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Book Review

Industrial Proteomics, Applications for Biotechnology and Pharmaceuticals; Daniel Figeys (Editor), John Wiley & Sons, Inc., Hoboken, New Jersey, 2005. Paperback (303 pages), ISBN: 0-471-45714-0

The proteome of an organism is defined as the sum of the proteins in existence either throughout its life cycle, or in response to changing conditions or a specific disease state. Proteomics, the large-scale study of the proteins within a particular proteome, is a dynamic and rapidly changing field of research. The sequencing of the human genome was a daunting task that found approximately 22,000 genes, but within the human proteome there are close to 400,000 proteins. This lack of correlation demonstrates that protein diversity cannot be fully characterized by gene expression analysis alone. The amount of protein in a cell can change dramatically without any change in RNA expression levels. Proteomics becomes a necessary tool for characterizing cells and tissues of interest.

The book *Industrial Proteomics* is aimed at those wishing to understand current proteomics technology. It is a compendium of functional and structural problems analyzed using a wide array of state-of-the-art proteomic techniques. Although the author describes the focus of the book to be on proteomics in industry, those new to the field can use the book to quickly catch up on applications of proteomics in a wide range of areas. Quality controls may be essential steps in current industrial proteomics processes, but any research can benefit from their application to produce statistically significant results. The book is also a great resource for literature and techniques for all proteomic applications.

The book begins with a well-composed overview of the field that covers both basic elements and the state-of-the-art proteomics. Each chapter is written by experts who review the literature and discuss current advantages of proteomic research. After the introductory first chapter, each of the next 10 chapters covers a different proteomic application. Functional proteomics techniques ranging from the two-hybrid technique to using mass spectrometry to map phosphorylation sites are covered in Chapters 2 and 3. The structural proteomic techniques of crystallography and hydrogen exchange are covered in the next two chapters. The next chapters cover health industry–related applications with excellent coverage of target discovery and biomarker discovery techniques. The final chapters address small molecule applications, bioinformatics, and protein arrays. This is not a cookbook. Proteomic theory and strategies are explained effectively without providing protocols or specific procedures. While having experts describe their field gives the most in-depth coverage possible, it also leads to some redundancy in rehashing the basics. This works, however, in that the chapters may be read out of order or as standalone articles.

Industrial Proteomics is as comprehensive as possible for a book in such a dynamic field. Editor and contributor Daniel Figeys, himself an expert in the field of industrial proteomics, has compiled a very nice resource for both the novice and experienced proteomic researcher. Though written from the perspective of industrial applications, this book is an excellent source for proteomics techniques that can be incorporated into traditional hypothesis-driven research.

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