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DNA Methylation

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Deadline for manuscript submissions:

closed (31 December 2017)

Message from the Guest Editors

Dear Colleagues,

Methylation of cytosine is a long-term epigenetic modification of the genome. Epigenetic deregulation of genes is achieved by aberrant DNA methylation of promoter sequences in different human malignancies, including cancer. The discovery of proteins that oxidase 5-methylcytosine (5mC) to 5-hydroxymethylcytosine (5hmC) has extended our knowledge of how aberrant DNA methylation is coupled to gene regulation in cancer and other human malignancies. Current models propose that 5hmC is an intermediate base in the DNA demethylation process, or a bivalent chromatin marker found in cancer and stem cells.

In this Special Issue of *IJMS* we invite you to submit an original research report or review article deciphering the role of DNA methylation in malignancies, aging or differentiation

Prof. Dr. Reinhard Dammann Assoc. Prof. Alexander Dobrovic Guest Editors













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Message from the Editor-in-Chief

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