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# Homology modeling of human NMDA receptor and studies of the channel symmetry using brownian dynamics simulation

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**Background and Aims:** Comparative homology modeling of human NMDA (N-methyl-D-aspartate) transmembrane domain was focused in this study. Two symmetrically possible models for the channel segment of human NMDA receptor (heterotetramer: NR1-NR2B) have been prepared using potassium channel crystal structure (PDB code: 1bl8) as template. The symmetry of arranged subunits was 2-fold in one model while arranged as 4-fold in the other. In order to investigate if potassium channel pore blockers can interact with any of these two models, Brownian dynamics simulation were performed on both models. Two known toxin blockers of potassium channels (1Ter, 1Pnh) have been used to study the interaction of channels and blockers.
**Methods:** The conventional homology modeling procedure was carried out to build transmembrane domain of NMDA receptor with Modeller 9v8 program. The high score model was selected for Brownian dynamic simulation study.
**Results:** It was observed that the complex of ligand-channel in two-fold symmetry is more favored than the four-fold state in terms of both frequency and energy of the triplets. The highest value of frequency for triplets was attributed to 12th conformation of 1-Ter toxin and two fold state of the protein (Frequency=119). The most stable complexes were also seen with the two fold symmetry of the channel in case of both toxins.
**Conclusions:** Since the known channel blocker of human NMDA receptor has shown higher affinity toward the two-fold model of channel, the two-fold symmetry could be assigned to channel segment of the human NMDA receptor.
**Keywords:** Brownian dynamics Simulation; NMDA receptor; Homology modeling