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Advances in the Mass Spectrometry-Based Proteomic Analysis of Complex Biological Specimens

Guest Editor:

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Deadline for manuscript submissions:
closed (31 January 2022)

Message from the Guest Editor

Recent advances in mass spectrometry-based proteomic technologies are poised to drive improvements in clinical and translational biomedical research. Indeed, such technologies and the associated analytical approaches have revolutionized cell biology and biochemistry by providing powerful new tools to characterize the proteomes of complex biological specimens. Novel developments have been made in areas such as post-translational modification analysis, isotopic and isobaric labeling, data-dependent and data-independent acquisition mass spectrometry methods, targeted mass spectrometry, and bioinformatics.

The goal of this Special Issue on “Advances in the Mass Spectrometry-Based Proteomic Analysis of Complex Biological Specimens” is to provide a forum for researchers to share the results from their studies and to give readers unique insight into the current state and future directions in this exciting area. Contributions to this Special Issue, in the form of original research or review articles, will be peer-reviewed and may cover all aspects of mass spectrometry-based proteomic analysis. Studies highlighting novel methods and applications are particularly welcome.

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Message from the Editor-in-Chief

As the premier open access journal dedicated to experimental organic chemistry, and now in its 25th year of publication, the papers published in *Molecules* span from classical synthetic methodology to natural product isolation and characterization, as well as physicochemical studies and the applications of these molecules as pharmaceuticals, catalysts and novel materials. Pushing the boundaries of the discipline, we invite papers on multidisciplinary topics bridging biochemistry, biophysics and materials science, as well as timely reviews and topical issues on cutting edge fields in all these areas.

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