Resource Summary Report

Generated by dkNET on Apr 29, 2025

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

Funding:

Availability: Artistic License, v2

Resource Name: flowTrans

Resource ID: SCR_002093

Alternate IDs: OMICS_05612

Record Creation Time: 20220129T080211+0000

Record Last Update: 20250420T014051+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 dkNET.

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.