**Supplementary Table 1.** Data acquisition and processing parameters. Related to Figures 2-4

|  |  |
| --- | --- |
| Microscope | Titan Krios |
| Detector  | Gatan K3 |
| V oltage | 300 kV |
| Electron Source  | Field Emission Gun  |
| Collecting Mode  | Counting  |
| Dose Rate (e-/Å2)  | 60.07  |
| Defocus range (μm) | -1.1 to -2.5 |
| Nominal Magnification | 105000x |
| Frames collected per exposure  | 75 |
| Frame alignment Software | MotionCor2 |
| CTF parameter estimationSoftware | Gctf |
| Total number of raw imagescollected | 4177 |
| Number of images used forparticle picking | 4168 |
| Initial particles picked | 1,301,452 |
| 2D classification software | Cryo-SPARC |
| Final reconstruction software | Relion 4.0 |
| Applied symmetry | C1 |
| Number of particles contributedfor the final reconstruction | 226320 |
| Resolution method | FSC 0.143 cut-off  |
| Map resolution (Å)  | 2.82  |
| Local resolution determining Software | Relion 4.0 |
| Map Visualization software  | Pymol/Chimera/ Chimera X/ Coot  |
| Deposit EMDB code  | 27138 |
| **Refinement parameters**  |  |
| CC (map\_model) (mask)  | 0.83 |
| RMSD (Bond lengths/Bond angles) | 0.006 Å /0.739° |
| Ramachandran plot (%) (Outlier/Allowed/Favored)  | (0.0/5.2/94.8) |
| Cβ Outliers (%)  | 0.0 |
| MolProbity Score  | 2.26 |
| Clash score | 25.8 |
| Rotamer outliers (%) | 0.0 |
| ADP (B-fator)Protein (min/mask/mean) Nucleotides (min/mask/mean) Zn (min/mask/mean) | Protein 0.00/74.8/31.5Nucleotides 0.00/131.1/40.9Zn 69.9/93.5/80.5 |
| dFSC model (0/0.143/0.5)  | 2.5/2.6/2.8 |
| Deposit PDB code  | 8D1V |