



# Virtual Issue: Technological Innovations\*

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The mission of *Molecular and Cellular Proteomics* since its creation in 2002 has been to “foster the development and applications of proteomics in both basic and translational research.” Our mission statement mandates that Research Articles “report significant new biological or clinical discoveries underpinned by proteomic observations across all kingdoms of life” and that “manuscripts must define the biological roles played by the proteins investigated or their mechanisms of action.” This governing principle still forms the basis of a Research Article’s acceptance in the journal.

However, the Editors have also long realized that these achievements in proteomics discoveries are only possible in the context of advances in enabling technologies. As such, the journal has always welcomed—but has recently reemphasized its interest in—important “new computational methods and technological advancements that will enable future discoveries.” In contrast to standard MCP Research Articles, “manuscripts describing such approaches do not have to include a solution to a biological problem, but must demonstrate that the technology works as described, is reproducible and is appropriate to uncover yet unknown protein/proteome function or properties using relevant model systems or publicly available data.”

Since our Editorial of January 2018 titled “Your technological advances belong here,” we have seen an increase in the submission of excellent experimental and computational technology papers. Those that we published have in turn garnered high interest from the community, both in terms of page access, Mendeley saves, online attention and even (despite their young age) citations.

This virtual issue celebrates some of the Technological Innovation manuscripts published in MCP since January 2018. We have selected several papers that represent the trends in improving the sensitivity in sample preparation, notably by coupling mass spectrometric analysis to laser microdissection (1) or Fluorescence Activated Cell Sorting (2), by developing streamlined and cost effective isobaric labeling protocols for multiplexing (3), and by developing new protein capture strategies for global proteome profiling (4). Some of the selected papers focus on sample analysis for specific applications, notably by overcoming common contaminants

in phosphopeptide enrichment (5), systematically investigating post-translationally modified spectra (6), expanding the acetyl proteome in plants (7) and enabling proximity dependent biotinylation across multiple cell types (8), and permitting multiplex protein profiling with DNA barcoded antibodies (9). Papers improving liquid chromatography (10, 11), adapting ion mobility workflows (12, 13), expanding Data Independent Acquisition (14) or defining new real-time quality control measurements (15) also exemplify the type of manuscripts that have been frequently accessed and/or cited. Lastly, a clear trend consistent with the need for new computational workflows, data sharing and the development of databases is that several computational or bioinformatics papers have been among the most read manuscripts at the journal since January 2018. Although several of these studies were published as part of our August 2019 Special Issue on Multi-Omics Data Integration (see the Editorial for this special issue (16)), we highlight here computational resources that facilitate comparison of data sets with the popular tool Skyline (17) or the analysis of phosphopeptides (18) and improve *de novo* sequencing (19).

The author versions of these research papers and all other MCP content are always freely available at [mcponline.org](http://mcponline.org). We hope you enjoy this collection and continue submitting your Technological Innovation manuscripts to MCP!

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