Resource Summary Report

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SINCERA Pipeline

RRID:SCR_016563
Type: Tool

Proper Citation

SINCERA Pipeline (RRID:SCR_016563)

Resource Information

URL: https://github.com/xu-lab/SINCERA

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Description: Software tool implemented in R S4 as an analytic pipeline for processing single-cell RNA-seq data from a whole organ or sorted cells. Used for Single Cell RNA-Seq profiling analysis.

Abbreviations: SINCERA

Synonyms: SINCERA, SINgle CEll RNA seq profiling Analysis

Resource Type: data processing software, software resource, data analysis software, software application, data analytics software

Defining Citation: PMID:26600239

Keywords: single, cell, RNA seq, data, sorted, whole, organ, profiling, analysis

Funding: NHLBI U01 HL110964;
NHLBI U01 HL122642;
NHLBI R01 HL105433

Availability: Free, Available for download, Freely available

Resource Name: SINCERA Pipeline

Resource ID: SCR_016563

Alternate URLs: https://research.cchmc.org/pbge/sincera.html

License: GNU General Public License v3

Record Creation Time: 20220129T080331+0000

Record Last Update: 20250428T054006+0000

Ratings and Alerts

No rating or validation information has been found for SINCERA Pipeline.

No alerts have been found for SINCERA Pipeline.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Goggin SM, et al. (2024) ESCHR: a hyperparameter-randomized ensemble approach for robust clustering across diverse datasets. Genome biology, 25(1), 242.

Wu G, et al. (2021) Short-term exposure to intermittent hypoxia leads to changes in gene expression seen in chronic pulmonary disease. eLife, 10.

Spakowicz D, et al. (2020) Approaches for integrating heterogeneous RNA-seq data reveal cross-talk between microbes and genes in asthmatic patients. Genome biology, 21(1), 150.

Wu H, et al. (2018) Comparative Analysis and Refinement of Human PSC-Derived Kidney Organoid Differentiation with Single-Cell Transcriptomics. Cell stem cell, 23(6), 869.