Supplementary File 2: Cryo-EM data collection, refinement and validation statistics

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|  | **Dodecamer Gln complex**(EMDB- 19730)(PDB 8S59) |
| **Data collection and processing** |  |
| Magnification  | 165,000 x |
| Voltage (kV) | 300 |
| Electron exposure (e–/Å2) | 55.0 |
| Defocus range (μm) | 0.25-2.0 |
| Pixel size (Å) | 0.72 |
| Symmetry imposed | D6 |
| Initial particle images (no.) | 1,243,001 |
| Final particle images (no.) | 878,308 |
| Map resolution (Å) FSC threshold | 2.390.143 |
| Map resolution range (Å) | 2.3-3.0 |
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| **Refinement** |  |
| Initial model used (PDB code) | *de novo,* AlphaFold |
| Model resolution (Å) FSC threshold | 2.50.5 |
| Model resolution range (Å) | 2.2-2.5 |
| Map sharpening *B* factor (Å2) | -80.1 |
| Model composition  Non-hydrogen atoms  Protein residues Ligands  | 469685352AKG: 12 |
| *B* factors (Å2) Protein  Ligand | 16.5815.64 |
| R.m.s. deviations Bond lengths (Å)  Bond angles (°) | 0.0030.602 |
|  Validation MolProbity score Clashscore Poor rotamers (%)  | 1.295.320.46 |
|  Ramachandran plot Favored (%) Allowed (%) Disallowed (%) | 98.221.560.23 |