

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

Bridger

RRID:SCR_017039

Type: Tool

Proper Citation

Bridger (RRID:SCR_017039)

Resource Information

URL: https://github.com/fmaguire/Bridger_Assembler

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Description: Software package as de novo transcriptome assembler for RNA-Seq data. Framework for de novo transcriptome assembly using RNA-seq data. Can assemble all transcripts from short reads without using reference. Input RNA-Seq reads in fasta or fastq format, and output all assembled candidate transcripts in fasta format. Operating system Unix/Linux.

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

Defining Citation: [PMID:25723335](#)

Keywords: de novo, transcripto, assembler, RNAseq, data, short, read, sequencing, bio.tools

Funding: NSFC 61432010;
NSFC 61272016;
NCRR P20 RR016460;
NIGMS P20 GM103429

Availability: Free, Available for download, Freely available

Resource Name: Bridger

Resource ID: SCR_017039

Alternate IDs: biotools:bridger, OMICS_07535

Alternate URLs: <https://bio.tools/bridger>

Record Creation Time: 20220129T080333+0000

Ratings and Alerts

No rating or validation information has been found for Bridger.

No alerts have been found for Bridger.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Wang Z, et al. (2022) Chromosome-level genome assembly of the black widow spider *Latrodectus elegans* illuminates composition and evolution of venom and silk proteins. *GigaScience*, 11.

Raghavan V, et al. (2022) A simple guide to de novo transcriptome assembly and annotation. *Briefings in bioinformatics*, 23(2).

Tang B, et al. (2020) Chromosome-level genome assembly reveals the unique genome evolution of the swimming crab (*Portunus trituberculatus*). *GigaScience*, 9(1).

Li Y, et al. (2019) Chromosome-level assembly of the mustache toad genome using third-generation DNA sequencing and Hi-C analysis. *GigaScience*, 8(9).

Cheng S, et al. (2019) Genomes of Subaerial Zygnematophyceae Provide Insights into Land Plant Evolution. *Cell*, 179(5), 1057.

Bushmanova E, et al. (2019) rnaSPAdes: a de novo transcriptome assembler and its application to RNA-Seq data. *GigaScience*, 8(9).