



Role of Epigenetic Modifications in Cancers

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Message from the Guest Editors

Dear Colleagues,

Cancer cells are simultaneously characterized by a massive overall loss of methylation in DNA and the acquisition of specific patterns of hypermethylation at CpG islands of certain gene promoters. Clearly established epigenetic mechanisms in human cancer, such as DNA methylation and histones methylation and acetylation, can reversibly or irreversibly alter gene function. Epigenetic abnormalities are set and maintained by multiple protein complexes and the interplay between their individual components, including DNA methylation machinery, histone modifiers, polycomb proteins and chromatin remodellers. Hence, DNA methylation mapping has revealed cancer-specific profiles of hypermethylated CpG islands (hypermethylomes) able to distinguish between different tumor types and to predict antineoplastic treatment responsiveness and patients' outcome. It has been made achievable, by the introduction of next-generation technologies that have led to the generation of a large amount of information, to better appreciate the role of the epigenomics of cancer in the clinical scenario.





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Message from the Editor-in-Chief

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