

Resource Summary Report

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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: nanoplot

Resource Type: software resource, software library, software toolkit

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/nanoplot/>, <https://nanoplot.bioinf.be/>

License: MIT License

Record Creation Time: 20230824T050212+0000

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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 [RRID](#) .

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 anelli*). *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.

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.

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

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.

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

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.

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

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.

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.

Chen GS, et al. (2025) Molecular and Histological Identification of Bovine Papillomavirus 1, 2 and a Novel Genotype in Cutaneous Papillomas of Dairy Cattle in Taiwan. *Transboundary and emerging diseases*, 2025, 5586786.

AbdulHak A, et al. (2025) The genomic configurations driving antimicrobial resistance and virulence in colistin resistant *Pseudomonas aeruginosa* from an Egyptian Tertiary Oncology Hospital. *PLOS global public health*, 5(8), e0004976.

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

Rahman MM, et al. (2025) Development of a culture-independent whole-genome sequencing of Nipah virus using the MinION Oxford Nanopore platform. *Microbiology spectrum*, 13(6), e0249224.