

SUPPLEMENTAL MATERIAL 1, Figs S1-4

Amino acid sequences of GlyR and cannabinoid receptors comparison

Local sequence alignment of CB1R, CB2R and GlyRs $\alpha 1$, $\alpha 2$ and β was generated with the web-based LALIGN/PLALIGN sequence alignment tools (Huang and Miller, 1991) available on the website of European Bioinformatics Institute (<http://fasta.bioch.virginia.edu>). Using LALIGN/PLALIGN-Local Alignment program we found that inspite of the low level of total sequence homology, some fragments of $\alpha 1$, $\alpha 2$ and β subunits of GlyR and CB1R/CB2R show quite high levels of identity (up to 60%) (Figs. S1-3). These fragments contain a number of residues (in particular residues 192, 195 and 282 in CBR1 and 112, 197 in CB2R) suggested to be responsible for cannabinoid agonist binding to CB1R or CB2R (Chin et al., 1999;Rhee et al., 2000;Song et al., 1999;Tao and Abood, 1998;Tao et al., 1999;Shim et al., 2003;McAllister et al., 2002;Mahmoudian, 1997). Local sequence alignments by dot matrix analysis were performed with PLALIGN (Fig. S4).

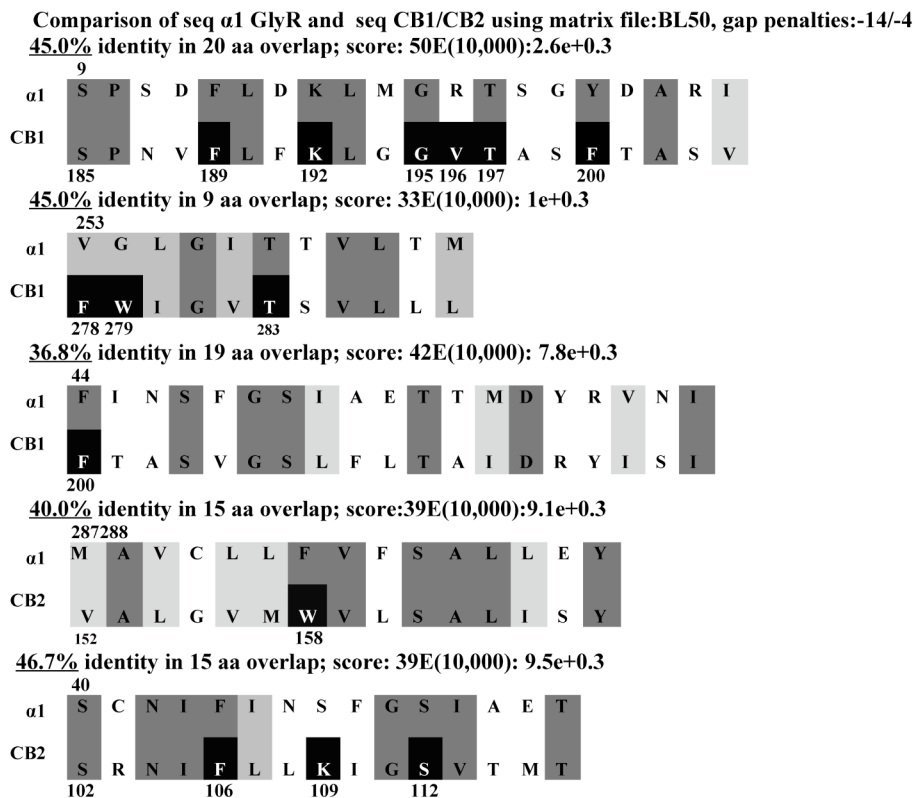


Figure S1. Local sequence alignment of CB1R, CB2R and GlyRs α 1 subunit. Blocks of amino acids (aa) of GlyR α 1 subunits that share at least 30% identity (as determined by the LALIGN program) with the corresponding sequences from CB1 or CB2 receptors. Both, here and below: gray shading demarcates identical and conserved amino acids in subunits of GlyR and CB1/CB2 receptors. Black shading indicates residues responsible for various cannabinoid agonists binding.

