



Protein Analysis by Mass Spectrometry

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Message from the Guest Editor

Dear Colleagues,

Mass spectrometry (MS), in conjunction with peripheral techniques such as chromatography, has become one of the most important analysis tools in the life sciences. It has revolutionized the detection of both low- and high-molecular-weight compounds, leading to the development of the so-called omics technologies, namely, the collective characterization of hundreds to thousands of substances. In particular, for the investigation of proteins or proteomes, mass spectrometry is invaluable as it generates qualitative and quantitative data that translate into structure and function—a fact which is reflected in the publication of more than 10,000 research papers annually since the year 2004, reaching twice as many in recent years. Research covers all fields from plants to microorganisms and mammals, from single cells to tissues and biofluids. Even though the analysis of proteins is the general goal, methods and applications differ to some extent depending on the sample type and the research question. In this Issue, the authors present a glimpse at the current state-of-the-art of this highly dynamic field.





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Message from the Editor-in-Chief

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