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Multi-Omics and Bioinformatics Approach to Identify Novel Disease Biomarker

Guest Editors:

Dr. Chih-Yang Wang
Program for Cancer Molecular Biology and Drug Discovery, College of Medical Science, Taipei Medical University, Taipei 11031, Taiwan

Dr. Wei-Jan Wang
Research Center for Cancer Biology, Department of Biological Science and Technology, China Medical University, Taichung 40604, Taiwan

Deadline for manuscript submissions:
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Message from the Guest Editors

High-throughput technologies are widely used as systemic approaches to explore differences in expressions of thousands of genes or metabolites for both biological and genomics systems. The proper and full utilization of these data from multi-omics would therefore accelerate the identification of important disease biomarkers as well as facilitate the development of improved molecular signatures. Bidirectional communication between the gut microbiota and the liver is conducted by the signals generated from genetic or dietary factors. It is also well recognized that many upregulated and downregulated genes or metabolites are associated with disease development. This Special Issue of *Separations* entitled "Multi-Omics and Bioinformatics Approach to Identify Novel Disease Biomarkers" seeks papers on the following topics:

- Metagenomics, metabolomics, genomics, epigenomics, transcriptomics;
- Systems biology and multimodal analysis, high throughput screening via mass spectrometry, microarray, RNAi, next-generation sequencing (NGS);
- Drug discovery and disease biomarkers, natural compounds, traditional Chinese medicine (TCM), complementary and alternative medicine (CAM).

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Special Issue

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Editor-in-Chief

Prof. Dr. Frank L. Dorman
Department of Chemistry,
Dartmouth College, Hanover, NH
03755, USA

Message from the Editor-in-Chief

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Contact Us

Separations Editorial Office
MDPI, Grosspeteranlage 5
4052 Basel, Switzerland

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