

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>

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

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

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: 20260903T235349+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 477 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Santos LBD, et al. (2026) Pangenome analysis of nine soybean cyst nematode genomes reveals hidden variation contributing to diversity and adaptation. BMC genomics, 27(1), 177.

Tomar S, et al. (2026) Molecular, serological, and epidemiological characterisation of a hepatitis A virus outbreak in Maharashtra, India, 2025. The Indian journal of medical research, 163(5), 671.

Davidovich A, et al. (2026) Non-Mendelian inheritance of DNA methylation patterns in mice. Nature genetics, 58(6), 1409.

López-Moyado IF, et al. (2026) Flanking DNA sequences determine DNA methylation maintenance in proliferation, cancer and aging. bioRxiv : the preprint server for biology.

Gouhier T, et al. (2026) Nonsense-mediated mRNA decay factors target short poly(A)-tailed mRNAs lacking a premature termination codon. Nature communications, 17(1).

Cheng G, et al. (2026) Raw signal segmentation for estimating RNA modification from Nanopore direct RNA sequencing data. eLife, 14.

Jiang Q, et al. (2026) Nanopore direct RNA sequencing reveals transmissible gastroenteritis virus epitranscriptomic and transcriptomic landscapes modulated by gene 7. Microbial genomics, 12(4).

Zhang L, et al. (2026) Exon skipping as a potential diagnostic biomarker in colorectal cancer: an integrated epigenomic-transcriptomic analysis?. Human genomics, 20(1).

Wang F, et al. (2026) Stoichiometry-preserving and stochasticity-aware identification of m6A from direct RNA sequencing. Briefings in bioinformatics, 27(2).

Chen D, et al. (2026) The Neijiang pig T2T genome reveals domestication history and germplasm traits of Southwest Chinese local breeds. Communications biology, 9(1), 278.

Shi Z, et al. (2026) Transcriptome and m6A epitranscriptome profiling reveal CCL20 as a key mediator of inflammation in Staphylococcus aureus-induced bovine mastitis. BMC microbiology, 26(1), 133.

Xiong L, et al. (2026) Dissecting the homeodomain MAT locus and engineering novel tripolar and bipolar mating systems in Cryptococcus amylo lentus. mBio, 17(4), e0005926.

Mackey AI, et al. (2026) Temperature and genetic background drive mobilization of diverse transposable elements in a global human fungal pathogen. *PLoS genetics*, 22(1), e1011979.

Zhao X, et al. (2026) m6AConquer: a consistently quantified and orthogonally validated database for the N6-methyladenosine (m6A) epitranscriptome. *Nucleic acids research*, 54(D1), D204.

Eura N, et al. (2026) Pathogenic CGG expansions in oculopharyngodistal myopathy exhibit distinct characteristics of each causative gene on the flanking sequences as well as methylation status. *Genome medicine*, 18(1).

Baptissart M, et al. (2026) TENT5C extends Odf1 poly(A) tail to sustain sperm morphogenesis and fertility. *Nature communications*, 17(1).

Guo A, et al. (2026) Impaired bone matrix turnover with selective small bone fragility in a child with TENT5A-associated osteogenesis imperfecta. *JBMR plus*, 10(4), zia029.

Fuhrmann E, et al. (2026) Extended poly(A) tails are a shared feature of herpesvirus mRNAs. *PLoS pathogens*, 22(6), e1014341.

Mitchell L, et al. (2026) Differential A-to-I editing of SINE B2 RNAs unveils an epitranscriptome response to A β neurotoxicity. *Life science alliance*, 9(9).

Chavarria-Pizarro T, et al. (2026) Genome-wide and gene-specific DNA methylation across developmental stages in *Pogonomyrmex californicus*: A socially polymorphic ant. *Insect molecular biology*, 35(3), 232.