Resource Summary Report

Generated by <u>dkNET</u> on May 6, 2025

Bandage

RRID:SCR_022772 Type: Tool

Proper Citation

Bandage (RRID:SCR_022772)

Resource Information

URL: http://rrwick.github.io/Bandage/

Proper Citation: Bandage (RRID:SCR_022772)

Description: Software tool for visualising de novo assembly graphs. By displaying connections which are not present in contigs file, opens up new possibilities for analysing de novo assemblies. Used for interactive visualization of de novo genome assemblies.

Synonyms: Bioinformatics Application for Navigating De novo Assembly Graphs Easily

Resource Type: software application, data analysis software, software resource, data processing software

Defining Citation: PMID:26099265

Keywords: interactive visualization, de novo genome assemblies, visualising de novo assembly graphs, analysing de novo assemblies

Funding:

Availability: Free, Available for download, Freely available

Resource Name: Bandage

Resource ID: SCR_022772

Alternate IDs: OMICS_09013

Alternate URLs: https://github.com/rrwick/Bandage, https://sources.debian.org/src/bandage/

License: GNU GPL v3

Record Creation Time: 20220922T050155+0000

Record Last Update: 20250505T054822+0000

Ratings and Alerts

No rating or validation information has been found for Bandage.

No alerts have been found for Bandage.

Data and Source Information

Source: <u>SciCrunch Registry</u>

Usage and Citation Metrics

We found 11 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>dkNET</u>.

Goldberg JK, et al. (2024) A long-read draft assembly of the Chinese mantis (Mantodea: Mantidae: Tenodera sinensis) genome reveals patterns of ion channel gain and loss across Arthropoda. G3 (Bethesda, Md.), 14(6).

Zhou Y, et al. (2024) Pan-genome analysis of Streptococcus suis serotype 2 highlights genes associated with virulence and antibiotic resistance. Frontiers in microbiology, 15, 1362316.

Fuga B, et al. (2024) Hybrid genome assembly of colistin-resistant mcr-1.5-producing Escherichia coli ST354 reveals phylogenomic pattern associated with urinary tract infections in Brazil. Journal of global antimicrobial resistance, 37, 37.

Peng D, et al. (2024) The telomere-to-telomere (T2T) genome provides insights into the evolution of specialized centromere sequences in sandalwood. GigaScience, 13.

Feng X, et al. (2023) Complete genome sequence of Mycolicibacterium mageritense strain H4_3_1 isolated from a hybrid biological-inorganic system reactor. Microbiology resource announcements, 12(10), e0023023.

Botelho J, et al. (2023) Phylogroup-specific variation shapes the clustering of antimicrobial resistance genes and defence systems across regions of genome plasticity in Pseudomonas aeruginosa. EBioMedicine, 90, 104532.

Volpe E, et al. (2023) The complete diploid reference genome of RPE-1 identifies human

phased epigenetic landscapes. bioRxiv : the preprint server for biology.

Colombini L, et al. (2023) The mobilome of Lactobacillus crispatus M247 includes two novel genetic elements: Tn7088 coding for a putative bacteriocin and the siphovirus prophage ?M247. Microbial genomics, 9(12).

Feng X, et al. (2023) Complete genome sequence of an Achromobacter xylosoxidans strain H1_3_1 isolated from a hybrid biological-inorganic system reactor. Microbiology resource announcements, 12(11), e0061223.

Yang T, et al. (2023) Chloroplast Genomes and Phylogenetic Analysis of Three Carthamus (Asteraceae) Species. International journal of molecular sciences, 24(21).

Zhang Y, et al. (2022) Improved microbial genomes and gene catalog of the chicken gut from metagenomic sequencing of high-fidelity long reads. GigaScience, 11.