2010 UVM Student Research Conference

Abstract for oral presentation by Liton Roy.

The dominant force in protein folding is the formation of a hydrophobic core; however it is not clear how the amino acid composition of the core determines stability and native structure. The only way to rigorously examine how core sequence corresponds to stability is to make all possible core variants and measure their biophysical parameters. Analysis of such large numbers of proteins is impossible. Our approach to this problem is to use dynamic libraries in which modest (100s) fragments are allowed to combine under thermodynamic control to give many (millions) of possible proteins. Fragment orientation in the protein assembly is controlled using metal-ligand chemistry that allows free exchange of fragments in the dynamic library, but is robust enough to allow isolation, characterization of the optimal self-selecting species. Dynamic libraries thus allow a complete coverage of sequence space.