

Special Issue

Molecular Impacts of DNA Methylation as Epigenetic Drivers of Disease Onset and Progression

Message from the Guest Editor

DNA methylation plays key roles in genome function and architecture, from modifications in promoter CpG islands that impact gene expression to higher-order silencing of chromosomal domains in heterochromatin packaging. In this Special Issue, manuscripts will be considered in two categories: (1) prospective work with human subjects or cell lines characterizing DNA methylation patterns and connecting those patterns to molecular epigenetic determinants of a disease; (2) retrospective computational work with human cohort data derived from publicly available databases to assess molecular biomarkers of disease demonstrating prognostic power relative to either early disease detection or patient disease progression/outcomes. The goals of this SI are as follows: (a) to establish a balance between “biological” lab work and “bioinformatic” computational work in order to emphasize how these dimensions are ultimately two sides of the same coin; (b) to survey the diversity of epigenetic disease mechanisms across cancers, neurodegenerative diseases, developmental diseases, environmental-driven diseases, etc.

Guest Editor

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Message from the Editor-in-Chief

Editor-in-Chief

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manuscripts are peer-reviewed and a first decision is provided to authors approximately 16.3 days after submission; acceptance to publication is undertaken in 2.8 days (median values for papers published in this journal in the second half of 2025).

Recognition of Reviewers:

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