

does not obstruct the understanding of the concept under discussion. With its detailed table of contents and index the book makes it easy to locate information. The contributing authors have done a very good job of balancing detail and demonstrating the concepts in a straightforward manner. Each chapter of the major sections is written by authoritative experts in their respective fields contains an introduction to the subject, an experimental design and methods section, followed by results and conclusions. Although the chapters are designed with the outline of a research paper, which makes them easy to follow owing to a layout familiar to scientists, the chapters are not mere replications or aggregations of collected research papers, which is a big plus for the book. Numerous figures and illustrations both in color and grayscale are provided, and the seemingly intended lack of experimental detail is compensated by citations of prior work to obtain further information if the reader desires.

The topics included are comprehensive, timely, and are explained well. The book is one of the best assemblies of information on recent advances in biomedical nanotechnology and its wide-ranging application in biology and medicine. I believe this book is indispensable not only to all those working in nanosciences and engineering, but also for those who are involved in life sciences and medical research and development, and who would like to get an idea about the promises of nanotechnology for their field. This book will also be of great interest to undergraduate and graduate students in such subdisciplines of engineering as biomedical, materials, electrical and optoelectronics, as well as those studying experimental biology, basic and applied medical sciences, and biotechnology. This would therefore be a handy reference book for educators in nanotechnologies.

In conclusion, this book gives a broad overview with specific examples of nano-biotechnology and applied nanomedical research while providing clear scientific and engineering principles of nanotechnology in the areas covered. It can therefore be recommended as a reference book for experts in experimental

nano-bioscience and as an excellent introductory book for new recruits into the field of nano-biotechnology.

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[1] R. A. Freitas, *Nanomedicine (Vol. IIA)*, Landes Bioscience, Austin, 2003..

Bioinformatics—From Genomes to Therapies

Edited by *Thomas Lengauer*.

Wiley-VCH, Weinheim 2007. 1732 pp. (3-vol. set), hardcover € 479.00.—ISBN 978-3-527-31278-8

This work is an encyclopedic three-volume set focused on all things bioinformatic. The work is very well edited and compiled by Thomas Lengauer with contributions from distinguished scientists from all over the world who use bioinformatics tools and techniques in their research. An exhaustive review of the work would not do it justice. The three volumes are intuitively organized as follows:

Volume 1 covers the basics of protein and nucleic acid sequence along with sequence analysis, alignment, protein secondary structure prediction and homology modeling.

Volume 2 covers interactions from hormone-receptor to drug-enzyme, as well as DNA microarray techniques (clinical microarray included), molecular docking (structure-based drug design), gene classification, and proteomics.

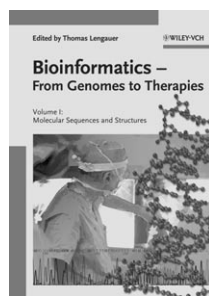
Volume 3 covers the relation of protein sequence and structure to function. Protein function prediction, genomics, evolution of drug resistance, database integration (biodatabases), and even biological data visualization techniques are

covered. Volume 3 has a cumulative index covering content in all three volumes of the set. The reader will find this index to be very helpful.

Each volume is subdivided into “parts” composed of chapters, each with their own bibliography. Each part addresses a specific area of bioinformatics research. For example, Part 4 of Volume 1 addresses the area of structure prediction. This part is composed of two chapters: Predicting Simplified Features of Protein Structure; Homology Modeling in Biology and Medicine. The first chapter provides a smooth introduction to the aspects of predicting protein secondary structure. This chapter gives a history of the techniques, their evolution, and has clear, concise figures describing their accuracy (comparison analysis). In addition, information about online resources is given in a table. An excellent discussion describing the problems with predicting and modeling transmembrane regions of proteins is a nice example of the many challenges in structural bioinformatics today.

The homology modeling chapter has an introduction into the basics of the techniques: template-based, side-chain modeling, and loop prediction, to name a few. The chapter provides a list of online resources and brief descriptions of the currently available homology modeling programs (such as Modeller and MolIDE). However, the author of this chapter spent too much time discussing his own homology modeling software package, and the list of software covered neglects to mention the popular GeneMine/Look software package. The Jackal suite of homology modeling tools developed at Columbia University was also absent in this discussion. The author’s homology modeling software package is an excellent tool, and the tutorial illustration is appreciated in this context. Nevertheless, a more balanced assessment of the available homology modeling tools would have been a better approach in this reviewer’s opinion.

The topics listed above are only a sample of what is available in each volume. Each chapter is a full-blown minireview of the subtopic covered. The chapters are well documented and intelligently written. In fact, the volume parts



taken as a composite of the chapters in this book are better than full reviews because they provide the basic fundamentals required for understanding the material covered in their introductory sections. Not all of the parts need be read in the order given. For a more global appreciation of bioinformatics in general, this set of reference books requires a

basic understanding of biochemistry, statistics, molecular biology, genetics, physical chemistry, and organic chemistry. However, specialists in these various disciplines will be pleased with the subtopics directed to their area(s) of expertise. This treatise on bioinformatics is an excellent reference set to use as additional reading in advanced undergraduate and

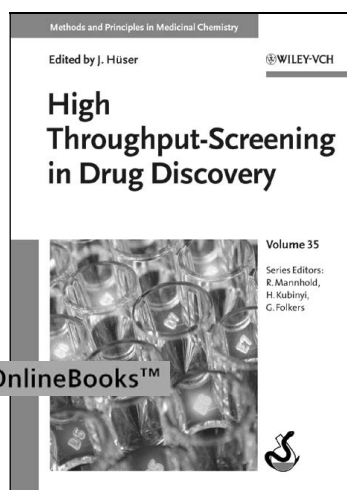
graduate courses or for any reference collection.

John E. Kerrigan

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DOI: 10.1002/cmdc.200700195

The professional guide for successful compound screening



2006. XVIII, 362 pages,
142 figures 13 in color, 11
tables. Hardcover.
ISBN: 978-3-527-31283-2
€ 139.- /£ 95.- /US\$ 180.-

*JÖRG HÜSER, Bayer HealthCare,
Wuppertal, Germany (ed.)*

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