

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 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: 20260905T132719+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 [Kravitz](#) .

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.