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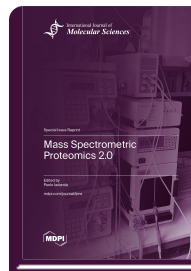
Special Issue Reprint

Mass Spectrometric Proteomics 2.0

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The high quality of the articles published in this Special Issue reflects the leadership of MS-based proteomics in handling the complexity of biological challenges. From these reports, it can be inferred that the peculiar features of this platform in terms of flexibility, reliability, and the speed of execution have so far not been demonstrated through any other technique. Altogether, the papers presented in this Special Issue Reprint demonstrate that the MS proteomics technique is a mature method that is available not only for listing the total proteins present in a sample, but, more importantly, for providing novel insights into the role played by those involved in specific human disorders.



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