Table S1 Cryo-EM data collection, refinement and validation statistics (Related to Fig. 3,4,5)

	(EMDB-0510) (PDB 6NTS)
Data collection and processing	
Magnification	130,000
Voltage (keV)	300
Electron exposure ($e^-/Å^2$)	40
Defocus range (um)	-1 ~ -3
Pixel Size (Å)	1.064
Symmetry imposed	C1
Initial particle images (no.)	869,372
Final particle images (no.)	83,784
Map resolution (Å)	3.6
FSC threshold	0.143
Map resolution range (Å)	3-5.5
Refinement	
Model resolution (Å)	3.8
FSC threshold	0.5
Model resolution range (Å)	
Map sharpening B factor ($Å^2$)	-86.2
Model composition	
Non-hydrogen atoms	10,040
Protein residues	1,250
Ligands	1
B factors ($Å^2$)	
Protein	80.68
Ligand	78.37
R.m.s deviations	
Bond length (Å)	0.01
Bond angles (Å)	0.98
Validation	
MolProbity score	1.62
Clashscore	3.86
Poor rotamers (%)	0.44
Ramachandran plot	
Favored (%)	93.12
Allowed (%)	6.88
Disallowed (%)	0.00