

# Resource Summary Report

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

## Fastphylo

RRID:SCR\_012068

Type: Tool

### Proper Citation

Fastphylo (RRID:SCR\_012068)

### Resource Information

**URL:** <http://fastphylo.sourceforge.net/>

**Proper Citation:** Fastphylo (RRID:SCR\_012068)

**Description:** A software package containing implementations of efficient algorithms for two common problems in phylogenetics: estimating DNA/protein sequence distances and reconstructing a phylogeny from a distance matrix.

**Resource Type:** software resource

**Defining Citation:** [PMID:24255987](#)

**Keywords:** applet

**Resource Name:** Fastphylo

**Resource ID:** SCR\_012068

**Alternate IDs:** OMICS\_04248

**Record Creation Time:** 20220129T080308+0000

**Record Last Update:** 20260912T195744+0000

### Ratings and Alerts

No rating or validation information has been found for Fastphylo.

No alerts have been found for Fastphylo.

### Data and Source Information

**Source:** [SciCrunch Registry](#)

## Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Barragan AC, et al. (2021) A Truncated Singleton NLR Causes Hybrid Necrosis in *Arabidopsis thaliana*. *Molecular biology and evolution*, 38(2), 557.

Kelemen RK, et al. (2018) Complex History and Differentiation Patterns of the t-Haplotype, a Mouse Meiotic Driver. *Genetics*, 208(1), 365.