

Supplementary information, Table S1
Cryo-EM data collection and image processing statistics

(A) Statistics of SARS-CoV S structure determination with C3 symmetry

Data collection	
Electron microscope	Titan Krios
Voltage (kV)	300
Electron detector	K2
Pixel size (Å)	1.32
Defocus range (µm)	1.0 – 3.8
Frames per movie	32
Dose rate (e ⁻ /Å ² ·s)	4.7
3D Reconstruction	
CTF estimation	CTFFIND4
Software	RELION 1.4
Particles for final refinement	34,152
Map sharpening B-factors (Å ²)	-140
Final Resolution (Å)	4.3
Model Refinement	
Software	PHENIX
Fourier Shell Correlation	0.71
Molprobit score	2.20
Rotamer outliers (%)	0.71
C-beta deviations	0
Clashscore	8.66
R.m.s. deviations	
Bonds length (Å)	0.0077
Bonds angles (°)	1.61
Ramachandran plot (%)	
Favored	80.26
Outliers	0.41

(B) Statistics of 3D reconstructions of SARS-CoV S of different conformations

	SARS-CoV S Conformation 1 (C3 symmetry)	SARS-CoV S Conformation 2 (C1 symmetry)	SARS-CoV S Conformation 3 (C1 symmetry)	SARS-CoV S Conformation 4 (C1 symmetry)
Particles	34,152	11,554	39,350	38,804
Final Resolution (Å)	4.3	7.3	5.7	6.8
Angle of CTD1 (°)	19	52	64	70
PHENIX CC*		0.951	0.925	0.937
Chimera CC [#]		0.968	0.949	0.959

The asymmetric CTD1 domain is masked out and the cross correlation is calculated between the masked maps of conformation 2-4 and conformation 1.

*Cross correlation calculated using *Phenix.get_cc_mtz_mtz* command.

Cross correlation calculated using Chimera *measure correlation* command.