

# Resource Summary Report

Generated by [dkNET](#) on Apr 24, 2025

## flowMeans

RRID:SCR\_002275

Type: Tool

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### Proper Citation

flowMeans (RRID:SCR\_002275)

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### 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

**Funding:**

**Availability:** Artistic License, v2

**Resource Name:** flowMeans

**Resource ID:** SCR\_002275

**Alternate IDs:** OMICS\_05603

**Record Creation Time:** 20220129T080212+0000

**Record Last Update:** 20250420T014057+0000

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## Ratings and Alerts

No rating or validation information has been found for flowMeans.

No alerts have been found for flowMeans.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 6 mentions in open access literature.

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

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.