Special Issue

MS-Based Protein Specific Analysis

Message from the Guest Editor

Proteins are essential macromolecules required in the structure, function, and regulation of many processes in living organisms. Assessing protein and proteoform variability is essential–yet challenging–in many research areas. Mass spectrometry (MS) has become the primary tool for the structural characterization of proteins and many different MS-based approaches–from bottom-up to intact and top-down approaches–are currently being used for protein identification and proteoform characterization. Thanks to recent technological developments in MS instrumentation, separation technology, and coupling options, online approaches are gaining a predominant position in the MS toolbox for protein analysis. This Special Issue will focus on MS-based protein analysis and will cover recent methodological developments and relevant applications. Applications may cover characterization of novel endogenous or recombinant proteins, biomarker discovery, or biologically relevant proteomic studies, among others. Original research work, communications as well as reviews in the field are welcome to this Special Issue.

Guest Editor

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The International Journal of Molecular Sciences (*IJMS*, ISSN 1422-0067) is an open access journal, which was established in 2000. The journal aims to provide a forum for scholarly research on a range of topics, including biochemistry, molecular and cell biology, molecular biophysics, molecular medicine, and all aspects of molecular research in chemistry. *IJMS* publishes both original research and review articles, and regularly publishes special issues to highlight advances at the cutting edge of research. We invite you to read recent articles published in *IJMS* and consider publishing your next paper with us.

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