1. Record Nr. UNINA9911020264403321

Autore	Kaltashov Igor A
Titolo	Mass spectrometry in biophysics : conformation and dynamics of biomolecules / / Igor A. Kaltashov, Stephen J. Eyles
Pubbl/distr/stampa	Hoboken, N.J., : John Wiley, 2005
ISBN	9786610275380 9781280275388 1280275383 9780470245118 0470245115 9780471705178 0471705179 9780471705161 0471705160
Descrizione fisica	1 online resource (480 p.)
Collana	Wiley-Interscience series on mass spectrometry
Altri autori (Persone)	EylesStephen J
Disciplina	572/.33
Soggetti	Mass spectrometry Biophysics Biomolecules - Spectra
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Description based upon print version of record.
Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	MASS SPECTROMETRY IN BIOPHYSICS; CONTENTS; Preface; 1 General Overview of Basic Concepts in Molecular Biophysics; 1.1. Covalent Structure of Biopolymers; 1.2. Noncovalent Interactions and Higher-order Structure; 1.2.1. Electrostatic Interaction; 1.2.2. Hydrogen Bonding; 1.2.3. Steric Clashes and Allowed Conformations of the Peptide Backbone: Secondary Structure; 1.2.4. Solvent-Solute Interactions, Hydrophobic Effect, Side Chain Packing, and Tertiary Structure; 1.2.5. Intermolecular Interactions and Association: Quaternary Structure; 1.3. The Protein Folding Problem 1.3.1. What Is Protein Folding?1.3.2. Why Is Protein Folding So Important; 1.3.3. What Is the Natively Folded Protein and How Do We Define a Protein Conformation?; 1.3.4. What Are Non-native Protein

Conformations? Random Coils, Molten Globules, and Folding Intermediates; 1.3.5. Protein Folding Pathways; 1.4. Protein Energy Landscapes and the Folding Problem; 1.4.1. Protein Conformational Ensembles and Energy Landscapes: Enthalpic and Entropic Considerations; 1.4.2. Equilibrium and Kinetic Intermediates on the Energy Landscape; 1.5. Protein Dynamics and Function
1.5.1. Limitations of the Structure-Function Paradigm1.5.2. Protein Dynamics Under Native Conditions; 1.5.3. Biomolecular Dynamics and Binding from the Energy Landscape Perspective; 1.5.4. Energy Landscapes Within a Broader Context of Nonlinear Dynamics: Information Flow and Fitness Landscapes; References; 2 Overview of "Traditional" Experimental Arsenal to Study Biomolecular Structure and Dynamics; 2.1. X-Ray Crystallography; 2.1.1. Fundamentals; 2.1.2. Crystal Structures at Atomic and Ultrahigh Resolution; 2.1.3. Crystal Structures of Membrane Proteins
2.1.4. Protein Dynamics and X-Ray Diffraction2.2. Solution Scattering Techniques; 2.2.1. Static and Dynamic Light Scattering; 2.2.2. Small-Angle X-Ray Scattering; 2.2.3. Cryo-Electron Microscopy; 2.2.4. Neutron Scattering; 2.3. NMR Spectroscopy; 2.3.1. Heteronuclear NMR; 2.3.2. Hydrogen Exchange by NMR; 2.4. Other Spectroscopic Techniques; 2.4.1. Cumulative Measurements of Higher Order Structure: Circular Dichroism; 2.4.2. Vibrational Spectroscopy; 2.4.3. Fluorescence: Monitoring Specific Dynamic Events; 2.5. Other Biophysical Methods to Study Macromolecular Interactions and Dynamics
2.5.1. Calorimetric Methods2.5.2. Analytical Ultracentrifugation; 2.5.3. Surface Plasmon Resonance; 2.5.4. Gel Filtration; 2.5.5. Gel Electrophoresis; References; 3 Overview of Biological Mass Spectrometry; 3.1. Basic Principles of Mass Spectrometry; 3.1.1. Stable Isotopes and Isotopic Distributions; 3.1.2. Macromolecular Mass: Terms and Definitions; 3.2. Methods of Producing Biomolecular Ions; 3.2.1. Macromolecular Ion Desorption Techniques: General Considerations; 3.2.2. Electrospray Ionization; 3.2.3. Matrix Assisted Laser Desorption/Ionization; 3.3. Mass Analysis
3.3.1. General Considerations: m/z Range and Mass Discrimination, Mass Resolution, Duty Cycle, Data Acquisition Rate

Sommario/riassunto

The first systematic summary of biophysical mass spectrometry techniquesRecent advances in mass spectrometry (MS) have pushed the frontiers of analytical chemistry into the biophysical laboratory. As a result, the biophysical community's acceptance of MS-based methods, used to study protein higher-order structure and dynamics, has accelerated the expansion of biophysical MS.Despite this growing trend, until now no single text has presented the full array of MS-based experimental techniques and strategies for biophysics. Mass Spectrometry in Biophysics expertly closes this gap i