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XG46EU - ERICKSON MORENO

This book will provide the most recent knowledge and advances in Sample Preparation Techniques for Separation Science. Everyone working in a laboratory must be familiar with the basis of these technologies, and they often involve elaborate and time-consuming procedures that can take up to 80% of the total analysis time. Sample preparation is an essential step in most of the analytical methods for environmental and biomedical analysis, since the target analytes are often not detected in their in-situ forms, or the results are distorted by interfering species. In the past decade, modern sample preparation techniques have aimed to comply with green analytical chemistry principles, leading to simplification, miniaturization, easy manipulation of the analytical devices, low costs, strong reduction or absence of toxic organic solvents, as well as low sample volume requirements. Modern Sample Preparation Approaches for Separation Science also provides an invaluable reference tool for analytical chemists in the chemical, biological, pharmaceutical, environmental, and forensic sciences.

Geneticists and molecular biologists have been interested in quantifying genes and their products for many years and for various reasons (Bishop, 1974). Early molecular methods were based on molecular hybridization, and were devised shortly after Marmur and Doty (1961) first showed that denaturation of the double helix could be reversed - that the process of molecular reassociation was exquisitely sequence dependent. Gillespie and Spiegelman (1965) developed a way of using the method to titrate the number of copies of a probe within a target sequence in which the target sequence was fixed to a membrane support prior to hybridization with the probe - typically a RNA. Thus, this was a precursor to many of the methods still in use, and indeed under development, today. Early examples of the application of these methods included the measurement of the copy numbers in gene families such as the ribosomal genes and the immunoglo bulin family. Amplification of genes in tumors and in response to drug treatment was discovered by this method. In the same period, methods were invented for estimating gene num bers based on the kinetics of the reassociation process - the so-called Cot analysis. This method, which exploits the dependence of the rate of reassociation on the concentration of the two strands, revealed the presence of repeated sequences in the DNA of higher eukaryotes (Britten and Kohne, 1968). An adaptation to RNA, Rot analysis (Melli and Bishop, 1969), was used to measure the abundance of RNAs in a mixed population.

This eBook is a collection of articles from a Frontiers Research Topic. Frontiers Research Topics are very popular trademarks of the Frontiers Journals Series: they are collections of at least ten articles, all centered on a particular subject. With their unique mix of varied contributions from Original Research to Review Articles, Frontiers Research Topics unify the most influential researchers, the latest key findings and historical advances in a hot research area! Find out more on how to host your own Frontiers Research Topic or contribute to one as an author by contacting the Frontiers Editorial Office: frontiersin.org/about/contact.

This book is devoted to the fascinating superfamily of plant ATP-binding cassette (ABC) transporters and their variety of transported substrates. It highlights their exciting biological functions, covering aspects ranging from cellular detoxification, through development, to symbiosis and defense. Moreover, it also includes a number of chapters that center on ABC transporters from non-Arabidopsis species. ABC proteins are ubiquitous, membrane-intrinsic transporters that catalyze the primary (ATP-dependent) movement of their substrates through biological membranes. Initially identified as an essential aspect of a vacuolar detoxification process, genetic work in the last decade has revealed an unexpectedly diverse variety of ABC transporter substrates, which include not only xenobiotic conjugates, but also heavy metals, lipids, terpenoids, lignols, alkaloids and organic acids. The discovery that members of the ABCB and ABCG family are involved in the movement of phytohormones has further sparked their exploration and provided a new understanding of the whole family. Accordingly, the trafficking, regulation and structure-function of ABCB-type auxin transporters are especially emphasized in this book.

During spontaneous food/beverage fermentations, the microbiota associated with the raw material has a considerable importance: this microbial consortium evolves in reason of the nutrient content and of the physical, chemical, and biological determinants present in the food matrix, shaping fermentation dynamics with significant impacts on the ‘qualities’ of final productions. The selection from the indigenous micro-biodiversity of ‘virtuous’ ecotypes that coupled pro-technological and biotechnological aptitudes provide the basis for the formulation of ‘tailored’ starter cultures. In the fermenting food and beverage arena, the wine sector is generally characterized by the generation of a high added value. Together with a pronounced seasonality, this feature strongly contributes to the selection of a large group of starter cultures. In the last years, several studies contributed to describe the complexity of grapevine-associated microbiota using both culture-dependent and culture-independent approaches. The grape-associated microbial communities continuously change during the wine-making process, with different dominances that correspond to the main biotechnological steps that take place in wine. In order to simplify, following a time trend, four major dominances can be mainly considered: non-Saccharomyces, Saccharomyces, lactic acid bacteria (LAB), and spoi-

lage microbes. The first two dominances come in succession during the alcoholic fermentation: the impact of Saccharomyces (that are responsible of key enological step of ethanol production) can be complemented/integrated by the contributions of compatible non-Saccharomyces strains. Lactic acid bacteria constitute the malolactic consortium responsible of malolactic fermentation, a microbial bioconversion often desired in wine (especially in red wine production). Finally, the fourth dominance, the undesired microbiota, represents a panel of microorganisms that, coupling spoilage potential to the resistance to the harsh conditions typical of wine environment, can cause important economic losses. In each of these four dominances a complex microbial biodiversity has been described. The studies on the enological significance of the micro-biodiversity connected with each of the four dominances highlighted the presence of a dichotomy: in each consortia there are species/strains that, in reason of their metabolisms, are able to improve wine 'qualities' (resource of interest in starter cultures design), and species/strains that with their metabolism are responsible of depreciation of wine. Articles describing new oenological impacts of yeasts and bacteria belonging to the four main categories above mentioned (non-Saccharomyces, Saccharomycetes, lactic acid bacteria, and spoilage microbes) are welcome. Moreover, in this Research Topic, we encourage mini-review submissions on topics of immediate interest in wine microbiology that link microbial biodiversity with positive/negative effects in wine.

Advances in Sustainable Viticulture and Winemaking Microbiology is an international scientific research eBook on the context of sustainable viticulture and winemaking development from the microbiological point of view. The Editors welcome the lectors to read multidisciplinary articles that bridge viticulture and winemaking with microbial ecology, environmental and social sciences. Manuscripts focus on novel findings underlining those relationships. The journal 'Frontiers in Microbiology' published original research articles that demonstrate a clear scientific breakthrough versus current knowledge. This eBook covers application fields such as sustainable viticulture, sustainable winemaking, the climatic global change, the preservation of natural resources and health, agriculture and biodiversity, ecological, economical and social impacts of beverages and food quality and security management and the geographical distribution of yeast and bacteria populations related to winemaking issues of agricultural changes. 'If wine was perfect, there would be no need for microorganisms for a sustainable viticulture and winemaking' - Gustavo Cordero-Bueso

This book provides a wide spectrum of methods to study RNA chaperones in vitro, at the single molecule level, and protocols useful for cell-based assays. Beginning with a section on a number of bacterial proteins for study, the volume also explores proteins from eukaryotic cells and how to delve into the complex interactions between RNA chaperones and the folding and unfolding of proteins. Written for the highly successful Methods in Molecular Biology series, 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, RNA Chaperones: Methods and Protocols serves as an ideal guide for scientists and students interested in RNA biology and RNA chaperones. Chapter 3 is available Open Access under a Creative Commons Attribution 4.0 International License via link.springer.com.

Microbial transmission, the processes by which microbes transit to new environments, is a significant and broad-reaching concept with applications throughout the biological sciences. This collection of reviews, edited by an international team of experts studying and working across a range of disciplines, explores transmission not just as an idea in disease but as a fundamental biological process that acts in all domains of nature and exerts its force on disparate size scales, from the micro to the macro, and across units of time as divergent as a single bacterial replication cycle and the entire course of evolution. In five sections, this overview Defines the concept of transmission and covers basic processes of transmission, including causality, control strategies, fitness costs, virulence, and selection Presents numerous combinations of transmission scenarios across the bacterial, animal, and human interface Examines transmission as the defining characteristic of infectious disease Presents methods for experimentally verifying and quantifying transmission episodes Concludes with important theoretical and modeling approaches Anyone studying or working in microbial colonization, evolution, pathogenicity, antimicrobial resistance, or public health will benefit from a deeper understanding of Microbial Transmission.

