

On Strengthening the MCP Editorial Leadership

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With this issue, a long-standing member of our Editorial Board, Natalie Ahn, becomes President of our Society. Also with this issue, I am delighted to announce a number of editorial changes designed to expand and broaden our scientific leadership. Although a revised Mission Statement follows, our core mission has not changed. MCP will continue to serve the proteomics community with original contributions that enhance our knowledge in the general areas of protein biology of living systems and the biomedical sciences. In parallel, we will report on innovative methodologies, software tools, and technologies that drive our growing insights on the workings of the machinery of cells from studies in proteomics and systems biology. This includes publishing reviews, perspectives, and data-rich resources for our community. In addition, we have revised the topics for manuscripts being considered to better reflect current and likely future areas of focus of the proteomics research of greatest importance (*vide infra*).

In addition we are considering the use of related categories that reflect research areas of relevance to the MCP readership including model organisms, evolutionary animal biology, plants and agriculture, host-pathogen interactions and microbiome, activity-based assays, genetic approaches to proteomic research, proteostasis, single cell proteomics, instrumentation, hardware and data standards, curation, and databases. We welcome suggestions in this area prior to instituting their use.

New MCP Deputy Editors and Associate Editors—

Steven A. Carr and Anne-Claude Gingras have agreed to assume new roles as Deputy Editors and will function with me as the new journal leadership and management team. This revised management structure will improve the efficiency of manuscript handling, with the goal to provide a faster review turnaround time without compromising on the manuscript quality. We are also very happy to announce the addition of Pierre Thibault and Thomas Neubert as new Associate Editors.

I would like to include some notes on their current research interests as follows:

- Steven A. Carr is Director of Proteomics at the Broad Institute of MIT and Harvard (Fig. 1). His laboratory fo-

cuses on the development and application of new technologies to quantify proteins, their modifications and interaction partners in health and disease, in order to understand the function of proteins and especially their response and resistance to drugs. Carr's group also has a major focus on the discovery and quantitative verification of biomarkers for major diseases including cancer, cardiovascular and infectious diseases.

- Anne-Claude Gingras is a Senior Investigator at the Lunenfeld-Tanenbaum Research Institute (formerly, Samuel Lunenfeld Research Institute), Mount Sinai Hospital, Toronto and a Professor in Molecular Genetics at the University of Toronto (Fig. 2). She is investigating mammalian protein complex assemblies and their regulation by signaling pathways. Together with collaborators she is developing computational tools to score, visualize, and archive protein-protein interactions and is using quantitative proteomics approaches to study deregulation of interactions in disease.
- Pierre Thibault is Professor of Chemistry and Director of the proteomics platform at the Institute for Research in Immunology and Cancer at Université de Montreal (Fig. 3). He has more than 20 years' experience in bioanalytical mass spectrometry and proteomics as a principal investigator in academic, government, and industry laboratories. His research interests encompass the development and application of quantitative proteomics to study the molecular mechanisms and the post-translational modifications regulating the functions of proteins involved in cell immunity and in the signaling of cancer cells.
- Thomas Neubert is Associate Professor of Pharmacology and Skirball Institute Program in Structural Biology, New York University School of Medicine (Fig. 4). He is especially interested developing and using variations of SILAC for global and phosphoproteomics to study signaling in primary neurons. He has been using mass spectrometry to study proteins and their modifications since 1991.

Finally, I am very pleased to announce that Muhammad Saddiq Zahari has joined my office to assume important new roles overseeing processes aimed at expediting manuscript flow and as a pro-active "ombudsman" to assure the streamlining our relationship with authors. He will also initiate steps to provide information for timely community awareness of new MCP scientific content.

Muhammad Saddiq Zahari is a Research Associate in the Department of Pharmaceutical Chemistry and Mass Spectrometry and Proteomic Resource, UCSF. He carried out his PhD thesis research with Akhilesh Pandey at Johns

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FIG. 1. Steven A. Carr, MCP Deputy Editor

Hopkins University School of Medicine on global analysis of the PI3K signaling pathways using mass spectrometry and proteomics.

MCP Mission Statement—

The mission of MCP is to foster the development and applications of proteomics in both basic and translational research. MCP will publish manuscripts that report significant new discoveries, supported by proteomics observations across all kingdoms of life. Manuscripts must define the biological roles played by proteins or their mechanisms of action or provide significant computational and methodological advancements that enable such discoveries.

Indeed MCP has been successful in its original mission to facilitate the development of enabling proteomics technology and to establish standards of performance and quality, and this mission continues. A major focus of proteomics, and therefore of MCP, has shifted toward reproducible quantification—rather than simple enumeration—of proteins and their modifications across biological samples in a range of states. These studies of the “proteotypes” present, their levels, and how they change constitute the proteomic basis of phenotypes underlying normal physiology, diseases, and the interplay of living systems and environment.

Scope of the Journal—

Proteotype determines phenotype. It is now possible to analyze proteotypes and thus to define the molecular deter-



FIG. 2. Anne-Claude Gingras, MCP Deputy Editor



FIG. 3. Pierre Thibault, MCP Associate Editor

minants of phenotypes. Much more progress must be made before it will be possible to measure proteotypes comprehensively: to determine the identity, quantity, post-translational modifications, tissue distributions, subcellular locations, interacting partners, and functional chemistry of every protein. Manuscripts that elucidate these detailed features of proteotypes and establish causal relationships with phenotypes will be given preference for publication. Because living systems are dynamic, studies that define the dynamics of proteotypes are especially important. Proteotypes reflect the interplay of genotype, development, environment, and interactions with other organisms. Publication preference will be given to manuscripts that establish the mechanistic bases of these relationships.

The flow of biological information from genotype to phenotype is particularly important in understanding gene function and how genomic abnormalities cause disease. Genomic data alone are often insufficient for inference from genotype to phenotype. Proteomics provides a key information layer to understand how genomic characteristics are expressed. Genomic and transcriptomic data present hypotheses that can be tested with proteomic measurements. The integration of proteomic data with genomic, transcriptomic, and phenotypic information presents important conceptual and computational challenges. Publication preference will be given to studies that describe new proteogenomic data



FIG. 4. Thomas Neubert, MCP Associate Editor

analysis approaches and that integrate combined genomic and proteomic data to describe physiology and disease processes.

Host-microbe and microbiome studies are important emerging areas in biology and health. Proteomics offers new opportunities to analyze these important systems at both the molecular and evolutionary levels. Publication preference will be given to manuscripts that describe studies in microbiome proteomics, host-microbe and host-pathogen interactions, and their roles in health and disease.

Metabolomics is focused on the analysis of small molecules in living systems and shares common analysis platforms with proteomics. The metabolome is both a functional output and regulator of the proteome and can provide important information about physiological and disease processes. Publication preference will be given to studies that integrate metabolomics and proteomics to understand functional connection between genes and phenotypes.

Topics - Manuscript Content—

Affinity and interaction proteomics
Assay development and automation
Bioinformatics, algorithms, and statistics
Biomarkers and clinical and translational proteomics
Cell and molecular biology
Chemical biology and chemoproteomics
Glycoproteomics
Imaging, mass spectrometry-based
Mechanisms of disease
Microarrays, combinatorics, and display technologies
Multiomics, systems biology, and integrative analysis
Post-translational modification analysis
Protein and peptide separation
Protein and peptide identification
Protein and peptide quantification (relative and absolute)
Protein structure and folding
Proteomics: intact proteins and protein complexes
Targeted mass spectrometry