

Resource Summary Report

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AgBase

RRID:SCR_007547

Type: Tool

Proper Citation

AgBase (RRID:SCR_007547)

Resource Information

URL: <http://www.agbase.msstate.edu/>

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Description: A curated, open-source, web-accessible resource for functional analysis of agricultural plant and animal gene products. Our long-term goal is to serve the needs of the agricultural research communities by facilitating post-genome biology for agriculture researchers and for those researchers primarily using agricultural species as biomedical models. AgBase provides tools designed to assist with the analysis of proteomics data and tools to evaluate experimental datasets using the GO. Additional tools for sequence analysis are also provided. We use controlled vocabularies developed by the Gene Ontology (GO) Consortium to describe molecular function, biological process, and cellular component for genes and gene products in agricultural species. AgBase will also accept annotations from any interested party in the research communities. AgBase develops freely available tools for functional analysis, including tools for using GO. We appreciate any and all questions, comments, and suggestions. AgBase uses the NCBI Blast program for searches for similar sequences. And the Taxonomy Browser allows users to find the NCBI defined taxon ID for or taxon name for different organisms.

Abbreviations: AgBase

Resource Type: data or information resource, database

Defining Citation: [PMID:21075795](#)

Keywords: gene ontology, agricultural species, biological process, cellular component for genes, molecular function, protein identification, animals, plants, microbes, parasites, bio.tools, FASEB list

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Extension Service 2007-35205-17941;

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NSF EPS 0903787

Resource Name: AgBase

Resource ID: SCR_007547

Alternate IDs: nif-0000-02537, biotools:agbase, r3d100012427

Alternate URLs: <https://bio.tools/agbase>, <https://doi.org/10.17616/R3P772>

Record Creation Time: 20220129T080242+0000

Record Last Update: 20260905T133140+0000

Ratings and Alerts

No rating or validation information has been found for AgBase.

No alerts have been found for AgBase.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 112 mentions in open access literature.

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

?eksteryt? V, et al. (2026) Antioxidant protein signatures in honey: botanical influence and proteomic variability. Food chemistry: X, 34, 103647.

Tanaka T, et al. (2025) Reference-based chromosome-scale assembly of Japanese barley (*Hordeum vulgare* ssp. *vulgare*) cultivar Hayakiso 2. DNA research : an international journal for rapid publication of reports on genes and genomes, 32(4).

Perveen A, et al. (2025) Integrative physiological, biochemical, and proteomic analysis of the leaves of two cotton genotypes under heat stress. PloS one, 20(1), e0316630.

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).

Lu F, et al. (2022) 2D-DIGE based proteome analysis of wheat-Thinopyrum intermedium 7XL/7DS translocation line under drought stress. BMC genomics, 23(1), 369.

Abdollahi H, et al. (2021) Coronavirus: proteomics analysis of chicken kidney tissue infected with variant 2 (IS-1494)-like avian infectious bronchitis virus. Archives of virology, 166(1), 101.

- Li T, et al. (2021) Label-Free Quantitative Proteome Analysis Reveals the Underlying Mechanisms of Grain Nuclear Proteins Involved in Wheat Water-Deficit Response. *Frontiers in plant science*, 12, 748487.
- Zhou X, et al. (2021) Identification and Functional Analysis of Tomato TPR Gene Family. *International journal of molecular sciences*, 22(2).
- Wimberley J, et al. (2020) De novo Sequencing and Analysis of *Salvia hispanica* Tissue-Specific Transcriptome and Identification of Genes Involved in Terpenoid Biosynthesis. *Plants (Basel, Switzerland)*, 9(3).
- Wang D, et al. (2020) Secretome Analysis of the Banana Fusarium Wilt Fungi Foc R1 and Foc TR4 Reveals a New Effector OASTL Required for Full Pathogenicity of Foc TR4 in Banana. *Biomolecules*, 10(10).
- Yamamoto KA, et al. (2020) Quantitative proteomic analysis of the tizoxanide effect in vero cells. *Scientific reports*, 10(1), 14733.
- Li F, et al. (2020) Comparative proteomics analysis of patients with quick development and slow development Chronic Obstructive Pulmonary Disease (COPD). *Life sciences*, 256, 117829.
- Liu X, et al. (2020) Genetic mapping and genomic selection for maize stalk strength. *BMC plant biology*, 20(1), 196.
- Paes VM, et al. (2020) Comparative Analysis of Porcine Follicular Fluid Proteomes of Small and Large Ovarian Follicles. *Biology*, 9(5).
- Zhang Y, et al. (2020) The genome of opportunistic fungal pathogen *Fusarium oxysporum* carries a unique set of lineage-specific chromosomes. *Communications biology*, 3(1), 50.
- 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.
- Paes VM, et al. (2019) Proteome changes of porcine follicular fluid during follicle development. *Journal of animal science and biotechnology*, 10, 94.
- Butsayawarapat P, et al. (2019) Comparative Transcriptome Analysis of Waterlogging-Sensitive and Tolerant Zombi Pea (*Vigna Vexillata*) Reveals Energy Conservation and Root Plasticity Controlling Waterlogging Tolerance. *Plants (Basel, Switzerland)*, 8(8).
- 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.
- Furci L, et al. (2019) Identification and characterisation of hypomethylated DNA loci controlling quantitative resistance in *Arabidopsis*. *eLife*, 8.