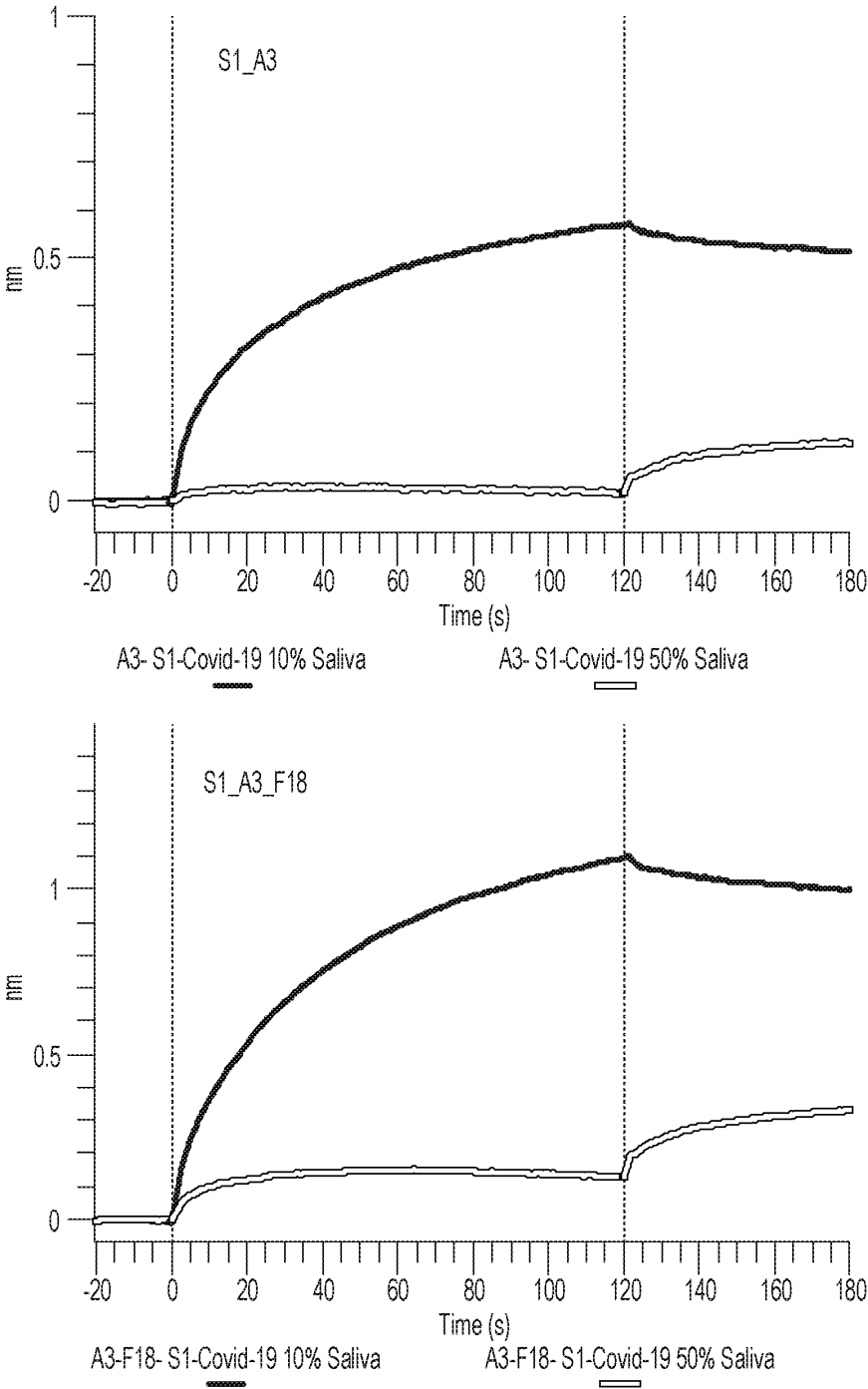


FIG. 9

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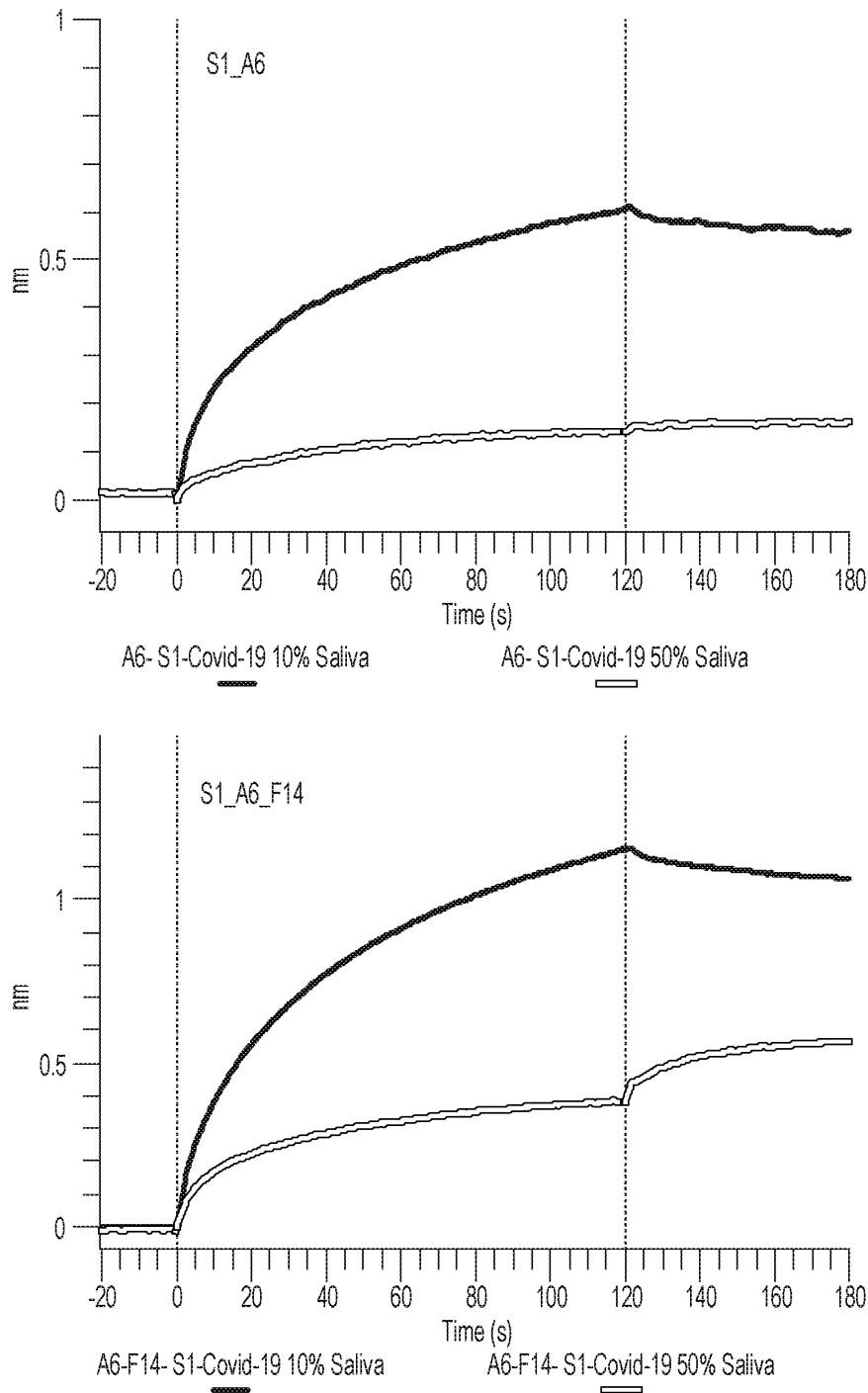


