

Resource Summary Report

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Oxford: Nanopore Technologies: PromethION

RRID:SCR_017987

Type: Tool

Proper Citation

Oxford: Nanopore Technologies: PromethION (RRID:SCR_017987)

Resource Information

URL: <https://nanoporetech.com/products/promethion>

Proper Citation: Oxford: Nanopore Technologies: PromethION (RRID:SCR_017987)

Description: System offers real-time, long-read, direct DNA and RNA sequencing by Oxford Nanopore Technologies. System suitable for large scale projects such as population-scale sequencing or plant genomics, or for large scale service offerings. PromethION 24 and PromethION 48 systems offer ability to run 24 and 48 flow cells respectively. System allows on demand sequencing, using any flow cell at any time. Users can start and stop running individual experiments as required, or deploy multiple flow cells onto single experiments for greater speed or throughput.

Synonyms: PromethION 24, PromethION 48

Resource Type: instrument resource

Keywords: sequencing machine, hardware, high-throughput sequencing, instrument, equipment

Availability: Restricted

Specification URL: https://raw.githubusercontent.com/SciCrunch/RRID-Instruments/main/PDF/SCR_017987.pdf

Resource Name: Oxford: Nanopore Technologies: PromethION

Resource ID: SCR_017987

Alternate URLs:

https://community.nanoporetech.com/requirements_documents/promethion-spec.pdf

Record Creation Time: 20220129T080338+0000

Record Last Update: 20260815T182544+0000

Ratings and Alerts

No rating or validation information has been found for Oxford: Nanopore Technologies: PromethION.

No alerts have been found for Oxford: Nanopore Technologies: PromethION.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 90 mentions in open access literature.

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

Wang K, et al. (2026) Silencing of BCL11A by disrupting enhancer-dependent epigenetic insulation. *Blood*, 147(13), 1470.

Ben Chehida Y, et al. (2026) Genetic parallelism underpins convergent mimicry coloration in Lepidoptera across 120 million years of evolution. *PLoS biology*, 24(4), e3003742.

Pang C, et al. (2026) Translating transcriptomics analysis into diagnostic workflows: clinical variant identification and interpretation in hypothesis-driven and hypothesis-free approaches. *EBioMedicine*, 128, 106313.

Buchthal J, et al. (2026) Non-invasive ovulation tracking enables genetic engineering in wild rodents. *Cell reports methods*, 6(2), 101311.

Fu ZH, et al. (2026) Synthetic rewriting of the IGH locus. *Cell genomics*, 6(6), 101252.

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

Chen Z, et al. (2025) The ZFHX3 GGC Repeat Expansion Underlying Spinocerebellar Ataxia Type 4 has a Common Ancestral Founder. *Movement disorders : official journal of the Movement Disorder Society*, 40(2), 363.

Funaguma S, et al. (2025) Retrotrans-genomics identifies aberrant THE1B endogenous retrovirus fusion transcripts in the pathogenesis of sarcoidosis. *Nature communications*, 16(1), 1318.

Culotta JA, et al. (2025) A reference genome for *Trichogramma kaykai*: a tiny desert-dwelling parasitoid wasp with competing sex-ratio distorters. *G3 (Bethesda, Md.)*, 15(8).

Kunigo K, et al. (2025) Targeted long-read methylation analysis using hybridization capture suitable for clinical specimens. *Cell reports methods*, 5(11), 101215.

Kuilman T, et al. (2025) Enabling next-generation engineered TCR-T therapies based on high-throughput TCR discovery from diagnostic tumor biopsies. *Nature communications*,

16(1), 649.

Liu D, et al. (2025) A practical DNA data storage using an expanded alphabet introducing 5-methylcytosine. *GigaByte* (Hong Kong, China), 2025, gigabyte147.

Yuan J, et al. (2025) A telomere-to-telomere genome assembly of koi carp (*Cyprinus carpio*) using long reads and Hi-C technology. *GigaScience*, 14.

Doyle PH, et al. (2025) Decoding the human PBMC isonome: Isoform-level resolution with single-cell long-read transcriptomics. *bioRxiv* : the preprint server for biology.

Wang Y, et al. (2025) Telomere-to-telomere genome of common bean (*Phaseolus vulgaris* L., YP4). *GigaScience*, 14.

Fanari O, et al. (2025) Protocol for differential analysis of pseudouridine modifications using nanopore DRS and unmodified transcriptome control. *STAR protocols*, 6(3), 103948.

Uematsu M, et al. (2025) Barcode-free multiplex plasmid sequencing using Bayesian analysis and nanopore sequencing. *eLife*, 12.

Li Z, et al. (2025) Phased high-quality genome of the gymnosperm Himalayan Yew assists in paclitaxel pathway exploration. *GigaScience*, 14.

Liu F, et al. (2025) The telomere-to-telomere gapless genome of grass carp provides insights for genetic improvement. *GigaScience*, 14.

Starcevic A, et al. (2025) Long-read metagenomic sequencing negates inferred loss of cytosine methylation in *Myxosporea* (Cnidaria: Myxozoa). *GigaScience*, 14.