Special Issue

Utilizing RNA-Seq and Genome Sequencing to Uncover Complexities of Genetic Disorders

Message from the Guest Editors

Mining this data by investigating mechanisms and variations in the genome can help us better understand how certain variants contribute to a phenotype and the genetic pathways involved to determine the underlying causes of a genetic disorder.Various NGS applications, particularly whole-genome (WGS) and exome sequencing, are powerful tools for diagnosing the underlying causes of genetic disorders. However, despite the recent advances in NGS technologies, their diagnostic rate is limited. Augmenting it with RNA-Seq can facilitate in resolving the genetic basis of unsolved diseases, narrowing the diagnostic gap. Additionally, RNA-Seq can detect a wide variety of RNA species, including pre-mRNA, mRNA, and non-coding RNAs (ncRNAs), allowing for a deeper understanding of their role in the progression of a genetic disorder. This Special Issue invites original research and reviews on topics utilizing the power of RNA-Seq in addition to other sequencing methods to determine causative variants in different diseases, including cancer, in research as well as in clinical applications.

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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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