

Supplementary Materials

GluR2 ligand-binding core (S1S2J) of AMPA-receptor was chosen as biological target. The crystal structure protein with aniracetam was downloaded from Protein Data Bank. Aniracetam redocking into the LBD-site correctly reproduced the mode of receptor and native ligand binding determined by X-ray crystallography (Figure A1). The root-mean-square deviation (RMSD) for ligand was 0.366

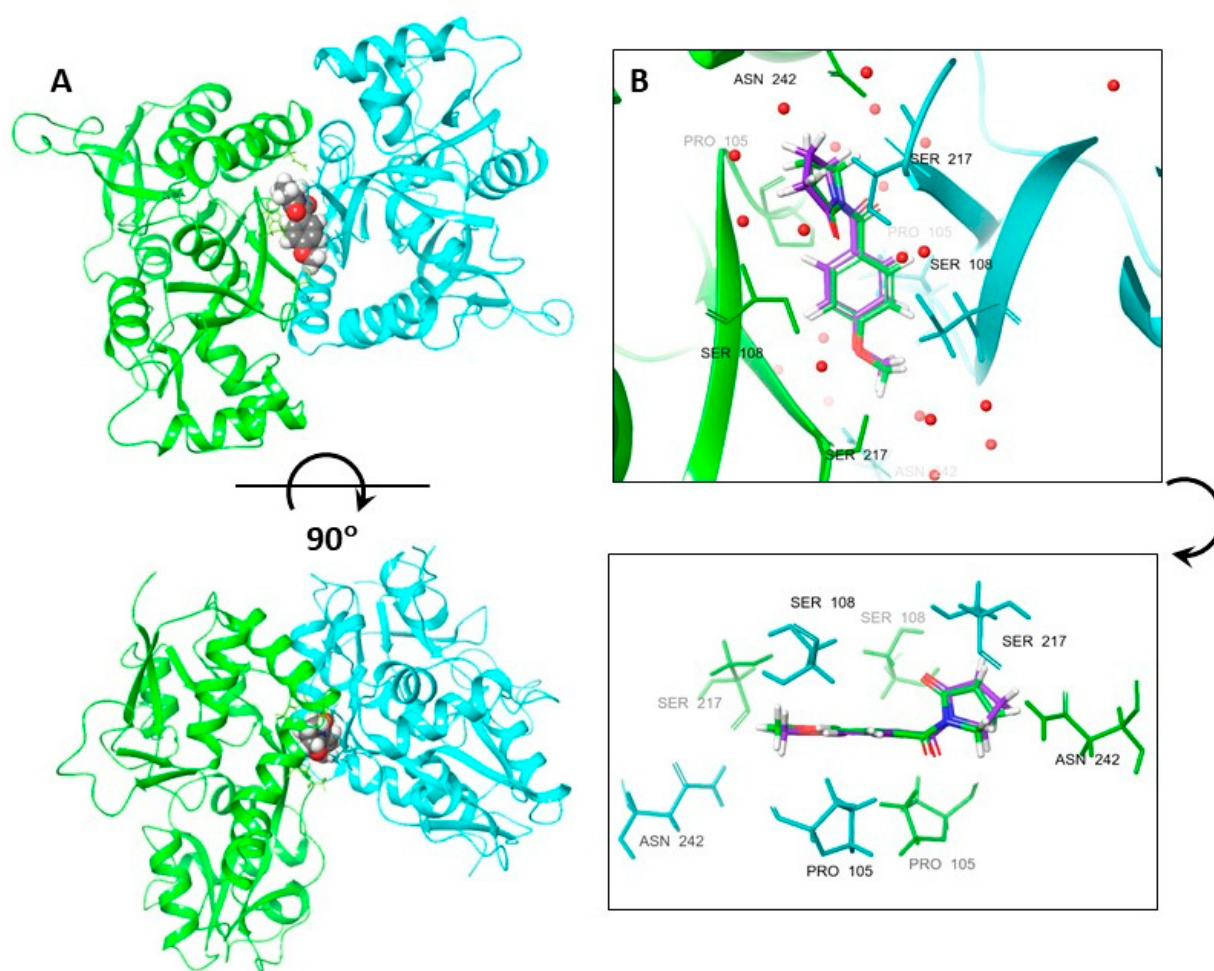


Figure-S1 Visualization of S1S2 LBD of AMPA-receptor: A – position of the aniracetam in the active site of the LBD (PDB code 2AL5); B – superimposition of two molecule of aniracetam: green molecule was downloaded from Protein Data Bank; violet was obtained as result of redocking procedure.

