**Cryo-EM data collection, refinement and validation statistics**

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| --- | --- | --- |
|  | #1 name  (EMDB-xxxx)  (PDB xxxx) | #2 name  (EMDB-xxxx)  (PDB xxxx) |
| **Data collection and processing** |  |  |
| Magnification |  |  |
| Voltage (kV) |  |  |
| Electron exposure (e–/Å2) |  |  |
| 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 *B* factor (Å2) |  |  |
| Model composition  Non-hydrogen atoms  Protein residues  Ligands |  |  |
| *B* factors (Å2)  Protein  Ligand |  |  |
| R.m.s. deviations  Bond lengths (Å)  Bond angles (°) |  |  |
| Validation  MolProbity score  Clashscore  Poor rotamers (%) |  |  |
| Ramachandran plot  Favored (%)  Allowed (%)  Disallowed (%) |  |  |