

Resource Summary Report

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BRIG

RRID:SCR_007802

Type: Tool

Proper Citation

BRIG (RRID:SCR_007802)

Resource Information

URL: <http://brig.sourceforge.net/>

Proper Citation: BRIG (RRID:SCR_007802)

Description: A cross-platform (Windows/Mac/Unix) application that can display circular comparisons between a large number of genomes, with a focus on handling genome assembly data.

Abbreviations: BRIG

Synonyms: BLAST Ring Image Generator

Resource Type: software resource

Defining Citation: [DOI:10.1186/1471-2164-12-402](https://doi.org/10.1186/1471-2164-12-402)

Keywords: bio.tools

Resource Name: BRIG

Resource ID: SCR_007802

Alternate IDs: OMICS_00929, biotools:brig

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

Record Creation Time: 20220129T080243+0000

Record Last Update: 20260905T132615+0000

Ratings and Alerts

No rating or validation information has been found for BRIG.

No alerts have been found for BRIG.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 561 mentions in open access literature.

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

Song H, et al. (2026) Emergence of Polymyxin Resistance Driven by a PhoQ Mutation in KPC-2-Producing *Klebsiella pneumoniae*. *Antibiotics* (Basel, Switzerland), 15(2).

Meng N, et al. (2026) A novel and evolutionarily distinct flavoprotein monooxygenase drives skatole degradation in *Rhodococcus*. *Applied and environmental microbiology*, 92(4), e0022826.

Liu D, et al. (2026) Characterization of phage AbpL with a terminally redundant genome and its therapeutic potential against drug-resistant *Acinetobacter baumannii* infections. *Frontiers in cellular and infection microbiology*, 16, 1760018.

Rivera I, et al. (2026) Phylogenomic framework and virulence gene boundaries of emerging Shiga toxin-producing *Escherichia coli* O118 informed by the comprehensive profiling of 359 O118 genomes. *Virulence*, 17(1), 2672206.

Wu J, et al. (2026) Translation control by altered start codon usage as a means of modulating the general stress response and virulence in *Listeria monocytogenes*. *PLoS genetics*, 22(4), e1011851.

Ruzickova M, et al. (2026) From ecology to evolution: plasmid- and colicin-mediated persistence of antibiotic-resistant *Escherichia coli* in gulls. *mSystems*, 11(2), e0166325.

Prasad S, et al. (2026) IncL plasmid-mediated dissemination of OXA-48 β -lactamase and bla CTX-M-15 gene amplification identified via long-read sequencing in carbapenem-resistant Enterobacterales. *JAC-antimicrobial resistance*, 8(1), dlaf254.

Safari M, et al. (2026) Comprehensive genomic analysis of a novel *Bacillus cereus* decomposing toluene potentially applicable in bioremediation. *Microbiology spectrum*, 14(1), e0289224.

Kumar R, et al. (2026) Pathogenesis and genome characterization of translucent post-larvae disease-causing *Vibrio parahaemolyticus* in *Litopenaeus vannamei*. *Current research in microbial sciences*, 11, 100634.

Shin GY, et al. (2026) Comparative genomics of *Pantoea allii* lineages and distribution of ecologically relevant traits. *Microbial genomics*, 12(2).

Xia P, et al. (2026) Within-host evolution drives the emergence of ceftazidime-avibactam resistance mediated by IncN plasmid-encoded blaNDM-1 and blaKPC-33 in ST11-KL64

hypervirulent *Klebsiella pneumoniae*. *Microbiology spectrum*, 14(4), e0236725.

Oforu Appiah F, et al. (2026) Genomic landscape of blaNDM-1- and blaOXA-181-carrying *Citrobacter portucalensis* sequence type 151 strains from hospital wastewater in Ghana. *Applied and environmental microbiology*, 92(4), e0210825.

de Larminat J, et al. (2026) Hemolytic Uremic Syndrome Outbreak in Adults and Shiga Toxin-Producing *Escherichia coli* Negative for Locus of Enterocyte Effacement, France, 2025. *Emerging infectious diseases*, 32(4), 592.

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).

Massacci FR, et al. (2026) Occurrence of oxazolidinone resistance genes in enterococci, staphylococci, and *Mammaliococcus sciuri* from swine slaughterhouse wastewater, Italy. *World journal of microbiology & biotechnology*, 42(5).

Chen T, et al. (2026) Genomic analyses identify nosocomial transmission of ST23 carbapenem-resistant hypervirulent *Klebsiella pneumoniae* mediated by a conjugative IncFIIK2 NDM-1 plasmid. *Virulence*, 17(1), 2668167.

Chu Y, et al. (2026) Swine wastewater drives dissemination of high-risk bla NDM-positive *Escherichia coli* clones. *Frontiers in microbiology*, 17, 1842719.

Tao J, et al. (2026) Identification of a novel SXT/R391 integrative and conjugative element harboring bla NDM-1 in a clinical *Providencia huaxiensis* isolate. *Frontiers in microbiology*, 17, 1818759.

Wan Y, et al. (2026) Genomic and molecular characterisation of a KPC-producing *Klebsiella pneumoniae* clinical isolate resistant to meropenem-vaborbactam, imipenem-relebactam, and ceftazidime-avibactam. *BMC genomic data*, 27(1).

Wei X, et al. (2026) Characterization and antibacterial efficacy of the broad-host-range phage P108 against biofilm-forming and methicillin-resistant *Staphylococcus aureus*. *Virus research*, 368, 199745.