

Resource Summary Report

Generated by SPARC SAWG on Aug 9, 2026

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: 20260808T190353+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 [SPARC SAWG](#) .

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.

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.

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

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.

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.

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.

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.

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.