

**Table S1. Cryo-EM Data Collection and Refinement Statistics, Related to Figures 1-2.**

SARS-CoV-2 S2P complex	1-57 Fab	2-7 Fab
<b>EMDB ID</b>	EMD-23506	EMD-23507
<b>PDB ID</b>	7LS9	7LSS
<u>Data Collection</u>		
Microscope	FEI Titan Krios	FEI Titan Krios
Voltage (kV)	300	300
Electron dose (e <sup>-</sup> /Å <sup>2</sup> )	41.92	51.69
Detector	Gatan K3 BioQuantum	Gatan K3 BioQuantum
Pixel Size (Å)	1.07	1.058
Defocus Range (µm)	-0.8/-2.5	-0.5/-2.5
Magnification	81000	81000
<u>Reconstruction</u>		
Software	cryoSPARC v2.15	cryoSPARC v2.15
Particles	89,601	165,576
Symmetry	C3	C1
Box size (pix)	420	384
Resolution (Å) (FSC <sub>0.143</sub> )	3.42	3.72
<u>Refinement</u>		
Software	Phenix 1.18	Phenix 1.18
Protein residues	4002	2783
Chimera CC	0.83	0.79
EMRinger Score	2.14	3.13
R.m.s. deviations		
Bond lengths (Å)	0.006	0.011
Bond angles (°)	1.11	1.066
<u>Validation</u>		
Molprobrity score	1.38	1.15
Clash score	4.32	1.08
Favored rotamers (%)	100	100
Ramachandran		
Favored regions (%)	97.0	95.09
Allowed regions (%)	3.0	4.91
Disallowed regions (%)	0	0