Methods For General And Molecular Microbiology

Science of Synthesis provides a critical review of the synthetic methodology developed from the early 1800s to date for the entire field of organic and organometallic chemistry. As the only resource providing full-text descriptions of organic transformations and synthetic methods as well as experimental procedures, Science of Synthesis is therefore a unique chemical information tool. Over 1000 world-renowned experts have chosen the most important molecular transformations for a class of organic compounds and elaborated on their scope and limitations. The systematic, logical and consistent organization of the synthetic methods for each functional group enables users to quickly find out which methods are useful for a particular synthesis and which are not. Effective and practical experimental procedures can be implemented quickly and easily in the lab.// The content of this e-book was originally published in November 2008.

This laboratory manual gives a thorough introduction to basic techniques. It is the result of practical experience, with each protocol having been used extensively in undergraduate courses or tested in the authors laboratory. In addition to detailed protocols and practical notes, each technique includes an overview of its general importance, the time and expense involved in its application and a description of the theoretical mechanisms of each step. This enables users to design their own modifications or to adapt the method to different systems. Surzycki has been holding undergraduate courses and workshops for many years, during which time he has extensively modified and refined the techniques described here.

Specialist Periodical Reports provide systematic and detailed review coverage of progress in the major areas of chemical research. Written by experts in their specialist fields the series creates a unique service for the active research chemist, supplying regular critical in-depth accounts of progress in particular areas of chemistry. For over 80 years the Royal Society of Chemistry and its predecessor, the Chemical Society, have been publishing reports charting developments in chemistry, which originally took the form of Annual Reports. However, by 1967 the whole spectrum of chemistry could no longer be contained within one volume and the series Specialist Periodical Reports was born. The Annual Reports themselves still existed but were divided into two, and subsequently three, volumes covering Inorganic, Organic and Physical Chemistry. For more general coverage of the highlights in chemistry they remain a 'must'. Since that time the SPR series has altered according to the fluctuating degree of activity in various fields of chemistry. Some titles have remained unchanged, while others have altered their emphasis along with their titles; some have been combined under a new name whereas others have had to be discontinued. The current list of Specialist Periodical Reports can be seen on the inside flap of this volume.

Our knowledge of biological macromolecules and their interactions is based on the application of physical methods, ranging from classical thermodynamics to recently developed techniques for the detection and manipulation of single molecules. These methods, which include mass spectrometry, hydrodynamics, microscopy, diffraction and crystallography, electron microscopy, molecular dynamics simulations, and nuclear magnetic resonance, are complementary; each has its specific advantages and limitations. Organised by method, this textbook provides descriptions and examples of applications for the key physical methods in modern biology. It is an invaluable resource for undergraduate and graduate students of molecular biophysics in science and medical schools, as well as research scientists looking for an introduction to techniques beyond their specialty. As appropriate for this interdisciplinary field, the book includes short asides to explain physics aspects to biologists and biology aspects to physicists.

The new edition of this popular book emphasizes the decisions that need to be made to select one procedure over another.

Science of Synthesis provides a critical review of the synthetic methodology developed from the early 1800s to date for the entire f ield of organic and organometallic chemistry. As the only resource providing full-text descriptions of organic transformations and s ynthetic methods as well as experimental procedures, Science of Synthesis is therefore a unique chemical information tool. Over 1000 world-renowned experts have chosen the most important molecular transformations for a class of organic compounds and elaborated on their scope and limitations. The systematic, logical and consistent organization of the synthetic methods for each functional group enables users to quickly find out which methods are useful for a particular synthesis and which are not. Effective and practical exp erimental procedures can be implemented quickly and easily in the lab. This enables the chemist to get started immediately with the design and planning of a synthesis. // The content of this e-book was origin

This manual provides general information about molecular techniques relevant to molecular ecological research. Attention is paid to the use of molecular methods for studying the fate of genetically modified and native microorganisms in the environment.

