

Resource Summary Report

Generated by [NIF](#) on Aug 27, 2026

[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, THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: agriGO

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

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

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

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Availability: THIS RESOURCE IS NO LONGER IN SERVICE

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: 20260821T193816+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 1743 mentions in open access literature.

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

Wu CC, et al. (2026) Serial Spatial Transcriptomes Reveal Regulatory Transitions in Maize Leaf Development. *Plant biotechnology journal*, 24(5), 2787.

Zhu Y, et al. (2026) BoLAG-BoIRPI2-BoIBAM4 Module Regulates the Bolting of Curd by Modulating Starch Metabolism in Broccoli (*Brassica oleracea* var. *italica*). *Plant biotechnology journal*, 24(3), 1465.

Lei C, et al. (2025) Chemical Glycoproteomic Profiling in Rice Seedlings Reveals N-glycosylation in the ERAD-L Machinery. *Molecular & cellular proteomics : MCP*, 24(2), 100883.

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).

Zluhan-Martinez 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.

Hong X, et al. (2025) Identification of key candidate genes regulating hundred-grain weight in the maize inbred line Ye107 from Southern China. *Plant cell reports*, 44(9), 206.

Hamid R, et al. (2025) Genome-wide identification and characterization of DUF789 genes in cotton: implications for fibre development. *BMC plant biology*, 25(1), 1192.

Wang Q, et al. (2025) Natural variation in ZmNRT2.5 modulates husk leaf width and promotes seed protein content in maize. *Plant biotechnology journal*, 23(4), 1039.

Zhang P, et al. (2025) Systems analysis of long-term heat stress responses in the C4 grass *Setaria viridis*. *The Plant cell*, 37(4).

Sun L, et al. (2025) Interspecific Hybridization Enhanced Tolerance to Salinity and Cadmium Stress Through Modifying Biochemical, Physiological, and Resistance Gene Levels, Especially in Polyploid Rice: A Sustainable Way for Stress-Resilient Rice. *Rice* (New York, N.Y.), 18(1), 19.

Adamik L, et al. (2025) Suboptimal pre-anthesis water status mitigates wheat susceptibility to fusarium head blight and triggers specific metabolic responses. *Scientific reports*, 15(1), 11773.

Cackett L, et al. (2025) Increased chloroplast area in the rice bundle sheath through cell-specific perturbation of brassinosteroid signaling. *Plant physiology*, 197(4).

Chen L, et al. (2025) ZmSSRP1, transactivated by OPAQUE11, positively regulates starch biosynthesis in maize endosperm. *Plant biotechnology journal*, 23(9), 3770.

Hao S, et al. (2025) FLL2 modulates Arabidopsis development and stress tolerance via polyadenylation and CPSF73 interaction. *iScience*, 28(6), 112579.

Yadav HK, et al. (2025) Telomere-to-telomere genome assembly of linseed (*Linum usitatissimum* L.) for functional genomics and accelerated genetic improvement. *Plant biotechnology journal*, 23(9), 3919.

Pradhan AK, et al. (2025) Predictive prioritization of genes significantly associated with biotic and abiotic stresses in maize using machine learning algorithms. *Frontiers in plant science*, 16, 1611784.

Kim EJ, et al. (2025) OsPRK1/2/3-mediated reactive oxygen species signaling is required for pollen tube germination in rice. *Journal of integrative plant biology*, 67(7), 1965.

Zhang L, et al. (2025) Chromosome-scale genome assembly of *Phyllanthus emblica* L. 'Yingyu'. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 32(2).

Hou N, et al. (2025) MdDSK2a-Like-MdMTA Module Functions in Apple Cold Response via Regulating ROS Detoxification and Cell Wall Deposition. *Advanced science* (Weinheim, Baden-Wurtemberg, Germany), 12(26), e2504405.

Ding G, et al. (2025) Identifications of Genes Involved in ABA and MAPK Signaling Pathways Positively Regulating Cold Tolerance in Rice. *Plants* (Basel, Switzerland), 14(4).