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BOOK REVIEWS

Utilization of Greenhouse Gases. Edited by Chang-jun Liu (Tianjin University), Richard G. Mallinson (University of Oklahoma), and Michele Aresta (University of Bari). American Chemical Society: Washington, DC (Distributed by Oxford University Press). 2003. xii + 412 pp. $145.00. ISBN 0-8412-3827-8.

This book was developed from a symposium of the same title held during the 223rd American Chemical Society National Meeting in Florida in April 2002. To quote from the Preface, the volume "focuses on the simultaneous utilization of greenhouse gases, innovative utilization technologies, and processes for the conversion of greenhouse gases." The 26 chapters are organized under the following headings: General Overview; Simultaneous Utilization; Organic Synthesis with CO_2 as a Reactant; Biochemical Fixation of CO_2; Methane Valorization; Conversion of Methane and Other Greenhouse Gases via Plasmas or Microwave Heating; Application of Supercritical CO_2; and Methane Combustion. An author and a subject index complete the book.

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ICP Emission Spectrometry: A Practical Guide. By Joachim Nölte (AnalytikSupport, Owingen, Germany). Wiley-VCH Verlag GmbH & Co. KGaA: Weinheim. 2003. xii + 268 pp. $49.50. ISBN 3-527-30672-2.

This short book, comprised of eight chapters, provides a wonderful collection of useful practical advice for the operation of ICP emission spectrometers. The book is designed as a tutorial guide for relatively inexperienced instrument operators, and it succeeds admirably as such. The approach taken in this book is to provide useful advice in an informal style, much as one would obtain from the installation and initial training courses provided to new users by instrument manufacturers. The areas of plasma generation, sample introduction, spectrometer optics, signal detection, method development, instrument preparation and calibration, and routine maintenance are covered in a general manner to include most of the commercially successful and a few of the research approaches that have been introduced in the past 40 years. Although a few noteworthy approaches are not included or only briefly mentioned, it is remarkable that there is such a wide coverage of most successful procedures in such a short book.

This book is written for the beginning instrument operator at the upper undergraduate level. It would be a useful supplemental text for an introductory-level graduate course in atomic spectroscopy. It purposely lacks the theoretical and technical details that can be found in many of the wide selection of books on ICP emission spectrometry and does not present sample preparation methods in enough depth to be used by itself as a teaching text. It does, however, present many useful points that are not included in more theoretical textbooks. There are 554 references, most of them from 1970−1990, reflecting the period of the most active development in the evolution of ICP emission instrumentation. This reviewer highly recommends this book as a guide that should be sitting beside every ICP instrument utilized in routine sample analysis.

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Nitrogen, Oxygen and Sulfur Ylide Chemistry. A Practical Approach in Chemistry. Edited by J. Stephen Clark (University of Nottingham). Oxford University Press: Oxford. 2002. xvi + 298 pp. $148.00. ISBN 0-19-850017-3.

This book covers the generation and reactions of nitrogen, oxygen and sulfur ylides in organic synthesis. Its 22 chapters, written by an international group of experts in the field, are organized under the following topics: Nitrogen, oxygen and sulfur ylides: an overview; Ammonium, oxonium and sulfonium ylides; Azomethine, carbonyl and thiocarbonyl ylides; and Nitrile ylides. A subject index completes the book.

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Compendium of Organic Synthetic Methods, Volume 11. By Michael B. Smith (University of Connecticut). John Wiley & Sons, Inc.: Hoboken, NJ. 2003. xxii + 796 pp. $115.00. ISBN 0-471-25965-9.

This book lists functional group transformations and carbon−carbon bond-forming reactions appearing in the literature from 1999 to 2001. It also contains a chapter devoted exclusively to difunctional compounds as well as a new section on cyclobutanations. To navigate the book, a helpful list of abbreviations, indices of monofunctional and difunctional compounds, and an author index have been provided.

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Advances in High Pressure Bioscience and Biotechnology II. Edited by Roland Winter (University of Dortmund). Springer-Verlag: Berlin, Heidelberg, New York. 2003. xvi + 490 pp. $279.00. ISBN 3-540-00977-9.

