**Supplementary file 1. Cryo-EM data collection and refinement statistics.**

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| **Data Collection** |   |
| Electron Microscope | Titan Krios G3 |
| Camera | Falcon 3EC |
| Voltage (kV) | 300 |
| Nominal Magnification | 75,000 |
| Calibrated physical pixel size (Å) | 1.06 |
| Total exposure (e/Å2) | 42.7 |
| Exposure rate (e/pixel/s) | 0.8 |
| Number of frames | 30 |
| Defocus range (µm) | 1.8 to 2.2 |
|   |  |
| **Image Processing** |   |
| Motion correction software | cryoSPARC v2, MontionCor2 |
| CTF estimation software | CTFFIND4,GCTF |
| Particle selection software | cryoSPARC v2, RELION |
| Micrographs used | 3600 |
| 3D map classification and refinement software | cryoSPARC v2, RELION |
|  |  |
| **Model building** |   |
| Modeling software | COOT, ROSETTA, PHENIX, ISOLDE |
| Particle images contributing to maps  | 71,350 |
| Applied symmetry  | C3 |
| Global resolution (FSC = 0.143, Å)  | 3.1 |
| RMS bond length (Å)  | 0.012 |
| RMS bond angle (°) | 1.77 |
| Ramachandaran outliers (%) | 0.0 |
| Ramachandran favoured (%) | 95.72 |
| Clashscore | 0.24 |
| MolProbity score | 0.89 |
| EMRinger score | 3.81 |
| Protein residue number | 2895 |
| Ligands  |  |
| BMA | 6 |
| NAG | 63 |
| MAN | 12 |