



Spatial, Bulk, and Cell-Type-Related Transcriptomics in Cancer Research

Guest Editors:

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Deadline for manuscript
submissions:
30 April 2025

Message from the Guest Editors

Current transcriptomic approaches based on bulk, single-cell and spatial RNA sequencing can be complemented by multi-level bioinformatics analysis to provide a complete picture of an individual tumor. Each type of analysis has its own unique advantages and pitfalls, and the proper use and combination of these techniques can provide a comprehensive picture of cancer.

We are pleased to invite you to submit manuscripts to this Special Issue that contribute to our understanding of tumor biology, pathophysiology, and drug sensitivity using modern transcriptomics.

Submissions of original research articles and reviews are welcome. We intend to focus on the following topics:

- 1) Methodological advances in transcriptomics for cancer research;
- 2) What modern transcriptomics has to offer to clinical oncologists;
- 3) Recent advances in single-cell, spatial, and bulk RNA sequencing of cancers;
- 4) Significant new discoveries in cancer biology using the above methods;
- 5) Useful bioinformatics tools that can equip us with new techniques to effectively study and fight cancer.





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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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