

Resource Summary Report

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NanoFilt

RRID:SCR_016966

Type: Tool

Proper Citation

NanoFilt (RRID:SCR_016966)

Resource Information

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

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Description: Software tool written in Python to perform its filtering based on mean read quality and GC content and read length. Used for filtering and trimming of long read sequencing data.

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

Keywords: filtering, trimming, long, sequencing, data, read

Availability: Free, Available for download, Freely available

Resource Name: NanoFilt

Resource ID: SCR_016966

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

License: GNU General Public License v3.0

Record Creation Time: 20220129T080332+0000

Record Last Update: 20260821T194100+0000

Ratings and Alerts

No rating or validation information has been found for NanoFilt.

No alerts have been found for NanoFilt.

Data and Source Information

Usage and Citation Metrics

We found 331 mentions in open access literature.

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

Kataoka K, et al. (2026) Chromosome-scale genome assembly and annotation of the two-spotted cricket *Gryllus bimaculatus* (Orthoptera: Gryllidae). *G3* (Bethesda, Md.), 16(4).

Pigeault R, et al. (2026) Within-Host Environmental Heterogeneity Is Associated With Phenotypic but Not Genomic Diversity in *Wolbachia* Endosymbionts. *Environmental microbiology reports*, 18(1), e70286.

Ding J, et al. (2026) Highly Resolved Community Sewage Metagenomics Unveiling Landscape and Transmission Patterns of Antibiotic Resistome in Hong Kong Populations. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(20), e08389.

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).

Pamornchainavakul N, et al. (2026) QoALa: A comprehensive workflow for viral quasispecies diversity comparison using long-read sequencing data. *PLoS computational biology*, 22(4), e1014208.

Roy FA, et al. (2026) Hybrid genome assembly of the cannabis powdery mildew agent *Golovinomyces ambrosiae* uncovers important resources for deciphering virulence factors. *BMC genomics*, 27(1).

Mbaya-Tshibangu F, et al. (2026) Low-Abundance and Fragmentary *Helicobacter pylori* DNA Detected in Phenotypically Negative Gastric Biopsies Using Targeted Sequencing. *Biomolecules*, 16(6).

Taniguchi I, et al. (2026) Global population structure of Shiga toxin-producing *Escherichia coli* O103:H2 and the variation in their major virulence factor-encoding genetic elements. *Microbial genomics*, 12(1).

Joel GS, et al. (2026) Genome sequencing reveals variation of African swine fever virus in Nigerian outbreaks and identification of two major West African viral lineages. *Microbial genomics*, 12(2).

K-Jánosi K, et al. (2026) Characterisation of *Salmonella* Typhimurium from a fatal equine nosocomial outbreak and retrospective analysis of equine clinic salmonellosis cases (2010-2025). *Scientific reports*, 16(1).

de Souza Araujo N, et al. (2026) Retroelement expansions underlie genome evolution in stingless bees. *BMC genomics*, 27(1), 160.

Xu Z, et al. (2026) The nucleoid-associated protein subunit HupA positively regulates the Pqs system and pyocyanin production in *Pseudomonas aeruginosa*. *Applied and environmental microbiology*, 92(4), e0242525.

Nagy NA, et al. (2026) Draft genomes of two *Lethrus* species. *Scientific data*, 13(1).

Vatansever C, et al. (2026) Emergence of carbapenem-resistant putative hypervirulent *Klebsiella pneumoniae* ST147 with a distinct hybrid plasmid in Türkiye. *Emerging microbes & infections*, 15(1), 2653280.

Won S, et al. (2026) *Mycobacterium tuberculosis* infection disrupts gut and respiratory microbial communities and networks with incomplete restoration after two months of treatment. *Gut pathogens*, 18(1).

Domingues Carvalho R, et al. (2026) Virulence gains in the *Puccinia striiformis* f. sp. *tritici* PstS10 lineage correlate with expression polymorphism in a candidate Avr effector. *Communications biology*, 9(1).

Beckett T, et al. (2026) Transcriptome Profiling of Leaves and Roots from Rooibos (*Aspalathus linearis*) Using Oxford Nanopore Sequencing. *Plants (Basel, Switzerland)*, 15(11).

Liu P, et al. (2026) Telomere-to-telomere genome of *Stylosanthes guianensis* uncovers symbiotic adaptation to phosphorus-deficient soils. *Genome biology*, 27(1).

Sauerborn E, et al. (2026) Resolving plasmid-encoded carbapenem resistance dynamics and reservoirs in a hospital setting through nanopore sequencing. *Microbial genomics*, 12(2).

Zhou S, et al. (2026) hnRNPM cooperates with BCAS2 to modulate alternative splicing during oocyte development. *Nature communications*, 17(1).