

Book Reviews

Microbial Transformation and Degradation of Toxic Organic Compounds. Edited by Lily Y. Young (Rutgers University) and Carl E. Cerniglia (National Center for Toxicological Research, Arkansas). Wiley: New York. 1995. xii + 654 pp. \$89.95. ISBN 0-471-52109-4.

The Editors have brought together contributions to environmental microbiology by an outstanding group of scientists and engineers. It is not surprising that there is some unevenness in presentation. However, on balance, this is an important source of current thinking and research results in bioremediation.

In the preface, the editors describe the strategy employed to create the volume and the rationale for sequential organization of chapters. The preface is too brief and does not deal adequately with the important and useful information that follows. The overly terse preface is followed by Chapter One; the latter is pretentious and inappropriate as a technical introduction for the remaining chapters of the volume. It contributes very little and may discourage the systematic reader. In the case of a "results-oriented" reader, clear chapter titles and a well-constructed table of contents make it possible to skip directly to a chapter containing subject matter of immediate interest.

Chapter Two of Part I has outstanding value; it catalogs the extent and diversity of synthetic organic chemical species in the environment. It establishes linkages between organic chemistry, chemical manufacturing, and chemical utilization in the U.S. and comparable highly developed societies. Table 2.1 includes essential background on applications that lead to production and dispersion of these chemicals. Similarly, Figure 2.1 is an excellent description of fates and mechanistic pathways in the environment. This information is too often presented in terms of either environmental protectionism or defense of manufacturing/use practices; the approach taken is factual and founded on sound, traditional science.

Chapter Three is an excellent and long-awaited update of the Atlas publications on petroleum hydrocarbons in soils. This chapter is generally applications-oriented and promises to be very useful in that context. It would have been better served as the first chapter of Part III (Applications) rather than as the first chapter of Part II (*Basic Microbiology*).

Chapter Four is a comprehensive review of anaerobic (reductive) dechlorination of polychlorinated biphenyls [PCBs]. More than 200 di- through octasubstituted congeners are possible. In addition, the synthesis of these compounds, for use as heat transfer agents and insulating fluids, yielded commercial mixtures of 60 or more congeners. Microbial activity in natural anaerobic environments has been inferred from weathering of these commercial mixtures, observed as changes in congener distribution. This chapter provides clear insight into the complex pathways and product patterns associated with degradation of PCBs. It is not possible to draw a distinction between microbiological fundamentals and field application, i.e., bioremediation. This is true of chlorinated aromatics compounds, as discussed in Chapters Four and Twelve. Several sections of the latter, especially 3.1, 3.2, and 5.3.3, are recommended as companion reading for Chapter Four.

Chapters Five through Nine present well-defined fundamentals on microbial processes relating to key environmental contaminants. Halogenated organic compounds do *not* represent important energy sources; thus, the cometabolic and gratuitous reactions described in Chapter Five are important. Chapter Six generalizes on reductive dechlorination of monocyclic aromatic halide species. Subsequent chapters address oxidation of polycyclic hydrocarbons, anaerobic degradation of substituted benzenes, and fungal processes.

Part III provides design and operating guidance for microbial processes to treat industrial wastewater and contaminated environmental media, i.e., soil and ground water. The chapters of Part III have immense value; this material represents the key to technology transfer for practical decontamination mediated by biochemical reactions. Information concerning petroleum releases and/or discharges and lighting gas manufacturing residues is immediately useful.

Part IV touches on speculative and controversial issues. The three chapters are well documented; however, the topics are subjects of intense current debate. Risk assessment is the focus of new federal legislation; genetic engineering has raised questions about control and monitoring in laboratory and field environments. Readers will note

that this part is relatively less authoritative and, perhaps, more thought provoking than earlier parts.

This book is a valuable addition to a functional bioremediation library. Chapters serve as brief, thoroughly documented summaries of microbial pathways and processes. They provide technical resources for microbiologists and non-microbiologists concerned with bioremediation strategy and implementation.

Robert C. Ahlert, Rutgers University

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Ion Exchange and Solvent Extraction. Volume 12. Edited by Jacob A. Marinsky (State University of New York at Buffalo) and Yizhak Marcus (The Hebrew University). Marcel Dekker: New York. 1995. xvi + 448 pp. \$195.00. ISBN 0-8247-9382-X.

This volume continues a tradition of excellence established in the first volume. The purpose of this series is to provide "...the reader with timely considerations of important aspects of the ion-exchange phenomenon...Significant applications of the ion-exchange phenomenon continue to be emphasized...[and] presentations continue to be broader and more informative than one ordinarily encounters in technical and review papers."

This series has yielded a number of contributions which continue to be referenced as standards, including *Extraction of Solvent-Impregnated Resins* by Abraham Warshawsky (Volume 7), *A Systematic Approach to Reactive Ion Exchange* by Gilbert E. Janauer, Robert E. Gibbons, Jr., and William E. Bernier (Volume 9), and *Liquid Membranes* by Richard D. Noble, J. Douglas Way, and Annett L. Bunge.

