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

Keywords: bio.tools

Funding:

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: 20250410T065625+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 457 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Pla-Díaz M, et al. (2025) Insights into Treponema pallidum genomics from modern and ancient genomes using a novel mapping strategy. BMC biology, 23(1), 7.

Liu R, et al. (2025) Biochemical properties and substrate specificity of GOB-38 in Elizabethkingia anophelis. Scientific reports, 15(1), 351.

Rodwell EV, et al. (2025) Hybrid strains of enterotoxigenic/Shiga toxin-producing Escherichia coli, United Kingdom, 2014-2023. Journal of medical microbiology, 74(1).

Elizondo-Reyna E, et al. (2025) Insights from a Genome-Wide Study of Pantoea agglomerans UADEC20: A Promising Strain for Phosphate Solubilization and Exopolysaccharides Production. Current issues in molecular biology, 47(1).

Zamunér CFC, et al. (2025) Evolution and spread of Xanthomonas citri subsp. citri in the São Paulo, Brazil, citrus belt inferred from 758 novel genomes. Microbial genomics, 11(1).

Wang W, et al. (2024) Emergence and genomic characteristics of multi-drug-resistant Salmonella in pet turtles and children with diarrhoea. Microbial genomics, 10(1).

Sattler J, et al. (2024) OXA-48-like carbapenemases in Proteus mirabilis - novel genetic environments and a challenge for detection. Emerging microbes & infections, 13(1), 2353310.

Moussa J, et al. (2024) Characterization of blaNDM-19-producing IncX3 plasmid isolated from carbapenem-resistant Escherichia coli and Klebsiellapneumoniae. Heliyon, 10(8), e29642.

Liu J, et al. (2024) Emergence of a novel sequence type carbapenem-resistant hypervirulent Klebsiella pneumoniae ST6417 harboring blaNDM-5 on the IncX3 plasmid. Microbiology spectrum, 12(10), e0098424.

Handy NB, et al. (2024) Hierarchical determinants in cytotoxic necrotizing factor (CNF) toxins driving Rho G-protein deamidation versus transglutamination. mBio, 15(7), e0122124.

Jiang L, et al. (2024) Analysis of the recombination and evolution of the new type mutant pseudorabies virus XJ5 in China. BMC genomics, 25(1), 752.

Böer T, et al. (2024) Isolation and characterization of novel acetogenic Moorella strains for employment as potential thermophilic biocatalysts. FEMS microbiology ecology, 100(9).

Burger NFV, et al. (2024) Host-specific co-evolution likely driven by diet in Buchnera aphidicola. BMC genomics, 25(1), 153.

Sattar F, et al. (2024) Analyzing Antibiotic Resistance in Bacteria from Wastewater in Pakistan Using Whole-Genome Sequencing. Antibiotics (Basel, Switzerland), 13(10).

Manfreda C, et al. (2024) Rare Plasmid-Mediated AmpC Beta-Lactamase DHA-1 Located on Easy Mobilized IS26-Related Genetic Element Detected in Escherichia coli from Livestock and Food in Germany. Microorganisms, 12(3).

Teng G, et al. (2024) Adaptive attenuation of virulence in hypervirulent carbapenem-resistant Klebsiella pneumoniae. mSystems, 9(6), e0136323.

Greig DR, et al. (2024) Genomic analysis of an outbreak of Shiga toxin-producing Escherichia coli O183:H18 in the United Kingdom, 2023. Microbial genomics, 10(5).

Vilela FP, et al. (2024) Comparative genomics reveals high genetic similarity among strains of Salmonella enterica serovar Infantis isolated from multiple sources in Brazil. PeerJ, 12, e17306.

Liu C, et al. (2024) Phenotypic and genomic characteristics of clinical IMP-producing Klebsiella spp. Isolates in China. Communications medicine, 4(1), 25.

Moura Q, et al. (2024) Genomic Features of an MDR Escherichia coli ST5506 Harboring an IncHI2/In229/blaCTX-M-2 Array Isolated from a Migratory Black Skimmer. Pathogens (Basel, Switzerland), 13(1).