

Special Issue

Advances in Mass Spectrometry-Based Proteomics: From Biomarker Discovery to Translational Applications

Message from the Guest Editor

This Special Issue aims to bring together cutting-edge research on quantitative proteomics, glycoproteomics, phosphoproteomics, and emerging mass spectrometry workflows, with a particular focus on biomedical and clinical applications. We welcome original research and reviews that highlight advances in the following areas:

Innovative Mass Spectrometry Techniques: DIA-MS, TIMS-MS, FAIMS, and ion mobility spectrometry; Quantitative Proteomics and PTMs: SILAC, TMT, iTRAQ, phosphoproteomics, and ubiquitinomics; Glycoproteomics and Glycomics: Site-specific glycosylation, lectin-based enrichment, and glycan profiling; Biomarker Discovery and Translational Applications: Cancer proteomics, neuroproteomics, and immunopectidomics; Advancements in Data Analysis and Computational Tools: MaxQuant, Proteome Discoverer, Spectronaut, and machine learning in proteomics.

Guest Editor

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Message from the Editor-in-Chief

The International Journal of Molecular Sciences (*IJMS*, ISSN 1422-0067) is an open access journal, which was established in 2000. The journal aims to provide a forum for scholarly research on a range of topics, including biochemistry, molecular and cell biology, molecular biophysics, molecular medicine, and all aspects of molecular research in chemistry. *IJMS* publishes both original research and review articles, and regularly publishes special issues to highlight advances at the cutting edge of research. We invite you to read recent articles published in *IJMS* and consider publishing your next paper with us.

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