

**Table S6. Statistics for cryo-EM analysis and model refinement.**

	Case
PDB ID	7YOJ
EMDB ID	EMD-33983
<b>Data collection and processing</b>	
Microscope	Titan Krios
Detector	Gatan K3 with GIF Quantum (20eV slit)
CS (mm)	0.01
Magnification	81K
Pixel size (Å)	0.856
Electron dose (e <sup>-</sup> / Å <sup>2</sup> )	50(32 frames)
Defocus range (µm)	-1.5 ~ -2.0
Micrographs collected	6,690
Micrographs used	6,690
<b>Reconstruction</b>	
Software	RELION-3.1, cryoSPARC-3.3.1
Particles picked	2,544,599
Particles refinement	39,500
Symmetry	C1
Resolution (Å)	3.4
Sharpening B-factor (Å <sup>2</sup> )	111.3
<b>Refinement</b>	
Software	PHENIX-1.20.1
Model composition	
Number of atoms	11,545
Protein residues	867
Nucleotides	216
Ligand	0/0
B factors (Protein/Nucleotide/Ligand)	113.04/191.67/0
Bonds RMSD	
Bonds lengths (Å)	0.004
Bonds angles (°)	0.681
<b>Validation</b>	
MolProbity score	2.02
Clash score	8
Rotamer outliers (%)	0.27
C-beta outliers (%)	0.00
Ramachandran plot	
Favored (%)	94%
Allowed (%)	6%
Outlier (%)	0
Model vs. Data	
CC mask/box	0.82/0.78