

Table S1. Cryo-EM data collection, model refinement, and validation statistics.

Data Collection and Processing	D1R-G_s- Rotigotine	D2R-G_i- Rotigotine	D3R-G_i- Rotigotine	D4R-G_i- Rotigotine	D5R-G_s- Rotigotine
EMDB accession number	EMD-35683	EMD-35684	EMD-35685	EMD-35686	EMD-35687
PDB accession number	8IRR	8IRS	8IRT	8IRU	8IRV
Magnification	46,296	46,296	46,685	49,310	49,310
Voltage (kV)	300	300	300	300	300
Electron exposure (e ⁻ /Å ²)	60	60	70	64	64
Defocus range (μm)	-1.2 to -2.2	-1.0 to -3.0	-1.2 to -2.2	-1.2 to -2.2	-1.2 to -2.2
Pixel size (Å)	1.08	1.045	1.071	1.08	1.071
Symmetry imposed	C1	C1	C1	C1	C1
Initial particle projections (no.)	2,685,434	7,064,860	8,770,602	4,333,829	7,900,346
Final particle projections (no.)	448,516	140,237	1,786,008	471,638	2,652,297
Map resolution (Å)	3.2	3.0	2.7	3.2	3.1
FSC threshold	0.143	0.143	0.143	0.143	0.143
Map resolution range (Å)	2.5-5.0	2.5-5.0	2.5-5.0	2.5-5.0	2.5-5.0
Refinement					
Initial model used	7JVQ	7JVR	7CMV	7CMV	7JVQ
Model resolution (Å)	3.2	3.2	2.7	3.3	3.3
FSC threshold	0.5	0.5	0.5	0.5	0.5
Model Composition					
Non-hydrogen atoms	8,249	8,764	8,768	9,007	7,465
Protein residues	1,032	1121	1,122	1,123	912
Ligands	1	1	1	1	1
Lipids	3	0	0	9	8
Waters	2	0	2	0	0
B factors (Å ²)					
Protein	71.64	69.16	32.81	74.96	45.37
Ligand	31.30	117.83	15.50	25.04	21.63
RMSD					
Bound lengths (Å)	0.012	0.012	0.012	0.012	0.013
Bound angles (°)	1.927	1.965	2.015	1.881	1.840
Validation					
MolProbity score	1.08	1.01	1.11	0.84	0.86
Clashscore	1.09	0.57	0.98	0.28	0.40
Rotamer outliers (%)	0	0	0	0	0
Ramachandran Plot					
Favored (%)	96.15	95.48	95.47	96.39	96.65
Allowed (%)	3.85	4.52	4.53	3.61	3.35
Disallowed (%)	0	0	0	0	0