Peptide Microarrays

Methods and Protocols

Edited by

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Preface

The ability to directly interrogate protein interactions in a high-throughput format provides an unprecedented opportunity to dissect the complex molecular architectures of living systems. Traditional molecular biology techniques provide valuable information on the expression, structure, and function of proteins; nonetheless, these methods are unable to provide the massively parallel analysis capacity which is essential to map an entire proteome or to accomplish the present-day drug discovery programs. Parallel sensing using arrayed systems has proved to be successful in genomic research where DNA microarrays are widely used for large-scale analysis of gene expression. However, the protein equivalent of the DNA microarrays poses a more difficult challenge, especially in the identification of suitable high-affinity capture ligands, which retain their specificity and functionality following immobilization on the arrayed sensor substrate. Synthetic peptides have some very interesting features as capture ligands in microarray experiments: they are easy to synthesize and manipulate, highly stable, and inexpensive. More importantly, since peptide ligands can be modeled to act as a binding site for almost any target structure of the proteome, they can mimic biological activities of proteins and provide a straightforward analytical approach in a variety of applications. Beyond their initial utility in protease profiling, researchers are adopting peptide microarrays for the comparative screening of many different classes of enzymes and proteins for the study of complex biological matrices and even living cells. The peptides on the arrays may serve to sense protein activity (as substrates) or act as small molecule ligands (for potential therapeutic leads) in profiling, detection or diagnostic applications. Due to these developments, along with the diminishing costs of library synthesis and the growing of commercial support, peptide microarrays will no longer remain just a research tool but also a versatile and powerful platform to be harnessed for wider drug discovery and point-of-care applications.

*Peptide Microarrays: Methods and Protocols* is a view on the peptide array technology, on its applications and technical issues. The book is divided into four sections:

i) The **Introduction** comprises four review chapters aimed at giving to the readers the broadest view of how peptides can characterize proteins and clarify, at the amino acid level, the molecular recognition events in which they are involved.

ii) **Section II** is dedicated to several practical applications of peptide arrays: to their production and use for enzyme and binding motifs characterization, epitope mapping and diagnostics.

iii) **Section III** is devoted to new technological advancements that can improve the state-of-the-art of peptide microarray methodologies and even pose the way toward new concepts in parallel analysis.

iv) **Section IV** is dedicated to software and Web tools for the design of peptide arrays and for the analysis of output data.
We hope that readers will take advantage of the unique insights and the novel solutions in peptide arrays technology offered by each chapter of this book.

We thank all the authors of this Volume for their valuable contributions and for their willingness in sharing their experience and knowledge. We thank Prof. John Walker for continuous support and editorial help and the staff of Humana Press for their professionalism.

Finally, we wish to express gratitude to the members of our group and to all the colleagues and friends who, despite the difficulties, stay beside us.

Marina Cretich
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