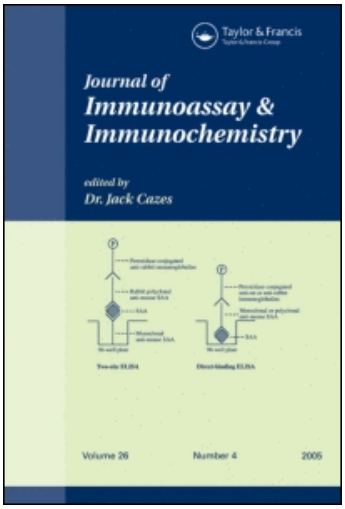

Journal of Immunoassay and Immunochemistry

Publication details, including instructions for authors and subscription information:
http://www.informaworld.com/smpp/title~content=t713597271

The Book Corner

To cite this Article (2006) 'The Book Corner', Journal of Immunoassay and Immunochemistry, 27: 3, 289 — 290
To link to this Article: DOI: 10.1080/15321810600735007
URL: http://dx.doi.org/10.1080/15321810600735007

Journal of Immunoassay & Immunochemistry, 27: 289–290, 2006

ISSN 1532-1819 print/1532-4230 online
DOI: 10.1080/15321810600735007

The Book Corner

The Evolution from Protein Chemistry to Proteomics Basic Science to Clinical Application, Roger L. Lundblad, CRC Taylor & Francis Group, New York, NY, 2006, 295 pages. Price: $139.95

In the first chapter of the book, the author, Dr. Lundbad introduces and defines proteome and proteomics. For the benefit of the reader, we quote here the first part of the introduction with which we agree. "Proteomics is an increasingly complex area of study that is expected to yield results important for the development of therapeutics, diagnostics and for the emerging discipline of theranostics, which emphasizes patient-specific therapeutics. What, however, exactly is proteomics? The term proteome dates back to 1995 when Humphrey-Smith and colleagues defined the proteome as "the total protein content of a genome." Genome is defined as "a complete single set of the genetic material of a cell or of an organism; the complete set of genes in a gamete."

It would follow that proteomics is the study of the proteome. A variety of other definitions have been proposed for proteomics. Morrison and coworkers define the proteome as "the entire complement of proteins expressed by a cell at a point in time." In such cases, proteomics would be the study of the proteome; however, this definition would exclude extracellular collections of proteins such as those found in blood plasma, urine, and lymphatic fluid. These latter studies use some of the tools of proteomics, such as two-dimensional electrophoresis and mass spectrometry, but are clearly different from studies where isotope-coded affinity tag (ICAT) technology is used to study differential protein expression and are used to identify biomarkers for diagnostics and therapeutics.

Whatever the precise definition, proteomics involves the study of complex mixtures of proteins and their interactions. This somewhat broader definition might be useful in that it extends the application of proteomics to diagnostics. The technologies that underlie proteomics quite likely will improve sufficiently in analytical capability to be valuable in personalized medicine."

According to the author, "The overall intent of the current book is to address issues that are not discussed in detail by others and to avoid, where

possible, redundancy in the coverage of information discussed in considerable detail in other sources. The use of chemical modification in proteomics will be covered in great detail as will sample preparation and sample prefractionation. There is limited discussion of the specific separation technologies (two-dimensional gel electrophoresis, capillary electrophoresis, and liquid chromatography) that result in the actual samples for mass spectrometry. There is little discussion of microarray technology other than chemistry associated with covalent linkage to a matrix. As noted above, microarray technology will only be of value when there is a better understanding of important analytes (biomarkers) and their importance to diagnosis and prognosis. Also, new technologies will be tied firmly to the concepts used in their development, both to present the unique qualities of proteomics and to indicate that proteomics is not "magic" and that other, perhaps older technologies can be equally useful. Success in the identification of tissue-based biomarkers will depend on the interplay of pathology and analaytical biochemistry, while the use of samples derived from serum or plasma will require the use of more traditional separation technologies prior to the analytical process."

The book consistes of eight chapters dealing with different aspects of proteome modifications to clinical proteomics. The book is very well referenced, for example Chapter 6, which gives an overview of the analytical technologies used in proteomic research, totals 24 pages of which 10 pages are references (a total of 197 citations). The book is recommended as a desk reference.

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Haleem J. Issaq, Ph.D.
Editor, The Book Corner