Special Issue

Reality and Perspectives for Single Cell RNA Sequencing

Message from the Guest Editors

Although recent large-scale transcriptomic studies have revealed aberrant regulatory pathways and disease subtypes of human cancers, most of these studies measure the expression profiles of tumors in bulk average. However, substantial evidence indicates that intratumoral heterogeneity among malignant and non-malignant cells, and their interactions within the tumor microenvironment are critical to understand diverse aspects of tumor biology. Transcriptomes of thousands of cells can be massively parallel characterized by the development of recent technology in single-cell RNA sequencing. Single-cell RNA sequencing would help to dissect tumor complexity by characterizing the molecular landscape by cellular components, which could deepen our understanding of tumor heterogeneity and the microenvironment. We invite authors to submit research or review articles describing recent findings in single-cell RNA sequencing in cancer.

Guest Editors

Prof. Hae-Ock Lee
College of Medicine, The Catholic University of Korea, Seoul, Korea

Prof. Dr. Yeun-Jun Chung
1. Department of Microbiology, College of Medicine, The Catholic University of Korea, Seoul 03083, Republic of Korea
2. Precision Medicine Research Center, Integrated Research Center for Genome Polymorphism, College of Medicine, The Catholic University of Korea, Seoul 03083, Republic of Korea

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Editorial Office
MDPI, Grosspeteranlage 5
4052 Basel, Switzerland
Tel: +41 61 683 77 34
biomolecules@mdpi.com

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Biomolecules is a multidisciplinary open-access journal that reports on all aspects of research related to biogenic substances, from small molecules to complex polymers. We invite manuscripts of high scientific quality that pertain to the diverse aspects relevant to organic molecules, irrespective of the biological question or methodology. We aim for a competent, fair peer review and rapid publication. Please look at some of the exciting work that has been published in *Biomolecules* so far. We would be delighted to welcome you as one of our authors.

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Prof. Dr. Peter E. Nielsen
Department of Cellular and Molecular Medicine, Faculty of Health and Medical Sciences, University of Copenhagen, Blegdamsvej 3C, DK-2200 Copenhagen, Denmark

Prof. Dr. Lukasz Kurgan
Department of Computer Science, Virginia Commonwealth University, Richmond, VA 23284, USA

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