

Resource Summary Report

Generated by [RRID](#) on Sep 18, 2026

Taiji

RRID:SCR_028464

Type: Tool

Proper Citation

Taiji (RRID:SCR_028464)

Resource Information

URL: <https://github.com/Taiji-pipeline/Taiji>

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Description: Software integrative analysis pipeline for analyzing bulk/single-cell ATAC-seq and RNA-seq data. Integrative multi-omics data analysis framework. It can be used as a standalone pipeline to analyze ATAC-seq, RNA-seq, single cell ATAC-seq or Drop-seq data. Used to integrate diverse datasets and use these information to construct regulatory network and identify candidate driver genes.

Resource Type: software resource, software toolkit, source code

Defining Citation: [PMID:30944857](#)

Keywords: integrative analysis, single-cell ATAC-seq data, RNA-seq data, identify driver transcription factors, construct regulatory network, identify candidate driver genes,

Funding: NHGRI R01HG009626;
NHGRI U54HG006997

Availability: Free, Available for download, Freely available

Resource Name: Taiji

Resource ID: SCR_028464

Alternate URLs: <https://taiji-pipeline.github.io/>

License: BSD-3-Clause

Record Creation Time: 20260519T054547+0000

Record Last Update: 20260912T200551+0000

Ratings and Alerts

No rating or validation information has been found for Taiji.

No alerts have been found for Taiji.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Pratt BM, et al. (2026) Single-cell gain-of-function mapping reveals latent regulatory programs governing CD8+ T cell fate. Research square.

Ainsworth RI, et al. (2022) Systems-biology analysis of rheumatoid arthritis fibroblast-like synoviocytes implicates cell line-specific transcription factor function. Nature communications, 13(1), 6221.

Li YE, et al. (2021) An atlas of gene regulatory elements in adult mouse cerebrum. Nature, 598(7879), 129.

Zhang K, et al. (2021) A single-cell atlas of chromatin accessibility in the human genome. Cell, 184(24), 5985.