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*Facilitating the innovation,
development, and application
of new spectroscopic methods*

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***in proteomics, Spectral
Techniques in Proteomics
provides a broad overview of
the spectroscopic toolbox that
can be used, either with
proteome or sub-proteome
mixtures or with***

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***individual/purified proteins
studied in parallel. It gives a
modest overview of
It has been known for over 150
years that hallmarks of
inflammation can be observed
in the wall of atherosclerotic***

vessels. It was, however, not clear if this inflammation is the cause or the consequence of atherogenesis. More recently, it has become evident that inflammation mediated both by innate and adaptive immunity

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is instrumental even in the earliest stages of the development of atherosclerotic lesions, i.e., that it plays an important pathogenetic role. In this volume, international experts

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***in the field discuss the
pathogenetic, diagnostic,
preventive and possible
therapeutic relevance of
inflammation in atherogenesis.
This book is intended for
researchers and physicians in***

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***the fields of vascular biology,
immunology and
atherosclerosis.***

***Precision medicine is a
disruptive innovation with a
fast-evolving pace in the
healthcare ecosystem.***

Precision medicine enables precise diagnosis and targeted treatment by considering individual variability in the abnormalities of causative genes and molecular drivers behind biochemical

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mechanisms. A vast amount of data created by advanced omics technologies is a foundation of precision medicine's success, and the implications of the findings from these technologies can

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***potentially improve clinical
outcomes. Recent Advances
in Molecular and Translational
Medicine: Updates in
Precision Medicine presents
essential information of
molecular and translational***

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***research in precision
medicine, with a specific focus
on pediatrics. This book
provides an accessible
introduction to omics
technologies, gives a detailed
explanation of bioinformatics***

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workflows to interpret high-throughput omics profiles for molecular diagnosis, and collects some of the cutting-edge research for precise therapeutics. Contributions to the book have been provided

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by experts in biomedical engineering and clinical practice, thus, bringing an informed perspective to the reader on each topic. The book is a valuable resource for postgraduate students,

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***researchers, data scientists
and clinicians interested in
precision medicine, as well as
researchers in the field of
genetics and pediatrics who
are interested in
understanding the role of***

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***precision medicine in clinical
practice.***

***Due to its enormous
sensitivity and ease of use,
mass spectrometry has grown
into the analytical tool of
choice in most industries and***

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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,

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***environmental science,
forensic science, clinical
analysis, polymers, oil
composition, doping, cellular
research, semiconductor,
ceramics, metals and alloys,
and homeland security. The***

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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

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**Spectral
industrial, environmental, and
clinical fields.**

**Recent Advances in Molecular
and Translational Medicine:
Updates in Precision Medicine
Advancements of Mass
Spectrometry in Biomedical**

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Research

Inflammation and

Atherosclerosis

Handbook of Schizophrenia

Spectrum Disorders, Volume I

Proteomics for Biological

Discovery

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***Integration of Omics
Approaches and Systems
Biology for Clinical
Applications***

**Proteomics, like other post-
genomics tools, has been
growing at a rapid pace and has**

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important applications in numerous fields of science. While its use in animal and veterinary sciences is still limited, there have been considerable advances in this field in recent years, in areas as

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diverse as physiology, nutrition and food of animal origin processing. This is mainly as a consequence of a wider availability and better understanding of proteomics methodologies by animal and

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veterinary researchers. This book provides a comprehensive, state-of-the-art account of the status of farm-animal proteomics research, focusing on the principles behind proteomics methodologies and

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**its specific applications and
offering clear example.**

**Introduces readers to the state
of the art of omics platforms and
all aspects of omics approaches
for clinical applications This
book presents different high**

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throughput omics platforms used to analyze tissue, plasma, and urine. The reader is introduced to state of the art analytical approaches (sample preparation and instrumentation) related to proteomics,

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**peptidomics, transcriptomics,
and metabolomics. In addition,
the book highlights innovative
approaches using
bioinformatics, urine miRNAs,
and MALDI tissue imaging in the
context of clinical applications.**

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Particular emphasis is put on integration of data generated from these different platforms in order to uncover the molecular landscape of diseases. The relevance of each approach to the clinical setting is explained

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and future applications for patient monitoring or treatment are discussed. Integration of omics Approaches and Systems Biology for Clinical Applications presents an overview of state of the art omics techniques. These

