

Resource Summary Report

Generated by [NIF](#) on Aug 13, 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: 20260808T185747+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 5 mentions in open access literature.

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

Kirino S, et al. (2026) Fetal reversion from diverse lineages sustains the intestinal stem cell pool and confers stress resilience. *Communications biology*, 9(1), 255.

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.