**Table 1. Cryo-EM and model statistics**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | THO-Sub2highRes(EMDB-11859)(PDB 7APX) | THO-Sub2 dimer(EMDB-11871)(PDB 7AQO) | THO-Sub2 bottom protomer(EMDB-11871) | THO-Sub2 top protomer(EMDB-11871) |
| **Data collection and processing** |  |  |  |  |
| Magnification  | 64,000 x |
| Voltage (kV) | 300 |
| Electron exposure (e–/Å2) | 55.0 |
| Defocus range (μm) | 0.5-3.0 |
| Pixel size (Å) | 1.38 |
| Symmetry imposed | C1 |
| Initial particle images (no.) | 922,935 |
| Final particle images (no.) | 298,657 | 113,076 |
| Map resolution (Å) FSC threshold | 3.400.143 | 3.930.143 | 3.690.143 | 4.010.143 |
| Map sharpening *B* factor (Å2) | -108.6 | -81.8 | -71.7 | -73.6 |
|  |  |  |  |  |
| **Refinement** |  |  |  |
| Initial model used (PDB code) | *de novo,* 5SUP | THO-Sub2highres |  |
| Model resolution (Å) FSC threshold | 3.50.143  |  4.5 0.143 |  |
| Model composition Non-hydrogen atoms Protein residues Ligands | 20574 2889 0 | 411735783 |  |
| *B* factors (Å2) Protein  Ligand | 135.92 | 600 |  |
| R.m.s. deviations Bond lengths (Å) Bond angles (°) |   0.006  0.739 |  0.010 1.026 |  |
|  Validation MolProbity score  Clashscore Poor rotamers (%) |  2.6 8.0 2.5 | 3.1253 |  |
|  Ramachandran plot Favored (%)  Allowed (%) Disallowed (%) | 93.56.350.18 | 92.63 6.850.32 |  |