FIG. 9 (continued)

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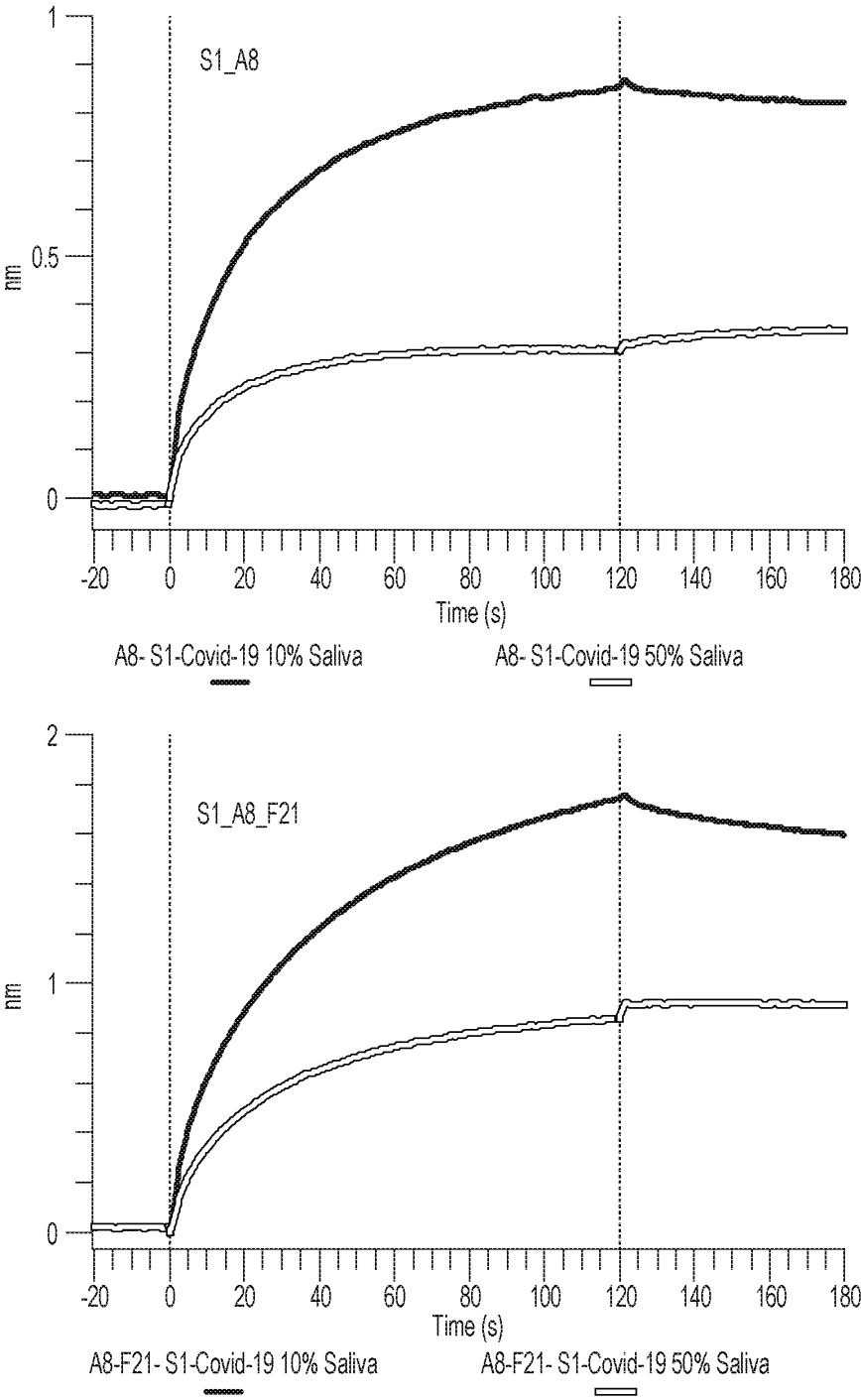


FIG. 9 (continued)

