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Predicting G-Protein Coupled Receptor Thermostability Conferred by Point Mutations

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Predicting G-Protein Coupled Receptor Thermostability Conferred by Point Mutations

Abstract

G-protein Coupled receptors (GPCRs) are cell surface receptors characterized by their 7 trans membrane helices connected by extra- and intra-cellular loops. GPCRs mediate cell signaling and control many important human biological functions. Because they are ubiquitous. They offer a broad pharmacueutical target in order to create a ligand (drugs) to affect a change in the receptor interface. We must be able to model that GPCR.

To divine the structure of a GPCR, we must isolate and purify that protein. But, as a transmembrane protein, GPCRs rely on the surrounding lipid membrane for stability removal of which can degrade the receptor and invalidates any subsequent crystallization. One method to maintain receptor integrity and stability is through point mutations.

The purpose of this research was to correlate data on the termostability of mutations of a GPCR(turkey beta-1-adrenergic receptor), with specific parameters. Given the serendipity of the generic strategy used for the isolation of there detergent-solubilized thermostable mutants, it would be convenient to provide a computational method that predicts GPCR thermostatbility. The generalizebility of the β-1adrenergic receptor themostable mutations to other class A GPCRs was also investigated. Future receptor themostable mutations to other class A GPCRs was also investigated. Future research will focus on the structural predictions of GPCR using mutagensis as a tool.

評語

此作品仍基於 2008 年論文之進一步研究，作者嘗試以不同的篩選方式找出決定性的因子，並已有不錯之結果，建議以更大更具代表性之 dataset 來驗證所提出之模型。