

Resource Summary Report

Generated by [kravitz2](#) on Aug 12, 2026

DENTIST

RRID:SCR_021856

Type: Tool

Proper Citation

DENTIST (RRID:SCR_021856)

Resource Information

URL: <https://github.com/a-ludi/dentist>

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Description: Software as automated pipeline method to close gaps in assemblies with long reads. Used to close assembly gaps using long reads at high accuracy.

Resource Type: software toolkit, software resource

Defining Citation: [DOI:10.1101/2021.02.26.432990](https://doi.org/10.1101/2021.02.26.432990)

Keywords: genome assembly, long sequencing reads, assembly gaps

Availability: Free, Available for download, Freely available

Resource Name: DENTIST

Resource ID: SCR_021856

Alternate IDs: biotools:dentist

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

License: MIT License

Record Creation Time: 20220129T080357+0000

Record Last Update: 20260810T040806+0000

Ratings and Alerts

No rating or validation information has been found for DENTIST.

No alerts have been found for DENTIST.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Ludwig A, et al. (2022) DENTIST-using long reads for closing assembly gaps at high accuracy. GigaScience, 11.