

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

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: 20260801T190531+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 81 mentions in open access literature.

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

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).

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.

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.

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.

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).

Goldstein S, et al. (2019) Evaluation of strategies for the assembly of diverse bacterial genomes using MinION long-read sequencing. *BMC genomics*, 20(1), 23.

Uribe RV, et al. (2019) Discovery and Characterization of Cas9 Inhibitors Disseminated across Seven Bacterial Phyla. *Cell host & microbe*, 25(2), 233.