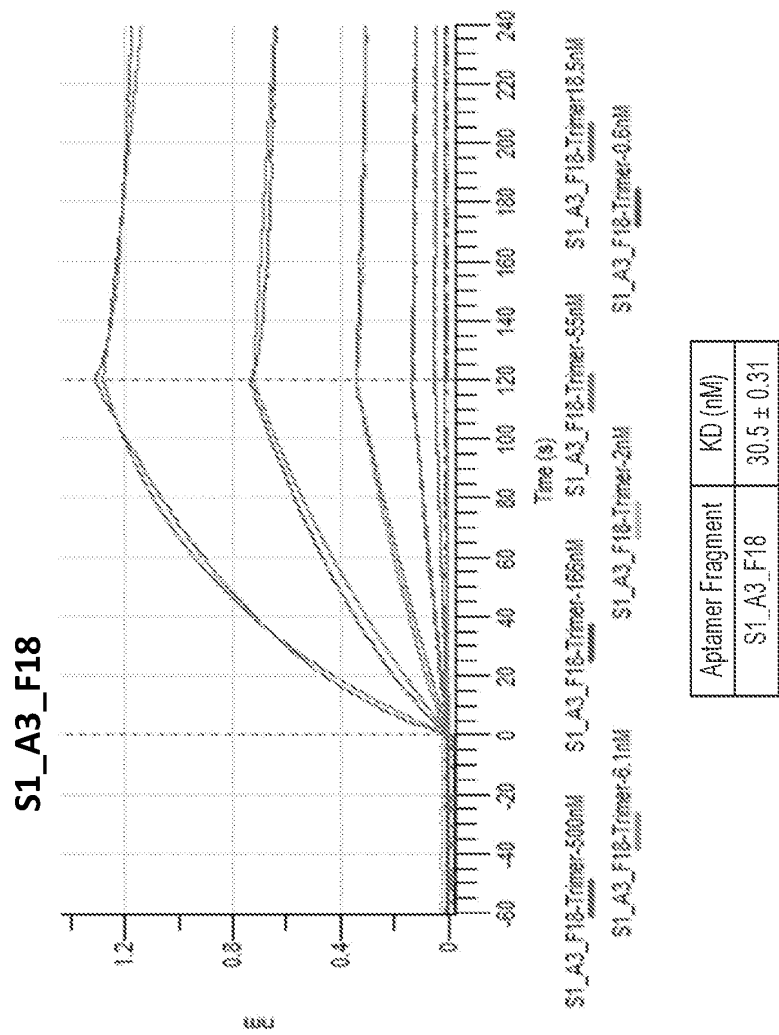


FIG. 10

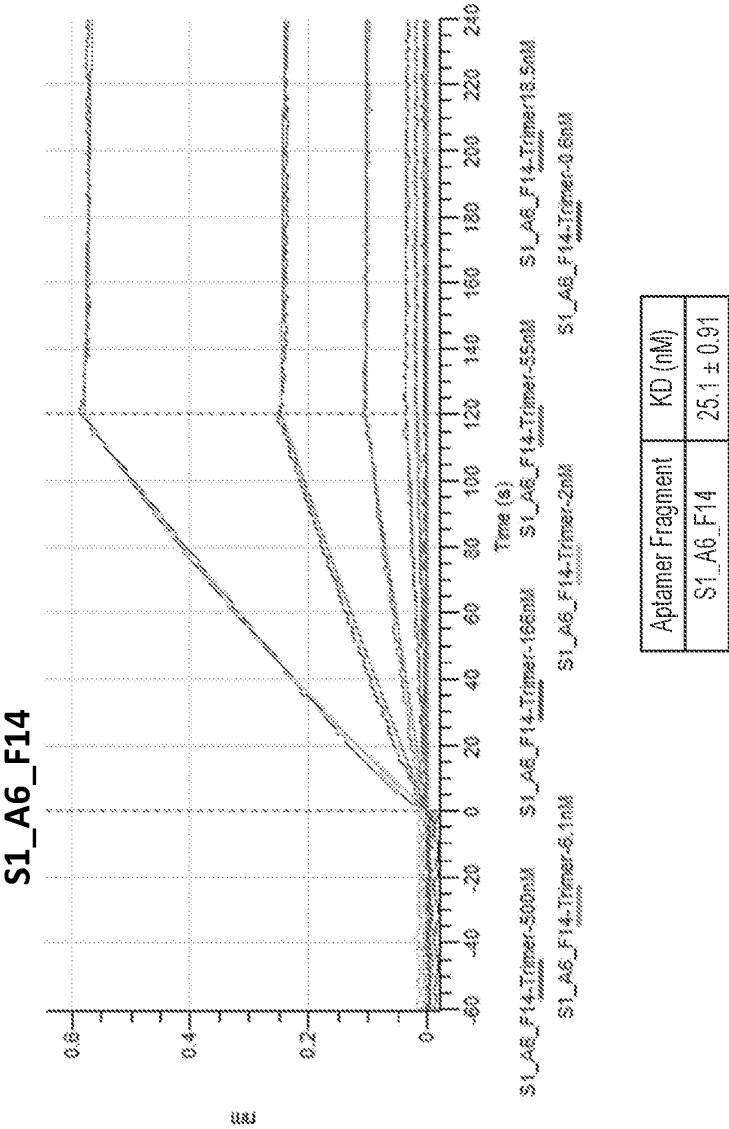


FIG.10 (continued)

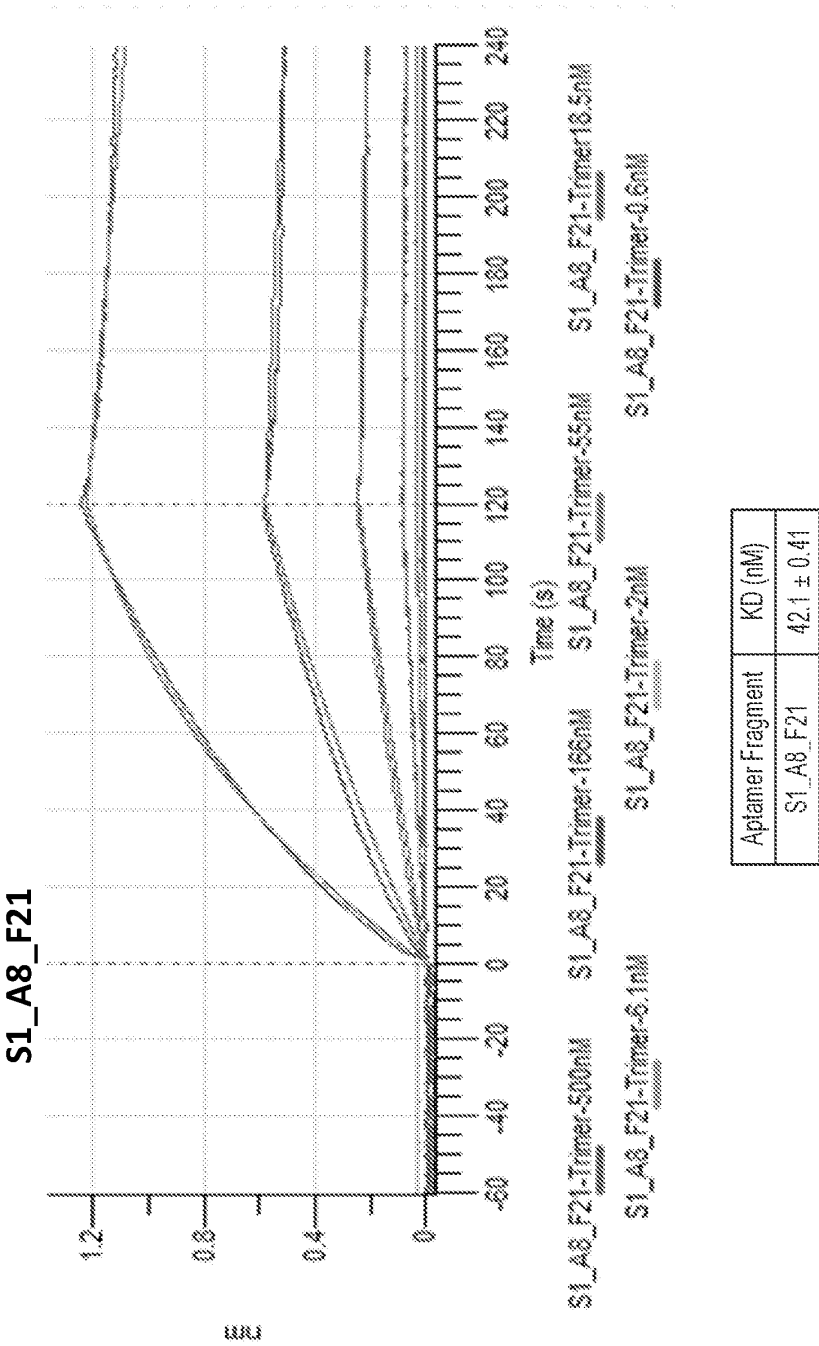


FIG. 10 (continued)

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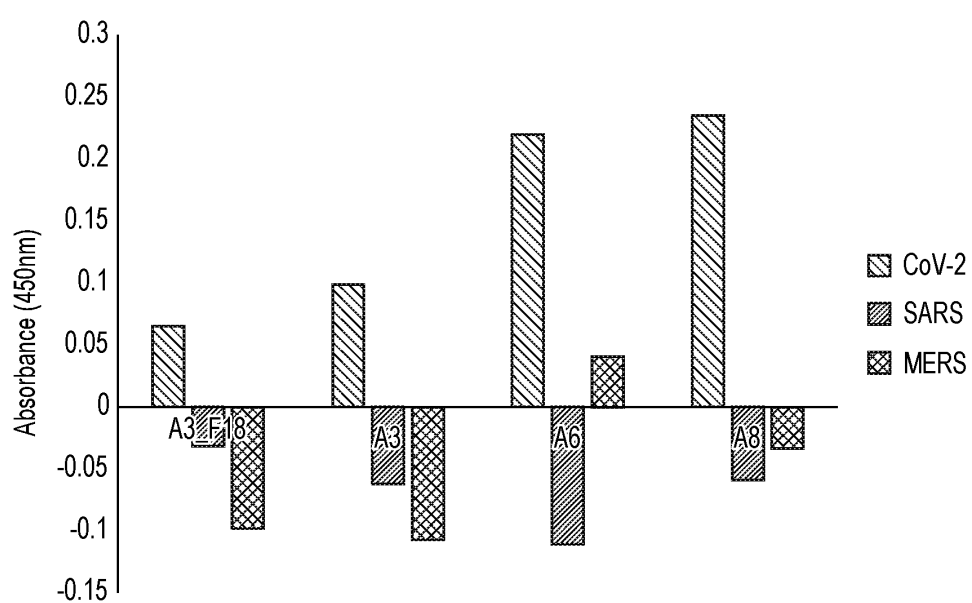


