

Resource Summary Report

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FlowCal

RRID:SCR_018140

Type: Tool

Proper Citation

FlowCal (RRID:SCR_018140)

Resource Information

URL: <https://github.com/taborlab/FlowCal>

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Description: Open source software tool for automatically converting flow cytometry data from arbitrary to calibrated units. Can be run using intuitive Microsoft Excel interface, or customizable Python scripts. Software accepts Flow Cytometry Standard (FCS) files as inputs and is compatible with different calibration particles, fluorescent probes, and cell types. Automatically gates data, calculates common statistics, and produces plots.

Synonyms: Python Flow Cytometry Calibration Library

Resource Type: data processing software, software application, software resource

Defining Citation: [PMID:27110723](#)

Keywords: Converting flow cytometry data, arbitrary unit, calibrated unit, data gating, statistic, plot, data, bio.tools

Funding: NDSEG Fellowship ;
NIAID R21 AI115014;
NSF Graduate Research Fellowship DGE 0940902;
NSF EFRI 1137266;
NSF MCB 1244135;
Office of Naval Research MURI N000141310074;
Office of Naval Research YIP N000141410487;
Welch Foundation

Availability: Free, Available for download, Freely available

Resource Name: FlowCal

Resource ID: SCR_018140

Alternate IDs: biotools:flowcal

Alternate URLs: <https://bio.tools/flowcal>

Record Creation Time: 20220129T080338+0000

Record Last Update: 20260905T133054+0000

Ratings and Alerts

No rating or validation information has been found for FlowCal.

No alerts have been found for FlowCal.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Nalley MJ, et al. (2025) Near 100% efficient homology-dependent genome engineering in the human fungal pathogen *Cryptococcus neoformans*. *G3* (Bethesda, Md.), 15(8).

Lazar JT, et al. (2025) A stationary phase-specific bacterial green light sensor for enhancing metabolite production. *Nature communications*, 17(1), 1071.

Thalén NB, et al. (2024) Mammalian cell display with automated oligo design and library assembly allows for rapid residue level conformational epitope mapping. *Communications biology*, 7(1), 805.

Armendariz DA, et al. (2023) CHD-associated enhancers shape human cardiomyocyte lineage commitment. *eLife*, 12.

Ho TYH, et al. (2021) A systematic approach to inserting split inteins for Boolean logic gate engineering and basal activity reduction. *Nature communications*, 12(1), 2200.

Moudgil A, et al. (2020) Self-Reporting Transposons Enable Simultaneous Readout of Gene Expression and Transcription Factor Binding in Single Cells. *Cell*, 182(4), 992.