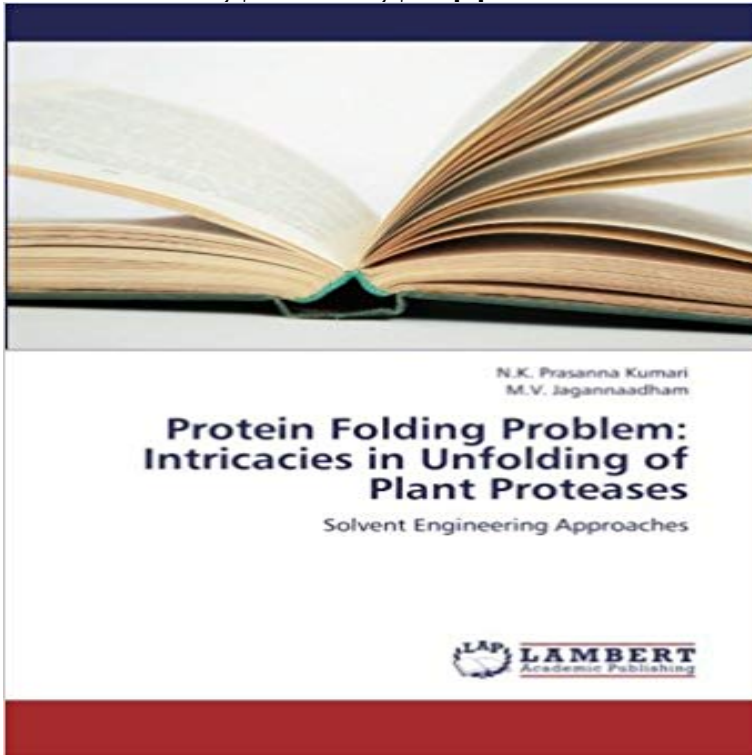


Protein Folding Problem: Intricacies in Unfolding of Plant Proteases: Solvent Engineering Approaches



The protein folding problem refers to the question how a protein molecule adopts the specific conformation given the vast number of conformations possible for a given polypeptide sequence as all the information is encoded in the amino acid sequence. An understanding of the protein-folding pathway requires the identification and structural analysis of the intermediate steps, if any, in the process. To investigate the folding behavior of multi-domain proteins, cryptolepain, heynein a well-characterized serine and thiol proteins with established structure is chosen as a model system in the present studies. In the present study, attempts were made to get an insight into the folding behavior of cryptolepain and heynein emphasizing the role of domains in its molecular structure. Specifically, the order of unfolding of domains in the sequential unfolding of domains was established. Further, the insight in to the role of domains in molecular structure of the protein is also attempted using the approach of solvent engineering. The importance of the findings are discussed in application point of view in biotechnology as domain interactions play an important role in the folding of various

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