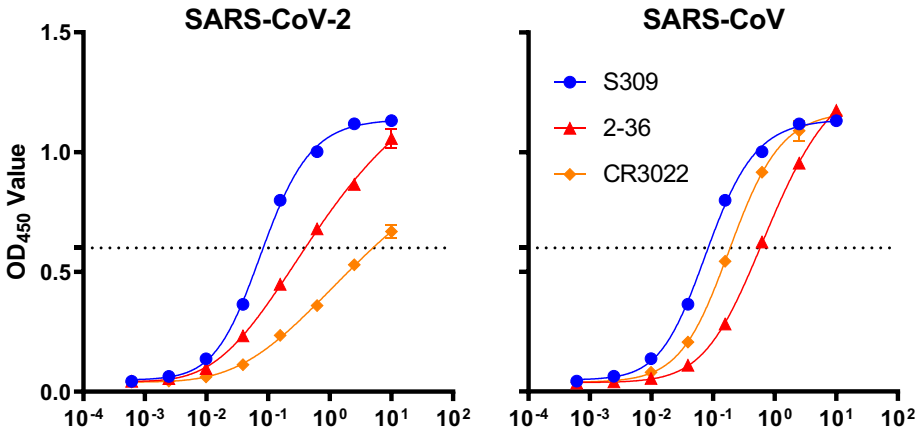
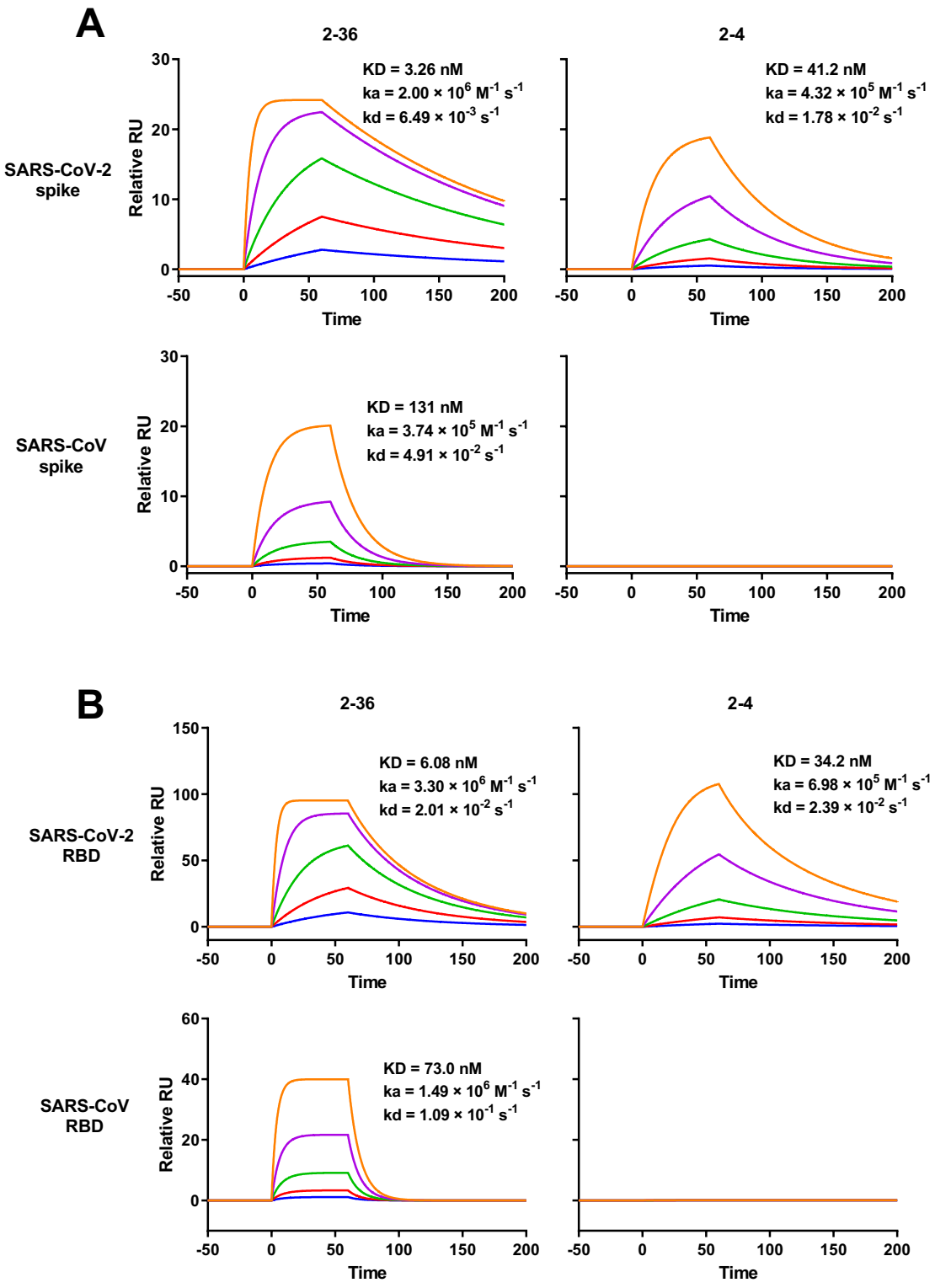
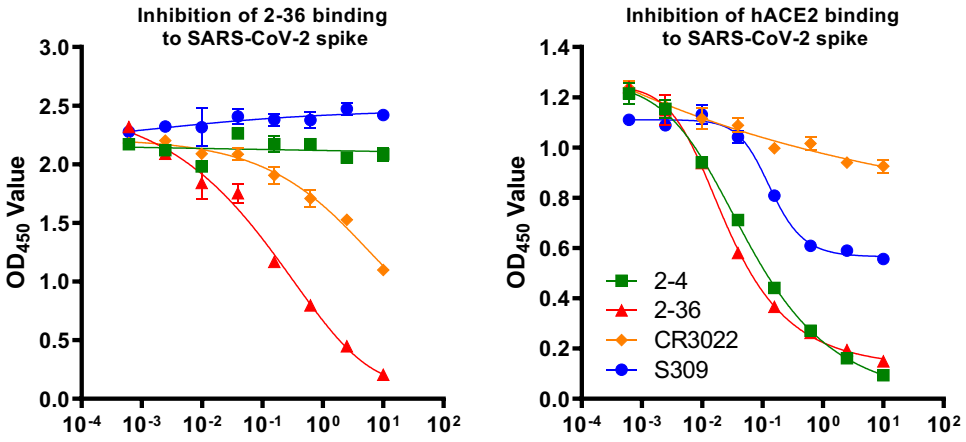


