
Preface

Recent developments in the field of proteomics have revolutionized the way that proteins, and their contribution to cellular functions, are studied. The subsequent increased understanding of the mechanisms of cellular function and malfunction will have particular impact in the area of medical research, where disease processes will be better understood, many new (protein) therapeutic targets identified, and novel therapeutic agents developed. At the basic research level, phenotype will be explained in terms of cellular mechanisms.

The completion of the sequences of an ever-widening range of genomes—not least of all, the human genome—has provided the molecular biologist with a wealth of data that needs to be analyzed and interpreted. For a variety of reasons (including alternative mRNA splicing, varying translational stop/start sites, frameshifting, and the inability to deduce posttranslational modifications), complete sequences of genomes are insufficient to elucidate the protein components of cells. The focus of attention has therefore turned to directly examining these protein components as the means of understanding cell function, as well as the cellular changes involved in disease states. However, the wealth of gene sequencing data now available has produced a glut of information that challenges the protein chemist to develop new tools to utilize this flood of genomic data.

From the beginning, the cornerstone of proteomics has been the use of two-dimensional gel electrophoresis to compare proteomes of different tissues (for example, normal and diseased tissue) with the subsequent identification of protein differences by the use of mass spectrometry and database searching. These still remain valuable techniques and receive appropriate coverage in this book. However, the term proteomics now encompasses a range of newly developed methodologies for determining the structure and function of a protein. I have therefore included in *The Proteomics Protocols Handbook* a number of novel mass spectrometry and LC-MS techniques, protein array technology, new bioinformatics tools, and the range of techniques central to structural and functional proteomics that are needed to deduce the function of newly discovered protein sequences. The use of these techniques, and no doubt further ones that will be developed in the coming years, will lead to achieving the ultimate goal of proteomics, namely to catalog the identity and function of all proteins in living organisms.

The Proteomics Protocols Handbook should prove a valuable resource for molecular biologists, protein chemists, clinical/medical researchers, structural chemists/biochemists, and microbiologists, as well as those involved in bioinformatics and structural/functional genomics.

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