

Mass Spectrometry In Cancer Research

Advancements of Mass Spectrometry in Biomedical Research
Cancer Research
Proteomic Applications in Cancer Detection and Discovery
Mass Spectrometry in Cancer Research
Cancer Systems Biology
Proteomic and Metabolomic Approaches to Biomarker Discovery
Genome and Proteome in Oncology
Handbook of Cancer Models with Applications
Issues in Chemistry and General Chemical Research: 2011 Edition
Advances in Cytochrome P-450 Enzyme System Research and Application: 2011 Edition
Lung Cancer: New Insights for the Healthcare Professional: 2011 Edition
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Advancements of Mass Spectrometry in Biomedical Research

Proteomics in Cancer Research covers both the basic principles of proteomics along with detailed presentations of new and emerging technology that represent promising breakthroughs in cancer prevention and treatment. The topics covered include: Basic concepts, including setting up a proteomics laboratory, mass spectrometry, protein separations, protein array technologies, and informatics tools Application of emerging technologies to proteomic analysis of cancer cells and tissues, including discussion of critical issues such as characteristics of cancer cell proteomes and protein-protein interactions Application of proteomics approaches in clinical cancer research and a forecast of future research and applications In most cases, applications of methods in basic and translational cancer research that are discussed in the text represent the first uses of these proteomics approaches to study any disease. Critical issues that readers in cancer research need to understand are covered in detail, including: Advantages and limitations of different technologies New approaches to the molecular classification of tumors Discovery of new biomarkers and imaging targets and development of new proteomic platforms for profiling and screening The unique proteomic features that characterize cancers offer new opportunities for disease prevention and treatment. Despite intense interest, however, proteomics is just beginning to become a part of the cancer research mainstream, as relatively few cancer researchers have training in proteomics methods and approaches. This book,

therefore, is both a timely and an essential guide that will help readers understand key concepts of proteomics and use its methods to search for ways to both cure and prevent cancer.

Cancer Research

Issues in Proteins and Peptides Research and Application: 2012 Edition is a ScholarlyEditions™ eBook that delivers timely, authoritative, and comprehensive information about Protein Science. The editors have built Issues in Proteins and Peptides Research and Application: 2012 Edition on the vast information databases of ScholarlyNews.™ You can expect the information about Protein Science in this eBook to be deeper than what you can access anywhere else, as well as consistently reliable, authoritative, informed, and relevant. The content of Issues in Proteins and Peptides Research and Application: 2012 Edition has been produced by the world's leading scientists, engineers, analysts, research institutions, and companies. All of the content is from peer-reviewed sources, and all of it is written, assembled, and edited by the editors at ScholarlyEditions™ and available exclusively from us. You now have a source you can cite with authority, confidence, and credibility. More information is available at <http://www.ScholarlyEditions.com/>.

Proteomic Applications in Cancer Detection and Discovery

This volume explores the use of mass spectrometry for biomedical applications. Chapters focus on specific therapeutic areas such as oncology, infectious disease and psychiatry. Additional chapters focus on methodology as well as new technologies and instrumentation. This volume provides readers with a comprehensive and informative manual that will allow them to appreciate mass spectrometry and proteomic research but also to initiate and improve their own work. Thus the book acts as a technical guide but also a conceptual guide to the newest information in this exciting field. Mass spectrometry is the central tool used in proteomic research today and is rapidly becoming indispensable to the biomedical scientist. With the completion of the human genome project and the genomic revolution, the proteomic revolution has followed closely behind. Understanding the human proteome has become critical to basic and clinical biomedical research and holds the promise of providing comprehensive understanding of human physiological processes. In addition, proteomics and mass spectrometry are bringing unprecedented biomarker discovery and are helping to personalize medicine.

Mass Spectrometry in Cancer Research

Cancer research is becoming multidisciplinary. The complex structural and therapeutic problems require synergistic approaches employing an assortment of biochemical manipulations, chromatographic or electrophoretic separations, sequencing strategies, and more and more mass spectrometry. Mass Spectrometry in Cancer Research provides a broad examination of current strategies and techniques and their application to the study of: (i) occupational and environmental carcinogens; (ii) antineoplastic and chemopreventive agents; (iii)

pertinent proteins, lipids, nucleic acids and glycoconjugates. Also included are a chapter on instrumentation and methodologies for biologists and physicians and a brief review of the relevant concepts of cancer biology and medicine for mass spectrometrists. This book is intended for: mass spectrometrists in research or those providing core services; researchers in biological, medical, pharmaceutical or environmental sciences; physicians in academic medicine; and academic/industrial research managers.

