

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

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: 20260812T044318+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 [dkNET](#) .

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.

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.

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

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).

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.

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.

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.

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).

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), ziag029.

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

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.