

Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

NanoFilt

RRID:SCR_016966

Type: Tool

Proper Citation

NanoFilt (RRID:SCR_016966)

Resource Information

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

Proper Citation: NanoFilt (RRID:SCR_016966)

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: software application, software resource, data processing software

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: 20260727T040651+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 268 mentions in open access literature.

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

Liang H, et al. (2025) Efficiently constructing complete genomes with CycloneSEQ to fill gaps in bacterial draft assemblies. GigaByte (Hong Kong, China), 2025, gigabyte154.

Álvarez-Narváez S, et al. (2025) Choosing the most suitable NGS technology to combine with a standardized viral enrichment protocol for obtaining complete avian orthoreovirus genomes from metagenomic samples. Frontiers in bioinformatics, 5, 1498921.

Rubalskii E, et al. (2025) Characterization and genome analysis of the novel virulent Burkholderia phage Bm1, which is active against pan-drug-resistant Burkholderia multivorans. Archives of virology, 170(5), 106.

Wang Y, et al. (2025) Telomere-to-telomere genome of common bean (*Phaseolus vulgaris* L., YP4). GigaScience, 14.

Ito Y, et al. (2025) Chromosome-scale whole genome assembly and annotation of the Jamaican field cricket *Gryllus assimilis*. Scientific data, 12(1), 826.

Cen JQ, et al. (2025) Co-infection with *Proteus mirabilis* and extraintestinal pathogenic *Escherichia coli* aggravated liver injury in chickens by disrupting the jejunal barrier. Poultry science, 104(8), 105369.

Chen X, et al. (2025) Chromosome-level genome assembly of the vegetable leafminer *Liriomyza sativae* (Diptera: Agromyzidae). Scientific data, 12(1), 1393.

Gopaulchan D, et al. (2025) A defined microbial community reproduces attributes of fine flavour chocolate fermentation. Nature microbiology, 10(9), 2130.

Harada S, et al. (2025) Genomic epidemiology and antimicrobial resistance of *Corynebacterium macclintockiae*, the predominant species of human pathogens within the *Corynebacterium jeikeium* complex. Journal of clinical microbiology, 63(8), e0050025.

Nappo A, et al. (2025) Biotechnological Potential of a Novel Strain of *Fusarium proliferatum*, a Terrestrial Fungus Adapted to Marine Environment. Environmental microbiology reports, 17(4), e70143.

Pongchaikul P, et al. (2025) Genomic analysis of contaminant *Stenotrophomonas maltophilia*, from placental swab culture, carrying antibiotic resistance: a potential hospital laboratory contaminant. Scientific reports, 15(1), 22323.

Zhang M, et al. (2025) Telomere-to-telomere genome assembly uncovers Wolbachia-driven recurrent male bottleneck effect and selection in a sawfly. Communications biology, 8(1), 1211.

Downing J, et al. (2025) Allele Level Sequencing of Killer Cell Immunoglobulin-Like Receptor Genes Using Oxford Nanopore Long Read Sequencing. *HLA*, 106(3), e70400.

Ye F, et al. (2025) Characteristics and filtering of low-frequency artificial short deletion variations based on nanopore sequencing. *GigaScience*, 14.

Wang Z, et al. (2025) Microbial diversity and community assembly in heavy metal-contaminated soils: insights from selenium-impacted mining areas. *Frontiers in microbiology*, 16, 1561678.

He T, et al. (2025) The endophytic fungus *Cosmosporella* sp. VM-42 from *Vinca minor* is a source of bioactive compounds with potent activity against drug-resistant bacteria. *Current research in microbial sciences*, 8, 100390.

Llarena AK, et al. (2025) DNA extraction protocols for animal fecal material on blood spot cards. *PloS one*, 20(5), e0313808.

Nolan JM, et al. (2025) Evaluation of Oxford Nanopore Technologies MinION Sequencer as a Novel Short Amplicon Metabarcoding Tool Using Arthropod Mock Sample and Irish Bat Diet Characterisation. *Ecology and evolution*, 15(5), e71333.

Apostolopoulou G, et al. (2025) The Impact of Tank Disinfectants on the Development of Microbiota in Gilthead Seabream (*Sparus aurata*) Larviculture Systems. *Microorganisms*, 13(6).

Nakanishi E, et al. (2025) Microbiome Associated with *Polypedilum* sp. (Diptera; Chironomidae), a Midge Adapted to an Extremely Acidic Environment. *Microbes and environments*, 40(2).