

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

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: 20260811T043549+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 [SPARC SAWG](#) .

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.

Jiménez-Castro L, et al. (2026) LUCID: An Integrative Approach for Target Discovery and dsRNA Design in Plant Fungal Pathogens. Plant biotechnology journal, 24(6), 3597.

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).

Barua A, et al. (2026) Estimates of molecular convergence reveal multiple genes with adaptive variation across teleost fish. *Molecular biology and evolution*, 43(1).

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

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.

Belay KH, et al. (2026) Genomic insights into *Ceratobasidium* sp. associated with vascular streak dieback of woody ornamentals in the United States using a metagenomic sequencing approach. *Microbiology spectrum*, 14(3), e0252325.

Gonzalez Ramos VM, et al. (2026) The Zn(II)₂Cys₆ transcription factor DsAce3 is a major activator of cellulases in the white-rot fungus *Dichomitus squalens*. *Applied and environmental microbiology*, 92(3), e0154825.

Boden S, et al. (2026) *Diutina cutanea* sp. nov.-phylogenomic-based analysis of a novel clinically relevant ascomycetous yeast. *Medical mycology*, 64(4).

Yamakawa S, et al. (2026) Multiple losses of ecdysone receptor genes in nematodes: an alternative evolutionary scenario of molting regulation. *Molecular biology and evolution*, 43(5).

Søndreli KL, et al. (2026) Transcriptomic and functional analyses uncover a conserved effector driving genotype-dependent virulence in the *Sphaerulina musiva*-*Populus trichocarpa* interaction. *mBio*, 17(5), e0312025.

Deng X, et al. (2026) Conserved and divergent gene regulatory networks for crop drought resistance. *Nature communications*, 17(1).

Wang B, et al. (2026) Global genomic diversity of the selfing nematode *Caenorhabditis tropicalis* correlates with geography. *bioRxiv* : the preprint server for biology.

Han L, et al. (2026) Chromosome-level genome provides new insights into the fatty acid biosynthesis and metabolism of the sea urchin *Strongylocentrotus intermedius*. *BMC genomics*, 27(1).