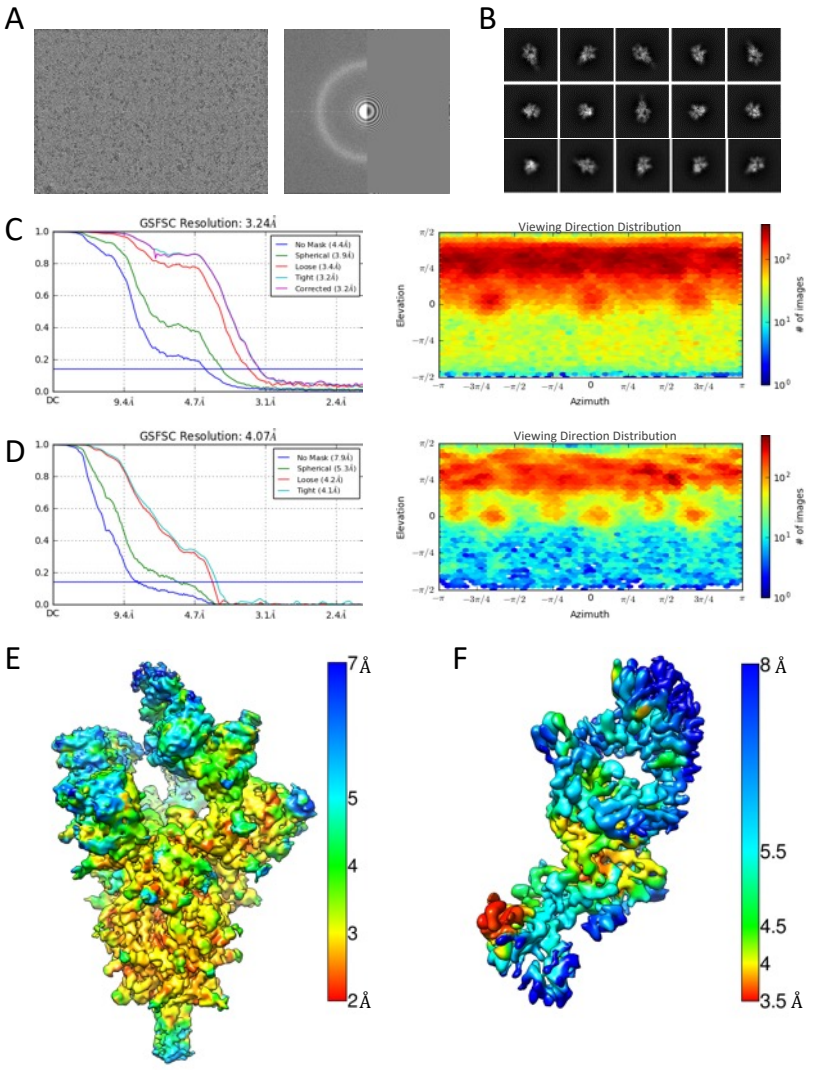
Supplementary Figure 1. Binding of 2-36 to SARS-CoV-2 and SARS-CoV spike as determined by ELISA.



