

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 8, 2026

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: 20260905T132711+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 310 mentions in open access literature.

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

Tchatchouang CK, et al. (2026) Whole-Genome Sequence Profiling of *Listeria innocua* From Different Sources: Implications for Public Health. *MicrobiologyOpen*, 15(2), e70274.

Virieux-Petit M, et al. (2026) Adaptive evolution of *Pseudomonas aeruginosa* ST299 population colonizing a hospital copper water network over a 2.5-year period. *Microbial genomics*, 12(1).

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

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

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.

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.

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.

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.

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.

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

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.

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.

Xu S, et al. (2025) The Complete Mitochondrial Genome of the Pest Beetle *Latheticus oryzae*: Assembly, Annotation, and Phylogenetic Analysis. *Ecology and evolution*, 15(12), e72717.

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.

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.

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 D, et al. (2025) Complete genome sequence and comparative analysis of *Bacillus velezensis* Lzh-5, a fungal antagonistic and plant growth-promoting strain. *BMC microbiology*, 25(1), 230.

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