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: software application, software resource, data processing software

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

Funding:

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: 20250412T060618+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 175 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Shutinoski B, et al. (2025) Complete genomes of Salmonella and draft genome of Escherichia isolates from oysters collected in Canada. Microbiology resource announcements, 14(1), e0058524.

Guro P, et al. (2025) Whole-genome sequence of non-rhizobial strain Tardiphaga sp. 709 isolated from the root nodule of Astragalus inopinatus Borris., growing on the Kamchatka Peninsula. Microbiology resource announcements, 14(1), e0092324.

Yoshizu D, et al. (2025) Genome sequences of three electrochemically active bacteria isolated from an anaerobic digester. Microbiology resource announcements, 14(1), e0113224.

Shin GY, et al. (2025) Complete genome sequences of Pantoea vagans strains GM1 and GM2, isolated from the leaves of garlic mustard. Microbiology resource announcements, 14(1), e0094324.

Toubiana W, et al. (2025) Functional monocentricity with holocentric characteristics and chromosome-specific centromeres in a stick insect. Science advances, 11(1), eads6459.

Zarra F, et al. (2025) Novel insights into insect mediated polystyrene biodegradation through bacterial genome analyses. Scientific reports, 15(1), 1047.

Olagoke O, et al. (2025) Whole-genome automated assembly pipeline for Chlamydia trachomatis strains from reference, in vitro and clinical samples using the integrated CtGAP pipeline. NAR genomics and bioinformatics, 7(1), lqae187.

Ofosu Appiah F, et al. (2025) Emergence of Carbapenem-Resistant blaPOM-1 Harboring Pseudomonas otitidis Isolated from River Water in Ghana. Antibiotics (Basel, Switzerland), 14(1).

Bryant JL, et al. (2025) Phenotypic and Complete Reference Whole Genome Sequence

Analyses of Two Paenibacillus spp. Isolates from a Gray Wolf (Canis lupus) Gastrointestinal Tract. Veterinary sciences, 12(1).

Zhao Q, et al. (2025) Near telomere-to-telomere genome assemblies of Silkie Gallus gallus and Mallard Anas platyrhynchos restored the structure of chromosomes and "missing" genes in birds. Journal of animal science and biotechnology, 16(1), 9.

Rodwell EV, et al. (2025) Hybrid strains of enterotoxigenic/Shiga toxin-producing Escherichia coli, United Kingdom, 2014-2023. Journal of medical microbiology, 74(1).

Liu S, et al. (2025) Complete genome sequence of Franconibacter pulveris SL.qac10, a putative QAC-resistant isolate from an indoor built environment. Microbiology resource announcements, 14(1), e0109624.

Bejaoui S, et al. (2025) Comparison of Illumina and Oxford Nanopore sequencing data quality for Clostridioides difficile genome analysis and their application for epidemiological surveillance. BMC genomics, 26(1), 92.

Nong Y, et al. (2024) Emergence and clonal expansion of a qacA-harbouring sequence type 45 lineage of methicillin-resistant Staphylococcus aureus. Communications biology, 7(1), 349.

Delandre O, et al. (2024) Long-Read Sequencing and De Novo Genome Assembly Pipeline of Two Plasmodium falciparum Clones (Pf3D7, PfW2) Using Only the PromethION Sequencer from Oxford Nanopore Technologies without Whole-Genome Amplification. Biology, 13(2).

McCabe CV, et al. (2024) Long-read sequencing for fast and robust identification of correct genome-edited alleles: PCR-based and Cas9 capture methods. PLoS genetics, 20(3), e1011187.

Nozick SH, et al. (2024) Phenotypes of a Pseudomonas aeruginosa hypermutator lineage that emerged during prolonged mechanical ventilation in a patient without cystic fibrosis. mSystems, 9(1), e0048423.

Scott A, et al. (2024) Complete genome sequence of Bradyrhizobium ottawaense strain MIAE 01942 isolated from soybean nodules grown in antibiotic-amended soil. Microbiology resource announcements, 13(4), e0000424.

Lam M, et al. (2024) Complete genome sequence of Klebsiella variicola subsp. variicola ML.9ba2, an endophytic strain isolated from aerial roots of Philodendron erubescens. Microbiology resource announcements, 13(4), e0116323.

Fuga B, et al. (2024) Hybrid genome assembly of colistin-resistant mcr-1.5-producing Escherichia coli ST354 reveals phylogenomic pattern associated with urinary tract infections in Brazil. Journal of global antimicrobial resistance, 37, 37.