# Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 14, 2025

# 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

**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.

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.

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.

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).

Lee C, et al. (2024) Comprehensive understanding of the mutant 'giant' Arthrospira platensis developed via ultraviolet mutagenesis. Frontiers in plant science, 15, 1369976.

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

Ma J, et al. (2024) Whole transcriptome sequencing analyses of islets reveal ncRNA regulatory networks underlying impaired insulin secretion and increased ?-cell mass in high fat diet-induced diabetes mellitus. PloS one, 19(4), e0300965.

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).

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).

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.

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.

Luo D, et al. (2024) Pulchinenoside B4 ameliorates oral ulcers in rats by modulating gut microbiota and metabolites. Applied microbiology and biotechnology, 108(1), 292.

Wang XJ, et al. (2024) A pipeline contributes to efficient identification of salivary proteins in short-headed planthopper, Epeurysa nawaii. Scientific reports, 14(1), 6225.

Qin Y, et al. (2024) Molecular mechanism of endophytic bacteria DX120E regulating polyamine metabolism and promoting plant growth in sugarcane. Frontiers in plant science, 15, 1334907.

Qiao J, et al. (2024) Graphene promotes the growth of Vigna angularis by regulating the nitrogen metabolism and photosynthesis. PloS one, 19(3), e0297892.

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).