

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

flowMeans

RRID:SCR_002275

Type: Tool

Proper Citation

flowMeans (RRID:SCR_002275)

Resource Information

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

Proper Citation: flowMeans (RRID:SCR_002275)

Description: Software that identifies cell populations in Flow Cytometry data using non-parametric clustering and segmented-regression-based change point detection.

Synonyms: flowMeans: Non-parametric Flow Cytometry Data Gating, flowMeans - Non-parametric Flow Cytometry Data Gating

Resource Type: software resource

Defining Citation: [PMID:21182178](#)

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

Availability: Artistic License, v2

Resource Name: flowMeans

Resource ID: SCR_002275

Alternate IDs: OMICS_05603

Record Creation Time: 20220129T080212+0000

Record Last Update: 20260725T190523+0000

Ratings and Alerts

No rating or validation information has been found for flowMeans.

No alerts have been found for flowMeans.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Mow RJ, et al. (2024) Harnessing a Safe Novel Lipid Nanoparticle: Targeted Oral Delivery to Colonic Epithelial and Macrophage Cells in a Colitis Mouse Model. *Nanomaterials* (Basel, Switzerland), 14(22).

Del Barrio E, et al. (2020) optimalFlow: optimal transport approach to flow cytometry gating and population matching. *BMC bioinformatics*, 21(1), 479.

Liu X, et al. (2019) A comparison framework and guideline of clustering methods for mass cytometry data. *Genome biology*, 20(1), 297.

Rahim A, et al. (2018) High throughput automated analysis of big flow cytometry data. *Methods* (San Diego, Calif.), 134-135, 164.

Li YH, et al. (2017) Scalable multi-sample single-cell data analysis by Partition-Assisted Clustering and Multiple Alignments of Networks. *PLoS computational biology*, 13(12), e1005875.

Chattopadhyay PK, et al. (2012) Cytometry: today's technology and tomorrow's horizons. *Methods* (San Diego, Calif.), 57(3), 251.