Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 11, 2025

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

Funding:

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: 20250411T055925+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

Source: SciCrunch Registry

Usage and Citation Metrics

We found 906 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Hauff L, et al. (2025) De Novo Genome Assembly for an Endangered Lemur Using Portable Nanopore Sequencing in Rural Madagascar. Ecology and evolution, 15(1), e70734.

Sokolova DD, et al. (2025) The Construction of Heterothallic Strains of Komagataella kurtzmanii Using the I-SceI Meganuclease. Biomolecules, 15(1).

Iliev I, et al. (2025) Characterization and Probiotic Potential of Levilactobacillus brevis DPL5: A Novel Strain Isolated from Human Breast Milk with Antimicrobial Properties Against Biofilm-Forming Staphylococcus aureus. Microorganisms, 13(1).

Krawczyk K, et al. (2025) Chromosome-scale telomere to telomere genome assembly of common crystalwort (Riccia sorocarpa Bisch.). Scientific data, 12(1), 77.

Huang D, et al. (2025) Adaptive modification of antiviral defense systems in microbial community under Cr-induced stress. Microbiome, 13(1), 34.

Mears HV, et al. (2025) Emergence of SARS-CoV-2 subgenomic RNAs that enhance viral fitness and immune evasion. PLoS biology, 23(1), e3002982.

Rodwell EV, et al. (2025) Hybrid strains of enterotoxigenic/Shiga toxin-producing Escherichia coli, United Kingdom, 2014-2023. Journal of medical microbiology, 74(1).

Ofosu Appiah F, et al. (2025) Emergence of Carbapenem-Resistant blaPOM-1 Harboring Pseudomonas otitidis Isolated from River Water in Ghana. Antibiotics (Basel, Switzerland), 14(1).

Baeza JA, et al. (2025) Assembly of Mitochondrial Genomes Using Nanopore Long-Read Technology in Three Sea Chubs (Teleostei: Kyphosidae). Molecular ecology resources, 25(1), e14034.

Zhao Q, et al. (2025) Near telomere-to-telomere genome assemblies of Silkie Gallus gallus and Mallard Anas platyrhynchos restored the structure of chromosomes and "missing" genes in birds. Journal of animal science and biotechnology, 16(1), 9.

Willemsen A, et al. (2025) Novel High-Quality Amoeba Genomes Reveal Widespread Codon Usage Mismatch Between Giant Viruses and Their Hosts. Genome biology and evolution, 17(1).

Gatins R, et al. (2024) Whole genome assembly and annotation of the King Angelfish (Holacanthus passer) gives insight into the evolution of marine fishes of the Tropical Eastern Pacific. GigaByte (Hong Kong, China), 2024, gigabyte115.

Ghoshal M, et al. (2024) Transcriptomic analysis using RNA sequencing and phenotypic analysis of Salmonella enterica after acid exposure for different time durations using adaptive laboratory evolution. Frontiers in microbiology, 15, 1348063.

Albuja-Quintana M, et al. (2024) Genome report: First reference genome of Vaccinium floribundum Kunth, an emblematic Andean species. G3 (Bethesda, Md.), 14(8).

Oberle A, et al. (2024) Evaluation of Nanopore Sequencing on Polar Bodies for Routine Pre-Implantation Genetic Testing for Aneuploidy. Clinical chemistry.

Kijner S, et al. (2024) CRISPR-Cas-based identification of a sialylated human milk oligosaccharides utilization cluster in the infant gut commensal Bacteroides dorei. Nature communications, 15(1), 105.

Benvenga V, et al. (2024) Historic methicillin-resistant Staphylococcus aureus: expanding current knowledge using molecular epidemiological characterization of a Swiss legacy collection. Genome medicine, 16(1), 23.

Sawaswong V, et al. (2024) Full-length 16S rDNA sequencing based on Oxford Nanopore Technologies revealed the association between gut-pharyngeal microbiota and tuberculosis in cynomolgus macaques. Scientific reports, 14(1), 3404.

Jonca J, et al. (2024) Comprehensive phenomic and genomic studies of the species, Pectobacterium cacticida and proposal for reclassification as Alcorniella cacticida comb. nov. Frontiers in plant science, 15, 1323790.

Wu W, et al. (2024) circAtlas 3.0: a gateway to 3 million curated vertebrate circular RNAs based on a standardized nomenclature scheme. Nucleic acids research, 52(D1), D52.