

Resource Summary Report

Generated by [dkNET](#) on Sep 12, 2026

HomoplasyFinder

RRID:SCR_017300

Type: Tool

Proper Citation

HomoplasyFinder (RRID:SCR_017300)

Resource Information

URL: <https://github.com/JosephCrispell/homoplasyFinder/wiki>

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Description: Software tool to identify and annotate homoplasies on phylogeny and sequence alignment. Used to automatically identify any homoplasies present in simulated and real phylogenetic data. Java application that can be used as standalone tool or within statistical programming environment R.

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

Defining Citation: [PMID:30663960](#)

Keywords: homoplasy, phylogeny, sequence, alignment, identify, data, annotate

Funding: Science Foundation Ireland

Availability: Free, Available for download, Freely available

Resource Name: HomoplasyFinder

Resource ID: SCR_017300

Alternate URLs: <https://github.com/JosephCrispell/homoplasyFinder>

License: GPL v3

Record Creation Time: 20220129T080334+0000

Record Last Update: 20260912T195851+0000

Ratings and Alerts

No rating or validation information has been found for HomoplasyFinder.

No alerts have been found for HomoplasyFinder.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6 mentions in open access literature.

Listed below are recent publications. The full list is available at [dkNET](#) .

Wu Y, et al. (2025) Hotspots of genetic change in *Yersinia pestis*. *Nature communications*, 16(1), 388.

Batisti Biffignandi G, et al. (2024) Optimising machine learning prediction of minimum inhibitory concentrations in *Klebsiella pneumoniae*. *Microbial genomics*, 10(3).

Dreyer V, et al. (2022) High fluoroquinolone resistance proportions among multidrug-resistant tuberculosis driven by dominant L2 *Mycobacterium tuberculosis* clones in the Mumbai Metropolitan Region. *Genome medicine*, 14(1), 95.

Merker M, et al. (2022) Transcontinental spread and evolution of *Mycobacterium tuberculosis* W148 European/Russian clade toward extensively drug resistant tuberculosis. *Nature communications*, 13(1), 5105.

Wan Y, et al. (2021) Alterations in chromosomal genes *nfsA*, *nfsB*, and *ribE* are associated with nitrofurantoin resistance in *Escherichia coli* from the United Kingdom. *Microbial genomics*, 7(12).

Crispell J, et al. (2019) Combining genomics and epidemiology to analyse bi-directional transmission of *Mycobacterium bovis* in a multi-host system. *eLife*, 8.