

1. Record Nr.	UNINA9910876503203321
Titolo	Protein conformation
Pubbl/distr/stampa	Chichester [England] ; ; New York, : Wiley, 1991
ISBN	1-282-34774-8 9786612347740 0-470-51414-0 0-470-51415-9
Descrizione fisica	1 online resource (288 p.)
Collana	Ciba Foundation symposium ; ; 161
Disciplina	574.19/245
Soggetti	Proteins - Conformation
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Proceedings of the Symposium on Protein Conformation, held Jan. 22-24, 1991 at the Ciba Foundation, London, England. "A Wiley-Interscience publication".
Nota di bibliografia	Includes bibliographical references and indexes.
Nota di contenuto	<p>PROTEIN CONFORMATION; Contents; Introduction; Mechanisms of enzyme catalysis from crystal structure analyses; Comparative analysis of protein three-dimensional structures and an approach to the inverse folding problem; Structural and genetic analysis of electrostatic and other interactions in bacteriophage T4 lysozyme; Simulation analysis of the stability mutants R96H of bacteriophage T4 lysozyme and I96A of barnase; Towards time-resolved diffraction studies with glycogen phosphorylase</p> <p>The application of computational methods to the study of enzyme catalysis by triose-phosphate isomerase and stabilities of variants of bacteriophage T4 lysozymeMultidimensional triple resonance NMR spectroscopy of isotopically uniformly enriched proteins: a powerful new strategy for structure determination; Six years of protein structure determination by NMR spectroscopy: what have we learned?; On deriving spatial protein structure from NMR or X-ray diffraction data; NMR spectroscopy and protein folding: studies of lysozyme and a-lactalbumin</p> <p>Experimental studies of pathways of protein foldingProtein stability and protein folding; Ca²⁺ binding in proteins of the calmodulin</p>

superfamily: cooperativity, electrostatic contributions and molecular mechanisms; Protein-protein interaction: an analysis by computer simulation; General discussion; Index of contributors; Subject index

Sommario/riassunto

How the amino acid sequence of a protein determines its three-dimensional structure is a major problem in biology and chemistry. Leading experts in the fields of NMR spectroscopy, X-ray crystallography, protein engineering and molecular modeling offer provocative insights into current views on the protein folding problem and various aspects for future progress.