FIG. 11

Round	pmol pool	Target change	Target excess	pmol Target	Negative beads	Extra salt	Matrix	+ve incub time (min)	-ve incub time (min)	Washes
2	27.7	0.5	11.25	311.63	2	0	0%	45	15	2
3	27.7	0.5	5.63	155.81	2	0	0%	30	30	2
4	27.7	0.5	2.81	77.91	4	220	0%	15	30	2
5	27.7	0.5	1.406	38.953	4	220	20%	15	30	4
6	27.7	0.5	0.703	19.477	6	220	20%	15	30	4
7	27.7	0.5	0.352	9.738	6	220	40%	15	30	4
8	27.7	0.5	0.176	4.869	8	220	60%	15	30	4
9	27.7	0.5	0.088	2.435	8	220	40%	10	45	6
10	27.7	0.5	0.044	1.217	8	220	60%	10	45	6
11	27.7	0.5	0.022	0.609	8	220	40%	10	45	6
12	27.7	0.5	0.011	0.304	8	220	60%	10	45	6
13	27.7	0.5	0.005	0.152	8	220	60%	10	45	6

FIG. 12

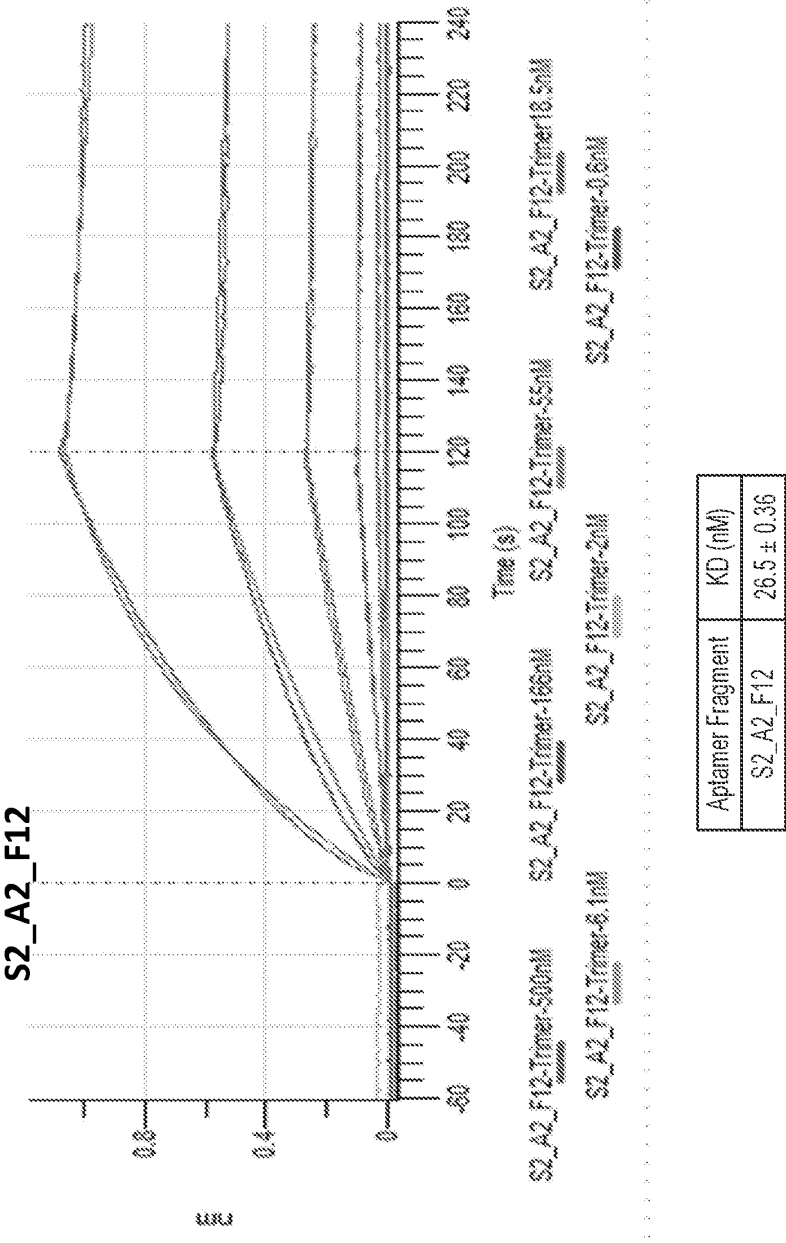


FIG. 13

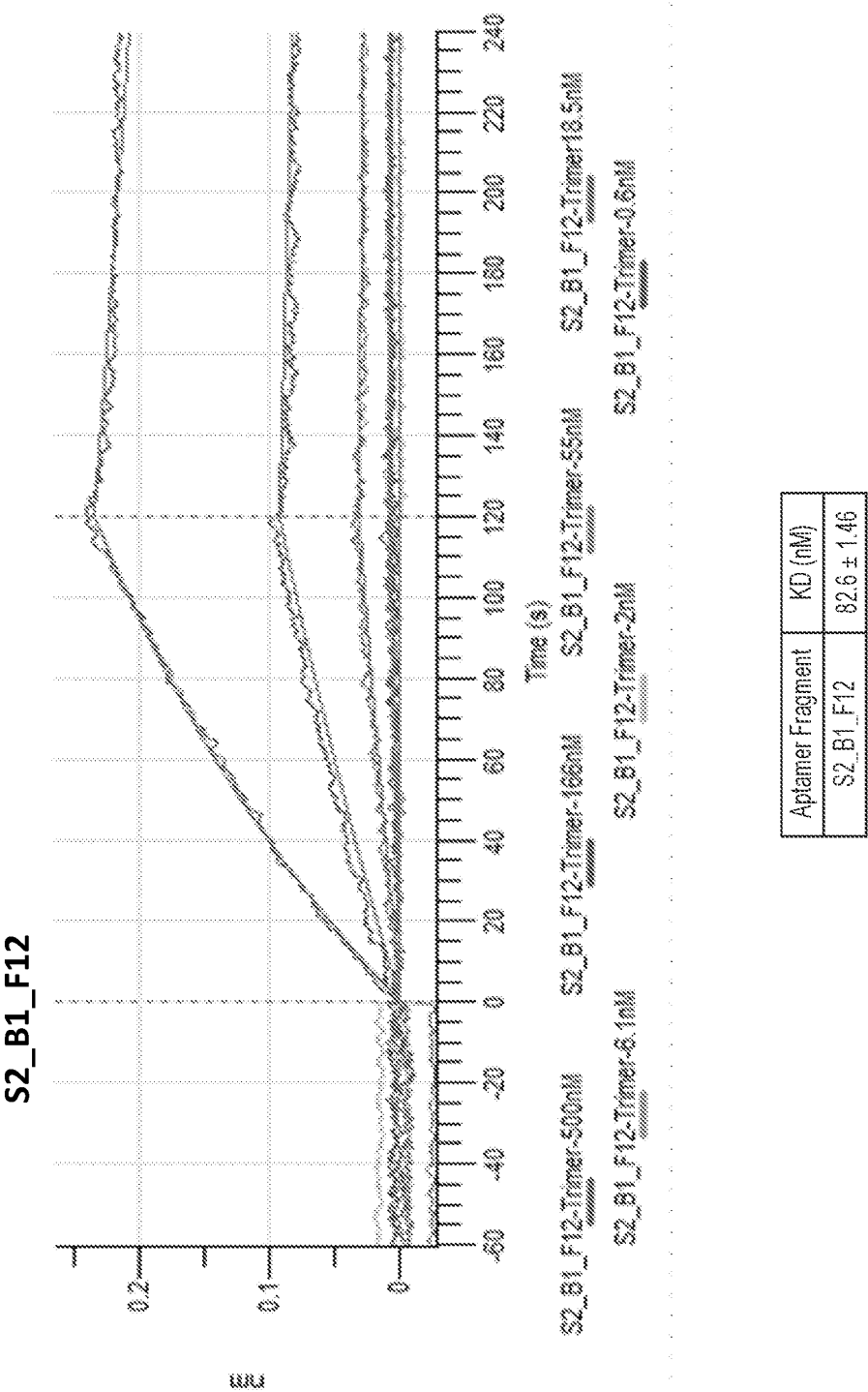


FIG. 13 (continued)

