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

|  |  |  |
| --- | --- | --- |
|  | TOROID  (helical reconstruction) | TOROID  (signal subtraction and SPA) |
|  | EMDB 13595 | EMDB 13594  PDB 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 | 9.10  0.143 | 3.85  0.143 |
|  |  |  |
| **Refinement** |  |  |
| Model resolution (Å) (masked)  FSC threshold | N.A. | 4.2  0.5 |
| Map sharpening *B* factor (Å2) | -979.5 | -123.7 |
| Model composition  Non-hydrogen atoms  Protein residues  Water  Ligands |  | 102,675  12.832  0  0 |
| *B* factors (Å-2)  Protein  Ligand |  | 127.1  - |
| R.m.s. deviations  Bond lengths (Å)  Bond angles (°) |  | 0.005  1.197 |
| Validation  MolProbity score  Clashscore  Poor rotamers (%) |  | 1.88  8.47  0.12 |
| Ramachandran plot  Favored (%)  Allowed (%)  Outliers (%)  Ramachandran-Z score  Whole  Helix  Sheet  Loop |  | 93.81  6.16  0.03  -1.40  -0.19  -0.53  -2.01 |