Cancer Systems Biology

Tandem Mass Spectrometry - Molecular Characterization presents a comprehensive coverage of theory, instrumentation and description of experimental strategies and MS/MS data interpretation for the structural characterization of relevant molecular compounds. The areas covered include the analysis of drugs, metabolites, carbohydrates and protein post-translational modifications. The book series in Tandem Mass Spectrometry serves multiple groups of audiences; professional (academic and industry), graduate students and general readers interested in the use of modern mass spectrometry in solving critical questions of chemical and biological sciences.

Proteomic and Metabolomic Approaches to Biomarker Discovery

Due to its enormous sensitivity and ease of use, mass spectrometry has grown into the analytical tool of choice in most industries and areas of research. This unique reference provides an extensive library of methods used in mass spectrometry, covering applications of mass spectrometry in fields as diverse as drug discovery, environmental science, forensic science, clinical analysis, polymers, oil composition, doping, cellular research, semiconductor, ceramics, metals and alloys, and homeland security. The book provides the reader with a protocol for the technique described (including sampling methods) and explains why to use a particular method and not others. Essential for MS specialists working in industrial, environmental, and clinical fields.

Genome and Proteome in Oncology

Recent advances in large scale DNA sequencing technology have made it possible to sequence the entire genome of an organism. Attention is now turning to the analysis of the product of the genome, the proteome, which is the set of proteins being expressed by a cell. Mass spectrometry is the method of choice for the rapid large-scale identification of these proteomes and their modifications. This is the first book to extensively cover the applications of mass spectrometry to proteome research.

Handbook of Cancer Models with Applications

Multivariate analysis is a mainstay of statistical tools in the analysis of biomedical data. It concerns with associating data matrices of n rows by p columns, with rows representing samples (or patients) and columns attributes of samples, to some

response variables, e.g., patients outcome. Classically, the sample size n is much larger than p , the number of variables. The properties of statistical models have been mostly discussed under the assumption of fixed p and infinite n . The advance of biological sciences and technologies has revolutionized the process of investigations of cancer. The biomedical data collection has become more automatic and more extensive. We are in the era of p as a large fraction of n , and even much larger than n . Take proteomics as an example. Although proteomic techniques have been researched and developed for many decades to identify proteins or peptides uniquely associated with a given disease state, until recently this has been mostly a laborious process, carried out one protein at a time. The advent of high throughput proteome-wide technologies such as liquid chromatography-tandem mass spectroscopy make it possible to generate proteomic signatures that facilitate rapid development of new strategies for proteomics-based detection of disease. This poses new challenges and calls for scalable solutions to the analysis of such high dimensional data. In this volume, we will present the systematic and analytical approaches and strategies from both biostatistics and bioinformatics to the analysis of correlated and high-dimensional data.

Issues in Chemistry and General Chemical Research: 2011 Edition

For many diseases, such as heart disease and cancer, early detection plays a pivotal role in the survival rate of the patient. When detected early, many such lethal diseases can be effectively treated with existing remedies. The difficulty remains, however, how to effectively detect such conditions at the earliest possible stage with a high enough positive predictive value so that they can be treated effectively without overwhelming the medical system with false positive diagnoses. What is required is the identification of more effective or additional biomarkers, as well as other types of technologies, that can aid in the diagnosis of early stage diseases. The challenge is how to identify more effective biomarkers or technologies that can provide an earlier indication of a disease with a higher positive predictive value than presently utilized methods. Proteomics, along with genomics and transcriptomics, has benefited greatly from the development of high-throughput methods to study thousands of proteins almost simultaneously. Based on the rate of interesting leads already being discovered using proteomics, it is likely that not only will biomarkers with better sensitivity and specificity be identified but individuals will be treated using customized therapies based on their specific protein profile. Since many of the proteomic technologies and data management tools are still in their infancy, the future of proteomics in disease diagnostics looks extremely promising.

Advances in Cytochrome P-450 Enzyme System Research and Application: 2011 Edition

This indispensable reference source contains the complete texts of the invited plenary and keynote lectures from the 13th International Mass Spectrometry Conference held in the autumn of 1994. It presents a comprehensive account of all methods and applications of mass spectrometry, covering the most important

developments that have occurred in all fields of this area within the past three years.

