



Proteomic Analysis of Kidney Diseases

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Message from the Guest Editor

Omics have changed the strategy for analysis of life sciences from hypothesis-based sciences to discovery-based sciences. Proteomics elucidates all proteins of a certain system (proteome), and the proteins are the most significant molecules to play biological functions and to correlate with pathological conditions. Therefore, proteomics is expected to disclose unknown mechanisms of the biology and pathology more directly than other omics. Methodologies for proteomics by mass spectrometry have recently progressed to catch up the preceding ones for genomics and metabolomics and made it possible not only to identify each protein of proteomes but also to quantitate their amounts. Human kidney diseases are good targets to apply proteomics because the pathophysiology is mostly unknown and materials such as urine samples and kidney biopsy tissues are not so difficult to obtain in clinics. In this Special Issue, several outstanding proteomics researchers, who have been employing proteomics to understand the pathophysiology of kidney diseases, will introduce methodologies for proteomics analysis of kidney tissues and urine samples and will also present the results of their research.





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Message from the Editor-in-Chief

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