

Supplementary information, Table. S1 | Cryo-EM data collection, refinement and validation statistics.

| GLP-2-GLP-2R-G _s complex | Value |
|---|-------------|
| Data collection and processing | |
| Magnification | 49310 |
| Voltage (kV) | 300 |
| Electron exposure (e ⁻ /Å ²) | 64 |
| Defocus range (μm) | -0.5 ~ -2.5 |
| Pixel size (Å) | 1.014 |
| Symmetry imposed | C1 |
| Initial particle projections (no.) | 1,498,893 |
| Final particle projections (no.) | 284,669 |
| Map resolution (Å) | 3.0 |
| FSC threshold | 0.143 |
| Map resolution range (Å) | 2.5-5.0 |
| Refinement | |
| Initial model used (PDB code) | 6NBF |
| Model resolution (Å) | 3.1 |
| FSC threshold | 0.5 |
| Model resolution range (Å) | 2.5-5.0 |
| Map sharpening <i>B</i> factor (Å ²) | -94.5881 |
| Model composition | |
| Non-hydrogen atoms | 8566 |
| Protein residues | 1070 |
| Water | 7 |
| <i>B</i> factors (Å ²) | |
| Protein | 58.72 |
| Water | 30.00 |
| R.M.S. deviations | |
| Bond lengths (Å) | 0.004 |
| Bond angles (°) | 0.648 |
| Validation | |
| MolProbity score | 1.77 |
| Clash score | 7.98 |
| Poor rotamers (%) | 0.76 |
| Ramachandran plot | |
| Favored (%) | 95.15 |
| Allowed (%) | 4.75 |
| Disallowed (%) | 0.10 |