Resource Summary Report

Generated by RRID on Apr 9, 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: 20250214T182911+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 RRID.

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.