

Resource Summary Report

Generated by [NIF](#) on Sep 3, 2026

Cross-species scaffolding

RRID:SCR_015932

Type: Tool

Proper Citation

Cross-species scaffolding (RRID:SCR_015932)

Resource Information

URL: <https://github.com/thackl/cross-species-scaffolding>

Proper Citation: Cross-species scaffolding (RRID:SCR_015932)

Description: Software that generates in silico mate-pair reads from single-/paired-end reads of your organism of interest, and a closely related reference genome. It can improve draft genomes by using preferred scaffolding software with the newly created read data. Software that generates in silico mate-pair reads from single-/paired-end reads of your organism of interest, and a closely related reference genome. It can improve draft genomes by using preferred scaffolding software with the newly created read data. Super-scaffolding of draft genome assemblies with in silico mate-pair libraries derived from (closely) related references.

Synonyms: cross-species-scaffolding

Resource Type: data analysis software, data processing software, sequence analysis software, software application, software resource, source code

Keywords: mate, pair, end, reference, genome

Availability: Free, Available for download, Freely available

Resource Name: Cross-species scaffolding

Resource ID: SCR_015932

Alternate IDs: SCR_016125

License: MIT License

Record Creation Time: 20220129T080328+0000

Record Last Update: 20260903T235339+0000

Ratings and Alerts

No rating or validation information has been found for Cross-species scaffolding.

No alerts have been found for Cross-species scaffolding.

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 [NIF](#) .

Grau JH, et al. (2018) Improving draft genome contiguity with reference-derived in silico mate-pair libraries. GigaScience, 7(5).