

Supplementary Table 2 | Cryo-EM data collection, refinement and validation statistics.

	Map 1 (EMD-10465) (PDB 6TDA)	Map 2 (EMD-10465)	Map 3 (EMD-10465)	Map 4 (EMD-10465)
Data collection and processing				
Magnification	130,000	130,000	130,000	130,000
Voltage (kV)	300	300	300	300
Electron exposure (e-/Å ²)	47.8 / 45.4*	47.8 / 45.4*	47.8 / 45.4*	39.0 [†] / 45.2 [†] / 54.9 [‡]
Defocus range (μm)	0.4 – 2.9	0.4 – 2.9	0.4 – 2.9	0.8 – 4.8
Pixel size (Å)	1.05	1.05	1.05	1.05
Symmetry imposed	C1	C1	C1	C1
Initial particle images (no.)	1,232,532	1,232,532	1,232,532	1,009,020
Final particle images (no.)	372,442	106,474	35,972	176,594
Map resolution (Å)	~15 [#]	3.6	4.3	3.8
FSC threshold		0.143	0.143	0.143
Map resolution range (Å)		3.4 – 5.3	3.7 – 7.8	3.7 – 4.5
Refinement				
Initial model used (PDB code)	5Z3U, 3LJW, 1UHR, 2FQ3, 2YUS, 1TOT, 4V3Q, 6AX5			
Model resolution (Å)				
FSC threshold				
Map sharpening <i>B</i> factor (Å ²)				
Model composition				
Non-hydrogen atoms	42,578			
Protein / Nucleotide residues	4817 / 320			
Ligands	1x Zn			
<i>B</i> factors (Å ²)				
Protein				
Ligand				
Nucleotide				
R.m.s. deviations				
Bond lengths (Å)	0.005			
Bond angles (°)	0.947			
Validation				
MolProbity score	1.82			
Clashscore	7.27			
Poor rotamers (%)	1.37			
Ramachandran plot				
Favored (%)	95.50			
Allowed (%)	4.27			
Disallowed (%)	0.23			

	Map 5 (EMD-10465)	Map 6 (EMD-10465)	Map 7 (EMD-10465) (PDB 6TDA) [§]	Map 8 (EMD-10465) (PDB 6TDA) [§]
Data collection and processing				
Magnification	130,000	130,000	130,000	130,000
Voltage (kV)	300	300	300	300
Electron exposure (e ⁻ /Å ²)	39.0 [†] / 45.2 [†] / 54.9 [‡]	39.0 [†] / 45.2 [†] / 54.9 [‡]	47.8 / 45.4*	39.0 [†] / 45.2 [†] / 54.9 [‡]
Defocus range (μm)	0.8 – 4.8	0.8 – 4.8	0.4 – 2.9	0.8 – 4.8
Pixel size (Å)	1.05	1.05	1.05	1.05
Symmetry imposed	C1	C1	C1	C1
Initial particle images (no.)	1,009,020	1,009,020	1,232,532	1,009,020
Final particle images (no.)	176,594	176,594	106,474 / 35,972	176,594
Map resolution (Å)	3.6	3.6	3.9	3.6
FSC threshold	0.143	0.143	0.143	0.143
Map resolution range (Å)	3.5 – 5.4	3.5 – 5.7	3.5 – 7.5	3.5 – 5.5
Refinement				
Initial model used (PDB code)			5Z3U	3LJW, 1UHR, 2FQ3, 2YUS, 1TOT, 4V3Q, 6AX5
Model resolution (Å)			3.6	3.7
FSC threshold			0.5	0.5
Map sharpening <i>B</i> factor (Å ²)			-152.1	-105.7
Model composition				
Non-hydrogen atoms			13,648	20,260
Protein / Nucleotide residues			1,274 / 246	2646 / -
Ligands			0	1x Zn
<i>B</i> factors (Å ²)				
Protein			106.52	68.91
Ligand				61.21
Nucleotide			119.35	
R.m.s. deviations				
Bond lengths (Å)			0.004	0.005
Bond angles (°)			0.749	0.995
Validation				
MolProbity score			1.17	1.77
Clashscore			3.79	7.26
Poor rotamers (%)			0.00	0.05
Ramachandran plot				
Favored (%)			98.07	94.57
Allowed (%)			1.93	5.39
Disallowed (%)			0.00	0.05