

Resource Summary Report

Generated by [PRECISE-TBI](#) on Jul 31, 2026

[flowTrans](#)

RRID:SCR_002093

Type: Tool

Proper Citation

flowTrans (RRID:SCR_002093)

Resource Information

URL: <http://www.bioconductor.org/packages/release/bioc/html/flowTrans.html>

Proper Citation: flowTrans (RRID:SCR_002093)

Description: Software for profile maximum likelihood estimation of parameters for flow cytometry data transformations.

Synonyms: flowTrans - Parameter Optimization for Flow Cytometry Data Transformation

Resource Type: software resource

Defining Citation: [PMID:21050468](#)

Keywords: software package, mac os x, unix/linux, windows, r, flow cytometry

Availability: Free, Available for download, Freely available

Resource Name: flowTrans

Resource ID: SCR_002093

Alternate IDs: OMICS_05612

License: Artistic License, v2

Record Creation Time: 20220129T080211+0000

Record Last Update: 20260725T190516+0000

Ratings and Alerts

No rating or validation information has been found for flowTrans.

No alerts have been found for flowTrans.

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 [PRECISE-TBI](#) .

Shichino S, et al. (2022) TAS-Seq is a robust and sensitive amplification method for bead-based scRNA-seq. Communications biology, 5(1), 602.

Kamatani T, et al. (2022) Human iPS cell-derived cartilaginous tissue spatially and functionally replaces nucleus pulposus. Biomaterials, 284, 121491.

López Hernández JF, et al. (2021) Diverse mating phenotypes impact the spread of wtf meiotic drivers in Schizosaccharomyces pombe. eLife, 10.

Theorell A, et al. (2019) Determination of essential phenotypic elements of clusters in high-dimensional entities-DEPECHE. PloS one, 14(3), e0203247.