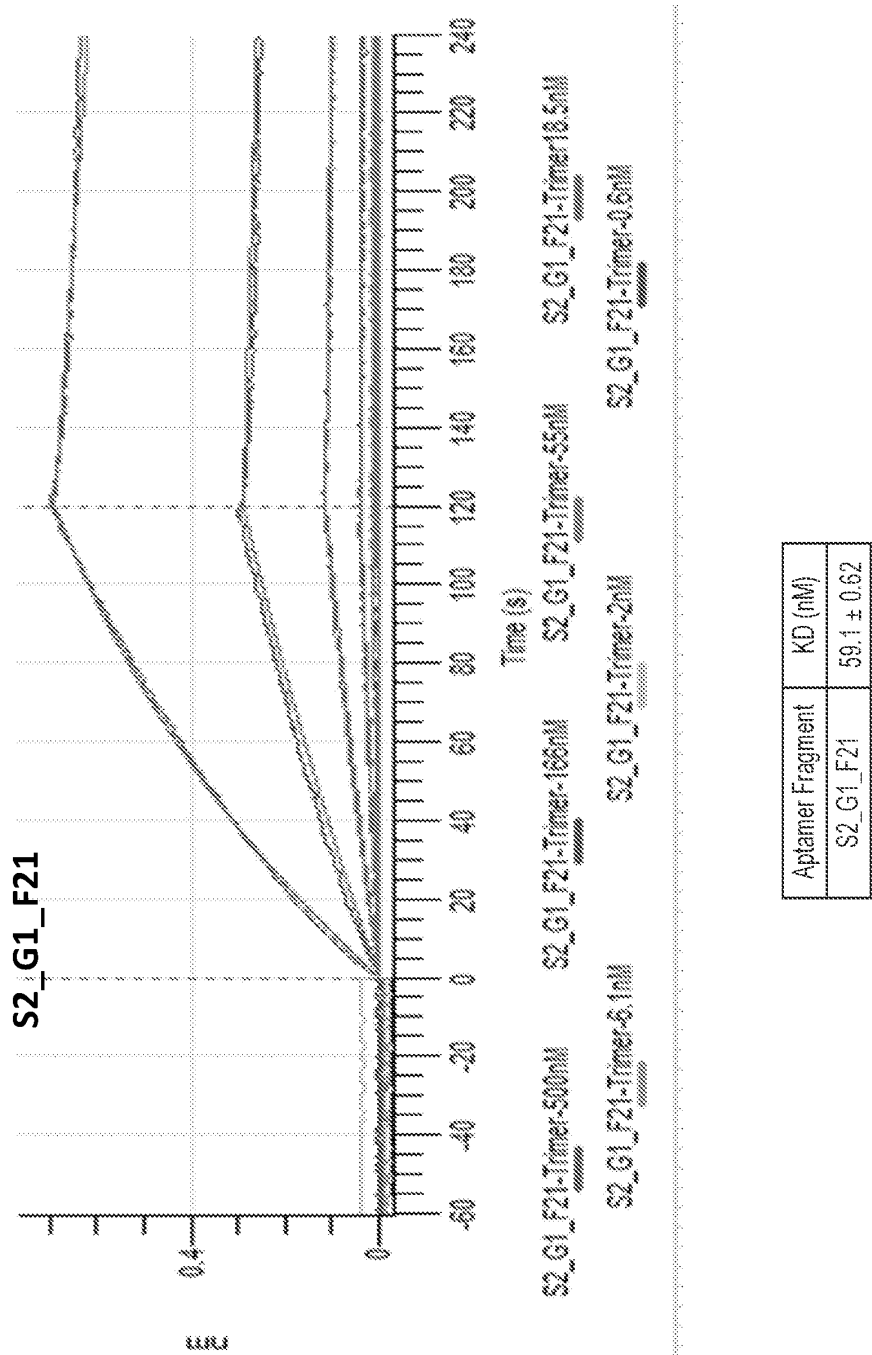
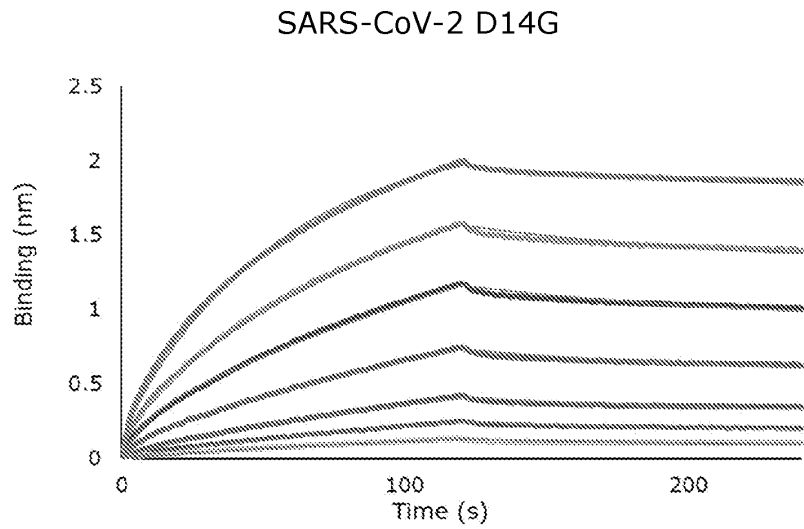
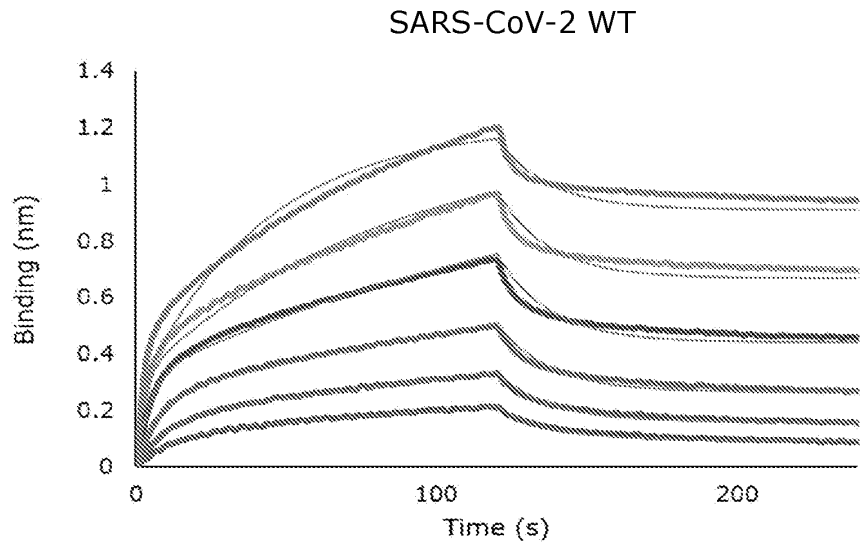


FIG. 13 (continued)

