

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 18, 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: 20260912T195539+0000

Ratings and Alerts

No rating or validation information has been found for flowMatch.

No alerts have been found for flowMatch.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

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.