

Resource Summary Report

Generated by [kravitz2](#) on Aug 21, 2026

[phyloscanner](#)

RRID:SCR_017400

Type: Tool

Proper Citation

phyloscanner (RRID:SCR_017400)

Resource Information

URL: <https://github.com/BDI-pathogens/phyloscanner>

Proper Citation: phyloscanner (RRID:SCR_017400)

Description: Software tool for analysing pathogen genetic diversity and relationships between and within hosts at once, in windows along genome. Inferring transmission from within and between host pathogen genetic diversity.

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

Defining Citation: [PMID:29186559](#)

Keywords: Analysing, pathogen, genetic, diversity, relationship, host, genome

Funding: Bill & Melinda Gates Foundation ;
ERC Advanced Grant ;
Medical Research Council

Availability: Free, Available for download, Freely available

Resource Name: phyloscanner

Resource ID: SCR_017400

License: GNU GPL v3

Record Creation Time: 20220129T080335+0000

Record Last Update: 20260821T194115+0000

Ratings and Alerts

No rating or validation information has been found for phyloscanner.

No alerts have been found for phyloscanner.

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 [kravitz2](#) .

Hall M, et al. (2026) The age and sex dynamics of heterosexual HIV transmission in Zambia: an HPTN 071 (PopART) phylogenetic and modelling study. medRxiv : the preprint server for health sciences.

Ratmann O, et al. (2020) Quantifying HIV transmission flow between high-prevalence hotspots and surrounding communities: a population-based study in Rakai, Uganda. The lancet. HIV, 7(3), e173.