The final review surveys recent developments in the exciting area of chemical genetics profiling that permit prioritization of crude extracts or rapid deconvolution of target pathways. Volume II concludes with four chapters compiled by industry experts that detail natural product-based (epothilones, artemisinin, FK228) or inspired (fingolimod) drug discovery programs. Each chapter provides an overview of the development process from crude extract to clinical trials, including discussions on discovery, mechanism of action, medicinal chemistry and large-scale production. For example, the final chapter (artemisinin) provides, in great detail (e.g. color photographs of artemisinin crystals of varying purity and a HPLC chromatogram of crude artemisinin), a behind the scenes look at the challenges encountered and overcome in developing an agriculturally produced drug substance and the global effort required to deliver over 100 million artemisinin-based combination therapies to African countries as part of the Roll Back Malaria initiative. These chapters provide tremendous insight into the drug discovery process, and are an excellent conclusion to this two-volume tour de force in natural product chemistry.

Together, Volumes I and II provide a detailed and up-to-date look at the state of the art and evolving practices in natural product-based drug discovery and highlight the bright future for natural compounds as drugs. The figures and schemes are clear, and through an excellent choice and organization of reviews, the editors accomplish their stated goals in demonstrating how natural products can be integrated into modern drug discovery programs and the incredible potential for natural compounds as drugs. Although the combined cost of these volumes may preclude their use as graduate-level textbooks, both volumes would be excellent resource material for a senior undergraduate or graduate course in natural products or drug discovery, or for faculty, students and industry professionals engaged in natural product research.

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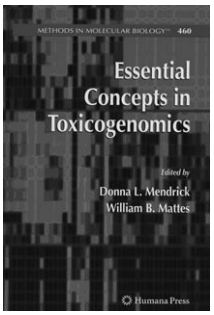
Essential Concepts in Toxicogenomics (Methods in Molecular Biology Series)

Edited by *Donna L. Mendrick* and *William B. Mattes.*

Humana Press, Totowa 2008. xi+277 pp., hardcover € 79.95.—ISBN 978-1-588-29-638-2



Toxicogenomics has now been with us for more than 10 years. It was first heralded as representing a "sea change" in the toxicological sciences, and there was considerable optimism that the ability to simultaneously interrogate toxicant-induced changes in many thousands of genes—or even the entire genome—would transform predictive and mechanistic toxicology overnight. After that first flush of enthusiasm had been tempered by experience, there was a period of consolidation and of re-evaluation of how best this technology might be deployed in the interests of toxicology. This period was characterised by the realisation that it is not always easy to translate data into knowledge—and that the problem is even greater when it is possible to generate vast amounts of data. In recent years, toxicogenomics has come of age—or at least is coming of age—and this excellent and very readable book reflects that growing maturity and the increasing utility of "omics" technologies.

The book is comprised of 12 separate chapters with many leading lights in the discipline as contributing authors. The book opens with an excellent piece by one of the editors (Donna Mendrick) that effectively and concisely sets the scene for the remainder of the volume. Thereafter all the key elements—theoretical and practical—that are required for the successful design, conduct and interpretation of toxicogenomic investigations are discussed in some detail. Included are considerations of the application of toxicogenomics to mechanistic toxicology and predictive testing, the identification of novel biomarkers, and preclinical drug development. Importantly, and in addition to coverage of these discrete scientific applications, there are extremely thoughtful and valuable chapters that examine, among other issues, the role of statistics in toxicogenomics, quality control, the use of and need for bioinformatics and gene annotation, the work of public consortia in toxicogenomics, and—in the concluding chapter—a regulatory perspective in the context of drug development.

Overall, this is an excellent book that will be of interest to all those who practice toxicology, and particularly those using microarray analyses. This reader would perhaps have liked to have heard a little more about some of the regulatory issues that are posed by the increasing use of toxicogenomics, but that is a minor quibble, and not one that prevents me from recommending this book unreservedly.

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New Antibiotic Targets

Edited by *W. Scott Champley.*

Humana Press, Totowa 2008. xi+274 pp., hardcover $ 99.00.—ISBN 978-1-588-29-915-4

Much has been written about the alarming rate at which pathogenic bacteria are becoming resistant to available antibiotics and the resulting clinical consequences and economic impact on the healthcare system. Whereas antibiotic resistance was once largely confined to hospitals and long-term care facilities, resistance has emerged in community settings and has escalated into one of the most pressing global public health concerns. Resistance is an unavoidable side effect of antibiotic use and this fact fuels the search for new antibiotic targets and novel therapeutic agents to treat drug-resistant organisms and emerging infectious diseases. *New Antibiotic Targets* is an attempt to assemble a broad selection of detailed methods for antibacterial

target assays that could be conducted in most laboratories focused on the identification of new antibiotic lead compounds.

The title of the book is somewhat deceptive inasmuch as the focus is not really on new antibiotic targets. Rather, the content primarily outlines various in vitro assays of established or well-known antibacterial targets, such as those inhibited by the β-lactam and fluoroquinolone antibiotics, that have proven successful for uncovering antibacterial lead compounds. There is one chapter that presents a nicely detailed yet brief description of the bioinformatics approach to mine whole-genome sequences for gene products that may be potential drug targets or occupy a role in pathogenesis. There are also a number of chapters that present improved assays for established targets such as mycobacterial fatty acid biosynthesis, or which cover known but still clinically unproven targets that warrant more attention. The latter group includes some very useful assays for such timely topics as Gram-negative lipopolysaccharide synthesis and for several poorly understood processes involved in bacterial protein biosynthesis. The book also includes four chapters that provide details for the analysis of widespread mechanisms of antibiotic resistance such as efflux pumps, aminoglycoside-modifying enzymes, or β-lactamases.

Viewed together, the topics covered by the 20 well-chosen chapters span a broad range of antibiotic mechanisms of action and provide a useful and detailed methods reference. The descriptions of the methods in most chapters are a strong point of the book, and most laboratory technicians and graduate students could readily conduct the assays and analyze the results without consulting the primary literature. Several of the chapters include very helpful illustrations that depict the type of data one should expect to see, or provide useful kinetic equations to analyze the data.

Overall, *New Antibiotic Targets* nicely assembles a diverse selection of assay methods for antibiotic discovery and analysis in one volume. The book would make a useful addition to the reference libraries of any institution, and the price will make it attractive for many individual laboratories engaged in screening compound libraries for antibacterial lead discovery.

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DOI: 10.1002/cmdc.200800419

