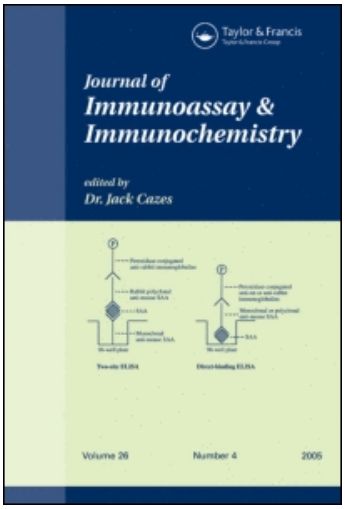

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Inter-Test Comparison Between Filter Paper Absorbed Blood Eluate and Serum for Malaria Serology by Enzyme Immunoassay: An Operational Feasibility

Sukla Biswas[a]
[a] Malaria Research Centre (ICMR), Delhi, India

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The Book Corner

Advances in Protein Chemistry, Volume 65, Proteome Characterization and Proteomics, Richard D. Smith and Timothy D. Veenstra, Eds., Academic Press, New York, 2003, 413 pages. Price: $130.00.

Proteome Characterization and Proteomics is a timely book that is written by experts in their fields. The book comprises 13 chapters totaling 413 pages. It is Volume 65 of *Advances in Protein Chemistry.*

The proteome describes the entire complement of proteins expressed by a cell at a point in time. Recently, there have been significant efforts to develop methods that will enable the analysis of cellular proteome. This is easier said than done. A cell may express up to 20,000 proteins with a concentration dynamic range of 10^{10}. No single chromatographic or electrophoretic procedure is capable of resolving such a complex mixture with varying physical and chemical properties.

Many attempts have been made using different electrophoretic, chromatographic, and a combination of both techniques in a two- or three-dimensional format, off-line or on-line, to separate such complex protein/peptide mixtures. Analytical chemists have attempted to develop sample fractionation, separation, concentration, and detection methods that possess sufficient resolution to separate large numbers of peptides/proteins, as well as be sensitive enough to detect those peptides of proteins that are present in low abundance; however, no method currently exists that can be used to separate, detect, and quantify all the proteins within a given proteome. Current liquid-phase proteome analysis strategies are based on initial digestion of the proteins into peptides, fractionation of the peptides, followed by a single- or two-dimensional separation procedure of each fraction, and

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mass spectrometry for peptide sequencing and identification. Fractionation is an important aspect of mass spectral detection of peptides because mass spectrometers can perform mass measurements on few but not on many co-eluting peptides.

The book summarizes the current state of proteome analysis and presents a wealth of information. It is recommended for protein chemists, biochemists, and analytical chemists. The editors are commended for a job well done.

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Reviewed by
Jack Cazes, Ph.D.
Florida Atlantic University
Boca Raton, Florida, USA