



OPEN ACCESS

EDITED AND REVIEWED BY

Liang Xu,
University of Kansas, United States

*CORRESPONDENCE

Linheng Li,
✉ lil@stowers.org

RECEIVED 16 January 2025

ACCEPTED 21 January 2025

PUBLISHED 20 February 2025

CITATION

Li L, Tang F and Deng H (2025) Editorial:
Exploring drug development with single cell
omics analytics and stem cell-based
disease models.

Front. Drug Discov. 5:1561985.

doi: 10.3389/fddsv.2025.1561985

COPYRIGHT

© 2025 Li, Tang and Deng. This is an open-
access article distributed under the terms of the
[Creative Commons Attribution License \(CC BY\)](https://creativecommons.org/licenses/by/4.0/).

The use, distribution or reproduction in other
forums is permitted, provided the original
author(s) and the copyright owner(s) are
credited and that the original publication in this
journal is cited, in accordance with accepted
academic practice. No use, distribution or
reproduction is permitted which does not
comply with these terms.

Editorial: Exploring drug development with single cell omics analytics and stem cell-based disease models

Linheng Li^{1,2*}, Fuchou Tang³ and Hongkui Deng⁴

¹Stem Cell, Stowers Institute for Medical Research, Kansas City, MO, United States, ²Department of Pathology, University of Kansas Medical Center, Kansas City, MO, United States, ³Biomedical Pioneering Innovation Center, Peking University, Beijing, China, ⁴MOE Engineering Research Center of Regenerative Medicine, School of Basic Medical Sciences, Peking University, Beijing, China

KEYWORDS

single-cell, multi-omics, drug discovery, drug candidates, drug screening

Editorial on the Research Topic

[Exploring drug development with single cell omics analytics and stem cell-based disease models](#)

In the dynamic realm of biological research, we are witnessing a transformative era that redefines our grasp of cellular functions, development processes, and disease complexities. Central to this scientific renaissance are leading-edge technologies like single-cell (sc)-omics-based analytics, encompassing single-cell multiomics, alongside innovative stem cell based approaches. These technologies have catalyzed a cascade of discoveries, opening new frontiers in our quest for knowledge and revolutionizing the landscape of scientific investigations.

The exploration of stem cells marks a significant chapter in this journey. Known for their remarkable capabilities of self-renewal and differentiation, stem cells are crucial for maintaining tissue equilibrium and enabling regeneration. This deeper understanding of their properties and biological processes has not only advanced the field of regenerative medicine but also introduced potential therapeutic strategies for combatting various diseases, providing new hope and possibilities for treatment across the globe.

Moreover, the process of reprogramming somatic cells into pluripotent stem cells stands as a particularly compelling advancement. This technique allows for the creation of diverse disease models by deriving cells from patients or by genetic engineering to reflect specific diseases, providing a powerful tool to explore disease mechanisms at a more personal and precise level. It also improved drug screening approaches from testing candidate drugs on a single type of cells to testing them on complex tissues with many types of cells well-organized together, which mimic better the real pathological conditions *in vivo*. Such insights into stem cell biology and disease modeling showcase a promising area ripe for breakthroughs, previously likened to the realms of science fiction.

This Research Topic of reviews explores the transformative impact of sc-sequencing technologies, particularly their expansion into sc-multiomics, using stem cells as a platform for advancing disease understanding, diagnosis and drug discovery. [Zhang et al.](#) address the persistent challenges in drug development, such as low success rates

and high costs, highlighting how sc-multiomics can refine drug target identification and improve preclinical models. [Ma et al.](#) examines advancements in sc-multiomics, focusing on genome-wide analyses that enhance drug research, improve understanding of drug responses and resistance, and pave the way for personalized treatment strategies. [Wang and Tang](#) highlight the application of sc-sequencing technologies into drug discovery, emphasizing the importance of post-injury lung regeneration mechanisms and recent sc-seq discoveries, which hold promise for developing drugs targeting lung diseases. Additionally [Ma et al.](#) summarizes recent progress in using sc-multiomics to improve drug research by examining drug-chromatin interactions and mechanisms of resistance, paving the way for personalized treatment approaches.

Through continued research and exploration within these innovative domains, we are not only enhancing our understanding of fundamental biology but are also bridging the gap between bench-side basic research and bed-side clinical applications, setting the stage for significant transformations in drug discovery, which will have a profound impact on medical treatment.

Author contributions

LL: Writing–original draft, Writing–review and editing. FT: Writing–review and editing. HD: Writing–review and editing.

Funding

The author(s) declare that no financial support was received for the research, authorship, and/or publication of this article.

Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Generative AI statement

The author(s) declare that Generative AI was used in the creation of this manuscript. We have used ChatGPT to edit our draft of Editorial with the purpose of improving English.

Publisher's note

All claims expressed in this article are solely those of the authors and do not necessarily represent those of their affiliated organizations, or those of the publisher, the editors and the reviewers. Any product that may be evaluated in this article, or claim that may be made by its manufacturer, is not guaranteed or endorsed by the publisher.