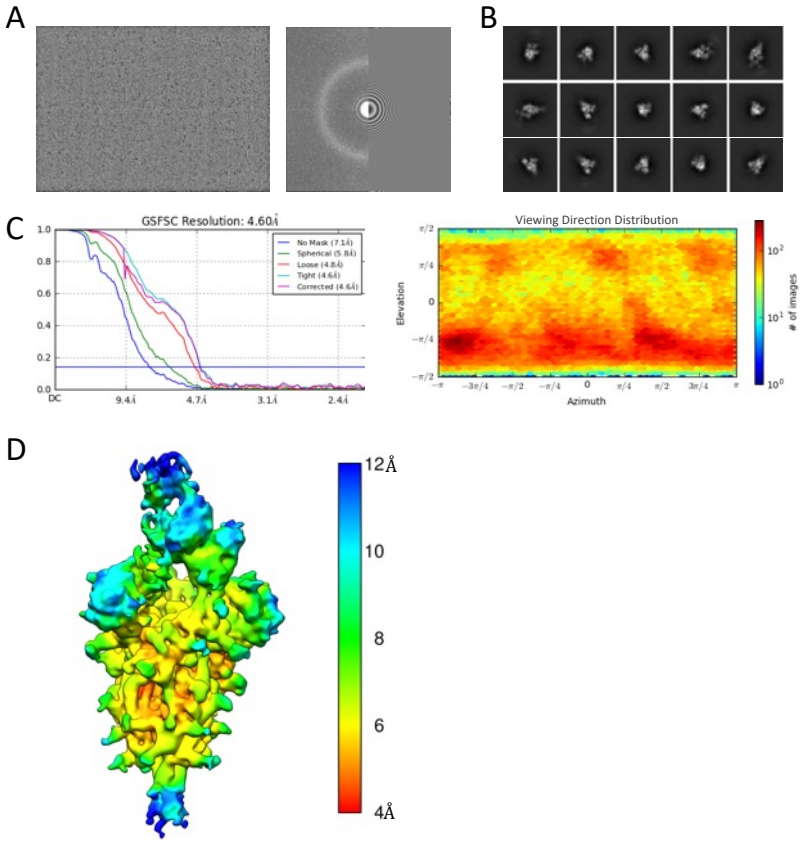
Supplementary Figure 2. 2-36 binding affinity to SARS-CoV-2 and SARS-CoV (a) spike or (b) RBD as measured by SPR.