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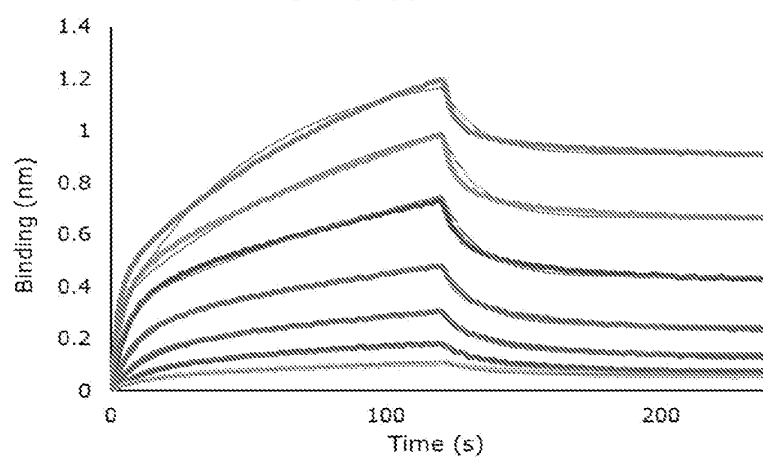


Protein	Variant	KD (nM)
S1-WT	WT	10.7 ± 0.057
S1-D14G	Denmark	19.8 ± 0.35

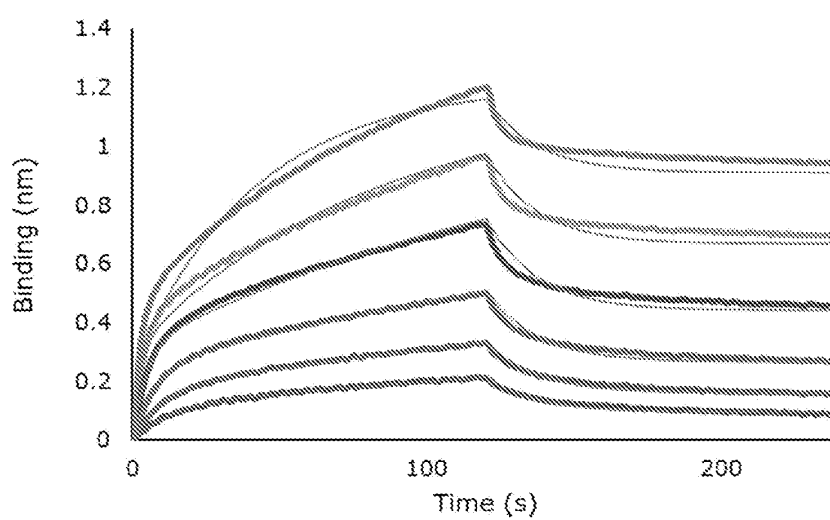
FIG. 14

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SARS-CoV-2 B.1.1.7



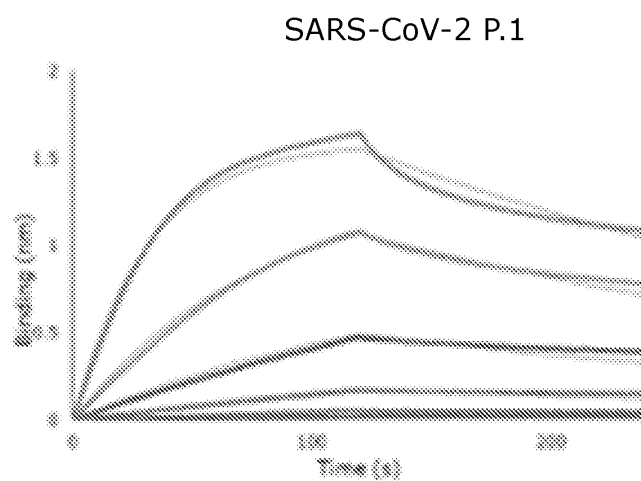
SARS-CoV-2 B.1.351



Protein	Variant	KD (nM)
S1-B.1.1.7	UK 'Kent'	62.6 ± 1.22
S1-B.1.351	South Africa	43.76 ± 1.24

FIG. 14 (continued)

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Protein	Variant	KD (nM)
S1-P.1	Brazil	19.52 ± 0.13

FIG. 14 (continued)

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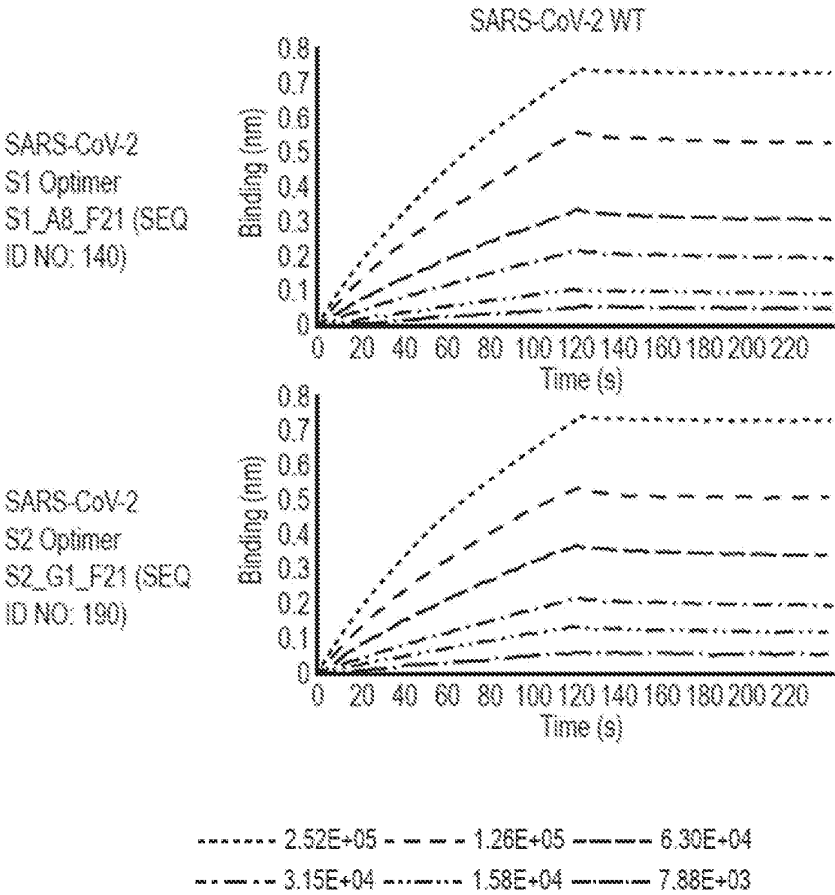
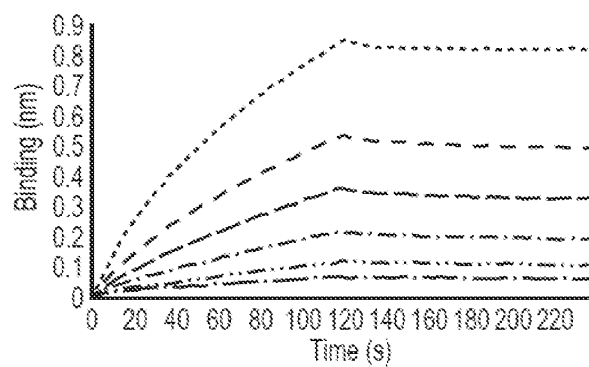


FIG. 15

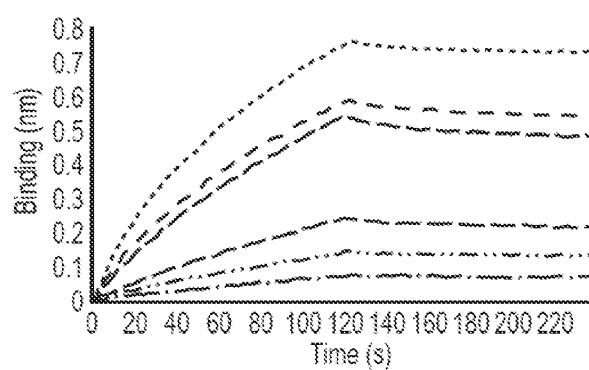
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SARS-CoV-2 B.1.1.7

