

Resource Summary Report

Generated by [kravitz2](#) on Sep 5, 2026

Centrifuge Classifier

RRID:SCR_016665

Type: Tool

Proper Citation

Centrifuge Classifier (RRID:SCR_016665)

Resource Information

URL: <http://www.ccb.jhu.edu/software/centrifuge/>

Proper Citation: Centrifuge Classifier (RRID:SCR_016665)

Description: Software for rapid and sensitive classification of metagenomic sequences. Used for the classification of DNA sequences from microbial samples and analysis of large metagenomics data sets on conventional desktop computers.

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

Defining Citation: [DOI:10.1101/gr.210641.116](https://doi.org/10.1101/gr.210641.116)

Keywords: classification, large, metagenomic, sequence, DNA, microbial, sample, analysis, data, desktop, computer, bio.tools

Funding: NHGRI R01 HG006677;
NIGMS R01 GM083873;
NSF ABI1356078;
U. S. Army Research Office W911NF1410490

Availability: Free, Available for download, Freely available

Resource Name: Centrifuge Classifier

Resource ID: SCR_016665

Alternate IDs: biotools:centrifuge, OMICS_12217

Alternate URLs: <https://github.com/infphilo/centrifuge>, <https://bio.tools/centrifuge>, <https://sources.debian.org/src/centrifuge/>

License: GNU General Public License v3.0

Record Creation Time: 20220129T080331+0000

Record Last Update: 20260903T235351+0000

Ratings and Alerts

No rating or validation information has been found for Centrifuge Classifier.

No alerts have been found for Centrifuge Classifier.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 10 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Tiwari D, et al. (2026) Molecular mechanisms of naturally encoded signaling bias at the complement anaphylatoxin receptors. *Molecular cell*, 86(13), 2586.

Nasr E, et al. (2025) PathoGFAIR: a collection of FAIR and adaptable (meta)genomics workflows for (foodborne) pathogens detection and tracking. *GigaScience*, 14.

Huang D, et al. (2025) Variations in salivary microbiome and metabolites are associated with immunotherapy efficacy in patients with advanced NSCLC. *mSystems*, 10(3), e0111524.

Leiendecker L, et al. (2023) Human Papillomavirus 42 Drives Digital Papillary Adenocarcinoma and Elicits a Germ Cell-like Program Conserved in HPV-Positive Cancers. *Cancer discovery*, 13(1), 70.

L??tter A, et al. (2022) Haplogenome assembly reveals structural variation in Eucalyptus interspecific hybrids. *GigaScience*, 12.

Pham GM, et al. (2020) Construction of a chromosome-scale long-read reference genome assembly for potato. *GigaScience*, 9(9).

Rousseau-Gueutin M, et al. (2020) Long-read assembly of the Brassica napus reference genome Darmor-bzh. *GigaScience*, 9(12).

Nikolaisen NK, et al. (2020) Employing MIC Data for Mink Pathogens to Propose Tentative Epidemiological Cut-Off Values: A Step Toward Rationalizing Antimicrobial Use in Mink. *Frontiers in veterinary science*, 7, 544594.

Nelson MT, et al. (2019) Human and Extracellular DNA Depletion for Metagenomic Analysis of Complex Clinical Infection Samples Yields Optimized Viable Microbiome Profiles. *Cell reports*, 26(8), 2227.

Watts GS, et al. (2019) Identification and quantitation of clinically relevant microbes in patient samples: Comparison of three k-mer based classifiers for speed, accuracy, and sensitivity. PLoS computational biology, 15(11), e1006863.