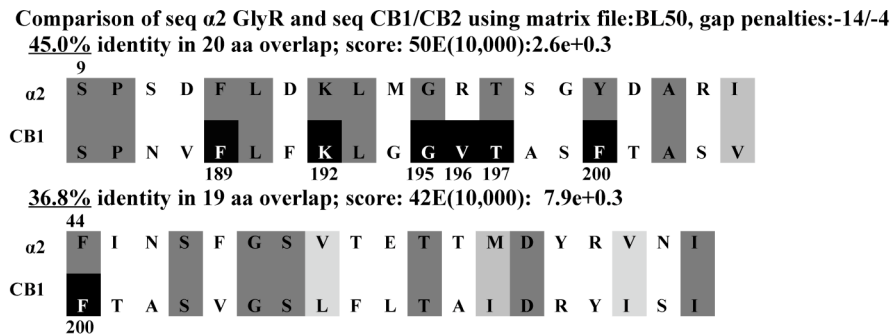


Figure S2. Local sequence alignment of CB1R, CB2R and GlyRs α 2 subunit.

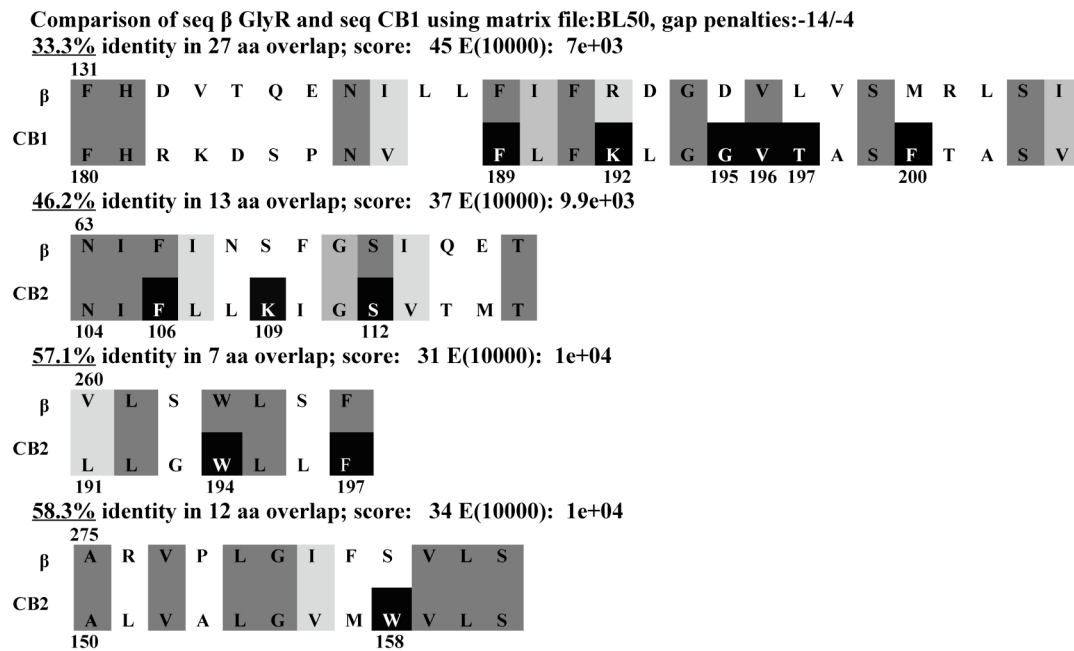


Figure S3. Local sequence alignment of CB1R, CB2R and GlyRs β subunit.

