

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: data processing software, software application, software resource

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: 20260905T133052+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 1350 mentions in open access literature.

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

Williams SE, et al. (2026) OSMAC guided bioprospecting of Atlantic sponges reveals novel bacterial species and evidence for the antimicrobial thiazole alkaloid agrochelin II. *Applied and environmental microbiology*, 92(3), e0187725.

Campos-Madueno EI, et al. (2026) Gut microbiota and resistome profiles of Swiss expatriates in Africa revealed by Nanopore metagenomics. *Scientific reports*, 16(1), 7016.

Ayala-Montaño S, et al. (2026) Mitigation and detection of putative microbial contaminant reads from long-read metagenomic datasets. *Microbial genomics*, 12(1).

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).

Ilieva L, et al. (2026) Potential of Fermented Food-Derived *Lactiplantibacillus* Cell-Free Supernatants to Control *Staphylococcus aureus* Growth and Biofilm Development. *International journal of molecular sciences*, 27(2).

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).

Salokas J, et al. (2026) Evaluation of commercial kits and purification approaches for DNA extraction from atmospheric samples for 3rd generation sequencing without amplification. *Scientific reports*, 16(1).

Chang L, et al. (2026) RP9 revisited; RP9 p.(H137L) remains a likely cause of dominant splicing factor-Retinitis Pigmentosa. *European journal of human genetics : EJHG*, 34(2), 227.

Aldeia C, et al. (2026) A commercial bacteriophage cocktail failed to decolonize *Zophobas morio* larvae and promoted overgrowth of an OXA-48-producing *Salmonella enterica*. *European journal of clinical microbiology & infectious diseases : official publication of the European Society of Clinical Microbiology*, 45(2), 363.

Arumugam K, et al. (2026) Draft genome of a member of ascomycotal fungal genus *Pseudopithomyces* (family *Didymosphaeriaceae*). *Microbiology resource announcements*, 15(1), e0017323.

Nakamura A, et al. (2026) A Novel *Paludibacterium* Species Isolated from Human Blood. *Microorganisms*, 14(2).

Brierley S, et al. (2026) Description of *Bartonella bennetti* sp. nov., a novel rodent-associated species, with comparative genomics of the *Bartonella* genus. *International journal of systematic and evolutionary microbiology*, 76(3).

Duduk B, et al. (2026) Microbial diversity of plant pathogens and insect endosymbionts in *Reptalus artemisiae*. *BMC microbiology*, 26(1).

Ofosu Appiah F, et al. (2026) Genomic landscape of blaNDM-1- and blaOXA-181-carrying *Citrobacter portucalensis* sequence type 151 strains from hospital wastewater in Ghana. *Applied and environmental microbiology*, 92(4), e0210825.

Oduor B, et al. (2026) Phenotypic and genomic profiling of multidrug-resistant *Escherichia coli* and *Klebsiella pneumoniae* isolated from Intensive Care Unit patients in Kenya. *BMC microbiology*, 26(1).

Cartairade L, et al. (2026) Optimizing a Novel eDNA-Based Framework for Reef Fish Biodiversity Monitoring Using an Autonomous Filtration System and in situ Nanopore Sequencing. *Ecology and evolution*, 16(3), e73254.

Flatau R, et al. (2026) Metabolic potential structures gill symbiont communities in two common shipworm species. *The ISME journal*, 20(1).

Wiradiputra MRD, et al. (2026) Genomic signatures of dominant clones and evolutionary divergence of *Acinetobacter baumannii* in Thailand. *Microbial genomics*, 12(5).

Ramalingam C, et al. (2026) Effect of sialidase inhibitors on a plaque community biofilm model. *Access microbiology*, 8(6).

Jo J, et al. (2026) Genomic and Phenotypic Evaluation of the Gliadin-Degrading Probiotic *Bacillus amyloliquefaciens* EG025 from Cheonggukjang for Celiac Disease Treatment. *Probiotics and antimicrobial proteins*, 18(3), 4012.