scope implied by the title, including the several chapters on microarray methods and the chapters on gene ontology and gene evolution. Some of the material in the later chapters might be better described as cheminformatics, and the chapter on protein design is a slight stretch, but these are minor quibbles. The chapters that really stretch the limits of the title include those on mass spectroscopy and NMR methods for drug discovery. Another sprawling but enjoyable chapter ("Receptor-Binding Sites", by Darren R. Flower) includes, among other topics, X-ray crystallography, homology modeling, molecular dynamics, pharmacophore- and structure-based docking, p$K_a$ prediction, and binding-site identification; only a few of these topics fit comfortably within a conventional, narrow definition of "bioinformatics". These chapters are well written and informative, and the book would be poorer without them. The editor finesses the issue of the title in the preface by defining the scope of the book to encompass "new, powerful technologies [for drug discovery] that have a prominent bioinformatic component". This statement would provide a more accurate, albeit awkward, title for the book. Whether the broad scope of the book is a strength or a weakness of this volume is, I suspect, a matter a taste. Bioinformaticists expecting to find in-depth discussions of topics more conventionally considered within the scope of their field might be disappointed. Readers looking for a broad overview of data-rich technologies for drug discovery will likely enjoy the volume quite a bit. By reading the whole volume, one can learn a great deal indeed.

The biggest strength of the book is that the chapters are written by active practitioners of the methods described, and the depth of their knowledge and enthusiasm are apparent. The overall feel of the book is a "from the trenches" view on various developing technologies for drug discovery. The detailed, step-by-step protocols distinguish this volume from other edited series. Lists of specific websites, and even examples of input files for specific analysis programs, are among the highlights. An inevitable corollary is that the focus on specific technology platforms narrows the scope; alternative programs/methods are sometimes omitted. Consistent with the broad scope of the book, roughly half of the detailed protocols describe experimental rather than computational techniques.

This compendium falls prey to common pitfalls of multiauthor volumes. There is considerable redundancy among the chapters, notably among the four chapters focused on microarray data, and among some of the later chapters that cover virtual compound libraries and their uses. The chapters also differ dramatically in style and organization. Some chapters are straightforward reviews of available technology. Some are case studies, highlighting how the authors have used bioinformatics and other technologies to solve a specific problem. The most satisfying are the chapters written as tutorials. Chapter 2, "Basic Microarray Analysis", written by Scott A. Ness, is a terse but lucid introduction to microarray methods, clearly written with non-experts (like myself) in mind. Chapter 14 is another short gem, providing a wealth of practical advice on chemical database preparation.

One final weakness of the book is the low quality of many of the figures. Many of the figures, particularly in the later chapters focused on structure-based methods for drug discovery, suffer from not being presented in color. In an age of elaborate Powerpoint presentations and color figures in essentially every journal, low-quality black-and-white images are jarring, and seem out of place in a reasonably pricey reference book.

After reading through the book, I find myself hoping that it will find a readership. The vast majority of titles in the *Methods in Molecular Biology* series describe experimental techniques. Introducing computational methods into this series is an important experiment, and I hope that other volumes will be forthcoming. The field of computational biology, including bioinformatics and other disciplines, can certainly benefit from an effort to reach out to a broad audience, by providing well-tested and -documented protocols that even novices can use profitably. This volume represents a worthwhile albeit imperfect step towards this goal.

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## Directory of Therapeutic Enzymes

Edited by *Barry McGrath* and *Gary Walsh.*

*CRC Press, Boca Raton 2005. 312 pp., hardcover $ 159.95.—ISBN 0-8493-2714-8*

The editors address the book to biochemists working in biotechnological research in industry, research institutions and universities. The book provides a concise review of the recombinant enzymes produced for analysis and therapy. Particular focus is set on applied enzymology and enzyme engineering in the first two general chapters, which are followed by 11 chapters dealing in detail with selected examples of important enzymes used in therapies of blood-clotting disorders, in the treatment of cancer and some genetic disorders. Most of the authors of the 13 chapters are industrial experts, and their research areas cover genomics, protein biochemistry and analysis, biotechnology and clinical applications.

The use of recombinant enzymes in clinical therapy is a steadily growing field. It should be noted that very soon the first generica of products such as tissue plasminogen adivator will be on the market. Furthermore, about 100 enzymes are used as diagnostic tools. The industrial use of proteases and carbohydrates in food technology and in laundry and the leather industry will expand permanently. In particular, new thermostable and oxidant-resistant enzymes as well as enzymes working in organic media, for example, for group transformation of chemicals, will be developed. The bioengineering of novel properties is summarized in a special chapter.

The book describes recent research efforts and offers an up-to-date review of classical therapeutic enzymes, as shown

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by a look to the references, which cover the literature of 2005.

The reader is only informed a little in a few chapters about the safety aspects and side effects, such as immune reactions observed in clinical studies with the therapeutic enzymes. This might deserve a separate general chapter in a future edition of the book. The keyword index is useful but should be improved by omitting a number of double and meaningless keywords. The abbreviation of L-asparaginase as L-Asp (aspartic acid) should be avoided. The table of contents does not contain the main subtitles only the titles of chapters.

In summary the book may find a broad readership in both academic and industrial research because it covers in a handy and well-weighted format all the different aspects and some hot-topics of therapeutic enzymes. The book provides concise information from the view of experts in the field with fast access to recent literature.

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