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methods are employed in order to obtain the comprehensive molecular profile of biological specimens. In addition, computational tools are used for organizing and integrating these multi-source data towards

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developing molecular models that reflect the pathophysiology of diseases. Investigation of chronic kidney disease (CKD) and bladder cancer are used as test cases. These represent multi-factorial, highly

heterogeneous diseases, and are among the most significant health issues in developed countries with a rapidly aging population. The book presents novel insights on CKD and bladder cancer obtained by

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omics data integration as an example of the application of systems biology in the clinical setting. Describes a range of state of the art omics analytical platforms Covers all aspects of the systems biology

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**approach—from sample
preparation to data integration
and bioinformatics analysis
Contains specific examples of
omics methods applied in the
investigation of human diseases
(Chronic Kidney Disease,**

Bladder Cancer) Integration of omics Approaches and Systems Biology for Clinical Applications will appeal to a wide spectrum of scientists including biologists, biotechnologists, biochemists, biophysicists, and

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**bioinformaticians working on the
different molecular platforms. It
is also an excellent text for
students interested in these
fields.**

**Proteomic Profiling and
Analytical Chemistry: The**

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Crossroads, Second Edition
helps scientists without a strong
background in analytical
chemistry to understand
principles of the multistep
proteomic experiment necessary
for its successful completion. It

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also helps researchers who do have an analytical chemistry background to break into the proteomics field. Highlighting points of junction between proteomics and analytical chemistry, this resource links

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**experimental design with
analytical measurements, data
analysis, and quality control.
This targeted point of view will
help both biologists and
chemists to better understand all
components of a complex**

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proteomic study. The book provides detailed coverage of experimental aspects such as sample preparation, protein extraction and precipitation, gel electrophoresis, microarrays, dynamics of fluorescent dyes,

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and more. The key feature of this book is a direct link between multistep proteomic strategy and quality control routinely applied in analytical chemistry. This second edition features a new chapter on SWATH-MS,

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substantial updates to all chapters, including proteomic database search and analytical quantification, expanded discussion of post-hoc statistical tests, and additional content on validation in

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**proteomics. Covers the
analytical consequences of
protein and peptide
modifications that may have a
profound effect on how and what
researchers actually measure
Includes practical examples**

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**illustrating the importance of
problems in quantitation and
validation of biomarkers Helps in
designing and executing
proteomic experiments with
sound analytics
The book “Advances in**

Biotechnology” is about recent advances in some of the important fields that are ongoing in certain biotechnological applications. Biotechnology has been quite helpful in keeping pace with the demands of every

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**increasing human population
and in improving the quality of
human life. Major
biotechnological achievements
associated with human welfare
have been from the fields like
genetic engineering; transgenic**

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plants and animals; genomics, proteomics, monoclonal antibodies for the diagnosis of disease, gene therapy etc. Fourteen authoritative chapters written by experts having experience in academics and

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research on current developments and future trends in biotechnology have been empathized. The book provides a detailed account of various methodologies used in biotechnology i.e. High capacity

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**vectors, DNA sequencing
dealing with next generation
sequencing, Molecular markers,
DNA microarray technology, as
well as Proteomics that have
revolutionized biotechnology
with a wide array of applications.**

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The book not only presents a well-founded explanation of the topics but also aims to present up-to-date reviews of current research efforts, some thoughtful discussions on the potential benefits and risks

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**involved in producing
biotechnological products and
the challenges of bringing such
products to market. It will prove
to be an excellent reference
work for both academicians and
researchers, indicating new**

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starting points to young researchers for new projects in the field. The book is intended for biotechnologist, biologist, researchers, teachers and students of Biosciences and Biotechnology.

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**Molecular Parasitology
Seed Development: OMICS
Technologies toward
Improvement of Seed Quality
and Crop Yield
Quantitative Methods in
Proteomics**

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Vol. 1

**Computational and Statistical
Methods for Protein
Quantification by Mass
Spectrometry
Functional Genomics
Perspectives, Volume 1**

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Stomata, the tiny pores on leaf surface, are the gateways for CO₂ uptake during photosynthesis as well as water loss in transpiration. Further, plants use stomatal closure as a defensive response, often

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triggered by elicitors, to prevent the entry of pathogens. The guard cells are popular model systems to study the signalling mechanism in plant cells. The messengers that mediate closure upon perception of

