Resource Summary Report

Generated by NIF on Apr 21, 2025

GOSlimViewer

RRID:SCR_005665
Type: Tool

Proper Citation

GOSlimViewer (RRID:SCR_005665)

Resource Information

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

Proper Citation: GOSlimViewer (RRID:SCR_005665)

Description: Service to summarize the GO function associated with a data set using prepared GO Slim sets. The input is a tab separated list of gene product IDs and GO IDs.

Abbreviations: GOSlimViewer

Synonyms: GO Slim Viewer, GOSlim Viewer

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

Defining Citation: PMID:17135208, PMID:16961921

Keywords: agriculture, browser, slimmer-type tool, gene ontology, gene, ontology, ontology or annotation browser

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: GOSlimViewer

Resource ID: SCR_005665

Alternate IDs: nlx_149103, OMICS_02270

Record Creation Time: 20220129T080231+0000

Record Last Update: 20250420T015523+0000

Ratings and Alerts

No rating or validation information has been found for GOSlimViewer.

No alerts have been found for GOSlimViewer.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 40 mentions in open access literature.

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

Coates BS, et al. (2023) A draft Diabrotica virgifera virgifera genome: insights into control and host plant adaption by a major maize pest insect. BMC genomics, 24(1), 19.

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 Abscisic Acid, and Cytokinin Contents. Frontiers in plant science, 12, 628167.

Xie Y, et al. (2020) Transcriptome differences in adipose stromal cells derived from pre- and postmenopausal women. Stem cell research & therapy, 11(1), 92.

Liu X, et al. (2020) Genetic mapping and genomic selection for maize stalk strength. BMC plant biology, 20(1), 196.

Human MP, et al. (2020) Time-Course RNAseq Reveals Exserohilum turcicum Effectors and Pathogenicity Determinants. Frontiers in microbiology, 11, 360.

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.

Marks RA, et al. (2019) Genome of the tropical plant Marchantia inflexa: implications for sex chromosome evolution and dehydration tolerance. Scientific reports, 9(1), 8722.

Rashmi D, et al. (2019) Integrative omics analysis in Pandanus odorifer (Forssk.) Kuntze reveals the role of Asparagine synthetase in salinity tolerance. Scientific reports, 9(1), 932.

Ma Y, et al. (2019) A pan-transcriptome analysis shows that disease resistance genes have undergone more selection pressure during barley domestication. BMC genomics, 20(1), 12.

Zhang C, et al. (2018) Transcriptional and physiological data reveal the dehydration memory behavior in switchgrass (Panicum virgatum L.). Biotechnology for biofuels, 11, 91.

Zhang C, et al. (2018) Long non-coding RNAs of switchgrass (Panicum virgatum L.) in multiple dehydration stresses. BMC plant biology, 18(1), 79.

Qin L, et al. (2017) Proteomic analysis of macrophage in response to Edwardsiella tarda-infection. Microbial pathogenesis, 111, 86.

Straub D, et al. (2017) Cross-Species Genome-Wide Identification of Evolutionary Conserved MicroProteins. Genome biology and evolution, 9(3), 777.

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.

Cheon SA, et al. (2017) A novel bZIP protein, Gsb1, is required for oxidative stress response, mating, and virulence in the human pathogen Cryptococcus neoformans. Scientific reports, 7(1), 4044.

Schwager EE, et al. (2017) The house spider genome reveals an ancient whole-genome duplication during arachnid evolution. BMC biology, 15(1), 62.

Nayak SN, et al. (2017) Aspergillus flavus infection triggered immune responses and host-pathogen cross-talks in groundnut during in-vitro seed colonization. Scientific reports, 7(1), 9659.

Malhotra S, et al. (2017) Decoding the similarities and differences among mycobacterial species. PLoS neglected tropical diseases, 11(8), e0005883.