Resource Summary Report

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PromethION

RRID:SCR_017987
Type: Tool

Proper Citation

PromethION (RRID:SCR_017987)

Resource Information

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

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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

Funding:

Availability: Restricted

Resource Name: PromethION

Resource ID: SCR_017987

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

Record Creation Time: 20220129T080338+0000

Record Last Update: 20250422T060040+0000

Ratings and Alerts

No rating or validation information has been found for PromethION.

No alerts have been found for PromethION.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 61 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

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.

Sigurpalsdottir BD, et al. (2024) A comparison of methods for detecting DNA methylation from long-read sequencing of human genomes. Genome biology, 25(1), 69.

Culotta J, et al. (2024) A reference genome for Trichogramma kaykai: A tiny desert-dwelling parasitoid wasp with competing sex-ratio distorters. bioRxiv : the preprint server for biology.

Wong B, et al. (2024) Streamlining remote nanopore data access with slow5curl. GigaScience, 13.

Bai M, et al. (2024) The telomere-to-telomere (T2T) genome of Peucedanum praeruptorum Dunn provides insights into the genome evolution and coumarin biosynthesis. GigaScience, 13.

Sarre LA, et al. (2024) DNA methylation enables recurrent endogenization of giant viruses in an animal relative. Science advances, 10(28), eado6406.

Leduque B, et al. (2024) Simultaneous profiling of chromatin accessibility and DNA methylation in complete plant genomes using long-read sequencing. Nucleic acids research, 52(11), 6285.

Makova KD, et al. (2024) The complete sequence and comparative analysis of ape sex chromosomes. Nature, 630(8016), 401.

Neale DB, et al. (2024) A genome sequence for the threatened whitebark pine. G3 (Bethesda, Md.), 14(5).

Cao S, et al. (2024) Gapless genome assembly and epigenetic profiles reveal gene regulation of whole-genome triplication in lettuce. GigaScience, 13.

Tan KT, et al. (2024) Neotelomeres and telomere-spanning chromosomal arm fusions in cancer genomes revealed by long-read sequencing. Cell genomics, 4(7), 100588.

Peng D, et al. (2024) The telomere-to-telomere (T2T) genome provides insights into the evolution of specialized centromere sequences in sandalwood. GigaScience, 13.

Huang M, et al. (2024) Comprehensive genetic analysis of facioscapulohumeral muscular dystrophy by Nanopore long-read whole-genome sequencing. Journal of translational medicine, 22(1), 451.

Tsouris A, et al. (2024) Diallel panel reveals a significant impact of low-frequency genetic variants on gene expression variation in yeast. Molecular systems biology, 20(4), 362.

Xiao B, et al. (2024) Combining optical genome mapping and RNA-seq for structural variants detection and interpretation in unsolved neurodevelopmental disorders. Genome medicine, 16(1), 113.

Unneberg P, et al. (2024) Ecological genomics in the Northern krill uncovers loci for local adaptation across ocean basins. Nature communications, 15(1), 6297.

LaFlamme CW, et al. (2024) Diagnostic utility of DNA methylation analysis in genetically unsolved pediatric epilepsies and CHD2 episignature refinement. Nature communications, 15(1), 6524.

Ballard JWO, et al. (2023) The Australasian dingo archetype: De novo chromosome-length genome assembly, DNA methylome, and cranial morphology. bioRxiv : the preprint server for biology.

Gaikwad K, et al. (2023) The chromosome-scale genome assembly of cluster bean provides molecular insight into edible gum (galactomannan) biosynthesis family genes. Scientific reports, 13(1), 9941.

Schall PZ, et al. (2023) Genome-wide methylation patterns from canine nanopore assemblies. G3 (Bethesda, Md.), 13(11).