Preface

Proteins are essential players in all cellular processes, facilitating various functions as enzymes and structure-forming or signal-transducing molecules. Their enormous versatility in primary structure, folding, and modification enables a complex, highly dynamic, but nevertheless robust, network carrying out all the necessary tasks to ensure proper function of each cell and concerted activity of cellular associations up to complex organisms. Therefore, proteins have always been, and presumably will always be, the target of all kinds of studies in biological sciences.

Protein purification and separation methods have a longstanding record as they were a prerequisite for enzymological studies and chemical protein identification methods such as Edman-sequencing. Thus, various elaborate and mostly time-consuming techniques for the isolation of distinct proteins have been developed often based on chromatography or electrophoresis, and the identification of the protein's primary structure was accomplished afterwards by no less intricate methods. However, the relatively recent development of MALDI- and ESI-ionization techniques for mass spectrometric analysis of large and fragile biomolecules enabled protein identification in an automated fashion, thereby speeding up protein identification by a multiple. This turned out to be a major breakthrough in protein analysis enabling high-throughput protein identification on a global scale, leading to approaches to study the entirety of all proteins of a cell, tissue, organ, etc.

In 1995, the term "Proteome" was introduced by Marc Wilkins and Keith Williams as the entirety of all proteins encoded in a single genome expressed under distinct conditions representing the turning point in the journey from studying genes to studying proteins, from "Genomics" to "Proteomics." Since then, great efforts have been undertaken to characterize a "healthy" or a "diseased" proteome, but it soon turned out that a proteome is far too complex and dynamic to be defined by such simple terms. The enormous progress that has been accomplished both technically and biologically has not only granted deeper insight into the cellular network but has also raised further questions and set further challenges to proteomic research.

The enormous range of protein abundance, dynamics, and interactions as well as the spatio-temporal distribution of a proteome gave rise to the evolution of several new fields like phospho-, glyco-, subcellular, and membrane proteomics, etc. Many techniques have been developed or significantly increased in these fields and will contribute to the understanding of the cellular networks in the future.

Leading scientists have contributed to this volume, which is intended to give an overview of the contemporary challenges and possibilities in the various areas of proteomics and to offer some detailed protocols as examples for successful analysis in proteomics studies. Therefore, we hope that this book can raise your interest in proteomics and be a valuable reference book for your laboratory work.