

Supplemental Table 1. CryoEM data collection, refinement and model parameters

	<i>TT-OAD2:GLP1R: Gs</i> (EMDB-20179) (PDB 6ORV)
<hr/>	
Data collection and processing	
Magnification	105,000 (indicated); 60,530 (actual)
Voltage (kV)	300
Electron exposure (e ⁻ /Å ²)	65.6 and 63.5 (super resolution)
Defocus range (μm)	0.7 – 1.5
Pixel size (Å)	0.826
Symmetry imposed	C1
Initial particle images (no.)	1,470,000
Final particle images (no.)	85,978
Map resolution (Å)	3.0
FSC threshold	0.143
Map resolution range (Å)	200-1.65
Refinement	
Initial model used (PDB code)	6B3J
Model resolution (Å)	3.0
FSC threshold	0.143
Model resolution range (Å)	999-1.65
Map sharpening <i>B</i> factor (Å ²)	-70
Model composition	
Non-hydrogen atoms	8041
Protein residues	997
Ligands	1
<i>B</i> factors (Å ²)	
Protein	38
Ligand	76
R.m.s. deviations	
Bond lengths (Å)	0.008
Bond angles (°)	0.857
Validation	
MolProbity score	1.56
Clashscore	4.89
Poor rotamers (%)	0
Ramachandran plot	
Favored (%)	95.7
Allowed (%)	4.3
Disallowed (%)	0
