Special Issue

Advances in LC-MS-Based Metabolomics: From (Un)targeted Screening to Structural Elucidation

Message from the Guest Editors

In the past few decades, advances in LC-MS technology have led to the expansion of metabolomics among the “omics” disciplines. On one hand, the unpaired sensitivity and versatility of MS platforms supported the development of analytical methods where tenths to hundreds of metabolites were successfully identified and quantified in a single run. On the other hand, the improvements in the field of separation science and the progressive increase in the employment of ion mobility MS provided further tools to address the unambiguous identification of isomeric species. Nowadays, the use of high-throughput LC-MS methods in combination with the latest bioinformatics tools can be reliably exploited to deepen our understanding of complex biological systems and improve the characterization of complex food matrices through targeted or untargeted metabolomics. This Special Issue focuses on the application of innovative LC-MS approaches for animal, plant metabolomic studies, and is also oriented toward the development and application of (un)targeted LC-MS methods for metabolomic qualitative and quantitative studies.

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Message from the Editor-in-Chief

The metabolome is the result of the combined effects of genetic and environmental influences on metabolic processes. Metabolomic studies can provide a global view of metabolism and thereby improve our understanding of the underlying biology. Advances in metabolomic technologies have shown utility for elucidating mechanisms which underlie fundamental biological processes including disease pathology. *Metabolites* is proud to be part of the development of metabolomics and we look forward to working with many of you to publish high quality metabolomic studies.

Editor-in-Chief

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