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Mass Spectrometric Proteomics 3.0

Guest Editor:

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Deadline for manuscript submissions:
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Message from the Guest Editor

Dear Colleagues,

Understanding how proteins function and interact with one another is another goal of proteomics that makes this approach even more intriguing. Because of their ability to handle the complexity of the events mentioned above, mass spectrometry (MS)-based methods have become the primary technology to identify proteins that may be separated by one- and two-dimensional gel electrophoresis (1- and 2-DE) and/or via liquid chromatographic techniques (1- and 2D-LC). Currently, proteomics relies mainly on MS, and the numerous applications thus far described have contributed heavily to providing new insights into the roles played by some proteins in human disorders.

The aim of this Special Issue is to attract contributions on all aspects of MS-based proteomics, with special emphasis on recent/novel technologies that, by pushing the boundaries of MS capabilities, are able to address biological problems that have not yet been resolved.

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Special Issue

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Message from the Editor-in-Chief

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