

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 8, 2026

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 analysis software, data processing 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: 20260905T133016+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 27 mentions in open access literature.

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

Gu YY, et al. (2026) The complete mitochondrial genome analysis of *Elachiptera decipiens* (Loew, 1863) (Diptera: Chloropidae). *Mitochondrial DNA. Part B, Resources*, 11(5), 599.

Duan M, et al. (2026) Mitochondrial genomes of two subspecies of *Citellophilus tesquorum*: Insights into the molecular evolution and phylogenetic analysis within Siphonaptera. *Frontiers in veterinary science*, 13, 1785674.

Colombini L, et al. (2026) The novel pseudo-compound transposon Tn7086 carries aminoglycoside resistance genes in *Enterococcus faecalis*. *Microbial genomics*, 12(4).

Tang S, et al. (2026) Mitogenomic analysis of *Palaeopsylla remota* and *Frontopsylla elata elata* with implications for the phylogeny of Siphonaptera. *Frontiers in veterinary science*, 13, 1722404.

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*.

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.

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

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

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

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

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

Cui X, et al. (2025) Description and phylogenetic analysis of the complete mitochondrial genome of Reeves' muntjac, *Muntiacus reevesi* Ogilby, 1839 (Artiodactyla; Cervidae), from Chongqing, China. *Mitochondrial DNA. Part B, Resources*, 10(12), 1126.

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

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

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

Zhai S, et al. (2024) Mitochondrial Genome Assembly and Comparative Analysis of *Chionanthus Retusus* (Oleaceae). *Genes*, 15(12).

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.