

Resource Summary Report

Generated by PRECISE-TBI on Sep 8, 2026

Filtlong

RRID:SCR_024020

Type: Tool

Proper Citation

Filtlong (RRID:SCR_024020)

Resource Information

URL: <https://github.com/rrwick/Filtlong>

Proper Citation: Filtlong (RRID:SCR_024020)

Description: Software tool for filtering long reads by quality.Can take set of long reads and produce smaller, better subset. Uses both read length and read identity when choosing which reads pass the filter.

Synonyms: filtlong

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

Keywords: filtering long reads by quality, read length, read identity, filtering reads,

Availability: Free, Available for download, Freely available

Resource Name: Filtlong

Resource ID: SCR_024020

Alternate URLs: <https://sources.debian.org/src/filtlong/>

License: GPL-3.0 license

Record Creation Time: 20230824T050211+0000

Record Last Update: 20260905T133028+0000

Ratings and Alerts

No rating or validation information has been found for Filtlong.

No alerts have been found for Filtlong.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 474 mentions in open access literature.

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

Loo EPI, et al. (2026) Removal of Transgenes and Evaluation of Yield Penalties in Genome Edited Bacterial Blight Resistant Rice Varieties. *Plant biotechnology journal*, 24(2), 939.

Tomita K, et al. (2026) Complete genome sequence of *Fundidesulfovibrio* sp. strain YSD1, an electroactive bacterium isolated from estuarine sediment. *Microbiology resource announcements*, 15(2), e0119325.

Huang X, et al. (2026) Pangenome Analysis Reveals Structural Variations Associated With Citric Acid Accumulation in *Prunus mume*. *Plant biotechnology journal*, 24(4), 2623.

Zhang J, et al. (2026) Cross-kingdom genomic variation in chicken gut microbiomes: insights from China's diverse local breeds. *Microbiome*, 14(1).

Yu Q, et al. (2026) Diversity and evolution of a phase-variable multi-locus antigen in *Neisseria gonorrhoeae*. *bioRxiv : the preprint server for biology*.

Rivas L, et al. (2026) *Yersinia fenwicki* sp. nov., isolated from human clinical cases in Aotearoa | New Zealand and Australia. *International journal of systematic and evolutionary microbiology*, 76(1).

Kawabata Y, et al. (2026) Antimicrobial susceptibility of *Escherichia coli* isolated from wild deer (*Cervus nippon yesoensis*) and fox (*Vulpes vulpes schrencki*) in Hokkaido: a pilot study on sustainable antimicrobial resistance monitoring. *The Journal of veterinary medical science*, 88(4), 642.

van Gorp E, et al. (2026) Ambler class C-type β -lactamases and porin alterations in *Enterobacter cloacae* complex and *Klebsiella aerogenes* in the Netherlands, 2012-2023. *BMC microbiology*, 26(1).

Velásquez AC, et al. (2026) Complete genome sequence of *Bradyrhizobium* sp. WCU1 isolated from lager beer. *Microbiology resource announcements*, 15(4), e0110625.

Bargheet A, et al. (2026) Metabolic reprogramming of the infant gut by bifidobacteria-based probiotics drives exclusion of antibiotic-resistant pathobionts. *Cell reports. Medicine*, 7(5), 102752.

Doi Y, et al. (2026) Draft genome sequence of *Labrys* sp. strain Lb11, an α -glucose-utilizing bacterium isolated from soil. *Microbiology resource announcements*, 15(5), e0009926.

Leonardo IC, et al. (2026) A novel temperate phage from *Alicyclobacillus*: first evidence in this genus of genomic identity to a sigK-integrated prophage. *Microbiology spectrum*, 14(5), e0374725.

Kumar R, et al. (2026) Comparative genomics and molecular insights into smooth and rough clinical isolates of *Mycobacterium abscessus*. *Microbial genomics*, 12(5).

Fakoya AO, et al. (2026) HapAsmbl: A reference-aided pipeline for assembling haplotypes in Nanopore amplicon sequence data of polymorphic populations. *Applications in plant sciences*, 14(3), e70062.

Ivanova M, et al. (2026) Human-associated NDM-5-producing multidrug-resistant *Escherichia coli* detected in retail beef and pork in Hungary, 2021. *Frontiers in bioinformatics*, 6, 1793862.

Søndreli KL, et al. (2026) Transcriptomic and functional analyses uncover a conserved effector driving genotype-dependent virulence in the *Sphaerulina musiva*-*Populus trichocarpa* interaction. *mBio*, 17(5), e0312025.

Wang B, et al. (2026) Global genomic diversity of the selfing nematode *Caenorhabditis tropicalis* correlates with geography. *bioRxiv* : the preprint server for biology.

Harmer CJ, et al. (2026) Mobilization of the AbGRI4 resistance island in *Acinetobacter baumannii*: IS26 action and homologous recombination both contribute. *Microbiology spectrum*, 14(6), e0038926.

Petrushin IS, et al. (2026) Genomic Features of the Micropredator *Lysobacter* sp. Hz25 Isolated from the Rhizosphere of *Hedysarum zundukii*. *International journal of molecular sciences*, 27(9).

Mancini A, et al. (2026) Genomic and functional analysis of stress-responsive prophages in *Lactobacillus helveticus*. *Frontiers in microbiology*, 17, 1819103.