
Preface

The folding/unfolding kinetics of a three-dimensional lattice protein was studied using a simple statistical mechanical model for protein folding that the authors had developed earlier. The model considers the specificity of an amino acid sequence and the native structure of a given protein. They calculated the characteristic relaxation rate on the free energy surface starting from a completely unfolded structure (or native structure) that is assumed to associate with a folding rate (or an unfolding rate). The chevron plot of these rates as a function of the inverse temperature was obtained for four lattice proteins, $a1$, $a2$, $b1$, and $b2$, in order to investigate the dependency of the folding and unfolding rates on their native structures and amino acid sequences. Proteins $a1$ and $a2$ fold to the same native structure, but their amino acid sequences differ. The same is true for proteins $b1$ and $b2$, but their native structure is different from that of $a1$ and $a2$. To elucidate the roles of individual amino acid residues in protein folding/unfolding kinetics, the authors calculated the kinetic properties for all possible single amino acid substitutions of these proteins and examined their responses. The results are discussed with respect to the roles of short- and long-range interactions and formation of a folding nucleus in the kinetics of protein folding/unfolding.