



Non-CpG Methylation

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Message from the Guest Editors

The DNA methylation represents the most known and most studied epigenetic mark, able to regulate the mRNA expression of the associated genes. Despite the very impressive bulk of studies related to DNA methylation mechanisms, dynamics, function and its physiological and even pathogenetic role, the scientific community has been stuck for years on the concept that >90% of DNA methylation in mammals occurs on the cytosines followed by a guanine. The possibility that DNA methylation at cytosines followed by other nucleotides, the so-called non-CpG methylation, remained confined to a small proportion of cytosines, considered non-functionally significant, except for embryonic tissues and stem cells. In the recent years, however, many evidences raised the possibility that the non-CpG methylation in adult and somatic tissues was underestimated due to technical biases and supported the idea that it could have functional role in driving gene expression.

The Special Issue is aimed at collecting research articles and reviews that can draw the state-of-the-art on the role of non-CpG methylation in mammal cells, its dynamic regulation, structural patterning and role in pathogenic mechanisms.





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Message from the Editor-in-Chief

In the past years the growth of the epigenetic field has been outstanding, from here the need of a journal where to centralize all new information on the subject. The term epigenetics is now broadly used to indicate changes in gene functions that do not depend on changes in the sequence of DNA. *Epigenomes* covers all areas of DNA modification from single cell level to multicellular organism as well as the epigenetics on human pathologies and behavior.

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