

Special Issue

Research Advances in Whole-Genome/Exome Sequencing (WGS/WES) and Next-Generation Sequencing

Message from the Guest Editor

Most inherited diseases form a clinically and genetically heterogeneous group of disorders, which generally manifests in many tissues or organs, causing irreversible progressing disease, e.g., cancer, systemic disease, and age-related disease. However, the use of next-generation sequencing such as whole-exome and whole-genome sequencing has improved the diagnostic yield in the search for disease-causing variants in inherited diseases. In current standard bulk analyses on DNA genomics or RNA whole-transcriptomics technologies, biologically relevant pathophysiology differences are not always picked up on. However, new technologies, such as long-read sequencing, are being developed for complex bioinformatic analyses in organs, tissue, or even cells, offering the possibility of determining the whole transcriptome, or whole genome, and also the complete epigenome sequence in less than a day. This Special Issue aims to provide a current overview of advanced research on whole-genome/exome sequencing (WGS/WES) and next-generation sequencing. Reviews and research papers are encouraged on relevant topics.

Guest Editor

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Message from the Editor-in-Chief

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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