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## Single-cell sequencing in stem cell biology

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4832540>

Apr 15, 2016 · **Tissue-specific stem cells.** Tissue-specific stem cells reside in developing or differentiated tissues. They also undergo self-renewal and have the potential to differentiate into a variety of specified cell types. In the past 2 years, **single-cell RNA-seq** methods have been applied to **tissue-specific stem cells**.

Cited by: 66

Author: Lu Wen, Fuchou Tang

Publish Year: 2016

## A practical guide to single-cell RNA-sequencing for ...

<https://genomemedicine.biomedcentral.com/articles/10.1186/s13073-017-0467-4> ▾

Aug 18, 2017 · General workflow of **single-cell RNA-sequencing** (scRNA-seq) experiments. A typical **scRNA-seq** workflow includes most of the following steps: 1) isolation of **single cells**, 2) cell lysis while preserving **mRNA**, 3) **mRNA** capture, 4) reverse **transcription** of primed **RNA** into complementary **DNA** ...

Cited by: 73

Author: Ashraful Haque, Jessica Engel, Sarah ...

Publish Year: 2017

## Single-cell RNA-seq of cultured human adipose-derived ...

<https://www.nature.com/articles/sdata201931>

Feb 26, 2019 · Adipose-derived mesenchymal **stem cells** (ADSCs) show considerable promise for clinical **applications** in regenerative medicine. We performed a large-scale **single-cell** transcriptomic **sequencing** of ...

Author: Xuanyu Liu, Qinqin Xiang, Fen Xu, Ji... Publish Year: 2019

Author: Xuanyu Liu

## [PDF] Single-Cell Research - Illumina | Sequencing and array ...

[https://www.illumina.com/.../research\\_reviews/single-cell-sequencing-research-review.pdf](https://www.illumina.com/.../research_reviews/single-cell-sequencing-research-review.pdf)

18 Single-cell Research For Research Use Only. Not for use in diagnostic procedures. activated earlier than the **endoderm** program. This result was also observed for expression of **endoderm** orthologs in frog (*Xenopus tropicales*), sea anemone (*Nematostella vectensis*), and sponge (*Amphimedon queenslandica*).

## Single-cell multi-omics sequencing of mouse early embryos ...

<https://www.nature.com/articles/cr201782>

Jun 16, 2017 · Combinatorial **analysis** of **epigenomic** signatures in mouse ES Cells. To our knowledge, this is the first time that the **ploidy** of a **single cell** has been measured using a **single-cell** sequencing strategy, as for all of the previous **single-cell** genome sequencing techniques, a cell was assumed to be either diploid or haploid.

Cited by: 65

Author: Fan Guo, Lin Li, Jingyun Li, Xinglong W...

Publish Year: 2017

Author: Fan Guo





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## Applications of single cell RNA sequencing to research of stem cells

Xiao Zhang, Lei Liu

### Abstract

Stem cells (SCs) with their self-renewal and pluripotent differentiation potential, show great promise for therapeutic applications to some refractory diseases such as stroke, Parkinsonism, myocardial infarction, and diabetes. Furthermore, as seed cells in tissue engineering, SCs have been applied widely to tissue and organ regeneration. However, previous studies have shown that SCs are heterogeneous and consist of many cell subpopulations. Owing to this heterogeneity of cell states, gene expression is highly diverse between cells even within a single tissue, making precise identification and analysis of biological properties difficult, which hinders their further research and applications. Therefore, a defined understanding of the heterogeneity is a key to research of SCs. Traditional ensemble-based sequencing approaches, such as microarrays, reflect an average of expression levels across a large population, which overlook unique biological behaviors of individual cells, conceal cell-to-cell variations, and cannot understand the heterogeneity of SCs radically. The development of high throughput single cell RNA sequencing (scRNA-seq) has provided a new research tool in biology, ranging from identification of novel cell types and exploration of cell markers to the analysis of gene expression and predicating developmental trajectories. scRNA-seq has profoundly changed our understanding of a series of biological phenomena. Currently, it has been used in research of SCs in many fields, particularly for the research of heterogeneity and cell subpopulations in early embryonic development. In this review, we focus on the scRNA-seq technique and its applications to research of SCs.

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Aug 18, 2017 · General workflow of single-cell RNA-sequencing (scRNA-seq) experiments. A typical **scRNA-seq workflow** includes most of the following steps: 1) isolation of single cells, 2) cell lysis while preserving mRNA, 3) **mRNA capture**, 4) reverse transcription of primed RNA into complementary DNA (cDNA...

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Author: Ashraful Haque, Jessica Engel, Sarah A. ...

Publish Year: 2017

## Single-cell sequencing in stem cell biology

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4832540>

Apr 15, 2016 · The **application** of these methods to different types of **stem cells**, including pluripotent **stem cells** and tissue-specific **stem cells**, has led to exciting new findings in the **stem cell** field. In this review, we discuss the recent progress as well as future perspectives in the methodologies and **applications of single-cell omic sequencing technologies**.

Cited by: 78

Author: Lu Wen, Fuchou Tang

Publish Year: 2016

## Single-cell RNA sequencing: Technical advancements and ...

<https://www.sciencedirect.com/science/article/pii/S0098299717300535>

Abstract. Cells are the basic building blocks of organisms and each cell is unique. Single-cell RNA sequencing has emerged as an indispensable tool to dissect the **cellular heterogeneity** and decompose tissues into cell types and/or cell states, which offers enormous potential for **de novo discovery**.

Cited by: 28

Author: Eva Hedlund, Qiaolin Deng

Publish Year: 2017

## Single-Cell RNA Sequencing of Human Embryonic Stem Cell ...

[https://www.cell.com/stem-cell-reports/fulltext/S2213-6711\(19\)30024-4](https://www.cell.com/stem-cell-reports/fulltext/S2213-6711(19)30024-4) ▾

Feb 28, 2019 · Here, we performed single-cell RNA sequencing (scRNA-seq) of human embryonic stem cell (hESC)-derived **embryoid body (EB)** in the presence or absence of nicotine. **Nicotine-induced lineage-specific responses** and dysregulated cell-to-cell communication in EBs, shedding light on the