Resource Summary Report

Generated by NIF on May 20, 2025

Phylogenetic Clusters of Orthologous Groups Ranking

RRID:SCR_008223
Type: Tool

Proper Citation

Phylogenetic Clusters of Orthologous Groups Ranking (RRID:SCR_008223)

Resource Information

URL: http://www.uni-wh.de/pcogr

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Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented on August 20,2019.The COG-database has become a powerful tool in the field of comparative genomics. The construction of this data-base is based on sequence homologies of proteins from different completely sequenced genomes. Highly homologous proteins are assigned to clusters of orthologous groups. The updated collection of orthologous protein sets for prokaryotes and eukaryotes is expected to be a useful platform for functional annotation of newly sequenced genomes, including those of complex eukaryotes, and genome-wide evolutionary studies. The availability of multiple, essentially complete genome sequences of prokaryotes and eukaryotes spurred both the demand and the opportunity for the construction of an evolutionary classification of genes from these genomes. Such a classification system based on orthologous relationships between genes appears to be a natural framework for comparative genomics and should facilitate both functional annotation of genomes and large-scale evolutionary studies. Here is a major update of the previously developed system for delineation of Clusters of Orthologous Groups of proteins (COGs) from the sequenced genomes of prokaryotes and unicellular eukaryotes and the construction of clusters of predicted orthologs for 7 eukaryotic genomes, which we named KOGs after eukaryotic orthologous groups. The COG collection currently consists of 138,458 proteins, which form 4873 COGs and comprise 75% of the 185,505 (predicted) proteins encoded in 66 genomes of unicellular organisms. The eukaryotic orthologous groups (KOGs) include proteins from 7 eukaryotic genomes: three animals (the nematode Caenorhabditis elegans, the fruit fly Drosophila melanogaster and Homo sapiens), one plant, Arabidopsis thaliana, two fungi (Saccharomyces cerevisiae and Schizosaccharomyces pombe), and the intracellular microsporidian parasite Encephalitozoon cuniculi. The current KOG set consists of 4852 clusters of orthologs, which include 59,838 proteins, or approximately 54% of the analyzed eukaryotic 110,655 gene products. Compared to the coverage of the prokaryotic genomes with COGs, a considerably smaller fraction of eukaryotic genes could be included into the KOGs; addition of new eukaryotic genomes is expected to result in substantial increase in the coverage of eukaryotic genomes with KOGs. Examination of the phyletic patterns of KOGs reveals a conserved core represented in all analyzed species and consisting of approximately 20% of the KOG set. This conserved portion of the KOG set is much greater than the ubiquitous portion of the COG set (approximately 1% of the COGs). In part, this difference is probably due to the small number of included eukaryotic genomes, but it could also reflect the relative compactness of eukaryotes as a clade and the greater evolutionary stability of eukaryotic genomes.

Synonyms: PCOGR

Resource Type: database, data or information resource

Keywords: elegans, encephalitozoon, eukaryote, evolutionary, fly, fruit, fungus, gene, general genomics databases, animal, arabidopsis, caenorhabditis, cerevisiae, classification, comparative, cuniculi, drosophila, genome, genomic, homo, homology, intracellular, melanogaster, microsporidian, nematode, organism, ortholog, orthologous, parasite, pattern, phyletic, phylogenetic, plant, pombe, prokaryote, protein, saccharomyces, sapiens, schizosaccharomyces, sequence, thaliana, tool, unicellular

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Phylogenetic Clusters of Orthologous Groups Ranking

Resource ID: SCR_008223

Alternate IDs: nif-0000-21313

Record Creation Time: 20220129T080246+0000

Record Last Update: 20250519T204758+0000

Ratings and Alerts

No rating or validation information has been found for Phylogenetic Clusters of Orthologous Groups Ranking.

No alerts have been found for Phylogenetic Clusters of Orthologous Groups Ranking.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Zhao H, et al. (2020) Mycoparasitism illuminated by genome and transcriptome sequencing of Coniothyrium minitans, an important biocontrol fungus of the plant pathogen Sclerotinia sclerotiorum. Microbial genomics, 6(3).

Ufarté L, et al. (2015) Discovery of new protein families and functions: new challenges in functional metagenomics for biotechnologies and microbial ecology. Frontiers in microbiology, 6, 563.

Meereis F, et al. (2004) PCOGR: phylogenetic COG ranking as an online tool to judge the specificity of COGs with respect to freely definable groups of organisms. BMC bioinformatics, 5, 150.