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Nota di contenuto	PROTEOMICS OF BIOLOGICAL SYSTEMS: Protein Phosphorylation Using Mass Spectrometry Techniques; CONTENTS; PREFACE; ACKNOWLEDGMENTS; ABOUT THE AUTHOR; 1: Posttranslational Modification (PTM) of Proteins; 1.1 OVER 200 FORMS OF PTM OF PROTEINS; 1.2 THREE MAIN TYPES OF PTM STUDIED BY MS; 1.3 OVERVIEW OF NANO-ELECTROSPRAY/NANOFLOW LC-MS; 1.3.1 Definition and Description of MS; 1.3.2 Basic Design of Mass Analyzer Instrumentation; 1.3.3 ESI; 1.3.4 Nano-ESI; 1.4 OVERVIEW OF NUCLEIC ACIDS; 1.5 PROTEINS AND PROTEOMICS; 1.5.1 Introduction to Proteomics; 1.5.2 Protein Structure and Chemistry
	1.5.3 Bottom-Up Proteomics: MS of Peptides1.5.3.1 History and Strategy; 1.5.3.2 Protein Identification through Product Ion Spectra; 1.5.3.3 High-Energy Product Ions; 1.5.3.4 De Novo Sequencing; 1.5.3.5 Electron Capture Dissociation (ECD); 1.5.4 Top-Down Proteomics: MS of Intact Proteins; 1.5.4.1 Background; 1.5.4.2 GP Basicity and Protein

| Sommario/riassunto | Phosphorylation is the addition of a phosphate (PO4) group to a protein or other organic molecule. Phosphorylation activates or deactivates many protein enzymes, causing or preventing the mechanisms of diseases such as cancer and diabetes. This book shows how to use mass spectrometry to determine whether or not a protein has been correctly modified by the addition of a phosphate group. It also provides a combination of detailed, step-by-step methodology for phosphoproteomic sample preparation, mass spectral instrumental analysis, and data interpretation approaches. Furthermore, it i |