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The Landscape of Transcriptomic Diversity in Oncology

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Deadline for manuscript
submissions:

30 August 2024

Message from the Guest Editors

Dear Colleagues,

Recently, the development of transcriptome analyses has been drastically accelerated, which is largely depends on the improved performance of next-generation sequencing. Big data collected from the analyses have not only provided information about aberrant gene expression in various cancer types but also enabled to discover thousands of the novel splice variants of annotated transcripts and unannotated long non-coding RNAs, providing new sources for identification of clinical biomarkers and druggable targets. Especially, cancer-related transcripts have attracted attention because there are still few cancer biomarkers and drugs with satisfactory effectiveness. In this Special Issue category, we highlight the landscape of transcriptomic diversity in oncology

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Guest Editors



mdpi.com/si/126783

Special Issue



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Message from the Editor-in-Chief

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