
Preface

Recently, mass spectrometry (MS) instrumentation and computational tools have witnessed significant advancements. Thus, MS-based proteomics continuously improved the way proteins are identified and functionally characterized. This book covers the most recent proteomics techniques, databases, bioinformatics tools, and computational approaches that are used for the identification and functional annotation of proteins and their structure. The most recent proteomic resources widely used in the biomedical scientific community for storage and dissemination of data are discussed. In addition, specific MS/MS spectrum similarity scoring functions and their application in the field of proteomics, statistical evaluation of labeled comparative proteomics using permutation testing, and methods of phylogenetic analysis using MS data are also described in detail.

This edition includes recent cutting-edge technologies and methods for protein identification and quantification using tandem MS techniques. The reader gets the details of both experimental and computational methods and strategies in the identifications and functional annotation of proteins. Readers are expected to have basic bioinformatics and computational skills for a clear understanding of this book.

We hope the scope of this book is useful for researchers who are beginners as well as advanced in the field of proteomics. We are extremely grateful to our colleagues who contributed high-quality chapters to this book. We thank the Springer publishers for their support and are grateful to Professor Emeritus John Walker.

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