

Resource Summary Report

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GORetriever

RRID:SCR_005633

Type: Tool

Proper Citation

GORetriever (RRID:SCR_005633)

Resource Information

URL: http://agbase.msstate.edu/cgi-bin/tools/goretriever_select.pl

Proper Citation: GORetriever (RRID:SCR_005633)

Description: GORetriever is used to find all of the GO annotations corresponding to a list of user-supplied protein identifiers. GORetriever produces a list of proteins and their annotations and a separate list of entries with no GO annotation. Platform: Online tool

Abbreviations: GORetriever

Synonyms: AgBase GORetriever

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

Defining Citation: [PMID:17135208](#), [PMID:16961921](#)

Keywords: gene, annotation, protein, ontology or annotation search engine

Funding: USDA ;
Mississippi State University; Mississippi; USA ;
MSU Office of Research ;
MSU Bagley College of Engineering ;
MSU College of College of Veterinary Medicine ;
MSU Life Science and Biotechnology Institute

Availability: Free for academic use

Resource Name: GORetriever

Resource ID: SCR_005633

Alternate IDs: nlx_149140

Record Creation Time: 20220129T080231+0000

Record Last Update: 20260919T195652+0000

Ratings and Alerts

No rating or validation information has been found for GORetriever.

No alerts have been found for GORetriever.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 13 mentions in open access literature.

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

Yan H, et al. (2024) GORetriever: reranking protein-description-based GO candidates by literature-driven deep information retrieval for protein function annotation. Bioinformatics (Oxford, England), 40(Suppl 2), ii53.

Escobar-Niño A, et al. (2023) The Adaptation of Botrytis cinerea Extracellular Vesicles Proteome to Surrounding Conditions: Revealing New Tools for Its Infection Process. Journal of fungi (Basel, Switzerland), 9(9).

Urban MO, et al. (2021) The Resistance of Oilseed Rape Microspore-Derived Embryos to Osmotic Stress Is Associated With the Accumulation of Energy Metabolism Proteins, Redox Homeostasis, Higher Absciscic Acid, and Cytokinin Contents. Frontiers in plant science, 12, 628167.

Hewel C, et al. (2019) Common miRNA Patterns of Alzheimer's Disease and Parkinson's Disease and Their Putative Impact on Commensal Gut Microbiota. Frontiers in neuroscience, 13, 113.

van der Pluijm I, et al. (2018) Decreased mitochondrial respiration in aneurysmal aortas of Fibulin-4 mutant mice is linked to PGC1A regulation. Cardiovascular research, 114(13), 1776.

Xue M, et al. (2017) Analysis of the spleen proteome of chickens infected with reticuloendotheliosis virus. Archives of virology, 162(5), 1187.

Urban MO, et al. (2017) Proteomic and physiological approach reveals drought-induced changes in rapeseeds: Water-saver and water-spender strategy. Journal of proteomics, 152, 188.

Lyon D, et al. (2016) Drought and Recovery: Independently Regulated Processes Highlighting the Importance of Protein Turnover Dynamics and Translational Regulation in

Medicago truncatula. Molecular & cellular proteomics : MCP, 15(6), 1921.

Ragupathy R, et al. (2016) Deep sequencing of wheat sRNA transcriptome reveals distinct temporal expression pattern of miRNAs in response to heat, light and UV. Scientific reports, 6, 39373.

Marie P, et al. (2015) Quantitative proteomics and bioinformatic analysis provide new insight into protein function during avian eggshell biomineralization. Journal of proteomics, 113, 178.

Davis RV, et al. (2015) Transcriptome analysis of post-hatch breast muscle in legacy and modern broiler chickens reveals enrichment of several regulators of myogenic growth. PloS one, 10(3), e0122525.

Liu L, et al. (2012) The human microbiome: a hot spot of microbial horizontal gene transfer. Genomics, 100(5), 265.

Fan Z, et al. (2012) Proteomics of DF-1 cells infected with avian leukosis virus subgroup J. Virus research, 167(2), 314.