## **Resource Summary Report**

Generated by FDI Lab - SciCrunch.org on May 15, 2025

# **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

**Funding:** 

Resource Name: Fastphylo

Resource ID: SCR\_012068

Alternate IDs: OMICS\_04248

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

**Record Last Update:** 20250420T014605+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 FDI Lab - SciCrunch.org.

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.