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Book Review

Microbial Proteomics. I. Humphrey-Smith and M. Hecker. Wiley & Sons Inc., Hoboken, NJ, 2006, Hardback, 512 pp. ISBN 0471699756

Proteomic techniques seek to understand the levels of global protein expression and post-translational modification, and represent a logical development of genomic technologies. However, while genomic technologies are greatly facilitated by printing complementary nucleic acid sequences in arrays and hybridization with sample, no such technologies are available for proteomics. The intrepid investigator must therefore separate and quantify hundreds or thousands of proteins by electrophoretic and/or chromatographic techniques, and identify what the protein is (not just done by array address) by complex mass spectrometry. Furthermore, interesting proteins or posttranslational modifications are often present at low abundances that severely test analytical systems. Despite these major technical difficulties, the field of proteomics has so much potential that a host of investigators world-wide have devoted the time and effort required to make these technologies work, and have great advances. The manageable sizes of microbial genomes predicts a similarly manageable proteome, and together with the array of elegant genetics available, in many ways make these systems ideal 'test beds' for the rigorous development of proteomic applications and approaches, while simultaneously providing key insights into the impacts of the studied microorganisms.

This multi-contributor edited book provides an elegant and efficient access point for those interested in studying microbial proteomics. The first five chapters provide overviews of the current state of the art in general proteomic techniques and analyses, showing what can be possible while detailing pitfalls and areas that still require the development of experimental approaches, e.g., Chapter 3 "Quest for complete proteome coverage." The next four chapters detail how proteomics have been applied to study bacterial physiology in response to stresses, such as low pH, starvation and how some bacteria use metals as terminal electron donors. The contributions of proteomics and future challenges in these fields are clear. Industrially-important micro-organisms are covered in the next three chapters, for example, the proteomics of *Corynebacterium glutamicum*, responsible for producing over a million tons of glutamate that enhances food as MSG, are covered. The next eight chapters cover specific pathogenic microorganisms, prefaced by an elegant review of the role of proteomics in understanding pathogenicity of organisms such as *M. tuberculosis, C. albicans* and *Brucella sp*. Finally, and quite appropriately, the last three chapters deal with how to analyze the torrent of data that a successful experiment produces, and how to derive key insights from such data streams. Indeed, as analytical techniques improve to provide more and higher-quality data, making sense of "too much information" will become a key task in "omics" techniques.

Overall, this is a well-written and well-edited book that can be recommended to a range of audiences: researchers wishing to enter this field or improve their current applications, or those interested in the proteomic specifics of their own "favorite" organisms.

Graham S. Timmins
University of New Mexico
College of Pharmacy
Albuquerque, NM
E-mail: gtimmins@salud.unm.edu

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