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elicitors or microbe associated molecular patterns (MAMPs) are quite similar to those during ABA effects. These components include reactive oxygen species (ROS), nitric oxide (NO), cytosolic pH and intracellular

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Ca²⁺. The main components are ROS, NO and cytosolic free Ca²⁺. The list extends to others, such as G-proteins, protein phosphatases, protein kinases, phospholipids and ion channels. The sequence of these signalling

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components and their interaction during stomatal signalling are complex and quite interesting. The present e-Book provides a set of authoritative articles from ' Special Research Topic ' on

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selected areas of stomatal guard cells. In the first set of two articles, an overview of ABA and MAMPs as signals is presented. The next set of 4 articles, emphasize the role of ROS, NO, Ca²⁺ as well as pH, as secondary

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messengers. The next group of 3 articles highlight the recent advances on post-translational modification of guard cell proteins, with emphasis on 14-3-3 proteins and MAPK cascades. The last article

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described the method to isolate epidermis of grass species and monitor stomatal responses to different signals. Our e-Book is a valuable and excellent source of information for all those interested in guard cell function

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as well as signal transduction in
plant cells.

Written as an advanced text for
toxicology students, this book is
much more than an
introduction and provides in-
depth information describing

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the underlying mechanisms through which toxicants produce their adverse responses. • Links traditional toxicology to modern molecular techniques, important for teaching to graduate courses

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and professional studies • Uses a didactic approach with basic biological or theoretical background for the methodology presented • Brings together and comprehensively covers a range

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of dynamic aspects in
biochemical and molecular
toxicology • Guides student
and professional toxicologists in
comprehending a broad range
of issues, compiled and
authored by a diverse group of

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experts • “ A good
introductory textbook covering
the biochemical toxicology of
organic substances and the
relevant methodology in some
detail.... It offers good value for
money and can be

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recommended as a textbook for
appropriate courses ” – BTS
Newsletter review of the 4th
edition

Precision Molecular Pathology
of Prostate Cancer Springer
Structural genomics is the

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systematic determination of 3-D
structures of proteins
representative of the range of
protein structure and function
found in nature. The goal is to
build a body of structural
information that will predict the

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structure and potential function for almost any protein from knowledge of its coding sequence. This is essential information for understanding the functioning of the human proteome, the ensemble of tens

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of thousands of proteins specified by the human genome. While most structural biologists pursue structures of individual proteins or protein groups, specialists in structural genomics pursue structures of

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proteins on a genome wide scale. This implies large-scale cloning, expression and purification. One main advantage of this approach is economy of scale. Examines the three dimensional structure of

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all proteins of a given organism,
by experimental methods such
as X-ray crystallography and
NMR spectroscopy Looks at
structural genomics as a
foundation of drug discovery as
discovering new medicines is

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becoming more challenging and
the pharmaceutical industry is
looking to new technologies to
help in this mission

Computational Medicine
Translational Biomedical
Informatics

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Mammalian Toxicology

Evolving Applications

Advances in Proinsulin Research
and Application: 2013 Edition

Experimental Strategies

***The discovery that
nitrogen monoxide or***

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nitric oxide (NO) is a biologically produced free radical has revolutionized our thinking about physiological and pathological processes. This discovery has ignited

enormous interest in the scientific community. When generated at low levels, NO is a signaling molecule, but at high concentration, NO is a cytotoxic molecule. The

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*physiological and
pathological processes of
NO production and
metabolism and its
targets, currently areas
of intensive research,
have important*

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***pharmacologic implications
for health and disease.
This book will cover
several topics to
elaborate how proteomics
may enhance agricultural
productivity. These***

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include crop and food proteomics, farm animal proteomics, aquaculture, microorganisms and insect proteomics. It will also cover several technical advances, which may

***address the current need
for comprehensive proteome
analysis. An emerging field
of the proteomics aim is
to integrate knowledge
from basic sciences and to
translate it into***

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***agricultural applications
to solve issues related to
economic values of farm
animals, crops, food
security, health, and
energy sustainability.
Given the wealth of***

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information generated and to some extent applied in agriculture, there is the need for more efficient and broader channels to freely disseminate the information to the

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***scientific community.
Abiotic stresses such as
high temperature, low-
temperature, drought, and
salinity limit crop
productivity worldwide.
Understanding plant***

