

Resource Summary Report

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Porechop

RRID:SCR_016967

Type: Tool

Proper Citation

Porechop (RRID:SCR_016967)

Resource Information

URL: <https://github.com/rrwick/Porechop>

Proper Citation: Porechop (RRID:SCR_016967)

Description: Software tool for finding and removing adapters from Oxford Nanopore reads.

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

Keywords: finding, removing, adapter, Oxford Nanopore, read, sequencing, data

Availability: Free, Available for download, Freely available

Resource Name: Porechop

Resource ID: SCR_016967

Alternate IDs: OMICS_17306

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

License: GNU GPL v3

Record Creation Time: 20220129T080333+0000

Record Last Update: 20260803T040724+0000

Ratings and Alerts

No rating or validation information has been found for Porechop.

No alerts have been found for Porechop.

Data and Source Information

Usage and Citation Metrics

We found 1100 mentions in open access literature.

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

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

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

Mehta I, et al. (2025) Control of pili synthesis and putrescine homeostasis in *Escherichia coli*. *eLife*, 13.

Park G, et al. (2025) NanoMnT: an STR analysis tool for Oxford Nanopore sequencing data driven by a comprehensive analysis of error profile in STR regions. *GigaScience*, 14.

Liu H, et al. (2025) A telomere-to-telomere gapless genome reveals *SIPRR1* control of circadian rhythm and photoperiodic flowering in tomato. *GigaScience*, 14.

Tizabi D, et al. (2025) Nanopore Sequencing of *Amoebophrya* Species Reveals Novel Collection of Bacteria Putatively Associated With *Karlodinium veneficum*. *Genome biology and evolution*, 17(3).

Park K, et al. (2025) Epidemiological surveillance and phylogenetic diversity of Orthohantavirus hantanense using high-fidelity nanopore sequencing, Republic of Korea. *PLoS neglected tropical diseases*, 19(2), e0012859.

Saati-Santamar??a Z, et al. (2025) Genetic and species rearrangements in microbial consortia impact biodegradation potential. *The ISME journal*, 19(1).

Koper P, et al. (2025) Comparative analysis of *Legionella lytica* genome identifies specific metabolic traits and virulence factors. *Scientific reports*, 15(1), 5554.

Navasca A, et al. (2025) Dispensable genome and segmental duplications drive the genome plasticity in *Fusarium solani*. *Frontiers in fungal biology*, 6, 1432339.

Mohamed AYA, et al. (2025) Genome-Resolved Metatranscriptomics Provide Insights on Immigration Influence in Structuring Microbial Community Assembly of a Full-Scale Aerobic Granular Sludge Plant. *Environmental science & technology*, 59(12), 6126.

Cousson A, et al. (2025) NanoASV: a snakemake workflow for reproducible field-based Nanopore full-length 16S metabarcoding amplicon data analysis. *Bioinformatics (Oxford, England)*, 41(3).

Ngomtcho SCH, et al. (2025) Continued T12 transmission and shared antibiotic resistance during 2018-2023 *Vibrio cholerae* outbreaks in Cameroon. *PLOS global public health*, 5(2), e0003763.

Kupke J, et al. (2025) Heteroresistance in *Enterobacter cloacae* complex caused by variation in transient gene amplification events. *npj antimicrobials and resistance*, 3(1), 13.

Howells G, et al. (2025) Co-Existence Slows Diversification in Experimental Populations of *E. coli* and *P. fluorescens*. *Environmental microbiology*, 27(2), e70061.

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.

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).

Yen EC, et al. (2025) Chromosome-level genome assembly and methylome profile yield insights for the conservation of endangered loggerhead sea turtles. *GigaScience*, 14.

Heo H, et al. (2025) Hydrogen-dependent dissimilatory nitrate reduction to ammonium enables growth of *Campylobacterota* isolates. *The ISME journal*, 19(1).