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BOOK REVIEWS

Catalysis in Asymmetric Synthesis, 2nd ed. By Vittorio Caprio (University of Auckland, New Zealand) and Jonathan M. J. Williams (University of Bath, U.K.). John Wiley and Sons, Ltd.: Chichester. 2009. xiv + 394 pp. $130. ISBN 978-1-4051-9091-6.

In this second edition of *Catalysis in Asymmetric Synthesis*, Caprio and Williams set out to bridge the gap between undergraduate textbook and cutting-edge review of asymmetric catalysis. In these goals, they have succeeded, and this volume should serve as a starting point for graduate students and those looking to become well-versed in this fast-moving and important field.

The first chapter presents a concise look at how chirality is assigned and how it is usually imparted to a molecule catalytically through controlled rehybridization of sp^2- to sp^3-centers. Subsequent chapters follow a logical sequence, starting with a thorough and well-documented look at the asymmetric reduction of alkenes, ketones, and imines. This is not limited to hydrogenation, with the enantioselective addition of organoelement species across alkenes, such as hydroboration, hydrosilylation, and hydroformylation, receiving adequate attention. Epoxidation, dihydroxylation, and other asymmetric oxidation reactions are presented carefully, followed by nucleophilic additions and cycloadditions. The authors make good use of the example of dialkyl zinc addition to aldehydes to broach the subject of chiral amplification, a topic that is clearly, if briefly, explained. A later chapter is dedicated to the emerging field of asymmetry in catalytic carbon−carbon bond forming reactions. As the cross coupling of sp^3-centers becomes accessible, the control of product configuration becomes increasingly important. The asymmetric Heck reaction, allylic substitution, and Kumada-type coupling of secondary nucleophiles are considered in Chapter 10, the most up-to-date chapter in the book. Throughout the book, special emphasis is placed on organocatalysis as an alternative to metal-catalyzed reactions. Indeed, a large number of the recent references stem from this topic. Notably, the use of non-racemic proline-based catalysts in various asymmetric transformations is highlighted.

On the whole, the book is well written and well compiled. Each chapter commences with a brief summary, outlining the relevance of the reaction in question and limitations that have recently been addressed. This gives the book perspective and often helps the reader follow the subsequent subtopics as part of an evolving body of work. The large number of examples, however, sometimes causes the reader to search for reaction schemes. As the examples listed are judiciously chosen and by no means superfluous, this is an acceptable inconvenience. It should also be noted that the mechanisms of some non-trivial reactions are omitted, surely in the interest of space and retaining focus. These would have been a useful addition for readers more interested in this aspect of catalysis. Because this book provides a useful compendium of synthetically important methods in asymmetric catalysis, is well organized, and well referenced, it will be a good resource for students and faculty interested in this important area.

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Computational Drug Design: A Guide for Computational and Medicinal Chemists. By David C. Young (Computer Sciences Corporation). John Wiley & Sons, Inc.: Hoboken, NJ. 2009. xxxvi + 308 pp. $100. ISBN 978-0-470-12685-1.

As the author states, "this book is very industry-centric" and was designed to explore the drug design process through the computational techniques that are used in a typical pharmaceutical industry. Part I covers the drug design process; Part II focuses on computational tools and techniques, such as homology model building, QSAR, and cheminformatics, to name a few; and Part III addresses a variety of new and emerging technologies, such as proteomics. Each chapter includes a bibliography of key references. A longer, more in-depth list of references is included on the accompanying CD. Along with a table of contents, the book opens with a "Book Abstract", providing short summaries of each of the 27 chapters. A glossary and subject index conclude the book.

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Protein Structure, Stability, and Interactions. Edited by John W. Shriver (University of Alabama, Huntsville). From the series, Methods in Molecular Biology, 490. Edited by John M. Walker (University of Hertsfordshire, U.K.). Humana Press (a part of Springer Science + Business Media): New York. 2009. x + 360 pp. $109. ISBN 978-1-58829-954-3.

Students of protein structure, and that includes life-long students of protein structure who may themselves have students, are sure to greet the latest offering of *Methods in Molecular Biology* with a sigh of relief. Simplicity at last has been given a front row seat. In the complex world of macromolecular biophysics, which is full of unsolved problems, hand-waving theories, and esoteric instrumentation, a generation of hard-won secrets will certainly die with their respective keepers unless detailed methods, protocols, and derivations are made available to the broadest audience of students and researchers. This book presents those details in 14 clearly labeled and logically arranged chapters, authored by 24 prominent protein biophysicists.

Protein Structure, Stability, and Interactions covers a thorough list of biophysical methods as applied to proteins and their environments in vivo, in vitro, and sometimes in silico. Notably omitted are X-ray crystallography and most of the structure

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solution part of NMR, methods that warrant textbooks of their own because of their sophistication. Purely computational methods are also not covered. The focus is on instrumentation, theory, and physical phenomena with regard to protein folding, flexibility, binding, and solvation. Each chapter begins with the roots, usually the biophysical equations of state for the phenomenon being measured. This is followed by stepwise instructions for executing the experiments or the analysis of experimental data, followed by prototypical case studies, a "Notes" section, i.e., think "footnotes" or "frequently asked questions", a conclusion, an extensive bibliography of archival and up-to-date references, and web resources. The chapters are surprisingly consistent in their tone and style, given the distributed authorship.

Readers should be well schooled in physical chemistry and biophysics, with some molecular biology as well, before attempting this text. This is not an introduction to proteins or protein structure, and there is no glossary of terms to explain the meaning of an α helix or any appendix containing the structures of the amino acids. The reader must be well beyond the basics. The chapters in this book deal with cutting-edge questions regarding protein interactions and stability and present the tools and protocols for answering these questions.

