



Mass Spectrometry: An Undeniable Tool in Current Microbiology 2.0

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Deadline for manuscript
submissions:

closed (15 October 2023)

Message from the Guest Editors

Dear Colleagues,

Mass spectrometry (MS) is an analytical tool in chemistry with a long history of constant technological progress regarding the mass resolution, accuracy, and acquisition speed of instruments and the software that allows them to operate. In the last two decades, MS has also become indispensable in the study of microorganisms. Among the MS techniques, MALDI-TOF MS offers a reliable and cost-effective method for microbial identification. Fingerprints obtained from ribosomal proteins and other small molecules, in the range of 2–20 kDa, are nowadays used to identify microorganisms in many laboratories all around the world.

We are interested in receiving papers that provide updates on the progress made in the last five years, not only in solving problems in the QA/QC of microbial identification using MS techniques, but also new applications of MS towards generating information about microbial traits and the deployment of data. We encourage authors to submit original research, opinions, and reviews to this Special Issue and demonstrate that MS in current microbiology is an essential tool.

Keywords: LC-MS; GC-MS; QA/QC





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Message from the Editor-in-Chief

"Microorganism" merges the idea of the very small with the idea of the evolving reproducing organism is a unifying principle for the discipline of microbiology. Our journal recognizes the broadly diverse yet connected nature of microorganisms and provides an advanced publishing forum for original articles from scientists involved in high-quality basic and applied research on any prokaryotic or eukaryotic microorganism, and for research on the ecology, genomics and evolution of microbial communities as well as that exploring cultured microorganisms in the laboratory.

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