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Experimental and Computational Methods to Determine Protein Structure and Stability

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Abstract

Proteins are versatile biological macromolecules that are involved in many essential processes and basic functions of a cell, including catalytic activity, storage, transport, cell structure, metabolism, cell signaling, and immunity. The functions of proteins are dictated by their structures. For instance, the shape, catalytic activity, and specificity of enzymes depend on both the sequence of amino acids in their active site to which the substrate or drug binds and the nature of protein folding. The stability of protein will determine if a protein is in native folded conformation or the unfolded or denatured state. The key role of drug designing is to enhance protein stability since the marginal stability of a protein could cause loss of protein function, increased degradation, and difficulty in synthesizing protein-based drugs. The folded

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