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responses to these stresses is essential for rational engineering of crop plants. In Arabidopsis, the signal transduction pathways for abiotic stresses, light,

several phytohormones and pathogenesis have been elucidated. A significant portion of plant genomes (most studies are Arabidopsis and rice genome) encodes for

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***proteins involves in
signaling such as
receptor, sensors,
kinases, phosphatases,
transcription factors and
transporters/channels.
Despite decades of***

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***physiological and
molecular effort,
knowledge pertaining to
how plants sense and
transduce low and high
temperature, low-water
availability (drought),***

water-submergence and salinity signals is still a major question before plant biologists. One major constraint hampering our understanding of these signal transduction

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processes in plants has been the lack or slow pace of application of molecular genomic and genetics knowledge in the form of gene function. In the post-genomic era, one

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***of the major challenges is
investigation and
understanding of multiple
genes and gene families
regulating a particular
physiological and
developmental aspect of***

plant life cycle. One of the important physiological processes is regulation of stress response, which leads to adaptation or adjustment in response to adverse

stimuli. With the holistic understanding of the signaling pathways involving not only one gene family but multiple genes or gene families, plant biologists can lay a

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*foundation for designing
and generating future
crops that can withstand
the higher degree of
environmental stresses
(especially abiotic
stresses, which are the*

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***major cause of crop loss
throughout the world)
without losing crop yield
and productivity.
Proteomics was thought to
be a natural extension
after the field of***

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genomics has deposited significant amount of data. However, simply taking a straight verbatim approach to catalog all proteins in all tissues of different organisms is not

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viable. Researchers may need to focus on the perspectives of proteomics that are essential to the functional outcome of the cells. In Integrative Proteomics, expert

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***researchers contribute
both historical
perspectives, new
developments in sample
preparation, gel-based and
non-gel-based protein
separation and***

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identification using mass spectrometry. Substantial chapters are describing studies of the sub-proteomes such as phosphoproteome or glycoproteomes which are

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*directly related to
functional outcomes of the
cells. Structural
proteomics related to
pharmaceutics development
is also a perspective of
the essence.*

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***Bioinformatics tools that
can mine proteomics data
and lead to pathway
analyses become an
integral part of
proteomics. Integrative
proteomics covers both***

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***look-backs and look-outs
of proteomics. It is an
ideal reference for
students, new researchers,
and experienced scientists
who want to get an
overview or insights into***

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*new development of the
proteomics field.*

*Signal Transduction in
Stomatal Guard Cells*

Theory and Protocols

*Proteomic Profiling and
Analytical Chemistry*

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***Mass Spectrometry in
Chemical Biology
Molecular and Biochemical
Toxicology
Proteomics in Domestic
Animals: from Farm to
Systems Biology***

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This volume focuses on our current understanding of the molecular underpinnings of prostate cancer and their potential application for precision medicine approaches. The emergence and applications of new

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technologies has allowed for a rapid expansion of our understanding of the molecular basis of prostate cancer and has revealed a remarkable genetic heterogeneity that may underlie the clinically

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variable behavior of the disease. The book consists of five sections which provide insight about the following: (1) General principles; (2) Molecular signatures of primary prostate cancer; (3)

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*Molecular signatures of
advanced prostate cancer;
(4) Key molecular pathways
in prostate cancer
development and progression;
(5) and Precision medicine
approach: Diagnosis,
treatment, prognosis.*

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*Precision Molecular
Pathology of Prostate Cancer
is an important resource for
the practicing oncologist,
urologist, and pathologist,
and will also be useful for
researchers in the prostate
cancer community.*

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*Introduction; Introduction
to mass spectrometry
instrumentation and methods
used in chemical biology;
Metabolomics; Proteomics;
Mass spectrometry to
discover natural products;
Applications of mass*

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*spectrometry in synthetic
biology; Studying enzyme
mechanisms using mass
spectrometry: Introduction;
Studying enzyme mechanisms
using mass spectrometry:
Applications; Databases;
Future perspectives;*

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Photosystem II is a 700-kDa membrane-protein super-complex responsible for the light-driven splitting of water in oxygenic photosynthesis. The photosystem is comprised of two 350-kDa complexes each

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made of 20 different polypeptides and over 80 co-factors. While there have been major advances in understanding the mature structure of this photosystem many key protein factors involved in the

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assembly of the complex do not appear in the holoenzyme. The mechanism for assembling this super-complex is a very active area of research with newly discovered assembly factors and subcomplexes requiring

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characterization.

