

# Resource Summary Report

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## DNAPlotter

RRID:SCR\_005006

Type: Tool

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### Proper Citation

DNAPlotter (RRID:SCR\_005006)

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### 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 application, software resource

**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:** 20260727T040348+0000

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### Ratings and Alerts

No rating or validation information has been found for DNAPlotter.

No alerts have been found for DNAPlotter.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 108 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [nidm-terms](#).

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

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.

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

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.

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

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.

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.

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.

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.

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

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

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

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.

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).

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.

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.