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Epigenetic Regulation of Gene Expression

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Message from the Guest Editor

Gene expression in cells is defined by the epigenetic status of the chromatin, including DNA methylation, histone modifications, RNA modifications and noncoding-RNA-mediated regulation. Epigenetic machinery is at the core of an organism's adaptation to a changing environment.

The precise mapping of the epigenome requires modern high-throughput profiling technologies and sophisticated analysis tools. The development of next-generation sequencing technologies and associated bioinformatics tools greatly facilitated investigations into epigenetics. The investigation of the epigenome at the systems level, however, requires the integration of data from other omics modalities, e.g., high-resolution imaging technology to visualize chromatin dynamics, genetic engineering to modify epigenomes and methods to integrate epigenomics with disease and physiology.

This Special Issue aims to present the latest research regarding the epigenetic regulation of gene expression, as well as the application of omics technologies and statistical and bioinformatic approaches to decipher epigenetic mechanisms. Both original research articles and comprehensive reviews are welcomed.

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Special Issue

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Message from the Editor-in-Chief

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