This book stems from the 2nd International Conference on High Pressure Bioscience and Biotechnology held in Dortmund, Germany in September 2002. The numerous chapters are

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grouped under the following headings: Proteins and Macromolecules − Biophysical Aspects; Protein Unfolding and Reaction; Proteins and High Pressure Enzymology; Protein Misfolding and Aggregation; Protein Crystallography; Nucleic Acids; Membranes and Lipid Mesophases; Microbiology; Biomedical Applications; and Food Science − Chemical and Technological Aspects. An author index completes the book.

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Protein NMR for the Millennium. Biological Magnetic Resonance, Volume 20. Edited by N. Rama Krishna (University of Alabama at Birmingham) and Lawrence J. Berliner (University of Denver). Kluwer Academic/Plenum Publishers: New York. 2003. xii + 342 pp. $135.00. ISBN 0-306-47448-4.

The recent award of the Nobel Prize in Chemistry (2002) to Kurt Wüthrich for his development of NMR techniques to determine the three-dimensional structure of biological macromolecules in solution highlights current advances made within this rapidly growing field. Determination of the solution structure of proteins up to 20−25 kDa has become almost routine now, in favorable cases, due to technical advances in commercially available NMR spectrometers, wide availability of robust software for data processing and analysis, efficient molecular dynamics-based software for calculating structures, and, to a growing extent, application of software that integrates and automates aspects of these steps. Several developments in recent years, however, are allowing the application of solution NMR spectroscopy to extend well beyond the "small protein" niche to systems as large as 0.9 MDa, as shown by Kurt Wüthrich for GroEL/ES. This timely book provides a review of recent developments in the study of large proteins by solution and solid-state NMR spectroscopy and offers detailed insights into the structure, dynamics, and function of multicomponent, biological systems.

The book is divided into three main sections covering the study of large proteins in solution and solid state, refinement of structures, and screening of bioactive ligands. The topics covered include TROSY, segmental isotope labeling of multidomain proteins, analysis of protein domain orientation and dynamics by NMR relaxation techniques, obtaining distance restraints using selective spin labeling, solid-state NMR studies of uniformly labeled proteins, protein encapsulation and dissolution in low viscosity solvents, structure refinement based on residual dipolar couplings, hydrogen bond scalar couplings, and NMR techniques used for the screening of bioactive ligands. The chapters were written by various leaders in their fields who have made significant contributions toward the development and application of state-of-the-art NMR techniques.

The theory and fundamental application of TROSY for the analysis of proteins having molecular masses of up to 110 kDa is discussed in Chapter 1. The recent introduction of this NMR technique has overcome the problem of rapid transverse spin relaxation that previously prohibited the structural analysis of proteins with a molecular mass greater than about 30 kDa. The concept and application of TROSY are presented in a clear and concise manner. Unfortunately, other aspects of the use of TROSY, such as with CRINEPT and CRIPT for polarization transfer in large proteins, for example, receive only a brief mention. The use of these methods, together with TROSY, has recently been applied to GroEL/ES (900 kDa, Wüthrich and co-workers) and p53/Hsp90 (200 kDa, Fersht and co-workers).

Clearly one of the major challenges confronting NMR spectral studies of large proteins and protein complexes not characterized by symmetry is extensive resonance overlap. Chapter 2 is a review of one strategy that may be used to overcome this problem, segmental isotopic labeling. This method involves the introduction of NMR active nuclei into selective regions, usually domains, of a protein. Expressed protein ligation and trans-splicing, two semisynthetic methods that can be used for segmental labeling, are discussed in detail. The authors then describe how segmentally labeled proteins can be used to study the interactions and orientations of domains by various NMR techniques. This section is nicely complemented by a review of NMR relaxation methods for determining interdomain orientations in Chapter 3. Proteins have evolved to have modular structure, and these two chapters illustrate how NMR spectroscopy can be applied to study such large, multidomain proteins in solution.

The application of TROSY to large proteins is optimal when aliphatic protons are replaced by deuterons, which has the side effect of drastically reducing the number and types of $^{1}H-^{1}H$ NOEs that can be analyzed for determination of structures. A solution to this problem through the site-specific incorporation of spin labels in large proteins or protein complexes is the subject of Chapter 4. Paramagnetic centers perturb nuclear relaxation rates in a distance-dependent manner, allowing long-range distance restraints to be determined. The authors review the basic concepts and practical aspects of this technique and then discuss its application to structure determination for large protein systems through numerous examples. This approach is a valuable complement to traditional NOE-based methods and has a promising future.

