



Proteomics and Metabolomics Approaches on Cancer Research

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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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Message from the Editor-in-Chief

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