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A computational prospective for isoform-selective CB2 inhibitors

Yi Zhao[a], Ying Wang[b], Huibin Wang[a], Baichun Hu[c,d], Zhaohu Luo[b], Fengjiao Zhang[b*]

a. School of Pharmacy, Shenyang Pharmaceutical University, Shenyang 110016, People's Republic of China

b. Wuya College of Innovation, Shenyang Pharmaceutical University, Shenyang 110016, People's Republic of China

c. Key Laboratory of Structure-Based Drug Design & Discovery of Ministry of Education, Shenyang Pharmaceutical University, Shenyang 110016, People's Republic of China

d. School of Pharmaceutical Engineering, Shenyang Pharmaceutical University, Shenyang 110016, People's Republic of China

Zhao Y. and Wang Y. contributed equally to this work.

Corresponding author: Fengjiao Zhang, E-mail: zhangfengjiao@syphu.edu.cn.

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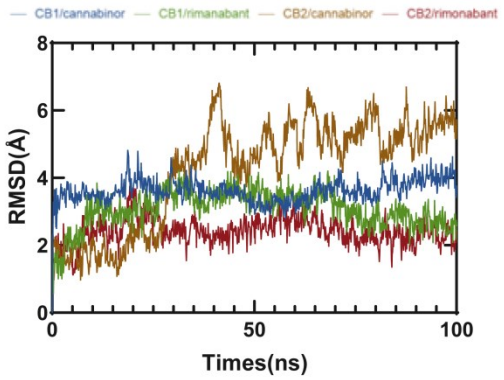

Figure S1. RMSD evaluation of ligands throughout the MD simulation referring to protein.

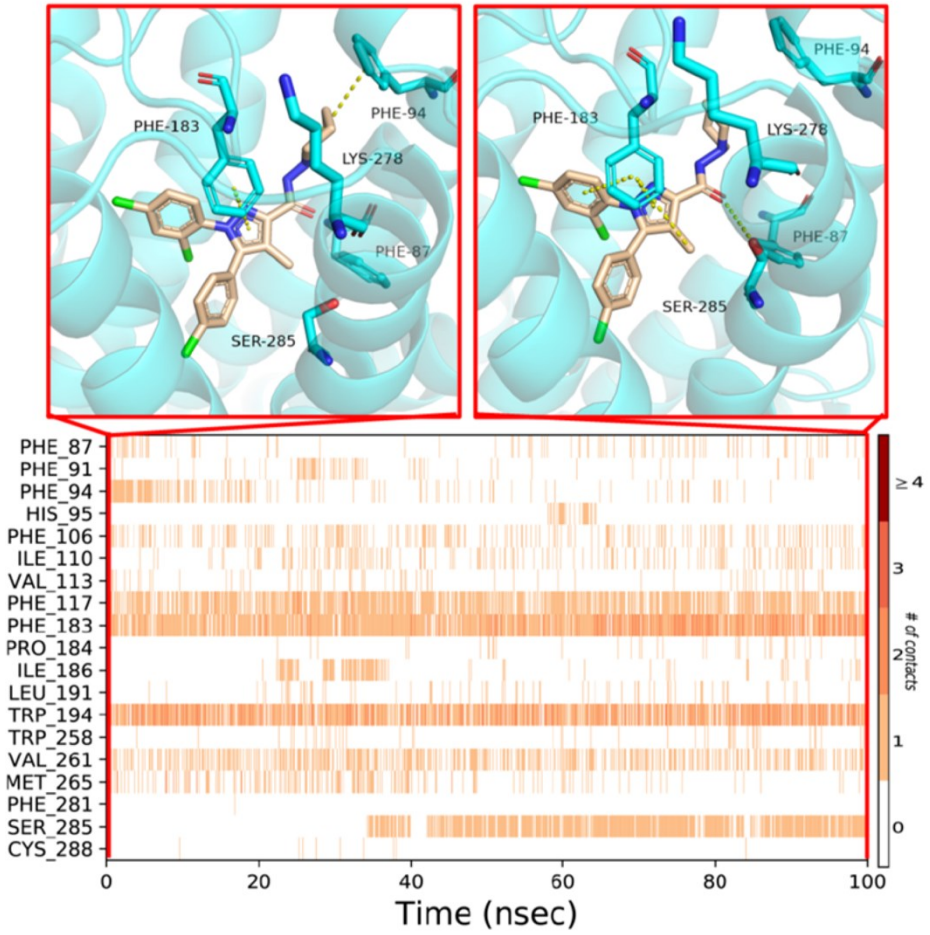

Figure S2 The protein-ligand interactions analysis of CB2/ rimonabant complex during MD simulation. The interactions were shown as a timeline representation, and the initial and final

conformation were displayed in the top panel.

