De Novo Modeling of GPCR Class A Structures

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Abstract

In this talk I will describe recent work to develop novel methods to model G protein-coupled receptor (GPCR) structures from their sequence information and statistically significant side chain contacts within a "template" structure. Our approach utilizes methods of bioinformatics to identify likely high confidence side chain side chain TM helical contacts and then reconstitutes the seven TM helical domain through a simulated annealing protocol with refinement using replica exchange and an implicit solvent/implicit membrane sampling scheme. Results will be presented for de novo prediction of the b2 adenergic receptor, the adenine receptor and a number of other amine receptors.