

Resource Summary Report

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OrthoFinder

RRID:SCR_017118

Type: Tool

Proper Citation

OrthoFinder (RRID:SCR_017118)

Resource Information

URL: <https://github.com/davidemms/OrthoFinder>

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Description: Software Python application for comparative genomics analysis. Finds orthogroups and orthologs, infers rooted gene trees for all orthogroups and identifies all of gene duplication events in those gene trees, infers rooted species tree for species being analysed and maps gene duplication events from gene trees to branches in species tree, improves orthogroup inference accuracy. Runs set of protein sequence files, one per species, in FASTA format.

Synonyms: OrthoFinder2, OrthoFinder

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

Defining Citation: [PMID:26243257](#), [DOI:10.1101/466201](#)

Keywords: comparative, genomic, analysis, find, orthogroup, ortholog, infer, gene, tree, duplicate, accuracy, protein, sequence, bio.tools

Funding: Bill and Melinda Gates Foundation ;
UKAID

Availability: Free, Available for download, Freely available

Resource Name: OrthoFinder

Resource ID: SCR_017118

Alternate IDs: biotools:OrthoFinder, OMICS_09733, BioTools:OrthoFinder

Alternate URLs: <https://bio.tools/OrthoFinder>, <https://bio.tools/OrthoFinder>,
<https://bio.tools/OrthoFinder>

License: GNU GPL v3

Record Creation Time: 20220129T080333+0000

Record Last Update: 20260905T133008+0000

Ratings and Alerts

No rating or validation information has been found for OrthoFinder.

No alerts have been found for OrthoFinder.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3413 mentions in open access literature.

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

Zeng L, et al. (2026) Functional genomics reveals key gene families and molecular pathways for extreme cold survival in the khapra beetle. BMC biology, 24(1).

Mao C, et al. (2026) Chromosome-level genome assembly and transcriptomes of the leaf insect Cryptophyllum westwoodii provide insights into the evolution of leaf-like masquerade. GigaScience, 15.

Liu H, et al. (2026) The genomes of 5 mantises provide insights into sex chromosome evolution and Mantodea phylogeny clarification. GigaScience, 15.

Yan L, et al. (2026) A NACHT domain-containing protein Ncp is required for appendage-associated unconventional protein secretion in the fungus Penicillium herquei. iScience, 29(7), 116464.

Nawae W, et al. (2026) Genome Assembly of Three Shrub Mangroves in the Genus Acanthus Reveals Two Polyploidy Events and Expansion of Genes Linked to Root Adaptation in Coastal Habitats. GigaScience, 15.

Szablińska-Piernik J, et al. (2026) Giant chromosomes of a tiny plant-the complete telomere-to-telomere genome assembly of the simple thalloid liverwort Apopellia endiviifolia (Jungermanniopsida, Marchantiophyta). GigaScience, 15.

Stratakis M, et al. (2026) Unravelling the thread of Podarcis omics; insights into the genome and transcriptome of the Cretan wall lizard. Genes & genomics, 48(1), 27.

Zhang T, et al. (2026) Phylogenomic profile of exon-intron organization across angiosperms, their relationships with protein domains, and functional implications. Nature communications, 17(1), 106.

Ma HY, et al. (2026) A pangenome insight into the genome divergence and flower color diversity among *Rhododendron* species. *BMC genomics*, 27(1), 101.

Kimbrel JA, et al. (2026) High-quality *Acinetobacter* genomes recovered from combat wounds via metagenomic sequencing resemble cultured isolate genomes. *Microbiology spectrum*, 14(1), e0187625.

Avni R, et al. (2026) A pangenome and pantranscriptome of hexaploid oat. *Nature*, 649(8095), 131.

Zhai J, et al. (2026) Genomic characteristics and risk factor analysis of carbapenem-non-susceptible *Pseudomonas aeruginosa* causing bacteremia in a tertiary hospital (2014-2023). *BMC microbiology*, 26(1).

Teramura A, et al. (2026) Silver chimaera genome highlights lineage-specific sex chromosome and opsin gene evolution in holocephalans. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 33(2).

Ploessl SG, et al. (2026) Evolutionary Transitions in Social Behavior are Associated With Convergent and Partially Reversible Expansions of Transcription Factor Binding Sites. *Genome biology and evolution*, 18(2).

Shao H, et al. (2026) Decoding the Pine Wood Nematode's survival mystery: Gene family expansion drives adaptation revealed by dual-omics. *PLoS pathogens*, 22(3), e1014033.

Akiyama M, et al. (2026) Cross-species gene redesign leveraging ortholog information and generative modeling. *Nature communications*, 17(1).

Shipova AA, et al. (2026) From Adam's rib: the Siberian moth's female W chromosome is derived from its Z counterpart. *Molecular biology and evolution*, 43(3).

Wolf M, et al. (2026) The genome of the relict earless monitor lizard, *Lanthanotus borneensis*, and the Toxicofera hypothesis. *BMC biology*, 24(1).

Katsuma S, et al. (2026) Identification of two *Wolbachia* genes with cell proliferation-inhibitory activity in *Ostrinia* cultured cells. *mBio*, 17(5), e0007426.

Wu Y, et al. (2026) Allelic structural variation at the NLR25-1 locus enhances defense against *Pseudomonas syringae* in kiwifruit. *Genome biology*, 27(1).