
Preface

The adaptive immune system is a complex system of cells, tissues, and organs that constantly samples proteins and peptides of the immune landscape as part of defense against disease. Antibodies directed against foreign proteins, or peptides derived from invading pathogens that activate B- and T-cells, are highly amenable to study by protein-based methods. Classical methods to study the immune response to disease have been used for many years, including agglutination, enzyme-linked immunoabsorbent assay, or Western blotting. Rapid advances in genomics and proteomics in the past two decades now allow characterization and quantification of protein and peptide targets of the immune response to disease. The collective study of the complement of proteins and peptides that stimulate an immune response has been termed “immunoproteomics.” Describing a broad and rapidly growing field, this umbrella term includes gel-based, array-based, mass spectrometry-based, DNA-based, and *in silico* approaches. Immunoproteomics is yielding an understanding of disease and disease progression, vaccine candidates, and biomarkers. The resulting information has potential to be used in diagnostics, disease progression, and vaccine correlates of protection analysis, to name but a few. This book provides a broad overview of the current diverse approaches and techniques that are being exploited to study the immunoproteome.

The book opens with an introduction to the immune system and a broad overview of some of the major techniques used in immunoproteomics. Following this, authors present techniques used for the study of the antibody targets of bacterial pathogens, viruses, and cancer. These include classical techniques such as serological proteome analysis and expression arrays, in addition to emerging approaches such as *in vivo* microbial antigen discovery, detection of glycoprotein antigens, and mass spectrometry differentiation of immune cells. Later chapters describe mass spectrometry-based approaches to characterize T-cell epitopes followed by the detection and relative quantification of cytokines in serum. *In silico* prediction of epitopes using sequence-based or modeling approaches has been important in immunological research for many years, and protocols are presented here to aid the experimental researcher in utilizing these approaches. Lastly, perspective upon translation and commercialization of immunoproteomic biomarkers, an increasingly important consideration for many researchers, is discussed in the closing chapter.

This book is aimed at scientists new to the field and those with years of experience in immunoproteomics. The variety of techniques presented provides not only an overview of the breadth of the field but valuable hands-on insights from specialists. Success stories will allow readers to transfer these techniques to their laboratories, in addition to providing a reference to guide researchers towards appropriate techniques.

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