Special Issue

Advancements in Proteomics: Identification and Application

Message from the Guest Editor

Proteomics technologies are progressing at a rapid pace and the last decade, in particular, has witnessed a huge advancement in mass spectrometry and data analysis tools. The development of data-(in)dependent acquisition, isobaric mass tags, label-free quantitation, and targeted proteomics approaches has provided a platform for the in-depth proteome analysis of different biological samples. Moreover, the development of low-protein enrichment techniques has further boosted the identification of biomarkers and other proteins which are usually not identified during whole-cell proteome analysis. In this Special Issue, articles employing gel-based and gel-free/shotgun proteomic approaches for a comparative proteome analysis, identification of post-translationally modified proteins and development of proteome maps/proteome atlases of all lifeforms are invited.

Guest Editor

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Deadline for manuscript submissions

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Message from the Editor-in-Chief

As the premier open access journal dedicated to molecular chemistry, now in its 29th year of publication, the papers published in *Molecules* span from classical synthetic methodology to natural product isolation and characterization, as well as physicochemical studies and the applications of these molecules as pharmaceuticals, catalysts, and novel materials. Pushing the boundaries of the discipline, we invite papers on all major fields of molecular chemistry and multidisciplinary topics bridging chemistry with biology, physics, and materials science, as well as timely reviews and topical issues on cutting-edge fields in all of these areas.

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