Special Issue

Transcriptional and Genetic Tumor Heterogeneity through ScRNA-seq

Message from the Guest Editor

With the quick progress of scRNA-seq technologies, including approaches to assess cell-level genetic heterogeneity, the anticipation is that scRNA-seq will soon be incorporated in the clinics. This process will greatly benefit from improved knowledge on tumor heterogeneity, the ability to interpret cell-level genetic and transcriptional variation, and, consequently, to distinguish and characterize sensitive and resistant clones. In the near future, this new knowledge is expected to be translated into better diagnosis and treatment of cancer patients.

We invite submissions of both methodological and original research papers assessing tumor heterogeneity through single-cell RNA sequencing. Special focus will be placed on research integrating genetic and transcriptional heterogeneity and identifying cell-level genetic determinants of phenotype. The overarching aim of this issue is to stimulate emerging and promising single-cell research, pursuing at the same time new exploratory and collaborative venues to address its challenges.

Guest Editor

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Deadline for manuscript submissions

closed (1 December 2021)

About the Journal

Message from the Editor-in-Chief

Genes is central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fast-moving field. There is a need for good quality, open access journals in this area, and the *Genes* team aims to provide expert manuscript handling, serious peer review, and rapid publication across the whole discipline of genetics. Starting in 2010, the journal is now well established and recognised. Why not consider *Genes* for your next genetics paper?

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