

Cell, Volume 183

Supplemental Information

Molecular Architecture of the SARS-CoV-2 Virus

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Table S1. Cryo-ET Data collection and reconstruction statistics. Related to Figure 1.

Data collection						
Microscope	Titan Krios					
Voltage (kV)	300					
Detector	Gatan K3					
Energy filter	Gatan GIF Quantum, 20 eV slit					
Pixel size (Å)	0.68 (super-resolution)					
Tilt schemes	Dose-symmetric scheme					
Number of tilt-series	319					
Number of virions	2,294					
Exposure (e ⁻ /Å ²)	131.2					
Defocus range (µm)	-1.7 ~ -5.0					
Software	SerialEM					
Reconstruction						
Software	Dynamo 1.1.333, Relion 2.0					
Data set	Prefusion S (RBD down)	Prefusion S (one RBD up)	Postfusion S	RNP (individual)	RNP (tetrahedron)	RNP (hexon)
Final number of particles	25,236	21,080	1,954	18,500	3,659	2,270
Symmetry imposed	C3	C1	C3	C1	C3	C6
Final Resolution (Å)	8.7	10.9	15.3	13.1	N/A	N/A
Gold-standard	yes	yes	yes	yes	no	no
FSC threshold	0.143	0.143	0.143	0.143	N/A	N/A
Final pixelsize (Å)	1.36	2.72	2.72	2.72	5.44	5.44
Map sharpening B-factor (Å ²)	-1200	-2000	N/A	N/A	N/A	N/A