

All in all, *Won for All* is for the general reader and should interest anyone wanting a glimpse into modern science with an intimate look at the politics, ethics, principles, theory, and advancement that make science what it is today.

Uzma Alam  
Department of Epidemiology  
and Public Health  
Yale University School of Medicine

***Genomics, Proteomics and Bioinformatics.*** By A. Malcolm Campbell and Laurie J. Heyer. 2nd edition. San Francisco: Benjamin Cummings; 2006, 464 pp. \$98.80 Paperback. ISBN: 978-0805382198.

*Genomics, Proteomics and Bioinformatics* is a guided tour to the new world of -omics. In contrast with most other books on the subject, the work by Campbell and Heyer invites the reader to walk the walk by following a problem-based approach. The descriptive chapters are logically constructed and carefully blended with the case studies, resulting in stimulating and scientifically enriching reading — it is Dr. House on paper.

The sequencing of the human genome and the boom in high-throughput methodology led to the foundation of genomics and modern systems biology. In parallel, increased availability of reliable and fast electronic communication made large quantities of data available to the global scientific community. The need to develop competences in the critical analysis and interpretation of these large scale data sets became pivotal in many fields of biomedical sciences. This book is ideal for all people interested in joining the -omics revolution and who need a solid starting point. The text is definitely more accessible for the scientists familiar with the data and methodology, but its high readability also makes it appropriate for colleagues with clinical background. Beginning researchers and those already at an advanced stage will be pleasantly surprised that one single book adequately tackles the major foundations of both genomics and pro-

teomics. Typically, the genome is not even discussed in the same volume as the proteome, not to mention the integration of both.

The book is divided in three parts. The first deals with the aspects of genome sequence, specifically, its acquisition and analysis. The reader will become familiarized with the essential notions of human genetics and the tools used in the generation of -omics data. Loaded with this basic and technical knowledge, the reader is then invited to take an overview of several model organisms (prokaryotes, yeast, mammals), culminating in a chapter discussing the variability of the human genome. The second part of the book is dedicated to gene expression. It describes the methodology of expression microarray analysis and its application and ends with a chapter fully devoted to proteomics. Finally, the third part approaches systems biology, attempting to integrate data from several dimensions (genomic, proteomic, etc.). Here, the most exciting aspects of the -omics revolution are given attention: single-gene circuits, a.k.a. regulation of gene expression, gene networks and network regulation. In summary, *Genomics, Proteomics and Bioinformatics* is a recommended read for those looking for a guide to the rapidly evolving fields of genomics and proteomics.

Ira Milosevic  
Department of Cell Biology  
Yale University School of Medicine

Nuno Raimundo  
Department of Pathology  
Yale University School of Medicine

***Genomics and Evolution of Microbial Eukaryotes.*** Edited by Laura A. Katz and Debashish Bhattacharya. New York: Oxford University Press; 2008, 256 pp. \$60 Paperback. ISBN: 978-0199229055.

In *Genomics and Evolution of Microbial Eukaryotes*, editors Laura Katz and Debashish Bhattacharya guide the reader through an introductory overview of the vast world of pro-