



## Mass Spectrometric Proteomics II

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### Message from the Guest Editors

The investigation of genome, including transcriptome, has been widely applied and has permitted us to improve our understanding of it; however, at the same time, it has increased the demand to characterize other -omes sectors.

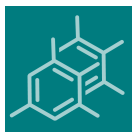
In addition, the improvements of both proteomics applications and related hyphenated techniques, have permitted us to develop the so-called mass spectrometry-based proteomics. Today, the MS-based approach has become the gold standard for proteomics study.

This Special Issue on “Mass Spectrometric Proteomics” will cover several topics, including but not limited to:

- Proteome analysis;
- Study of protein–protein interactions;
- Clinical proteomics;
- Proteomics for biomarker discovery;
- Proteomics for amyloid investigations;
- Quantitative proteomics by label-free or label-based approaches;
- Mass spectrometry analysis for the identification and the characterization of post-translational modifications (PTMs);
- Study of protein structure by mass spectrometry;
- MS-based proteomics imaging;
- Development of new analytical MS-based methods.

We warmly invite our colleagues to submit their original contributions to this Special Issue.





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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 22nd 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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