

Resource Summary Report

Generated by PRECISE-TBI on Jul 30, 2026

Marvel

RRID:SCR_017621

Type: Tool

Proper Citation

Marvel (RRID:SCR_017621)

Resource Information

URL: <https://github.com/schloi/MARVEL>

Proper Citation: Marvel (RRID:SCR_017621)

Description: Software set of tools that facilitate overlapping, patching, correction and assembly of noisy long reads.

Resource Type: software application, software toolkit, software resource, data processing software, alignment software, image analysis software

Keywords: Overlapping, patching, correction, assembly, noisy, long, read, sequence, align

Availability: Free, Available for download, Freely available

Resource Name: Marvel

Resource ID: SCR_017621

License: <https://github.com/schloi/MARVEL/blob/master/LICENSE>

Record Creation Time: 20220129T080336+0000

Record Last Update: 20260729T044431+0000

Ratings and Alerts

No rating or validation information has been found for Marvel .

No alerts have been found for Marvel .

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 [PRECISE-TBI](#) .

Meyer A, et al. (2021) Giant lungfish genome elucidates the conquest of land by vertebrates. Nature, 590(7845), 284.

Wang W, et al. (2020) The draft nuclear genome assembly of Eucalyptus pauciflora: a pipeline for comparing de novo assemblies. GigaScience, 9(1).