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Non-coding RNA Markers and Epigenetic Modifications in Tumor Identification

Guest Editor:

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Deadline for manuscript submissions:

closed (25 April 2022)

Message from the Guest Editor

Non-coding RNAs perform an important role in post-transcriptional regulation by inhibiting gene expression. Their tissue-specific expression and stable structure make them ideal candidates that may allow identifying tumor subtypes in an accurate manner. They potentially act as biomarkers for diagnostic, prognostic purposes and therapeutic targets for this disease. During the last decade, the discovery of ncRNAs' deregulation in different cancer cells has been the focus of attention for numerous investigations. The emergence of deep sequencing technologies has generated a high amount of public data available to further explore the role of ncRNAs in early diagnostics and classification of patients. Therefore, there is a large amount of interest in the study of ncRNAs to personalize clinical practice and be able to apply more specific and effective treatments to cancer patients.

This Special Issue aims to shed some light on the use of novel candidates for tumor identification and strategies involving non-coding RNAs, as well as describe new advances obtained in clinics. Original research manuscripts and comprehensive reviews are welcome to this call.



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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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