

Resource Summary Report

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eggNOG-mapper

RRID:SCR_021165

Type: Tool

Proper Citation

eggNOG-mapper (RRID:SCR_021165)

Resource Information

URL: <http://eggno-mapper.embl.de>

Proper Citation: eggNOG-mapper (RRID:SCR_021165)

Description: Software tool for functional annotation of large sets of sequences based on fast orthology assignments using precomputed eggNOG v5.0 clusters and phylogenies.

Synonyms: eggNOG-mapper v2, eggNOG v5.0

Resource Type: software resource

Defining Citation: [PMID:28460117](#)

Keywords: Functional annotation, sequences large sets, fast orthology assignments, eggNOG v5.0 clusters, phylogenies

Funding:

Resource Name: eggNOG-mapper

Resource ID: SCR_021165

Record Creation Time: 20220129T080354+0000

Record Last Update: 20250420T015109+0000

Ratings and Alerts

No rating or validation information has been found for eggNOG-mapper.

No alerts have been found for eggNOG-mapper.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 220 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Yi L, et al. (2025) Chromosome-level genome assemblies of sunflower oilseed and confectionery cultivars. *Scientific data*, 12(1), 24.

Oriowo TO, et al. (2025) A chromosome-level, haplotype-resolved genome assembly and annotation for the Eurasian minnow (Leuciscidae: Phoxinus phoxinus) provide evidence of haplotype diversity. *GigaScience*, 14.

Almeida-Santos AC, et al. (2025) The healthy human gut can take it all: vancomycin-variable, linezolid-resistant strains and specific bacteriocin-species interplay in *Enterococcus* spp. *Applied and environmental microbiology*, 91(1), e0169924.

Hooykaas MJG, et al. (2025) Crown Gall Induced by a Natural Isolate of *Brucella* (*Ochrobactrum*) *pseudogrignonense* Containing a Tumor-Inducing Plasmid. *Microorganisms*, 13(1).

Wu X, et al. (2025) Genome-Wide Identification, Phylogenetic Evolution, and Abiotic Stress Response Analyses of the Late Embryogenesis Abundant Gene Family in the Alpine Cold-Tolerant Medicinal *Notopterygium* Species. *International journal of molecular sciences*, 26(2).

Li Z, et al. (2025) Structure and metabolic function of spatiotemporal pit mud microbiome. *Environmental microbiome*, 20(1), 10.

Wu F, et al. (2025) Comparative genomic analysis of ten *Elizabethkingia anophelis* isolated from clinical patients in China. *Microbiology spectrum*, 13(1), e0178024.

Zhu Z, et al. (2025) Integrative multi-omics analysis reveals the translational landscape of the plant-parasitic nematode *Meloidogyne incognita*. *Communications biology*, 8(1), 140.

Denoeud F, et al. (2024) Evolutionary genomics of the emergence of brown algae as key components of coastal ecosystems. *Cell*, 187(24), 6943.

Niu YH, et al. (2024) Comparative transcriptomic evidence of physiological changes and potential relationships in vertebrates under different dormancy states. *Zoological research*,

45(2), 341.

Dong Z, et al. (2024) Genome-Wide Analysis of the TCP Transcription Factor Gene Family in Pepper (*Capsicum annuum* L.). *Plants* (Basel, Switzerland), 13(5).

Entila F, et al. (2024) Commensal lifestyle regulated by a negative feedback loop between *Arabidopsis* ROS and the bacterial T2SS. *Nature communications*, 15(1), 456.

Isla A, et al. (2024) Advancements in rapid diagnostics and genotyping of *Piscirickettsia salmonis* using Loop-mediated Isothermal Amplification. *Frontiers in microbiology*, 15, 1392808.

He L, et al. (2024) Unveiling Antibiotic Resistance: Genome Sequencing of Streptomycin-Resistant *Erwinia amylovora* Isolate. *Microorganisms*, 12(12).

Xia X, et al. (2024) Genomic Epidemiology of *Clostridioides difficile* ST81 in Multiple Hospitals in China. *Infection and drug resistance*, 17, 5535.

Quiroz-Castañeda RE, et al. (2024) Molecular Identification and Bioinformatics Analysis of *Anaplasma marginale* Moonlighting Proteins as Possible Antigenic Targets. *Pathogens* (Basel, Switzerland), 13(10).

Tang J, et al. (2024) Synergistic pectin deconstruction is a prerequisite for mutualistic interactions between honeybee gut bacteria. *Nature communications*, 15(1), 6937.

Li R, et al. (2024) Genome-wide characterization and evolution analysis of miniature inverted-repeat transposable elements in Barley (*Hordeum vulgare*). *Frontiers in plant science*, 15, 1474846.

Wang H, et al. (2024) The overall regulatory network and contributions of ABC(D)E model genes in yellowhorn flower development. *BMC plant biology*, 24(1), 1081.

Arthofer P, et al. (2024) A giant virus infecting the amoeboflagellate *Naegleria*. *Nature communications*, 15(1), 3307.