Determining the structure of molecules is a fundamental skill that all chemists must learn. Structural Methods in Molecular Inorganic Chemistry is designed to help readers interpret experimental data, understand the material published in modern journals of inorganic chemistry, and make decisions about what techniques will be the most useful in solving particular structural problems. Following a general introduction to the tools and concepts in structural chemistry, the following topics are covered in detail: • computational chemistry • nuclear magnetic resonance spectroscopy • electron paramagnetic resonance spectroscopy • Mössbauer spectroscopy • rotational spectra and rotational structure • vibrational spectroscopy • electronic characterization techniques • diffraction methods • mass spectrometry The final chapter presents a series of case histories, illustrating how chemists have applied a broad range of structural techniques to interpret and understand chemical systems. Throughout the textbook a strong connection is made between theoretical topics and the real world of practicing chemists. Each chapter concludes with problems and discussion questions, and a supporting website contains additional advanced material. Structural Methods in Molecular Inorganic Chemistry is an extensive update and sequel to the successful textbook Structural Methods in Inorganic Chemistry by Ebsworth, Rankin and Cradock. It is essential reading for all advanced students of chemistry, and a handy reference source for the professional chemist.

With the application of new analytical techniques, the field of food fermentation has grown in recent years. This book provides the latest information and relevant advances on the microbial ecology of fermented foods and the application of molecular methods. This book serves as a guide for students and researchers on the most advanced techniques to identify bacteria and helps in choosing the most appropriate tools to study fermented food from a microbiological point of view.

This book presents tutorial overviews for many applications of variational methods to molecular modeling. Topics discussed include the Gibbs-Bogoliubov-Feynman variational principle, square-gradient models, classical density functional theories, self-consistent-field theories, phase-field methods, Ginzburg-Landau and Helfrich-type phenomenological models, dynamical density functional theory, and variational Monte Carlo methods. Illustrative

examples are given to facilitate understanding of the basic concepts and quantitative prediction of the properties and rich behavior of diverse many-body systems ranging from inhomogeneous fluids, electrolytes and ionic liquids in micropores, colloidal dispersions, liquid crystals, polymer blends, lipid membranes, microemulsions, magnetic materials and high-temperature superconductors. All chapters are written by leading experts in the field and illustrated with tutorial examples for their practical applications to specific subjects. With emphasis placed on physical understanding rather than on rigorous mathematical derivations, the content is accessible to graduate students and researchers in the broad areas of materials science and engineering, chemistry, chemical and biomolecular engineering, applied mathematics, condensed-matter physics, without specific training in theoretical physics or calculus of variations.

The mucins (mucus glycoproteins) have long been a complex corner of glycoprotein biology. While dramatic advances in the separation, structural an- ysis, biosynthesis, and degradation have marked the progress in general glycop- tein understanding, the mucins have lagged behind. The reasons for this lack of progress have always been clear and are only now being resolved. The mucins are very large molecules; they are difficult to separate from other molecules present in mucosal secretions or membranes; they are often degraded owing to natural protective functions or to isolation methodology and their peptide and oligos- charide structures are varied and complex. Understanding these molecules has demanded progress in several major areas. Isolation techniques that protect the intact mucins and allow dissociation from other adsorbed but discrete molecules needed to be developed and accepted by all researchers in the field. Improved methods for the study of very large molecules with regard to their aggregation and polymerization were also needed. Structural analysis of the peptide domains and the multitude of oligosaccharide chains was required for smaller sample sizes, for multiple samples, and in shorter time. In view of these problems it is perhaps not surprising that the mucins have remained a dilemma, of obvious biological importance and interest, but very difficult to analyze.

In the United States, hospitals annually report over 5 million cases of infectious-disease-related illnesses: clinical microbiology laboratories in these hospitals are engaged in detecting and identifying the pathogenic microorganisms in clinical specimens collected from these patients with suspected infections. Clearly, the timely and accurate detection/identification of these microbial pathogens is critical for patient treatment decisions and outcomes for millions of patients each year. Despite an appreciation that the outcome of an infectious-disease-related illness is directly related to the time required to detect and identify a microbial pathogen, clinical microbiology laboratories in the United States as well as worldwide have long been hampered by traditional culture-based assays, which may require prolonged incubation time for slowly growing microorganisms such as Mycobacterium tuberculosis. Moreover, traditional culture-based assays often require multiple steps with additional time needed for discernment of species and/or detection of antimicrobial

