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| Collana | Wiley-Interscience series in mass spectrometry |
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| Nota di contenuto | PROTEOMICS TODAY; CONTENTS; PREFACE TO PART I; ACKNOWLEDGMENT; I INTRODUCTION TO PART I; 1 INSTRUMENTATION AND DEVELOPMENTS; 1.1 Introduction; 1.2 Ionization Techniques for Macromolecules; 1.2.1 (252)Cf Plasma Desorption Ionization; 1.2.2 Fast Atom/Ion Bombardment; 1.2.3 Type of Fragment Ions and Nomenclature; 1.3 Examples on Analytical Solutions Based on FAB-MS; 1.3.1 Detection of Abnormalities in Hemoglobin; 1.3.2 Glycoprotein Structure Determination; 1.3.3 Early Scanning Functions on Sector Machines; 1.4 Electrospray Ionization; 1.5 Matrix-Assisted Laser Desorption Ionization 1.5.1 MALDI at High Pressure1.5.2 Desorption Ionization on Silicon |

(DIOS); 1.5.3 Delayed Extraction; 1.6 Ion Detection; 1.6.1 Microchannel Plates (MCPs); 1.6.2 Cryogenic Detectors; 1.6.2.1 Superconducting Tunnel Junction; 1.6.2.2 Thermal Detectors; 1.7 Types of Analyzers; 1.7.1 Quadrupole Mass Filter; 1.7.2 Three-Dimensional Quadrupole Ion Trap; 1.7.3 Linear Ion Trap; 1.7.4 Time of Flight; 1.7.5 Fourier Transform Ion Cyclotron Resonance; 1.8 Hybrid Analyzers; 1.8.1 Quadrupole Time of Flight; 1.8.2 Ion Mobility-TOF; 1.8.3 Linear Ion Trap-FT-ICR; 1.8.4 Ion Trap-TOF; 1.9 Tandem Mass Spectrometry 1.9.1 Postsource Decay 1.9.2 MS-MS Measurements; 1.9.3 Collisional Activation; 1.10 Current MS Instrumentation in Proteome Analyses; 1.10.1 MALDI-TOF; 1.10.2 MALDI-TOF-TOF; 1.10.3 FT-ICR-MS; 1.10.4 ION Mobility-MS; 1.11 Current MS-Based Proteomics; 1.11.1 Delivering Peptides to Ion Source; 1.11.2 Peptide Sequencing and Database Searching; 1.11.3 Peptide Mass Fingerprinting; 1.11.4 Searching with MS-MS Data; 1.11.5 Databases for MS Data Search; 1.12 Recent Achievements and Future Challenges; 1.12.1 Current Applications; 1.12.2 Signal Transduction Pathways; 1.13 Concluding Remarks; References

2 PROTEOMICS IN CANCER RESEARCH 2.1 Introduction; 2.1.1 Two-Dimensional Gel Electrophoresis; 2.1.2 Surface-Enhanced Laser Desorption Ionization; 2.1.3 Protein Microarrays; 2.1.4 Getting More Than Just Simple Change in Protein Expression; 2.1.5 Laser Capture Microdissection; 2.2 Pancreatic Ductal Adenocarcinoma; 2.2.1 Analyses Based on Chip Technology; 2.2.2 SELDI Analysis of Pancreatic Ductal Adenocarcinoma; 2.2.3 Protein Profiling Following Treatment with DNA Methylation/Histone Deacetylation Inhibitors; 2.2.4 Proteomic Profiling of PDAC Following Treatment with Trichostatin A 2.2.5 Proteomic Profiling of PDAC Following Treatment with 5 -aza-2 -deoxycytidine 2.3 Proteomic Analysis of Human Breast Carcinoma; 2.3.1 Two-DE Analysis in Breast Cancer; 2.3.2 Proteomic Profiling of Breast Cancer Cell Membranes; 2.3.3 Proteomic Analysis on Selected Tissue Samples; 2.4 Proteomic Profiling of Chemoresistant Cancer Cells; 2.4.1 Protein Alterations in Pancreas Carcinoma Cells Exposed to Anticancer Drug; 2.4.2 Proteomic Profiling of Cervix Squamous Cell Carcinoma Treated with Cisplatin; 2.5 Signal Pathway Profiling of Prostate Cancer 2.6 Emerging Role of Functional and Activity-Based Proteomics in Disease Understanding

Sommario/riassunto

The last few years have seen an unprecedented drive toward the application of proteomics to resolving challenging biomedical and biochemical tasks. Separation techniques combined with modern mass spectrometry are playing a central role in this drive. This book discusses the increasingly important role of mass spectrometry in proteomic research, and emphasizes recent advances in the existing technology and describes the advantages and pitfalls as well.* Provides a scientifically valid method for analyzing the approximate 500,000 proteins that are encoded in the human genome* Explains t