Resource Summary Report

Generated by RRID on Apr 9, 2025

ascend

RRID:SCR_017257
Type: Tool

Proper Citation

ascend (RRID:SCR_017257)

Resource Information

URL: https://github.com/powellgenomicslab/ascend

Proper Citation: ascend (RRID:SCR_017257)

Description: Software R package for analysis of single cell RNA-seq expression, normalization and differential expression data. Provides framework to perform cell and gene filtering, quality control, normalization, dimension reduction, clustering, differential expression, and visualization functions.

Synonyms: Normalization and Differential expression, ASCEND, Analysis of Single Cell Expression

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

Defining Citation: PMID:31505654

Keywords: analysis, single, cell, RNAseq, expression, normalization, data, gene, filtering, quality, control, dimension, reduction, clustering, visualization, bio.tools

Funding:

Availability: Free, Available for download, Freely available

Resource Name: ascend

Resource ID: SCR_017257

Alternate IDs: biotools:ascend

Alternate URLs: https://bio.tools/ascend

Record Creation Time: 20220129T080334+0000

Record Last Update: 20250409T061501+0000

Ratings and Alerts

No rating or validation information has been found for ascend.

No alerts have been found for ascend.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 2 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

Shim WJ, et al. (2020) Conserved Epigenetic Regulatory Logic Infers Genes Governing Cell Identity. Cell systems, 11(6), 625.

Senabouth A, et al. (2019) ascend: R package for analysis of single-cell RNA-seq data. GigaScience, 8(8).