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Research Abstract

Remote Homologs of Pharmaceutically Important
Membrane Proteins

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G-protein coupled receptors are the largest family of proteins and they play an integral role in cell signaling. They are present in practically every organ and play a vital role in several physiological activities. Hence present a wide range of opportunities as drug targets. But these proteins pose problems for physical extraction. Hence there is a need for computationally determining structure and function of these proteins as a first step towards developing novel drug molecules.

In this project, we try to identify possible relationships between the GPCR families. We postulate that some of the known or orphan GPCRs would have arisen due to exon shuffling and /or exon duplication. Here the strategy is to shuffle the transmembrane segments of the selected GPCRs and supply them as query sequences to the BLAST tool, which searches for similar sequences among the database of protein sequences. This can help us find novel relationships between the GPCRs i.e. instances of shuffled homologs or homologs arising out of exon duplication.

In our study, we shuffled the transmembrane domains of seven Class A and Class B GPCRs and analyzed the output of the shuffled sequences. Our preliminary studies indicate that there are four instances of probable exon shuffling and eight instances of probable exon duplication among the Class A and Class B GPCRs.

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