

**Table S1. Cryo-EM data collection and refinement statistics.**

<b>Data collection</b>						
Magnification	81,000					
Voltage (kV)	300					
Electron Microscope	Krios-GIF-K3					
Defocus (um)	-1.0 to -2.0					
Total exposure time (s)	2.6					
Energy filter width (eV)	20					
Pixel size (Å)	1.08 (0.54)					
Total dose (e <sup>-</sup> / Å <sup>2</sup> )	40					
Number of frames	40					
Does rate (e <sup>-</sup> / Å <sup>2</sup> /phys. Pixel)	18.02					
Number of micrographs	5,669					
Initial particle images (no.)	2,188,223					
Final particle images (no.)	982,491					
<b>Refinement</b>	<b>AdeB-I</b>	<b>AdeB-II</b>	<b>AdeB-III</b>	<b>AdeB-Et-I</b>	<b>AdeB-Et-II</b>	<b>AdeB-Et-III</b>
Total Particles (no.)	16,223	95,552	25,060	93,835	10,137	9,781
GS-FSC Resolution (0.143, Å)	3.64	3.21	3.42	2.97	3.79	3.34
FSC-model Resolution after Density Modification (0.5, Å)	3.59	3.13	3.27	2.96	3.55	3.21
Symmetry	C3	C1	C3	C1	C1	C1
<u>Model composition</u>						
Protein residues	3,060	3,060	3,060	3,060	3,060	3,060
Ligands	6	3	0	9	5	6
<u>RMSD</u>						
Bond lengths (Å)	0.006	0.005	0.006	0.006	0.005	0.005
Bond angles (°)	1.222	1.058	1.110	1.115	1.079	1.065
<b>Validation</b>	<b>AdeB-I</b>	<b>AdeB-II</b>	<b>AdeB-III</b>	<b>AdeB-Et-I</b>	<b>AdeB-Et-II</b>	<b>AdeB-Et-III</b>
MolProbity score	1.70	1.37	1.59	1.25	1.49	1.40
Clash score	9.40	6.66	9.04	4.37	9.15	7.35
<u>Ramachandran plot</u>						
Favored (%)	97.87	98.56	97.44	99.05	98.26	98.06
Allowed (%)	2.13	1.44	2.56	0.95	1.74	1.94
Disallowed (%)	0.00	0.00	0.06	0.00	0.00	0.00
CC Mask	0.71	0.79	0.74	0.82	0.72	0.78