

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](https://pubmed.ncbi.nlm.nih.gov/12969510/), [PMID:9381173](https://pubmed.ncbi.nlm.nih.gov/9381173/)

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

Funding:

Resource Name: COG

Resource ID: SCR_007139

Alternate IDs: OMICS_01688, nif-0000-02672

Record Creation Time: 20220129T080240+0000

Record Last Update: 20250412T055147+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 1090 mentions in open access literature.

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

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

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.

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.

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

Yang S, et al. (2025) Deciphering the Proteome and Phosphoproteome of Peanut (*Arachis hypogaea* L.) Pegs Penetrating into the Soil. *International journal of molecular sciences*, 26(2).

Wang L, et al. (2024) Fecal PCR survey and genome analysis of *Lawsonia intracellularis* in China. *Frontiers in veterinary science*, 11, 1324768.

- Jin S, et al. (2024) Effects of Alkalinity Exposure on Antioxidant Status, Metabolic Function, and Immune Response in the Hepatopancreas of *Macrobrachium nipponense*. *Antioxidants* (Basel, Switzerland), 13(1).
- Lee C, et al. (2024) Comprehensive understanding of the mutant 'giant' *Arthrospira platensis* developed via ultraviolet mutagenesis. *Frontiers in plant science*, 15, 1369976.
- Ma J, et al. (2024) Whole transcriptome sequencing analyses of islets reveal ncRNA regulatory networks underlying impaired insulin secretion and increased β -cell mass in high fat diet-induced diabetes mellitus. *PloS one*, 19(4), e0300965.
- Cheng C, et al. (2024) A *Bacillus velezensis* strain isolated from oats with disease-preventing and growth-promoting properties. *Scientific reports*, 14(1), 12950.
- Li XT, et al. (2024) *Acidithiobacillus acidisediminis* sp. nov., an acidophilic sulphur-oxidizing chemolithotroph isolated from acid mine drainage sediment. *International journal of systematic and evolutionary microbiology*, 74(5).
- Wang F, et al. (2024) Evaluation of the Immune Response of Patulin by Proteomics. *Biosensors*, 14(7).
- Guo G, et al. (2024) Genome-wide identification of GA2ox genes family and analysis of PbrGA2ox1-mediated enhanced chlorophyll accumulation by promoting chloroplast development in pear. *BMC plant biology*, 24(1), 166.
- Liu F, et al. (2024) Transcriptome analysis reveals regulatory mechanisms of different drought-tolerant *Gleditsia sinensis* seedlings under drought stress. *BMC genomic data*, 25(1), 29.
- Lyu S, et al. (2024) Isolation and characterization of a novel temperate bacteriophage infecting *Aeromonas hydrophila* isolated from a *Macrobrachium rosenbergii* larvae pond. *Virus research*, 339, 199279.
- Liao T, et al. (2024) Full-length transcriptome characterization of *Platyclusus orientalis* based on the PacBio platform. *Frontiers in genetics*, 15, 1345039.
- Luo D, et al. (2024) Pulchrenoside B4 ameliorates oral ulcers in rats by modulating gut microbiota and metabolites. *Applied microbiology and biotechnology*, 108(1), 292.
- Xi BX, et al. (2024) Antennal Transcriptome Evaluation and Analysis for Odorant-Binding Proteins, Chemosensory Proteins, and Suitable Reference Genes in the Leaf Beetle Pest *Diorhabda rybakowi* Weise (Coleoptera: Chrysomelidae). *Insects*, 15(4).
- Ning Y, et al. (2024) Comparative transcriptomics analysis of tolerant and sensitive genotypes reveals genes involved in the response to cold stress in bitter melon (*Momordica charantia* L.). *Scientific reports*, 14(1), 16564.
- Chen H, et al. (2024) Quality changes of whitespotted conger (*Conger myriaster*) based physicochemical changes and label-free proteomics analysis during frozen storage. *Current*

research in food science, 8, 100779.