

Resource Summary Report

Generated by [ASWG](#) on Aug 25, 2026

PAFScaff

RRID:SCR_017976

Type: Tool

Proper Citation

PAFScaff (RRID:SCR_017976)

Resource Information

URL: <https://github.com/slimsuite/pafscaff>

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Description: Software as Pairwise mApping Format reference based Scaffold anchoring and super scaffolding tool. Dsigned for mapping genome assembly scaffolds to closely related chromosome level reference genome assembly.

Synonyms: Pairwise mApping Format reference-based Scaffold

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

Keywords: Pairwise, mapping, reference, scaffold, genomics, scaffolding, assembly, genome, chromosome, bio.tools

Availability: Free, Freely available

Resource Name: PAFScaff

Resource ID: SCR_017976

Alternate IDs: biotools:PAFScaff

Alternate URLs: <https://github.com/slimsuite/pafscaff/blob/master/PAFScaff.md>, <https://slimsuite.github.io/pafscaff/>, <https://bio.tools/PAFScaff>

License: GNU General Public License v3.0

Record Creation Time: 20220129T080338+0000

Record Last Update: 20260821T194127+0000

Ratings and Alerts

No rating or validation information has been found for PAFScaff.

No alerts have been found for PAFScaff.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Field MA, et al. (2022) The Australian dingo is an early offshoot of modern breed dogs. Science advances, 8(16), eabm5944.

Edwards RJ, et al. (2021) Chromosome-length genome assembly and structural variations of the primal Basenji dog (Canis lupus familiaris) genome. BMC genomics, 22(1), 188.

Martin BT, et al. (2021) ClineHelpR: an R package for genomic cline outlier detection and visualization. BMC bioinformatics, 22(1), 501.

Field MA, et al. (2020) Canfam_GSD: De novo chromosome-length genome assembly of the German Shepherd Dog (Canis lupus familiaris) using a combination of long reads, optical mapping, and Hi-C. GigaScience, 9(4).