

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 18, 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: data or information resource, database

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: 20260912T200126+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 4095 mentions in open access literature.

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

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

She J, et al. (2026) DOO: integrated multi-omics resources for deep ocean organisms. *Nucleic acids research*, 54(D1), D1031.

Wang Z, et al. (2026) Optimization of culture conditions for enhanced antibacterial metabolite production by *Bacillus velezensis* TL and evaluation of its efficacy against necrotic enteritis in broilers. *Poultry science*, 105(3), 106439.

Wang Y, et al. (2026) Comparative metagenomic characterization of gut microbiota and antibiotic resistome in multi-facility SPF mice. *BMC microbiology*, 26(1).

Bai M, et al. (2026) RrMYB2 Regulates Drought Stress via RrJM12-Dependent Epigenetic Modification in *Rosa rugosa*. *Plant biotechnology journal*, 24(3), 1578.

Martin JA, et al. (2026) High-quality de novo genome assembly for the Galápagos endemic lava gull using Oxford Nanopore Technologies. *G3 (Bethesda, Md.)*, 16(3).

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

Lizcano-Salas AF, et al. (2026) First genome assemblies of Neotropical *Thoracobombus* bumblebees *Bombus pauloensis* and *Bombus pullatus*. *G3 (Bethesda, Md.)*, 16(3).

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

Hemmati R, et al. (2026) Draft genome sequence of *Talaromyces trachyspermus*, a biocontrol fungus isolated from broomrape. *G3 (Bethesda, Md.)*, 16(4).

Aikawa Y, et al. (2026) Plant Immunity-Activating Endophytic Bacteria Induce Dynamic Metabolic Changes in Cultured Plant Cells Without Inhibiting Their Growth. *Microbial biotechnology*, 19(1), e70297.

Zhu J, et al. (2026) Ectomycorrhizal fungi recruit hyphae-associated bacteria that metabolize thiamine to promote pine symbiosis. *The ISME journal*, 20(1).

Cui J, et al. (2026) Chromosome-level genome assembly and annotation of two Asian bumble bees. *Scientific data*, 13(1), 248.

Hariharan J, et al. (2026) Biogeographical and phylogenetic constraints on horizontal gene transfer and genome evolution in *Streptomyces*. *Microbiology spectrum*, 14(2), e0295825.

Tang Y, et al. (2026) A chromosome level genome assembly of *Homatula variegata* from the Yangtze River basin. *Scientific data*, 13(1).

Young V, et al. (2026) Effector-host interactome map links type III secretion systems in healthy gut microbiomes to immune modulation. *Nature microbiology*, 11(2), 442.

Mao S, et al. (2026) Physiological and transcriptomic cooperative regulatory mechanisms of *Cotinus Coggygria* in response to drought and rewatering processes. *BMC plant biology*, 26(1), 343.

Sessi IR, et al. (2026) First whole-genome assembly of the Galápagos Petrel (*Pterodroma phaeopygia*) using Oxford Nanopore sequencing to advance conservation genomics in a critically endangered seabird. *G3 (Bethesda, Md.)*, 16(3).

Sun X, et al. (2026) Physiological and transcriptomic analyses provide new insights into the effects of 1-MCP and ethephon treatments on apricot fruit during storage. *Frontiers in plant science*, 17, 1744757.

Kiran S, et al. (2026) Segmented filamentous bacteria are worldwide human gut commensals. *Nature communications*, 17(1).