Special Issue

Single Cell RNA Sequencing in Breast Cancer

Message from the Guest Editor

One of the most common types of cancer in women is breast cancer, which encompasses many diseases defined by their heterogeneity. Using single-cell RNA sequencing (scRNA-Seq), complex heterogeneous tumors can be analyzed at individual cell resolution, which overcomes the limitations of bulk RNA sequencing. This emerging method can determine molecular characteristics, explore the mechanisms of breast cancer metastasis, and, most importantly, lead to novel therapeutic targets and precise treatment management that are urgently needed in breast cancer treatment. We are pleased to invite you to contribute to this Special Issue of *Cancers,* which aims to provide research leading to novel insights into breast cancer single-cell RNA sequencing. In this Special Issue, original research articles and reviews are welcome. Research areas may include (but are not limited to) the following:

- Single-cell transcriptional sequencing;
- Tumor heterogeneity;
- Genetic heterogeneity and phenotypic variation of breast cancer cells;
- Novel biomarkers;
- Mechanisms of drug resistance;
- New therapeutic targets;
- The breast cancer microenvironment;
- Breast cancer metastasis.

Guest Editor

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About the Journal

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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