

Resource Summary Report

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[chopper](#)

RRID:SCR_026486

Type: Tool

Proper Citation

chopper (RRID:SCR_026486)

Resource Information

URL: <https://github.com/wdecoster/chopper>

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Description: Software tool that combines the utility of NanoFilt and NanoLyse, for filtering sequencing reads based on quality, length, and contaminating sequences, delivers 7-fold speed up compared to the Python implementation, making use of the Rust-Bio library and Rust bindings to minimap2.

Resource Type: source code, software resource

Defining Citation: [PMID:37171891](#)

Keywords: filtering sequencing reads, quality, length, contaminating sequences,

Funding: Flanders Institute for Biotechnology ;
Belgium ;
University of Antwerp

Availability: Free, Available for download, Freely available

Resource Name: chopper

Resource ID: SCR_026486

License: MIT license

Record Creation Time: 20250301T060334+0000

Record Last Update: 20260810T040929+0000

Ratings and Alerts

No rating or validation information has been found for chopper.

No alerts have been found for chopper.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Meyer D, et al. (2026) Unlocking the full potential of nanopore sequencing: tips, tricks, and advanced data analysis techniques. *Nucleic acids research*, 54(3).

Huang Y, et al. (2026) Long-read sequencing and proteomics reveal blood transcriptome and protein expression profiles in multiple primary lung cancers. *BMC cancer*, 26(1).

Liu L, et al. (2026) ACP4 Variants in Hypoplastic Amelogenesis Imperfecta. *Calcified tissue international*, 117(1).

Suarez-Silva R, et al. (2026) Exploring the Algarrobo Decline in the Pómac Forest: Unraveling the Relationship between the Endomicrobiome of *Neltuma pallida* and *Enallodiplosis discordis*. *Microbial ecology*, 89(1).

Panattoni A, et al. (2026) Exploring the functional microbiome of pigs within the porcine respiratory disease complex: viral-bacterial co-infections and virulence factor profiling. *Microbiology spectrum*, 14(3), e0191025.

Fiesinger A, et al. (2026) The genome of the reef-building coral *Porites harrisoni* from the southern Persian/Arabian Gulf. *GigaByte (Hong Kong, China)*, 2026, gigabyte174.

Bergman LA, et al. (2025) Checklist of ichthyoplankton of NORI-D polymetallic nodule exploration claim (eastern Clarion-Clipperton Zone) during winter 2021. *Biodiversity data journal*, 13, e137744.

Tucci M, et al. (2025) Magnetite Nanoparticles Enhancing H₂-Driven Biomethanation in a Mixed Microbial Community. *Global challenges (Hoboken, NJ)*, 9(9), e00367.

Mencius J, et al. (2025) Restoring flowcell type and basecaller configuration from FASTQ files of nanopore sequencing data. *Nature communications*, 16(1), 4102.

Gauthier J, et al. (2025) Leveraging artificial intelligence community analytics and nanopore metagenomic surveillance to monitor early enteropathogen outbreaks. *Frontiers in public health*, 13, 1675080.

Estes BJG, et al. (2025) Development of circular AAV cargos for targeted seamless insertion with large serine integrases. *Molecular therapy. Methods & clinical development*,

33(2), 101490.

Pagano L, et al. (2025) Evaluation of Illumina and Oxford Nanopore Sequencing for the Study of DNA Methylation in Alzheimer's Disease and Frontotemporal Dementia. *International journal of molecular sciences*, 26(9).

Bird E, et al. (2025) BALROG-MON: a high-throughput pipeline for Bacterial Antimicrobial Resistance annotation of Genomes-Metagenomic Oxford Nanopore. *microPublication biology*, 2025.

El-Sayed ER, et al. (2024) Enhancing bioprocessing of red pigment from immobilized culture of gamma rays mutant of the endophytic fungus *Monascus ruber* SRZ112. *Journal of biological engineering*, 18(1), 44.