

## Special Issue

# Multimomics 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

Prof. Dr. Sergei Moshkovskii

1. Pirogov Russian National Research Medical University, 1, Ostrovityanova, 117997 Moscow, Russia
2. Federal Research and Clinical Center of Physical-Chemical Medicine, 1a, Malaya Pirogovskaya, 119435 Moscow, Russia

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## International Journal of Molecular Sciences

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Editorial Office  
MDPI, Grosspeteranlage 5  
4052 Basel, Switzerland  
Tel: +41 61 683 77 34  
[ijms@mdpi.com](mailto:ijms@mdpi.com)

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### Message from the Editor-in-Chief

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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### Editor-in-Chief

Prof. Dr. Maurizio Battino

Department of Odontostomatologic and Specialized Clinical Sciences,  
Sez-Biochimica, Faculty of Medicine, Università Politecnica delle  
Marche, Via Ranieri 65, 60100 Ancona, Italy

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