The current volume is divided into nine chapters. Each chapter has been very carefully edited to ensure a uniformity between the contributions and clarity within each contribution. Chapters written by authors whose native language is not English have been worked on with much care and are extremely readable. All chapters but one have lists of references with the latest citation being 1992 or 1993.

Chapter 1 (High Pressure Ion Exchange Separation of Rare Earths; Liguang Chen, Wenda Xin, Changfa Dong, Wangsuo Wu, and Sujun Ye) consists of 28 pages and 12 references. It focuses on a comparison of classical with high-pressure ion exchange chromatography, the latter utilizing beads with diameters of 5–10 μm . Chapter 2 (Ion Exchange in Countercurrent Columns; Vladimír I. Gorshkov; 63 pages; 93 references) has as its central point that the "use of countercurrent columns enables one...to employ ion exchanger capacity more effectively, to reduce expenditures for resin regeneration, and to decrease the amount of waste." Chapter 3 (Recovery of Valuable Mineral Components from Seawater by Ion Exchange and Sorption Methods; Ruslan Khamizov, Dmitri N. Muraviev, and Abraham Warshawsky; 55 pages; 301 references) discusses the different sorbents capable of complexing magnesium, potassium, bromine, lithium, uranium, rubidium, and boron from seawater. Chapter 4 (Investigation of Intraparticle Ion-Exchange Kinetics in Selective Systems; A. I. Kalinitchev; 47 pages; 73 references) presents the author's model for ion exchange kinetics in selected systems, and a comparison is made between intraparticle diffusion kinetics for conventional vs selective ion exchange. Chapter 5 (Equilibrium Analysis of Complexation in Ion Exchangers Using Spectroscopic and Distribution Methods; Hirohiko Waki; 31 pages; 29 references) explores the ionic interactions which define selective ion exchange. Chapter 6 (Ion Exchange Kinetics in Heterogeneous Systems; K. Bunzl; 45 pages; 38 references) details the ion exchange kinetics "...for the case where diffusion of the ions across a hydrostatic boundary layer (Nernst film) surrounding the particle is the rate controlling step...". Chapter 7 (Evaluation of the Electrostatic Effect on Metal Ion-Binding Equilibria in Negatively Charged Polyion Systems; Tohru Miyajima; 76 pages; 76 references) presents the thermodynamic equations for correlating microscopic binding equilibria at the reaction site to the macroscopic binding data. Chapter 8 (Ion Exchange Equilibria of Amino Acids; Zuyi Tao; 26 pages; 33 references) describes the mechanism of amino acid complexation by ion exchangers. Chapter 9 (Ion Exchange Selectivities of Inorganic Ion Exchangers; Mitsuo Abe; 59 pages; 211 references) examines through representative examples the selectivities displayed

by inorganic ion exchangers and compares their behavior to those of more conventional organic exchangers.

Each chapter describes in a thorough manner the aspect of ion exchange described in its title and is well worth investigating by those interested in the physical chemistry of the ion exchange process.

Spiro D. Alexandratos, *University of Tennessee at Knoxville*

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Membrane Protein Structure: Experimental Approaches.

Edited by Stephen H. White (University of California, Irvine). Oxford University Press: New York, 1994. x + 395 pp. \$65.00. ISBN 0-19-507112-3.

This book consists of 16 multiauthored chapters on various aspects of membrane protein structures with an aim to provide a compact volume describing the experiences of experts in critical areas of membrane protein structure. This volume is not an exhaustive compendium relevant to membrane protein structures, but rather highlights major aspects of the field. The book does a superb job of attaining its goal, and the result is a comprehensive, well-documented, pertinent, and readable reference work which will be of great value to all students and experts with interests in membrane structures.

The volume is divided into four major sections with several chapters in each. The first section—The Nature of the Membrane Protein Structure Problem—defines the features of membrane proteins needed for successful structure prediction. Chapter 1 by D. C. Rees et al., Membrane Protein Structure and Stability: Implications of the First Crystallographic Analysis, focuses on structural analysis of globular, integral membrane proteins with emphasis on the analyses of the photosynthetic reaction center. Chapter 2 by G. von Heijne, Decoding the Signals of Membrane Protein Sequences, is organized around three main sections: introduction to the general problem of intracellular protein sorting, how proteins insert into membranes and how their transmembrane topology is determined, and implications for membrane protein structure prediction. Chapter 3 by J.-L. Popot et al., Folding and Assembly of Integral Membrane Proteins: An Introduction, highlights the problems of protein folding and assembly of integral membrane proteins and is highlighted by specific examples. Chapter 4 by S. H. White, Hydrophathy Plots and the Prediction of Membrane Protein Topology, presents hydrophathy plot analysis as a tool for the construction of testable hypothesis of structure. Throughout the reader is frequently warned of the major pitfalls of these methods demonstrated with many examples.

