Book Reviews

Medicinal Natural Products. A Biosynthetic Approach. 2nd Edition. By Paul M. Dewick. John Wiley & Sons, New York. 2002. xii + 507 pp. 19 × 25.5 cm. ISBN 0-471-49640-5. $115.00.

The author opens this edition with a brief chapter entitled "About This Book and How To Use It". He states that "the book is user friendly, suitable for a modular course, a starting point for later project and dissertation work, designed to be forward looking, and gives possible leads to new drugs". It is this and much more. The user is admonished to concentrate on understanding the broad features of the sequences that are emphasized. Furthermore, the author states that the mechanistic explanations for the processes used are the essence of the book. Each chapter ends with a list of references that are topic-related and often consist of separate lists of books, reviews, and some articles from the primary literature. This reviewer found the lack of direct insertion of references into the text to be something of a drawback, and he would have appreciated additional detailed primary references for some compounds. The book is organized into eight main sections: (1) About This Book and How To Use It; (2) Secondary Metabolism: The Building Blocks and Construction Mechanisms; (3) The Acetate Pathway: Fatty Acids and Polyketides; (4) The Shikimate Pathway: Aromatic Amino Acids and Phenylpropanoids; (5) The Mevalonate and Deoxyxylulose Phosphate Pathways: Terpinoids and Steroids; (6) Alkaloids; (7) Peptides, Proteins, and Other Amino Acid Derivatives; and (8) Carbohydrates. Sections 5 and 6 are each over 100 pages long. The text is remarkable for the paucity of mistakes and for the numerous excellent choices of compounds used as product examples for the pathways. Significant examples are highlighted in gray-tone offset boxes that provide the reader with information on their uses, sources, commercial production, toxicity, pharmacology, and/or economic importance. For example, some of the Chapter 3 (on the acetate pathway) examples include poison ivy and poison oak (urushiol), mevastatin, the cannabinoids, macrolides, and prostaglandins while Chapter 4 (Shikimate) includes folic acid, flavonoids, isoflavonoids, and vitamins E and K. The terpene chapter has extensive tables and examples that include popular dietary supplements, antineoplastics, forskolin, and steroids. The alkaloid chapter is classically organized around major precursor amino acids with similar classic examples, yet emphasis is still present in the examples of substances of abuse and some marine toxins (saxitoxin, tetrodotoxin). Chapter 7 (on peptides) covers its topics on the basis of initial pathway considerations, and then the remainder is organized directly on examples: peptide hormones and antibiotics, toxins such as the amanitins, lactams, and the cyanogenetic glycosides, glusinolates, and cysteine sulfoxides. The final chapter (on carbohydrates) is organized similarly from monosaccharides to polysaccharides (cellulose, chitin, various gums, mucilages, and heparin), ending with discussions of acarbose, lincomycin/clindamycin, and the aminoglycoside antibiotics.

The strengths of this book lie in its readability, organization, plethora of structures, and relevancy of its examples. It is very timely in its discussions of polyketide synthase enzymes and genetic manipulation of the acetate pathway and of the deoxyxylulose phosphate pathway. It is an extremely timely text for an era deeply immersed in determination of the genetic codes of many organisms, since it enables students to understand the ultimate consequences of this effort. The book is highly recommended to all medicinal and natural products chemists and to any others involved with the products of these pathways. Although the hard-cased edition is expensive, a paperback edition is planned for students. They will both prove to be favored lasting additions to personal libraries.

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Reviews in Computational Chemistry. Volume 17. Edited by Kenny B. Lipkowitz and Donald B. Boyd. Wiley-VCH, New York. 2001. xxxv + 399 pp. 16 × 24.5 cm. ISBN 0-471-39845-4. $150.00.

This is volume 17 in a series that has covered most significant aspects of computational chemistry since it was started. Over the years, these reviews have dealt with cutting edge academic subjects to the applications of computational chemistry to life or material sciences, didactically, with balance and impeccable scientific rigor. This volume is no exception to those rules. The pervasive nature of computational chemistry that allows it to make an impact on multiple areas of research is reflected in its four chapters and appendix.

The preface contains a discussion of the accuracy of the information in chemical literature databases, with some interesting observations by the editors. It is followed by a tribute to the many prominent colleagues who passed away since the series began, with particular attention to Michael Zerner's contributions.

The first two chapters provide overviews on the problem of docking, that is, the computational techniques that study the mode in which molecules interact (sampling) and the algorithms that quantify how well they do it (scoring). The issue is particularly important for computer-aided drug design, where one of the molecules is typically a protein. The first chapter written by Muegge and Rarey covers the docking of small molecules to proteins. An overview of the sampling problem and the different techniques for its automation starts the chapter. Strategies for scoring are at the front line in this area and are sensibly described by the authors. The application of docking methodologies in virtual screening and the selection of potential ligands for biological evaluation end the chapter.

Protein−protein docking is discussed by Ehrlich and Wade in the second chapter. Protein−protein interactions are very significant in biological systems, as stated in the chapter. In turn, that importance transfers to computational chemistry because of its role in multidisciplinary projects. Sampling and scoring are also revisited in this case, but the techniques utilized are drastically different from small-molecule docking. The chapter contains an account of different attempts to dock barnase to barstar to illustrate methods and their limitations.

A more basic aspect of theoretical chemistry is covered by Marian in a chapter on spin−orbit coupling in molecules. The chapter starts from the beginning with a description of the Stern−Gerlach experiment and the Zeeman effect. In particular, the first part of the chapter could make good reading for students in a quantum chemistry course. The chapter also presents an outline of the approaches used to compute spin−orbit couplings. Radiative and nonradiative spin-forbidden transitions are depicted, and examples are provided. The chapter closes with an outlook on the challenges in this area, namely, the integration of spin−orbit and electron correlation effects.

Kier, Cheng, and Seybold provide the final chapter to this volume with a description of the use of cellular automata models for aqueous solution systems. This chapter reminds us that computational chemistry extends beyond the molecular realm to the study of aggregates. Cellular automata provide an alternative to the more common molecular dynamics and Monte Carlo techniques to examine condensed-phase phenomena. The chapter provides a description of cellular automata algorithms and their workings and provides examples of their uses, in particular regarding water solutions and enzymatic kinetic models.

As with many of the preceding volumes, the editors close with an appendix with varied information for the practitioners. In this case, the appendix provides a compilation of over 1600 book titles that have been published in the field of computational chemistry, subdivided into 9 tables by subdiscipline.

Overall, volume 17 is true to the spirit of most the collection, covering a diversity of aspects in computational chemistry. The emphasis on docking procedures makes this volume particularly valuable to those involved in computer-aided drug (ligand) design.

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