Special Issue

Deciphering Epigenetic Signature in Human Health and Disease

Message from the Guest Editors

Epigenetic modifications, including DNA methylation, histone modifications, chromatin remodeling, and noncoding RNAs, represent the regulatory network at the basis of development and differentiation. The fundamental role in gene expression puts epigenetics at the head of many diseases related to both development and cancer progression. Aberrant DNA methylation is a cause of altered development and is liable for tumors and several diseases. In recent years, the methylation signature has been the focus of numerous studies for the early diagnosis of diseases, given the advantage of being able to detect DNA methylation through free circulating DNA analysis. The genome and epigenome in single-cell sequencing have enabled deciphering some of the epigenetic codes underlying both development and severe diseases. The aim of this Special Issue is to provide a broad overview of the topic of epigenetic signatures that mark development and cells differentiation. It will give attention to the genomic distribution of DNA methylation at high resolution in various organisms, cell types, and diseases.

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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?

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