

Resource Summary Report

Generated by [SPARC SAWG](#) on Jul 30, 2026

Rascaf

RRID:SCR_022014

Type: Tool

Proper Citation

Rascaf (RRID:SCR_022014)

Resource Information

URL: <https://github.com/mourisl/Rascaf>

Proper Citation: Rascaf (RRID:SCR_022014)

Description: Software tool for scaffolding with RNA-seq read alignments. Used for improving genome assembly with RNA sequencing data.

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

Defining Citation: [DOI:10.3835/plantgenome2016.03.0027](https://doi.org/10.3835/plantgenome2016.03.0027)

Keywords: Scaffolding, RNA-seq data, scaffolding with RNAseq read alignments, improving genome assembly, RNA sequencing data

Funding: NSF IOS1339134

Availability: Free, Available for download, Freely available

Resource Name: Rascaf

Resource ID: SCR_022014

License: GPL-2.0 License

Record Creation Time: 20220421T050138+0000

Record Last Update: 20260727T040740+0000

Ratings and Alerts

No rating or validation information has been found for Rascaf.

No alerts have been found for Rascaf.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Miller J, et al. (2022) Chromosome-level genome and the identification of sex chromosomes in *Uloborus diversus*. *GigaScience*, 12.

Pickett BD, et al. (2022) Genome assembly of the roundjaw bonefish (*Albula glossodonta*), a vulnerable circumtropical sportfish. *GigaByte* (Hong Kong, China), 2022, gigabyte44.

Pickett BD, et al. (2022) The genome of a giant (trevally): *Caranx ignobilis*. *GigaByte* (Hong Kong, China), 2022, gigabyte67.