

Resource Summary Report

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[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: database, data or information resource

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: 20260805T044253+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 999 mentions in open access literature.

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

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).

Hirase S, et al. (2026) Ancestral Origin and Structural Characteristics of Non-Syntenic Homologous Chromosomes in Abalones (*Haliotis*). *Molecular ecology resources*, 26(1), e70057.

Bekavac M, et al. (2026) De novo genome assembly of Ansell's mole-rat (*Fukomys ansellii*). *G3* (Bethesda, Md.), 16(1).

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

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.

Fogg LG, et al. (2026) The visual system of the longest-living vertebrate, the Greenland shark. *Nature communications*, 17(1), 39.

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.

Tørresen OK, et al. (2025) A chromosome-level genome assembly of the common eider, *Somateria mollissima* (Linnaeus, 1758). *The Journal of heredity*, 116(3), 363.

Zakerzade R, et al. (2025) Diversification and recurrent adaptation of the synaptonemal complex in *Drosophila*. *PLoS genetics*, 21(1), e1011549.

Huang YH, et al. (2025) Molecular evolution of dietary shifts in ladybird beetles (Coleoptera: Coccinellidae): from fungivory to carnivory and herbivory. *BMC biology*, 23(1), 67.

- Jetha P, et al. (2025) Discovery of Cortinarius O-methyltransferases for the heterologous production of dermolutein and physcion. *Biotechnology for biofuels and bioproducts*, 18(1), 25.
- Zhao X, et al. (2025) Chromosome-level genome assembly of an endoparasitoid *Cotesia ruficrus*. *Scientific data*, 12(1), 508.
- Toubiana W, et al. (2025) Functional monocentricity with holocentric characteristics and chromosome-specific centromeres in a stick insect. *Science advances*, 11(1), eads6459.
- Li Y, et al. (2025) Structural insights into spliceosome fidelity: DHX35-GPATCH1-mediated rejection of aberrant splicing substrates. *Cell research*, 35(4), 296.
- Robertson C, et al. (2025) Spiral phyllotaxis predicts left-right asymmetric growth and style deflection in mirror-image flowers of *Cyanella alba*. *Nature communications*, 16(1), 3695.
- Baird RB, et al. (2025) Faster adaptation but slower divergence of X chromosomes under paternal genome elimination. *Nature communications*, 16(1), 5288.
- Tittarelli E, et al. (2025) Transposable element dynamics in *Xenopus laevis* embryogenesis: a tale of two coexisting subgenomes. *Mobile DNA*, 16(1), 17.
- Chen D, et al. (2025) Largest genome assembly in Brassicaceae: retrotransposon-driven genome expansion and karyotype evolution in *Matthiola incana*. *Plant biotechnology journal*, 23(9), 4109.
- Zheng J, et al. (2025) Genome mining and OSMAC strategies unveil diverse secondary metabolites from the endophytic fungus *Diaporthe kyushuensis* ZMU-48-1 with antifungal activity. *Frontiers in microbiology*, 16, 1604639.
- Ryan K, et al. (2025) New Genome Assemblies for Poeciliidae: A Foundation for Adaptation Studies. *Genome biology and evolution*, 17(6).