**Supplementary File 2**

**Cryo-EM data collection, refinement, and validation statistics.**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | CsGSIbDec (PDB 7V4I)  | CsGS1bPen (I) (PDB 7V4J) | CsGSIbPen (II)(PDB 7V4K) | CsGSIbPen (III) (PDB 7V4L) |  GmGSβ2 (PDB 7V4H) |
| Data collection |
| Magnification | 29000 x | 29000 x | 29000 x | 29000 x | 29000 x |
| Voltage (kV) | 300 | 300 | 300 | 300 | 300 |
| Electron exposure (e−/Å2 ) | 51 | 51 | 51 | 51 | 51 |
| Defocus range (μm) | -1.6 ~ -2.3 | -1.6 ~ -2.3 | -1.6 ~ -2.3 | -1.6 ~ -2.3 | -1.6 ~ -2.3 |
| Pixel size (Å) | 0.505 | 0.505 | 0.505 | 0.505 | 0.505 |
|  |
| Reconstruction and Model composition |
| Symmetry imposed | D5 | C5 | C5 | C5 | D5 |
| Chains | 10 | 5 | 5 | 5 | 10 |
| Nonhydrogen atoms | 27680 | 9850 | 9260 | 8966 | 27340 |
| Protein residues | 3560 | 1275 | 1195 | 1140 | 3520 |
|  |
| Refinement |
| R.m.s. deviations |
|   Bond lengths (Å) | 0.003 | 0.003 | 0.004 | 0.004 | 0.004 |
|   Bond angles (°) | 0.585 | 0.670 | 0.660 | 0.696 | 0.589 |
| Model-to-map fit (CC) | 0.74 | 0.52 | 0.64 | 0.57 | 0.82 |
| Map resolution (Å) | 3.3 | 3.5 | 3.6 | 3.4 | 2.9 |
| FSC threshold | 0.143 | 0.143 | 0.143 | 0.143 | 0.143 |
|  |
| Validation |
| MolProbity score | 1.91 | 2.28 | 1.98 | 2.24 | 1.63 |
| Clashscore | 10.27 | 19.49 | 17.27 | 17.81 | 7.07 |
| Rotamers outliers (%) | 0.00 | 0.00 | 0.20 | 0.00 | 0.00 |
| Ramachandran plot |
|   Favored (%) | 94.46 | 91.84 | 96.33 | 91.87 | 96.37 |
|  Allowed (%) | 5.54 | 8.16 | 3.67 | 8.13 | 3.63 |
|   Outliers (%) | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |