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In response to environmental stresses, or during development, plant cells will produce lipids that will act as intracellular or intercellular mediators. Glycerophospholipid and/or sphingolipid second messengers resulting from the action of lipid metabolizing enzymes (e.g. lipid-kinases or lipases) are commonly found within cells. The importance of such mediating lipids in plants has become increasingly apparent. Responses to biotic and abiotic stresses, and to plant hormones, all appear to involve and require lipid signals. Likewise, developmental processes, in particular polarized growth, seem also to involve signalling lipids. Amongst these lipids, phosphatidic acid (PA) has received the most attention. It can be produced by phospholipases D, but also by diacylglycerol kinases coupled to phospholipases C. Proteins that bind phosphatidic acid, and for which the activity is altered upon binding, have been identified. Furthermore, other lipids are also important in signalling processes. PA can be phosphorylated into diacylglycerol-pyrophosphate, and plants are one of the first biological models where the production of this lipid has been reported, and its implication in signal transduction have been demonstrated. PA can also be deacylated into lyso- phosphatidic acid. The phosphorylated phosphatidylinositols, i.e. the phosphoinositides, can act as substrate of phospholipases C, but are also mediating lipids per se, since proteins that bind them have been identified. Other important lipid mediators belong to the sphingolipid family such the phosphorylated phytosphingosine, or long-chain bases. Many questions remain unanswered concerning lipid signalling in plants. Understanding and discussing current knowledge on these mechanisms will provide insights into plant mechanisms in response to constraints, either developmental or environmental.

Gas chromatography continues to be one of the most widely used analytical techniques, since its applications today expand into fields such as biomarker research or metabolomics. This new practical textbook enables

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the reader to make full use of gas chromatography. Essential fundamentals and their implications for the practical work at the instrument are provided, as well as details on the instrumentation such as inlet systems, columns and detectors. Specialized techniques from all aspects of GC are introduced ranging from sample preparation, solvent-free injection techniques, and pyrolysis GC, to separation including fast GC and comprehensive GCxGC and finally detection, such as GC-MS and element-specific detection. Various fields of application such as enantiomer, food, flavor and fragrance analysis, physicochemical measurements, forensic toxicology, and clinical analysis are discussed as well as cutting-edge application in metabolomics is covered.

This volume features a comprehensive set of protocols featuring a range of both old and new technologies that can be used to analyze drugs of abuse, including prescription drugs, new psychoactive substances and psychoactive plants. Chapters guide readers through the application of color tests, light microscopy-based particle imaging, GC-MS, Raman spectroscopy, capillary electrophoresis, ultra-high performance LC-tandem MS, DART-MS, MALDI-mass spectrometry imaging, LC-MS/MS and HPLC-ESI-MS/MS to the analysis of abused drugs in wastewater, hair, urine and plant-derived materials, among other matrices. 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, *Analysis of Drugs of Abuse* aims to ensure successful results in the further study of this vital field.

Miriam, a freshman Calculus student at Louisiana State University, made 37.5% on her first exam but 83% and 93% on the next two. Matt, a first year General Chemistry student at the University of Utah, scored 65%

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and 55% on his first two exams and 95% on his third—These are representative of thousands of students who decisively improved their grades by acting on the advice described in this book. What is preventing your students from performing according to expectations? Saundra McGuire offers a simple but profound answer: If you teach students how to learn and give them simple, straightforward strategies to use, they can significantly increase their learning and performance. For over a decade Saundra McGuire has been acclaimed for her presentations and workshops on metacognition and student learning because the tools and strategies she shares have enabled faculty to facilitate dramatic improvements in student learning and success. This book encapsulates the model and ideas she has developed in the past fifteen years, ideas that are being adopted by an increasing number of faculty with considerable effect. The methods she proposes do not require restructuring courses or an inordinate amount of time to teach. They can often be accomplished in a single session, transforming students from memorizers and regurgitators to students who begin to think critically and take responsibility for their own learning. Saundra McGuire takes the reader sequentially through the ideas and strategies that students need to understand and implement. First, she demonstrates how introducing students to metacognition and Bloom ' s Taxonomy reveals to them the importance of understanding how they learn and provides the lens through which they can view learning activities and measure their intellectual growth. Next, she presents a specific study system that can quickly empower students to maximize their learning. Then, she addresses the importance of dealing with emotion, attitudes, and motivation by suggesting ways to change students ' mindsets about ability and by providing a range of strategies to boost motivation and learning; finally, she offers guidance to faculty on partnering with campus learning centers. She pays particular attention to academically unprepared students, noting that the strategies she offers for this particular population are equally beneficial for all students. While stressing that there are many ways to teach effectively, and that readers can be flexible in picking and choosing among the strategies

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she presents, Sandra McGuire offers the reader a step-by-step process for delivering the key messages of the book to students in as little as 50 minutes. Free online supplements provide three slide sets and a sample video lecture. This book is written primarily for faculty but will be equally useful for TAs, tutors, and learning center professionals. For readers with no background in education or cognitive psychology, the book avoids jargon and esoteric theory.

Biogenic amines are bioactive compounds distributed in foods of all origins. Apart from their fundamental role in many bodily functions, there has recently been great interest in their toxicological potential, much research is being carried out to understand their occurrence related to both desired and undesired fermentative phenomena, chemical spoilage, low hygienic conditions, wrong handling, and criticism about technological factors of process and storage conditions. All these causes can contribute to a higher content of biogenic amines in food, particularly of those hazardous to human health. This book aims to collect scientific studies looking for new tools to limit the over-production of biogenic amines in food, search for new food sources of biogenic amines, and to spotlight the concept of safe food and bioactive amines content.

Amino Acid Analysis (AAA) is an integral part of analytical biochemistry. In a relatively short time, the variety of AAA methods has evolved dramatically with more methods shifting to the use of mass spectrometry (MS) as a detection method. Another new aspect is miniaturization. However, most importantly, AAA in this day and age should be viewed in the context of Metabolomics as a part of Systems Biology. Amino Acid Analysis: Methods and Protocols presents a broad spectrum of all available methods allowing for readers to choose the method that most suits their particular laboratory set-up and analytical needs. In this volume, a reader can find chapters describing general as well as specific approaches to the

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sample preparation. A number of chapters describe specific applications of AAA in clinical chemistry as well as in food analysis, microbiology, marine biology, drug metabolism, even archeology. Separate chapters are devoted to the application of AAA for protein quantitation and chiral AAA. Written in the highly successful Methods in Molecular Biology™ series format, chapters contain introductions to their respective topics, lists of the necessary materials and reagents, step-by-step, readily reproducible laboratory protocols, and notes on troubleshooting and avoiding known pitfalls. Authoritative and accessible, Amino Acid Analysis: Methods and Protocols provides crucial techniques that can be applied across multiple disciplines by anyone involved in biomedical research or life sciences.

In this Festschrift celebrating the career of Thom H. Dunning, Jr., selected researchers in theoretical chemistry present research highlights on major developments in the field. Originally published in the journal Theoretical Chemistry Accounts, these outstanding contributions are now available in a hardcover print format, as well as a special electronic edition. This volume provides valuable content for all researchers in theoretical chemistry and will especially benefit those research groups and libraries with limited access to the journal.

This volume explores the different approaches and techniques used by researchers to study the recent challenges and developments in metabolic profiling. This book is divided into IV parts. Part I contains chapters that highlight basic concepts, such as experimental design, data treatment, metabolite identification, and harmonization. Part II describes experimental protocols for both targeted and untargeted metabolomics covering the basic analytical technologies: LC-MS, GC-MS, NMR and CE-MS. In addition the protocols describe methods for the study of tissues, feces, blood and other types of biological samples as well as the

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application of chemical derivatization for GC-MS. Parts III and IV present the use of metabolomics in the study of food, plants and the life sciences, with examples from the quest for the discovery of disease biomarkers, physical exercise omics and metabolic profiling of food, fruit and wine. 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 thorough, *Metabolic Profiling: Methods and Protocols* is a valuable resource for researchers who are interested in expanding their knowledge of this rapidly developing field.

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.

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