

Supplemental Data Table 1. Cryo-EM data collection, refinement and validation statistics

	#1 name (EMDB-xxxx) (PDB xxxx)
Data collection and processing	
Magnification	47170
Voltage (kV)	300
Electron exposure (e-/Å ²)	50e/Å ²
Defocus range (μm)	0.5
Pixel size (Å)	1.06
Symmetry imposed	C1
Initial particle images (no.)	614883
Final particle images (no.)	184672
Map resolution (Å)	3.26
FSC threshold	0.143
Map resolution range (Å)	3.1-3.5
Refinement	
Initial model used (PDB code)	5VAI, 3C5T, 3SN6
Model resolution (Å)	
FSC threshold	0.143
Model resolution range (Å)	3.26
Map sharpening <i>B</i> factor (Å ²)	-50
Model composition	
Protein residues	1083
<i>B</i> factors (Å ²)	82-193 (avr. 128)
R.m.s. deviations	
Bond lengths (Å)	0.008
Bond angles (°)	1.217
Validation	
MolProbity score	1.5
Clashscore	4.31
Poor rotamers (%)	0
Ramachandran plot	
Favored (%)	95.8
Allowed (%)	4.2
Disallowed (%)	0