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Nota di contenuto	PROTEOMIC APPLICATIONS IN CANCER DETECTION AND DISCOVERY; CONTENTS; PREFACE; ACKNOWLEDGMENTS; 1 SYSTEMS BIOLOGY; 1.1 INTRODUCTION; 1.2 WHAT IS SYSTEMS BIOLOGY?; 1.3 WHAT SYSTEMS DO WE NEED TO STUDY?; 1.3.1 Genomics; 1.3.2 Transcriptomics; 1.3.3 Proteomics; 1.3.4 Metabolomics; 1.4 CANCER IS A SYSTEMS BIOLOGY DISEASE; 1.5 MODELING SYSTEMS BIOLOGY; 1.6 DATA INTEGRATION; 1.6.1 Integrating Transcriptomics and Proteomics; 1.7 CONCLUSIONS; REFERENCES; 2 MASS SPECTROMETRY INCANCER RESEARCH; 2.1 INTRODUCTION; 2.2 MASS SPECTROMETRY: THE TECHNOLOGY DRIVING CANCERPROTEIN BIOMARKER DISCOVERY 2.2.1 Ion Sources2.2.2 Electrospray Ionization; 2.2.3 Matrix-Assisted Laser Desorption/Ionization; 2.3 TYPES OF MASS SPECTROMETERS; 2.3.1 Ion-Trap Mass Spectrometer; 2.3.2 Fourier Transform Ion Cyclotron Resonance MS; 2.3.3 Orbitrap Mass Spectrometer; 2.3.4 TOF Mass Spectrometer; 2.3.5 Triple-Quadrupole Mass Spectrometer; 2.3.6 Triple-Quadrupole TOF Mass Spectrometer; 2.4 PROTEIN

FRACTIONATION; 2.4.1 Polyacrylamide Gel Electrophoresis; 2.4.2 Liquid Chromatography; 2.5 IMPACT OF MS IN CANCER; 2.5.1 Identification of a Drug Target; 2.6 CONCLUSIONS; REFERENCES; 3 QUANTITATIVE PROTEOMICS
3.1 INTRODUCTION3.2 WHAT IS BEING MEASURED IN QUANTITATIVE PROTEOMICS?; 3.3 TWO-DIMENSIONAL POLYACRYLAMIDE GEL ELECTROPHORESIS; 3.4 TWO-DIMENSIONAL DIFFERENCE GEL ELECTROPHORESIS; 3.5 SOLUTION-BASED QUANTITATIVE METHODS; 3.5.1 Stable Isotope Labeling; 3.5.2 Isotope-Coded Affinity Tags; 3.5.3 Isobaric Tag for Relative and Absolute Quantitation; 3.5.4 Stable Isotope Labeling of Amino Acids in Culture; 3.6 NONISOTOPIC SOLUTION-BASED QUANTITATION; 3.6.1 Subtractive Proteomics-Peptide Counting; 3.6.2 Subtractive Proteomics-Peak Intensity; 3.7 CONCLUSIONS; REFERENCES
4 PROTEOMIC ANALYSIS OF POSTTRANSLATIONAL MODIFICATIONS4.1 INTRODUCTION; 4.2 PHOSPHORYLATION; 4.2.1 Identification of Phosphorylated Proteins; 4.2.2 Phosphopeptide Mapping; 4.2.3 Collision-Induced Dissociation; 4.2.4 Electron Capture and Electron Transfer Dissociation; 4.2.5 Electron Transfer Dissociation; 4.2.6 Enrichment of Phosphopeptides; 4.2.7 Immunoaffinity Chromatography; 4.2.8 Immobilized Metal Affinity Chromatography; 4.2.9 Metal Oxide Affinity Chromatography; 4.3 GLYCOSYLATION; 4.3.1 Mass Spectrometry Characterization; 4.3.2 Electron Capture and Electron Transfer Dissociation
4.3.3 Targeted Identification of Glycoproteins4.3.4 Proteome-Wide Identification of Glycoproteins; 4.4 OTHER POSTTRANSLATIONAL MODIFICATIONS; 4.5 CONCLUSIONS; REFERENCES; 5 CHARACTERIZATION OF PROTEIN COMPLEXES; 5.1 INTRODUCTION; 5.2 METHODS FOR ISOLATING PROTEIN COMPLEXES; 5.2.1 Optimizing Protein Complex Isolation; 5.2.2 Importance of Optimizing Isolation Conditions; 5.2.3 Oligoprecipitation; 5.3 PROTEOME SCREENING USING TANDEM AFFINITY PURIFICATION; 5.4 YEAST TWO-HYBRID SCREENING; 5.5 QUICK LC-MS METHOD TO IDENTIFY SPECIFICALLY BOUND PROTEINS; 5.6 PROTEIN ARRAYS
5.7 FLUORESCENCE MICROSCOPY

Sommario/riassunto

"Bridging the knowledge gap between scientists that develop and apply proteomics technologies and oncologists who focus on understanding the biological basis behind cancer manifestation and progression, Proteomic Applications in Cancer Detection and Discovery provides an up-to-date account of how the multiple facets of proteomics have been applied to cancer. By balancing the treatment of technologies and applications, the book enables analytical scientists and oncologists, post-doctoral researchers, major research or medical centers, cancer researchers, pharmaceutical researchers, chemists, and biologists to better understand both"--