SARS-CoV-2
S1 Optimiser
S1_A8_F21 (SEQ
ID NO: 140)



SARS-CoV-2
S2 Optimiser
S2_G1_F21 (SEQ
ID NO: 190)

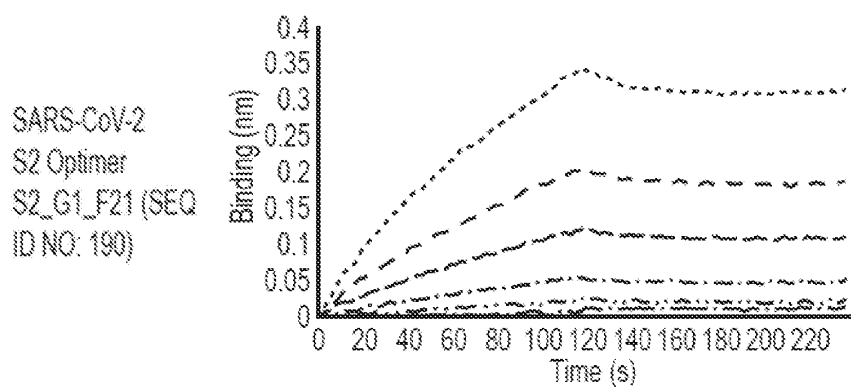
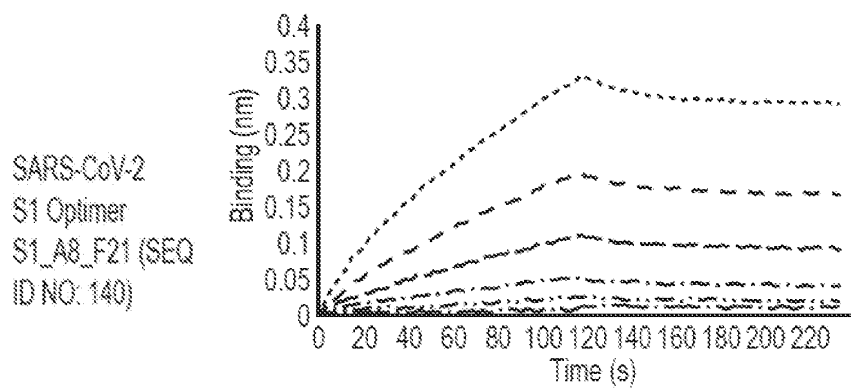


----- 2.52E+05 ----- 1.26E+05 ----- 6.30E+04
----- 3.15E+04 ----- 1.58E+04 ----- 7.88E+03

FIG. 15 (continued)

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SARS-CoV-2 B.1.351



----- 2.52E+05 ----- 1.26E+05 ----- 6.30E+04
----- 3.15E+04 ----- 1.58E+04 ----- 7.88E+03

FIG. 15 (continued)