From an evolutionary perspective, our species has relied upon physical activity for most of its history to survive and has had to escape from predators, to scavenge for food, and to use physique to work or build necessary means for everyday life. Physical activity has been part of our evolution and progress since the very beginning and, consequently, our entire body has been programmed to be active physically. In the last 20 years, scientific research has increasingly shown that our ancient survival principle has beneficial effects not only on the cells and organs involved in physical activities but on the metabolism of the entire organism, influencing the homeostasis and integration of all bodily functions, likely stimulating the production of hormones and other regulatory molecules, with each affecting vital signalling pathways. Most of the web of factors involved in molecular signalling upon exercise are suspected to be centrally controlled by the brain, which has been reported to be deeply modified by physical activity. Such complexity requires a multifaceted approach to shed light on the molecular interactions that occur between physical activity and its outcome at a cellular level.

Genetics and Improvement of Barley Malt Quality presents up-to-date developments in barley production and breeding. The book is divided into nine chapters, including barley production and consumption, germplasm and utilization, chemical composition, protein and protein components, carbohydrates and sugars, starch degrading enzymes, endosperm cell walls and malting quality, genomics and malting quality improvement, and marker-assisted selection for malting quality. The information will be especially useful to barley breeders, malsters, brewers, biochemists, barley quality specialists, molecular geneticists, and biotechnologists. This book may also serve as reference text for post-graduate students and barley researchers. The authors for each chapter are the experts and frontier researchers in the specific areas. Professor Guoping Zhang is a barley breeder and crop physiologist in Department of Agronomy, Zhejiang University of China. Dr. Chengdao Li is a senior molecular geneticist and barley breeder in Department of Agriculture & Food, Western Australia. He is also an adjunct professor in Murdoch University of Australia and Zhejiang University of China.

This book is a printed edition of the Special Issue "Antioxidants in Health and Disease" that was published in Nutrients

This book thoroughly reviews our current scientific understanding of the significant role that mobile genetic elements play in the evolution and function of genomes and organisms–from plants and ani-

mals to humans. Highly-regarded geneticist Haig Kazazian offers an accessible intellectual history of the field’s research strategies and concerns, explaining how advances opened up new questions, and how new tools and capabilities have encouraged progress in the field. Kazazian introduces the key strategies and approaches taken in leading laboratories (including his own) to gain greater insight into the large proportion of our genome that derives from mobile genetic elements, including viruses, plasmids, and transposons. He also presents intriguing insights into long-term research strategies that may lead to an even deeper understanding.

This book provides a comprehensive but concise overview on the economically important emerging cattle pox virus derived Lumpy Skin Disease, including the characteristics of causative agent, description of clinical signs in cattle, pathology and histopathology, immunity, geographical distribution, epidemiology and transmission pathways, control and eradication of the disease. In addition the recent developments in vaccination, mathematical modeling and risk assessment are discussed. Lumpy Skin Disease currently spreads aggressively across the Middle and Near East. The first incursion to the European Union territory occurred in Greece in autumn 2015. The book targets clinicians and field veterinarians in Lumpy Skin Disease affected regions, veterinary authorities as well as advanced students in veterinary medicine and virology.

Until the mid 1980s, the detection and quantification of a specific mRNA was a difficult task, usually only undertaken by a skilled molecular biologist. With the advent of PCR, it became possible to amplify specific mRNA, after first converting the mRNA to cDNA via reverse transcriptase. The arrival of this technique—termed reverse transcription-PCR (RT-PCR)—meant that mRNA suddenly became amenable to rapid and sensitive analysis, without the need for advanced training in molecular biology. This new accessibility of mRNA, which has been facilitated by the rapid accumulation of sequence data for human mRNAs, means that every biomedical researcher can now include measurement of specific mRNA expression as a routine component of his/her research plans. In view of the ubiquity of the use of standard RT-PCR, the main objective of RT-PCR Protocols is essentially to provide novel, useful applications of RT-PCR. These include some useful adaptations and applications that could be relevant to the wider research community who are already familiar with the basic RT-PCR protocol. For example, a variety of different adaptations are described that have been employed to obtain quantitative data from RT-PCR. Quantitative RT-PCR provides the ability to accurately measure changes/imb- ances in specific mRNA expression between normal and diseased tissues.