resistance. Finally, these traditional, slow multistep culture-based assays are labor-intensive and required skilled clinical microbiologists at the bench. Over the past several decades, advanced molecular techniques in diagnostic microbiology quietly have been revolutionizing the practice of clinical microbiology in the hospital setting. Indeed, molecular diagnostic testing in general and nucleic-acid-based amplification methods in particular have been heralded as diagnostic tools for the new millennium. There is no question that the development of rapid molecular techniques for nucleic acid amplification/characterization combined with automation and user-friendly software has greatly broadened the diagnostic capabilities of the clinical microbiology laboratory. These technical advances in molecular microbiology over the first decade of the 21st Century have profoundly influenced the physical structure of clinical microbiology laboratories as well as their staffing patterns, workflow, and turnaround time. These molecular microbiology advances have also resulted in the need for a revised and updated second edition of Advanced Techniques in Diagnostic Microbiology. This second edition again provides an updated and comprehensive description of the ongoing evolution of molecular methods for the diagnosis of infectious diseases. In addition, many new chapters have been added, including a chapter on the clinical interpretation and relevance of advanced technique results. The second edition, like the first edition, includes both a “techniques” section describing the latest molecular techniques and an “applications” section describing how these advanced molecular techniques are being used in the clinical setting. Finally, the second edition, like the first edition, utilizes a diverse team of authors who have compiled chapters that provide the reader with comprehensive and useable information on advanced molecular microbiology techniques.

Methods for General and Molecular MicrobiologyAmerican Society for Microbiology Press

This volume presents a collection of methods that have contributed to the current understanding of bacterial persisters. Chapters in the book detail general guidelines for measuring persister levels in bacterial cultures, strategies to enrich and resuscitate persister subpopulations, single-cell approaches for visualizing and characterizing persisters, omics techniques and cellular and animal models for studying persistence. Written in the highly successful Methods in Molecular Biology series format, chapters include introductions to their respective topics, lists of the necessary materials and reagents, step-by-step, readily reproducible laboratory protocols, and tips on troubleshooting and avoiding known pitfalls. Authoritative and cutting-edge, Bacterial Persistence: Methods and Protocols, Second Edition aims to be a useful practical guide to researchers to help further their study in this field.

Science of Synthesis provides a critical review of the synthetic methodology developed from the early 1800s to date for the entire field of organic and organometallic chemistry. As the only resource providing full-text descriptions of organic transformations and synthetic methods as well as experimental procedures, Science of Synthesis is therefore a unique

chemical information tool. Over 1000 world-renowned experts have chosen the most important molecular transformations for a class of organic compounds and elaborated on their scope and limitations. The systematic, logical and consistent organization of the synthetic methods for each functional group enables users to quickly find out which methods are useful for a particular synthesis and which are not. Effective and practical experimental procedures can be implemented quickly and easily in the lab.// The content of this e-book was originally published in December 2007.

Over the past 40 years the field of molecular simulations has evolved from picosecond studies of isolated macromolecules in vacuum to studies of complex, chemically heterogeneous biological systems consisting of millions of atoms, with the simulation time scales spanning up to milliseconds. In Biomolecular Simulations: Methods and Protocols, expert researchers illustrate many of the methods commonly used in molecular modelling of biological systems, including methods for electronic structure calculations, classical molecular dynamics simulations and coarse-grained techniques. A selection of advanced techniques and recent methodological developments, which rarely find coverage in traditional textbooks, is also introduced. Written in the highly successful Methods in Molecular Biology series format, chapters include general introductions to well-established computational methodologies, applications to real-world biological systems, as well as practical tips and general protocols on carrying out biomolecular simulations. Special emphasis is placed on simulations of proteins, lipids, nucleic acids, and carbohydrates. Authoritative and practical, Biomolecular Simulations: Methods and Protocols seeks to aid scientists in further simulation studies of biological systems.

A comprehensive state-of-the-art collection of the most frequently used techniques for plant cell and tissue culture. Readily reproducible and extensively annotated, the methods range from general methodologies, such as culture induction, growth and viability evaluation, and contamination control, to such highly specialized techniques as chloroplast transformation involving the laborious process of protoplast isolation and culture. Most of the protocols are currently used in the research programs of the authors or represent important parts of business projects aimed at the generation of improved plant materials. Two new appendices explain the principles for formulating culture media and the composition of the eight most commonly used media formulations, and list more than 100 very useful internet sites.

