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This handbook describes experimental techniques to monitor and manipulate individual biomolecules, including fluorescence detection, atomic force microscopy, and optical and magnetic trapping. It includes single-molecule studies of physical properties of biomolecules such as folding, polymer physics of protein and DNA, enzymology and biochemistry, single molecules in the membrane, and single-molecule techniques in living cells.

Several milestones in biology have been achieved since the first publication of the Handbook of Molecular and Cellular Methods in Biology and Medicine. This is true particularly with respect to genome-level sequencing of higher eukaryotes, the invention of DNA microarray technology, advances in bioinformatics, and the development of RNAi technology. Now in its third edition, this volume provides researchers with an updated tool kit that incorporates conventional as well as modern approaches to tackle biological and medicinal research in the post-genomics era. Significantly revised to address these recent changes, the editors have evaluated, revised, and sometimes replaced protocols with more efficient, more reliable, or simpler ones. The book has also been reorganized with section headings focusing on different biological levels connected to one another, taking into account the central dogma of biology (DNA RNA protein metabolites). The book first explores traditional approaches and then moves to the modern "omics" approaches, including genomics, proteomics, and metabolomics. It also discusses the manipulation of biological systems (including RNAi) and macromolecular analyses, focusing on the use of microscopy. In each chapter, various notes and cautionary considerations are presented for potentially hazardous reagents. Filled with diagrams, tables, and figures to clarify methods, most chapters also contain Troubleshooting Guides indicating problems, possible causes, and solutions that may be incurred in carrying out the procedures. Researchers and scientists who master the techniques in this book are putting themselves at the cutting edge of biological and medicinal research.

Since the publication of the best-selling Handbook of Molecular and Cellular Methods in Biology and Medicine, the field of biology has experienced several milestones. Genome sequencing of higher eukaryotes has progressed at an unprecedented speed. Starting with baker's yeast (*Saccharomyces cerevisiae*), organisms sequenced now include human (*Homo sa*

In the first volume, Fundamental Concepts in Biophysics, the authors lay down a foundation for biophysics study. Rajiv Singh opens the book by pointing to the central importance of " Mathematical Methods in Biophysics ". William Fink follows with a discussion on " Quantum Mechanics Basic to Biophysical Methods ". Together, these two chapters establish some of the principles of mathematical physics underlying many biophysics techniques. Because computer modeling forms an intricate part of biophysics research, Subhadip Raychaudhuri and colleagues introduce the use of computer modeling in " Computational Modeling of Receptor – Ligand Binding and Cellular Signaling Processes ". Yin Yeh and coworkers bring to the reader 's attention the physical basis underlying the common use of fluorescence spectroscopy in biomedical research in their chapter " Fluorescence Spectroscopy ". Electrophysiologists have also applied biophysics techniques in the study of membrane proteins, and Tsung-Yu Chen et al. explore stochastic processes of ion transport in their " Electrophysiological Measurements of Membrane Proteins ". Michael Saxton takes up a key biophysics question about particle distribution and behavior in systems with spatial or temporal inhomogeneity in his chapter " Single – Particle Tracking ". Finally, in " NMR Measurement of Biomolecule Diffusion ", Thomas Jue explains how magnetic resonance techniques can map biomolecule diffusion in the cell to a theory of respiratory control. This book thus launches the Handbook of Modern Biophysics series and sets up for the reader some of the fundamental concepts underpinning the biophysics issues to be presented in future volumes.

The enormous complexity of biological systems at the molecular level must be answered with powerful computational methods. Computational biology is a young field, but has seen rapid growth and advancement over the past few decades. Surveying the progress made in this multidisciplinary field, the Handbook of Computational Molecular Biology of

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Handbook of Molecular Gastronomy: Scientific Foundations and Culinary Applications presents a unique overview of molecular gastronomy, the scientific discipline dedicated to the study of phenomena that occur during the preparation and consumption of dishes. It deals with the chemistry, biology and physics of food preparation, along with the physiology of food consumption. As such, it represents the first attempt at a comprehensive reference in molecular gastronomy, along with a practical guide, through selected examples, to molecular cuisine and the more recent applications named note by note cuisine. While several books already exist for a general audience, either addressing food science in general in a "light" way and/or dealing with modern cooking techniques and recipes, no book exists so far that encompasses the whole molecular gastronomy field, providing a strong interdisciplinary background in the physics, biology and chemistry of food and food preparation, along with good discussions on creativity and the art of cooking. Features: Gives A – Z coverage to the underlying science (physics, chemistry and biology) and technology, as well as all the key cooking issues (ingredients, tools and methods). Encompasses the science and practice of molecular gastronomy in the most accessible and up-to-date reference available. Contains a final section with unique recipes by famous chefs. The book is organized in three parts. The first and main part is about the scientific discipline of molecular and physical gastronomy; it is organized as an encyclopedia, with entries in alphabetical order, gathering the contributions of more than 100 authors, all leading scientists in food sciences, providing a broad overview of the most recent research in molecular gastronomy. The second part addresses educational applications of molecular gastronomy, from primary schools to universities. The third part provides some innovative recipes by chefs from various parts of the world. The authors have made a particular pedagogical effort in proposing several educational levels, from elementary introduction to deep scientific formalism, in order to satisfy the broadest possible audience (scientists and non-scientists). This new resource should be very useful to food scientists and chefs, as well as food and culinary science students and all lay people interested in gastronomy.

Dyneins are molecular motors that are involved in various cellular processes, such as cilia and flagella motility, vesicular transport, and mitosis. Since the first edition of this book was published in 2012, there has been a significant breakthrough: the crystal structures of the motor domains of cytoplasmic dynein have been solved and the previously unknown details of this huge and complex molecule have been unveiled. This new edition contains 14 chapters written by researchers in the US, Europe, and Asia, including 3 new chapters that incorporate new fields. The other chapters have also been substantially updated. Compared with the earlier edition, this book focuses more on the motile mechanisms of dynein, especially by biophysical methods such as cryo-EM, X-ray crystallography, and single-molecule nanometry. It is a major handbook for frontline researchers as well as for advanced students studying cell biology, molecular biology, biochemistry, biophysics, and structural biology.

"a gem of a textbook which manages to produce a genuinely fresh, concise yet comprehensive guide" – Mark Leske, University of York "destined to become a standard reference... Not just a ' how to ' handbook but also an accessible primer in the essentials of kinetic theory and practice." – Michael Geeves, University of Kent "covers the entire spectrum of approaches, from the traditional steady state methods to a thorough account of transient kinetics and rapid reaction techniques, and then on to the new single molecule techniques" – Stephen Halford, University of Bristol This illustrated treatment explains the methods used for measuring how much a reaction gets speeded up, as well as the framework for solving problems such as ligand binding and macromolecular folding, using the step-by-step approach of numerical integration. It is a thoroughly modern text, reflecting the recent ability to observe reactions at the single-molecule level, as well as advances in microfluidics which have given rise to femtoscale studies. Kinetics is more important now than ever, and this book is a vibrant and approachable entry for anyone who wants to understand mechanism using transient or single molecule kinetics without getting bogged down in advanced mathematics. Clive R. Bagshaw is Emeritus Professor at the University of Leicester, U.K., and Research Associate at the University of California at Santa Cruz, U.S.A.

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