# **Resource Summary Report**

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# **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: software application, software resource, data processing software

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: 20250502T060425+0000

## **Ratings and Alerts**

No rating or validation information has been found for ScaffMatch.

No alerts have been found for ScaffMatch.

## Data and Source Information

Source: <u>SciCrunch Registry</u>

#### **Usage and Citation Metrics**

We found 1 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>NIF</u>.

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