Printed Edition of the Special Issue Published in Entropy

The amount of information that can be obtained by using molecular techniques in evolution, systematics and ecology has increased exponentially over the last ten years. The need for more rapid and efficient methods of data acquisition and analysis is growing accordingly. This manual presents some of the most important techniques for data acquisition developed over the last years. The choice and justification of data analysis techniques is also an important and critical aspect of modern phylogenetic and evolutionary analysis and so a considerable part of this volume addresses this

important subject. The book is mainly written for students and researchers from evolutionary biology in search for methods to acquire data, but also from molecular biology who might be looking for information on how data are analyzed in an evolutionary context. To aid the user, information on web-located sites is included wherever possible. Approaches that will push the amount of information which systematics will gather in the

Science of Synthesis provides a critical review of the synthetic methodology developed from the early 1800s to date for the entire field of organic and organometallic chemistry. As the only resource providing full-text descriptions of organic transformations and synthetic methods as well as experimental procedures, Science of Synthesis is therefore a unique chemical information tool. Over 1000 world-renowned experts have chosen the most important molecular transformations for a class of organic compounds and elaborated on their scope and limitations. The systematic, logical and consistent organization of the synthetic methods for each functional group enables users to quickly find out which methods are useful for a particular synthesis and which are not. Effective and practical experimental procedures can be implemented quickly and easily in the lab. // The content of this e-book was originally published in December 2001.

A first source for traditional methods of microbiology as well as commonly used modern molecular microbiological methods. • Provides a comprehensive compendium of methods used in general and molecular microbiology. • Contains many new and expanded chapters, including a section on the newly important field of community and genomic analysis. • Provides step-by-step coverage of procedures, with an extensive list of references to guide the user to the original literature for more complete descriptions. • Presents methods for bacteria, archaea, and for the first time a section on mycology. • Numerous schematics and illustrations (both color and black and white) help the reader to easily understand the topics presented.

The QM/MM method, short for quantum mechanical/molecular mechanical, is a highly versatile approach for the study of chemical phenomena, combining the accuracy of quantum chemistry to describe the region of interest with the efficiency of molecular mechanical potentials to represent the remaining part of the system. Originally conceived in the 1970s by the influential work of the the Nobel laureates Martin Karplus, Michael Levitt and Arieh Warshel, QM/MM techniques have evolved into one of the most accurate and general approaches to investigate the properties of chemical systems via computational methods. Whereas the first applications have been focused on studies of organic and biomolecular systems, a large variety of QM/MM implementations have been developed over the last decades, extending the range of applicability to address research questions relevant for both solution and solid-state chemistry as well. Despite approaching their 50th anniversary in 2022, the formulation of improved QM/MM methods is still an active field of research, with the aim to (i) extend the applicability to address an even broader range of research questions in chemistry

and related disciplines, and (ii) further push the accuracy achieved in the QM/MM description beyond that of established formulations. While being a highly successful approach on its own, the combination of the QM/MM strategy with other established theoretical techniques greatly extends the capabilities of the computational approaches. For instance the integration of a suitable QM/MM technique into the highly successful Monte-Carlo and molecular dynamics simulation protocols enables the description of the chemical systems on the basis of an ensemble that is in part constructed on a quantum-mechanical basis. This eBook presents the contributions of a recent Research Topic published in Frontiers in Chemistry, that highlight novel approaches as well as advanced applications of QM/MM method to a broad variety of targets. In total 2 review articles and 10 original research contributions from 48 authors are presented, covering 12 different countries on four continents. The range of research questions addressed by the individual contributions provide a lucid overview on the versatility of the QM/MM method, and demonstrate the general applicability and accuracy that can be achieved for different problems in chemical sciences. Together with the development of improved algorithms to enhance the capabilities of quantum chemical methods and the continuous advancement in the capacities of computational resources, it can be expected that the impact of QM/MM methods in chemical sciences will be further increased already in the near future.

Applications of Numerical Methods in Molecular Spectroscopy provides a mathematical background, theoretical perspective, and review of spectral data processing methods. The book discusses methods of complex spectral profile separation into bands, factor analysis methods, methods of quantitative analysis in molecular spectroscopy and reflectance spectroscopy, and new data processing methods. Mathematical methods in special areas of molecular spectroscopy, such as color science, electron spin resonance, and nuclear magnetic resonance spectroscopies are also covered. The book will benefit researchers and postgraduate students in fields of chemistry, physics, and biology.

Science of Synthesis provides a critical review of the synthetic methodology developed from the early 1800s to date for the entire field of organic and organometallic chemistry. As the only resource providing full-text descriptions of organic transformations and synthetic methods as well as experimental procedures, Science of Synthesis is therefore a unique chemical information tool. Over 1000 world-renowned experts have chosen the most important molecular transformations for a class of organic compounds and elaborated on their scope and limitations. The systematic, logical and consistent organization of the synthetic methods for each functional group enables users to quickly find out which methods are useful for a particular synthesis and which are not. Effective and practical experimental procedures can be implemented quickly and easily in the lab.// The content of this e-book was originally published in December 2006.

