

Supplemental information

Antibody evasion by the P.1 strain of SARS-CoV-2

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Table S1 Data collection and refinement statistics of RBD complexes, related to X-ray data collection, structure determination and refinement, STAR Methods

Structure	RBD-EY6A-222	K417N-RBD-EY6A-222	K417T-RBD-EY6A-222	B.1.1.7-RBD-EY6A-222	P.1-RBD-EY6A-222	B.1.351-RBD-EY6A-222	P.1-RBD-ACE2
PDB ID	7NX6	7NX7	7NX8	7NX9	7NXB	7NXA	7NXC
Data collection							
Space group	P2 ₁ 2 ₁ 2 ₁	P2 ₁ 2 ₁ 2 ₁	P2 ₁ 2 ₁ 2 ₁	P2 ₁ 2 ₁ 2 ₁	P2 ₁ 2 ₁ 2 ₁	P2 ₁ 2 ₁ 2 ₁	P4 ₁ 2 ₁ 2
Cell dimensions							
a, b, c (Å)	54.4, 120.1, 211.7	54.7, 122.4, 213.7	54.8, 122.7, 213.9	54.3, 120.9, 210.2	54.7, 122.8, 212.3	54.2, 120.4, 211.6	103.5, 103.5, 225.9
a, b, g (°)	90, 90, 90	90, 90, 90	90, 90, 90	90, 90, 90	90, 90, 90	90, 90, 90	90, 90, 90
Resolution (Å)	120–2.25 (2.29–2.25) ^a	81–2.30 (2.30–2.34)	81–1.95 (1.98–1.95)	79–2.40 (2.44–2.40)	80–2.67 (2.72–2.67)	61–2.50 (2.54–2.50)	70–3.14 (3.27–3.14)
R _{merge}	0.438 (---)	0.245 (---)	0.120 (0.990)	0.257 (---)	0.365 (---)	0.401 (---)	0.500 (---)
R _{pim}	0.073 (0.767)	0.039 (0.367)	0.034 (0.972)	0.051 (0.547)	0.072 (1.176)	0.080 (1.086)	0.100 (1.087)
I/s(I)	4.3 (0.3)	7.7 (0.4)	12.0 (0.4)	7.7 (0.6)	7.0 (0.4)	4.6 (0.3)	5.3 (0.5)
CC _{1/2}	0.991 (0.320)	0.997 (0.664)	0.996 (0.354)	0.995 (0.584)	0.997 (0.344)	0.992 (0.360)	0.992 (0.306)
Completeness (%)	99.8 (95.8)	100 (99.7)	100 (99.6)	100 (98.5)	100 (97.7)	99.9 (94.2)	100 (98.1)
Redundancy	34.8 (17.3)	39.6 (36.0)	13.4 (13.2)	26.6 (25.8)	26.3 (27.5)	26.3 (27.1)	25.7 (27.1)
Refinement							
Resolution (Å)	106–2.25	81–2.30	81–1.95	79–2.40	80–2.67	61–2.50	70–3.14
No. reflections	61666/3310	6175/3233	100792/5255	52327/2727	39534/2103	45980/2393	20278/1904
R _{work} / R _{free}	0.207/0.248	0.208/0.239	0.223/0.246	0.200/0.229	0.213/0.251	0.205/0.253	0.226/0.278
No. atoms							
Protein	8014	8004	8017	8012	8025	8014	6405
Ligand/ion/water	386	373	389	345	182	192	70
B factors (Å ²)							
Protein	67	87	78	72	91	77	90
Ligand/ion/water	60	72	50	67	84	92	102
r.m.s. deviations							
Bond lengths (Å)	0.002	0.003	0.002	0.002	0.002	0.002	0.003
Bond angles (°)	0.5	0.6	0.5	0.5	0.5	0.5	0.6

^aValues in parentheses are for highest-resolution shell.

