

Table S6. Cryo-EM Data Collection, Refinement, and Validation Statistics, Related to Figure 3

	1-18-BG505-10-1074	1-55-RC1-10-1074
	(EMDB-20739)	(EMDB-20740)
	(PDB 6UDJ)	(PDB 6UDK)
Data collection and processing		
Magnification	130,000x	73,000x
Voltage (kV)	300	200
Microscope	Titan Krios	Talos Arctica
Electron exposure (e-/Å ²)	60	39.1
Defocus range (µm)	1 - 2.6	1 - 3.4
Pixel size (Å)	1.057	1.40
Symmetry imposed	C3	C3
Initial particle images (no.)	352,598	160,254
Final particle images (no.)	230,924	110,126
Map resolution (Å)	2.5	3.9
FSC threshold	0.143	0.143
Refinement		
Initial model used (PDB code)	ab initio	5T3Z
Model resolution (Å)	2.5	3.9
FSC threshold	0.143	0.143
Map sharpening <i>B</i> factor (Å ²)	-71.0	-272.3
Model composition		
Non-hydrogen atoms (no.)	26,592	25,724
Protein residues (no.)	3,090	3,129
Ligands	BMA: 27 NAG: 105 MAN: 45	BMA: 8 NAG: 57 MAN: 23
<i>B</i> factors		
Protein (Å ²)	42.53	42.31
Ligand (Å ²)	62.19	48.20
R.m.s. deviations		
Bond lengths (Å)	0.010	0.004
Bond angles (°)	1.071	0.809
Validation		
MolProbity score	1.39	1.62
Clashscore	3.07	4.88
Poor rotamers (%)	0.41	0.52
Ramachandran plot		
Favored (%)	95.83	94.71
Allowed (%)	4.11	5.22
Disallowed (%)	0.07	0.07