Chapter 5 is a concise review of the determination of protein structure by solid-state NMR. This area is rapidly evolving and, as pointed out by the author, could potentially contribute significantly to current efforts in structural genomics. The reason for this is that many proteins that cannot be studied by X-ray crystallography or solution NMR because they are either insoluble (e.g., amyloid fibrils) or difficult to crystallize can be readily studied by solid-state NMR. Unfortunately, there is only a very brief discussion of the fundamental principles underlying this promising method. Readers are referred to the recent work of Oschkinat, Griffin, and Opella and their co-workers, as well as others, for recent and very exciting developments in this emerging area of NMR spectroscopy.

As proteins become larger, they tumble more slowly in solution. Wand and co-workers reduced the adverse impact of this phenomenon on the NMR spectra of proteins by encapsulating proteins in reverse micelles and dissolving these aggregates in low viscosity organic solvents; the net effect was to increase the molecular tumbling rate with respect to that for the protein alone in aqueous solution. This subject is very thoroughly reviewed in Chapter 6, which covers the basic principles involved and their application to proteins. While this approach to the study of large proteins is technically demanding, it is

beginning to receive broader application and fits well with the other topics discussed in this book.

Chapters 7 and 8 present a thorough review of the fundamentals and practical use of residual dipolar couplings (RDCs) for structural refinement. The theory and measurement of RDCs using liquid crystalline media, filamentous phage, or anisotropic materials are discussed in detail. The wonderful presentation of this powerful technique is easy to read and should be considered essential reading for any novice considering this technique. As solution NMR is applied to larger and larger systems, the use of partial alignment to measure RDCs is playing an increasingly important role by providing restraints for calculations of structure. Importantly, these restraints allow the alignment of distant regions of a protein to be related to a common molecular alignment frame and help overcome limitations associated with the local nature of NOE-based distance restraints.

It has been shown recently that many NMR active nuclei exhibit scalar coupling across hydrogen bonds in biomolecules; their occurrence in nucleic acids, proteins, and complexes of the two is the topic of Chapter 9. The largest number of examples is available for nucleic acids, and these are thoroughly reviewed. The examples for proteins are fewer in number because of the difficulties in measuring the couplings, which are quite small. Although the characterization of the heavy atom partners in H-bonds does provide an additional source of restraints for determining biomolecular structures, as systems become larger, the small couplings become increasingly difficult to measure; therefore, these studies are currently limited to relatively small systems. As cryogenic NMR probes become more widely available, these techniques may receive wider application. Size issues aside, the measurement of scalar couplings across H-bonds provides unique insights into the physical chemistry of these bonds and their roles in stabilizing biomolecules and in catalytic mechanisms. This chapter provides an up-to-date review of this important topic.

The final chapter of the book is a discussion of the use of NMR spectroscopy to study the interactions between small molecules and proteins. Methods centered on monitoring the effects of these interactions on protein NMR spectra and on small-molecule spectra are separately discussed. These approaches are in widespread use in both academia and industry and contribute meaningfully to the area of drug discovery and rational drug design. This chapter provides a good introduction to these widely used NMR techniques.

In summary, this book assumes a basic knowledge of protein NMR spectroscopy and is thus geared toward graduate students and researchers. The exciting topics that are discussed cover a wide range of areas and are generally reviewed in detail. However, as may be expected with a field that has seen major advances over the past few years, several recent studies are not discussed, as mentioned above. Nevertheless, the references are timely (up to and including 2001) and adequately cover the topics discussed in each chapter. The book is generally easy to read for those with an appreciable knowledge of protein NMR spectroscopy. However, one important topic is not covered, the key role played by isotope labeling in studies of large proteins, for example, the use of extensive deuteration and methyl protonation à la Gardner and Kay. Despite this shortcoming, this book presents a timely review of many recently developed techniques for the study of large proteins by NMR spectroscopy. We highly recommend it as a reference for anyone with an active interest in this field.

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