

SPECIAL ISSUE: DECIPHERING TUMOR COMPLEXITY VIA SINGLE-CELL MULTI-OMICS

OPEN LIFE SCIENCES

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GUEST EDITORS:

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Scope

Single-cell sequencing technologies are revolutionizing cancer research by enabling scientists to resolve cellular heterogeneity and functional variation in unprecedented depth. These advancements have increased our understanding of human cancers, with a particular emphasis on the interconnections between various cell types. Through the use of single-cell multi-omics, this field is making headway in updating current knowledge, notably in precision medicine, where the study of cellular subpopulations might offer insight into responses to anti-tumor treatment.

Deep learning is an effective method for organizing the high-dimensional data produced by single-cell profiling. It does imputation, batch correction, and grouping, as well as improving signal-to-noise ratios. Despite advances in single-cell multi-omics and deep learning, the science continues to provide exciting difficulties and new viewpoints.

We encourage contributions on the most latest developments in single-cell multi-omics research, which will provide readers with a complete review of the state of the art in single-cell multi-omics and its influence on cancer research.

*In case of any questions please contact:
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Managing Editor, Open Life Sciences*

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We are looking for papers that highlight the use of single-cell multi-omics in cancer research for this collection. The issue will include, but is not limited to, the following topics:

- Elucidating the relationships between multi-omics layers at the single-cell level using integrative techniques on single-cell multi-omics data.
- Using state-of-the-art algorithms to analyze single-cell profiling data and detect patterns in cellular heterogeneity are deep learning approaches.
- Using single-cell multi-omics sequencing and machine learning to identify interesting cancer biomarkers.
- Utilizing single-cell multi-omics data to develop new therapeutic approaches and improve current cancer therapies.
- Applying single-cell multi-omics to next-generation immunotherapy and targeted cancer therapy.
- Understanding the genetic characteristics of metastatic and therapy-resistant tumor subpopulations using single-cell multi-omics technology.
- Integration of single-cell sequencing data with clinical pathology information for developing novel diagnostic and prognostic biomarkers and potential therapeutic targets.
- Molecular characterization of circulating tumor cells using a variety of single-cell omics approaches.
- Elucidating the relationships between multi-omics layers at the single-cell level, including spatial transcriptomics and proteomics, to map the tumor microenvironment and understand the spatial heterogeneity within tumors.

Please note that studies consisting solely of bioinformatic investigation of publicly available datasets will not be considered unless accompanied by experimental data. Submitted manuscripts to this Special Issue must go beyond the analysis of pre-existing datasets and provide significant insight into the process being investigated.

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How to submit

Authors are kindly invited to submit their contribution via online submission system Editorial Manager available at:

<https://www.editorialmanager.com/openbiol/default1.aspx>

Please remember to select: SI: Multi-omics to ensure that your manuscript will be processed with the highest priority.

Before completing their manuscript, authors should carefully read the journal's Instruction for Authors located at:

https://www.degruyter.com/publication/journal_key/BIOL/downloadAsset/BIOL_Instruction%20for%20Authors.pdf

Contributors to the Special Issue will benefit from:

- indexation in Web of Science, PubMed, SCOPUS, DOAJ, Google Scholar
- quick and constructive peer review provided by experts in the field
- no space constraints
- convenient, web-based paper submission and tracking system – Editorial Manager
- quick online publication upon completing the publishing process
- better visibility due to Open Access
- long-term preservation of the content (articles archived in Portico)

***Deadline for submissions:
October 31st, 2024***



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