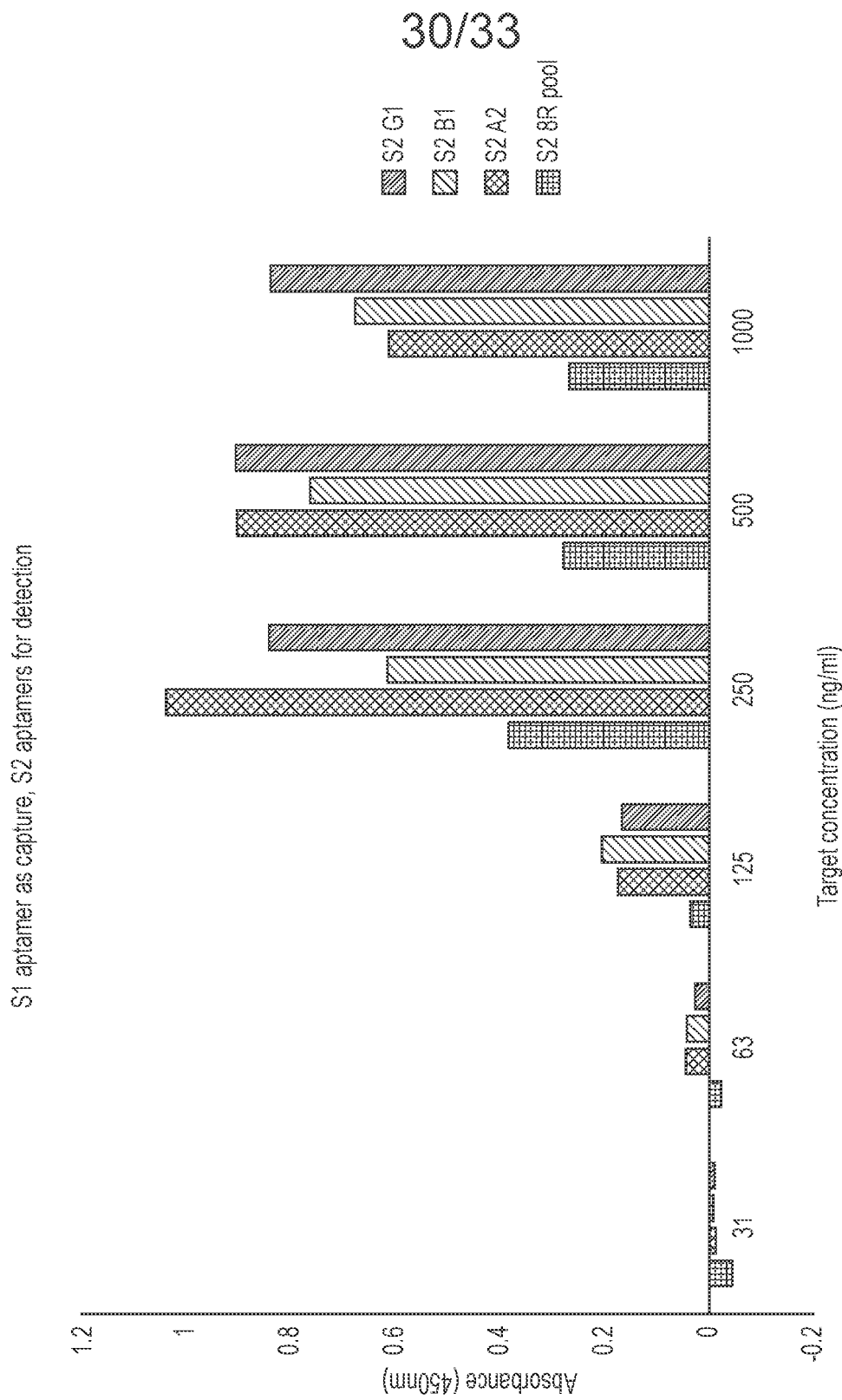


FIG. 16

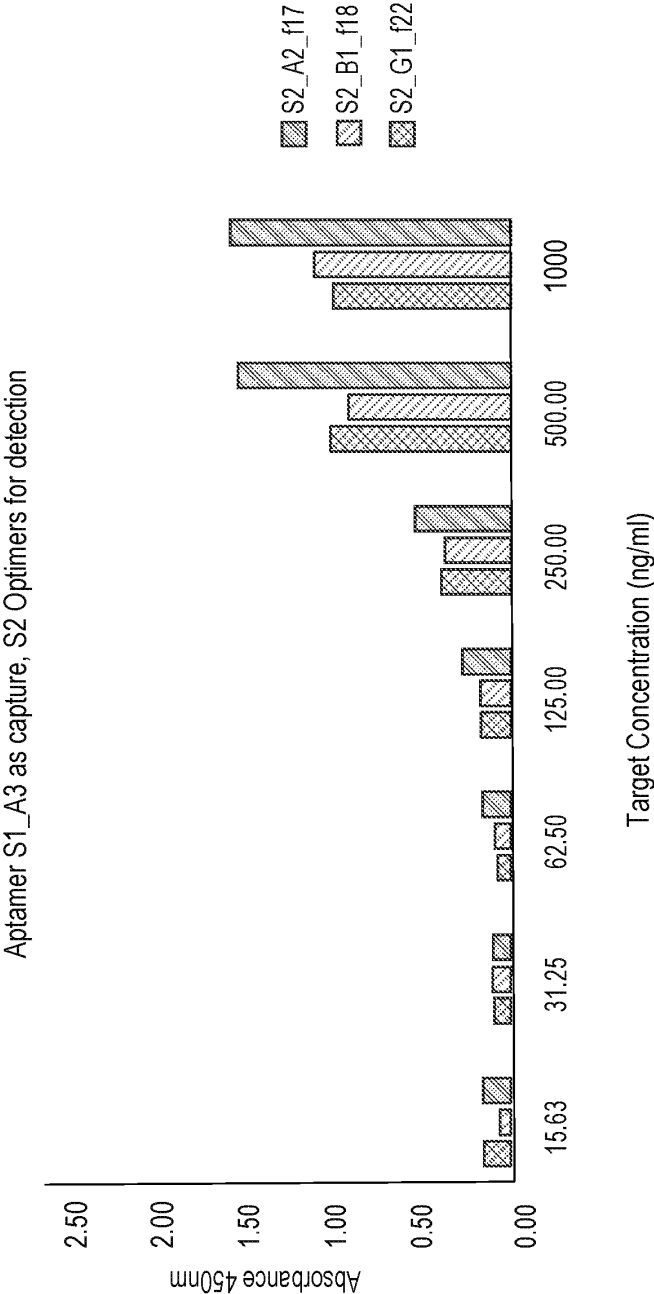


FIG. 17

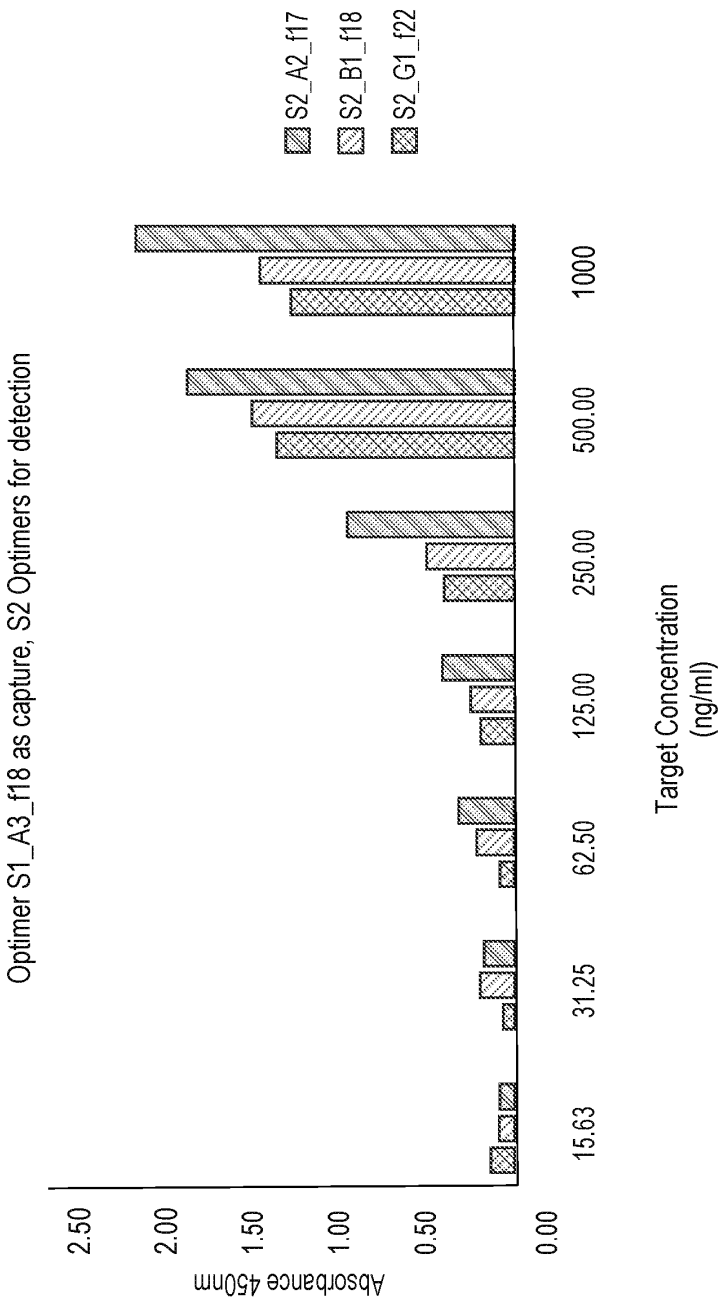


FIG. 17 (continued)

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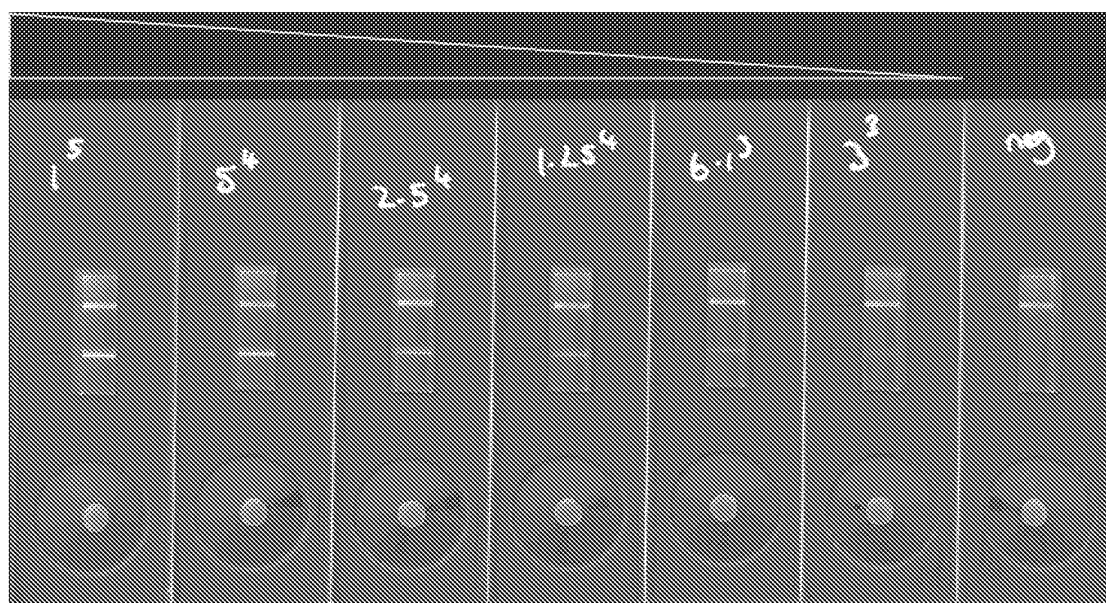


FIG. 18