Electronic Supplementary Material (ESI) for Molecular BioSystems.

Exploration of antagonist CP-376395 escape pathway for the corticotropin-releasing factor receptor 1 by random acceleration molecular dynamics simulations

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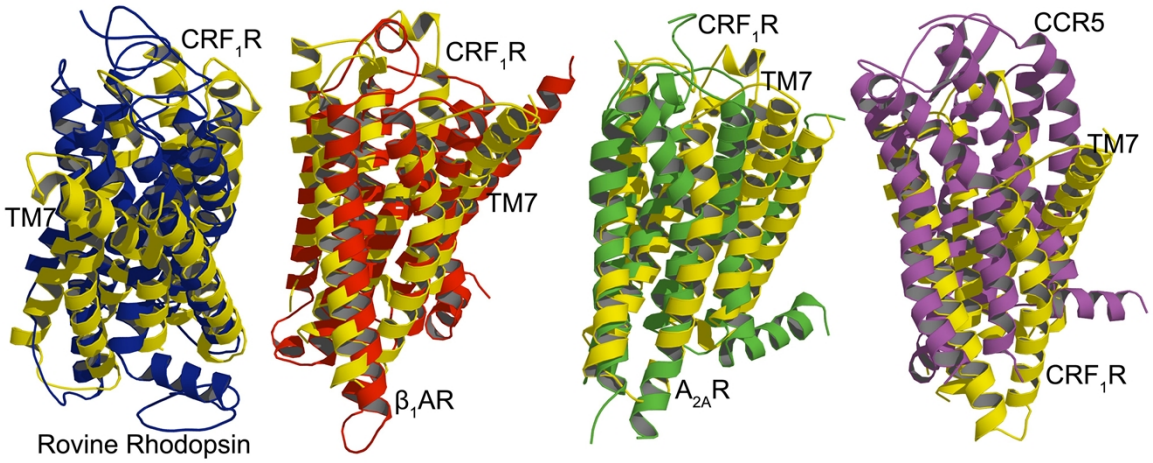

Figure S1: The structural alignment bween the bovine rhodopsin (PDB ID: 1U19), β1 adrenergic receptor (β_1AR, PDB ID: 3ZPQ), Adenosine A2a receptor (A_{2A}R, PDB ID: 3EML), C-C chemokine receptor type 5 (CCR5, PDB ID: 4MBS) and CRF_1R. The cartoon structure of CRF_1R is shown with yellow color in the four alignment structure, and others receptors correspond the remaining colors.

