

Resource Summary Report

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Poretools

RRID:SCR_015879

Type: Tool

Proper Citation

Poretools (RRID:SCR_015879)

Resource Information

URL: <https://www.github.com/arg5x/poretools>

Proper Citation: Poretools (RRID:SCR_015879)

Description: Software toolkit for analyzing nanopore sequence data.

Resource Type: sequence analysis software, software resource, data analysis software, software toolkit, data processing software, software application

Defining Citation: [PMID:25143291](#)

Keywords: nanopore, sequence, python, oxford nanopore, MinION, quality control, downstream analysis, bio.tools

Funding: Medical Research Council ;
NHGRI R01 HG006693

Availability: Open source, Free, Available for download

Resource Name: Poretools

Resource ID: SCR_015879

Alternate IDs: biotools:poretools

Alternate URLs: <https://bio.tools/poretools>

License: MIT License

Record Creation Time: 20220129T080327+0000

Record Last Update: 20260807T042845+0000

Ratings and Alerts

No rating or validation information has been found for Poretools.

No alerts have been found for Poretools.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 83 mentions in open access literature.

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

van Gorp E, et al. (2026) Ambler class C-type β -lactamases and porin alterations in *Enterobacter cloacae* complex and *Klebsiella aerogenes* in the Netherlands, 2012-2023. *BMC microbiology*, 26(1).

Vishwanatha A, et al. (2025) *Plasmodium falciparum* DNA repair dynamics reveal unique roles for TLS polymerases and PfRad51 in genome diversification. *Nucleic acids research*, 53(21).

Priyadarshini A, et al. (2025) Whole genome sequencing of a hypermucoviscous, multidrug-resistant *Klebsiella pneumoniae* subsp. *pneumoniae* K219 isolated from human sputum. *Scientific reports*, 16(1), 1237.

Kim JH, et al. (2025) Higher Microbial Abundance and Diversity in Bronchus-Associated Lymphoid Tissue Lymphomas Than in Non-cancerous Lung Tissues. *Cancer research and treatment*, 57(2), 580.

Talsma DT, et al. (2024) Nosocomial transmission of tet(x3), bla NDM-1 and bla OXA-97-carrying *Acinetobacter baumannii* conferring resistance to eravacycline and omadacycline, the Netherlands, March to August 2021. *Euro surveillance : bulletin Europeen sur les maladies transmissibles = European communicable disease bulletin*, 29(28).

Maestri S, et al. (2024) Benchmarking of computational methods for m6A profiling with Nanopore direct RNA sequencing. *Briefings in bioinformatics*, 25(2).

Tian R, et al. (2023) HPV integration generates a cellular super-enhancer which functions as ecDNA to regulate genome-wide transcription. *Nucleic acids research*, 51(9), 4237.

McHugh MP, et al. (2022) Presence of optrA-mediated linezolid resistance in multiple lineages and plasmids of *Enterococcus faecalis* revealed by long read sequencing. *Microbiology (Reading, England)*, 168(2).

Zheng R, et al. (2021) *Pseudodesulfovibrio cashew* sp. Nov., a Novel Deep-Sea Sulfate-Reducing Bacterium, Linking Heavy Metal Resistance and Sulfur Cycle. *Microorganisms*, 9(2).

Pirzadian J, et al. (2021) National surveillance pilot study unveils a multicenter, clonal outbreak of VIM-2-producing *Pseudomonas aeruginosa* ST111 in the Netherlands between 2015 and 2017. *Scientific reports*, 11(1), 21015.

Hendrickx APA, et al. (2021) blaOXA-48-like genome architecture among carbapenemase-producing *Escherichia coli* and *Klebsiella pneumoniae* in the Netherlands. *Microbial genomics*, 7(5).

Lisotto P, et al. (2021) Molecular Characterisation of Vancomycin-Resistant *Enterococcus faecium* Isolates Belonging to the Lineage ST117/CT24 Causing Hospital Outbreaks. *Frontiers in microbiology*, 12, 728356.

Chen C, et al. (2021) *Prevotella copri* increases fat accumulation in pigs fed with formula diets. *Microbiome*, 9(1), 175.

Janssen AB, et al. (2020) Nonclonal Emergence of Colistin Resistance Associated with Mutations in the BasRS Two-Component System in *Escherichia coli* Bloodstream Isolates. *mSphere*, 5(2).

Sia CM, et al. (2020) The characterization of mobile colistin resistance (mcr) genes among 33?000 *Salmonella enterica* genomes from routine public health surveillance in England. *Microbial genomics*, 6(2).

Valsalan R, et al. (2020) Draft genome of *Meyerozyma guilliermondii* strain vka1: a yeast strain with composting potential. *Journal, genetic engineering & biotechnology*, 18(1), 54.

Molina-Mora JA, et al. (2020) High quality 3C de novo assembly and annotation of a multidrug resistant ST-111 *Pseudomonas aeruginosa* genome: Benchmark of hybrid and non-hybrid assemblers. *Scientific reports*, 10(1), 1392.

Monika S, et al. (2020) Smokeless Tobacco Products (STPs) Harbour Bacterial Populations with Potential for Oral Carcinogenicity. *Asian Pacific journal of cancer prevention : APJCP*, 21(3), 815.

Hendrickx APA, et al. (2020) Plasmid diversity among genetically related *Klebsiella pneumoniae* blaKPC-2 and blaKPC-3 isolates collected in the Dutch national surveillance. *Scientific reports*, 10(1), 16778.

Bayjanov JR, et al. (2019) *Enterococcus faecium* genome dynamics during long-term asymptomatic patient gut colonization. *Microbial genomics*, 5(7).