Special Issue

Multiomics Approaches in Biomedicine

Message from the Guest Editor

Up to now, the most efficient mode of proteome profiling was based on a search with the use of genomic sequence for the corresponding species. Since proteomics was able to quantify thousands of gene products, integration of transcriptome and proteome data became feasible, which provided new possibilities for system description and modelling of cellular processes. Furthermore, routine use of high-resolution mass spectrometry in proteomics made it possible to study the production of protein-coding genomic variants at the proteome level, which is especially important in cancer research, where mutations serve as drivers of malignant transformation. Integration of omics data for nucleic acids and proteins, called, sensu lato, proteogenomics, turned into a valuable instrument for biomedical research. Instruments and applications of proteogenomics are to be collected in the Special Issue. For this Special Issue, we invite authors to contribute original research articles, method papers, as well as review articles that will address recent developments in the area of proteogenomics in the broad sense of this term.

Guest Editor

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The *International Journal of Molecular Sciences* (*IJMS*) 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, and molecular biophysics. *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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