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## Preface

Proteins are involved in almost any aspect of cellular function. The cellular proteome is subjected to a steady flow of dynamic changes, and therefore is a very suitable readout for the functional properties of a cell or an organism. Proteins, for example, build the cellular architecture, and are essential components of membranous compartments confining a cell, as well as subcellular organelles. Networks of tightly regulated enzymes are in command of the energy supply, and provide molecular building blocks, such as carbohydrates, lipids, and nucleic acids. Other proteins are involved in replication and transcriptional processes, and assist in the translation of new proteins. Proteins in extracellular fluids maintain the communication between cells of a tissue as well as within an organism and may serve as disease biomarkers. The number of different proteins encoded by the genome is increased by at least an order of magnitude, due to the introduction of posttranslational modifications, such as glycosylation, lipid-modifications, acetylation, and by protein phosphorylation which is the best-studied mode of cellular regulation.

Understanding protein function and the regulation of signaling networks requires large-scale efforts which enable the dynamic analysis of numerous samples in parallel. Progress in functional proteomics has been limited for a long time, partially because of limitations in assay sensitivity and sample capacity. Protein microarrays have the ability to overcome these limitations so that a highly parallel analysis of hundreds of proteins in thousands of samples is attainable. Advancements in the field of robotics and signal detection have facilitated an increase in sensitivity and sample capacity and, therefore, have contributed to the evolution of an increasing number of robust protein microarray applications. Thus, due to the robustness and flexibility of this experimental platform, diverse applications can now be implemented in principles of different types of biochemical assays.

This volume presents an up-to-date collection of robust strategies in the field of protein microarrays, and summarizes recent advantages in the field of printing technologies, the development of suitable surface materials, as well as detection and quantification technologies. Parallel to the advancement of wet-lab techniques, new software tools were developed for data analysis in order to deal with large data sets generated by protein microarray applications.

Thanks to all article authors for taking the time to prepare a chapter for this book, the series editor for shaping the idea for this volume, people at Springer for their uncomplicated and helpful advice, and special thanks to my family for their patience and cooperation while I edited the articles in this book to their completion.

I am confident that this book will stimulate the application and further advancement of this powerful technology in labs worldwide. I am very much looking forward to the future of protein microarray-based applications.

*Heidelberg, Germany*

*Ulrike Korf*



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