

Resource Summary Report

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Bandage

RRID:SCR_022772

Type: Tool

Proper Citation

Bandage (RRID:SCR_022772)

Resource Information

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

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

Defining Citation: [PMID:26099265](#)

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

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: 20260801T190801+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: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 21 mentions in open access literature.

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

Rahman SIA, et al. (2025) Genomic insights into a diarrheal outbreak in Bangladesh reveal novel ETEC lineages and expansion of CS23 colonization factor. *Microbiology spectrum*, 13(10), e0331524.

Nowbandegani PS, et al. (2025) Defining and cataloging variants in pangenome graphs. *bioRxiv : the preprint server for biology*.

Kumar V, et al. (2025) Whole genome sequencing and assembly of the house sparrow, *Passer domesticus*. *GigaByte (Hong Kong, China)*, 2025, gigabyte161.

Colombini L, et al. (2025) A 69.9-kb long inverted repeat increases genome instability in a strain of *Lactobacillus crispatus*. *NAR genomics and bioinformatics*, 7(2), lqaf085.

Arcari G, et al. (2025) Post-pandemic upsurge in Group A *Streptococcus* infections at an Italian tertiary university hospital. *Microbiology spectrum*, 13(5), e0249424.

Zaman SAU, et al. (2025) Whole genome of petroleum hydrocarbon degrading *Rhodococcus indonesiensis* isolated from Nacharam, Hyderabad, India. *Scientific reports*, 16(1), 165.

Spurgeon K, et al. (2025) Complete genome sequence of *Prevotella histicola* T05-04. *Microbiology resource announcements*, 14(6), e0014425.

Zhang S, et al. (2025) Mitochondrial genome assembly and comparative analysis of decaploid *Camellia hainanica*. *Frontiers in plant science*, 16, 1556379.

Volpe E, et al. (2025) The reference genome of the human diploid cell line RPE-1. *Nature communications*, 16(1), 7751.

Sia CM, et al. (2025) Distinct adaptation and epidemiological success of different genotypes within *Salmonella enterica* serovar Dublin. *eLife*, 13.

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.

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.

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).

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 ϕ M247. *Microbial genomics*, 9(12).

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

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.