The second section—Biochemical and Molecular Biological Approaches: Protein Topology—emphasizes the need to determine the correct topology of the membrane proteins. Chapter 5 by D. S. Cafiso, Experimental Determination of the Topography of Membrane Proteins: Lessons from the Nicotinic Acetylcholine Receptor, a Multi-subunit Polytropic Protein, reviews methods for testing topology including antibody studies, enzymatic digestion or labeling, chemical labeling, and a novel, reliable method that uses proteolysis and mass spectrometry. Chapter 6 by D. Boyd, Use of Gene Fusions to Determine Membrane Protein Topology, describes gene fusion methods for proteins expressed in *Escherichia coli* and discusses the use of glycosylation sites to determine topology. Chapter 7 by L. M. Amzel et al., Structure of F_0F_1 ATPases Determined by Direct and Indirect Methods, shows by a case study of the F_0F_1 ATPase complex how hydrophathy and topology analyses can be combined to derive a reasonable model for membrane proteins.

Section three—Direct Structural Approaches—describes several methods, some indirect, such as circular dichroism, infrared spectroscopy, nuclear magnetic resonance, and two-dimensional electron diffraction, to gain direct structural information. Because of the special nature of membrane proteins, the applications of these techniques are not straightforward and special problems exist in the interpretation of their results. Chapter 8 by R. W. Williams, Experimental Determination of Membrane Protein Secondary Structure Using Vibrational and CD Spectroscopies, points out the critical need for measurements to be reliable and specific enough to distinguish between competing models.

Recent developments in three common methods used to measure membrane protein secondary structure (FTIR, Raman, and CD) are highlighted, along with a more complete outline of several other techniques. Special problems associated with the presence of lipids are considered in detail. Chapter 9 by W. Kuhlbrandt, High-Resolution Electron Crystallography of Membrane Proteins, describes the use of two-dimensional electron diffraction techniques on the structure of a light harvesting complex. While this technique is still in its infancy, rapid advances in methods for growth of two-dimensional crystals, for protein refinement and for microscope design, make it an even more powerful tool in determining the structure of membrane proteins. Chapter 10 by W. L. Hubbell and C. Altenbach, Site-Directed Spin Labeling of Membrane Proteins, describes the use of nitroxide spin labels attached to cysteine residues which have been added to the membrane proteins by site-directed mutagenesis techniques. These labels become powerful tools for providing dynamic and structural information on lipids in membranes. Strategies for the selective incorporation of nitroxide in the sequence without disruption of the structure are highlighted with several examples. Chapter 11 by S. J. Opella, Nuclear Magnetic Resonance Approaches to Membrane Protein Structure, describes the pertinent aspects of solid-state and multidimensional solution NMR spectroscopy for membrane peptides and the interpretation of molecular dynamics of these peptides on the NMR time scale. Examples of these techniques are illustrated by studies of the Pf1 viral coat protein. Chapter 12 by J. K. Blasie, Structure of Integral Membrane Proteins within Membranes via X-Ray and Neutron Diffraction: From Oriented Multilayers to a Single Monolayer, reviews the techniques of using oriented arrays of the photosynthetic reaction center in lipid multilayers to determine the structure profile projected normal to the bilayer. Newer refinements in the method now make it possible to obtain useful diffraction data from oriented protein monolayers.

The final section of the book—Model and Physicochemical Approaches—describes specific examples to test models for membrane protein structures. Chapter 13 by L. K. Tamm, Physical Studies of Peptide-Bilayer Interactions, reviews experiments conducted to characterize the thermodynamics and structural features of the interactions of synthetic and natural peptides with lipid bilayers. Studies of model systems with 20–30 residues help to understand relevant contributions to peptide-bilayer interactions. These data also delineate the basic issues related to protein folding in membranes and the mechanism of biologically active peptides. Chapter 14 by G. A. Woolley and B. A. Wallace, Membrane Protein Structure: Lessons from Gramacidin, provides a forum to illustrate the organization and function of sodium, potassium, and other ion channels. Chapter 15 by J. D. Lear et al., Use of Synthetic Peptides for the Study of Membrane Protein Structure, is concerned with channels formed by small peptides in order to engineer peptides designed to have structural features thought important in natural proteins and to test basic principles. These data have shown that a sequence length greater than 14 is important, that amino acid sequence can affect channel conductance characteristics, and that significant cation conductance can be attained without charged residues in the sequence. Chapter 16 by I. L. Karle, Diffraction Studies of Model and Natural Helical Peptides, summarizes structural data for a large series of peptide crystal structures which reveal favorable packing arrangements driven by van der Waals interactions and that, somewhat surprisingly, water molecules can participate in backbone hydrogen bonds of hydrophobic helices.

This volume is clearly written in a crisp, readable style, and each chapter is punctuated with useful tips of the many pitfalls that can befall the unwary to membrane structure determination. The strengths and limitations of each method for determining membrane structure are presented so that even the novice can evaluate the appropriateness of the techniques to solve the question at hand. Overall, this book gives great value for its cost, which by today's standards is very inexpensive; a must for everyone interested in membrane protein structure, whether expert or student.

Vivian Cody, *Hauptman-Woodward Medical Research Institute*

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