Display technologies have become a very powerful way of generating therapeutic lead molecules and specific reagents

for increasing our understanding of biology; however, despite being first described shortly after phage display, the use of ribosome display and related methods have been much less widespread. Since this is in part due to the complexity of the methods, Ribosome Display and Related Technologies: Methods and Protocols seeks to extend their use by collecting expert contributions describing these detailed protocols. The protocols described range from well-established methods that have been used for a decade to generate high affinity antibodies, which are already in the clinic, to methods that are in their early stages of application such as display of peptides incorporating non-canonical amino acids. Written in the highly successful Methods in Molecular BiologyTM series format, chapters include introductions to their respective topics, lists of the necessary materials and reagents, step-by-step, readily reproducible laboratory protocols, and tips on troubleshooting and avoiding known pitfalls. Invaluable and easy to use, Ribosome Display and Related Technologies: Methods and Protocols will be of great benefit to those with general molecular biology or protein engineering experience who wish to select peptides or proteins by display, those with phage display experience who would benefit from the application of ribosome display, as well as those with some ribosome display experience who would like to expand the range of applications to which they are applying the technology.

First published in 2004. Routledge is an imprint of Taylor & Francis, an informa company.

There are numerous books on cellular and molecular protocols for general use in cell biology but very few are exclusively devoted to neurobiology. This book fills this gap and explains in a clear and consistent manner, some of the more commonly used protocols in neuroscience research. Each chapter is written by either the person who invented the procedure or an expert in the field. The format is uniform: "Overview," "Background," "Protocols," and "results and discussion." Each protocol begins with the principle of the technique, studies in cell culture, materials and reagents, and, lastly, step-by-step outline of the procedure itself. This highly practical book is also well illustrated (with 17 four color plates) to make the concepts and procedures easy to understand and perform.

Science of Synthesis provides a critical review of the synthetic methodology developed from the early 1800s to date for the entire field of organic and organometallic chemistry. As the only resource providing full-text descriptions of organic transformations and synthetic methods as well as experimental procedures, Science of Synthesis is therefore a unique chemical information tool. Over 1000 world-renowned experts have chosen the most important molecular transformations for a class of organic compounds and elaborated on their scope and limitations. The systematic, logical and consistent organization of the synthetic methods for each functional group enables users to quickly find out which methods are useful for a particular synthesis and which are not. Effective and practical experimental procedures can be implemented quickly and easily in the lab.// The content of this e-book was originally published in May 2007.

In recent years, advanced molecular techniques in diagnostic microbiology have been revolutionizing the practice of clinical microbiology in the hospital setting. Molecular diagnostic testing in general and nucleic acid-based amplification methods in particular have been heralded as diagnostic tools for the new millennium. This third edition covers not only the most recent updates and advances, but details newly invented omic techniques, such as next generation sequencing. It is divided into two distinct volumes, with Volume 1 describing the techniques, and Volume 2 addressing their applications in the field. In addition, both volumes focus more so on the clinical relevance of the test results generated by these techniques than previous editions.

The molecular modeling perspective in drug design. (N. Calude Cohen). Molecular graphics and modeling: tools of the trade. (Roderick E. Hubbard). Molecular modeling of small molecules. (Tamara Gund). Computer assisted new lead design. (Akiko Itai, Miho Yamada Mizutani, Yoshihiko Nishibata, and Nubuo Tomioka). Experimental techniques and data banks. (John P. Priestle and C. Gregory Paris). Computer-assisted drug discovery. (Peter Gund, Gerald Maggiora, and James P. Snyder). Modeling drug-receptor interactions. (Konrad F. Koehler, Shashidhar N. Rao, and James P. Snyder). Glossary of terminology. (J. P. Tollenaere).

