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Bioinformatic Approaches in Cancer

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Deadline for manuscript
submissions:

closed (20 May 2023)

Message from the Guest Editors

You are invited to contribute to a Special Issue of *Genes* that will focus on a Multi-omics Approach in Cancer. The advent of high-throughput technologies has enabled the development of methods for genome-wide characterization and detection of global transcript levels. Recently, bioinformatics tools have been developed and applied to the integration of the massive amount of data across multiple omics layers. Each type of omics data provides high-dimensional and meaningful information on the molecular mechanisms underlying the disease. An integrative approach provides a basis for the development of targeted cancer therapies.

In this Special Issue of *Genes*, we welcome reviews, new methods, and original research articles that apply different layers of multi-omics data (i.e., genome, transcriptome, epigenome, proteome, metabolome) for cancer research.

We look forward to receiving your contributions.



mdpi.com/si/141618

Special Issue



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Message from the Editor-in-Chief

Genes is central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fast-moving 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. Why not consider *Genes* for your next genetics paper?

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