

# Resource Summary Report

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## Filtlong

RRID:SCR\_024020

Type: Tool

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### Proper Citation

Filtlong (RRID:SCR\_024020)

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### 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:** 20260731T043153+0000

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### 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 [NIF](#) .

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.

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.

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.

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.

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).

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.

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

Pich?? LC, et al. (2025) Evolutionary responses of Escherichia coli to phage pressure: insights into mucoidy and colanic acid overexpression. BMC genomics, 26(1), 448.

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.

Koong J, et al. (2025) Genomic characteristics of the multiresistant Acinetobacter baumannii global clone 1 reference strain A297/RUH875. The Journal of antimicrobial chemotherapy, 80(7), 1988.

Rojas SM, et al. (2025) Complete and draft genome sequences of clinical *Mycobacterium tuberculosis* isolates from the Philippines. *Microbiology resource announcements*, 14(7), e0030525.

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

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.

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.

Cordeiro NF, et al. (2025) First Report in the Americas of *S. enterica* Var. Enteritidis Carrying bla<sub>NDM-1</sub> in a Putatively New Sub-Lineage of IncC2 Plasmids. *Antibiotics (Basel, Switzerland)*, 14(6).

Sia CM, et al. (2025) Distinct adaptation and epidemiological success of different genotypes within *Salmonella enterica* serovar Dublin. *eLife*, 13.

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.

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.