# Resource Summary Report

Generated by RRID on Apr 11, 2025

# Fastphylo

RRID:SCR_012068
Type: Tool

## Proper Citation

Fastphylo (RRID:SCR_012068)

## Resource Information

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

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**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

**Funding:**

**Resource Name:** Fastphylo

**Resource ID:** SCR_012068

**Alternate IDs:** OMICS_04248

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

**Record Last Update:** 20250410T070228+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 RRID.

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.