

Resource Summary Report

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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: 20260801T190824+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 309 mentions in open access literature.

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

Le VH, et al. (2025) Metabolites derived from bacterial isolates of the human skin microbiome inhibit *Staphylococcus aureus* biofilm formation. *Microbiology spectrum*, 13(9), e0130625.

Nittami T, et al. (2025) Genome sequences of two *Escherichia coli* bacteriophages isolated from activated sludge in domestic wastewater treatment plants. *Microbiology resource announcements*, 14(9), e0028525.

Ahn J, et al. (2025) Complete genome sequence of *Neobacillus* sp. strain OS1-2, a denitrifying bacterium isolated from apple orchard soil. *Microbiology resource announcements*, 14(2), e0111424.

Ledoux JB, et al. (2025) Chromosome-Level Genome Assembly and Annotation of *Corallium rubrum*: A Mediterranean Coral Threatened by Overharvesting and Climate Change. *Genome biology and evolution*, 17(2).

Ziegler FMR, et al. (2025) A full genome assembly reveals drought stress effects on gene expression and metabolite profiles in blackcurrant (*Ribes nigrum* L.). *Horticulture research*, 12(2), uhae313.

Zhang K, et al. (2025) A telomere-to-telomere genome assembly of the protandrous hermaphrodite blackhead seabream, *Acanthopagrus schlegelii*. *Scientific data*, 12(1), 350.

Allemann MN, et al. (2025) Laboratory evolution in *Novosphingobium aromaticivorans* enables rapid catabolism of a model lignin-derived aromatic dimer. *Applied and environmental microbiology*, 91(2), e0208124.

Chow LKY, et al. (2025) Complete genome sequences of two strains of *Pseudomonas fragi*, isolated from feces of a domestic rabbit (*Oryctolagus cuniculus*). *Microbiology resource announcements*, 14(11), e0098425.

Gasser MT, et al. (2025) Complete genome sequences of two shipworm endosymbiont strains, *Teredinibacter turnerae* SR01903 and SR02026. *Microbiology resource announcements*, 14(6), e0026525.

Xu L, et al. (2025) Mobilome-mediated transcriptional activation of biosynthetic gene clusters and its impact on strain competitiveness in food fermentation microbiomes. *Microbiome*, 13(1), 191.

Pradel N, et al. (2025) Complete genome sequence of *Nitratireductor aquimarinus* strain MNA2.1 isolated from sediments of the Berre lagoon, France. *Microbiology resource*

announcements, 14(10), e0025925.

Turroni F, et al. (2025) Quorum Sensing via Autoinducer-2 Promotes Colonisation and Host Adaptation in *B. bifidum* PRL2010. *Microbial biotechnology*, 18(9), e70231.

Stefan M, et al. (2025) Recurrence following invasive GAS infections in adults: Triumph of virulence or failure of immunity? *Virulence*, 16(1), 2563765.

Gotze CR, et al. (2025) Genomic prediction of symbiotic interactions between two *Endozoicomonas* clades and their coral host, *Acropora loripes*. *Animal microbiome*, 7(1), 94.

Nuncio-Garc??a LA, et al. (2025) Complete genome sequence of *Serratia marcescens* strain CH31 isolated from a *Periplaneta americana* associated with a tertiary hospital setting. *Microbiology resource announcements*, 14(10), e0061125.

Zhang K, et al. (2025) A telomere-to-telomere gap-free genome assembly of the endangered humphead wrasse (*Cheilinus undulatus*). *Scientific data*, 12(1), 1194.

Perault AI, et al. (2025) *Enterobacter hormaechei* replaces virulence with carbapenem resistance via porin loss. *Proceedings of the National Academy of Sciences of the United States of America*, 122(8), e2414315122.

Hurtado A, et al. (2025) A One Health approach for the genomic characterization of antibiotic-resistant *Campylobacter* isolates using Nanopore whole-genome sequencing. *Frontiers in microbiology*, 16, 1540210.

Jiang D, et al. (2025) The telomere-to-telomere genome of flowering cherry (*Prunus campanulata*) reveals genomic evolution of the subgenus *Cerasus*. *GigaScience*, 14.

Pardons M, et al. (2025) Blood and tissue HIV-1 reservoirs display plasticity and lack of compartmentalization in virally suppressed people. *Nature communications*, 16(1), 2173.