*Additionally the ability to
split water is inseparable
from light-induced
photodamage that arises from
radicals and reactive O₂
species generated by
Photosystem II chemistry.*

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Consequently, to sustain water splitting, a “self repair” cycle has evolved whereby damaged protein is removed and replaced so as to extend the working life of the complex.

Understanding how the

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biogenesis and repair processes are coordinated is among several important questions that remain to be answered. Other questions include: how and when are the inorganic cofactors inserted during the assembly

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and repair processes and how are the subcomplexes protected from photodamage during assembly? Evidence has also been obtained for Photosystem II biogenesis centers in cyanobacteria but do these also exist in

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plants? Do the molecular mechanisms associated with Photosystem II assembly shed fresh light on the assembly of other major energy-transducing complexes such as Photosystem I or the cytochrome b6/f complex or

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indeed other respiratory complexes? The contributions to this Frontiers in Plant Science Research Topic are likely to reveal new details applicable to the assembly of a range of membrane-protein complexes, including

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aspects of self-assembly and solar energy conversion that may be applied to artificial photosynthetic systems. In addition, a deeper understanding of Photosystem II assembly – particularly in response to changing

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*environmental conditions –
will provide new knowledge
underpinning photosynthetic
yields which may contribute
to improved food production
and long-term food security.
Proteomic and Metabolomic
Approaches to Biomarker*

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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

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*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*

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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

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*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,*

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*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*

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*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*

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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

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*biochemists, biologists,
analytical chemists,
bioanalytical chemists,
clinical and medical
technicians, researchers in
pharmaceuticals and graduate
students*

Handbook of Pharmacogenomics

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and Stratified Medicine

Nitric Oxide, Part F

Integrative Proteomics

Oxidative Stress and Oxygen

Radicals

Protein and Peptide Analysis

by LC-MS

Handbook of Research on

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Computational Grid

Technologies for Life

Sciences, Biomedicine, and

Healthcare

Epigenetic modifications
underlie all aspects of
human physiology, including

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stem cell renewal, formation of cell types and tissues. They also underlie environmental impacts on human health, including aging and diseases like cancer. Consequently, cracking the epigenetic

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"code" is considered a key challenge in biomedical research. Chromatin structure and function are modified by protein complexes, causing genes to be turned "on" or "off" and controlling other aspects of

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DNA function. Yet while there has been explosive growth in the epigenetics field, human chromatin-modifying machines have only recently started to be characterized. To meet this challenge, our book explores

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complementary experimental tracks, pursued by expert international research groups, aimed at the physical and functional characterization of the diverse repertoire of chromatin protein machines -

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namely, the "readers,
writers and erasers" of
epigenomic marks. These
studies include the
identification of RNA
molecules and drugs that
interact selectively with
components of the chromatin

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machinery. What makes this book distinctive is its emphasis on the systematic exploration of chromatin protein complexes in the context of human development and disease networks.

"This book provides

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methodologies and
developments of grid
technologies applied in
different fields of life
sciences"--Provided by
publisher.

Written by recognized
experts in the study of

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proteins, Proteomics for Biological Discovery begins by discussing the emergence of proteomics from genome sequencing projects and a summary of potential answers to be gained from proteome-level research. The tools of

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proteomics, from conventional to novel techniques, are then dealt with in terms of underlying concepts, limitations and future directions. An invaluable source of information, this title also

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provides a thorough overview of the current developments in post-translational modification studies, structural proteomics, biochemical proteomics, microfabrication, applied proteomics, and

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bioinformatics relevant to proteomics. Presents a comprehensive and coherent review of the major issues faced in terms of technology development, bioinformatics, strategic approaches, and applications Chapters offer

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a rigorous overview with
summary of limitations,
emerging approaches,
questions, and realistic
future industry and basic
science applications
Discusses higher level
integrative aspects,

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including technical
challenges and applications
for drug discovery
Accessible to the novice
while providing experienced
investigators essential
information Proteomics for
Biological Discovery is an

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essential resource for
students, postdoctoral
fellows, and researchers
across all fields of
biomedical research,
including biochemistry,
protein chemistry, molecular
genetics, cell/developmental

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biology, and bioinformatics.
The first book to offer a
blueprint for overcoming the
challenges to successfully
quantifying biomarkers in
living organisms The demand
among scientists and
clinicians for targeted

