

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: data processing software, software resource, software application

Defining Citation: [PMID:25890305](https://pubmed.ncbi.nlm.nih.gov/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: 20250423T060940+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: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

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