**Figure 2-figure supplement 2-Source Data 1 : Data collection and processing statistics of the cryo-EM structure**

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| **Data collection** | |
| Microscope | FEI Titan Krios |
| Voltage (kV) | 300 |
| Camera | Gatan K2 Summit |
| Camera mode | Super-resolution |
| Energy Filter | Gatan postcolumn quantum energy filter (20 eV slit) |
| Nominal Magnification | 58’180 |
| Pixel Size (Å) | 0.4297 (in super-resolution)  0.8594 (for reconstruction) |
| Defocus range (μm) | -0.5 to -1.5 |
| Total electron dose (e/Å2) | 67 |
| Number of movies | ~2000 |
| **Data processing** | |
| Software | RELION 2.1 and RELION 3.0 |
| Initial number of particles | 1’331’906 |
| Final number of particles | 55’245 |
| Symmetry | C1 |
| Map resolution (Å)  FSC threshold | 3.38  0.143 |
| Map resolution range (Å) | 3.4 to 3.8 |
| Resolution of sharpened map (Å) | 3.38 |
| Resolution of unsharpened map (Å) | 3.44 |
| Map sharpening B-factor (Å2) | -111 |
| **Refinement** | |
| Refinement package | Phenix (Real-space refinement at 3.40Å) |
| Initial model used (PDB code) | 5YJ6 |
| Map-model CC | |
| CC\_mask | 0.73 |
| CC\_volume | 0.68 |
| CC\_peaks | 0.56 |
| CC\_box | 0.62 |
| Model composition | |
| Non-hydrogen atoms | 5180 |
| Protein residues | 636 |
| Ligands | 0 |
| *B* factors (Å2) (mean) | |
| Protein | 14.14 |
| R.M.S. deviations |  |
| Bond lengths (Å) | 0.004 (0) |
| Bond angles (°) | 0.616 (0) |
| Validation | |
| MolProbity score | 1.45 |
| Clashscore | 3.51 |
| Rotamer outliers (%) | 0.56 |
| Ramachandran plot | |
| Favored (%) | 95.58 |
| Allowed (%) | 4.26 |
| Outliers (%) | 0.16 |
| Cb boutliers (%) | 0 |
| CaBLAM outliers (%) | 2.06 |