The last few years have seen the rapid development of new methodology in the field of molecular biology. New techniques have been regularly introduced and the sensitivity of older techniques greatly improved upon. Developments in the field of genetic engineering in particular have contributed a wide range of new techniques. The purpose of this book therefore is to introduce the reader to a selection of the more advanced analytical and preparative techniques which the editors consider to be frequently used by research workers in the field of molecular biology. In choosing techniques for this book we have obviously had to be selective, and for the sake of brevity a knowledge of certain basic biochemical techniques and terminology has been assumed. However, since many areas of molecular biology are developing at a formidable rate and constantly generating new terminology, a glossary of terms has been included. The techniques chosen for this book are essentially based on those used in a series of workshops on 'techniques in molecular biology' that have been held at The Hatfield Polytechnic in recent years. In choosing these chapters we have taken into account many useful suggestions and observations made by participants at these workshops. Each chapter aims to describe both the theory and relevant practical details for a given technique, and to identify both the potential and limitations of the technique. Each chapter is written by authors who regularly use the technique in their own laboratories.

This book presents a range of fundamentally new approaches to solving problems involving traditional molecular models. Fundamental molecular symmetry is shown to open new avenues for describing molecular dynamics beyond standard perturbation techniques. Traditional concepts used to describe molecular dynamics are based on a few fundamental

assumptions, the ball-and-stick picture of molecular structure and the respective perturbative treatment of different kinds of couplings between otherwise separate motions. The book points out the conceptual limits of these models and, by focusing on the most essential idea of theoretical physics, namely symmetry, shows how to overcome those limits by introducing fundamentally new concepts. The book begins with an introduction to molecular symmetry in general, followed by a discussion of nuclear spin symmetry. Here, a new correlation between identical particle exchange and spin angular momentum symmetry of nuclei is exhibited. The central part of the book is the discussion of extremely floppy molecules, which are not describable in the framework of traditional theories. The book introduces a fundamentally new approach to describing the molecular dynamics of these molecules - the super-rotor model, which is based on a five-dimensional symmetry that has never been observed in molecules before. By applying the super-rotor theory to the prototype of floppy molecules, protonated methane, this model can consistently predict the symmetry and energy of low-energy states, which were characterized experimentally only a few years ago. The theoretical predictions agree with the experimental results, which makes the prospect of further developing the super-rotor theory and applying it to other molecules a promising one. In the final section, the book also covers the topic of ultrafast rotations, where usual quantum calculations reach their natural limits. A semi-classical method for determining rotational energies, developed in the early 1990s, is shown to be attachable to quantum calculations of the vibrational states. This new combined method is suitable for efficiently calculating ro-vibrational energies, even for molecular states with large angular momentum.

Science of Synthesis provides a critical review of the synthetic methodology developed from the early 1800s to date for the entire field of organic and organometallic chemistry. As the only resource providing full-text descriptions of organic transformations and synthetic methods as well as experimental procedures, Science of Synthesis is therefore a unique chemical information tool. Over 1000 world-renowned experts have chosen the most important molecular transformations for a class of organic compounds and elaborated on their scope and limitations. The systematic, logical and consistent organization of the synthetic methods for each functional group enables users to quickly find out which methods are useful for a particular synthesis and which are not. Effective and practical experimental procedures can be implemented quickly and easily in the lab.// The content of this e-book was originally published in December 2005.

Molecular systems are assemblies of molecules designed to possess special qualities and desired functionality. Such systems are important because they provide materials with novel properties, and they will be particularly useful for minimizing electronic devices. Molecular systems often form organized molecular crystals, polymers, or thin films that are significantly more complex than current materials. To provide a sound basis for understanding these levels of complexity, this book provides an analysis of the fundamentals of electronic structures, dynamic processes in condensed phases,

and the unique properties of organic molecular solids and the environmental effects on these properties. Also covered are the latest methods in physical chemistry that are particularly useful for deriving and controlling the functionality of molecular systems. A second volume subtitled From Molecular Systems to Molecular Devices is also being published. Science of Synthesis provides a critical review of the synthetic methodology developed from the early 1800s to date for the entire field of organic and organometallic chemistry. As the only resource providing full-text descriptions of organic transformations and synthetic methods as well as experimental procedures, Science of Synthesis is therefore a unique chemical information tool. Over 1000 world-renowned experts have chosen the most important molecular transformations for a class of organic compounds and elaborated on their scope and limitations. The systematic, logical and consistent organization of the synthetic methods for each functional group enables users to quickly find out which methods are useful for a particular synthesis and which are not. Effective and practical experimental procedures can be implemented quickly and easily in the lab.// The content of this e-book was originally published in December 2003.

Prominent multinational contributors present articles on condensed matter physics, quantum biology and quantum chemistry. Among the topics covered: reactive molecular collisions, density-functional theory, atomic and molecular phenomena in astrophysics, non-Born-Oppenheimer methods, thin films and surfaces.