

S3 Table. Cryo-EM data collection and refinement statistics

CH505.N279K.G458Y.SOSIP.664 +CH235 UCA2	
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Data Collection	
Microscope	FEI Titan Krios
Voltage (kV)	300
Electron dose (e ⁻ /Å ²)	42
Detector	Falcon 3
Pixel Size (Å)	1.08
Defocus Range (µm)	~1.5-3
Magnification	75000
Reconstruction	
Software	cryoSparc
Particles	22093
Symmetry	C3
Box size (pix)	320
Resolution (Å) (FSC0.143) [§]	4.2
Refinement (Phenix)	
Protein residues	3054
Chimera CC	0.85
R.m.s. deviations	
Bond lengths (Å)	0.006
Bond angles (°)	0.946
Validation	
Molprobit score	1.0
Clash score	1.4
Favored rotamers (%)	99.0
Ramachandran	
Favored regions (%)	97.1
Disallowed regions (%)	0.5
EMRinger score	1.47
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¹Resolutions are reported according to the FSC 0.143 gold-standard criterion