# **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 CEII RNA seg profiling Analysis

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

analysis software, software application

**Defining Citation: PMID:26600239** 

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

Funding Agency: NHLBI, NHLBI, NHLBI

Availability: Free, Available for download, Freely available

Resource Name: SINCERA Pipeline

Resource ID: SCR\_016563

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

### 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 3 mentions in open access literature.

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

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.