Timothy D. Veenstra & John R. Yates: Proteomics for Biological Discovery

A Jack-Of-All-Trades?

Multiple-author books have their advantages and disadvantages.
How does this new textbook on proteomics, written by 29 proven experts, measure up?

This book's content is as ambiguous as its title. What do we have here? A description of the current state of proteomic methodology? A collection of proteomic methods? A guide to the uses of proteomics? It is a Jack-of-all-trades and a master of none. Furthermore, the 29-author tome ***Proteomics for Biological Discovery*** has a lot of the disadvantages of multiple-author books and only some of the advantages.

Old references and lots of repetition

First, the disadvantages. References are rather old. Most papers date from the last century and only a few from the year before the book was published (2006). Also, in multiple-author books contributors have little incentive to produce something original in style and content, since only editors make it onto the cover and there are no other rewards. So, authors submit a rehashed standard text, which is usually churned out in dull academic prose. Finally, since no author knows what the others have written, there is a lot of repetition. Thus in *Proteomics for Biological Discovery* one reads a dozen times that membrane proteins are difficult to work with and you have dozens of lightweight and cliché-studded introductions pointing out the importance of proteomics.

The advantage of a multiple-author approach is that you can hire specialists to write each chapter. The chapter may be obsolete but at least it is competently written. Also, if each author writes in an original style the book can be as varied as an illustrated paper and as interesting to read.

Engaging style

The chapters of this book are indeed competently written. Some of them are even written in an engaging style, such as the first half of Thierry Rabilloud's chapter, entitled "Protein fractionation methods for proteomics". This chapter contained methods that I had overlooked in the literature. I was unaware of endosome preparation methods which preincubate the cells with Triton WR-1339 and use magnetite-dextran to change the buoyant density of the organelles and thus improve their purification. The Triton method dates (shame on me) from 1967. Other examples are Hisabori *et al.*'s anionic detergent system, which enables electrophoresis of membrane proteins in their native state, and Rigaut *et al.*'s tandem affinity purification. Rabilloud is good at pointing out the very different conditions in viscosity, dielectric constant and ionic strength for proteins in the intact cell and in solution after cell lyses.

Analysing the proteome of a single cell

Chapter 12, "Single cell proteomics" by Norman Dovichi *et al.*, is also interesting. The authors are attempting a daunting task: analysing the proteome of a single cell (the protein mass of the average mammalian cell is only around 50 pg). Here I learned that the first analysis of a single cell was performed in 1953 by Jan Erik Edstrom, who analysed RNA using electrophoresis on a fibre of silk. In contrast, Dovici *et al.* used capillary electrophoresis in polyethylene oxide, laser-induced fluorescence detection and various other tricks. They managed to achieve a resolution similar to that of SDS-gels. With two dimensional capillary electrophoresis they even got two-dimensional intensity plots from the proteins of a single cell.

Although this is technically stunning, I doubt whether it will be of much use in biological research. Imaging techniques on single live cells have a greater potential since both the concentration and the distribution of a single protein, perhaps labelled with green fluorescent protein, can be observed continuously during a cell's life. Incidentally, the book has a 20-page chapter entitled "Protein localization by cell imaging" by Eric Müller and Trisha Davis.

The editors are Timothy Veenstra and John Yates, the latter famous for the development of the Mudpit technique. For them, *Proteomics for Biological Discovery* must have meant a lot of work. First, the writing: they are the authors of chapter one (mass spectrometry, the foundation of proteomics), chapter four (mass spectrometric characterization of post translational modifications), chapter five (technologies for large-scale proteomic tandem mass spectrometry) and chapter 14 (automation in proteomics); and second, the management of the 27 other authors. Why on earth did they do it?

John R. Yates, one of the editors of *Proteomics for Biological Discovery*, is a full professor at the Scripps Research Institute in San Diego, California, and an expert in tandem mass spectrometry.

It's certainly not for the money

Certainly not for the money. There is little money in publishing nowadays and after Wiley takes its cut the profits will be divided by 29. Fame is also unlikely: this is not a Crighton novel and the regurgitation of previously-published science affords little credit. Perhaps the editing of multiple-author books is a form of networking.

Altogether, this is a reasonably useful book. However, those after new methods will find it cheaper, quicker and more efficient to browse original literature on the net.

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