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Cancer Risk and Gene Variations

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Deadline for manuscript submissions:
closed (25 January 2024)

Message from the Guest Editors

The advancing of genomic technologies has allowed the identification of a great number of genetic variations associated with cancer development and has thus allowed us to deepen our knowledge of the genetic architecture of cancer risk. This knowledge has helped in the establishment of public health strategies to reduce cancer prevalence and to improve early molecular diagnostics.

This Special Issue aims to describe the state of the art of the current research performed in genetic and genomic risk in cancer. Contributions are expected to highlight genomic variations that underly genetic risk for specific types of cancers, explore genetic modifying factors in people exposed to known environmental carcinogens, characterize the functional effects of genetic variants on cellular models, evaluate the impact of genetic variation in pathophysiology mechanisms, and describe genomic variants as biomarkers of prognosis and treatment response.

Contributions in the form of research papers and critical reviews are all welcome.

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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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