Lung Cancer: New Insights for the Healthcare Professional: 2011 Edition

This title is the collected abstracts from the 33rd annual meeting of the International Society for Oncodevelopmental Biology and Medicine.

Proteomics in Diagnostics

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Modern Molecular Biology:

The metabolomics approach, defined as the study of all endogenously-produced low-molecular-weight compounds, appeared as a promising strategy to define new cancer biomarkers. Information obtained from metabolomic data can help to highlight disrupted cellular pathways and, consequently, contribute to the development of new-targeted therapies and the optimization of therapeutics. Therefore, metabolomic research may be more clinically translatable than other omics approaches, since metabolites are closely related to the phenotype and the metabolome is sensitive to many factors. Metabolomics seems promising to identify key metabolic pathways characterizing features of pathological and physiological states. Thus, knowing that tumor metabolism markedly differs from the metabolism of normal cells, the use of metabolomics is ideally suited for biomarker research. Some works have already focused on the application of metabolomic approaches to different cancers, namely lung, breast and liver, using urine, exhaled breath and blood. In this Special Issue we contribute to a more complete understanding of cancer disease using metabolomics approaches.

Mass Spectrometry Handbook

Catechols: Advances in Research and Application: 2011 Edition is a ScholarlyPaper™ that delivers timely, authoritative, and intensively focused information about Catechols in a compact format. The editors have built Catechols:

Advances in Research and Application: 2011 Edition on the vast information databases of ScholarlyNews.™ You can expect the information about Catechols in this eBook to be deeper than what you can access anywhere else, as well as consistently reliable, authoritative, informed, and relevant. The content of Catechols: Advances in Research and Application: 2011 Edition has been produced by the world's leading scientists, engineers, analysts, research institutions, and companies. All of the content is from peer-reviewed sources, and all of it is written, assembled, and edited by the editors at ScholarlyEditions™ and available exclusively from us. You now have a source you can cite with authority, confidence, and credibility. More information is available at <http://www.ScholarlyEditions.com/>.

Advances in Mass Spectrometry

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Advances in Cancer Research

Applications of Mass Spectrometry Imaging to Cancer, the latest volume in the Advances in Cancer Research provides invaluable information on the exciting and fast-moving field of cancer research. This volume presents original reviews on applications of mass spectrometry imaging to cancer. Provides information on cancer research Offers outstanding and original reviews on a range of cancer research topics Serves as an indispensable reference for researchers and students alike

Unravelling Cancer Signaling Pathways: A Multidisciplinary Approach

This volume explores the use of mass spectrometry for biomedical applications. Chapters focus on specific therapeutic areas such as oncology, infectious disease and psychiatry. Additional chapters focus on methodology as well as new technologies and instrumentation. This volume provides readers with a comprehensive and informative manual that will allow them to appreciate mass spectrometry and proteomic research but also to initiate and improve their own

work. Thus the book acts as a technical guide but also a conceptual guide to the newest information in this exciting field. Mass spectrometry is the central tool used in proteomic research today and is rapidly becoming indispensable to the biomedical scientist. With the completion of the human genome project and the genomic revolution, the proteomic revolution has followed closely behind. Understanding the human proteome has become critical to basic and clinical biomedical research and holds the promise of providing comprehensive understanding of human physiological processes. In addition, proteomics and mass spectrometry are bringing unprecedented biomarker discovery and are helping to personalize medicine.

Plasma Source Mass Spectrometry

Mass spectrometry is fast becoming an indispensable field for medical professionals. The mass spectrometric analysis of metabolites and proteins promises to revolutionize medical research and clinical diagnostics. As this technology rapidly enters the medical field, practicing professionals and students need to prepare to take full advantage of its capabilities. Medical Applications of Mass Spectrometry addresses the key issues in the medical applications of mass spectrometry at the level appropriate for the intended readership. It will go a long way to help the utilization of mass spectrometry in medicine. The book comprises five parts. A general overview is followed by a description of the basic sampling and separation methods in analytical chemistry. In the second part a solid foundation in mass spectrometry and modern techniques of data analysis is presented. The third part explains how mass spectrometry is used in exploring various classes of biomolecules, including proteins and lipids. In the fourth section mass spectrometry is introduced as a diagnostic tool in clinical treatment, infectious pathogen research, neonatal diagnostics, cancer, brain and allergy research, as well as in various fields of medicine: cardiology, pulmonology, neurology, psychiatric diseases, hemato-oncology, urologic diseases, gastrointestinal diseases, gynecology and pediatrics. The fifth part covers emerging applications in biomarker discovery and in mass spectrometric imaging.

