Supporting information

Molecular interaction between distal C-terminal domain of the CB_1 cannabinoid receptor and Cannabinoid Receptor Interacting Proteins (CRIP1a/CRIP1b)

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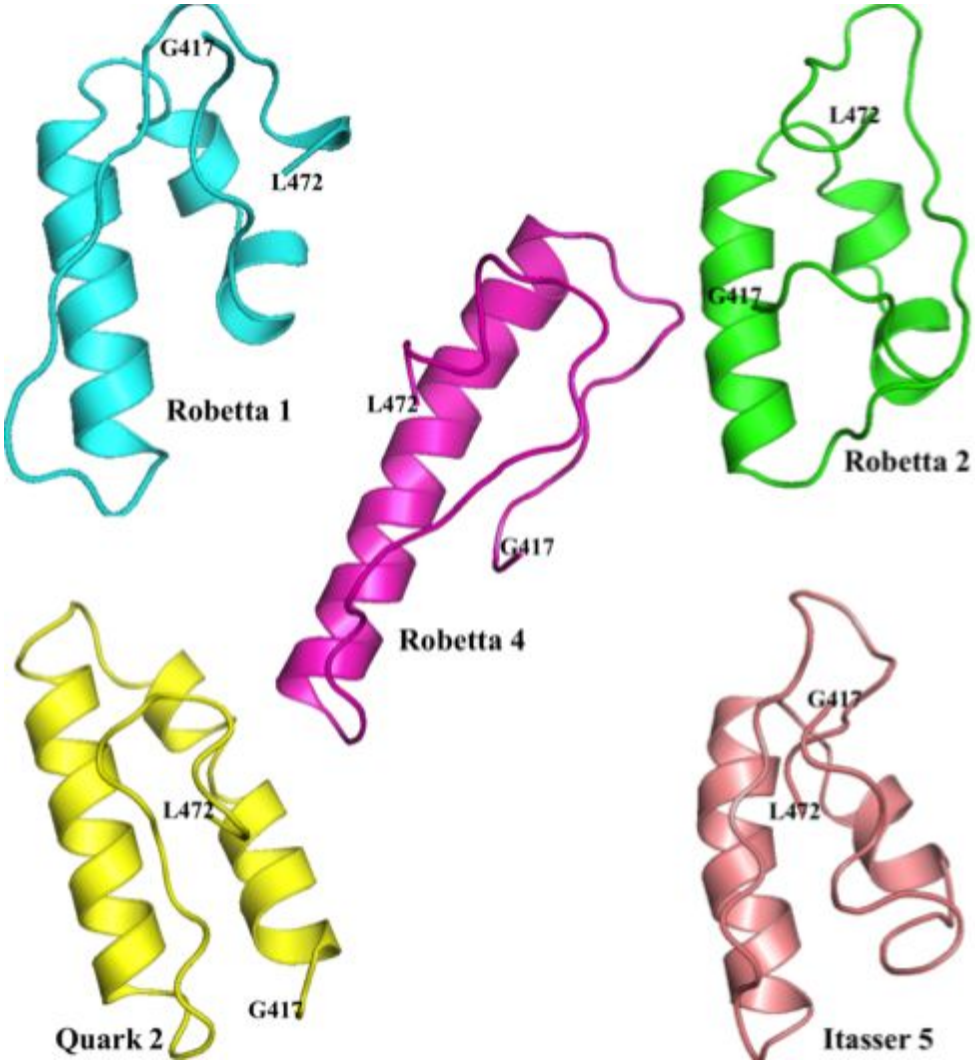

Figure S1: Top scoring three-dimensional models of CB_1 receptor C-terminal domain.

The last 56 residues of CB_1 receptor sequence (G^{417}-L^{472}) were subjected to *ab initio* prediction by using different algorithms, and were ranked according to their zDOPE scores. Each server predicted multiple models, which are named according to their server name followed by a number.