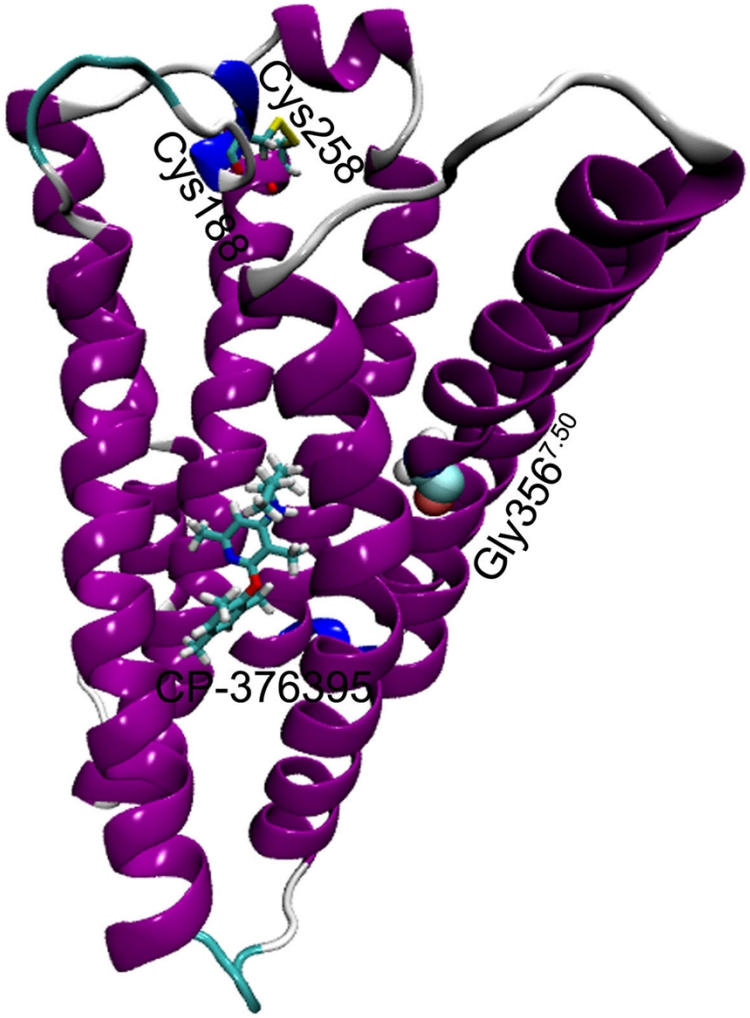

Figure S2: The antagonist CP-376395 and key residues of CRF_1R.

