



Multi-Omics and Bioinformatics Approach to Identify Novel Disease Biomarker

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Deadline for manuscript submissions:

closed (10 April 2022)

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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Message from the Editor-in-Chief

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