/seqprg/slib/bin/plalign -N 5000 -s BL50 -E 10 -f -12 -g -2 -w 75

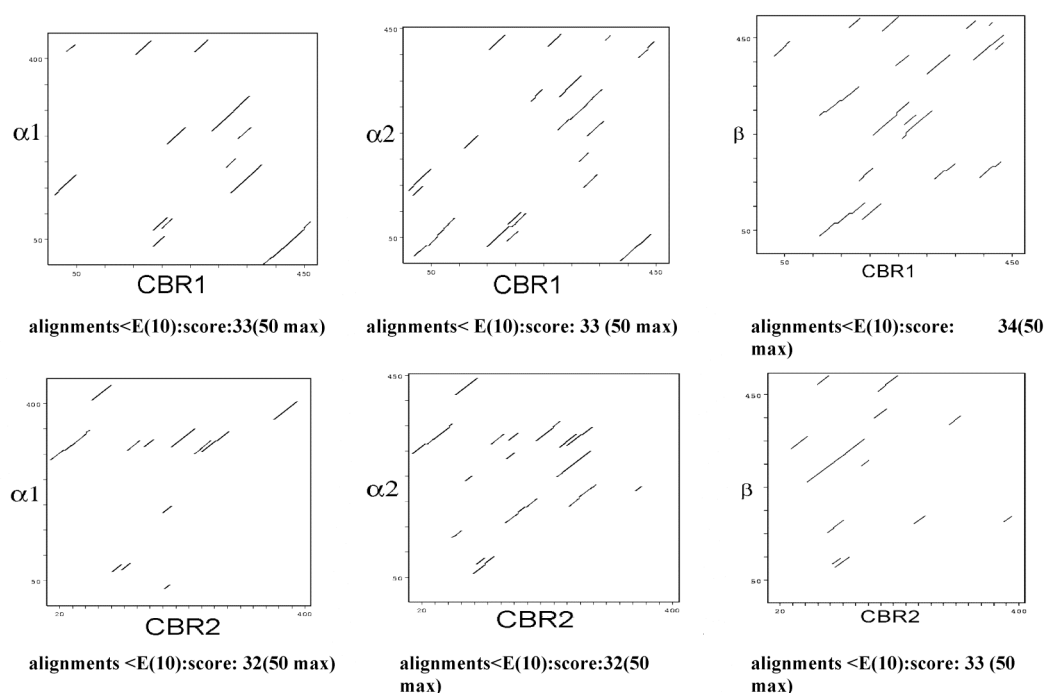


Figure S4. Graphic "dotplot" output of the alignments

Reference List

1. Chin CN, Murphy JW, Huffman JW, Kendall DA (1999) The third transmembrane helix of the cannabinoid receptor plays a role in the selectivity of aminoalkylindoles for CB2, peripheral cannabinoid receptor. *J Pharmacol Exp Ther* 291: 837-844.
2. Huang X, Miller W (1991) A Time-efficient, Linear-Space Local Similarity Algorithm. *Adv Appl Math* 12: 373-381.
3. Mahmoudian M (1997) The cannabinoid receptor: computer-aided molecular modeling and docking of ligand. *J Mol Graph Model* 15: 149-53, 179.
4. McAllister SD, Tao Q, Barnett-Norris J, Buehner K, Hurst DP, Guarnieri F, Reggio PH, Nowell Harmon KW, Cabral GA, Abood ME (2002) A critical role for a tyrosine residue in the cannabinoid receptors for ligand recognition. *Biochem Pharmacol* 63: 2121-2136.
5. Rhee MH, Nevo I, Bayewitch ML, Zagoory O, Vogel Z (2000) Functional role of tryptophan residues in the fourth transmembrane domain of the CB(2) cannabinoid receptor. *J Neurochem* 75: 2485-2491.
6. Shim JY, Welsh WJ, Howlett AC (2003) Homology model of the CB1 cannabinoid receptor: sites critical for nonclassical cannabinoid agonist interaction. *Biopolymers* 71: 169-189.
7. Song ZH, Slowey CA, Hurst DP, Reggio PH (1999) The difference between the CB(1) and CB(2) cannabinoid receptors at position 5.46 is crucial for the selectivity of WIN55212-2 for CB(2). *Mol Pharmacol* 56: 834-840.

8. Tao Q, Abood ME (1998) Mutation of a highly conserved aspartate residue in the second transmembrane domain of the cannabinoid receptors, CB1 and CB2, disrupts G-protein coupling. *J Pharmacol Exp Ther* 285: 651-658.
9. Tao Q, McAllister SD, Andreassi J, Nowell KW, Cabral GA, Hurst DP, Bachtel K, Ekman MC, Reggio PH, Abood ME (1999) Role of a conserved lysine residue in the peripheral cannabinoid receptor (CB2): evidence for subtype specificity. *Mol Pharmacol* 55: 605-613.