

Resource Summary Report

Generated by [kravitz2](#) on Sep 5, 2026

Glimmer

RRID:SCR_011931

Type: Tool

Proper Citation

Glimmer (RRID:SCR_011931)

Resource Information

URL: <http://ccb.jhu.edu/software/glimmer/index.shtml>

Proper Citation: Glimmer (RRID:SCR_011931)

Description: A software system for finding genes in microbial DNA, especially the genomes of bacteria, archaea, and viruses.

Abbreviations: Glimmer

Synonyms: Glimmer - Microbial Gene-Finding System

Resource Type: analysis service resource, data analysis service, production service resource, service resource, software resource

Defining Citation: [DOI:10.1093/nar/26.2.544](https://doi.org/10.1093/nar/26.2.544)

Keywords: microbial, gene, bio.tools

Availability: Open unspecified license, OSI certified

Resource Name: Glimmer

Resource ID: SCR_011931

Alternate IDs: OMICS_01486, biotools:glimmer

Alternate URLs: <https://bio.tools/glimmer>, <https://sources.debian.org/src/tigr-glimmer/>

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260903T235141+0000

Ratings and Alerts

No rating or validation information has been found for Glimmer.

No alerts have been found for Glimmer.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 687 mentions in open access literature.

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

Kushwaha P, et al. (2026) Isolation and genomic characterization of a lytic bacteriophage against multidrug-resistant *Proteus mirabilis*. *Applied microbiology and biotechnology*, 110(1).

Peng S, et al. (2026) Development and Assessment of Heavy Oil-Degrading Fungal Consortia (*Aspergillus* and *Alternaria*) for Soil Bioremediation. *Journal of fungi* (Basel, Switzerland), 12(3).

Liu S, et al. (2026) Isolation and characterization of a novel strain, *Paenibacillus lacisediminis* sp. nov., exhibiting both biomacromolecule degradation and plant growth-beneficial activities. *BMC microbiology*, 26(1).

Akanbi TM, et al. (2026) Isolation and characterization of TayeBlu, a novel bacteriophage of *Azotobacter vinelandii*. *Microbiology spectrum*, 14(1), e0128625.

Leal K, et al. (2026) Exploration of inactive metabolic pathways in Antarctic *Pseudogymnoascus australis* through elicitation: a genomic and metabolomic approach to investigate its biotechnological potential. *IMA fungus*, 17, e156018.

Sheng Q, et al. (2026) Silicate minerals enhance the expression of genes related to mineral dissolution by *Priestia aryabhattai* strain C4-10. *Applied and environmental microbiology*, 92(2), e0255425.

Zrelavs N, et al. (2026) Genomic and experimental characterization of unique Antarctic temperate phage Perkons reveals multiple integrases and complex lysogenic dynamics in *Psychrobacillus* sp. L4. *BMC microbiology*, 26(1).

Han Q, et al. (2026) *Massilia* strains facilitate root growth and reshape root microbiota through diverse salicylic acid hydrolysis pathways. *The ISME journal*, 20(1).

Hu S, et al. (2026) Transmission and genomic insights into *Elizabethkingia miricola*: A zoonotic pathogen with intrinsic resistance and nosocomial outbreak potential. *One health* (Amsterdam, Netherlands), 22, 101465.

Garza DR, et al. (2026) Characterization of genomic diversity in bacteriophages infecting *Rhodococcus*. *PloS one*, 21(6), e0352686.

Wang X, et al. (2026) Integrated multi-omics and phenotypic validations reveal biocontrol mechanisms of *Bacillus velezensis* XM18-5 against potato common scab. *Frontiers in microbiology*, 17, 1748645.

Baek K, et al. (2026) Genomic and in vitro characterization of two lytic bacteriophages infecting multidrug-resistant *Erwinia* sp. strain AnSW2-5. *Scientific reports*, 16(1).

Liu J, et al. (2026) Zoonotic *Bordetella bronchiseptica* infection at the swine-human interface: unveiling the evolutionary path from an animal to a human pathogen. *Emerging microbes & infections*, 15(1), 2637286.

Pedersen JS, et al. (2026) The first single-stranded DNA virus targeting *Pectobacterium* belongs to the family Microviridae and demonstrates a broad host range to *Pectobacterium brasiliense* soft rot pathogens. *Archives of virology*, 171(3).

Cui Q, et al. (2026) Isolation, identification, and plant growth-promoting mechanisms of strain BN5, with a focus on exogenously Trp-independent IAA biosynthesis, and its impact on cucumber cultivation. *Current research in microbial sciences*, 10, 100549.

Ge G, et al. (2026) Isolation, identification and genomic analysis of *Mycobacterium caprae* strain SY-1 from Chinese sika deer (*Cervus nippon*). *BMC genomics*, 27(1), 184.

Xia P, et al. (2026) Within-host evolution drives the emergence of ceftazidime-avibactam resistance mediated by IncN plasmid-encoded bla_{NDM-1} and bla_{KPC-33} in ST11-KL64 hypervirulent *Klebsiella pneumoniae*. *Microbiology spectrum*, 14(4), e0236725.

Chen EY, et al. (2026) Mitogenomic organization and characteristics of deep-sea pelagic ostracods from both polar regions. *BMC genomics*, 27(1).

Wan J, et al. (2026) Evolutionary and Mobile Genetic Element Analysis of a Multidrug-Resistant ST398-MRSA-Vc Isolate from Ready-to-Eat Pork Products. *Antibiotics (Basel, Switzerland)*, 15(3).

Choi A, et al. (2026) Genomic Insights into *Dechloromonas* sp. TW-R-39-2: A Dual-Function Bacterium for Heavy Metal Sequestration and Chlorinated Organic Degradation. *Microorganisms*, 14(2).