The examination of the human fallopian tubes was, until recently, restricted to observations on gross anatomical disposition and tubal patency. These studies, for decades, were the domain of doctors and physiologists whose primary interest was population control and family planning, funded largely by organisations and agencies seek ing alternatives to steroidal contraceptives. For a "worrying" but short period after the birth of Louise Brown in 1978 as the conse quence of successful in-vitro fertilisation and embryo transfer, the fallopian tube was considered to be "dispensable" given that the metabolic milieu in which human fertilisation takes place could be effortlessly reproduced in a Petri dish, in in-vitro fertilisation procedures. However, a number of factors have acted together to renew in terest in the fallopian tube, namely new techniques in cell biology, microinstrument developments (in particular in imaging), an inter disciplinary transfer of skills from interventional radiology and car diology to gynaecology, the surgeon's wish to improve surgical tech niques, and better techniques to monitor early pregnancy. These factors have led surgeons to develop the new diagnostic and ther apeutic strategies and techniques listed here. This volume contains contributions from the majority of keynote speakers at a conference held in London in April 1992 from which its title is derived. Better diagnostic procedures should lead to the implementation of rational effective treatments.

Antioxidant use in health promotion and disease prevention either through dietary intake or supplementation is controversial. This book reviews the latest evidence-based research in the area, principally through prospective cohort studies and randomized controlled trials. It assesses major dietary antioxidants and discusses their use in diseases such as cancer, diabetes, stroke, coronary heart disease, HIV/AIDS, and neurodegenerative and immune diseases. The use of antioxidants in health is also discussed along with common adverse effects associated with antioxidant use.

Microfluidic Devices for Biomedical Applications, Second Edition provides updated coverage on the fundamentals of microfluidics, while also exploring a wide range of medical applications. Chapters review materials and methods, microfluidic actuation mechanisms, recent research on droplet microfluidics, applications in drug discovery and controlled-delivery, including micro needles, consider applications of microfluidic devices in cellular analysis and manipulation, tissue engineering and their role in developing tissue scaffolds, and cover the applications of microfluidic devices in diagnostic sensing, including genetic analysis, low-cost bioassays, viral detection, and radio chemical synthesis. This book is an essential reference for medical device manufacturers, scientists and researchers concerned with microfluidics in the field of biomedical applications and life-science industries. Discusses the fundamentals of microfluidics or lab-on-a-chip (LOC) and explores a wide range of medical applications Considers materials and methods for microfabrication, microfluidic actuation mechanisms and digital microfluidic technologies Details applications of microfluidic devices in cellular analysis and manipulation, tissue engineering and its role in developing tissue scaffolds, and stem cell engineering

PCR has been successfully utilized in every facet of basic, cli- cal, and applied studies of the life sciences, and the impact that PCR has had on life science research is already staggering. C- comitant with the essentially universal use of PCR has been the creative and explosive development of a wide range of PCR-based techniques and applications. These increasingly numerous pro- cols have each had the general effect of facilitating and acceler- ing research. Because PCR technology is relatively easy and inexpensive, PCR applications are well within the reach of every research lab. In this sense, PCR has become the "equalizer" between "small" and "big" labs, since its use makes certain projects, especially those related to molecular cloning, now far more feasible for the small lab with a modest budget. This new volume on PCR Protocols does not attempt the impossible task of representing all PCR-based protocols. Rather, it presents a range of protocols, both analytical and preparative, that provide a solid base of knowledge on the use of PCR in many c- mon research problems. The first six chapters provide some basic information on how to get started. Chapters 7-19 represent primarily analytical uses of PCR, both for simple DNA and RNA detection, as well as for more complex analyses of nucleic acid (e. g. , DNA footprin ting, RNA splice site localization). The remaining chapters represent "synthetic," or preparative, uses of PCR.

