

Resource Summary Report

Generated by T1D on Aug 1, 2026

dcGO

RRID:SCR_014392

Type: Tool

Proper Citation

dcGO (RRID:SCR_014392)

Resource Information

URL: <http://supfam.org/SUPERFAMILY/dcGO/>

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Description: A database of domain-centric ontologies on functions, phenotypes, diseases and more. As a biomedical ontology resource, dcGO integrates functional, phenotypic, disease, and drug information. As a protein domain resource, it includes annotations to both the individual domains and supra-domains. Domain classifications and ontologies are organized in hierarchies, and dcGO includes the facility to browse the hierarchies: SCOP Hierarchy for browsing domains, GO Hierarchy for browsing GO terms, and BO Hierarchy for browsing other terms (mostly phenotypes). Users can mine and browse through resources.

Resource Type: data or information resource, database

Defining Citation: [PMID:23161684](#)

Keywords: database, mining, domain centric ontology, phenotype, human disease, drug, biomedical ontology, protein domain, hierarchy

Availability: Acknowledgement required, Both flat files and MySQL tables are available for download

Resource Name: dcGO

Resource ID: SCR_014392

Record Creation Time: 20220129T080320+0000

Record Last Update: 20260801T191024+0000

Ratings and Alerts

No rating or validation information has been found for dcGO.

No alerts have been found for dcGO.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 27 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Yu J, et al. (2025) Transcriptome-wide decoding the roles of aberrant splicing in melanoma MAPK-targeted resistance evolution. *EMBO reports*, 26(16), 4180.

Bao C, et al. (2023) The dcGO Domain-Centric Ontology Database in 2023: New Website and Extended Annotations for Protein Structural Domains. *Journal of molecular biology*, 435(14), 168093.

Fricke J, et al. (2023) Adaptations of Pseudoxylaria towards a comb-associated lifestyle in fungus-farming termite colonies. *The ISME journal*, 17(5), 733.

Gómez Borrego J, et al. (2022) Analysis of Host-Bacteria Protein Interactions Reveals Conserved Domains and Motifs That Mediate Fundamental Infection Pathways. *International journal of molecular sciences*, 23(19).

Caña-Bozada V, et al. (2022) De novo transcriptome assembly and identification of G-Protein-Coupled-Receptors (GPCRs) in two species of monogenean parasites of fish. *Parasite (Paris, France)*, 29, 51.

Nelson DR, et al. (2021) Large-scale genome sequencing reveals the driving forces of viruses in microalgal evolution. *Cell host & microbe*, 29(2), 250.

Wang M, et al. (2021) The completed genome sequence of the pathogenic ascomycete fungus *Penicillium digitatum*. *Genomics*, 113(2), 439.

Illescas-Zárate D, et al. (2020) Potential Impact of the Nonessential Energy-Dense Foods Tax on the Prevalence of Overweight and Obesity in Children: A Modeling Study. *Frontiers in public health*, 8, 591696.

Batugedara G, et al. (2020) The chromatin bound proteome of the human malaria parasite. *Microbial genomics*, 6(2).

Garcia MO, et al. (2020) Soil Microbes Trade-Off Biogeochemical Cycling for Stress Tolerance Traits in Response to Year-Round Climate Change. *Frontiers in microbiology*, 11, 616.

Arimoto A, et al. (2019) A siphonous macroalgal genome suggests convergent functions of homeobox genes in algae and land plants. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 26(2), 183.

Wang M, et al. (2019) Genomic Sequencing of *Phyllosticta citriasiana* Provides Insight Into Its Conservation and Diversification With Two Closely Related *Phyllosticta* Species Associated With Citrus. *Frontiers in microbiology*, 10, 2979.

Evans JD, et al. (2018) Interactions Among Host-Parasite MicroRNAs During *Nosema ceranae* Proliferation in *Apis mellifera*. *Frontiers in microbiology*, 9, 698.

Alborzi SZ, et al. (2017) ECDomainMiner: discovering hidden associations between enzyme commission numbers and Pfam domains. *BMC bioinformatics*, 18(1), 107.

Thirugnanasambandam R, et al. (2017) De novo assembly and annotation of the whole genomic analysis of *Vibrio campbellii* RT-1 strain, from infected shrimp: *Litopenaeus vannamei*. *Microbial pathogenesis*, 113, 372.

Plett KL, et al. (2017) Root morphogenic pathways in *Eucalyptus grandis* are modified by the activity of protein arginine methyltransferases. *BMC plant biology*, 17(1), 62.

Nguyen TT, et al. (2017) Computational Identification and Comparative Analysis of Secreted and Transmembrane Proteins in Six *Burkholderia* Species. *The plant pathology journal*, 33(2), 148.

Ryu T, et al. (2016) Hologenome analysis of two marine sponges with different microbiomes. *BMC genomics*, 17, 158.

Bunnik EM, et al. (2016) The mRNA-bound proteome of the human malaria parasite *Plasmodium falciparum*. *Genome biology*, 17(1), 147.

Linkeviciute V, et al. (2015) Function-selective domain architecture plasticity potentials in eukaryotic genome evolution. *Biochimie*, 119, 269.