Table S2 Monoclonal antibody neutralization and binding data, related to Figures 2 and 3

mAb	IC50 (ug/ml)				FRNT ⁵⁰ ratio			KD (nM)					Immunoglobulin gene usage		
	Victoria	B.1.1.7	B.1.351	P.1	B.1.1.7/ Victoria	B.1.351/ Victoria	P.1/ Victoria	Native RBD	K417T	K417N	E484K	RBD P.1	IGHV	K/ λ	IGLV
40	0.026 ± 0.007	0.035 ± 0.008	0.738 ± 0.311	0.153 ± 0.037	1.4	28.6	5.9	1.33±0.03	38.90±0.89	56.7±1.18	7.31±0.03	38.20±0.95	3-66	K	1-33 or 1D-33
55	0.095 ± 0.015	0.348 ± 0.044	0.127 ± 0.014	0.306 ± 0.046	3.7	1.3	3.2	2.66±0.05	4.60±0.12	4.21±0.09	3.82±0.02	11.10±0.37	1-58	K	3-20
58	0.041 ± 0.003	0.116 ± 0.029	0.136 ± 0.010	0.236 ± 0.075	2.8	3.3	5.7	1.46±0.04	1.83±0.02	2.75±0.03	0.97±0.04	2.84±0.03	3-9	λ	3-21
88	0.033 ± 0.001	0.058 ± 0.008	>10	>10	1.8	>307.6	>307.6	2.90±0.03	Knocked out	Knocked out	5.37±0.06	Knocked out	4-61	λ	1-36
132	0.048 ± 0.000	0.337 ± 0.048	>10	>10	7.0	>208.4	>208.4	2.93±0.10	1846±364	2495±1095	29.80±0.36	1338±452	4-34	λ	7-46
150	0.012 ± 0.000	0.139 ± 0.019	0.350 ± 0.010	0.040 ± 0.003	12.0	30.0	3.4	0.40±0.01	1.64±0.02	3.35±0.03	1.83±0.03	8.90±0.13	3-53	K	1-9
158	0.031 ± 0.004	0.254 ± 0.109	>10	>10	8.3	>327.5	>327.5	1.89±0.03	4.83±0.06	9.35±0.11	3.03±0.10	18.20±0.31	3-53	K	1-9
159	0.011 ± 0.000	0.061 ± 0.020	>10	1.434 ± 0.804	5.7	>928.4	133.2	N/A	N/A	N/A	N/A	N/A	3-30	K	3-20
165	0.034 ± 0.004	0.212 ± 0.004	0.054 ± 0.013	0.241 ± 0.030	6.3	1.6	7.2	2.15±0.03	2.62±0.06	3.29±0.05	3.49±0.03	7.10±0.15	1-58	K	3-20
170	0.025 ± 0.004	0.105 ± 0.050	>10	>10	4.2	>402.2	>402.2	5.23±0.02	6.24±0.04	6.95±0.05	Knocked out	463.4±25.4	5-51	K	2D-29
175	0.026 ± 0.000	0.575 ± 0.280	>10	3.881 ± 0.738	22.5	>391.5	151.9	1.36±0.01	3.17±0.02	8.60±0.04	10.8±0.07	68.30±0.50	3-53	K	1-33 or 1D-33
222	0.019 ± 0.000	0.014 ± 0.002	0.017 ± 0.005	0.008 ± 0.003	0.7	0.9	0.4	1.36±0.08	3.96±0.11	5.16±0.12	2.25±0.04	1.92±0.01	3-53	K	3-20
253	0.055 ± 0.008	0.126 ± 0.018	0.109 ± 0.055	0.137 ± 0.005	2.3	2.0	2.5	1.15±0.03	5.99±0.11	6.11±0.11	2.66±0.03	4.25±0.11	1-58	K	3-20
269	0.030 ± 0.000	>10	>10	>10	>337.5	>337.5	>337.5	0.76±0.02	6.69±0.04	8.88±0.04	1.29±0.03	Knocked out	3-53	K	1-9
278	0.014 ± 0.007	0.307 ± 0.149	0.160 ± 0.018	0.245 ± 0.042	22.5	11.7	17.9	4.16±0.03	5.21±0.03	6.37±0.03	6.95±0.27	16.20±0.17	1-18	K	1-39 or 1D-39
281	0.005 ± 0.001	0.012 ± 0.000	>10	>10	2.5	>2026.3	>2026.3	0.97±0.03	0.68±0.02	4.42±0.03	3.54±0.08	Knocked out	3-7	K	2-24
