

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, software application, data processing software

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: 20260801T190847+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 [RRID](#) .

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

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

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

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.

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

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

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.

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.

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).

Khongkool K, et al. (2025) Characterization and Evaluation of *Lactobacillus plantarum* LC5.2 Isolated from Thai Native Pigs for its Probiotic Potential in Gut Microbiota Modulation and Immune Enhancement. *Journal of microbiology and biotechnology*, 35, e2503028.

Nousias O, et al. (2025) Shotgun sequencing of airborne eDNA achieves rapid assessment of whole biomes, population genetics and genomic variation. *Nature ecology & evolution*, 9(6), 1043.

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).

Böer T, et al. (2025) Isolation and characterization of *Sporomusa carbonis* sp. nov.: a carboxydophilic hydrogenogen in the genus of *Sporomusa* isolated from a charcoal-burning pile. *International journal of systematic and evolutionary microbiology*, 75(4).

Schwarz EM, et al. (2025) Genomes of the entomopathogenic nematode *Steinernema hermaphroditum* and its associated bacteria. *Genetics*, 231(3).

Lai GKK, et al. (2025) Complete genome sequence of *Methylobacterium radiotolerans* NYY1 isolated from Hong Kong soil. *Microbiology resource announcements*, 14(10), e0041225.

Lu Y, et al. (2025) Comparative genomics of *Nocardia tsunamensis* IFM 10818, a new source of the antibacterial macrolide nargenicin A1. *Microbiology spectrum*, 13(12), e0122025.

Luo S, et al. (2025) Long-read RNA sequencing dataset of human pancreatic cancer cell lines. *Scientific data*, 12(1), 1653.