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Nota di contenuto	PROTEIN SEQUENCING AND IDENTIFICATION USING TANDEM MASS SPECTROMETRY; CONTENTS; Series Preface; Preface; Chapter 1. An Introduction to Protein Sequencing Using Tandem Mass Spectrometry; 1.1. Introduction; 1.2. References; Chapter 2. The Primary Structure of Proteins and a Historical Overview of Protein Sequencing; 2.1. Protein and Peptide Structure; 2.2. Edman Degradation; 2.2.1. The Edman Reaction; 2.2.2. Incorporation of the Edman Degradation Reaction into Automated Protein Sequenators; 2.2.3. Edman Degradation in Proteomic Research; 2.3. Tandem Mass Spectrometry 2.3.1. A Brief History of the Application of Mass Spectrometry to Protein Sequencing2.3.2. Sequence Analysis of Peptides Using Electron Ionization Mass Spectrometry; 2.3.3. The Utilization of Fast Atom Bombardment with Tandem Mass Spectrometry to Sequence Peptides; 2.3.4. Internal Sequence Analysis of Proteins Using Electrospray Ionization-Tandem Mass Spectrometry and Matrix-Assisted Laser

Desorption/Ionization-Time-of- Flight Mass Spectrometry; 2.4. Summary; 2.5. References; Chapter 3. Fundamental Mass Spectrometry; 3.1. An Overview of the Instrumentation; 3.2. Ionization Methods 3.2.1. Electrospray Ionization3.2.2. Nanospray and Microspray Ionization; 3.2.3. Matrix-Assisted Laser Desorption/ Ionization; 3.3. Mass Analyzers; 3.3.1. Fundamental Parameters of Mass Analysis; 3.3.2. Quadrupole Mass Filters (3.20); 3.3.3. Ion Trap Mass Analyzers (3.21-3.23); 3.3.4. Time-of-Flight Mass Analyzers (3.5); 3.4. Tandem Mass Spectrometry; 3.4.1. Collisionally Induced Dissociation; 3.4.2. Tandem Mass Spectrometers; 3.4.3. Types of Tandem Mass Spectrometry Experiments; 3.5. Data Systems; 3.6. Summary; 3.7. References

Chapter 4. Collisionally Induced Dissociation of Protonated Peptide Ions and the Interpretation of Product Ion Spectra4.1. Introduction; 4.2. Peptide Fragmentation Chemistry; 4.2.1. Collisionally Induced Dissociation of Peptide Ions Formed by Electrospray Ionization; 4.2.2. Fragmentation of Protonated Peptide Ions Formed by Matrix-Assisted Laser Desorption/Ionization; 4.3. Interpretation of the Product Ion Spectra of Tryptic Peptides; 4.3.1. Tabulated Values Used in the Interpretation; 4.3.2. A Strategy for the Interpretation of Product Ion Spectra of Tryptic Peptides

4.3.3. Sample Interpretation Problem Number One4.3.4. Sample Interpretation Problem Number Two; 4.3.5. A Summary of Interpretation Problems One and Two; 4.3.6. Examples of More Difficult Product Ion Spectra That Cannot Be Completely Interpreted; 4.3.7. Interpretation of Product Ion Spectra from Triply Charged Ions; 4.4. Summary; 4.5. References; Chapter 5. Basic Polyacrylamide Gel Electrophoresis; 5.1. Introduction; 5.2. The Principles of Gel Electrophoresis; 5.2.1. Protein Movement and Separation; 5.2.2. Protein Detection

5.3. The Basic Steps in a Polyacrylamide Gel Electrophoresis Experiment

Sommario/riassunto

How to design, execute, and interpret experiments for protein sequencing using mass spectrometry The rapid expansion of searchable protein and DNA databases in recent years has triggered an explosive growth in the application of mass spectrometry to protein sequencing. This timely and authoritative book provides professionals and scientists in biotechnology research with complete coverage of procedures for analyzing protein sequences by mass spectrometry, including step-by-step guidelines for sample preparation, analysis, and data interpretation. Michael Kinter and Nicholas Sherman