- * Provides a broad look at how the medical field is benefiting from advances in mass spectrometry.
- * Guides the reader from basic principles and methods to cutting edge applications.
- * There is NO comparable book on the market to fill this fast growing field.

Applications of Mass Spectrometry Imaging to Cancer

Helps researchers in proteomics and oncology work together to understand, prevent, and cure cancer. Proteomic data is increasingly important to understanding the origin and progression of cancer; however, most oncologic researchers who depend on proteomics for their studies do not collect the data themselves. As a result, there is a knowledge gap between scientists, who devise proteomic techniques and collect the data, and the oncologic researchers, who are expected to interpret and apply proteomic data. Bridging the gap between proteomics and oncology research, this book explains how proteomic technology can be used to address some of the most important questions in cancer research. Proteomic Applications in Cancer Detection and Discovery enables readers to understand how proteomic data is acquired and analyzed and how it is interpreted.

Author Timothy Veenstra has filled the book with examples—many based on his own firsthand research experience—that clearly demonstrate the application of proteomic technology in oncology research, including the discovery of novel biomarkers for different types of cancers. The book begins with a brief introduction to systems biology, explaining why cancer is a systems biology disease. Next, it covers such topics as: Mass spectrometry in cancer research Application of proteomics to global phosphorylation analysis Search for biomarkers in biofluids Rise and fall of proteomic patterns for cancer diagnostics Emergence of protein arrays Role of proteomics in personalized medicine The final chapter is dedicated to the future prospects of proteomics in cancer research. By guiding readers through the latest proteomic technologies and their applications in cancer research, *Proteomic Applications in Cancer Detection and Discovery* enhances the ability of researchers in proteomics and researchers in oncology to collaborate in order to better understand cancer and develop strategies to prevent and treat it.

Proteomic Applications in Cancer Detection and Discovery

With usage of mass spectrometry continually expanding, an increasing number of scientists, technicians, students, and physicians are coming into contact with this valuable technique. Mass spectrometry has many uses, both qualitative and quantitative, from analyzing simple gases to environmental contaminants, pharmaceuticals, and complex biopolymers

Advancements of Mass Spectrometry in Biomedical Research

This issue of *Clinics in Laboratory Medicine*, Guest Edited by Nigel Clarke, MD, and Andrew Hoofnagle, MD, will focus on Mass Spectrometry, with topics including: Proteins; Peptides; Small Molecules: Toxicology; Small Molecules: Diagnostics; and Regulatory Considerations.

Medical Applications of Mass Spectrometry

Cancer Metabolomics 2018

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Mass Spectrometry, An Issue of Clinics in Laboratory Medicine - E-Book

Proteomic and Metabolomic Approaches to Biomarker Discovery, Second Edition covers techniques from both proteomics and metabolomics and includes all steps involved in biomarker discovery, from study design to study execution. The book describes methods and presents a standard operating procedure for sample selection, preparation and storage, as well as data analysis and modeling. This new standard effectively eliminates the differing methodologies used in studies and creates a unified approach. Readers will learn the advantages and disadvantages of the various techniques discussed, as well as potential difficulties inherent to all steps in the biomarker discovery process. This second edition has been fully updated and revised to address recent advances in MS and NMR instrumentation, high-field NMR, proteomics and metabolomics for biomarker validation, clinical assays of biomarkers and clinical MS and NMR, identifying microRNAs and autoantibodies as biomarkers, MRM-MS assay development, top-down MS, glycosylation-based serum biomarkers, cell surface proteins in biomarker discovery, lipidomics for cancer biomarker discovery, and strategies to design studies to identify predictive biomarkers in cancer research. Addresses the full range of proteomic and metabolomic methods and technologies used for biomarker discovery and validation Covers all steps involved in biomarker discovery, from study design to study execution Serves as a vital resource for biochemists, biologists, analytical chemists, bioanalytical chemists, clinical and medical technicians, researchers in pharmaceuticals and graduate students

