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Collana	Wiley series on surface and interfacial chemistry
Altri autori (Persone)	RusoJuan M (Ruso Beiras, Juan Manuel) PineiroAngel <1973->
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Nota di contenuto	PROTEINS IN SOLUTION AND AT INTERFACES; CONTENTS; PREFACE; CONTRIBUTORS; PART I; 1 X-RAY CRYSTALLOGRAPHY OF BIOLOGICAL MACROMOLECULES: FUNDAMENTALS AND APPLICATIONS; 1.1 INTRODUCTION; 1.2 FUNDAMENTALS OF X-RAY DIFFRACTION; 1.2.1 X-Ray Radiation and Interaction with Matter; 1.2.2 Crystals and Symmetry; 1.2.3 Diffraction by Crystals; 1.2.4 Real and Reciprocal Space; 1.2.5 Structure Factors; 1.2.6 Fourier Synthesis and Transform; 1.2.7 The Phase Problem; 1.3 THE STRUCTURE DETERMINATION PROCESS; 1.3.1 Sample Production and Conditioning; 1.3.2 Crystallization; 1.3.3 Data Collection and Processing 1.3.4 Structure Determination 1.3.5 Electron Density Map Interpretation: Model Construction; 1.3.6 Model Refinement; 1.3.7 Validation; 1.4 STRUCTURAL ANALYSIS AND BIOLOGICAL IMPLICATIONS; 1.4.1 Structural Analysis; 1.4.2 Biological Implications; 1.5 FUTURE PROSPECTS; ACKNOWLEDGMENTS; REFERENCES; 2 NUCLEAR MAGNETIC RESONANCE METHODS FOR STUDYING SOLUBLE, FIBROUS, AND MEMBRANE-EMBEDDED PROTEINS; 2.1 INTRODUCTION AND BACKGROUND; 2.1.1 Nuclear Angular Momentum; 2.1.2 Chemical Shifts; 2.1.3 Nuclear Spin Interactions; 2.1.4 Relaxation; 2.1.5 Isotopic Labeling; 2.1.6 Samples; 2.2 STRUCTURAL DATA

2.2.1 Resonance Assignment; 2.2.2 Distance Measurements; 2.2.3 Angular Information; 2.2.4 Residual Dipolar Couplings; 2.2.5 Use of Paramagnetic Agents; 2.2.6 Oriented Samples; 2.2.7 Structure Calculations; 2.3 DYNAMICS; 2.3.1 Fast (ps-ns) Motions; 2.3.2 Slow (s-ms) Motions; 2.3.3 Motions in Solids; 2.4 INTERMOLECULAR INTERACTIONS; 2.4.1 Identification of Interaction Surfaces; 2.4.2 Structural Restraints; 2.5 DISCUSSION; 2.5.1 Large Protein Systems; 2.5.2 Advantages and Disadvantages of Solution and Solid-State MAS NMR; 2.5.3 Complementary Techniques; 2.6 CONCLUSION; REFERENCES

3 SMALL-ANGLE X-RAY SCATTERING APPLIED TO PROTEINS IN SOLUTION

3.1 INTRODUCTION; 3.2 SAXS THEORY; 3.2.1 General Equations; 3.2.2 Isotropy; 3.2.3 Homogeneous Scattering Particles (Two-Phase Model); 3.2.4 Model-Independent Shape Analysis: Kratky's Representation, Guinier's Law, and Porod's Invariant; 3.2.5 Methods to Calculate  $P(q)$ ; 3.2.6 Protein-Protein Interaction:  $S(q)$  Evaluation; 3.3 EXAMPLES; 3.3.1  $R_g$ ,  $p(r)$ , Kratky's Representation and Shape Reconstruction: Analysis of Protein TcOYE; 3.3.2 Guinier's Analysis and Multipole Expansion Shape Reconstruction: The Replication Factor C Case

3.3.3 Partial Folded and Unfolded Protein: Analysis of the Protein Bovine Serum Albumin, BSA, Under the Influence of Denaturing Agents

3.4 PROTEIN INTERACTION: BSA CASE; 3.5 PROTEIN AGGREGATION; 3.6 CONCLUSION; ACKNOWLEDGMENTS; REFERENCES;

4 ANALYZING THE SOLUTION STATE OF PROTEIN STRUCTURE, INTERACTIONS, AND LIGANDS BY SPECTROSCOPIC METHODS; 4.1 INTRODUCTION; 4.1.1 Overview; 4.1.2 Protein Secondary Structures and Motifs; 4.1.3 Structure Determination: Spectroscopic Methods; 4.2 ULTRAVIOLET-VISIBLE ABSORPTION SPECTROSCOPY; 4.2.1 Background

4.2.2 Lambert-Beer Law: Determination of Protein Concentration

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Sommario/riassunto

"Proteins in solution and at interfaces are increasingly used in exciting new applications, from biomimetic materials to nanoparticle patterning. This book surveys the state-of-the-art in the field, providing scientists in diverse areas with a comprehensive and modern analysis of the techniques used in protein characterization, as well as insight into the most important applications. Topics include protein and protein aggregate structure; computational and experimental techniques for the study of protein structure, aggregation, and adsorption; proteins in non-standard conditions; and biotechnological applications"--

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