

Resource Summary Report

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IKAP

RRID:SCR_017417

Type: Tool

Proper Citation

IKAP (RRID:SCR_017417)

Resource Information

URL: <https://github.com/NHLBI-BCB/IKAP>

Proper Citation: IKAP (RRID:SCR_017417)

Description: Software tool for identifying K mAjor cell population groups in single-cell RNA-seq analysis. Algorithm identifying major cell groups that improves differentiating by tuning parameters for clustering. Using multiple datasets improves identification of major cell types and facilitates cell ontology curation.

Synonyms: Identifying K mAjor cell Population

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

Defining Citation: [DOI:10.1101/596817](https://doi.org/10.1101/596817)

Keywords: Identify, cell, population, group, single, cell, RNAseq, analysis, clustering, dataset

Availability: Free, Available for download, Freely available

Resource Name: IKAP

Resource ID: SCR_017417

License: MIT license

Record Creation Time: 20220129T080335+0000

Record Last Update: 20260912T195852+0000

Ratings and Alerts

No rating or validation information has been found for IKAP.

No alerts have been found for IKAP.

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 [NIF](#) .

Liu S, et al. (2021) MultiK: an automated tool to determine optimal cluster numbers in single-cell RNA sequencing data. Genome biology, 22(1), 232.

Chen YC, et al. (2019) IKAP-Identifying K mAjor cell Population groups in single-cell RNA-sequencing analysis. GigaScience, 8(10).