Building a Homology Model of the Human Glycine α-1 Receptor Based on the Nicotinic Acetylcholine Receptor
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The glycine alpha 1 receptor is a member of the superfamily of ligand-gated ion channels which are essential to the transfer of information within the nervous system. Since the glycine alpha 1 receptor is a transmembrane protein, it tends to denature when removed from the membrane environment, so x-ray crystallography cannot be used to determine its native folded state. Other methods which could be used to predict structure, such as cryo-electron microscopy, could only give images of intermediate resolution at best. In this project, we use homology modeling to develop a model of the transmembrane domain of the glycine alpha 1 receptor based on the refined structure of the nicotinic acetylcholine receptor at 4Å, which was found using cryo-electron microscopy. The two proteins are in the same superfamily, thereby suggesting similar structures. The programs used to model and analyze the structure include ClustalW, Modeller, VMD, and PROCHECK.