Special Issue

Utilizing High-Throughput Sequencing and Deep Learning to Uncover Disease Epigenetic Mechanisms

Message from the Guest Editors

The completion of the Human Genome Project marked a pivotal milestone in biomedical research, providing a comprehensive catalog of genes essential for human life. However, it has become increasingly evident that gene sequences alone do not fully explain the intricate regulatory mechanisms underlying development and disease. Epigenetic modifications, which influence gene expression without altering DNA sequences, play a crucial role in governing cellular identity, differentiation, and response to environmental stimuli. Among these, DNA methylation, histone modifications, chromatin remodeling, non-coding RNA-mediated regulation, and 3D chromatin interactions have emerged as key players in disease pathogenesis.

By bringing together advances in high-throughput sequencing and deep learning, this Special Issue aims to provide a comprehensive perspective on how these powerful tools are transforming our understanding of epigenetic mechanisms in disease. We invite contributions from researchers exploring novel methodologies, computational innovations, and translational applications in this rapidly evolving field.

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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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