1. Record Nr. UNINA9910821926703321 Autore Veenstra Timothy Daniel <1966-> **Titolo** Proteomic applications in cancer detection and discovery / / Timothy D. Veenstra Hoboken, NJ,: John Wiley & Sons, Inc., c2013 Pubbl/distr/stampa **ISBN** 9781118634417 1118634411 9781118634493 1118634497 9781118634561 111863456X Edizione [1st ed.] Descrizione fisica 1 online resource (320 p.) Classificazione SCI029000 Disciplina 616.99/4042 Soggetti Biochemical markers Cancer - Genetic aspects **Proteomics** Lingua di pubblicazione Inglese **Formato** Materiale a stampa Livello bibliografico Monografia Note generali Includes index. 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

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"--

Protein Complex Isolation: 5.2.2 Importance of Optimizing Isolation

5.5 QUICK LC-MS METHOD TO IDENTIFY SPECIFICALLY BOUND

PROTEINS; 5.6 PROTEIN ARRAYS 5.7 FLUORESCENCE MICROSCOPY

Conditions; 5.2.3 Oligoprecipitation; 5.3 PROTEOME SCREENING USING TANDEM AFFINITY PURIFICATION; 5.4 YEAST TWO-HYBRID SCREENING;