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quantitation experiments has experienced explosive growth in recent years. While there are a few books dedicated to bioanalysis and biomarkers in general, until now there were none devoted exclusively to addressing

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critical issues surrounding this area of intense research. Targeted Biomarker Quantitation by LC-MS provides a detailed blueprint for quantifying biomarkers in biological systems. It uses numerous

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real-world cases to exemplify key concepts, all of which were carefully selected and presented so as to allow the concepts they embody to be easily expanded to future applications, including new biomarker

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development. Targeted Biomarker Quantitation by LC-MS primarily focuses on the assay establishment for biomarker quantitation—a critical issue rarely treated in depth. It offers comprehensive coverage of

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three core areas of
biomarker assay
establishment: the
relationship between the
measured biomarkers and
their intended usage;
contemporary regulatory
requirements for biomarker

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assays (a thorough understanding of which is essential for producing a successful and defensible submission); and the technical challenges of analyzing biomarkers produced inside a living

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organism or cell. Covers the theory of and applications for state-of-the-art mass spectrometry and chromatography and their applications in biomarker analysis Features real-life examples illustrating the

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challenges involved in
targeted biomarker
quantitation and the
innovative approaches which
have been used to overcome
those challenges Addresses
potential obstacles to
obtain effective biomarker

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level and data

interpretation, such as
specificity establishment
and sample collection

Outlines a tiered approach
and fit-for-purpose assay
protocol for targeted
biomarker quantitation

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Highlights the current state of the biomarker regulatory environment and protocol standards Targeted Biomarker Quantitation by LC-MS is a valuable resource for bioanalytical scientists, drug metabolism and

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pharmacokinetics scientists,
clinical scientists,
analytical chemists, and
others for whom biomarker
quantitation is an important
tool of the trade. It also
functions as an excellent
text for graduate courses in

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pharmaceutical,
biochemistry, and chemistry.

Tools and Challenges

Elucidation of Abiotic

Stress Signaling in Plants

Crops, Horticulture, Farm

Animals, Food, Insect and

Microorganisms

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Methods and Protocols

Precision Molecular

Pathology of Prostate Cancer

Advances in Protein

Chemistry and Structural

Biology

In the past years, genome
projects for numerous human

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parasites have been completed and now allow first in depth comparisons and evolutionary conclusions. The genomes of parasites reflect the coevolution with their host, metabolic capacities

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depending on their
respective habitat in the
host. Gut parasites usually
have an anaerobic
metabolism, while blood
parasites have an aerobic
metabolism, intracellular
parasites escape the immune

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system, while extracellular parasites evade the immune system, usually by antigenic variation. Comprehensive genome data now being available allow us to address profound scientific questions, such as which

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traits enable the parasite to survive in the human host, which to cause disease and which can be used as drug targets. This book intends to give an overview of the state of knowledge on “the molecules” of protozoan

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parasites - on their
genomes, proteomes, glycomes
and lipidomes.

Computational methodologies
and modeling play a growing
role for investigating
mechanisms, and for the
diagnosis and therapy of

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human diseases. This progress gave rise to computational medicine, an interdisciplinary field at the interface of computer science and medicine. The main focus of computational medicine lies in the

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development of data analysis methods and mathematical modeling as well as computational simulation techniques specifically addressing medical problems. In this book, we present a number of computational

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medicine topics at several scales: from molecules to cells, organs, and organisms. At the molecular level, tools for the analysis of genome variations as well as cloud computing resources for

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medical genetics are reviewed. Then, an analysis of gene expression data and the application to the characterization of microbial communities are highlighted. At the protein level, two types of analyses

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for mass spectrometry data are reviewed: labeled quantitative proteomics and lipidomics, followed by protein sequence analysis and a 3D structure and drug design chapter. Finally, three chapters on clinical

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applications focus on the integration of biomolecular and clinical data for cancer research, biomarker discovery, and network-based methods for computational diagnostics.

