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Epigenetics of Melanoma

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Message from the Collection Editor

The melanoma mutational landscape also includes genetic alterations in a number of epigenetic regulators. There is accumulating evidence that genetic alterations and changes in the expression or activity of ATP-dependent chromatin-modifying enzymes, histone modifying enzymes, and readers of the histone code, can drive melanoma pathogenesis. Re-wired transcriptional programs that drive tumorigenesis often involve interactions between chromatin regulators, oncogenic signaling pathways, and transcription factors.

This Topical Collection is focused on epigenetic reprogramming by ATP-dependent chromatin remodeling enzymes, histone-modifying enzymes and readers, in the regulation of gene expression involved in melanoma metabolism, proliferation, metastasis, and the response to anti-cancer drugs.

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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.

Epigenomes (ISSN 2075-4655) is a fully peer-reviewed publication outlet with a rapid and economical route to open access publication. All articles are peer-reviewed and the editorial focus is on determining that the work is scientifically sound rather than trying to predict its future impact.

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