

# Resource Summary Report

Generated by SPARC SAWG on Jul 28, 2026

## flowUtils

RRID:SCR\_001879

Type: Tool

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### Proper Citation

flowUtils (RRID:SCR\_001879)

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### 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:** 20260725T190512+0000

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### Ratings and Alerts

No rating or validation information has been found for flowUtils.

No alerts have been found for flowUtils.

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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 [SPARC SAWG](#) .

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.

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

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.