



BioMed Research International

Special Issue on

Emerging Proteomics Technologies

CALL FOR PAPERS

By most recent estimates, there are 37 trillion cells in the human body. Counting all of the cells in the human body under the microscope, even at the rate of 100 cells per second, would take over 11,000 years. Moreover, this number does not include the trillions of “hitchhikers” that constitute the microbial flora of the human body. Nearly 60,000 miles of blood vessels infiltrate every tissue of body, making blood an ideal “tissue” for biopsy of the human condition.

The complexity of the cellular proteome challenges current technologies, since protein concentration ranges can span over twelve orders of magnitude. Hence, the identification and reliable quantitation of extremely low abundance proteins of biological importance will necessarily require technological advances that improve detection sensitivity. These will with no doubt involve strategies such as affinity enrichment and depletion schemes that lessen sample complexity and the analytical burden.

Improvements in sample preparation methods are also much needed since proteins that are not recovered, are recovered with bias, or are damaged or changed during the recovery process render downstream analyses dismissible. Many biological processes, including cancer, are governed by proteins whose role is poorly understood and, potentially, by proteins that have only been predicted from genomic sequence or inferred at the transcriptional level. Posttranslational modifications (PTMs) alter protein charge, structure, and function and regulate many normal, aging, and disease processes but are not accurately predicted from genomic or transcriptomic analyses. Methods are required which ensure the preservation of labile PTMs such as phosphorylation and dephosphorylation, which can change on microsecond time scales, in order to derive accurate results.

This special issue calls for papers on new and developing technologies advancing the field of proteomics, accepting original research papers, reviews, and editorials on clinical and basic research.

Potential topics include but are not limited to the following:

- ▶ Blood and blood cell proteomics
- ▶ Microbiome and microbial proteomics
- ▶ Membrane proteomics
- ▶ Phosphoproteomics, glycoproteomics, and lipoproteomics
- ▶ Subcellular proteomics
- ▶ Clinical proteomics
- ▶ Metaproteomics
- ▶ Sample preparation methods
- ▶ Affinity enrichment and depletion
- ▶ Electrophoresis
- ▶ Mass spectrometry

Authors can submit their manuscripts through the Manuscript Tracking System at <http://mts.hindawi.com/submit/journals/bmri/molecular.biology/eptl/>.

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First Round of Reviews

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