

Resource Summary Report

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[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: 20260905T133118+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 [RRID](#) .

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

Liu M, et al. (2026) Physiological, Transcriptomic, and Metabolomic Responses of *Brachiaria decumbens* Roots During Symbiosis Establishment with *Piriformospora indica*. *Biology*, 15(3).

Liu Z, et al. (2026) Chromosome-Level Genome and Organ-Specific Transcriptome of *Alnus glutinosa* Uncover Lineage-Specific Innovations in Root Nodule Symbiosis. *Plant, cell & environment*, 49(6), 3003.

Zhang X, et al. (2026) Integrative transcriptomic and metabolomic analysis of *Drynaria roosii* reveals genes involved in the biosynthesis of medicinal compounds. *Scientific reports*, 16(1).

Kritsky AA, et al. (2026) An ancient *Erysipelothrix rhusiopathiae* genome recovered from 1400-year-old human remains in the Northern Caucasus. *Scientific reports*, 16(1), 7097.

Thangaraj S, et al. (2026) Depth Resolved Metagenomic Dataset from Surface and Deep Chlorophyll Maximum Layers in the Western Pacific Ocean. *Scientific data*, 13(1).

Kirsche L, et al. (2026) Gut microbial signatures expose the westernized lifestyle of urban Ethiopian children. *Communications biology*, 9(1).

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 Coggygia* in response to drought and rewatering processes. *BMC plant biology*, 26(1), 343.

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

Enagbonma BJ, et al. (2026) Effects of legume-based rotation on subsequent sorghum rhizosphere microbial communities and their drought tolerance-related genes. *Environmental microbiome*, 21(1).

Rodrigues GVP, et al. (2026) ViralQuest: a user-friendly interactive pipeline for viral-sequences analysis and curation. *BMC bioinformatics*, 27(1).

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

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

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.

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.

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

Li X, et al. (2026) Integrative epigenomic and transcriptomic profiling reveals organ-specific and coordinated cold stress responses in the brain and gill of Nile tilapia. *Stress biology*, 6(1), 4.

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