**Supplementary Table 1. Cryo-EM data collection, refinement and validation statistics**

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| --- | --- | --- |
|  | TOROID(helical reconstruction) | TOROID(signal subtraction and SPA) |
|  | EMDB 13595 | EMDB 13594PDB 7PQH |
| **Data collection and processing** |  |  |
| Magnification  | 37.000 | 37.000 |
| Voltage (kV) | 300 | 300 |
| Electron exposure (e–/Å2) | 20 | 20 |
| Defocus range (μm) | 1.0 – 2.5 | 1.0 – 2.5 |
| Pixel size (Å) | 1.35 | 1.35 |
| Symmetry imposed | D1 | D1 |
| Initial particle images (no.) | 219,455 | 219,455 |
| Final particle images (no.) | 219.455 | 213,808 |
| Map resolution (Å) FSC threshold | 9.100.143 | 3.850.143 |
|  |  |  |
| **Refinement** |  |  |
| Model resolution (Å) (masked) FSC threshold | N.A. | 4.20.5 |
| Map sharpening *B* factor (Å2) | -979.5  | -123.7  |
| Model composition Non-hydrogen atoms Protein residues Water Ligands |  | 102,67512.83200 |
| *B* factors (Å-2) Protein Ligand |  | 127.1- |
| R.m.s. deviations Bond lengths (Å) Bond angles (°) |  | 0.0051.197 |
| Validation MolProbity score Clashscore Poor rotamers (%)  |  | 1.888.470.12 |
| Ramachandran plot Favored (%) Allowed (%) Outliers (%)Ramachandran-Z scoreWholeHelixSheetLoop |  | 93.816.160.03-1.40-0.19-0.53-2.01 |