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Nota di contenuto	Protein and Peptide Mass Spectrometry in Drug Discovery; CONTENTS; PREFACE; CONTRIBUTORS; PART I: METHODOLOGY; 1 Ionization Methods in Protein Mass Spectrometry; 1.1 History of the Development of Protein Mass Spectrometry; 1.2 Laser-Based Ionization Methods for Proteins; 1.2.1 Matrix-Assisted Laser Desorption/Ionization (MALDI); 1.2.2 Atmospheric Pressure Matrix-Assisted Laser Desorption/Ionization (AP-MALDI); 1.2.3 Surface-Enhanced Laser Desorption/Ionization (SELDI); 1.2.4 Nanostructure-Initiator Mass Spectrometry (NIMS); 1.3 Spray-Based Ionization Methods for Proteins 1.3.1 Electrospray Ionization (ESI)1.3.2 Sonic Spray Ionization (SSI); 1.3.3 Electrosonic Spray Ionization (ESSI); 1.4 Ambient Ionization Methods; 1.4.1 Desorption Electrospray Ionization (DESI); 1.4.2 Fused-Droplet Electrospray Ionization (FD-ESI); 1.4.3 Electrospray-Assisted Laser Desorption Ionization (ELDI); 1.4.4 Matrix-Assisted Laser Desorption Electrospray Ionization (MALDESI); 1.5 Conclusions;

Acknowledgments; References; 2 Ion Activation and Mass Analysis in Protein Mass Spectrometry; 2.1 Introduction; 2.1.1 Mass Accuracy; 2.1.2 Mass Resolving Power; 2.1.3 Mass Range; 2.1.4 Scan Speed; 2.1.5 Tandem MS Analysis; 2.2 Ion Activation and Tandem MS Analysis; 2.2.1 Introduction: Fragmentation in Protein MS; 2.2.2 Collisional Activation Methods; 2.2.3 Photodissociation; 2.2.4 Electron-Induced Dissociation; 2.2.5 Other Radical-Induced Fragmentation Methods; 2.3 Mass Analyzers; 2.3.1 Time-of-Flight Mass Analyzer; 2.3.2 Quadrupole Mass Analyzer and Quadrupole Ion Trap; 2.3.3 Fourier-Transform Ion Cyclotron Resonance Mass Spectrometer; 2.3.4 Orbitrap; 2.3.5 Ion-Mobility Instruments; References; 3 Target Proteins: Bottom-up and Top-down Proteomics; 3.1 Mass Spectral Approaches to Targeted Protein Identification; 3.2 Bottom-up Proteomics; 3.2.1 Peptide Mass Fingerprinting; 3.2.2 Bottom-up Proteomics Using Tandem MS: GeLC-MS/MS and Shotgun Digests; 3.2.3 GeLC-MS/MS; 3.2.4 Shotgun Digest; 3.3 Top-down Approaches; 3.4 Next-Generation Approaches; References; 4 Quantitative Proteomics by Mass Spectrometry; 4.1 Introduction; 4.2 In-Cell Labeling; 4.2.1 <sup>15</sup>N Metabolic Labeling; 4.2.2 Stable Isotope Labeling by Amino Acid (SILAC); 4.3 Quantitation via Isotopic Labeling of Proteins; 4.3.1 2D PAGE-Based Quantitation; 4.3.2 Proteolytic Labeling Using <sup>18</sup>O Water; 4.3.3 Quantitative Labeling by Chemical Tagging; 4.4 Quantitation via Isotopic Labeling on Peptides; 4.4.1 ICAT; 4.4.2 iTRAQ; 4.4.3 SoPIL; 4.4.4 Absolute Quantitation; 4.5 Label-Free Quantitation; 4.6 Conclusions; Acknowledgment; References; 5 Comparative Proteomics by Direct Tissue Analysis Using Imaging Mass Spectrometry; 5.1 Introduction; 5.2 Conventional Comparative Proteomics; 5.3 Comparative Proteomics Using Imaging MS; 5.3.1 Biomarker Discovery: Breast Cancer; 5.3.2 Biomarker Discovery: Toxicity; 5.3.3 Correlating Drug and Protein Distributions; 5.4 Conclusions

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Sommario/riassunto

The book that highlights mass spectrometry and its application in characterizing proteins and peptides in drug discovery. An instrumental analytical method for quantifying the mass and characterization of various samples from small molecules to large proteins, mass spectrometry (MS) has become one of the most widely used techniques for studying proteins and peptides over the last decade. Bringing together the work of experts in academia and industry, Protein and Peptide Mass Spectrometry in Drug Discovery highlights current analytical approaches, industry practices, and modern s

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