

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 processing software, data analysis 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: 20260801T190743+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 2899 mentions in open access literature.

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

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

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.

Zhou Z, et al. (2026) Chromosome-level genome provides novel insights into the starch metabolism regulation and evolutionary history of *Tetraselmis helgolandica*. *Journal of advanced research*, 79, 251.

Tørresen OK, et al. (2026) Comparison of whole-genome assemblies of European river lamprey (*Lampetra fluviatilis*) and brook lamprey (*Lampetra planeri*). *The Journal of heredity*, 117(1), 96.

Dockman RL, et al. (2026) Improved chromosome-level genome assembly of the American cockroach, *Periplaneta americana*. *G3 (Bethesda, Md.)*, 16(1).

Nachtigall PG, et al. (2026) The Golden Lancehead Genome Reveals Distinct Selective Processes Acting on Venom Genes of an Island Endemic Snake. *Genome biology and evolution*, 18(1).

Shi T, et al. (2026) Revisiting ancient whole-genome duplications in the seed and flowering plants through the lens of dosage-sensitive genes. *Science advances*, 12(1), eaea9797.

Maurstad MF, et al. (2026) The green lacewing venom system and the complex mechanisms underlying its evolution. *Molecular biology and evolution*, 43(1).

Medvedeva S, et al. (2026) Widespread and intron-rich mirusviruses are predicted to reproduce in nuclei of unicellular eukaryotes. *Nature microbiology*, 11(1), 228.

García JF, et al. (2026) Intraspecies sequence-graph analysis of the *Phytophthora theobromicola* genome reveals a dynamic structure and variable effector repertoires. *G3* (Bethesda, Md.), 16(1).

Hägglund E, et al. (2026) Origin and Evolution of Key Enzymes in the Anammox Pathway Revisited. *Genome biology and evolution*, 18(1).

Gao C, et al. (2026) High-Quality Genome Assembly of *Diplocarpon coronariae* Unveils LTR Retrotransposon-Driven Structural Dynamics in Fungi Evolution. *Molecular ecology resources*, 26(1), e70070.

Wang T, et al. (2025) Multiomics analysis provides insights into musk secretion in muskrat and musk deer. *GigaScience*, 14.

Javier MCF, et al. (2025) Draft genome of the endangered visayan spotted deer (*Rusa alfredi*), a Philippine endemic species. *GigaByte* (Hong Kong, China), 2025, gigabyte150.

Wang ZF, et al. (2025) Chromosome-scale assemblies of three *Ormosia* species: repetitive sequences distribution and structural rearrangement. *GigaScience*, 14.

Bergheim BG, et al. (2025) Molecular dynamics of the matrisome across sea anemone life history. *eLife*, 14.

Bharti S, et al. (2025) Single-cell transcriptome atlas of adult male and female human hookworm *Ancylostoma ceylanicum*. *iScience*, 28(11), 113846.

Oriowo TO, et al. (2025) A chromosome-level, haplotype-resolved genome assembly and annotation for the Eurasian minnow (*Leuciscidae: Phoxinus phoxinus*) provide evidence of haplotype diversity. *GigaScience*, 14.

Wang G, et al. (2025) Genomic evidence for hybridization and introgression between blue peafowl and endangered green peafowl and molecular foundation of leucistic plumage of blue peafowl. *GigaScience*, 14.

Zhou Y, et al. (2025) Telomere-to-telomere genome and resequencing of 254 individuals reveal evolution, genomic footprints in Asian icefish, *Protosalanx chinensis*. *GigaScience*, 14.