

gies. These topics are well-covered in a number of chapters, resulting in a comprehensive treatment. The book concludes with a salient discussion of the many important applications of the DuPHOS class of chiral ligands in asymmetric hydrogenations.

This valuable reference should be most useful to the process chemist who is facing the difficult challenges associated with devising an economic and scalable synthesis of a complex chiral molecule. In addition, the impressive collection of over 1800 references contained in the 18 chapters coupled with a comprehensive index are additional noteworthy features of this volume.

**Pat N. Confalone**

*Senior Vice President  
Chemical Process R&D  
DuPont Pharmaceuticals  
Wilmington, Delaware 19880-0500*

JM990300V

10.1021/jm990300v

**Molecular Modeling of Nucleic Acids.** Edited by Neocles B. Leontis and John SantaLucia, Jr. ACS Symposium Series 682. American Chemical Society, Washington, D.C. 1998. x + 435 pp. 15.5 x 23.5 cm. ISBN 0-8412-3541-4. \$129.95.

This is a multiauthor volume based on a symposium the editors organized 2 years ago at the American Chemical Society National Meeting, San Francisco, CA, April 13-17, 1997. The book appeared at the beginning of 1998, but it was not received for review until April 1999. It contains some literature citations from 1997.

Of the 399 papers and posters organized at the San Francisco meeting under the auspices of the Computers in Chemistry Division, over 60 were related to the Symposium on Molecular Modeling and Structure Determination in Nucleic Acids. Of these, 26 became chapters in the book. About half of the chapters have titles different from the talks, and many chapters have had co-authors added or dropped.

The editors brought together as wide a range of approaches to nucleic acid modeling as possible. The book is about more than just molecular modeling in the computational chemistry sense. As the editors explain in their introduction, the conception of the original DNA double helix by Watson and Crick was a molecular modeling exercise, i.e., using available experimental information to construct a three-dimensional structure. Not all modeling need be done on a computer. The editors emphasize that precision at the atomic level is not necessarily the most important element; the success of a model can be judged by how well it integrates existing experimental data and whether it suggests new experiments. The introduction puts the book in context for the expert. The reader is directed to a 1989 reference giving terminology for helical parameters. The book has a long subject index (19 pages) and an index of its 97 authors but, following standard practice in ACS books, no index of cited authors.

The book is organized into sections covering basic computational issues, crystallography, spectroscopy, secondary structure prediction, molecular dynamics

simulations, and modeling with low-resolution data. It includes experimental studies in X-ray diffraction, NMR and Raman spectroscopy, thermodynamics, and kinetics. Among the specific topics are RNA folding, modeling a ribosome, fuzzy logic, a scripting language for model building, simulations in the presence of counterions, and simulating folding by genetic algorithms (an appropriate topic for a book about DNA). There is little in the book on intercalators or on molecules that regulate gene expression. Antisense drugs are briefly mentioned. Only three of the chapters have authors associated with pharmaceutical companies.

Several of the chapters serve merely as gateways to the literature and would have benefited by being more independent and giving more mathematical details. The chapters are journal-length (8-28 pages). As is typical for a book prepared from camera-ready typescripts, there is variability in how well the authors adhered to the instructions given them. Thus, a few of the chapters lack an abstract. Some of the stereodiagrams have the pairs too widely separated to be properly viewed. One chapter has a color plate, whereas a few of the other chapters could have benefited from color.

The book is a rich source of information about DNA and RNA and will help the reader appreciate the wide panorama of experimental and computational research directions. This volume should be in complete collections of books on computational chemistry or nucleic acids.

**Donald B. Boyd**

*Indiana University—Purdue University at Indianapolis  
402 North Blackford Street  
Indianapolis, Indiana 46202-3274*

JM990302F

10.1021/jm990302f

**Neuronal Nicotinic Receptors. Pharmacology and Therapeutics Opportunities.** Edited by Stephen P. Arneric and Jorge D. Brioni. Wiley-Liss, Inc., New York. 1999. xii + 421 pp. 16 x 24 cm. ISBN 0-471-24743-X. \$175.00.

A book that has a retail price of \$175.00 had better be good. This book is good and might even be worth the exorbitant purchase price. Topics covered range between an overview of neuronal nicotinic receptors to in-depth discussions of the structure, function, and regulation of neuronal nicotinic receptors to a discussion of the chemistry of nicotinic ligands to discussions of the potential therapeutic benefit of nicotinic compounds. The book consists of a collection of 23 reviews of "things nicotinic" written by many, indeed I would argue most, of the world's leaders in this field. Nearly without exception the chapters are chock full of valuable information. Better yet, at least half of the reviews are truly critical reviews of the literature. Nearly all of the authors did a commendable job of discussing the inevitable inconsistencies in the literature, and many had the courage to take sides on controversial issues. Of greater importance, many of these authors clearly identified questions and issues that need investigation.