

Resource Summary Report

Generated by [ASWG](#) on Aug 25, 2026

FACS

RRID:SCR_000055

Type: Tool

Proper Citation

FACS (RRID:SCR_000055)

Resource Information

URL: <https://github.com/SciLifeLab/facs>

Proper Citation: FACS (RRID:SCR_000055)

Description: Software for classification of Sequences using Bloom filters that can accurately and rapidly align sequences to a reference sequence.

Abbreviations: FACS

Synonyms: Fast and Accurate Classification of Sequences

Resource Type: software resource

Defining Citation: [PMID:20472541](#)

Keywords: unix/linux, sequence, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: FACS

Resource ID: SCR_000055

Alternate IDs: OMICS_02147, biotools:facs

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

License: MIT License

Record Creation Time: 20220129T080159+0000

Record Last Update: 20260815T182140+0000

Ratings and Alerts

No rating or validation information has been found for FACS.

No alerts have been found for FACS.

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 [ASWG](#) .

Choe M, et al. (2025) Preclinical Evaluation of Folate Receptor-? Chimeric Antigen Receptor T Cells Exhibits Highly Efficient Antitumor Activity against Osteosarcoma. Cancer research communications, 5(9), 1701.

Xiong W, et al. (2025) Zanubrutinib plus Ixazomib and Dexamethasone in Newly Diagnosed Symptomatic Waldenström Macroglobulinemia: A Phase II Study. Clinical cancer research : an official journal of the American Association for Cancer Research, 31(10), 1856.

Nooij S, et al. (2018) Overview of Virus Metagenomic Classification Methods and Their Biological Applications. Frontiers in microbiology, 9, 749.

Jia Y, et al. (2016) Anti-NDV activity of baicalin from a traditional Chinese medicine in vitro. The Journal of veterinary medical science, 78(5), 819.

Kawulok J, et al. (2015) CoMeta: classification of metagenomes using k-mers. PloS one, 10(4), e0121453.

Chu J, et al. (2014) BioBloom tools: fast, accurate and memory-efficient host species sequence screening using bloom filters. Bioinformatics (Oxford, England), 30(23), 3402.