

Resource Summary Report

Generated by [NIF](#) on Aug 12, 2026

[flowUtils](#)

RRID:SCR_001879

Type: Tool

Proper Citation

flowUtils (RRID:SCR_001879)

Resource Information

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

Proper Citation: flowUtils (RRID:SCR_001879)

Description: Software that provides utilities for flow cytometry data.

Synonyms: flowUtils - Utilities for flow cytometry

Resource Type: software resource

Keywords: software package, mac os x, unix/linux, windows, r, cell based assay, flow cytometry, decision tree, infrastructure

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: flowUtils

Resource ID: SCR_001879

Alternate IDs: OMICS_05614

License: Artistic License, v2

Record Creation Time: 20220129T080210+0000

Record Last Update: 20260808T185735+0000

Ratings and Alerts

No rating or validation information has been found for flowUtils.

No alerts have been found for flowUtils.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Kang H, et al. (2025) Optimization of a Cas12a-Driven Synthetic Gene Regulatory Network System. ACS synthetic biology, 14(5), 1732.

Grøndal SM, et al. (2024) Targeting AXL cellular networks in kidney fibrosis. Frontiers in immunology, 15, 1446672.

Grøndal SM, et al. (2024) Dynamic changes in immune cell populations by AXL kinase targeting diminish liver inflammation and fibrosis in experimental MASH. Frontiers in immunology, 15, 1400553.

Kang H, et al. (2023) SGRN: A Cas12a-driven Synthetic Gene Regulatory Network System. bioRxiv : the preprint server for biology.

White S, et al. (2021) FlowKit: A Python Toolkit for Integrated Manual and Automated Cytometry Analysis Workflows. Frontiers in immunology, 12, 768541.

Wong N, et al. (2021) K-means quantization for a web-based open-source flow cytometry analysis platform. Scientific reports, 11(1), 6735.

Platon L, et al. (2018) A computational approach for phenotypic comparisons of cell populations in high-dimensional cytometry data. Methods (San Diego, Calif.), 132, 66.