316	0.018 ± 0.007	0.024 ± 0.005	>10	>10	1.4	>563.6	>563.6	4.81±0.05	4.96±0.06	5.17±0.08	Knocked out	Knocked out	1-2	λ	2-8
318	0.029 ± 0.008	0.185 ± 0.037	0.019 ± 0.008	0.083 ± 0.032	6.3	0.7	2.8	4.43±0.04	4.96±0.04	5.35±0.04	6.05±0.02	9.30±0.03	1-58	K	3-20
384	0.004 ± 0.001	0.005 ± 0.002	>10	>10	1.1	>2398.4	>2398.4	1.19±0.02	1.30±0.03	1.80±0.03	1.75±0.04	Knocked out	3-11	K	1-27
398	0.091 ± 0.004	0.180 ± 0.001	>10	>10	2.0	>110.2	>110.2	4.63±0.04	10.40±0.10	13.60±0.24	Knocked out	Knocked out	3-66	λ	2-8
AZD1061	0.013 ± 0.003	0.012 ± 0.002	0.014 ± 0.002	0.007 ± 0.002	0.9	1.1	0.5	5.13±0.07	8.00±0.12	6.14±0.08	7.66±0.05	2.27±0.03	N/A	N/A	N/A
AZD8895	0.005 ± 0.001	0.011 ± 0.002	0.046 ± 0.031	0.046 ± 0.016	2.2	8.9	8.8	2.18±0.04	2.96±0.05	3.56±0.06	8.50±0.05	7.35±0.15	N/A	N/A	N/A
AZD7442	0.009 ± 0.000	0.007 ± 0.001	0.012 ± 0.001	0.006 ± 0.003	0.8	1.4	0.7	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
REGN10987	0.032 ± 0.007	0.028 ± 0.003	0.007 ± 0.001	0.013 ± 0.002	0.9	0.2	0.4	1.35±0.03	1.61±0.03	1.84±0.04	1.39±0.05	1.38±0.02	N/A	N/A	N/A
REGN10933	0.004 ± 0.002	0.014 ± 0.002	3.284 ± 2.014	6.177 ± 1.914	3.3	773.7	1455.2	0.97±0.02	1.99±0.02	1.70±0.01	1.92±0.02	308.7±10.0	N/A	N/A	N/A
ADG10	0.006 ± 0.000	0.010 ± 0.001	0.011 ± 0.001	0.003 ± 0.000	1.8	1.9	0.5	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
ADG20	0.004 ± 0.001	0.006 ± 0.000	0.010 ± 0.001	0.009 ± 0.000	1.4	2.5	2.2	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
ADG30	0.007 ± 0.002	0.016 ± 0.001	0.029 ± 0.003	0.002 ± 0.001	2.5	4.4	0.3	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
LY-CoV555	0.006 ± 0.002	0.009 ± 0.000	>10	>10	1.5	>1545.3	>1545.3	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
LY-CoV16	0.034 ± 0.007	3.225 ± 1.030	>10	>10	1.5	>291.2	>291.2	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
S309	0.040 ± 0.005	0.078 ± 0.069	0.082 ± 0.002	0.076 ± 0.014	1.5	2.0	1.9	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
222H+222L	0.017 ± 0.001	0.011 ± 0.002	0.016 ± 0.001	0.009 ± 0.000	0.6	1.0	0.5	N/A	N/A	N/A	N/A	N/A	3-53	K	3-20
150H+222L	0.016 ± 0.003	0.010 ± 0.001	0.007 ± 0.001	0.003 ± 0.000	0.6	0.4	0.2	N/A	N/A	N/A	N/A	N/A	3-53	K	3-20
158H+222L	0.033 ± 0.003	0.014 ± 0.001	0.056 ± 0.015	0.019 ± 0.000	0.4	1.7	0.6	N/A	N/A	N/A	N/A	N/A	3-53	K	3-20
175H+222L	>10	0.399 ± 0.012	>10	>10	<0.04	N/A	N/A	N/A	N/A	N/A	N/A	N/A	3-53	K	3-20
269H+222L	0.552 ± 0.085	0.024 ± 0.001	>10	>10	0.04	>18.1	>18.1	N/A	N/A	N/A	N/A	N/A	3-53	K	3-20

