

# Resource Summary Report

Generated by [nidm-terms](#) on Aug 15, 2026

## IKAP

RRID:SCR\_017417

Type: Tool

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### Proper Citation

IKAP (RRID:SCR\_017417)

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### 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 processing software, software application, data analysis software, 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:** 20260815T042805+0000

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### Ratings and Alerts

No rating or validation information has been found for IKAP.

No alerts have been found for IKAP.

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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 [nidm-terms](#) .

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).