

Resource Summary Report

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Nanopolish

RRID:SCR_016157

Type: Tool

Proper Citation

Nanopolish (RRID:SCR_016157)

Resource Information

URL: <https://github.com/jts/nanopolish>

Proper Citation: Nanopolish (RRID:SCR_016157)

Description: Software package for signal-level analysis of Oxford Nanopore sequencing data.

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

Keywords: Signal level analysis, Oxford Nanopore, sequencing data, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: Nanopolish

Resource ID: SCR_016157

Alternate IDs: OMICS_16545, biotools:nanopolish

Alternate URLs: <https://bio.tools/nanopolish>, <https://sources.debian.org/src/nanopolish/>

License: MIT License

Record Creation Time: 20220129T080329+0000

Record Last Update: 20260804T043618+0000

Ratings and Alerts

No rating or validation information has been found for Nanopolish.

No alerts have been found for Nanopolish.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 426 mentions in open access literature.

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

Guo W, et al. (2025) Single-molecule m6A detection empowered by endogenous labeling unveils complexities across RNA isoforms. *Molecular cell*, 85(6), 1233.

Park D, et al. (2025) Long-read RNA sequencing reveals allele-specific N 6-methyladenosine modifications. *Genome research*, 35(4), 999.

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.

Liu C, et al. (2025) Decoding the m6A epitranscriptomic landscape for biotechnological applications using a direct RNA sequencing approach. *Nature communications*, 16(1), 798.

Klimek D, et al. (2025) Insights into the phylogenetic and metabolic diversity of Planctomycetota in anaerobic digesters and the isolation of novel Thermoguttaceae species. *FEMS microbiology ecology*, 101(4).

Barker CR, et al. (2025) Characterization of a *Listeria monocytogenes* plasmid with antibiotic and stress resistance genes. *Microbial genomics*, 11(7).

Ma?dziarz MA, et al. (2025) Poly(A) tail dynamics, non-adenine incorporation and alternative polyadenylation shape the host transcriptome in COVID-19 pathogenesis. *Scientific reports*, 15(1), 37986.

AbdulHak A, et al. (2025) The genomic configurations driving antimicrobial resistance and virulence in colistin resistant *Pseudomonas aeruginosa* from an Egyptian Tertiary Oncology Hospital. *PLOS global public health*, 5(8), e0004976.

Spangenberg J, et al. (2025) The RMaP challenge of predicting RNA modifications by nanopore sequencing. *Communications chemistry*, 8(1), 115.

Bertocchi U, et al. (2025) Write and Read: Harnessing Synthetic DNA Modifications for Nanopore Sequencing. *ACS nano*, 19(44), 38553.

Wright G, et al. (2025) Saskemycin, a potent and selective antimycobacterial agent targeting a unique site on the ribosome. *Research square*.

Turmel M, et al. (2025) Comparative Genomics of *Chloropicon primus* and *Chloropicon roscoffensis* Provide Insights into the Evolutionary Dynamics and Ecological Success of These Tiny Green Algae in Marine Environments. *Genome biology and evolution*, 17(7).

Porter VL, et al. (2025) Rearrangements of viral and human genomes at human papillomavirus integration events and their allele-specific impacts on cancer genome regulation. *Genome research*, 35(4), 653.

Riquelme-Barrios S, et al. (2025) Direct RNA sequencing of the *Escherichia coli* epitranscriptome uncovers alterations under heat stress. *Nucleic acids research*, 53(6).

Li BP, et al. (2025) Transposable elements shape the landscape of heterozygous structural variation in a bird genome. *Zoological research*, 46(1), 75.

Prajapati HK, et al. (2025) The yeast genome is globally accessible in living cells. *Nature structural & molecular biology*, 32(2), 247.

Lu B, et al. (2025) Comprehensive comparison of the third-generation sequencing tools for bacterial 6mA profiling. *Nature communications*, 16(1), 3982.

García-González P, et al. (2025) APOE Haplotype Phasing Using ONT Long-Read Sequencing Reveals Two Common ?3 and ?4 intragenic haplotypes in the Spanish Population. *medRxiv : the preprint server for health sciences*.

Mackiewicz Z, et al. (2025) Excretory gland cell and NSPC genes in *C. elegans*: investigating their physiological roles. *Genetics*, 231(1).

Ren Z, et al. (2025) Isoform characterization of m6A in single cells identifies its role in RNA surveillance. *Nature communications*, 16(1), 5828.