



Modifications of Molecular Structure and Interactions in Epigenome 3.0

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Message from the Guest Editors

Epigenetic regulation involves heritable changes in gene expression that occur independent of changes in the primary DNA sequence. Such changes in gene expression are coupled to the chromatin structure. Modifications of its components, like DNA methylation, covalent histone modifications, nucleosome positioning, histone variants, and miRNAs, adds up to combinatorial patterns collectively termed as epigenome. The regulatory machinery also involves numerous enzymes and other proteins interacting with chromatin components. The understanding and precise description of such molecular interactions is key to the mapping of the epigenome, and to the design of new molecules interfering with epigenetic diseases. The present Special Issue welcomes manuscripts on molecular interactions of epigenetic regulation, including new methodological approaches and applications of established techniques.





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Message from the Editor-in-Chief

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