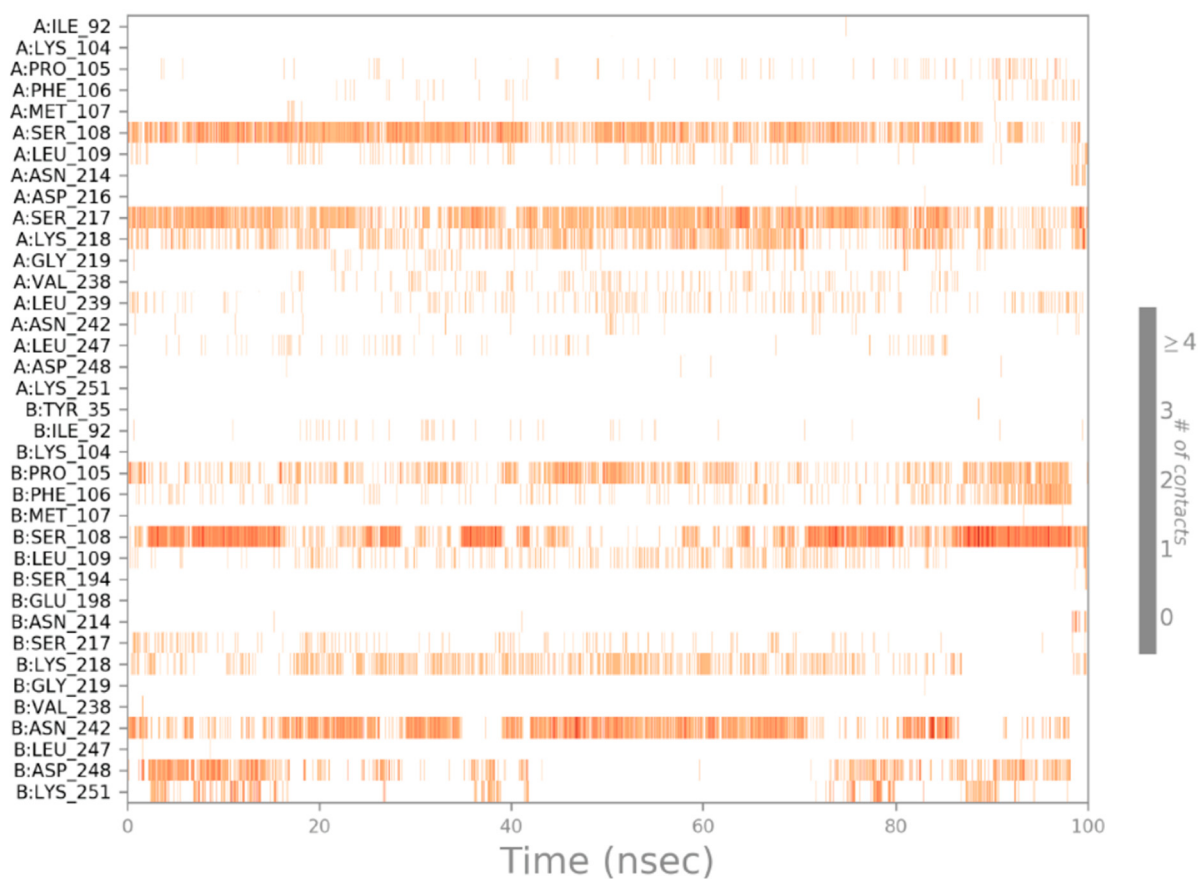


Figure-S2 Intensity of ligand-protein contacts in the system

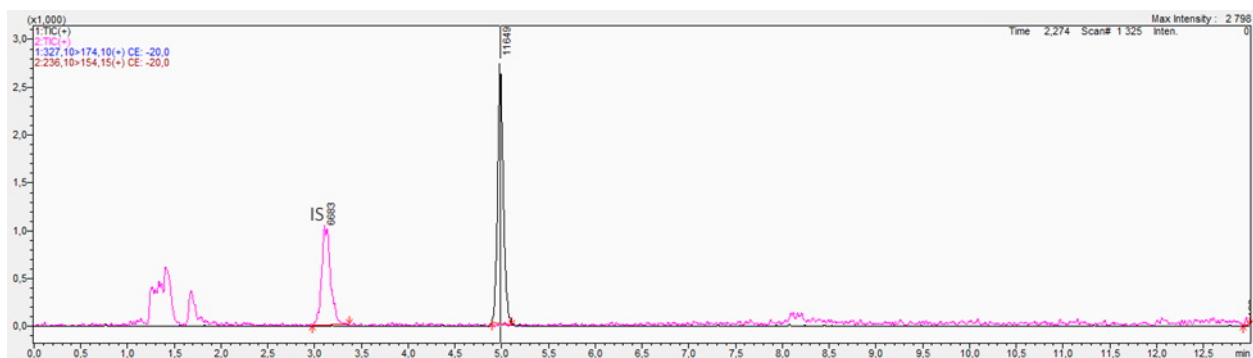


Figure-S3 Chromatograms of compound 1 with IS in brain homogenate

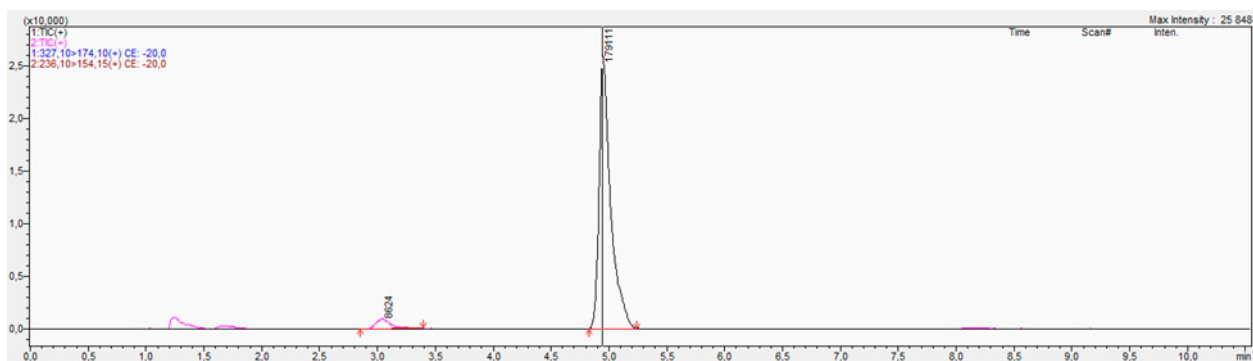


Figure-S4 Chromatograms of compound 1 with IS in brain homogenate from animal with MCAO.