# **Resource Summary Report**

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# **MinION**

RRID:SCR\_017985 Type: Tool

**Proper Citation** 

MinION (RRID:SCR\_017985)

#### **Resource Information**

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

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**Description:** Portable, real time device for DNA and RNA sequencing, putting you in control of your sequence data. Portable DNA/RNA sequencing by Oxford Nanopore Technologies.

Resource Type: instrument resource

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

Funding:

Availability: Restricted

Resource Name: MinION

Resource ID: SCR\_017985

Alternate URLs: https://nanoporetech.com/sites/default/files/s3/literature/MinION-Mk1C-brochure.pdf

Record Creation Time: 20220129T080338+0000

Record Last Update: 20250420T014846+0000

**Ratings and Alerts** 

No rating or validation information has been found for MinION.

No alerts have been found for MinION.

### Data and Source Information

Source: SciCrunch Registry

## **Usage and Citation Metrics**

We found 91 mentions in open access literature.

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

Xiao S, et al. (2024) New Vibrio cholerae sequences from Eastern and Southern Africa alter our understanding of regional cholera transmission. medRxiv : the preprint server for health sciences.

Kasianova AM, et al. (2024) Trans2express - de novo transcriptome assembly pipeline optimized for gene expression analysis. Plant methods, 20(1), 128.

Nakamura K, et al. (2024) Diversity of Shiga toxin transducing phages in Escherichia coli O145:H28 and the different Shiga toxin 2 production levels associated with short- or long-tailed phages. Frontiers in microbiology, 15, 1453887.

Holmes MJ, et al. (2024) HaplotagLR: An efficient and configurable utility for haplotagging long reads. PloS one, 19(3), e0298688.

Bamou R, et al. (2024) Pathogens spread by high-altitude windborne mosquitoes. bioRxiv : the preprint server for biology.

Gatins R, et al. (2024) Whole genome assembly and annotation of the King Angelfish (Holacanthus passer) gives insight into the evolution of marine fishes of the Tropical Eastern Pacific. GigaByte (Hong Kong, China), 2024, gigabyte115.

Lai J, et al. (2024) Relative efficacy of masks and respirators as source control for viral aerosol shedding from people infected with SARS-CoV-2: a controlled human exhaled breath aerosol experimental study. EBioMedicine, 104, 105157.

Zimoch M, et al. (2024) Mosquito-independent milk-associated transmission of zoonotic Wesselsbron virus in sheep. PLoS pathogens, 20(12), e1012751.

Young R, et al. (2024) Improved reference quality genome sequence of the plastic-degrading greater wax moth, Galleria mellonella. G3 (Bethesda, Md.), 14(6).

Takahashi T, et al. (2024) Comparative Genomic Analysis of Staphylococcal Cassette Chromosome mec Type V Staphylococcus aureus Strains and Estimation of the Emergence of SCCmec V Clinical Isolates in Korea. Annals of laboratory medicine, 44(1), 47.

Makhoul M, et al. (2024) Novel PHOTOPERIOD-1 gene variants associate with yield-related and root-angle traits in European bread wheat. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 137(6), 125.

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.

Grandi C, et al. (2024) Decoupled degradation and translation enables noise modulation by poly(A) tails. Cell systems, 15(6), 526.

Yano B, et al. (2023) Dynamic changes in Shiga toxin (Stx) 1 transducing phage throughout the evolution of O26:H11 Stx-producing Escherichia coli. Scientific reports, 13(1), 4935.

Charles C, et al. (2023) Features of Mycobacterium bovis Complete Genomes Belonging to 5 Different Lineages. Microorganisms, 11(1).

Tsouris A, et al. (2023) Diallel panel reveals a significant impact of low-frequency genetic variants on gene expression variation in yeast. bioRxiv : the preprint server for biology.

Souza UJB, et al. (2023) Circulation of Dengue Virus Serotype 1 Genotype V and Dengue Virus Serotype 2 Genotype III in Tocantins State, Northern Brazil, 2021-2022. Viruses, 15(11).

Takahashi K, et al. (2023) Emergence of putative energy parasites within Clostridia revealed by genome analysis of a novel endosymbiotic clade. The ISME journal, 17(11), 1895.

Hassouneh SA, et al. (2023) Antigen test swabs are comparable to nasopharyngeal swabs for sequencing of SARS-CoV-2. Scientific reports, 13(1), 11255.

Kuntová L, et al. (2023) Staphylococcus aureus Prophage-Encoded Protein Causes Abortive Infection and Provides Population Immunity against Kayviruses. mBio, 14(2), e0249022.