
Preface

Protein modifications and changes to them as well as the quantities of expressed proteins can define the various functional stages of the cell. Accordingly, perturbations can lead to various diseases and disorders. Consequently, it became paramount to be able to detect and monitor posttranslational modifications and to measure the abundance of proteins within the cell with extreme sensitivity. Thus, protein analysis has acquired an importance that goes well beyond protein identification per se.

Today, protein identification is an almost routine requirement. However, reliable techniques for quantifying unmodified proteins (including those that escape detection under standard conditions, such as protein isoforms and membrane proteins) as well as the detection and quantification of posttranslational protein modifications are still far from being a matter of routine. Hence, there is a need for a profound understanding of the principles underlying modern protein analysis, in order to apply and improve established and novel methods successfully.

This book gives a detailed survey of “Quantitative Methods in Proteomics” addressing topics and methods from statistical issues when planning proteomics experiments (Chapter 1), gel-based (Chapters 2–6) to mass spectrometry-based applications including relative and absolute quantification using enzymatic, chemical, and metabolic labeling as well as label-free approaches (Chapters 7–20). In a specialized section, the quantification of posttranslational modifications (phosphorylation, glycosylation, ubiquitination, nitrosylation, and oxidation) is addressed (Chapters 21–27). This is followed by the “hot” topics of software and data analysis (Chapters 28–31). Besides the detailed description of individual protocols, which are a necessary and utmost important part of any compendium of *Methods in Molecular Biology*, general overview articles (Chapters 1, 2, 7, 28, 29) provide a comprehensive overview of existing methods in quantitative proteomics.

As the guest editor of this volume “Quantitative Methods in Proteomics” I would like to thank all of the authors and coauthors for sharing their experience, knowledge, and time to make this book possible. I hope that the reader will take advantage for his/her research work of this comprehensive and competent overview of the important and still-growing field of quantitative proteomics. Enjoy!

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