

# Resource Summary Report

Generated by [SPARC SAWG](#) on Aug 1, 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, data analysis software, software application, software resource

**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:** 20260801T042926+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 [SPARC SAWG](#) .

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).