

Resource Summary Report

Generated by [RRID](#) on Aug 4, 2026

PHYLOG

RRID:SCR_024487

Type: Tool

Proper Citation

PHYLOG (RRID:SCR_024487)

Resource Information

URL: <http://pbil.univ-lyon1.fr/software/phylog/>

Proper Citation: PHYLOG (RRID:SCR_024487)

Description: Software tool to simultaneously build gene and species trees when gene families have undergone duplications and losses. Can analyze thousands of gene families in dozens of genomes simultaneously.

Resource Type: data processing software, software application, software resource, data analysis software

Defining Citation: [PMID:23132911](#)

Keywords: probabilistic model, reconstruct species tree and all corresponding gene trees, build gene and species trees, gene families analysis, genomes analysis simultaneously, gene families duplications and losses,

Availability: Free, Freely available

Resource Name: PHYLOG

Resource ID: SCR_024487

Record Creation Time: 20231002T161336+0000

Record Last Update: 20260805T044531+0000

Ratings and Alerts

No rating or validation information has been found for PHYLOG.

No alerts have been found for PHYLOG.

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 [RRID](#) .

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).