

Resource Summary Report

Generated by [kravitz2](#) on Sep 5, 2026

OrthoDB

RRID:SCR_011980

Type: Tool

Proper Citation

OrthoDB (RRID:SCR_011980)

Resource Information

URL: <https://www.orthodb.org/>

Proper Citation: OrthoDB (RRID:SCR_011980)

Description: Database of orthologous protein coding genes across vertebrates, arthropods, fungi, basal metazoans, and bacteria.

Synonyms: OrthoDB: Database of Orthologous Groups, OrthoDB v7, OrthoDB - The Hierarchical Catalog of Orthologs, OrthoDB v10

Resource Type: data or information resource, database

Defining Citation: [PMID:23180791](#)

Keywords: Hierarchical catalog, ortholog, protein coding genes, mapping genomics to functional data, FASEB list

Funding: Swiss National Foundation

Availability: Free, Freely available

Resource Name: OrthoDB

Resource ID: SCR_011980

Alternate IDs: OMICS_01692

Alternate URLs: <http://cegg.unige.ch/orthodb7>

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Record Creation Time: 20220129T080307+0000

Record Last Update: 20260904T000304+0000

Ratings and Alerts

No rating or validation information has been found for OrthoDB.

No alerts have been found for OrthoDB.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1143 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

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

Webster J, et al. (2026) Buscogeny: A BUSCO leveraged phylogenomic tree builder. *International microbiology : the official journal of the Spanish Society for Microbiology*, 29(2), 255.

Dani M, et al. (2026) Species delimitation within the *Achnanthidium minutissimum* complex (Bacillariophyta), based on morphological, molecular, and ecophysiological approaches. *Journal of phycology*, 62(1), 25.

Zhou X, et al. (2026) Synthetic Raphanobrassica Genome Reveals Functional and Evolutionary Insights Into Clubroot Resistance Genes on Chromosome R5. *Plant biotechnology journal*, 24(6), 3534.

de Souza Araujo N, et al. (2026) Retroelement expansions underlie genome evolution in stingless bees. *BMC genomics*, 27(1), 160.

Ivancevic A, et al. (2026) Whole-genome sequences of the dwarf honey bee subgenus *Micrapis*: *Apis andreniformis* and *Apis florea*. *G3 (Bethesda, Md.)*, 16(3).

Saenko S, et al. (2026) Annotation of 200 Insect Genomes with BRAKER for Consistent Comparisons across Species. *Scientific data*, 13(1).

Wang M, et al. (2026) Chromosome-level genome assembly of the alpine extremophyte Tibetan snow lotus, *Saussurea hypsipeta* Diels. *Scientific data*, 13(1).

Baalsrud HT, et al. (2026) Chromosomal fusions shaped the genome of the greater hornwrack bryozoan (*Flustra foliacea*) (Linnaeus, 1758). *The Journal of heredity*, 117(4), 750.

Ros-Rocher N, et al. (2026) Clonal-aggregative multicellularity tuned by salinity in a choanoflagellate. *Nature*, 651(8107), 974.

Voges K, et al. (2026) *Anopheles (Kerteszia) cruzii*, the main malaria vector in the Brazilian Atlantic Forest, is a complex of at least five cryptic species. *Communications biology*, 9(1).

Liao C, et al. (2026) Phylogenetic and Divergence Time Estimation of Muscomorpha with Low-Coverage Whole-Genome Sequencing of Syrphidae (Diptera: Brachycera). *Biology*, 15(5).

Xue D, et al. (2026) Chromosome-level genome assembly and annotation of the lesser grain borer, *Rhyzopertha dominica* (Fabricius) (Coleoptera: Bostrycidae). *Scientific data*, 13(1).

Marková S, et al. (2026) Chromosome-level genome of the bank vole (*Clethrionomys glareolus*): a resource for eco-evo-disease research. *Scientific data*, 13(1).

Sanchez G, et al. (2026) Rapid mid-Cretaceous diversification of squid and cuttlefish preceded radiation into coastal niches. *Nature ecology & evolution*, 10(4), 662.

Kim S, et al. (2026) *Tetraopes* Milkweed Beetle Genomes Elucidate the Adaptive Basis of a Temperate Coevolutionary Radiation. *Molecular ecology resources*, 26(3), e70117.

Malbranke C, et al. (2026) ProteomeLM: A proteome-scale language model enables accurate and rapid prediction of protein-protein interactions and gene essentiality across taxa. *Proceedings of the National Academy of Sciences of the United States of America*, 123(21), e2524201123.

Hsu SY, et al. (2026) Genomic and metabolic uniformity across diverse observed ecological contexts suggest that interactions of *Pestalotiopsis formosana* and *P. neolitseae* are context-dependent. *IMA fungus*, 17, e192779.

Olivas-Bernal CA, et al. (2026) Transcriptomic Meta-Analysis as a Framework for Robust Cross-Study Biological Inference. *International journal of molecular sciences*, 27(11).

Tørresen OK, et al. (2026) Chromosome-level genome assembly of Norwegian wild alpine reindeer (*Rangifer tarandus tarandus*). *The Journal of heredity*, 117(3), 557.