

Special Issue

Application of Metabolomics, Lipidomics and Exposomics Based on LC-MS

Message from the Guest Editors

Liquid chromatography–mass spectrometry (LC-MS) and high-resolution mass spectrometry (HRMS) have transformed the analysis of metabolites, lipids, and environmental chemicals with unprecedented sensitivity and scale. The integration of metabolomics, lipidomics, and exposomics provides a powerful framework for deep phenotyping, studying host–environment interactions, and uncovering mechanisms of disease and toxicological responses. Despite advances in instrumentation, translating complex LC-MS data into biological insight remains challenging due to issues in spectral processing, MS/MS annotation, multi-omics integration, and covariate adjustment in cohort studies. This Special Issue, “Application of Metabolomics, Lipidomics and Exposomics Based on LC-MS,” highlights methodological developments and biological applications in this multidisciplinary field. Topics include bioinformatics tools, statistical workflows, targeted and untargeted LC-MS/MS analysis, biomarker discovery, exposomics, dose–response modeling, causal inference, and integrative multi-omics approaches linking metabolome and exposome data with other omics layers.

Guest Editors

Dr. Zhiqiang Pang

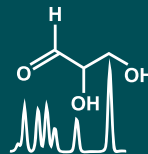
1. Faculty of Medicine and Health Sciences, McGill University, Ste-Anne-de-Bellevue, Montreal, QC H9X 3V9, Canada
2. Département de Médecine Moléculaire, Université Laval, Québec, QC G1V 0A6, Canada

Dr. Jianguo (Jeff) Xia

Institute of Parasitology, McGill University, 21111 Lakeshore Road, Ste Anne de Bellevue, Montreal, QC H9X 3V9, Canada

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Metabolites
Editorial Office
MDPI, Grosspeteranlage 5
4052 Basel, Switzerland
Tel: +41 61 683 77 34
metabolites@mdpi.com

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About the Journal

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

Dr. Amedeo Lonardo
Internal Medicine, Ospedale Civile di Baggiovara, Azienda Ospedaliero-
Universitaria, 41126 Modena, Italy

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