Resource Summary Report

Generated by NIF on May 20, 2025

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: database, data or information resource

Defining Citation: PMID:23161684

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

Funding:

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: 20250519T204822+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 26 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

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.

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

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.

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.

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.

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.

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.

Dorden S, et al. (2015) Functional prediction of hypothetical proteins in human adenoviruses. Bioinformation, 11(10), 466.