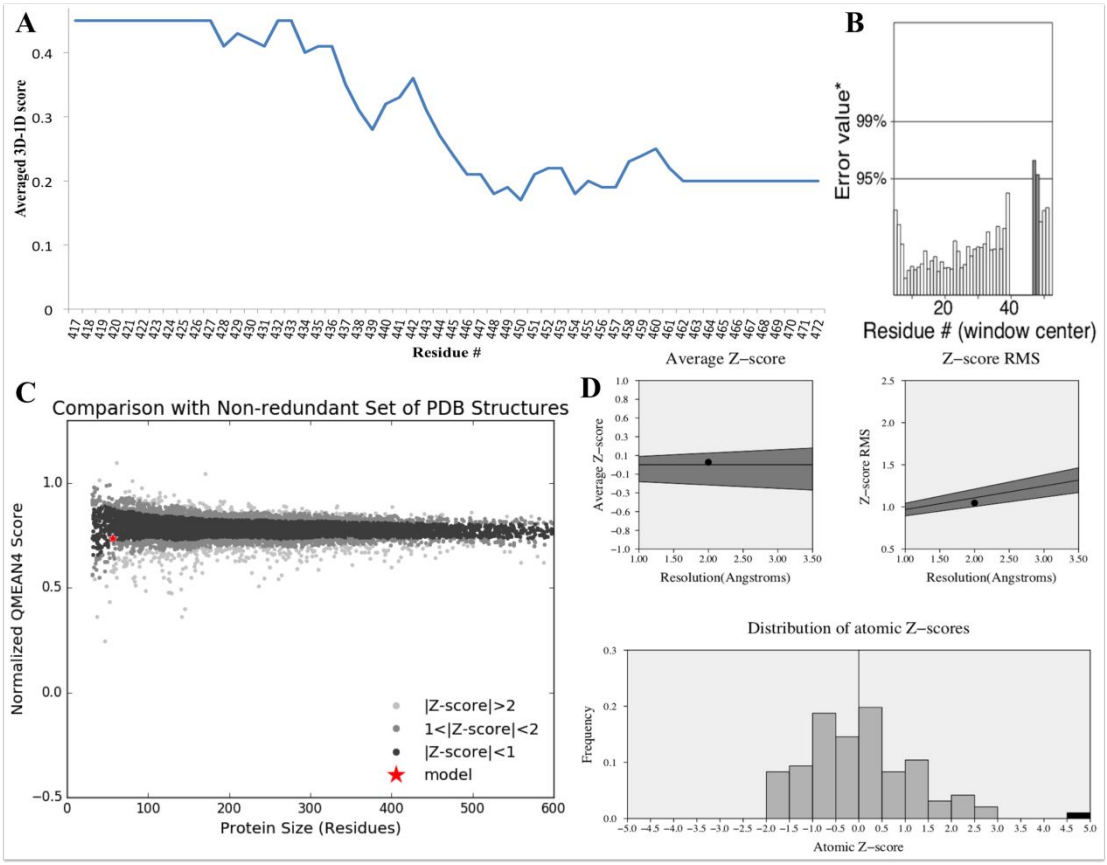

Figure S2: Validation for CB1R C-terminal domain model by different methods. The significant Verify3D (A), QMean(B), Errat (C) and Prove(D) scores validated the model.

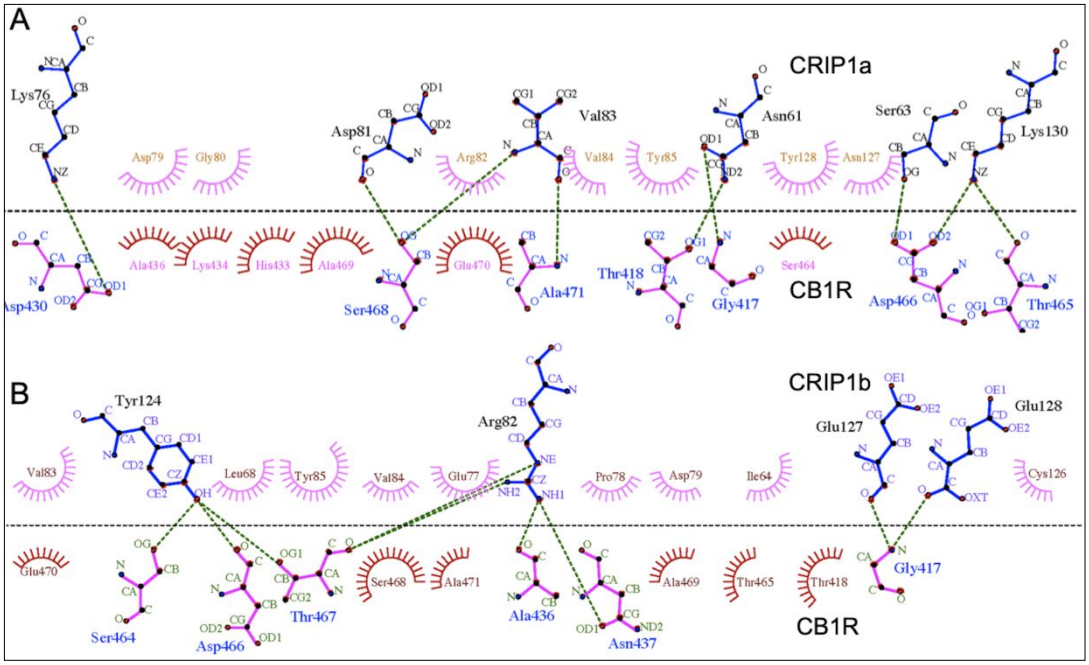

Figure S3: 2D interaction plot depicting key interactions between CB1R C-terminal domain with CRIP1a(A) and CRIP1b(B).
Key hydrogen bonds are represented by green dashed-lines; the hydrophobic residues present near interface are surrounded in colored semi-circles and the interfaces between the proteins are represented by black dashed-lines. The image was prepared using DIMPLOT program under LigPlot+ suit*.

*Laskowski, R. A.; Swindells, M. B. LigPlot+: Multiple Ligand–Protein Interaction Diagrams for Drug Discovery. *J. Chem. Inf. Model.* **2011**, *51* (10), 2778–2786. https://doi.org/10.1021/ci200227u.