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BOOK REVIEWS

Molecular Networks. Edited by Mir Wais Hosseini (Université de Strasbourg, France). From the series, Structure and Bonding, 132. Series edited by D. M. P. Mingos (Oxford University, U.K.). Springer-Verlag: Berlin, Heidelberg. 2009. xii + 166 pp. $189.00. ISBN 978-3-642-01366-9.

This book gives an overview of some recent developments in crystal engineering of molecular and metalloorganic solids in five, essentially independent chapters written by different authors. The main discussions are on charge-assisted hydrogen bonding (Chapter 1), polymorphism in molecular crystals (Chapter 2), and design and application of metal−organic frameworks (Chapters 3 and 4), plus a detailed case study of bipyridine-*N*,*N*′-dioxide-based assemblies (Chapter 5). Obviously, a comprehensive coverage of the recent literature was not the editor's intention (nor is it the goal of the *Structure and Bonding* series), although the subfields that are covered in these five chapters are thoroughly reviewed, with the main focus being approximately on the period 2000−2007. Still, I was surprised *not* to see any mention of two-dimensional molecular networks on surfaces in a book with such a general title. Studies of such networks by scanning tunneling microscopy have recently grown into a major research area at the interface of crystal engineering and surface science. Throughout the book, sufficient general information is given so that anyone with a chemistry degree can follow the discussion and appreciate the significance of the problems at hand. I particularly enjoyed the logic and quality of the illustrations in Chapter 1 by Ward portraying the hydrogen-bonding motif in crystal engineering. There is some duplication between Chapters 3 and 4 where the same class of porous crystalline materials — metal−organic frameworks and porous coordination polymers — are discussed under different names. The coverage is not entirely redundant, however: the focus of Chapter 3 is shifted toward gas adsorption/storage while more structural aspects, from the general perspective of inorganic porous materials, are discussed in Chapter 4. On the other hand, the space could have been used to discuss the latest breakthrough on closely related covalent organic frameworks (see Cote, et al. *Science* **2005**, *310*, 1166 for the first report).

All in all, this book makes good reading material that can appeal to nonexperts by showcasing some recent developments in the field of crystal engineering, as well as to some experts seeking a detailed overview of a specific subfield, such as a comprehensive account of all possible assemblies of bipyridine-dioxide in Chapter 5. The reader should not expect, however, to get a reference handbook on molecular networks in a mere 165 pages.

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Proteins: Energy, Heat, and Signal Flow. Edited by David M. Leitner (University of Nevada, Reno) and John E. Straub (Boston University). From the series "Computation in Chemistry." Edited by Peter Gill (Australian National University). CRC Press (an imprint of Taylor & Francis Group): Boca Raton, FL. 2009. xx + 396 pp. $103.96. ISBN 978-1-4200-8703-1.

This book provides a comprehensive survey of the state of the art in the relatively new field of computational structural biology, or in other words the study of the relationship between the structure and dynamics of biological macromolecules, as inferred from computer simulations, and their function. The primary focus is on energy flow in proteins, considered here to include vibrational relaxation, heat transport, allostery, the coupling of binding to conformational change in molecular motors, and the coupling of protein and solvent dynamics. A broad range of theoretical models is discussed, encompassing different levels of detail and computational expense, from phenomenological kinetic models to all-atom molecular dynamics simulations.

Part 1 comprises four chapters that focus on molecular motors, with reviews of recent theoretical studies of kinesin, dynein, the myosin motor domain, and cytochrome *c* oxidase, which is considered to be a motor by virtue of its ability to perform proton translocation. Part 2 focuses on vibrational relaxation and, in particular, on photoinduced conformational changes. It also presents work on the photoactive yellow protein found in the bacterium *E. halophila* and photoinduced energy flow in azobenzene peptides, as well as energy flow in deoxyhemoglobin and myoglobin bound to carbon monoxide. Part 3 extends the previous section by focusing on vibrational relaxation through methods based on normal modes and other harmonic or quasiharmonic models, such as elastic network models. The final four chapters in Part 4 cover coupling between protein and solvent dynamics and methods for studying protein conformational changes that take place on too long a time scale for molecular dynamics simulations.

Overall, this book is a useful guide for practitioners of molecular dynamics, theorists interested in structural biology, and users of modeling software seeking to understand the methods in more depth. The book is well organized, produced, and edited. References are up-to-date and comprehensive. Several figures are presented both in black and white and in color, in a separate insert.

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