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Epigenetic DNA Modifications as Cancer Biomarkers

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Deadline for manuscript submissions:
closed (30 September 2018)

Message from the Guest Editors

Epigenetic changes in cancer tissues have been often-reported in recent years. There may be a temptation to view such changes as little more than mechanistic regulators of gene expression, but they can also be biomarkers in the broadest sense of the word.

Modifications, such as DNA methylation, have a role to play in processes, such as:

- defining sub-classes of disease at a molecular level
- providing targets for liquid biopsies or in-situ imaging
- physical markers of cell turnover and chromatin accessibility
- elucidating the life-history of disease
- clarifying the interpretation of somatic mutation signatures in DNA

In addition, through regulation of transcription they can explain the biology behind many aspects of gene-expression-based biomarkers and counsel as to the bounds at which those biomarkers cease to be useful. Or through competition for metabolic resources they can inform about processes that are often at the heart of cancer biology.

This Special Issue is focused on studies relating to epigenetic DNA modifications in cancer, and in particular their use to make inference about other aspects of the disease, whether prognostic, retrospective or diagnostic.

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Special Issue

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Message from the Editor-in-Chief

Genes are central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fastmoving field. There is a need for good quality, open access journals in this area, and the *Genes* team aims to provide expert manuscript handling, serious peer review, and rapid publication across the whole discipline of genetics. Starting in 2010, the journal is now well established and recognised.

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