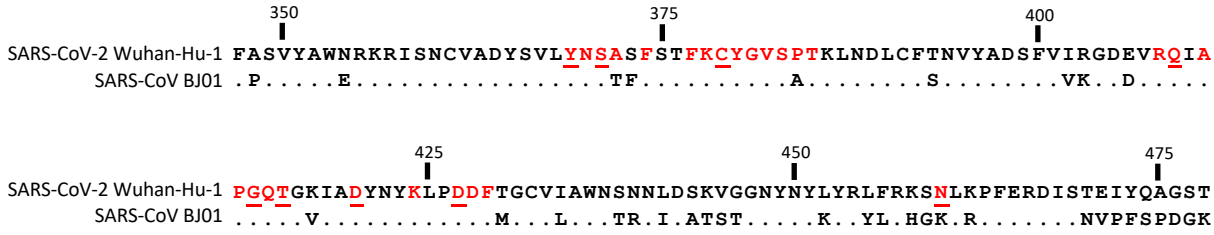
Supplementary Figure 3. 2-36 binding to SARS-CoV-2 spike is inhibited by CR3022; 2-36 inhibits hACE2 binding to SARS-CoV-2 spike.



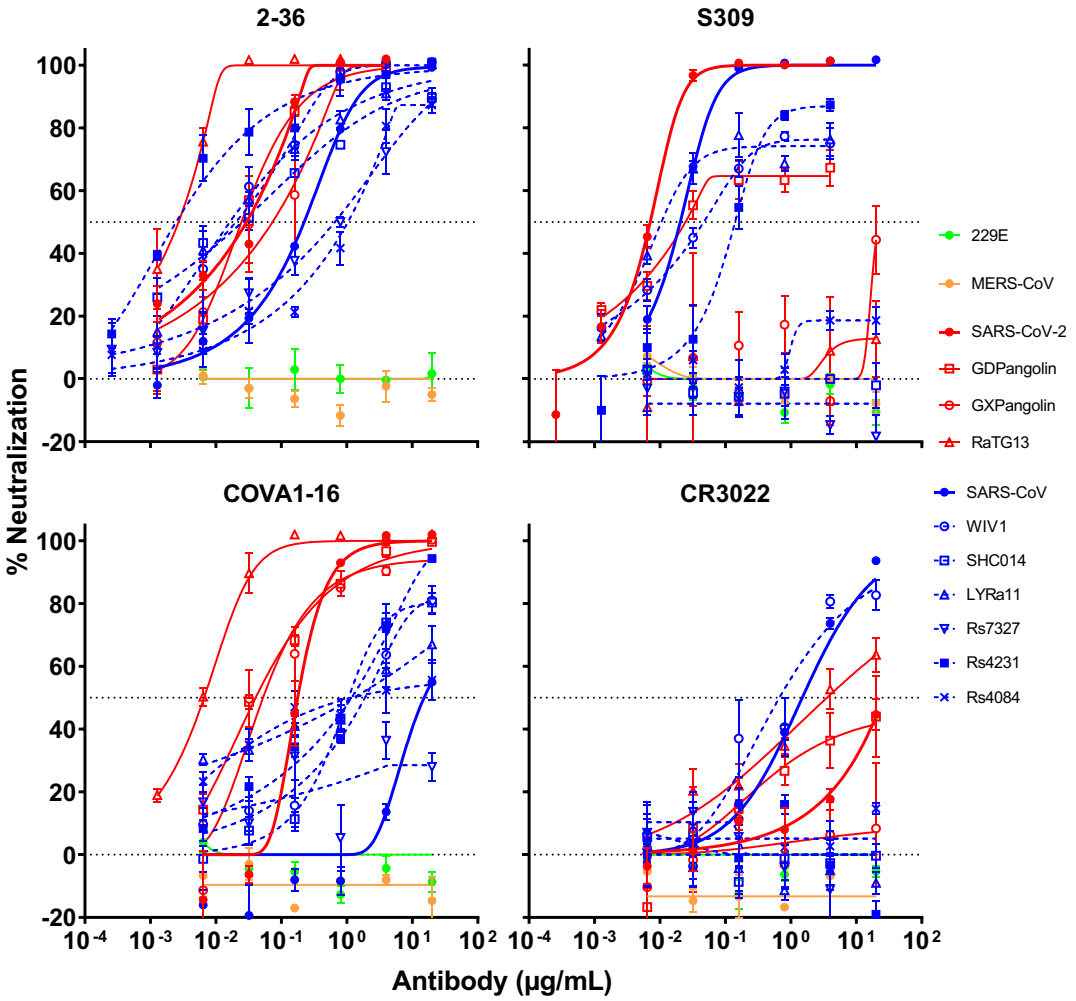
Supplementary Figure 4. Cryo-EM data processing for antibody 2-36 in complex with the SARS-CoV-2 S trimer.