The book begins with a tutorial on microcalorimetry by Privalov, followed by a chapter on useful protocols for urea denaturation curves and one on equations for analysis of two-state, multistate, and multimeric protein folding. Ultracentrifugation for the analysis of interactions is covered well in Chapter 4, followed by two chapters dedicated to the specialized applications of NMR to the detection of interactions and the location of flexible joints in proteins. Some previous experience with NMR is required. The editor has contributed two chapters covering the equations for the coupled equilibria of folding, ligand binding, and multimer association. Gierasch offers a protocol for monitoring unfolding in vivo. Two more chapters address the effects of solvent, molecular crowding, and steric effects on stability and interactions, and another two chapters explore the role of surface electrostatics, using molecular dynamics and rational design. Finally, the last two chapters outline the use of single-molecule FRET for folding studies and the characterization of the denatured state ensemble.

As a whole, this book would work as a text for an advanced course in biophysical methods or as a reference book for a biophysics laboratory.

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Anthracycline Chemistry and Biology I: Biological Occurrence and Biosynthesis, Synthesis and Chemistry. Edited by Karsten Krohn (Universität Paderborn, Germany). Springer: Berlin, Heidelberg. 2008. xiv + 324 pp. $339. ISBN 978-3-540-75814-3.

This book, Volume 282 of the renowned series *Topics in Current Chemistry*, covers many different aspects of the origin, chemistry, and biosynthesis of one of the oldest but most important classes of anticancer agents. Daunorubicin and doxorubicin, the prototype agents of the anthracyclines, have become the key components of curative regimens for multiple human neoplasms, demonstrating the clinical utility of this class of compounds. In addition to these drugs, epirubicin and idarubicin are also in clinical use, and there are several new analogues in preclinical and clinical development. Arguably, doxorubicin is the most recognized and representative member of this class of drugs and is also a molecule of choice for numerous biological studies, including understanding its mechanism of action, synthesis of new analogues, and investigation of its combination with different targeted therapies and delivery systems. This book is an important update on the field, which was last reviewed comprehensively in 1995.

Part I of the book focuses on the biological occurrence and biosynthesis of anthracyclines and should be very useful to both newcomers and investigators currently working in the fields of anthracycline chemistry and biology, since it provides an understanding of the robustness of this class of antibiotics. Chapter 1, entitled "Naturally Occurring Anthracyclines", covers the known natural products in a very systematic way and provides an impressive tabulated review of all the interesting structural features of these fascinating molecules. An impressive list of 283 references is also provided, which will allow easy access to the primary data.

Part II comprises selected reviews of the chemistry of both the antracyclinone chromophore and sugar moieties. Readers will find these chapters useful because the synthetic schemes and their descriptions allow for easy comparison of many different synthetic approaches. The other chapters may appeal to scientists interested in the exploration of glycosides in polyaromatic compounds, with the underlying intention of imitating the anthracycline scaffold.

In summary, the book is nicely produced, very well edited, and should serve as a valuable source of information that is difficult to locate, even for people familiar with the field. This book will serve as an inspiration for scientists and students in the areas of chemistry, drug discovery, and biological evaluation. It should be an essential addition to institutional library collections; however, a more attractive price or special discounts for those in academia would make it an appealing addition to the personal libraries of scientists and students.

Waldemar Priebe, *The University of Texas*

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Mass Spectrometry in Drug Metabolism and Pharmacokinetics. Edited by Ragu Ramanathan (Bristol-Myers Squibb Pharmaceutical Research Institute, Princeton, NJ). John Wiley & Sons, Inc.: Hoboken, NJ. 2009. xii + 390 pp. $125. ISBN: 978-0-471-75158-8.

Although mass spectrometry (MS) has long been a useful tool in drug metabolism and pharmacokinetics, beginning about 1995, it became the essential tool against which all others were measured. This occurred because electrospray ionization coupled to the much improved quadrupole hardware and software made quantitative measurements via liquid chromatography/mass spectrometry feasible, reliable, and highly economical. There has been no turning back. The richness of the art of mass spectrometry has continued to evolve to the point that we should no longer consider MS as a detector for chromatography. Rather chromatography serves as an accessory for preparing samples for MS, which in itself is a multistage separating device, a chemical reactor, a means of assessing mass with great accuracy,

and a tool for quantitative analysis. Time-of-flight, Fourier-transform, and ion-trap spectrometers were curiosities not very long ago but today are readily available in a variety of configurations and combinations. These are given full consideration in this volume.

The history of instrumentation is such that the more we are capable of doing, the more we are asked to do. Nowhere is this made more clear than in the regulated sciences of drugs, food, and the environment. Modern drugs are more potent and are composed of larger molecules. Drugs are now quantified at lower amounts in smaller volumes over longer periods of time, postdose where the concentration has diminished. Minor metabolites, invisible earlier, are now a concern. The tools improve, but the workload grows faster. With all this as a background, this book is an excellent overview of MS strategies for drug metabolism and pharmacokinetics of traditional organic drugs. The majority of the authors are from the industrial world and are well grounded in expectations of the industry and the FDA. It will be especially valuable to mass spectroscopists entering the world of drug metabolism and to scientists working in this field and wishing to learn more about new options in mass spectrometry. Of particular relevance here is the role of high mass resolution, which is quickly moving from the exotic to the routine. Strategies for identifying metabolites are especially well described. Early chapters provide efficient pedagogy for both groups, but the strength of this volume is in the many excellent examples of drug metabolism. The chapters are timely and of consistent quality. Two brief chapters at the end cover the rapidly evolving techniques of desorption ionization that are beginning to come into vogue. All in all, the book delivers on its promises to introduce and review the current art of mass spectrometry for the related disciplines of drug metabolism and pharmacokinetics. I highly recommend it.

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