"Reviews in Pharmaceutical

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and Biomedical Analysis
contains coverage and review
of new trends and
applications in all areas of
pharmaceutical, biomedical
and analytical chemistry.
Authors have contributed
review articles according to

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their expertise on var"

The book is about the seed development in the model and crop plants. Seed development is a key step of the plant life cycle that determines the nutrient value of seeds - the life

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for human civilization,
growth, and development. The
nutrient value of seeds is
mainly due to storage
reserve products such as
carbohydrates, lipids
(triacylglycerols), and
proteins. The book primarily

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focuses on application of the 21st century high-throughput technologies transcriptomics, proteomics, metabolomics, and systems biology in near complete understanding of the various processes involved in seed

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development in different crop plants. The book reveals how such technologies have revolutionized our understanding of the multilayer processes and regulations involved therein

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by generating large-scale datasets. Accumulated datasets provide basic knowledge to develop integrated strategies to eventually improve the nutritional value of plant seed and crop yield, a

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critical goal in food security issues around the globe.

Proteomic and Metabolomic Approaches to Biomarker Discovery

Systems Analysis of Chromatin-Related Protein

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Complexes in Cancer

A Precision Medicine

Perspective

Advances in Biotechnology

Targeted Biomarker

Quantitation by LC-MS

Assembly of the Photosystem

II Membrane-Protein Complex

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of Oxygenic Photosynthesis
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which thousands of proteins can be
simultaneously identified,
quantified and characterized in a

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high throughput manner. Beginning with the history of proteomics centered on the vital role of mass spectrometry in its development, this detailed volume continues with chapters on sample pre-fractionation, in vivo and in vitro stable isotope labeling, label-free

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date guide for researchers seeking to understand the proteome of any given species.

The definitive introduction to data analysis in quantitative proteomics

This book provides all the necessary knowledge about mass spectrometry based

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proteomics methods and computational and statistical approaches to pursue the planning, design and analysis of quantitative proteomics experiments. The author's carefully constructed approach allows readers to easily make the transition into the field of

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quantitative proteomics.

Through detailed descriptions of wet-lab methods, computational approaches and statistical tools, this book covers the full scope of a quantitative experiment, allowing readers to acquire new knowledge as well as acting as a

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useful reference work for more advanced readers. Computational and Statistical Methods for Protein Quantification by Mass Spectrometry: Introduces the use of mass spectrometry in protein quantification and how the bioinformatics challenges in this

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field can be solved using statistical methods and various software programs. Is illustrated by a large number of figures and examples as well as numerous exercises. Provides both clear and rigorous descriptions of methods and approaches. Is thoroughly

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various methods and approaches, this book is accessible to biologists, informaticians, and statisticians alike and is aimed at readers across the academics spectrum, from advanced undergraduate students to post doctorates entering the field.

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Mammalian Toxicology surveys chemical agents and examines how such chemicals impact on human health, emphasizing the importance in minimizing environmental exposure to chemical and physical hazards in our homes, communities and workplaces through such media

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as contaminated water, soil and air. Starting with the basic principles on a wide range of toxicagents, this textbook describes how they enter the body, theirmechanisms of action once inside, and strategies for diagnosis,prevention and

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treatment. Topics covered include:
General principles of toxicology:
pharmacological and toxicological
principles underpinning the study
of toxicology, risk assessments
and mechanisms of cell death
Disposition: routes of chemical
exposures, entry into the body and

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various tissues, storage, metabolic biotransformation and elimination, with examples from various toxicants. Toxic agents: the occurrences, disposition in the body, health effects, toxic mechanisms, antidotes and treatments of a range of agents

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including pesticides, metals, solvents, gases, nanomaterials, food components and additives, pharmaceuticals, drugs of abuse, natural toxins, endocrine disruptors, radiation, and warfare weapons. Toxic effects: including neurotoxicity,

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developmental toxicity,
immunotoxicity, teratogenicity,
male and female reproductive
toxicity, mutagenicity,
carcinogenicity, pulmonary
toxicity, cardiovascular toxicity,
hepatotoxicity, gastrointestinal
toxicity and cardiovascular toxicity

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Toxicology and society:
epidemiological studies of chemical-
induced diseases in human
populations, and a vision
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Mammalian Toxicology is an
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toxicology, biochemistry, biology,

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medicine and chemistry. It is also appropriate for professional toxicologists in research or regulatory affairs, and anyone who needs to understand the adverse effects of toxic agents on the human body.

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This book was written for graduate and medical students, as well as clinicians and postdoctoral researchers. It describes the theory of alternative pre-mRNA splicing in twelve introductory chapters and

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then introduces protocols and their theoretical background relevant for experimental research. These 43 practical chapters cover: Basic methods, Detection of splicing events, Analysis of alternative pre-mRNA splicing in vitro and in vivo,

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*Manipulation of splicing events, and
Bioinformatic analysis of alternative
splicing. A theoretical introduction
and practical guide for molecular
biologists, geneticists, clinicians and
every researcher interested in
alternative splicing. Website:*

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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

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*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*

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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

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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.