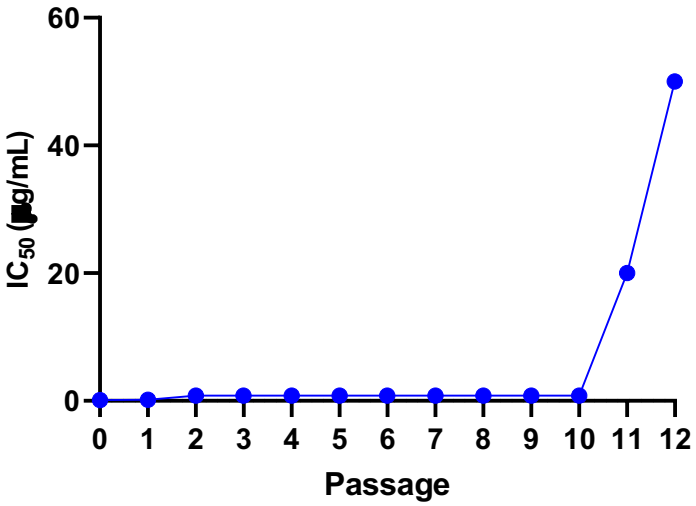
Supplementary Figure 5. Cryo-EM data processing for antibody 2-36 in complex with the SARS-CoV S trimer.



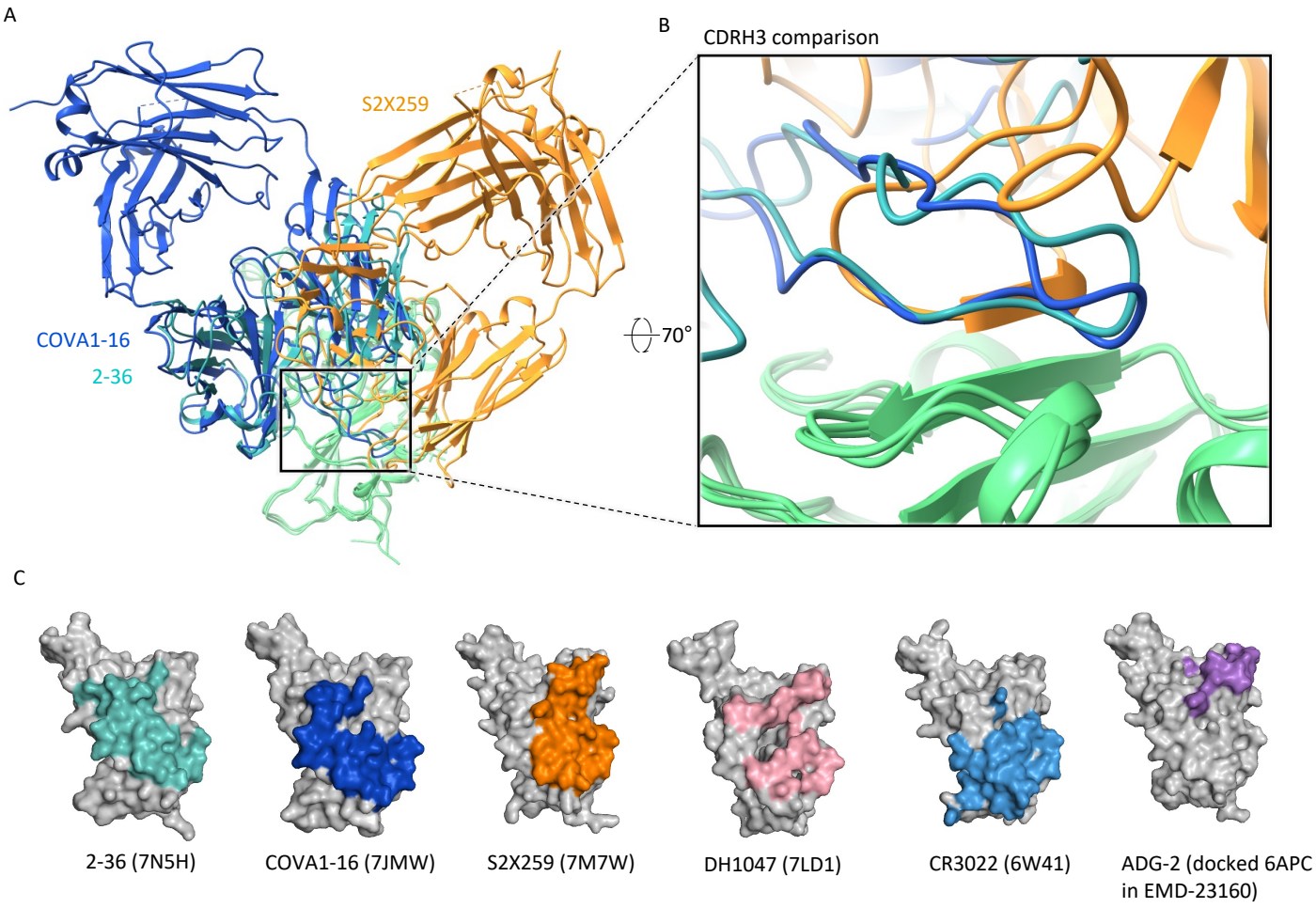
Supplementary Figure 6. Sequence alignment for SARS-CoV-2 and SARS-CoV RBD binding interface of 2-36.



