

Resource Summary Report

Generated by [ASWG](#) on Aug 4, 2026

NanoPlot

RRID:SCR_024128

Type: Tool

Proper Citation

NanoPlot (RRID:SCR_024128)

Resource Information

URL: <https://github.com/wdecoster/NanoPlot>

Proper Citation: NanoPlot (RRID:SCR_024128)

Description: Software package as plotting tool for long read sequencing data and alignments.

Synonyms: nanoplots

Resource Type: software library, software toolkit, software resource

Keywords: plotting tool, long read sequencing data and alignments,

Availability: Free, Available for download, Freely available,

Resource Name: NanoPlot

Resource ID: SCR_024128

Alternate URLs: <https://sources.debian.org/src/nanoplots/>, <https://nanoplots.bioinf.be/>

License: MIT License

Record Creation Time: 20230824T050212+0000

Record Last Update: 20260803T040911+0000

Ratings and Alerts

No rating or validation information has been found for NanoPlot.

No alerts have been found for NanoPlot.

Data and Source Information

Usage and Citation Metrics

We found 299 mentions in open access literature.

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

Littel HR, et al. (2026) The impact of Hnrnp1 deficiency on transcriptional patterns of developing muscle cells. *FEBS open bio*, 16(1), 178.

Kirkland C, et al. (2026) Chromosome-Level Genomics and Historical Museum Collections Reveal New Insights Into the Population Structure and Chromosome Evolution of Waterbuck. *Molecular ecology*, 35(1), e70218.

Bekavac M, et al. (2026) De novo genome assembly of Ansell's mole-rat (*Fukomys anselli*). *G3 (Bethesda, Md.)*, 16(1).

Chen J, et al. (2026) Genomic and transcriptomic analysis of yield enhancement mechanism of lipopeptide iturin W by tryptone supplementation. *Microbiology spectrum*, 14(1), e0324725.

Lee S, et al. (2025) Chromosome-scale genome assembly of Korean goosegrass (*Eleusine indica*). *Scientific data*, 12(1), 156.

Luk-In S, et al. (2025) Inhibitory effects of benzyl isothiocyanate on widespread mcr-1-harbouring IncX4 plasmid transfer. *Scientific reports*, 15(1), 12892.

Yu YH, et al. (2025) *Pseudomonas* Species Isolated From Lotus Nodules Are Genetically Diverse and Promote Plant Growth. *Environmental microbiology*, 27(3), e70066.

Salvà-Serra F, et al. (2025) Description of *Pseudomonas imrae* sp. nov., carrying a novel class C β -lactamase gene variant, isolated from gut samples of Atlantic mackerel (*Scomber scombrus*). *Frontiers in microbiology*, 16, 1530878.

Saavedra-Tralma D, et al. (2025) Functional and Genomic Evidence of L-Arginine-Dependent Bacterial Nitric Oxide Synthase Activity in *Paenibacillus nitricinens* sp. nov. *Biology*, 14(6).

López L, et al. (2025) Oral and parenteral treatment with a third-generation cephalosporin promotes the proliferation of diverse ESBL-producing *Escherichia coli* in the chicken intestinal tract. *mSphere*, 10(7), e0022725.

Pongchaikul P, et al. (2025) Genomic analysis of contaminant *Stenotrophomonas maltophilia*, from placental swab culture, carrying antibiotic resistance: a potential hospital laboratory contaminant. *Scientific reports*, 15(1), 22323.

Castelló-Sanjuán M, et al. (2025) Persistent viral infections impact key biological traits in *Drosophila melanogaster*. *PLoS biology*, 23(10), e3003437.

Frail S, et al. (2025) Genomes of nitrogen-fixing eukaryotes reveal an alternate path for organellogenesis. *Proceedings of the National Academy of Sciences of the United States of America*, 122(33), e2507237122.

Liu X, et al. (2025) SMART-RNA-Metavirome: a practical RNA metavirome platform compatible with high-throughput sequencing of both short and long reads. *Infectious diseases of poverty*, 14(1), 101.

Patarapuwadol S, et al. (2025) Whole-genome sequencing of *Burkholderia glumae* strains from Thailand reveals potential horizontal gene transfer with *Burkholderia pseudomallei*. *PloS one*, 20(12), e0340071.

Goodman RN, et al. (2025) Comparative genomics of blood and faecal *E. coli* and *K. pneumoniae* isolates from neonates with bloodstream infections in Tanzania. *Communications biology*, 8(1), 1603.

Choi S, et al. (2025) Chromosome-level genome assembly of *Salvia sclarea*. *Scientific data*, 12(1), 14.

Bednarczuk L, et al. (2025) Phenotypic and genetic heterogeneity of *Acinetobacter baumannii* in the course of an animal chronic infection. *Microbial genomics*, 11(2).

Mohamed AYA, et al. (2025) Genome-Resolved Metatranscriptomics Provide Insights on Immigration Influence in Structuring Microbial Community Assembly of a Full-Scale Aerobic Granular Sludge Plant. *Environmental science & technology*, 59(12), 6126.

Otron DH, et al. (2025) Improvement of Nanopore sequencing provides access to high quality genomic data for multi-component CRESS-DNA plant viruses. *Virology journal*, 22(1), 78.