Table S3 Results of PDB BLAST for the majority of the mAb 222 light chain sequence, PDB codes shown and residue 30 (within CDR L1) outlined in red. Related to Figure 4.

Accession	Sequence	Residue 30
222	MTOSPGTLLSLSPPERATLSCRASQSV	PSS
7JMO_L	MTOSPGTLLSLSPPERATLSCRASQSV	SSS
4LRN_L	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
7K43_D	MMOSPGTLLSLSPPERATLSCRASQSV	SSS
40B5_L	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
60L6_L	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
6026_B	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
4M62_L	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
5FT5_L	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
60L5_L	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
5J0F_B	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
7LAB_L	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
6GHG_B	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
6041_A	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
6W10_B	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
5117_A	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
4NP4_L	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
4HWB_L	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
6CA9_A	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
7CDI_L	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
7K8N_B	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
6BKC_L	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
4HWE_L	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
7LK9_B	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
6XE1_L	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
7K8M_B	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
7D0C_F	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
6025_B	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
5GMQ_C	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
3QEG_L	MMOSPGTLLSLSPPERATLSCRASQSV	SSS
5IBT_L	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
7K45_L	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
6J09_L	MTOSPGTLLSLSPPERATLSCRASQSV	SSS
6MVL_L	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
11QD_A	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
5Y2L_J	MTOSPGTLLSLSPPERATLSCRASQSV	SSS
7ND9_L	MTOSPGTLLSLSPPERATLSCRASQSV	SSS
5XMH_C	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
5WK0_B	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
7BEO_D	MTOSPGTLLSLSPPERATLSCRASQSV	SSS
4YPG_A	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
5W19_E	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
6028_B	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
7K3Q_L	LTOTPGTLLSLSPPERATLSCRASQSV	SSS
5D1Q_D	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
6CA7_L	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
5K9J_L	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
7NDB_L	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
5K9K_B	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
5J03_B	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
5UAX_L	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
6B0A_L	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
7NDC_E	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
5TRU_L	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
6WPS_D	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
6EHV_X	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
6B3D_D	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
5W1K_C	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
6XC4_L	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
6CMG_B	MTOSPGTLLSLSPPERATLSCRASQSV	SSS
7KN6_L	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
4F0L_L	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
5X8M_C	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
5XJ4_L	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
5Y0A_E	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
1U6A_L	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
6W56_B	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
6B9J_B	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
4KXZ_I	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
7BEN_F	MTOSPGTLLSLSPPERATLSCRASQSV	SSS
7K8U_L	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
3S03_B	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
4QXG_L	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
6BK6_L	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
5D1X_D	LTOTPATLLSLSPPERATLSCRASQSV	SSS
3W9D_B	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
4KV5_E	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
4IDJ_L	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
4N90_E	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
6W04_L	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
6029_L	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
5WYM_A	LTOSPATLLSLSPPERATLSCRASQSV	SSS
7J00_L	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
5V7R_L	MTOSPGTLLSLSPPERATLSCRASQSV	SSS
7AH1_A	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
35DY_L	MTOSPGTLLSLSPPERATLSCRASQSV	SSS
6N7J_B	MTOSPGTLLSLSPPERATLSCRASQSV	SSS
1DN0_A	LTOSPATLLSLSPPERATLSCRASQSV	SSS
5UJZ_G	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
6MTQ_L	LTOSPATLLSLSPPERATLSCRASQSV	SSS
6GFE_L	LTOSPATLLSLSPPERATLSCRASQSV	SSS
7CH5_L	LTOSPATLLSLSPPERATLSCRASQSV	SSS
5CSZ_B	LTOSPATLLSLSPPERATLSCRASQSV	SSS
6BKD_L	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
5IBU_B	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
1RH4_H	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
6W1Y_L	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
6W1Z_L	LTOSPGTLLSLSPPERATLSCRASQSV	SSS
5GS1_A	LTOSPATLLSLSPPERATLSCRASQSV	SSS
5W4L_C	LTOSPGTLLSLSPPERATLSCRASQSV	SSS

Table S4A Neutralization of Victoria and P.1 virus by convalescent plasma (infection with original Victoria-like virus), related to Figure 6

