

Resource Summary Report

Generated by [nidm-terms](#) on Aug 30, 2026

DepthSizer

RRID:SCR_021232

Type: Tool

Proper Citation

DepthSizer (RRID:SCR_021232)

Resource Information

URL: <https://github.com/slimsuite/depthsizer>

Proper Citation: DepthSizer (RRID:SCR_021232)

Description: Software tool for read-depth based genome size prediction. Wrapper for genome size estimate methods of Diploidocus. Uses long read depth of coverage and BUSCO single copy orthologue prediction to estimate genome size.

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

Keywords: Genome size prediction, genome size estimate wrapper, estimate genome size

Availability: Free, Available for download, Freely available

Resource Name: DepthSizer

Resource ID: SCR_021232

License: GNU GPL v3.0

Record Creation Time: 20220129T080354+0000

Record Last Update: 20260829T182714+0000

Ratings and Alerts

No rating or validation information has been found for DepthSizer.

No alerts have been found for DepthSizer.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

M??rquez R, et al. (2025) A draft genome assembly for the dart-poison frog *Phyllobates terribilis*. GigaByte (Hong Kong, China), 2025, gigabyte157.

Chen SH, et al. (2022) A high-quality pseudo-phased genome for *Melaleuca quinquenervia* shows allelic diversity of NLR-type resistance genes. GigaScience, 12.