

Resource Summary Report

Generated by [RRID](#) on Aug 15, 2026

Dorado

RRID:SCR_025883

Type: Tool

Proper Citation

Dorado (RRID:SCR_025883)

Resource Information

URL: <https://github.com/nanoporetech/dorado>

Proper Citation: Dorado (RRID:SCR_025883)

Description: Software tool as Oxford Nanopore basecaller. Used to determine nucleotide sequence.

Resource Type: software application, software resource, source code

Keywords: Oxford Nanopore, basecaller, determine nucleotide sequence,

Availability: Free, Available for download, Freely available

Resource Name: Dorado

Resource ID: SCR_025883

Record Creation Time: 20241015T053249+0000

Record Last Update: 20260815T042920+0000

Ratings and Alerts

No rating or validation information has been found for Dorado.

No alerts have been found for Dorado.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 370 mentions in open access literature.

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

Szablińska-Piernik J, et al. (2026) Giant chromosomes of a tiny plant-the complete telomere-to-telomere genome assembly of the simple thalloid liverwort *Apopellia endiviifolia* (Jungermanniopsida, Marchantiophyta). *GigaScience*, 15.

Karlsson O, et al. (2026) Loss of SETDB1-mediated H3K9me3 in human neural progenitor cells leads to transcriptional activation of L1 retrotransposons. *Nucleic acids research*, 54(4).

Mortazavi M, et al. (2026) Long-read genome sequencing improves detection and functional interpretation of structural and repeat variants in autism. *Cell genomics*, 6(5), 101186.

Banik P, et al. (2026) Targeted antisense oligonucleotide therapy rescues PRPF31 expression in retinitis pigmentosa caused by a splicing mutation. *Molecular therapy : the journal of the American Society of Gene Therapy*.

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

Abdollahzadeh E, et al. (2026) Dogme: a nextflow pipeline for reprocessing nanopore RNA and DNA modifications. *Bioinformatics (Oxford, England)*, 42(3).

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

Lean SS, et al. (2026) Of Commensals and Opportunists: Genomics of Coagulase-Negative Staphylococci During Sequential Ear and Eye Infections in a Healthy Adult. *MicrobiologyOpen*, 15(2), e70277.

Centofanti F, et al. (2026) The novel (TCTG)_n motif in CNBP expanded alleles: composition, dynamics and genotype-phenotype correlation in Myotonic dystrophy type 2 (DM2). *Human genomics*, 20(1).

Dias HM, et al. (2026) Reproducible Emu-Based Workflow for High-Fidelity Soil and Plant Microbiome Profiling on HPC Clusters. *Bio-protocol*, 16(2), e5577.

Pushkova EN, et al. (2026) Progress in Flax Genome Assembly from Nanopore Sequencing Data. *Plants (Basel, Switzerland)*, 15(1).

Christoffersen SN, et al. (2026) Arctic Insects Show a Highly Dynamic Microbiome Shaped by Abiotic and Biotic Variables. *Microbial ecology*, 89(1), 43.

Luna N, et al. (2026) Ecological insights into the cross-domain microbiome interactions in the hematophagous bat *Desmodus rotundus*. *Animal microbiome*, 8(1), 22.

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

Stanojević D, et al. (2026) Telomere-to-telomere assembly using HERRO-corrected Nanopore Simplex reads. *Nature*, 655(8121), 158.

Virtuoso FAS, et al. (2026) DIY: A Practical Field-to-Sequencer Workflow for Metabarcoding the Diet of Terrestrial Carnivore Species. *Molecular ecology resources*, 26(4), e70144.

Kousar A, et al. (2026) Biological control of *Botrytis cinerea* in tomato and *Fusarium graminearum* in wheat using the novel species *Burkholderia mycopellens* and *Burkholderia crassaminum*. *Frontiers in microbiology*, 17, 1776517.

Snell LB, et al. (2026) Antibody escape drives emergence of diverse spike haplotypes resembling variants of concern in persistent SARS-CoV-2 infections. *Cell reports. Medicine*, 7(2), 102587.

Xiao PX, et al. (2026) Haplotype-resolved and near telomere-to-telomere assembly of the autotetraploid potato genome. *Genome biology*, 27(1).

Synowiec A, et al. (2026) Antiviral effect of poly(styrene 4-sulfonate) (PSSNa) on feline calicivirus oral infections in cats-field study. *The veterinary quarterly*, 46(1), 2616395.