

PREFACE

Biological and cellular processes are incredibly complex and result from a large number of exceptionally well fine-tuned and interconnected individual events. Although investigation of these events at individualistic level and in isolated context typically provides important functional insights, their study at systems level and in global context is absolutely essential to decipher the inner workings of cellular and biological phenomena. This has been one of the key challenges in the modern era of biology; however, recent surge of proteomics strategies and approaches have made it possible. A combination of well-established and continuously evolving proteomics methodologies has started not only to reveal the molecular basis of a whole range of biological phenomena and regulation, but it has also emerged as a major engine to open new translational and therapeutic opportunities. The field of proteomics has evolved exceptionally rapidly in the last decade or so, and it is a monumental task and near impractical to cover every aspect in a couple of book volumes. Therefore, we have made the selection of chapters to cover a range of conventional approaches and well-established platforms, a few recent breakthroughs with respect to discovery of novel experimental framework, and finally, a few chapters highlighting the untapped potential of proteomics approaches with a futuristic outlook.

Many of the proteomics protocols have been standardized across different laboratories and published in many primary research articles, and therefore, they are mostly accessible to any interested researcher in the field. We have included a few chapters in these two volumes of *Methods in Enzymology* that briefly describe routine sample preparation strategies and then focus more on recent modifications that have been tested and validated experimentally. One of the key areas that has immensely benefited from the recent applications of proteomics is the identification, quantitation, and analysis of post-translational modifications such as glycosylation, phosphorylation, and acetylation. Here, we have collected a number of chapters describing the application of proteomics approaches in studying a wide range of post-translational modifications, either in the form of generic protocols or with a particular biological target as a case example. Proteomics-based studies typically generate large body of data which on one hand represent goldmine for extracting novel functional insights but on the other pose a major challenge in terms of unbiased, careful, and rigorous analysis. These large proteomics

data sets offer unique possibilities as a hypothesis generation platform to design subsequent experimental strategies to gain novel functional insights into biological processes. Considering that data handling and analysis represents an absolutely critical component in proteomics pipeline, we have included a number of chapters in these two volumes that specifically focus on recent trends in proteomics data analysis and interpretation.

One of the powers of proteomics approaches has been the possibility of studying the biological processes at organellar and organism levels. This has opened up the possibilities of obtaining a global and holistic view of biological processes in physiologically relevant context instead of in isolation. A number of chapters in these two volumes cover this aspect, for example, analysis of body fluid degradomics, global assessment of protein synthesis in *C. elegans*, comprehensive analysis of *E. coli* membrane proteins, and a few others. These chapters underline the robust platform that proteomics can provide for generating important systems-wide clues in biology. Another important application of proteomics, in addition to being a discovery engine for basic biology, is that it can open up new possibilities in disease etiology and therapeutics, for example, by identifying novel biomarkers or by presenting a comparative proteome-wide view of pathological vs normal tissues. We have incorporated a number of chapters that specifically highlight the power of proteomics-based approaches in disease models such as identification of novel biomarkers, quantitative proteome profiling of tumor tissues, and identifying key aspects of host-pathogen interactions. These chapters categorically underscore the emerging utility of proteomics approaches in translational biology and highlight a frontier where a major focus of the field is headed currently.

I take this opportunity to sincerely thank all the authors for their excellent contributions which have made these two volumes possible. I also express my gratitude to the editorial and production team of *Methods in Enzymology* for beautifully coordinating this project. On behalf of the entire *Methods in Enzymology* team, I present two volumes entitled "Proteomics in Biology: Part A" and "Proteomics in Biology: Part B." I sincerely hope that you find the content of these two volumes extremely useful and I welcome your feedback and comments.

With best compliments

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