Book Reviews

Comparative Genomics and Proteomics in Drug Discovery. Edited by J. Parrington and K. Coward. Taylor and Francis, New York. 2007. vii + 182 pp. 16 × 24 cm. ISBN 978-0-415-39653-0. $198.00.

For many years a promise has been made, or implied, that the era of genomics and related fields will significantly advance the discovery of disease-specific genes, drugable targets, and new drugs. The stated purpose of this book is to present research and views on the contributions of genomics and proteomics in drug discovery research. While many of the seven chapters do not fulfill this purpose as related to drug discovery, some chapters provide valuable discussions of disease-target identification leading to drug discovery.

The first three chapters focus on the etiology of diseases caused by the protozoan parasites *Trypanosomes* and *Plasmodium*. These chapters should be of interest to those specializing in these organisms, but there was little presented on the drug-discovery front, and thus, there was not much to generalize to other drug-discovery efforts.

Chapters 4 and 5 focus on two gene families, nicotinic receptors and sodium channel proteins, presenting genomic analyses and comparisons across family members. These chapters offer a discovery research framework that is applicable to other gene families and target discovery. The family members of nicotinic receptors are presented with an emphasis on comparisons across species genomes to elucidate function. The roles in disease for sodium channel proteins are discussed in Chapter 5, along with discussions of mechanisms for existing sodium channel blockers. We get a taste of functional and drug specificity profiles across family members and the potential for new discoveries relating structure, function, and small-molecule interactions.

Chapters 6 and 7 should appeal to a broad audience, with discussions of how one utilizes genomic and related data to advance diagnostics, target discovery, and improve existing disease treatment. Chapter 6 tackles the issues of applying various "omic" fields, such as genomics, to diagnostics and treatment management, with a well-deserved evaluation of the challenges and problems encountered. Chapter 7 lays out one paradigm for applying omics data to target identification involving the shift from "wet" bench research to computer-based research for drug-target discovery. A survey of data, summary results, and sources, ranging from genomics to drug databases, along with tools for analysis is presented for assembly into an informatics-based approach to discovering new drug targets.

In summary, the chapters do not mesh with the title of the book, but they do present the state of research for a wide range of topics focused on disease etiology, genomics, and potential drug targets, as well as the challenges ahead and logical solutions.

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JM7010645

10.1021/jm7010645