



Advancements in Proteomics: Identification and Application

Guest Editor:

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Message from the Guest Editor

Dear Colleagues,

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.

Dr. Ravi Gupta

Guest Editor





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Message from the Editor-in-Chief

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