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Homology Modeling of Metabotropic Glutamate Receptor 2.

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Many studies show involvement of metabotropic glutamate receptors (mGluRs) in synaptic excitation transudation. The mGluR family consists of eight proteins divided into three groups corresponding to sequence similarities, pharmacology and physiological role. These groups are: I (mGluR1, -5), II (mGluR2, -3) and III (mGluR4, -6, -7, -8). Group II lies in field of our interest due to its potential as therapeutic target for stroke and pain drugs. Primary goal of this research is to create viable virtual model of transmembrane domain of mGluR2 receptor capable of binding reference ligands. This model will be used for further research.

Our approach is based on homology modeling. Since mGluRs are part of superfamily of G protein coupled receptors (GPCRs) and thus their sequence is similar to Rhodopsin, we have chosen Rhodopsin crystal structure as a template for homology modeling of mGluR2 receptor. We have prepared sequence alignment of mGluR family with Rhodopsin and confronted it with alignments available in literature. Created models were verified using mutagenesis data available.

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