Convalescent plasma	FRNT50 (Reciprocal plasma dilution)		Victoria/P.1 ratio
	Victoria	P.1	
Convalescent 1	61	25	2.5
Convalescent 2	689	49	14.2
Convalescent 3	526	173	3.0
Convalescent 4	409	356	1.1
Convalescent 5	369	105	3.5
Convalescent 6	1270	556	2.3
Convalescent 7	274	80	3.4
Convalescent 8	633	223	2.8
Convalescent 9	667	126	5.3
Convalescent 10	124	34	3.7
Convalescent 11	102	30	3.4
Convalescent 12	339	74	4.6
Convalescent 13	331	240	1.4
Convalescent 14	438	95	4.6
Convalescent 15	6397	3261	2.0
Convalescent 16	44	39	1.1
Convalescent 17	1115	87	12.8
Convalescent 18	242	64	3.8
Convalescent 19	29	20	1.4
Convalescent 20	154	136	1.1
Convalescent 21	487	165	3.0
Convalescent 22	438	241	1.8
Convalescent 23	381	83	4.6
Convalescent 24	1647	390	4.2
Convalescent 25	913	322	2.8
Convalescent 26	1880	825	2.3
Convalescent 27	1464	206	7.1
Convalescent 28	361	81	4.4
Convalescent 29	2859	1010	2.8
Convalescent 30	1109	477	2.3
Convalescent 31	811	274	3.0
Convalescent 32	395	130	3.0
Convalescent 33	1144	207	5.5
Convalescent 34	676	201	3.4

Table S4B Neutralization of Victoria and P.1 virus by B.1.1.7 plasma, related to Figure 6

B.1.1.7 plasma	Day post symptom onset	FRNT50 (Reciprocal plasma dilution)		Victoria/P.1 ratio
		Victoria	P.1	
B.1.1.7 P3	11	440	116	3.8
B.1.1.7 P4	18	136884	48440	2.8
B.1.1.7 P5	45	1506	787	1.9
B.1.1.7 P6	31	370	259	1.4
B.1.1.7 P7	33	2250	267	8.4
B.1.1.7 P8	25	2999	2261	1.3
B.1.1.7 P9	26	970	861	1.1
B.1.1.7 P10	18	3735	861	4.3
B.1.1.7 P11	24	2193	1116	2.0
B.1.1.7 P13	29	<20	67	<0.3
B.1.1.7 P14	21	1700	168	10.1
B.1.1.7 P15	16	168	414	0.4

Table S5 Neutralisation of Victoria and P.1 viruses by immune serum from vaccinees, related to Figure 7

Vaccine samples	Day Post-boost	FRNT50 (Reciprocal serum dilution)		Victoria/P.1 ratio
		Victoria	P.1	
Pfizer1	7	1149	396	2.9
Pfizer2	7	<20	36	<0.6
Pfizer3	7	1727	698	2.5
Pfizer4	8	2234	712	3.1
Pfizer5	7	3016	1033	2.9
Pfizer6	7	1521	302	5.0
Pfizer7	7	609	294	2.1
Pfizer8	7	4340	2119	2.0
Pfizer9	7	1467	361	4.1
Pfizer10	7	1757	343	5.1
Pfizer11	7	860	424	2.0
Pfizer12	7	1749	452	3.9
Pfizer13	7	1851	669	2.8
Pfizer14	7	407	294	1.4
Pfizer15	8	1285	571	2.3
Pfizer16	8	1286	311	4.1
Pfizer17	8	1810	304	6.0
Pfizer18	8	1198	282	4.3
Pfizer19	8	466	229	2.0
Pfizer20	8	1539	693	2.2
Pfizer21	9	184	52	3.5
Pfizer22	11	1061	491	2.2
Pfizer23	12	1658	355	4.7
Pfizer24	12	1155	569	2.0
Pfizer25	15	8092	5029	1.6
AstraZeneca 1	28	495	265	1.9
AstraZeneca 2	28	580	429	1.4
AstraZeneca 3	28	253	<20	>12.6
AstraZeneca 4	28	183	102	1.8
AstraZeneca 5	28	432	215	2.0
AstraZeneca 6	28	764	111	6.9
AstraZeneca 7	28	133	29	4.5
AstraZeneca 8	28	257	116	2.2
AstraZeneca 9	28	501	97	5.2
AstraZeneca 10	28	357	133	2.7
AstraZeneca 11	14	334	115	2.9
AstraZeneca 12	14	250	94	2.7
AstraZeneca 13	14	122	40	3.1
AstraZeneca 14	14	212	110	1.9
AstraZeneca 15	14	789	281	2.8
AstraZeneca 16	14	538	181	3.0
AstraZeneca 17	14	1159	359	3.2
AstraZeneca 18	14	353	85	4.1
AstraZeneca 19	14	975	382	2.6
AstraZeneca 20	14	169	74	2.3
AstraZeneca 21	14	155	87	1.8
AstraZeneca 22	14	152	98	1.5
AstraZeneca 23	14	126	67	1.9
AstraZeneca 24	14	293	151	1.9
AstraZeneca 25	14	94	25	3.8