Identifying Unfolding Pathways of G Protein-Coupled Receptor Protein Structures

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G protein-coupled receptors (GPCRs) have important functionality in cell signaling processes by external affects such as light, smell, taste, and hormones. The conformational changes in structures of GPCR’s play vital role in signaling processes. The understanding of conformational changes is useful to determine basis of certain diseases that are related to malfunctioning of these proteins. The study of structures of GPCRs, however, is challenging since GPCR proteins are not sufficiently stable for crystallization.

In this study a new computational method for analyzing protein structures is proposed to assess their stability. The method is based on computational unfolding of proteins utilizing the Gaussian network model framework that represent protein structure by network of springs. The unfolding of a protein is represented by removal of springs so as to increase the conformational entropy in an appropriate fashion.

This new method is tested on several GPCR protein structures to determine their folding cores and important residue-ligand interactions.