

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 8, 2026

[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, data processing software, software application, software resource

Defining Citation: [PMID:31505654](#)

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

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: 20260905T132821+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 [PRECISE-TBI](#) .

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).