

Resource Summary Report

Generated by [NIF](#) on Sep 3, 2026

GMcloser

RRID:SCR_000646

Type: Tool

Proper Citation

GMcloser (RRID:SCR_000646)

Resource Information

URL: <http://sourceforge.net/projects/gmcloser/>

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Description: Software that fills and closes the gaps present in scaffold assemblies, especially those generated by the de novo assembly of whole genomes with next-generation sequencing (NGS) reads. Unlike other gap-closing tools that use only NGS reads, GMcloser uses preassembled contig sets or long read sets as the sequences to close gaps and uses paired-end (PE) reads and a likelihood-based algorithm to improve the accuracy and efficiency of gap closure. The efficiency of gap closure can be increased by successive treatments with different contig sets.

Abbreviations: GMcloser

Synonyms: Gmcloser - Closing the gaps in scaffolds with preassembled contigs

Resource Type: software resource

Defining Citation: [PMID:26261222](#)

Keywords: scaffolding, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: GMcloser

Resource ID: SCR_000646

Alternate IDs: biotools:gmcloser, OMICS_00042

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

Record Creation Time: 20220129T080202+0000

Record Last Update: 20260829T182033+0000

Ratings and Alerts

No rating or validation information has been found for GMcloser.

No alerts have been found for GMcloser.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Shirasawa K, et al. (2021) A chromosome-scale draft genome sequence of horsegram (*Macrotyloma uniflorum*). GigaByte (Hong Kong, China), 2021, gigabyte30.

Xu M, et al. (2020) TGS-GapCloser: A fast and accurate gap closer for large genomes with low coverage of error-prone long reads. GigaScience, 9(9).

Roscito JG, et al. (2018) The genome of the tegu lizard *Salvator merianae*: combining Illumina, PacBio, and optical mapping data to generate a highly contiguous assembly. GigaScience, 7(12).