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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

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*spectrometry are bringing
unprecedented biomarker discovery
and are helping to personalize
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*This book is the first example in
presenting LC-MS strategies for the
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with detailed information and hints about the needs and problems described from experts on-the-job. The best advantage is -for sure- the practical insight of experienced analysts into their novel protein analysis techniques. Readers

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Special Issue "Oxidative Stress and Oxygen Radicals" that was published in Biomolecules

This book introduces readers to essential methods and applications in translational biomedical informatics, which include biomedical big data,

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cloud computing and algorithms for understanding omics data, imaging data, electronic health records and public health data. The storage, retrieval, mining and knowledge discovery of biomedical big data will be among the key challenges for

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future translational research. The paradigm for precision medicine and healthcare needs to integratively analyze not only the data at the same level – e.g. different omics data at the molecular level – but also data from different levels – the molecular,

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cellular, tissue, clinical and public health level. This book discusses the following major aspects: the structure of cross-level data; clinical patient information and its shareability; and standardization and privacy. It offers a valuable guide for all biologists,

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biomedical informaticians and clinicians with an interest in Precision Medicine Informatics.

A few disorders have some of the same symptoms as schizophrenia including schizoaffective disorders, schizophreniform disorder,

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schizotypal and schizoid personality disorders, delusional disorder, and autism (schizophrenia spectrum disorders). Since the 2000 there has been significant progress in our understanding of the early presentations, assessment, suspected

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neuropathology, and treatment of these disorders. Recent technological breakthroughs in basic sciences hold promise for advancing our understanding of the pathophysiology of schizophrenia spectrum disorders. This collective monograph reviews

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recent researches regarding the origins, onset, course, and outcome of schizophrenia spectrum disorders. In particular, this book will be illustrate new developments in terms of conceptual models, and research methodology, genetics and genomics,

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brain imaging and neurochemical studies, neurophysiology and information processing in schizophrenia spectrum disorders patients. Also will be highlighted new developments in our understanding of the childhood psychosis, prodromal

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and first-episode states, in treatment and rehabilitation. Thus, the purpose of this book is to provide up-to-date overview of the rapid advances made in the clinical and basic science studies supporting our understanding of the relationship between cerebral

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processes and clinical, cognitive and other presentations of the schizophrenia spectrum disorders. In addition, this book aims to monitor important research developments, which may be relevant to treatment, and rehabilitation of patients.

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Handbook of Pharmacogenomics and Stratified Medicine is a comprehensive resource to understand this rapidly advancing field aiming to deliver the right drug at the right dose to the right patient at the right time. It is designed to provide a detailed, but

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accessible review of the entire field from basic principles to applications in various diseases. The chapters are written by international experts to allow readers from a wide variety of backgrounds, clinical and non-clinical (basic geneticists,

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pharmacologists, clinicians, trialists, industry personnel, ethicists) to understand the principles underpinning the progress in this area, the successes, failures and the challenges ahead. To be accessible to the widest range of readers, the

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clinical application section introduces the disease process, existing therapies, followed by pharmacogenomics and stratified medicine details. Medicine is the cornerstone of modern therapeutics prescribed on the basis that its benefit should outweigh its

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risk. It is well known that people respond differently to medications and in many cases the risk-benefit ratio for a particular drug may be a gray area. The last decade has seen a revolution in genomics both in terms of technological innovation and

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discovering genetic markers associated with disease. In parallel there has been steady progress in trying to make medicines safer and tailored to the individual. This has occurred across the whole spectrum of medicine, some more than others. In

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In addition there is burgeoning interest from the pharmaceutical industry to leverage pharmacogenomics for more effective and efficient clinical drug development. Provides clinical and non-clinical researchers with practical information normally

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beyond their usual areas of research or expertise Includes an basic principles section explaining concepts of basic genetics, genetic epidemiology, bioinformatics, pharmacokinetics and pharmacodynamics Covers newer

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technologies– next generation sequencing, proteomics, metabolomics Provides information on animal models, lymphoblastoid cell lines, stem cells Provides detailed chapters on a wide range of disease conditions, implementation and regulatory issues

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Includes chapters on the global
implications of pharmacogenomics