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Preface

Conventional protein analyses, based primarily on immunological methods, have been successfully used to study proteins for many years. However, these methods can be used to study only a small number of proteins in replicates of single experiments and are frequently limited by the availability of specific antibodies to proteins. *Proteomics* is an emerging area of science that attempts to study proteins on a massively parallel scale. The field of proteomics is relatively new as demonstrated by the fact that Marc Wilkins first introduced the term *proteome* to the public in 1994. Proteomics is a field or a subject to study the proteome (set of **PROTE**ins expressed by the **genOME**). Quantitative and qualitative proteomic analyses can be performed using various gel-based and gel-free methods. In general, mass spectrometry is used to identify the proteins by either direct sequence analysis or pattern matching of peptide fragments. Using state-of-the-art proteomic techniques, a large number of proteins can be studied at once and analyses of thousands of proteins can be completed within a few months.

The application of proteomic approaches is growing rapidly as demonstrated by the increasing number of published articles that use proteomic techniques. The first article, specifically related to proteomic research, appeared in the PubMed in 1995, although many similar protein chemistry studies were published earlier without using the term 'proteomics'. The number of published proteomic articles has grown dramatically since 1997 (see figure 1 in chapter 1), especially since the completion of the draft human genome database. During the year 2002, approximately 1,400 articles related to proteomic research were published. The number of publications related to proteomics through the first

quarter of 2003 is approximately 3,400, indicating the rapid acceleration of interest in this field. Most of the early publications in the field dealt with development of proteomic techniques, especially mass spectrometry. The following phase we observe is application of the newly developed techniques to understand normal physiology, pathophysiology of the diseases, and biomarker discovery. To date, cancer biology comprises the largest number of citations of articles that use proteomic techniques in clinical applications or studies of diseases mechanisms. The pattern of citations in PubMed clearly indicates that the application of proteomics to nephrology and renal physiology is in its early phase.

As nephrologists and scientists who daily use proteomic techniques, we believe that proteomics has remarkable potential to help us better understand renal physiology and the pathophysiology of renal diseases. This volume is a collection of papers provided by individuals who we believe are some of the leaders in applying proteomics to nephrology. The book has three main parts, including an overview of proteomics, principles of commonly used proteomic techniques, and applications of proteomics to nephrology. Not only the advantages, but also the disadvantages and limitations of proteomic techniques are discussed in this book. The applications section focuses on proteomic analyses of the kidneys, urine, dialysate, and the isolated intrarenal structures including mesangial cells, podocytes, glomeruli, intrarenal vessels and tubular cells. While proteomic analyses of cells and tissues may provide information about the pathogenesis and pathophysiology of the diseases, analyses of the urine, dialysate and plasma may lead to biomarker discovery that can be applied to the clinical practice. We have also included chapters that demonstrate that proteomic analysis can be applied to non-hypothesis-driven research. In these approaches, proteomic methods are used to ask open-ended questions that in turn generate data that suggest tightly focused hypotheses. Using this approach, previously hidden mechanisms of the diseases can be explored.

As the guest editors, we wish to thank all the contributors who made this book possible. We hope that this book will provide the readers some basics and new insights into their own research. Our goal is to further introduce a novel technology to the nephrology community and to encourage nephrologists to become actively involved in this field. Finally, we hope that the knowledge obtained from proteomic study will improve therapeutic outcomes and benefit all patients with renal diseases.

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