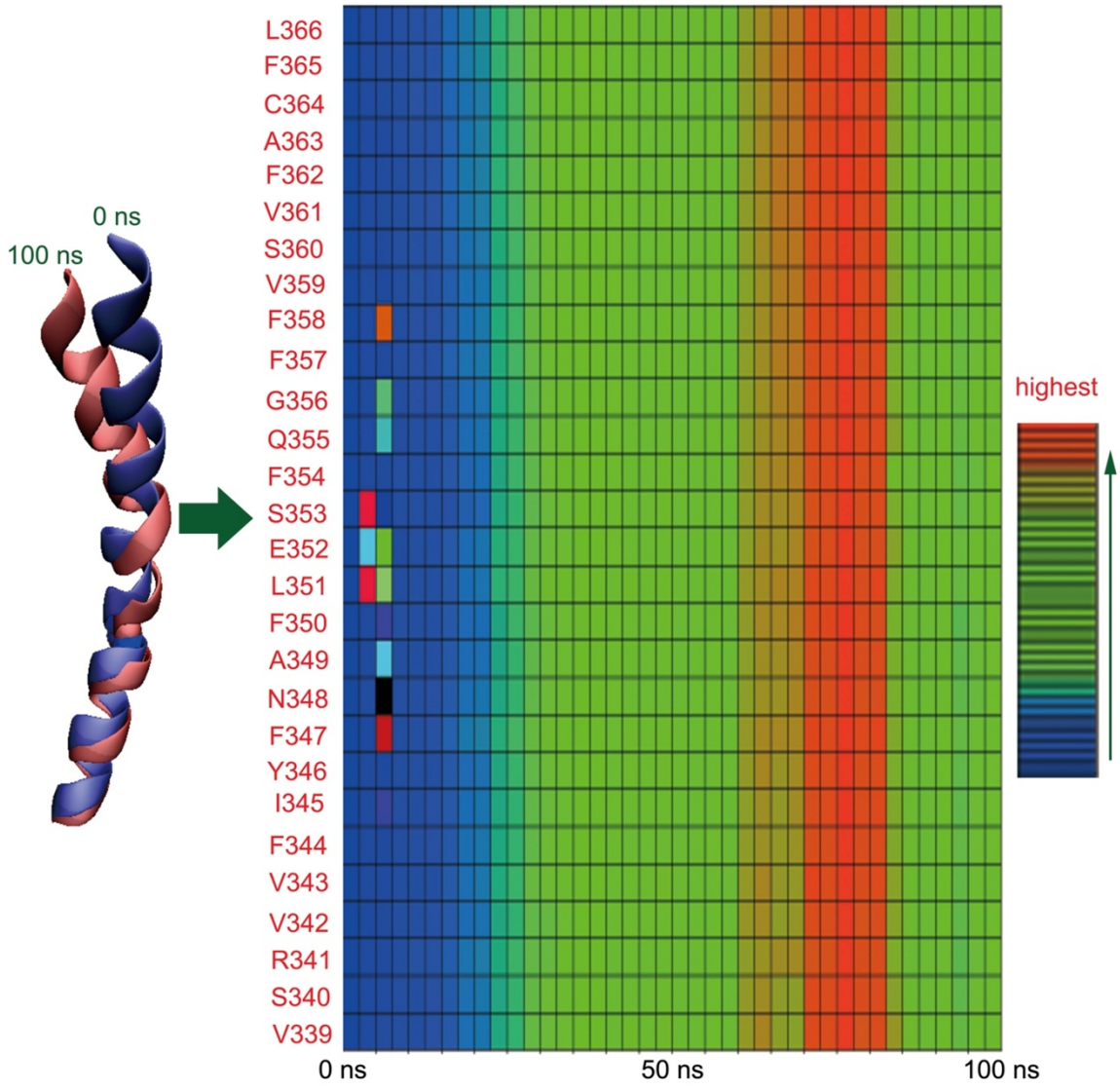

Figure S3: The RMSD of backbone atoms of the residues of TM7.

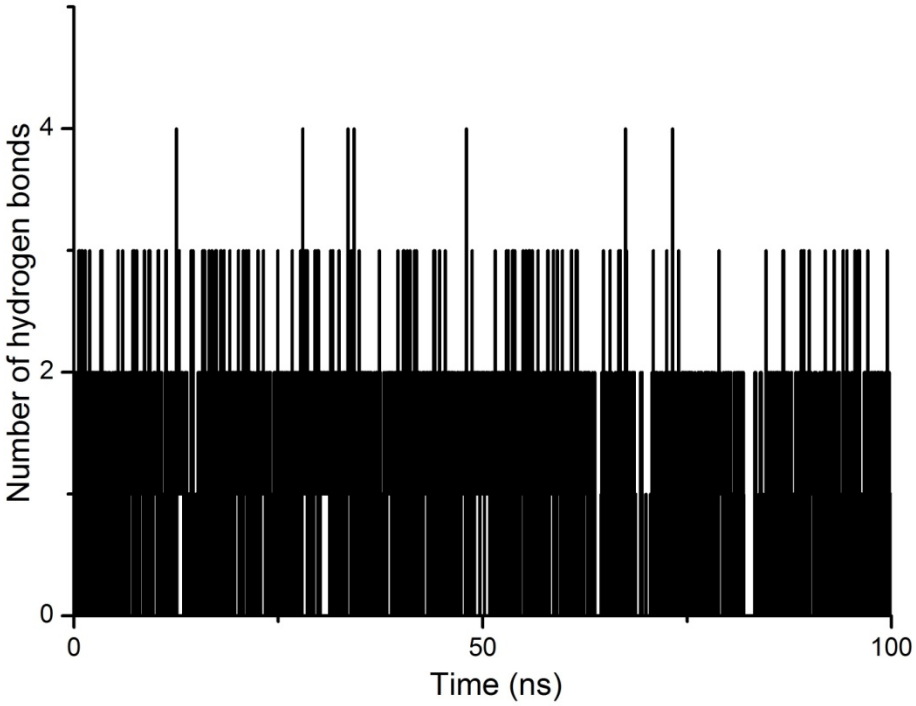

Figure S4: Total number of hydrogen bonds between the residues of CRF_1R and the antagonist CP-376395 during the 100 ns MD simulations.

