Special Issue

The Landscape of Transcriptomic Diversity in Oncology

Message from the Guest Editors

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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Deadline for manuscript submissions

closed (30 August 2024)

Cancers

an Open Access Journal by MDPI

Impact Factor 4.4
CiteScore 8.8
Indexed in PubMed

mdpi.com/si/126783

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Message from the Editor-in-Chief

Cancers is an international online journal addressing both clinical and basic science issues related to cancer research. The journal is publishing in Open Access format, which will certainly evolve to ensure that the journal takes full advantage of the rapidly changing world of information and knowledge dissemination. It publishes high-quality clinical, translational, and basic science research on cancer prevention, initiation, progression, and treatment, as well as other related topics, particularly to capture the most seminal studies in the rapidly growing area of immunology, immunotherapy, and tumor microenvironment.

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