

Resource Summary Report

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pod5

RRID:SCR_028166

Type: Tool

Proper Citation

pod5 (RRID:SCR_028166)

Resource Information

URL: <https://github.com/nanoporetech/pod5-file-format>

Proper Citation: pod5 (RRID:SCR_028166)

Description: File format for storing nanopore DNA data in an easily accessible way. High performance file format for nanopore reads.

Synonyms: POD5, pod5-file-format

Resource Type: source code, software resource

Keywords: File format, storing nanopore DNA data, DNA data, nanopore reads,

Availability: Free, Available for download, Freely available

Resource Name: pod5

Resource ID: SCR_028166

License: Mozilla Public License v 2.0

Record Creation Time: 20260319T071826+0000

Record Last Update: 20260810T040952+0000

Ratings and Alerts

No rating or validation information has been found for pod5.

No alerts have been found for pod5.

Data and Source Information

Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Ma?dziarz MA, et al. (2026) Epitranscriptomic signatures of m5C, m6A, and pseudouridine in COVID-19 reveal host RNA modifications involved in viral pathogenesis. *Microbiology spectrum*, 14(3), e0256125.

Suarez-Silva R, et al. (2026) Exploring the Algarrobo Decline in the Pómac Forest: Unraveling the Relationship between the Endomicrobiome of *Neltuma pallida* and *Enallodiplosis discordis*. *Microbial ecology*, 89(1).

Castelli R, et al. (2026) Efficient lossless compression of nanopore sequencing signals. *Bioinformatics advances*, 6(1), vbag157.

Cuypers WL, et al. (2026) SquiDBase: a community resource of raw nanopore data from microbes. *NAR genomics and bioinformatics*, 8(1), lqaf213.

White RT, et al. (2026) Decentralized nanopore genomics reveals diverse *Klebsiella pneumoniae* and no evidence of patient-patient transmission in a New Zealand hospital. *Microbial genomics*, 12(4).

Bowerman KL, et al. (2026) Metagenomic analysis of fecal microbiomes reveals genetic potential for diverse hydrogen management strategies in marsupials. *mSystems*, 11(2), e0160825.

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

Paivandy A, et al. (2026) Flexible and rapid validation of structural variation using adaptive sampling. *European journal of human genetics : EJHG*, 34(5), 649.

Xu ZS, et al. (2025) High-throughput analysis of microbiomes in a meat processing facility: are food processing facilities an establishment niche for persisting bacterial communities? *Microbiome*, 13(1), 25.

Emiliani FE, et al. (2025) Nanopore-based random genomic sampling for intraoperative molecular diagnosis. *Genome medicine*, 17(1), 6.

Nyaga DM, et al. (2024) Benchmarking nanopore sequencing and rapid genomics feasibility: validation at a quaternary hospital in New Zealand. *NPJ genomic medicine*, 9(1), 57.