

Special Issue

Proteomic Analysis of Kidney Diseases

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.

Guest Editor

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Deadline for manuscript submissions

closed (20 December 2023)



International Journal of Molecular Sciences

an Open Access Journal
by MDPI

Impact Factor 4.9
CiteScore 9.0
Indexed in PubMed



mdpi.com/si/133639

*International Journal of
Molecular Sciences*
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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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