**MASTER THESIS**

Identification of the inter-subunit interactions that maintains the trimeric structure of P2X receptors by using computational modeling.

**ABSTRACT**

The ATP gated cationic P2X receptors has homomeric or heterotrimeric structure. It consists of seven subunits P2X1-P2X7. Based on the available PDB(Protein data bank) structures the inter subunit contacts are mostly present in the extracellular domain. The Biochemical data suggested that block alanine mutation at certain positions of rP2X1 and hP2X4 caused complete trimeric disturbance or weak interactions of different subunits. The main aim of this thesis is to identify the interaction sites that plays a key role in maintaining the trimeric structure and to find out the loss of which electrostatic interaction resulted in the trimeric disturbance by computational modeling.

My hypothesis is that if an interaction site is present in both open and closed state of the receptor then that might be important for maintaining the oligomeric state. The plan for this project is to do few nanosecond MD simulation using GROMACS on the homology models of the rP2X1 and hP2X4 both in open and closed state and analyze for the presence of the electrostatic interactions like Hydrogen bonds and salt bridges between different subunits during the complete simulation. These analyses are done using gromacs tools or pymol tools. Also, to calculate RMSD and free energy calculations between the wild and mutated structure.