

# Resource Summary Report

Generated by [kravitz2](#) on Sep 17, 2026

## [ascend](#)

RRID:SCR\_017257

Type: Tool

### Proper Citation

ascend (RRID:SCR\_017257)

### Resource Information

**URL:** <https://github.com/powellgenomicslab/ascend>

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**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:** 20260912T195850+0000

### Ratings and Alerts

No rating or validation information has been found for ascend.

No alerts have been found for ascend.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 2 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [kravitz2](#) .

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).