

Resource Summary Report

Generated by PRECISE-TBI on Sep 8, 2026

LMAS

RRID:SCR_022251

Type: Tool

Proper Citation

LMAS (RRID:SCR_022251)

Resource Information

URL: <https://github.com/B-UMMI/LMAS>

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Description: Automated workflow enabling benchmarking of traditional and metagenomic prokaryotic de novo assembly software using defined mock communities. Results are presented in interactive HTML report where selected global and reference specific performance metrics can be explored.

Synonyms: Last (Meta)Genomic Assembler Standing

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

Keywords: Shotgun metagenomics, genomic assembler

Availability: Free, Available for download, Freely available

Resource Name: LMAS

Resource ID: SCR_022251

License: GNU GPL v3.0

Record Creation Time: 20220506T050143+0000

Record Last Update: 20260905T133012+0000

Ratings and Alerts

No rating or validation information has been found for LMAS.

No alerts have been found for LMAS.

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 [PRECISE-TBI](#) .

Mendes CI, et al. (2022) LMAS: evaluating metagenomic short de novo assembly methods through defined communities. GigaScience, 12.