Resource Summary Report

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agriGO

RRID:SCR_006989
Type: Tool

Proper Citation

agriGO (RRID:SCR_006989)

Resource Information

URL: http://bioinfo.cau.edu.cn/agriGO/

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Description: A web-based tool and database for the gene ontology analysis. Its focus is on agricultural species and is user-friendly. The agriGO is designed to provide deep support to agricultural community in the realm of ontology analysis. Compared to other available GO analysis tools, unique advantages and features of agriGO are: # The agriGO especially focuses on agricultural species. It supports 45 species and 292 datatypes currently. And agriGO is designed as an user-friendly web server. # New tools including PAGE (Parametric Analysis of Gene set Enrichment), BLAST4ID (Transfer IDs by BLAST) and SEACOMPARE (Cross comparison of SEA) were developed. The arrival of these tools provides users with possibilities for data mining and systematic result exploration and will allow better data analysis and interpretation. # The exploratory capability and result visualization are enhanced. Results are provided in different formats: HTML tables, tabulated text files, hierarchical tree graphs, and flash bar graphs. # In agriGO, PAGE and SEACOMPARE can be used to carry out cross-comparisons of results derived from different data sets, which is very important when studying multiple groups of experiments, such as in time-course research. Platform: Online tool

Abbreviations: agriGO

Synonyms: agriGO -- GO Analysis Toolkit and Database for Agricultural Community

Resource Type: data or information resource, analysis service resource, production service resource, service resource, data analysis service, database

Defining Citation: PMID:20435677

Keywords: browser, gene, online tool, visualization, statistical analysis, term enrichment, text mining, ontology or annotation browser, ontology or annotation visualization, database or data warehouse, bio.tools

Funding: Ministry of Science and Technology of China 90817006;
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Availability: Free for academic use

Resource Name: agriGO

Resource ID: SCR_006989

Alternate IDs: nlx_149099, OMICS_02265, biotools:agrigo

Alternate URLs: https://bio.tools/agrigo

Record Creation Time: 20220129T080239+0000

Record Last Update: 20250513T060853+0000

Ratings and Alerts

No rating or validation information has been found for agriGO.

No alerts have been found for agriGO.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1663 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Zluhan-Martínez E, et al. (2025) The MADS-box gene XAANTAL1 participates in Arabidopsis thaliana primary root growth and columella stem cell patterns in response to ROS, via direct regulation of PEROXIDASE 28 and RETINOBLASTOMA-RELATED genes. Journal of experimental botany, 76(2), 411.

Murithi A, et al. (2025) Global Transcriptomic Analysis of Inbred Lines Reveal Candidate Genes for Response to Maize Lethal Necrosis. Plants (Basel, Switzerland), 14(2).

Ma S, et al. (2025) OsBRW1, a novel blast-resistant gene, coded a NBS-LRR protein to

interact with OsSRFP1 to balance rice growth and resistance. Plant biotechnology journal, 23(1), 250.

Luo Y, et al. (2025) Characterization and functional analysis of conserved non-coding sequences among poaceae: insights into gene regulation and phenotypic variation in maize. BMC genomics, 26(1), 46.

Hemara LM, et al. (2025) Identification and Characterization of Innate Immunity in Actinidia melanandra in Response to Pseudomonas syringae pv. actinidiae. Plant, cell & environment, 48(2), 1037.

Kolesnikova A, et al. (2025) Drought Response in the Transcriptome and Ionome of Wild and Domesticated Lablab purpureus L. Sweet, an Underutilized Legume. Plant-environment interactions (Hoboken, N.J.), 6(1), e70027.

Korek M, et al. (2025) Strigolactone insensitivity affects differential shoot and root transcriptome in barley. Journal of applied genetics, 66(1), 15.

Gholami Z, et al. (2025) Comparative Proteomics of Resistant and Susceptible Strains of Frankliniella occidentalis to Abamectin. Electrophoresis, 46(1-2), 112.

Li Y, et al. (2025) Epitranscriptome profiles reveal participation of the RNA methyltransferase gene OsMTA1 in rice seed germination and salt stress response. BMC plant biology, 25(1), 115.

Yuan X, et al. (2025) The SUMO-conjugating enzyme OsSCE1a from wild rice regulates the functional stay-green trait in rice. Plant biotechnology journal, 23(2), 615.

Dziubek D, et al. (2024) NTRC and thioredoxins m1/m2 underpin the light acclimation of plants on proteome and metabolome levels. Plant physiology, 194(2), 982.

Zhang Y, et al. (2024) Antibody array-based proteome approach reveals proteins involved in grape seed development. Plant physiology, 195(1), 462.

Panahi B, et al. (2024) Global transcriptome analysis identifies critical functional modules associated with multiple abiotic stress responses in microalgae Chromochloris zofingiensis. PloS one, 19(8), e0307248.

Chun J, et al. (2024) Cytokinin-mediated enhancement of potato growth and yield by Verticillium Dahliae effector VDAL under low temperature stress. BMC plant biology, 24(1), 1115.

Li J, et al. (2024) ZmELP1, an Elongator complex subunit, is required for the maintenance of histone acetylation and RNA Pol II phosphorylation in maize kernels. Plant biotechnology journal, 22(5), 1251.

Armendariz I, et al. (2024) Rhytidome- and cork-type barks of holm oak, cork oak and their hybrids highlight processes leading to cork formation. BMC plant biology, 24(1), 488.

Itoh H, et al. (2024) Real-time emulation of future global warming reveals realistic impacts on the phenological response and quality deterioration in rice. Proceedings of the National Academy of Sciences of the United States of America, 121(21), e2316497121.

Jackson AC, et al. (2024) Genomics of ecological adaptation in Canary Island Descurainia (Brassicaceae) and comparisons with other Brassicaceae. Ecology and evolution, 14(8), e70144.

Chen Y, et al. (2024) Telomere-to-telomere genome assembly of Eleocharis dulcis and expression profiles during corm development. Scientific data, 11(1), 869.

Soulé S, et al. (2024) The root-knot nematode effector MiEFF12 targets the host ER quality control system to suppress immune responses and allow parasitism. Molecular plant pathology, 25(7), e13491.