Proteome Research: Mass Spectrometry

Genomics research has made significant advances in recent years. In this book, a team of internationally-renowned researchers share the most up-to-date information in a field that has in recent years switched emphasis from gene identification to functional genomics and the characterization of genes and gene products. This volume approaches this complex subject with a broad perspective to supply the reader with a vital overview of genomics and its derivative fields, with a focus on pivotal issues such as data analysis. Expansive and current, this book is a comprehensive research guide that describes both the key new techniques and more established methods. Every chapter discusses the merits and limitations of the various approaches and then provides selected tried-and-tested protocols, as well as a plethora of good practical advice for immediate use at the bench. Key features: Provides a broad introduction to current practices and techniques for lab-based research in genomics Explains clearly and precisely how to carry out selected techniques in addition to background information on the various approaches Chapters are written by a leading international authorities in the field and cover both well-known and new, tried and tested, methods for working in genomics Includes troubleshooting guide and reviews of alternative techniques An essential laboratory manual for students and researchers at all levels

Applications of Mass Spectrometry Imaging to Cancer

Unravelling the intricate cell signalling networks and their significance in cancer

poses major intellectual challenge. Keeping this in mind, the book aims at understanding the mechanism of action of different proteins and their complexes in the cancer signalling pathways. Hence, the proposed book that comprises 20 chapters provides a comprehensive introduction on cell signalling, its alterations in cancer, molecules that have been popular targets as well as the ones that are emerging as targets. In addition, it discusses different forms of therapy that are coming up for its treatment. Other than that, a major portion of the book is focused on studying different disciplines at the interface of biology and other areas of science that are being used to understand cancer biology in depth.

Cancer Biomarkers

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Mass Spectrometry for the Novice

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Tumor Biology

The nature of cancer disease, its probable causes, and the molecular and cellular mechanisms through which malignant tumours develop, have only recently begun to be understood in any appreciable detail. Cancer is fundamentally a disease of the genome, arising from dynamic changes occurring within DNA during the lifetime of the cell e.g. deletions, amplifications, point mutations, translocations that can occur in any cell and that may interact in a variety of cellular pathways. The imbalance in the interplay between genetic and environmental factors can initiate malignancy. The determination of the human genome sequence is acclaimed as one of the great achievements made possible by the rapid progress in the available molecular biology tools achieved during the last few years. The sequence of the human genome promises to unveil invaluable information useful for the development of novel approaches in the diagnosis and treatment of cancer disease. This book includes part of the work of international experts on the most up-to-date developments of various aspects of research on genome and proteome in oncology. the number of genes but in how gene parts are used to build different products in a process of the mRNA transcript called alternative splicing.

Cirrhosis of the Liver: New Insights for the Healthcare Professional: 2011 Edition

This book comprises protocols describing systems biology methodologies and computational tools, offering a variety of ways to analyze different types of high-throughput cancer data. Chapters give an overview over data types available in large-scale data repositories and state-of-the-art methods used in the field of cancer systems biology. Written in the highly successful Methods in Molecular Biology series format, chapters include introductions to their respective topics, lists of the necessary materials and reagents, step-by-step, readily reproducible laboratory protocols, and tips on troubleshooting and avoiding known pitfalls. Authoritative and practical, *Cancer Systems Biology : Methods and Protocols* aims to ensure successful results in the further study of this vital field. The chapters "Identifying Genetic Dependencies in Cancer by Analyzing siRNA Screens in Tumor Cell Line Panels", "Perseus: A Bioinformatics Platform for Integrative Analysis of Proteomics Data in Cancer Research" and "Phosphoproteomics-based Profiling of Kinase Activities in Cancer Cells" are available open access under a CC BY 4.0 license via link.springer.com.

Research Awards Index

Tools, techniques, and progress in cancer biomarkers discovery The completion of a number of gene sequencing projects, recent advances in genomic and proteomic technologies, and the availability of powerful bioinformatics tools have led to promising new avenues and approaches in the search for cancer biomarkers. This book provides a comprehensive overview of current methodologies and technologies. It discusses biomarker discovery as a whole, rather than focusing on one specific marker or cancer. With information on both existing and potential biomarkers, *Cancer Biomarkers: Analytical Techniques for Discovery*: * Provides insights into the current technological platforms for biomarker discovery, including mass spectrometry combined with multidimensional chromatography, DIGE, and various chip technologies * Includes a detailed discussion of protein networks and protein phosphorylation in cancer * Details the use of imaging mass spectrometry, laser capture microdissection, serial analysis of gene expression, enzyme-linked immunosorbent assays, protein microarrays, antibody-based microarrays, and bioinformatics * Covers the emerging role of surface-enhanced laser desorption ionization (SELDI) and various tagging and labeling strategies * Discusses related regulatory and ethical issues With a wealth of information that can be applied to a broad spectrum of biomarker research projects, this is a core reference for biomarker researchers, scientists working in proteomics and bioinformatics, pharmaceutical scientists, oncologists, biochemists, biologists, and chemists.

