GOblet

RRID:SCR_006998
Type: Tool

Proper Citation

GOblet (RRID:SCR_006998)

Resource Information

URL: http://goblet.molgen.mpg.de/cgi-bin/goblet2008/goblet.cgi

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Description: Tool that performs annotation based on GO and pathway terms for anonymous cDNA or protein sequences. It uses the species independent GO structure and vocabulary together with a series of protein databases collected from various sites, to perform a detailed GO annotation by sequence similarity searches. The sensitivity and the reference protein sets can be selected by the user. GOblet runs automatically and is available as a public service on our web server. GOblet expects query sequences to be in FASTA-Format (with header-lines). Protein and nucleotide sequences are accepted. Total size of all sequences submitted per request should not be larger than 50kb currently. For security reasons: Larger post's will be rejected. Due to limited capacities the queries may be processed in batches depending on the server load. The output of the BLAST job is filtered automatically and the relevant hits are displayed. In addition, the respective GO-terms are shown together with the complete GO-hierarchy of parent terms.

Abbreviations: GOblet

Resource Type: software application, analysis service resource, data analysis service, software resource, production service resource, service resource

Defining Citation: PMID:20134064, PMID:15215401, PMID:12824400

Keywords: gene, sequence, cdna, ontology or annotation browser, pathway, term enrichment, clustering, virus, genomic, protein, nucleotide

Funding: BMBF

Availability: Free, Public

Resource Name: GOblet

Resource ID: SCR_006998

Alternate IDs: nif-0000-30624, OMICS_02271

Old URLs: http://goblet.molgen.mpg.de

Record Creation Time: 20220129T080239+0000

Record Last Update: 20250423T060334+0000

Ratings and Alerts

No rating or validation information has been found for GOblet.

No alerts have been found for GOblet.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Via A, et al. (2019) A new pan-European Train-the-Trainer programme for bioinformatics: pilot results on feasibility, utility and sustainability of learning. Briefings in bioinformatics, 20(2), 405.

Schedina IM, et al. (2018) The gonadal transcriptome of the unisexual Amazon molly Poecilia formosa in comparison to its sexual ancestors, Poecilia mexicana and Poecilia latipinna. BMC genomics, 19(1), 12.

Schedina IM, et al. (2014) Comparative analysis of the gonadal transcriptomes of the all-female species Poecilia formosa and its maternal ancestor Poecilia mexicana. BMC research notes, 7, 249.

Hori TS, et al. (2010) Heat-shock responsive genes identified and validated in Atlantic cod (Gadus morhua) liver, head kidney and skeletal muscle using genomic techniques. BMC genomics, 11, 72.

Lockyer AE, et al. (2007) Biomphalaria glabrata transcriptome: identification of cell-signalling, transcriptional control and immune-related genes from open reading frame expressed sequence tags (ORESTES). Developmental and comparative immunology, 31(8), 763.

Fernández P, et al. (2003) Differential representation of sunflower ESTs in enriched organ-specific cDNA libraries in a small scale sequencing project. BMC genomics, 4(1), 40.