

Preface to the second edition

When I wrote the first edition of *Principles of Proteomics* in 2003, it was the first book that had attempted to cover the entire field of proteomics in broad strokes rather than focusing on specialized individual technologies. The first edition was published when proteomics was an emerging discipline, still unsure of its footing although confident in its abilities, with many technology platforms jostling for attention and consideration. Nearly a decade later, writing the second edition has proven a significant challenge. Although proteomics has stabilized, with certain technologies becoming unshakably established and others becoming obsolete, the cutting edge still boasts a rich and diverse source of novel technology platforms seeking to capture the proteome in ever more detail and on a scale barely conceived at the beginning of the millennium. But proteomics has also become increasingly commercialized. It is a billion-dollar industry, with many companies vying for attention, providing technologies, solutions, and contract research to other companies, who are in turn interested in using proteomics to find disease biomarkers, drug targets, vaccine candidates, novel chemical inhibitors, improved enzymes for industrial processes, and products to protect plants, the food chain, and the environment. Keeping up with the pace of change while still being aware of the fundamental aspects of proteomics, the core principles that make it possible in the first place, is a difficult task made more difficult by the dominant position of proprietary technologies, and the explosion in patents relating to proteomic technologies and strategies for processing proteomics data.

Despite the above, we must remember that proteomics is still about the global analysis of proteins. It seeks to achieve what genomics cannot—that is, a complete description of living cells in terms of all their functional components, brought about by the direct analysis of those components rather than the genes that encode them. Proteins offer a rich source of data, including sequences, structures, and biochemical and biological functions, which are influenced by modifications, subcellular localization, and, perhaps most important of all, the interactions among proteins and with other molecules. If genes are the instruction carriers, proteins are the molecules that execute those instructions. Genes are the instruments of change over evolutionary timescales, but proteins are the molecules that define which changes are accepted and which are discarded. It is from proteins that we shall learn how living cells and organisms are built and maintained and what leads to their dysfunction.

Although now firmly established, proteomics is still a difficult subject to penetrate for those not familiar with the terminology and technology, including experts in one area of proteomics venturing into another. There is still a great deal of jargon and many hyphenated acronyms that make sense once explained but otherwise remain mystifying; and there is still a high turnover of methods at the cutting edge, making it difficult to keep up. This situation is exacerbated by the increasing integration of proteomics with other areas of large-scale biology as researchers attempt to model cellular processes by looking not only at the functional components, but also at the information (genes, transcripts) and the outputs (metabolites, phenotypes) and how these are linked into networks and systems.

As I stated in the preface to the first edition, it is my hope that this book will be useful to those who need a broad overview of proteomics and what it has to offer. It is not meant to provide expertise in any particular area: there are plenty of other books that deal with specific technologies and their applications, the processing and archiving of proteomic data, and the integration of proteomics with other disciplines. The aim of this book is to pull together the different proteomics technologies and their applications, and present them in what I hope is a simple, logical, and user-friendly manner. After a brief introductory chapter providing an updated perspective on the history of proteomics since the turn of the millennium, the major proteomics technologies are discussed in more detail: two-dimensional gel electrophoresis, multidimensional liquid chromatography, mass spectrometry, sequence analysis, structural analysis, methods for studying protein interactions and modifications, and the development and applications of protein microarrays. These chapters have been broadened to account for new developments since the first edition, but I have made every effort to keep the material as concise as possible, since the brevity of the first edition was one of its strengths. I have assumed necessarily that the reader has a working knowledge of molecular biology and biochemistry. Each chapter has a short bibliography listing classic papers and useful reviews that will help the interested reader delve deeper into the literature.

The second edition would not have been possible without the help and support of the editorial team at Garland Science, so I extend special thanks to Gina Almond, David Borrowdale, and Ioana Moldovan for their dedication and assistance during the writing and revision process. I would also like to thank friends and colleagues who provided feedback on the first edition or suggestions for the second edition or who pointed out errors and omissions.

As ever, this book is dedicated with love to my parents, Peter and Irene, to my children, Emily and Lucy, and to Hannah, Joshua, and Dylan.

Richard M. Twyman

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