# Special Issue

# Bioinformatics and Genetics of Human Diseases

**Message from the Guest Editors**

Thanks to rapid advances in high-throughput sequencing technology (i.e., whole-exome sequencing), the sharp increase in genome data and methodology have accelerated the identification of candidate genes and associated variants in human genetic diseases.

In the current scenario of rapid progress, we believe more and more disease-associated variants will be prioritized by whole-genome sequencing and third-generation sequencing in the near future. Specifically, we believe that studies combining omics technologies (genomics, transcriptomics, epigenomics, proteomics, metabolomics, and metagenomics) with biotechnologies (molecular biology, cell biology, neurosciences, and animal model) will provide novel insights into the pathogenesis of human diseases.

Researchers are invited to contribute original articles, new methods, or reviews that address current advances in bioinformatics and the genetics of human diseases. If you would like more information about the Special Issue, or have any other questions, please feel free to contact us.


**Guest Editors**

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**Deadline for manuscript submissions**

closed (25 December 2022)


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## Message from the Editor-in-Chief

*Genes* is central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fast-moving field. There is a need for good quality, open access journals in this area, and the *Genes* team aims to provide expert manuscript handling, serious peer review, and rapid publication across the whole discipline of genetics. Starting in 2010, the journal is now well established and recognised. Why not consider *Genes* for your next genetics paper?

## Editor-in-Chief

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