

# Resource Summary Report

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

## ScaffMatch

RRID:SCR\_017025

Type: Tool

### Proper Citation

ScaffMatch (RRID:SCR\_017025)

### Resource Information

**URL:** <https://github.com/mandricigor/ScaffMatch>

**Proper Citation:** ScaffMatch (RRID:SCR\_017025)

**Description:** Software tool as scaffolding algorithm based on maximum weight matching able to produce high quality scaffolds from next generation sequencing data (reads and contigs). Able to handle reads with both short and long insert sizes.

**Resource Type:** data processing software, software application, software resource

**Defining Citation:** [PMID:25890305](#)

**Keywords:** scaffolding, algorithm, maximum, weight, matching, next, generation, sequencing, data, read, contig, bio.tools

**Funding:** NSF IIS 0916401

**Availability:** Free, Available for download, Freely available

**Resource Name:** ScaffMatch

**Resource ID:** SCR\_017025

**Alternate IDs:** biotools:scaffmatch, OMICS\_08198

**Alternate URLs:** <http://alan.cs.gsu.edu/NGS/?q=content/scaffmatch>,  
<https://bio.tools/scaffmatch>

**License:** MIT License

**Record Creation Time:** 20220129T080333+0000

**Record Last Update:** 20260905T133052+0000

### Ratings and Alerts

No rating or validation information has been found for ScaffMatch.

No alerts have been found for ScaffMatch.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Parisot N, et al. (2021) The transposable element-rich genome of the cereal pest Sitophilus oryzae. BMC biology, 19(1), 241.