Supplementary information, Table S2

Cryo-EM data collection, refinement and validation statistics

	Inactive GABA$_B$ receptor	**Active GABA$_B$ receptor**
Data collection and processing		
Magnification	4,9310	4,9310
Voltage (kV)	300	300
Electron exposure (e–/Å^2)	62	62
Defocus range (μm)	-0.5 ~ -2.5	-0.5 ~ -2.5
Pixel size (Å)	1.014	1.014
Symmetry imposed	C1	C1
Initial particle images (no.)	2,969,413	3,075,533
Final particle images (no.)	374,589	237,606
Map resolution (Å)		
(Overall/VFT/TM)	2.9/2.8/3.0	3.0/2.9/3.0
FSC threshold	0.143	0.143
Map resolution range (Å)	2.2-4.0	2.2-4.0
Refinement		
Initial model used (PDB code)	4MR7	inactive GABA$_B$ structure
Model resolution (Å)	2.9	3.3
FSC threshold	0.5	0.5
Model resolution range (Å)	2.5-4.0	2.5-4.0
Map sharpening *B* factor (Å^2)		
(Overall/VFT/TM)	83.6/84.1/67.6	78.5/80.9/190.3
Model composition		
Non-hydrogen atoms	10915	10894
Protein residues	1355	1348
Ligands	9	10
B factors (Å^2)		
Protein	61.64	66.88
Ligand	63.76	88.08
R.m.s. deviations		
Bond lengths (Å)	0.006	0.004
Bond angles (°)	0.741	0.684
Validation		
MolProbity score	1.69	1.65
Clashscore	8.01	7.15
Poor rotamers (%)	0.00	0.00
Ramachandran plot		
Favored (%)	96.27	96.18
Allowed (%)	3.73	3.82
Disallowed (%)	0.00	0.00