
Preface

Protein Arrays: Methods and Protocols is an introduction to protein array technology and its application to the multiplexed detection of proteins. Although protein array technology has some roots in gene array technology, it can only be described as a distant relative. Unlike DNA, with its established rules of base pairing, and therefore predictable biochemical behavior, proteins are rich with diversity. Proteins can be large or small, compact or extended, basic or acidic, hydrophobic or hydrophilic, and so on. Just as importantly, their behavior is determined by the environment in which they reside, and so the composition of the buffer in which experiments are performed has a dramatic impact on the outcome of the experiment.

Thus, if the goal is to simultaneously measure the expression of a large number of proteins, these variables must be addressed. Not to be deterred, scientists have created a variety of solutions to successfully detect and characterize multiple proteins simultaneously. It is the intent of this volume to introduce to the reader a set of technological solutions to the diversity problem as well as to provide the reader with some examples of practical applications of these technologies.

Like the gene array, the protein array requires an immobilized capture reagent (such as antibody, aptamer, or chromatographic substrate) to which the experimental sample is bound. Following a wash step to remove nonspecific bound materials, the specifically bound material is visualized using, for example, fluorescence or mass spectrometry. The first task in designing a protein array is to create and immobilize the capture substrate, which often is a collection of a large number of distinct probes, and this task is described in Chapters 1–10. Although antibodies are the most typically used affinity capture reagents, other capture reagents include biotin (Chapters 7 and 8), chemical reagents (Chapters 9 and 10), and chromatographic substrates (Chapter 22). Once the affinity capture reagent is chosen, the arrays themselves must be constructed. Though some of the above-mentioned chapters describe methods to construct these arrays, Chapters 11–14 describe other methods. The remaining chapters describe more specific applications of protein arrays. These include identifying proteins that bind to specific protein domains (Chapters 15 and 16), analyzing protein kinase activity (Chapters 17 and 18), assessing protein families (Chapters 19–21), and probing serum for diagnostic information (Chapters 22 and 23).

In reality, this overview is too simplistic, since most of the chapters provide unique methodologies for each of the steps of protein array construction and use. Indeed, this is the richness and reward of participating in an emerging field, where creative approaches have been taken to solve difficult problems. Each contributor to *Protein Arrays: Methods and Protocols* has provided unique insight into the task of studying proteins in a high-throughput manner. This is the new protein chemistry, and it is hoped that readers of our book will learn from these insights and, more importantly, create novel solutions of their own that may appear in future editions.

I thank the authors of the chapters first for their willingness to share their insight and experiences and second for their patience with me. I also would like to express my gratitude to John Walker for his expert editorial opinion and to the staff of Humana Press for taking the final steps to publication. Finally, many thanks to Ka'imilani Alvarado and Amy Jacobs for their outstanding administrative assistance.

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