

Two-dimensional electrophoresis protocols**David Sheehan & Raymond Tyther (Eds)****Humana press, Totowa, NJ, USA****Series: Springer Protocols****Methods in Molecular Biology,****Volume 519, 2009****Pages: 560; €74.95****ISBN: 978-1-58829-937-6**

It is worthy to buy this series of protocols on a classical well established technique, especially for those being newcomer users: I say this because today quite often the youngest colleagues are totally devoted to smashing techniques, forgetting those classical still essential to get the right answer from an experiment. Just think how the youngest among us are overwhelmed by the tremendous capacity of the microarray analysis or by the high-throughput technologies (sometimes even because a fashion: if you don't use them you don't get published in high impact factor journals....is the wrong message). Even the two editors stress the fact that their effort to produce the book was mainly devoted to present a still powerful technique (undoubtedly one of the most widely used) to the youngest colleagues. Thus, a great collection of protocols, some upgraded (the book was devised as the update of the "2DE protocols" edited by Andrew Link) and some totally new to reflect proteomics analysis in a growing number of biological topics is welcome by the whole scientific community. The book is divided in two parts:

the first (few chapters, seven) highlights by review-type papers essential step of the technique (solubilization of proteins in 2DE, selection of pH ranges, immunoblotting 2DE membranes, organelle proteomics, etc); the second presents a long list of protocols (twenty-nine protocols, 29 chapters!) devoted to the key steps of the technique (from sample preparation to bioinformatics, from staining to post-translational modification). The reader will for sure find out at least few of them to be of great interest and help to improve his own results. I say this because the protocols widely range both as for the organism studied (including *Caenorabditis* and, just to mention something less classical, the interesting "analysis of proteins from marine molluscs", that is that of a deep sea hydrothermal vent mussel and that of a coastal clam !) and for the techniques presented (from high-resolution large-gel 2DE till in-gel isoelectric focusing and tandem mass-spectrometry). Last two protocols (i.e., chapters) are devoted to bioinformatics: "database interrogation algorithms for identification of proteins in proteomic separations" and "creating 2DE databases for the WWW"; I spent nearly one entire week-end on them, I was captured and I can't stop to go through, it was like to play the master role in a game always giving a result. Hope to publish it !

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