High-Dimensional Data Analysis in Cancer Research

Written by an experienced and well-published individual, this unique reference source takes a forward-looking approach. It describes the concepts and practice of protein phosphorylation analysis by tandem mass spectrometry and related techniques. These include purification, enrichment, database searching, other software tools, synthesis, phosphatase treatment, phospho-specific staining methods, isoelectric focusing and element mass spectrometry. The book then goes on to cover the fragmentation behaviour of phosphopeptides in tandem MS (pos+neg ions) and the implementation of the particular features into an analytical strategy. The book ends with a summary and discussion of useful internet and

software tools currently available.

Protein Phosphorylation Analysis by Electrospray Mass Spectrometry

Composed of contributions from an international team of leading researchers, this book pulls together the most recent research results in the field of cancer modeling to provide readers with the most advanced mathematical models of cancer and their applications. Topics included in the book cover oncogenetic trees, stochastic multistage models of carcinogenesis, effects of ionizing radiation on cell cycle and genomic instability, induction of DNA damage by ionizing radiation and its repair, epigenetic cancer models, bystander effects of radiation, multiple pathway models of human colon cancer, and stochastic models of metastasis. The book also provides some important applications of cancer models to the assessment of cancer risk associated with various hazardous environmental agents, to cancer screening by MRI, and to drug resistance in cancer chemotherapy. An updated statistical design and analysis of xenograft experiments as well as a statistical analysis of cancer occult clinical data are also provided. The book will serve as a useful source of reference for researchers in biomathematics, biostatistics and bioinformatics; for clinical investigators and medical doctors employing quantitative methods to develop procedures for cancer diagnosis, prevention, control and treatment; and for graduate students.

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Proteomics in Cancer Research

This book provides a snapshot of the current state-of-the-art of the understanding of the fundamentals of ICPMS, instrumental development, methods development, spectral interpretation and applications. It covers a diverse range of topics including: bioanalytical applications (immunoassay, state of phosphorylation, metallo-drugs); environmental applications (drinking water, groundwater, seawater, speciation); reaction cells and collision cells (theory and applications);

archaeology; laser ablation; isotope ratio analysis; and the performance, characterization and applications of multicollector instruments. Written by international contributors who emphasize their current perceptions and understanding of the subject, *Plasma Source Mass Spectrometry: Applications and Emerging Technologies* offers a current perspective on elemental analysis by plasma source mass spectrometry that is not to be found elsewhere. Researchers and professionals in many areas will welcome this book, particularly those in the fields of bioanalytical, environmental and geological chemistry.

Tandem Mass Spectrometry

Advances in Cancer Research provides invaluable information on the exciting and fast-moving field of cancer research. Here, once again, outstanding and original reviews are presented on a variety of topics

Genomics

Molecular biology has rapidly advanced since the discovery of the basic flow of information in life, from DNA to RNA to proteins. While there are several important and interesting exceptions to this general flow of information, the importance of these biological macromolecules in dictating the phenotypic nature of living creatures in health and disease is paramount. In the last one and a half decades, and particularly after the completion of the Human Genome Project, there has been an explosion of technologies that allow the broad characterization of these macromolecules in physiology, and the perturbations to these macromolecules that occur in diseases such as cancer. In this volume, we will explore the modern approaches used to characterize these macromolecules in an unbiased, systematic way. Such technologies are rapidly advancing our knowledge of the coordinated and complicated changes that occur during carcinogenesis, and are providing vital information that, when correctly interpreted by biostatistical/bioinformatics analyses, can be exploited for the prevention, diagnosis, and treatment of human cancers. The purpose of this volume is to provide an overview of modern molecular biological approaches to unbiased discovery in cancer research. *Advances in molecular biology* allowing unbiased analysis of changes in cancer initiation and progression will be overviewed. These include the strategies employed in modern genomics, gene expression analysis, and proteomics.

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