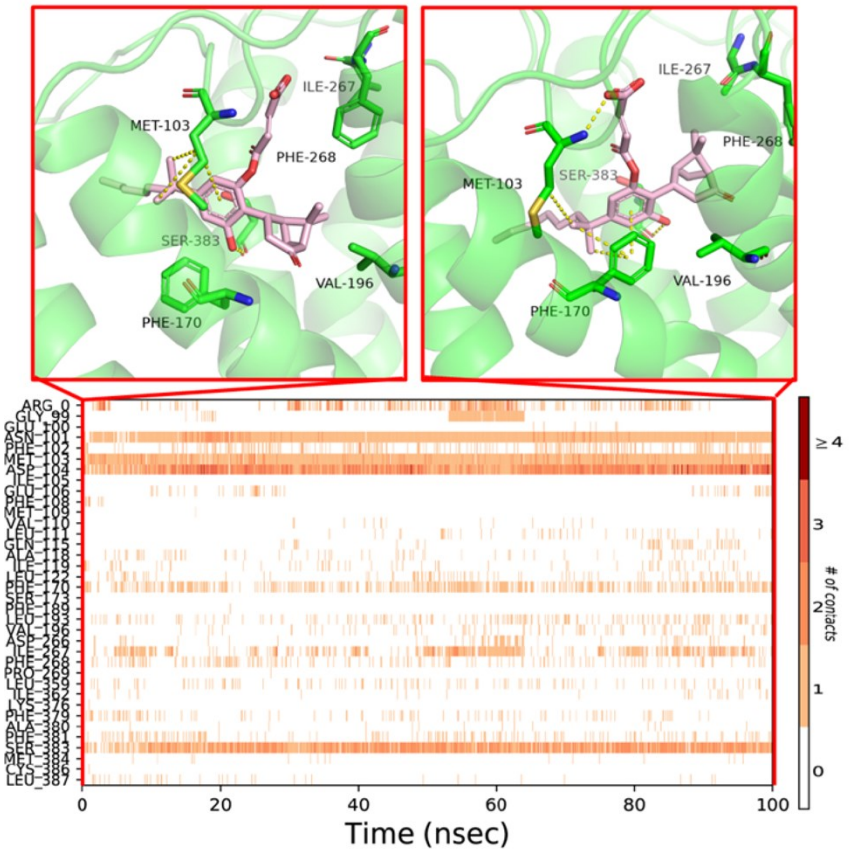

Figure S3 The protein-ligand interactions analysis of CB1/cannabinor complex during MD simulation. The interactions were shown as a timeline representation, and the initial and final conformation were displayed in the top panel.

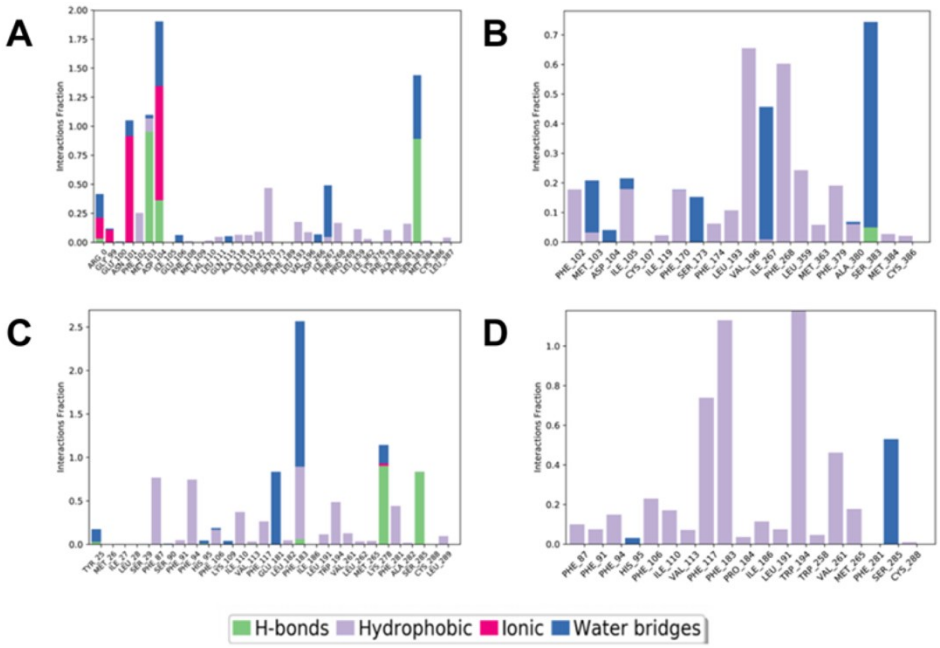

Figure S4. Sustainability of protein-ligand interaction during the MD simulation. Protein-ligand interactions of CB1/cannabinor (A), CB1/rimonabant (B), CB2/cannabinor (C) and CB2/rimonabant (D) by simulation.

Table S1. Alanine scanning mutagenesis analysis of CB1.

Residues	102	103	105	170	173	196	268	359	379	383
rimonabant	27.14	32.33	20.24	17.12	2.65	13.96	25.22	16.35	24.78	1.38
cannabinor	21.68	26.80	9.94	18.65	3.67	12.79	23.60	15.77	15.27	0.49

Table S2. Alanine scanning mutagenesis analysis of CB2.

Residues	87	94	110	117	183	194	278	281	285
rimonabant	21.57	24.01	25.73	13.71	23.66	31.70	10.72	20.01	2.47
cannabinor	23.75	19.91	24.53	16.25	28.80	31.75	9.63	23.66	5.81