High-throughput sequencing technologies are widely used to study microbial ecology across species

and habitats in order to understand the impacts of microbial communities on host health, metabolism, and the environment. Due to the dynamic nature of microbial communities, longitudinal microbiome analyses play an essential role in these types of investigations. Key questions in microbiome studies aim at identifying specific microbial taxa, enterotypes, genes, or metabolites associated with specific outcomes, as well as potential factors that influence microbial communities. However, the characteristics of microbiome data, such as sparsity and skewedness, combined with the nature of data collection, reflected often as uneven sampling or missing data, make commonly employed statistical approaches to handle repeated measures in longitudinal studies inadequate. Therefore, many researchers have begun to investigate methods that could improve incorporating these features when studying clinical, host, metabolic, or environmental associations with longitudinal microbiome data. In addition to the inferential aspect, it is also becoming apparent that visualization of high dimensional data in a way which is both intelligible and comprehensive is another difficult challenge that microbiome researchers face. Visualization is crucial in both the analysis and understanding of metagenomic data. Researchers must create clear graphic representations that give biological insight without being overly complicated. Thus, this Research Topic seeks to both review and provide novels approaches that are being developed to integrate microbiome data and complex metadata into meaningful mathematical, statistical and computational models. We believe this topic is fundamental to understanding the importance of microbial communities and provides a useful reference for other investigators approaching the field.

During the last two decades, our view of the role of reactive oxygen species (ROS) in inflammatory processes has changed dramatically. ROS that are constantly produced at lower levels by living cells metabolizing oxygen contribute to normal cellular function and tissue homeostasis. ROS are produced at higher levels in inflammation and regulate the inflammatory response in specific ways. The role of ROS in inflammation is complex and primarily determined by their relative amount, chemical properties, reactivity, subcellular localization and molecular environment, specificity for their biological targets, and availability and mechanisms of antioxidant defense systems. This eBook comprises twelve reviews and original articles that provide new findings on the role of ROS in the regulation of inflammatory processes, highlight emerging topics in redox signaling, describe new ROS detection techniques and discuss alternative therapeutic strategies to treat inflammatory disorders. The editorial that precedes the published articles briefly summarizes the main findings of each research paper. We hope that this collection of research articles contribute to a better understanding of ROS in inflammation.

This detailed volume provides a comprehensive collection of protocols for epigenomic research, powering our ability to analyze epigenetic modifications across the entire genome. Beginning with methods used to investigate epigenomic modifications such as DNA methylation, histone modifications, and chromatin structure, the book continues with methods for manipulating the epigenome, including platforms for epigenome editing, inducible systems for epigenome editing, and epigenetically modified animals. Written for the highly successful Methods in Molecular Biology series, chapters feature introductions to their respective topics, lists of the necessary materials and reagents, step-by-step and readily reproducible laboratory protocols, and tips on troubleshooting and avoiding known pitfalls. Authoritative and practical, Epigenomics: Methods and Protocols serves as an ideal resource for researchers looking to further expand the utility and scope of epigenomics research.

This volume provides experimental and bioinformatics approaches related to different aspects of gene expression analysis. Divided in three sections chapters detail wet-lab protocols, bioinformatics approaches, single-cell gene expression, highly multiplexed amplicon sequencing, multi-omics techniques, and targeted sequencing. 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 cutting-edge, Gene Expression Analysis: Methods and Protocols aims provide useful information to researchers worldwide.

The "Stress and Immunity" Research Topic includes two distant and seemingly unrelated forms of stress: physicochemical stress and psychological stress. In both forms of stress the body adapts to the changes in the environment. The different chapters of this eBook deal with aspects relevant for the fascinating interplay of various distinct stressors with the immune system.