

## Special Issue

# Epigenetic Connections between the Gene Regulatory Network and Chromatin Dynamics

### Message from the Guest Editor

Cells in tissues have different phenotypes and functions determined by lineage-specific and signal-responsive gene expression patterns. Activation or repression of gene transcription is facilitated by epigenetic mechanisms controlling the accessibility of DNA in nuclear chromatin. Transcription factors and histone- and DNA-modifying enzymes cooperate in gene regulatory networks that act on individual genes or genomic domains in the nucleus and can maintain gene expression patterns through cell divisions. This Special Issue focuses on gene regulation mechanisms involving transcription factors, epigenetic modifying and chromatin remodelling complexes acting at specific genomic loci or altering chromosomal dynamics. A better understanding of how cell types and cell states are defined will advance further insight into cell differentiation and cell function in normal tissues and in disease.

### Guest Editor

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## International Journal of Molecular Sciences

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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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