

# Resource Summary Report

Generated by [RRID](#) on Aug 4, 2026

## [flowMatch](#)

RRID:SCR\_002283

Type: Tool

### Proper Citation

flowMatch (RRID:SCR\_002283)

### Resource Information

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

**Proper Citation:** flowMatch (RRID:SCR\_002283)

**Description:** Software for matching cell populations and building meta-clusters and templates from a collection of flow cytometry (FC) samples.

**Synonyms:** flowMatch - Matching and meta-clustering in flow cytometry

**Resource Type:** software resource

**Defining Citation:** [PMID:22536861](#)

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

**Availability:** Free, Available for download, Freely available

**Resource Name:** flowMatch

**Resource ID:** SCR\_002283

**Alternate IDs:** OMICS\_05602

**License:** Artistic License, v2

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

**Record Last Update:** 20260801T190203+0000

### Ratings and Alerts

No rating or validation information has been found for flowMatch.

No alerts have been found for flowMatch.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Hsiao C, et al. (2016) Mapping cell populations in flow cytometry data for cross-sample comparison using the Friedman-Rafsky test statistic as a distance measure. Cytometry. Part A : the journal of the International Society for Analytical Cytology, 89(1), 71.