

Resource Summary Report

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DNAPlotter

RRID:SCR_005006

Type: Tool

Proper Citation

DNAPlotter (RRID:SCR_005006)

Resource Information

URL: <http://www.sanger.ac.uk/resources/software/dnaplotter/>

Proper Citation: DNAPlotter (RRID:SCR_005006)

Description: Software application used to generate images of circular and linear DNA maps to display regions and features of interest. The images can be inserted into a document or printed out directly. As this uses Artemis it can read in the common file formats EMBL, GenBank and GFF3.

Abbreviations: DNAPlotter

Synonyms: DNAPlotter: circular and linear interactive genome visualization

Resource Type: software resource, software application

Defining Citation: [PMID:18990721](#)

Keywords: java, circular, linear, plot, genome, macosx, unix, windows

Availability: GNU General Public License

Resource Name: DNAPlotter

Resource ID: SCR_005006

Alternate IDs: OMICS_00906, nlx_96278

Record Creation Time: 20220129T080227+0000

Record Last Update: 20260801T191050+0000

Ratings and Alerts

No rating or validation information has been found for DNAPlotter.

No alerts have been found for DNAPlotter.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 108 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Catalano Gonzaga O, et al. (2025) Gene-trait matching among Bifidobacterium dentium strains reveals various glycan metabolism loci including a strain-specific fucosyllactose utilization cluster. *Frontiers in microbiology*, 16, 1584694.

Hsu TK, et al. (2025) Characterization and genome analysis of a novel phage BP15 infecting *Vibrio parahaemolyticus*. *Scientific reports*, 15(1), 2801.

Yacoub E, et al. (2025) A sweeping view of avian mycoplasmas biology drawn from comparative genomic analyses. *BMC genomics*, 26(1), 24.

McDonnell B, et al. (2025) Lactococcal mobile genetic elements harbour a diverse phage defenseome rich in restriction-modification systems. *Nucleic acids research*, 53(17).

Rojas-Villalobos C, et al. (2025) MOBHunter: a data integration platform for identification and classification of mobile genetic elements in microbial genomes. *Nucleic acids research*, 53(W1), W398.

Papadimitriou K, et al. (2025) Genome Analysis of the Multidrug-Resistant *Campylobacter coli* BCT3 of the Sequence Type (ST) 872 Isolated from a Pediatric Diarrhea Case. *Microorganisms*, 13(6).

Trebino MA, et al. (2025) Parallel regulatory circuits orchestrate biofilm formation in response to c-di-GMP levels and growth phase. *PLoS genetics*, 21(9), e1011870.

Petushkova E, et al. (2024) The Complete Genome of a Novel Typical Species *Thiocapsa bogorovii* and Analysis of Its Central Metabolic Pathways. *Microorganisms*, 12(2).

Hong HX, et al. (2024) Virulence plasmid with IroBCDN deletion promoted cross-regional transmission of ST11-KL64 carbapenem-resistant hypervirulent *Klebsiella pneumoniae* in central China. *BMC microbiology*, 24(1), 400.

Guo X, et al. (2023) Phenotypic Characterization and Comparative Genomic Analyses of Mycobacteriophage WIVsmall as A New Member Assigned to F1 Subcluster. *Current issues in molecular biology*, 45(8), 6432.

Bhattacharyya M, et al. (2023) Molecular evaluation of the metabolism of estrogenic di(2-ethylhexyl) phthalate in *Mycobacterium* sp. *Microbial cell factories*, 22(1), 82.

Zlatohurska M, et al. (2023) Broad-host-range lytic *Erwinia* phage Key with exopolysaccharide degrading activity. *Virus research*, 329, 199088.

Pinheiro Y, et al. (2023) A thermophilic chemolithoautotrophic bacterial consortium suggests a mutual relationship between bacteria in extreme oligotrophic environments. *Communications biology*, 6(1), 230.

Cambroner-Heinrichs JC, et al. (2023) *Erwiniaceae* bacteria play defensive and nutritional roles in two widespread ambrosia beetles. *FEMS microbiology ecology*, 99(12).

Sharma V, et al. (2023) Systematic analysis of prophage elements in actinobacterial genomes reveals a remarkable phylogenetic diversity. *Scientific reports*, 13(1), 4410.

Tang SK, et al. (2023) Cellular differentiation into hyphae and spores in halophilic archaea. *Nature communications*, 14(1), 1827.

Zhang Z, et al. (2023) Plastoquinone synthesis inhibition by tetrabromo biphenyldiol as a widespread algicidal mechanism of marine bacteria. *The ISME journal*, 17(11), 1979.

Kalizang'oma A, et al. (2023) Novel Multilocus Sequence Typing and Global Sequence Clustering Schemes for Characterizing the Population Diversity of *Streptococcus mitis*. *Journal of clinical microbiology*, 61(1), e0080222.

Chino de la Cruz CM, et al. (2023) Complete genome sequence and characterization of a novel *Enterococcus faecium* with probiotic potential isolated from the gut of *Litopenaeus vannamei*. *Microbial genomics*, 9(3).

Martinez J, et al. (2022) Genome sequencing and comparative analysis of *Wolbachia* strain wAlbA reveals *Wolbachia*-associated plasmids are common. *PLoS genetics*, 18(9), e1010406.