

result in disease. Instead, they prefer to study the complex interplay between host and parasite that more accurately predicts the outcome of disease or health. Content also reflects the change in medical school curricula where microbiology is no longer taught as a separate discipline but is integrated with pathology, immunology and clinical studies.

There is an opening section that describes the microbial adversaries: bacteria, viruses, fungi, parasites, prions and the host-parasite relationship. Host defences are described in the next section: innate and adaptive responses, cellular adaptive immune responses. The third section describes the conflicts and battlegrounds of infective disease. The fourth section describes the groupings of disease by organ infection and vectorborne infections. The last section describes diagnosis and control in the familiar world of the microbiology laboratory where chemotherapy, immunotherapy, vaccination, hospital infections, sterilisation and disinfection still reign.

Each of the 36 subsections concludes with a summary of key facts, questions (not easy unless one looks at the 'Answers' section) and suggested further reading. Many readers will be pleased to see a closing 70-page 'pathogen parade' that provides brief but comprehensive descriptions of the major pathogens that attack humankind.

When the reader finally puts down this book, will they be wiser or merely better informed? Both, is this reviewer's opinion. □

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Proteomics in Nephrology

V. Thongboonkerd and J. B. Klein (eds). Basel: Karger, 2004: pp 335. ISBN 3-8055-7636-6. \$198.25.

This book, volume 141 in the 'Contributions to Nephrology' series, provides a welcome addition to the available literature on the practical applications of proteomics techniques. It is divided into three parts: first, a brief overview/introduction to proteomics and its application in nephrology; second, a series of articles describing the principles of techniques commonly used in proteomics; and third (the major section), specialist articles on applications of proteomics in nephrology.

In Part II, the article on sample preparation for two-dimensional gel electrophoresis (2-DE), which is written by the editors, is particularly useful to readers who intend to start work in this area. Experimental procedures are described in sufficient detail to enable them to be carried out readily. Articles on 2-DE, applications of mass spectrometry in proteomics and mass spectrometric strategies for quantitative proteomics provide good introductions to the techniques but lack the level of technical detail of the sample preparation article.

However, the final article in this section, entitled 'Practical Bioinformatics for Proteomics', again by the editors, is a gem. Using worked examples, bioinformatics tools for the identification of the protein, the presence of post-translational modifications, sequence similarities and homology, transmembrane domains, function and subcellular location are all described. URLs for the software used are given, together with examples of graphical outputs. Once again, a major strength of this chapter is that it gives sufficient detail for the procedures to be followed and utilised easily.

Part III contains 14 articles that either describe actual applications or discuss the potential of proteomics in nephrology. Articles are included that cover major kidney diseases such as cancer, hypertension, renal Fanconi syndrome and diabetic nephropathy. Descriptions of the proteomics techniques for the identification of biomarkers of glomerular disease, and for use in the study of proteins removed by dialysis, are also included. Other articles in this section describe the use of proteomics for the study of nephrotoxicity and kidney cell types (including techniques for the study of the post-translational modification of proteins within them). The final article in this section is entitled 'Proteomics and Drug Discovery' and seems a little out of place; nonetheless, it is interesting in its own right.

Overall, this volume will be of interest to both beginners and practitioners in the field, the broad coverage of the topics offering something for a wide range of readers, from analytical scientists to medical practitioners. As I work at the analytical end of the proteomics spectrum, learning the context of, for example, projects to identify post-translational modification of kidney proteins was particularly interesting. □

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