

# Resource Summary Report

Generated by [FDI Lab - SciCrunch.org](#) on May 4, 2025

## 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:** image analysis software, alignment software, software application, software resource, data processing software, software toolkit

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

**Funding:**

**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:** 20250503T060728+0000

### Ratings and Alerts

No rating or validation information has been found for Marvel .

No alerts have been found for Marvel .

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 2 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [FDI Lab - SciCrunch.org](#).

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).