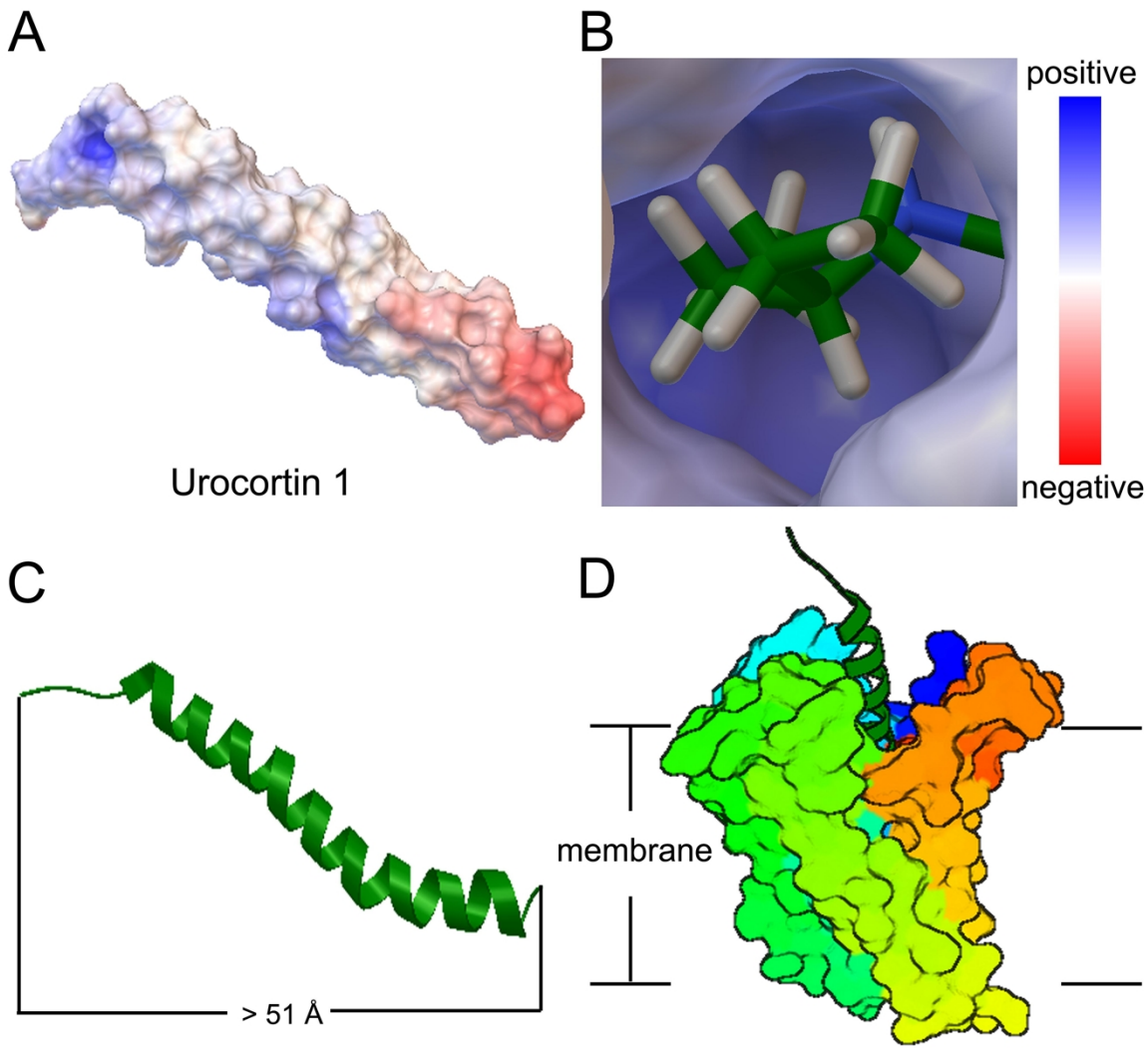

Figure S5: The agonist urocortin 1 of CRF_1R. (A) The electrostatic potential of urocortin 1. (B) The electrostatic potential of CRF_1R pocket. (C) The length of urocortin 1 (PDB ID: 2RMF). (D) Assumed model of CRF_1R in complex with urocortin 1.

Table S1. Occurrence number of three pathways in different constant forces

Pathway	20 (kcal/mol•Å)	50 (kcal/mol•Å)	100 (kcal/mol•Å)
PW1	1	2	8
PW2	0	1	6
PW3	19	17	6