

Resource Summary Report

Generated by [FDI Lab - SciCrunch.org](#) on Apr 21, 2025

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

Funding:

Availability: MIT License

Resource Name: FACS

Resource ID: SCR_000055

Alternate IDs: OMICS_02147, biotools:facs

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

Record Creation Time: 20220129T080159+0000

Record Last Update: 20250420T013926+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 4 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

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.