

Special Issue

Immunotherapy for Cancer: Immune Checkpoint Inhibitors or Single-Cell RNA Sequencing Approaches

Message from the Guest Editors

Based on the global cancer burden, 19.3 million new cancer cases and almost 10.0 million cancer deaths occurred in 2020. Single-cell RNA sequencing (scRNA-seq) solves the drawbacks of conventional RNA sequencing by measuring the entire transcriptome at a single-cell resolution and discriminating between distinct cell types by clustering various cells in tumor tissue. Additionally, this offers a better understanding of the molecular pathways that promote cancer progression and identifies somatic mutations throughout malignancy. The application of these technologies has a significant impact on cancer immunotherapy, such as identification of novel immune checkpoints and revealing the expression pattern of immune checkpoint inhibitors in the specific cancer type and also in the individual cells, which allows for a deeper understanding of the molecular and cellular interactions between cancer and the immune system. Single-cell technologies applied to tumor and blood samples have been generated. It will continue to create lots of new data with a direct effect on translational clinical research, leading to the identification of potential biomarkers.

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