

Special Issue

DNA Methylation and Histone Modifications in Cellular Homeostasis

Message from the Guest Editor

Current research on chromatin-mediated dysregulation of gene transcription faces significant constraints, lacking comprehensive frameworks to dissect its molecular mechanisms. Emerging technologies have enabled high-resolution chromatin state mapping, but critical gaps remain in linking epigenetic landscapes to transcriptional outcomes across various cellular contexts. This Special Issue focuses on two key epigenetic mechanisms—DNA methylation dynamics and histone post-translational modifications—which regulate eukaryotic cellular homeostasis. By presenting a curated collection of mechanistic studies and computational models, we aim to elucidate the roles of these epigenetic "gatekeepers." Special attention is given to resolving long-standing paradoxes. By integrating advanced epigenome analysis techniques, this Special Issue seeks to pioneer multidimensional approaches to decode the epigenetic logic of cellular equilibrium, with implications for cellular homeostasis and eukaryotic evolution.

Guest Editor

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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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