A Specific Aims

Realization of novel molecular function requires the ability to alter molecular complex formation. Enzymatic function can be altered by changing enzyme-substrate interactions via modification of an enzyme's active site. A redesigned enzyme may either perform a novel reaction on its native substrates or its native reaction on novel substrates. We propose a novel algorithm for protein redesign, which searches over possible active site mutations and combines a statistical mechanics-derived ensemble-based approach to computing the binding constant with the speed and completeness of a branch-and-bound pruning algorithm. We will develop an efficient. . .