

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: data or information resource, database

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: 20260905T133138+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 1278 mentions in open access literature.

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

Zhou F, et al. (2026) Protein corona proteomics characterizes low-abundance plasma protein signatures and highlights ferroptosis-associated signals in uremic hemodialysis patients. *Clinical proteomics*, 23(1).

Xi Y, et al. (2026) Genomic Map of Escherichia coli and Single Nucleotide Polymorphism Markers in Colorectal Cancer. *Microbial biotechnology*, 19(6), e70397.

Yang W, et al. (2026) Therapeutic efficacy of phage vB_SaP_NW15 and cinnamaldehyde against drug-resistant Salmonella Enteritidis in a chicken infection model. *Poultry science*, 105(3), 106327.

Hou J, et al. (2026) Whole-genome sequencing reveals the genomic characterization and evolution of carbapenem-resistant Klebsiella pneumoniae in Gansu, China. *Frontiers in cellular and infection microbiology*, 16, 1749978.

Liang Y, et al. (2026) Transcriptomic analysis of tigecycline-induced colistin collateral sensitivity in carbapenem-resistant Enterobacter cloacae complex. *mSphere*, 11(3), e0090325.

Cheng J, et al. (2026) PpZAT12 from a native Kentucky bluegrass (Poa pratensis L.) confers drought tolerance through regulating antioxidant defense system and multiple metabolic pathways. *BMC plant biology*, 26(1), 253.

Xu T, et al. (2026) Isolation and therapeutic potential of phage vB_EcoM_GXW16 against a drug-resistant avian pathogenic Escherichia coli strain. *Poultry science*, 105(6), 106701.

Wang Y, et al. (2026) A chromosome level genome, as well as transcriptomes and metabolomes, insights into genome evolution and the biosynthesis of kaempferol and kaempferol derivatives in Impatiens balsamina (Balsaminaceae). *Frontiers in plant science*, 17, 1725789.

Liu J, et al. (2026) Integrative Transcriptome and Metabolome Analysis Reveals the Regulatory Networks and Key Biosynthetic Pathway Genes of Wild and Cultivated Gentiana macrophylla Pall. *Metabolites*, 16(3).

Zhang Y, et al. (2026) Salivary proteomics of patients with type 2 diabetes identify potential biomarkers for diabetes and highlight significant role of immune response. *Clinical and experimental medicine*, 26(1), 103.

Wang YD, et al. (2026) Characterization of the full-length transcriptome of female *Eucolus annulatus* and comparative transcriptomic analysis of its head, middle, and tail body sections. *Parasites & vectors*, 19(1).

Yin Y, et al. (2026) Integrative Phenotypic and Genomic Analysis Reveals Antimicrobial and Stress-Resistance Mechanisms of *Lactocaseibacillus rhamnosus* MG0718 as a Promising Probiotic Candidate for Food Applications. *Microorganisms*, 14(6).

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.

Madushani MA, et al. (2025) From genome to field: *Bacillus halotolerans* BJ-3 as a novel biocontrol solution for grapevine *Botryosphaeria dieback*. *Current research in microbial sciences*, 9, 100483.

Yang L, et al. (2025) Full-length transcriptome profiling of *Gentiana straminea* Maxim. provides new insights into iridoid biosynthesis pathway. *PeerJ*, 13, e20136.

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.

Zhu X, et al. (2025) Polymyxin-resistant hypervirulent *Klebsiella pneumoniae* clinical isolates from a tertiary hospital in China: molecular mechanisms, antimicrobial susceptibility, and virulent phenotypes. *Frontiers in microbiology*, 16, 1705471.

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

Jiang L, et al. (2025) Analysis of Gene Regulatory Networks of Taro (*Colocasia esculenta* (L.) Schott.) Soluble Starch Synthase Based on DeGN and KASP Marker Development. *International journal of genomics*, 2025, 9953367.