



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

Guest Editor:

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Message from the Guest Editor

Dear Colleagues,

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.

Dr. Rick Kamps
Guest Editor





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Message from the Editor-in-Chief

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