

# Resource Summary Report

Generated by [dkNET](#) on Sep 17, 2026

## FastMulRFS

RRID:SCR\_024505

Type: Tool

### Proper Citation

FastMulRFS (RRID:SCR\_024505)

### Resource Information

**URL:** <https://github.com/ekmolloy/fastmulrfs>

**Proper Citation:** FastMulRFS (RRID:SCR\_024505)

**Description:** Software pipeline for estimating species trees from multi copy gene trees.

**Resource Type:** software resource, software toolkit

**Defining Citation:** [PMID:32657396](#)

**Keywords:** estimating species trees, multi copy gene trees,

**Availability:** Free, Available for download, Freely available

**Resource Name:** FastMulRFS

**Resource ID:** SCR\_024505

**License:** 3-Clause BSD

**Record Creation Time:** 20231002T161336+0000

**Record Last Update:** 20260912T200118+0000

### Ratings and Alerts

No rating or validation information has been found for FastMulRFS.

No alerts have been found for FastMulRFS.

### 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 [dkNET](#) .

Morel B, et al. (2022) SpeciesRax: A Tool for Maximum Likelihood Species Tree Inference from Gene Family Trees under Duplication, Transfer, and Loss. Molecular biology and evolution, 39(2).