Special Issue

Proteomics and Metabolomics Approaches on Cancer Research

Message from the Guest Editors

High-throughput technologies provide a great amount of data at multiple levels capable of revealing the complexity of cancer cells and their micro- and macro-environment, whereas the analyses of single data layers provide only causal relations. Therefore, multi-omics data integration strategies, including genome, epigenome, transcriptome, proteome, metabolome, microbiomes, lipidome and miRNome, also with bioinformatics and systems biology approaches, offer fantastic opportunities to understand the biology behind complex diseases, such as cancer. In recent years, multi-omics approaches have been applied to many cancer studies for better identification of clinical subtypes or drug resistance, and the discovery of novel biomarkers able to predict the cancer progression, the patient’s outcome and the efficacy of new drugs and combination therapies. The aim of this Special Issue is to present the latest research and new studies based on proteomics and metabolomics approaches applied to cancer research on different biological matrices such as cancer cells, tissues and biological fluids.

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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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