

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

Mapsembler2

RRID:SCR_024102

Type: Tool

Proper Citation

Mapsembler2 (RRID:SCR_024102)

Resource Information

URL: <http://colibread.inria.fr/software/mapsembler2/>

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Description: Targeted assembly software. It takes as input any number of NGS raw read sets and starter set of input sequences. May be used to Validate assembled sequence, Check if known enzyme is present in metagenomic NGS read set, Enrich unmappable reads by extending them, Check what happens at the extremities of a contig, Check the presence / absence and quantify RNA seq splicing events, Check presence/absence of SNPs or structural variants.

Synonyms: mapsembler2, Mapsembler

Resource Type: software library, software resource, software toolkit

Defining Citation: [PMID:22443449](#)

Keywords: Targeted assembly, NGS raw read, input sequences,

Availability: Free, Available for download, Freely available,

Resource Name: Mapsembler2

Resource ID: SCR_024102

Alternate IDs: OMICS_18310

Alternate URLs: <https://sources.debian.org/src/mapsembler2/>

License: GNU Affero General Public License

Record Creation Time: 20230824T050212+0000

Record Last Update: 20260905T133104+0000

Ratings and Alerts

No rating or validation information has been found for Mapsembler2.

No alerts have been found for Mapsembler2.

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 [Kravitz](#) .

Sass C, et al. (2016) Revisiting the Zingiberales: using multiplexed exon capture to resolve ancient and recent phylogenetic splits in a charismatic plant lineage. PeerJ, 4, e1584.