

# METHODS IN MOLECULAR BIOLOGY

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# Proteomics

## Methods and Protocols

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## Preface

In the catalog of biochemical techniques, proteomics has barely reached its adolescent stage, and a very immature adolescent at that. Like any teen, potential still overshadows realized accomplishment, but the future is still bright with potential. This particular adolescent has shown quite a level of promise. Indeed, for a number of tasks, proteomics is fully proficient—determining the identity of a small number of proteins, providing absolute quantitation of a similar number of proteins. For others, it is still testing its limits: How many proteins? How many orders of magnitude of sensitivity? And we begin to doubt, but it is not impossible to imagine the realization of the full parental dream—given a sample, what are the concentrations and identity of every protein and every modification on those proteins. And then there are the unexpected questions we can answer—our teenager has shown potential in areas we never first imagined: What is the three-dimensional structure of a protein? How do proteins interact? What is the turnover rate of various post-translational modifications?

We view proteomics as a pipeline with four discrete components: The isolation of material from a biological specimen, sample preprocessing, sample analysis, and data interpretation.

Recognizing proteomic analysis almost always is a collaborative effort and that specialized analyses will always require domain-specific knowledge, our goals with this book are to provide step-by-step protocols on a wide range of biochemical methods, analytical approaches, and bioinformatics tools developed to analyze the proteome. Here are our specific goals for this book:

1. Accessible. Most scientists in the life sciences will be able to employ the methods described in this book. Aside from basic mass spectrometers, we have avoided unusual and/or expensive equipment and reagents. (Specialists do not consult books as a primary reference.)
2. Practical. The techniques herein described are broadly applicable, commonly employed protocols.
3. Current. Mature well-established protocols will be referenced and briefly described. “State-of-the-art” emerging standard protocols will be clearly and completely described—common wisdom included at no extra charge!
4. One stop. Recognizing that proteomics is often a collaborative effort, this book shall describe, as we see it, the complete proteomic pipeline, upfront biology through data analysis. For analysis that has become or is emerging as routine, our hopes are for this to be *the* “go to” reference.

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