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

	ACTH-MC2R-G$_s$-MRAP1
Data collection	
Voltage (kV)	300
Magnification	81,000 x
Pixel size (Å)	1.04
Total electron dose (e^-/Å^2)	50
Defocus range (μm)	-0.5~-3.0
Micrographs collected	7,131
3D reconstruction	
Total extraced particles	4,347,219
Particles for final 3D reconstruction	59,170
Symmetry imposed	C1
Resolution range (Å)	2.86-10.45
Map resolution (Å) (FSC=0.143)	3.35
Refinement and validation	
Model resolution (Å) (FSC=0.5)	3.30
Model composition	
Non-hydrogen atoms	7,670
Protein residues	968
Map-model CC	0.77
B factors (Å^2)	30-137
R.M.S deviations	
Bonds lengths (Å)	0.004
Bonds angles (°)	0.756
MolProbity score	1.86
Clash score	10.37
Rotamer outliers (%)	0.96
Cβ outliers (%)	0.22
CaBLAM outliers (%)	2.98
Ramachandran plot statistics	
Preferred (%)	95.39
Allowed (%)	4.61
Outlier (%)	0.00
PDB accession number	**8GY7**
EMDB accession number	**EMD-34371**