

Review of “Protein Microarrays” Edited by Mark Schena

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Proteins interacting with diverse ligands—proteins, peptides, or DNA—are the basic principles underlying many biological processes, such as antigen-antibody binding, signal transduction, or receptor binding. Protein microarrays offer the opportunity to study the full spectrum of protein characteristics in a massively parallel, miniaturized, and automated fashion. Protein microarrays provide a means for high-throughput identification and quantification of proteins from different biological samples in health and disease. Protein microarrays are providing new insight at the cell and organism levels. The analysis of the proteome using protein microarrays will increase dramatically in the near future.

This book, edited by Mark Schena (Jones and Bartlett Publishers), represents a nice collection of articles that review approaches and technologies useful in the analysis of global protein expression, or proteomics, more precisely in the emerging and evolving field of protein microarrays. The book comprises 24 contributions that are intended as a guide both for novices and for experienced practitioners who want to try the newer protein microarrays techniques. The contributions guide researchers through the complete process of working with protein microarrays assay systems, from generating proteins, labeling them,

immobilizing proteins on microarrays (slide preparation, printing, binding reactions), detection to finally identifying the proteins. The volume includes also some detailed protocols for generating protein microarrays. Some chapters include a description of the protocol, the basic theory behind it, a list of the equipment and reagents necessary for the protocol, a step-by-step guide to the experiment, and hints for dealing with problems.

Written for both graduate students and experienced investigators, this collection of contributions from researchers with wide spectrum of research interests describes the general principles, analytical methods, and protocols involved in the study of the proteome using microarrays. The state of the art is described in detail in some chapters, together with an extensive coverage of the detection methods available. Sufficient detail is given to allow the readers to apply these technologies to their own particular requirements.

The list of authors consisting of world leading experts provide a roadmap for solving the complex challenges that are currently faced while monitoring protein-protein interactions over a wide range of microarray platforms. In doing so, they also offer a comprehensive overview of microarray surface chemistry, detection technologies, fabrication options for array development, and data analysis of numerous types of protein. In addition, detailed protocols for peptide synthesis, and the analysis of protein-protein, protein-DNA interactions as well as epitope mapping are presented in this book. It is ideally suited not only for basic research laboratories but also for diagnostic and therapeutic applications since many diseases are related to dysfunctions in protein recognition and binding.

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