BOOK REVIEW

Handbook of proteomic methods, edited by P. Michael Conn. 2003. Totowa, NJ: Humana Press. 524 pp. \$135 (hardcover)

This methods book is timely, addressing the growing needs for robust and novel methodologies in proteome research. The editor has been able to collect a palette of articles describing a variety of technologies, going from conventional two-dimensional (2D)-gel-based proteomics to the more advanced multidimensional chromatographic systems and protein-chip-based developments. Some of these contributions are gems loaded with valuable details, destined to become reference articles in the field.

An important part of the book is dedicated to aspects of posttranslational modifications, in particular phospho- and glycoproteomics.

With this book, the reader will readily acquire a general update of proteome methodologies, illustrated with a large number of applications in medicine, microbiology, and plant sciences.

The last chapter of the book deals with data analyses, one of the most important issues in future proteomics. Methods to obtain qualitative and quantitative information on protein expressions in 2D-gels are described and discussed. Means

for automated protein identification based on MS/MS-spectra are provided. Finally, methods describing the construction of protein-protein interaction networks are clearly presented. The last chapter alone makes the book worth buying.

In summary, the *Handbook of Proteomic Methods* provides an excellent overview of rapidly evolving technologies. The articles are contributed by leading researchers in the field, providing a state-of-the-art description and analysis, combined with solutions for future challenges in proteomics. The work is highly recommended not only to beginners in the field because of the broad coverage, but also to scientists seeking detailed information that is not always available in the original papers.

There is always a risk that books published in a fast evolving field may rapidly fade away being buried under a flood of novel papers. *Handbook of Proteomics Methods* contains excellent articles that may stay interesting for several years and may even become classics in their fields.

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