

Resource Summary Report

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COG

RRID:SCR_007139

Type: Tool

Proper Citation

COG (RRID:SCR_007139)

Resource Information

URL: <http://www.ncbi.nlm.nih.gov/COG>

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Description: A database for phylogenetic classification for proteins encoded in complete genomes. Clusters of Orthologous Groups of proteins (COGs) were delineated by comparing protein sequences encoded in complete genomes, representing major phylogenetic lineages. Each COG consists of individual proteins or groups of paralogs from at least 3 lineages and thus corresponds to an ancient conserved domain. Please be aware that COGs hasn't been updated in many years and will not be.

Abbreviations: COG, COG Cluster, COG Function, COG Pathway

Synonyms: COG Database, Clusters of Orthologous Groups of proteins, COGs, COGs - Clusters of Orthologous Groups of proteins, COGs - Phylogenetic classification of proteins encoded in complete genomes, COG Cluster, COG Pathway, COG Function

Resource Type: database, data or information resource

Defining Citation: [PMID:12969510](#), [PMID:9381173](#)

Keywords: ortholog, protein, cog, conserved protein sequence, unicellular cluster, genome, order, class, phyla, eukaryotic cluster, gold standard

Resource Name: COG

Resource ID: SCR_007139

Alternate IDs: OMICS_01688, nif-0000-02672

Record Creation Time: 20220129T080240+0000

Record Last Update: 20260803T040458+0000

Ratings and Alerts

No rating or validation information has been found for COG.

No alerts have been found for COG.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1117 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Kuang C, et al. (2025) HL-IR mediates cinnamaldehyde repellency behavior in parthenogenetic *Haemaphysalis longicornis*. *PLoS neglected tropical diseases*, 19(3), e0012877.

Gu S, et al. (2025) Siderophore synthetase-receptor gene coevolution reveals habitat- and pathogen-specific bacterial iron interaction networks. *Science advances*, 11(3), eadq5038.

Li L, et al. (2025) Isolation, characterization, and genomic analysis of a novel phage WSPA with lytic activity against *Serratia marcescens*. *Microbiology spectrum*, 13(9), e0271624.

Ouidir T, et al. (2025) Large scale identification of pellicle and cell-free liquid phase associated proteins in *Bacillus amyloliquefaciens* L-17. *Current research in microbial sciences*, 8, 100387.

Song G, et al. (2025) The First Isolation of Multiple Antifungal-Drug-Resistant *Trichophyton Rubrum* in China and the Novel Resistance Mechanism. *Mycoses*, 68(11), e70128.

Xu L, et al. (2025) Genomic Insights into the Pathogenicity of Hypervirulent *Aeromonas hydrophila* Strain D4 Isolated from Diseased Blunt Snout Bream with the Epidemic Sequence Type 251 Clones. *Pathogens (Basel, Switzerland)*, 14(6).

Jin S, et al. (2025) Investigation of the Effects of Salinity Exposure on Immune Defense, Morphology, and Gene Expression in the Gills of *Macrobrachium nipponense*. *Antioxidants (Basel, Switzerland)*, 14(6).

Hu G, et al. (2025) The HOG signal pathway contributes to survival strategies of the piezo-tolerant fungus *Aspergillus sydowii* DM1 in hadal sediments. *Applied and environmental microbiology*, 91(9), e0092125.

Kumari K, et al. (2025) In-depth genome and comparative genome analysis of a metal-resistant environmental isolate *Pseudomonas aeruginosa* S-8. *Frontiers in cellular and infection microbiology*, 15, 1511507.

He R, et al. (2025) Cooperative mechanisms of LexA and HtpG in the regulation of virulence gene expression in *Pseudomonas plecoglossicida*. *Current research in microbial sciences*, 8, 100351.

Hu TB, et al. (2025) Analysis of salivary proteins in gall-inducing psylla and their potential influence on host plants. *BMC genomics*, 26(1), 786.

Sun H, et al. (2025) Integrated transcriptomic and metabolomic analysis of Jinggang honey pomelo yellow spot disease to reveal the disease resistance mechanism. *PloS one*, 20(9), e0330626.

Kang Y, et al. (2025) Molecular and genetic features of a blaNDM-1 and blaSHV-12 coharboring hypermucoviscous *Klebsiella pneumoniae* of serotype K2 and ST65. *Annals of clinical microbiology and antimicrobials*, 24(1), 19.

Zhang X, et al. (2025) Transcriptomic analysis reveals the growth of *Populus Schneideri* in different light qualities. *BMC genomics*, 26(1), 871.

Alami NH, et al. (2025) Functional and genomic characterization of polyethylene degrading yeast *Meyerozyma carpophila* M6.0.2 isolated from marine plastic debris in East Java Indonesia. *Scientific reports*, 15(1), 40437.

Wang X, et al. (2025) Cell Wall Remodeling and pH Stress Coordinately Regulate *Monascus* Pigment Biosynthesis Through Transcriptional Reprogramming. *Foods (Basel, Switzerland)*, 14(21).

Mu Y, et al. (2025) Müller cells are activated in response to retinal outer nuclear layer degeneration in rats subjected to simulated weightlessness conditions. *Neural regeneration research*, 20(7), 2116.

Zhou Y, et al. (2025) Metabolic and transcriptional analysis of tuber expansion in *Curcuma kwangsiensis*. *Scientific reports*, 15(1), 1588.

Wang S, et al. (2025) Joint Analysis of Multiple Omics to Describe the Biological Characteristics of Resistant Hypertension. *Journal of clinical hypertension (Greenwich, Conn.)*, 27(1), e14961.

Jia S, et al. (2025) Transcriptome analysis reveals defense responses of alfalfa seedling roots to *Sclerotium rolfsii*. *Frontiers in plant science*, 16, 1561723.