**Supplemental File 1.** Cryo-EM data collection, refinement, and validation statistic.

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|  | GmCesA1(EMDB-43244)(PDB: 8VHZ) | GmCesA3(EMDB-43241)(PDB: 8VHT) | GmCesA6(EMDB-43245)(PDB 8VI0) |
| **Data collection and processing** |  |  |  |
| Microscope | Titan Krios | Titan Krios | Titan Krios |
| Camera | GIF K3 | GIF K3 | GIF K3 |
| Magnification  | 81,000 | 81,000 | 81,000 |
| Voltage (kV) | 300 | 300 | 300 |
| Electron exposure (e–/Å2) | 50 | 50 | 50 |
| Defocus range (μm) | -1.1 to -2.2 | -1.1 to -2.2 | -1.1 to -2.2 |
| Pixel size (Å) | 1.08 | 1.08 | 1.08 |
| Symmetry imposed | C3 | C3 | C3 |
| Initial particle images (no.) |  |  |  |
| Final particle images (no.) | 181,101 | 237,568 | 192,666 |
| Map resolution (Å) FSC threshold | 3.30.143 | 3.20.143 | 3.00.143 |
| Map resolution range (Å) | 3.3 -  | 3.2 - | 3.0 - |
|  |  |  | ­­ |
| **Refinement** |  |  |  |
| Initial model used | AlphaFold generated | AlphaFold generated | AlphaFold generated |
| Map sharpening *B* factor (Å2) | -117.5 | -105.1 | -92.4 |
| Model composition Non-hydrogen atoms Protein residues Ligand | 171902139 | 166442064BGC | 176942172BGC |
| Mean *B* factors (Å2) Protein Ligand | 39.47 | 56.4085.27 | 38.0372.40 |
| R.m.s. deviations Bond lengths (Å) Bond angles (°) | 0.0030.603 | 0.0020.53 | 0.0020.499 |
|  Ramachandran plot Favored (%) Allowed (%) Disallowed (%) | 96.883.120.00 | 97.052.950.00 | 97.72.30.00 |
|  Validation MolProbity score Clashscore Poor rotamers (%) | 1.526.320.16 | 1.424.910.00 | 1.586.870.00 |
| Overall correlation coefficients CC (mask) CC (peaks) CC (volume) | 0.760.620.74 | 0.820.790.66 | 0.850.740.83 |