



Advances in Mass Spectrometry-Based Proteomics

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Message from the Guest Editors

Mass spectrometry is the core technology at the heart of proteome research. While it is now widely employed by researchers in (among others) biological and biomedical research, significant advances in sample preparation, in mass spectrometric instrumentation, and in bioinformatics are still opening up completely new lines of research ranging from the classification of archaeological artifacts to single-cell analysis of engineered tissues. We cordially invite researchers from the fields of analytical chemistry, instrument development, biological and biomedical sciences, as well as bioinformatics to highlight this progress by contributing to this Special Issue, specifically with contributions in the following areas and technologies:

- Low-input proteomics;
- Ion-mobility-enhanced mass spectrometry techniques;
- Data-independent acquisition mass spectrometry;
- Next-generation data processing and statistical approaches.

In addition to conventional research articles and reviews, we also welcome commentaries, opinions, and perspectives on the progress and applications of mass spectrometric proteome analysis.





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Message from the Editor-in-Chief

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