

Resource Summary Report

Generated by T1D on Aug 5, 2026

eggNOG

RRID:SCR_002456

Type: Tool

Proper Citation

eggNOG (RRID:SCR_002456)

Resource Information

URL: <http://eggnog.embl.de>

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Description: A database of orthologous groups of genes. The orthologous groups are annotated with functional description lines (derived by identifying a common denominator for the genes based on their various annotations), with functional categories (i.e derived from the original COG/KOG categories). eggNOG's database currently counts 1.7 million orthologous groups in 3686 species, covering over 7.7 million proteins (built from 9.6 million proteins). (Jan 30, 2014)

Abbreviations: eggNOG

Synonyms: eggNOG: evolutionary genealogy of genes: Non-supervised Orthologous Groups, eggNOG (evolutionary genealogy of genes: Non-supervised Orthologous Groups), evolutionary genealogy of genes: Non-supervised Orthologous Groups

Resource Type: database, data or information resource

Defining Citation: [PMID:24297252](#), [PMID:22096231](#)

Keywords: orthologous gene, ortholog, gene, function, FASEB list

Funding: BMBF ;
European Union FP6

Availability: Free, Available for download, Freely available

Resource Name: eggNOG

Resource ID: SCR_002456

Alternate IDs: nif-0000-02789, OMICS_01689

Record Creation Time: 20220129T080213+0000

Record Last Update: 20260805T044040+0000

Ratings and Alerts

No rating or validation information has been found for eggNOG.

No alerts have been found for eggNOG.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3564 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

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

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

Yun Y, et al. (2026) Gut microbiome plasticity explains the altitudinal distribution pattern and adaptability in a small mammal species (*Apodemus draco*). *Microbiology spectrum*, 14(1), e0238825.

Yeki S, et al. (2026) Sex-Specific doublesex Regulation Targeting the Color-Patterning Gene h Underlies the Evolution of Wing Sexual Dimorphism in the Harlequin Ladybug *Harmonia axyridis*. *Evolution & development*, 28(1), e70028.

Mantzana-Oikonomaki V, et al. (2026) Pigments, Chromatophore Structure, and Gene Expression Underlying Colour Polytypy of a Panamanian Poison Frog. *Molecular ecology*, 35(1), e70214.

Pan S, et al. (2025) A holistic genome dataset of bacteria and archaea of mangrove sediments. *GigaScience*, 14.

van Hooff JJE, et al. (2025) Repeated duplications and losses shaped SMC complex evolution from archaeal ancestors to modern eukaryotes. *Cell reports*, 44(7), 115855.

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

Wang Z, et al. (2025) A high-quality assembly revealing the PMEL gene for the unique plumage phenotype in Liancheng ducks. *GigaScience*, 14.

- Menozzi E, et al. (2025) Exploring the relationship between GBA1 host genotype and gut microbiome in the GBA1 L444P/WT mouse model: implications for Parkinson's disease pathogenesis. *Frontiers in neuroscience*, 19, 1546203.
- Carrillo-Carrasco VP, et al. (2025) Auxin and tryptophan trigger common responses in the streptophyte alga *Penium margaritaceum*. *Current biology : CB*, 35(9), 2078.
- Conn T, et al. (2025) Genome assembly and annotation of *Acropora pulchra* from Mo'orea French Polynesia. *GigaByte (Hong Kong, China)*, 2025, gigabyte153.
- Kotsovolos N, et al. (2025) Sequence- and structure-based bioinformatic screening for potential *Theileria parva* transport-related proteins. *Computational biology and chemistry*, 120(Pt 1), 108653.
- Lee A, et al. (2025) Genetic adaptation despite high gene flow in a range-expanding population. *Molecular ecology*, 34(15), e17511.
- Liu Z, et al. (2025) Ecological features of microbial community linked to stochastic and deterministic assembly processes in acid mine drainage. *Applied and environmental microbiology*, 91(1), e0102824.
- Bousquet L, et al. (2025) Life cycle and morphogenetic differentiation in heteromorphic cell types of a cosmopolitan marine microalga. *The New phytologist*, 245(5), 1969.
- Zhou Z, et al. (2025) Chromosome-level assembly and gene annotation of *Kappaphycus striatus* genome. *Scientific data*, 12(1), 249.
- Monteiro LMO, et al. (2025) Metabolic profiling of two white-rot fungi during 4-hydroxybenzoate conversion reveals biotechnologically relevant biosynthetic pathways. *Communications biology*, 8(1), 224.
- Sharma P, et al. (2025) De novo Transcriptomic analysis to unveil the deltamethrin induced resistance mechanisms in *Callosobruchus chinensis* (L.). *Scientific reports*, 15(1), 5163.
- Valentina M, et al. (2025) Comparative transcriptomics reveals different profiles between diflubenzuron-resistant and -susceptible phenotypes of the mosquito *Culex pipiens*. *Pest management science*, 81(6), 3370.