

Resource Summary Report

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LIGER

RRID:SCR_018100

Type: Tool

Proper Citation

LIGER (RRID:SCR_018100)

Resource Information

URL: <https://bioinformaticshome.com/tools/rna-seq/descriptions/LIGER.html>

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Description: Software R package for integrating and analyzing multiple single-cell datasets. It relies on integrative non-negative matrix factorization to identify shared and dataset-specific factors. Used for analysis of multiple scRNA-seq data sets.

Synonyms: Linked Inference of Genomic Experimental Relationships

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

Defining Citation: [PMID:31178122](#)

Keywords: Single cell genomic, data integration, dataset, cell identity, integrative analysis, gene regulation, disease state, scRNA seq analysis, shared factor among data set,

Funding: NIH

Availability: Free, Available for download, Freely available

Resource Name: LIGER

Resource ID: SCR_018100

Alternate URLs: <https://github.com/MacoskoLab/liger>

License: GNU GPL v3

Record Creation Time: 20220129T080338+0000

Record Last Update: 20260903T235451+0000

Ratings and Alerts

No rating or validation information has been found for LIGER.

No alerts have been found for LIGER.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Jones J, et al. (2025) Gut commensal microbiota drive tailored macrophage responses. *Cell reports*, 44(8), 116157.

Gao C, et al. (2024) Integrating single-cell multimodal epigenomic data using 1D-convolutional neural networks. *bioRxiv : the preprint server for biology*.

Agrawal A, et al. (2024) NiCo identifies extrinsic drivers of cell state modulation by niche covariation analysis. *Nature communications*, 15(1), 10628.

Tiwari V, et al. (2024) Innate immune training restores pro-reparative myeloid functions to promote remyelination in the aged central nervous system. *Immunity*, 57(9), 2173.

Wang S, et al. (2024) 3D reconstruction of the mouse cochlea from scRNA-seq data suggests morphogen-based principles in apex-to-base specification. *Developmental cell*, 59(12), 1538.

O'Toole SM, et al. (2023) Molecularly targetable cell types in mouse visual cortex have distinguishable prediction error responses. *Neuron*, 111(18), 2918.

Widmer FC, et al. (2022) NMDA receptors in visual cortex are necessary for normal visuomotor integration and skill learning. *eLife*, 11.

Osorno T, et al. (2022) Candelabrum cells are ubiquitous cerebellar cortex interneurons with specialized circuit properties. *Nature neuroscience*, 25(6), 702.

Larouche JA, et al. (2021) Murine muscle stem cell response to perturbations of the neuromuscular junction are attenuated with aging. *eLife*, 10.

Li G, et al. (2021) ExpressHeart: Web Portal to Visualize Transcriptome Profiles of Non-Cardiomyocyte Cells. *International journal of molecular sciences*, 22(16).

Yao Z, et al. (2021) A transcriptomic and epigenomic cell atlas of the mouse primary motor cortex. *Nature*, 598(7879), 103.

van Dijk D, et al. (2018) Recovering Gene Interactions from Single-Cell Data Using Data Diffusion. *Cell*, 174(3), 716.