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# Preface

Ever since its first definition, proteomics has been referred to as the study of the full set of proteins encoded by a genome, and qualitative and quantitative comparisons of proteomes under different conditions to further unravel biological processes. Initially, proteomics was mainly a technology-driven field, centered on two-dimensional gels/mass spectrometry and LC-MS/MS approaches, which offered the ability to detect hundreds of proteins in a single analysis. Proteomics has since evolved into a wide-ranging discipline that includes a plethora of technologies and approaches whose subject is the study of proteins. However, as proteomics is entering into the realms of clinical and diagnostic applications, the enabling techniques are coming under an increased level of scrutiny. Significant weaknesses in some technological aspects have thus become apparent. As a result, new and improved proteomics techniques are being developed and propagated.

It is the intent of *New and Emerging Proteomic Techniques* to present some of the newer and still developing proteomics tools and techniques that enable enhanced protein analyses. The techniques span the entire spectrum of top-down and bottom-up approaches, and in their sum offer a clear example of how proteomics has embraced essentially all techniques that contend with protein analysis. From microarrays and gels, to chromatography and affinity separations, the proteomics techniques described in this book are addressing every aspect of the human proteome, both quantitative and qualitative. The methods of protein detection utilized are also very diverse, ranging from fluorescence and resonance light scattering, to surface plasmon resonance and mass spectrometry. Furthermore, several chapters describe a combination of two or more distinct techniques, resulting in enabling approaches for proteome analysis. There are also three chapters that describe advanced bioinformatics approaches, as they are becoming increasingly important in the analysis of the complex proteomics data.

*New and Emerging Proteomic Techniques* is aimed at both beginners and more experienced practitioners in the field of proteomics. Beginners will find it very useful to have such a diverse set of techniques assembled in a single book, serving as a valuable reference when choosing a technique that can address a specific proteomics question. For experienced proteomics researchers, the book offers protocols and know-how from the pioneers and the expert users of each of these techniques, with details that are usually not found in a typical research publication. We are well aware that there are other proteomics

approaches that are not represented in this book. However, we feel that the fifteen chapters included describe some of the most promising new and emerging proteomics techniques, and hope that at least some of them will become proteomics mainstays in the years to come.

Finally, we would like to thank all of our colleagues who kindly contributed their time and expertise for the assembly of *New and Emerging Proteomic Techniques*.

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