Supplementary Figure 7. 2-36 Neutralizes SARS-like coronaviruses using hACE2.



Supplementary Figure 8. 2-36 neutralization IC_{50} (μg/mL) on the serially passaged virus**.**



Supplementary Figure 9. Structural comparison between antibody 2-36 in complex with SARS CoV-2 RBD and other published antibody structures.

Supplementary Table 1. Cryo-EM data collection, processing, and model refinement and validation statistics. Related to Figure 2 and 4.

	SARS-CoV-2 S2P + 2-36 Fab	SARS-CoV S2P + 2-36 Fab
EMDB ID	24190	
PDB ID	7N5H	
Data Collection		
Microscope	FEI Titan Krios	FEI Titan Krios
Voltage (keV)	300	300
Magnification	81000	81000
Defocus Range (μm)	-0.8/-2.5	-0.8/-2.5
Camera	Gatan K3 BioQuantum	Gatan K3 BioQuantum
Pixel Size (Å/pix)	1.07	1.07
Recording Mode	counting	counting
Dose Rate (e-/pixel/s)	16	16
Elctron Dose (e-/Å^2)	42	42
Data Processing		
Software	cryoSPARC v2.15	cryoSPARC v2.15
Micrographs used	4,226	3835
Number of Particles	171,897	80112
Symmetry	C1	C1
Box Size (pix)	440	440
Global Map FSC$_{0.143}$ (Å)	3.24	4.60
Local Map FSC$_{0.143}$ (Å)	4.07	
Refinement and Validation		
Software	Phenix 1.18	
Initial Model Used	6BE2 (Fab), 7BZ5 (RBD), 6VXX (spike)	
Number of Atoms	29,691	
Protein Residues	3,739	
Ligands	NAG: 41	
Model vs. Data CC (mask)	0.72	
RMS deviations		
Bond lengths (Å) (# >4σ)	2	
Bond angles (°) (# >4σ)	17	
MolProbity Score	1.20	
Clashscore (all atom)	4.20	
Poor rotamers (%)	0.18	
Ramachandran plot		
Favored (%)	98.34	
Allowed (%)	1.66	
Outliers (%)	0.00	