

Cryo-EM data collection, refinement and validation statistics

	#1 name (EMDB-xxxx) (PDB xxxx)	#2 name (EMDB-xxxx) (PDB xxxx)
Data collection and processing		
Magnification		
Voltage (kV)		
Electron exposure (e-/Å ²)		
Defocus range (µm)		
Pixel size (Å)		
Symmetry imposed		
Initial particle images (no.)		
Final particle images (no.)		
Map resolution (Å)		
FSC threshold		
Map resolution range (Å)		
Refinement		
Initial model used (PDB code)		
Model resolution (Å)		
FSC threshold		
Model resolution range (Å)		
Map sharpening <i>B</i> factor (Å ²)		
Model composition		
Non-hydrogen atoms		
Protein residues		
Ligands		
<i>B</i> factors (Å ²)		
Protein		
Ligand		
R.m.s. deviations		
Bond lengths (Å)		
Bond angles (°)		
Validation		
MolProbity score		
Clashscore		
Poor rotamers (%)		
Ramachandran plot		
Favored (%)		
Allowed (%)		
Disallowed (%)		