

Resource Summary Report

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CGView

RRID:SCR_011779

Type: Tool

Proper Citation

CGView (RRID:SCR_011779)

Resource Information

URL: <http://wishart.biology.ualberta.ca/cgview/>

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Description: A Java package for generating high quality, zoomable maps of circular genomes. Its primary purpose is to serve as a component of sequence annotation pipelines, as a means of generating visual output suitable for the web., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: CGView

Synonyms: Circular Genome Viewer

Resource Type: software resource

Defining Citation: [DOI:10.1093/bioinformatics/bti054](https://doi.org/10.1093/bioinformatics/bti054)

Keywords: bio.tools

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: CGView

Resource ID: SCR_011779

Alternate IDs: OMICS_00905, biotools:cgview

Alternate URLs: <https://bio.tools/cgview>, <https://sources.debian.org/src/cgview/>

Record Creation Time: 20220129T080306+0000

Record Last Update: 20260801T190417+0000

Ratings and Alerts

No rating or validation information has been found for CGView.

No alerts have been found for CGView.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 304 mentions in open access literature.

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

Park JS, et al. (2025) Characterization of the complete chloroplast genome of a woody invasive species, *Leucaena leucocephala* in Korea. Mitochondrial DNA. Part B, Resources, 10(8), 725.

Lan N, et al. (2025) Metagenomic insights into resistance trends related to microbial VB12 synthesis in eutrophic urban lakes. Scientific reports, 15(1), 20599.

Gurung S, et al. (2025) Comparative Genome Analysis of Three *Halobacillus* Strains Isolated From Saline Environments Reveal Potential Salt Tolerance and Algicidal Mechanisms. Environmental microbiology reports, 17(3), e70121.

Kim J, et al. (2025) Isolation and Characterization of a *Bacillus amyloliquefaciens* Bacteriophage JBA6 and Its Endolysin PlyJBA6. Journal of microbiology and biotechnology, 35, e2502026.

Felton EA, et al. (2025) Emergence of ST3390: A non-pigmented HA-MRSA clone with enhanced virulence. bioRxiv : the preprint server for biology.

Li H, et al. (2025) Complete mitochondrial genome assembly and comparative analysis of *Colocasia esculenta*. BMC plant biology, 25(1), 67.

Miga M, et al. (2025) Complete mitochondrial genome data and phylogenetic analysis of the Plain Banded Awl, *Hasora vitta* (Lepidoptera: Hesperidae: Coeliadinae) from Malaysia. Mitochondrial DNA. Part B, Resources, 10(6), 528.

Muhammad N, et al. (2025) Comparative genome analyses reveal insights into the marine adaptation of a novel bacterium *Pontimicrobium maritimus* sp. nov., isolated from seawater. Scientific reports, 15(1), 24027.

Nobthai P, et al. (2025) The Co-Existence of mcr-1.1 and mcr-3.5 in *Escherichia coli* Isolated from Clinical Samples in Thailand. Antibiotics (Basel, Switzerland), 14(6).

Hu Q, et al. (2025) Lytic bacteriophages targeting multidrug-resistant *Pseudomonas aeruginosa* in *Moschus berezovskii*: isolation, characterization, and therapeutic efficacy against bacteremia. Virology journal, 22(1), 285.

Wang Y, et al. (2025) Emergence of highly virulent *Aeromonas dhakensis* in channel catfish aquaculture: Genomic insights into pathogenicity and antimicrobial resistance. *Virulence*, 16(1), 2525933.

Li Q, et al. (2025) Characterization and genomics of phage Henu2_3 against K1 *Klebsiella pneumoniae* and its efficacy in animal models. *AMB Express*, 15(1), 112.

Kim EJ, et al. (2025) Bacteriophage cocktail LEC2-LEC10 for broad-spectrum control of pathogenic and uncharacterized *Escherichia coli* in fresh produce. *Frontiers in microbiology*, 16, 1594533.

Chai J, et al. (2025) Isolation, characterization, and application of the novel polyvalent bacteriophage vB_EcoM_XAM237 against pathogenic *Escherichia coli*. *Veterinary research*, 56(1), 90.

Cui H, et al. (2025) Branched-chain amino acid metabolism supports *Roseobacteraceae* positive interactions in marine biofilms. *Applied and environmental microbiology*, 91(3), e0241124.

Yang R, et al. (2025) The *Klebsiella pneumoniae* tellurium resistance gene *terC* contributes to both tellurite and zinc resistance. *Microbiology spectrum*, 13(5), e0263424.

Born P, et al. (2025) Complete genome sequence data of *Clostridium isatidis* BK32, a lignocellulose-degrading bacterium isolated from compost. *Data in brief*, 61, 111874.

Zhao K, et al. (2024) Genome Analysis for Cholesterol-Lowing Action and Bacteriocin Production of *Lactiplantibacillus plantarum* WLPL21 and ZDY04 from Traditional Chinese Fermented Foods. *Microorganisms*, 12(1).

Takahashi T, et al. (2024) Comparative Genomic Analysis of Staphylococcal Cassette Chromosome *mec* Type V *Staphylococcus aureus* Strains and Estimation of the Emergence of SCC*mec* V Clinical Isolates in Korea. *Annals of laboratory medicine*, 44(1), 47.

Buysse M, et al. (2024) Detection of *Anaplasma* and *Ehrlichia* bacteria in humans, wildlife, and ticks in the Amazon rainforest. *Nature communications*, 15(1), 3988.