

Special Issue

Epigenetic and Transcriptional Dysregulation in Cancer and Therapeutic Opportunities

Message from the Guest Editor

Epigenetic and transcriptional dysregulation—including DNA methylation, histone modifications, chromatin remodeling, and altered transcription-factor networks—drives cancer initiation, progression, and therapy resistance. Advanced molecular techniques such as whole-genome bisulfite sequencing, ATAC-seq, Hi-C, and single-cell multi-omics now reveal these mechanisms in unprecedented detail, uncovering new therapeutic opportunities. This Special Issue invites original research and reviews that provide molecular insights into epigenetic and transcriptional changes across cancers and connect them to diagnostic, prognostic, or therapeutic applications. We especially encourage studies grounded in genomic, epigenomic, transcriptomic, or structural data, including work on epigenetic drugs, chromatin-targeting agents, and molecular biomarkers. We look forward to your contributions to advancing the mechanistic and translational understanding of the cancer epigenome.

Guest Editor

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