

Special Issue

Proteomics and Nucleotide Profiling as Tools for Biomarker and Drug Target Discovery

Message from the Guest Editors

Separate developments of a wide variety of techniques including two-dimensional gel electrophoresis (2D-PAGE), mass spectrometry (MS), construction of databases with structural information as well as the development of software applications and computer science formed the basis for the field of proteomics some decades ago. The field has shown tremendous advancement ever since, especially more recently. Proteins originate from protein-coding RNA. More recently, non-coding RNAs have been shown to be important regulators of cell function, biomarkers of pathology and as putative clinical interventions.

This Special Issue addresses the challenges in the application of proteomic analysis and nucleotide profiling to support clinical decisions based on the mapping of disease-associated protein and nucleotide changes that may highlight protein and nucleotide candidates as biomarkers or drug targets.

This Special Issue calls for papers that describe the current knowledge and future perspectives in the development of proteomics and nucleotide-based techniques to reveal candidate biomarkers or drug targets for diseases.

Guest Editors

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Deadline for manuscript submissions

closed (31 October 2020)



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Message from the Editor-in-Chief

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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