

Resource Summary Report

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MaizeGDB

RRID:SCR_006600

Type: Tool

Proper Citation

MaizeGDB (RRID:SCR_006600)

Resource Information

URL: <http://www.maizegdb.org>

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Description: Collection of data related to crop plant and model organism Zea mays. Used to synthesize, display, and provide access to maize genomics and genetics data, prioritizing mutant and phenotype data and tools, structural and genetic map sets, and gene models and to provide support services to the community of maize researchers. Data stored at MaizeGDB was inherited from the MaizeDB and ZmDB projects. Sequence data are from GenBank. Data are searchable by phenotype, traits, Pests, Gel Pattern, and Mutant Images.

Abbreviations: MaizeGDB

Synonyms: Maize Genetics and Genomics Database, MaizeGDB, MaizeGDB Locus

Resource Type: analysis service resource, data analysis service, data or information resource, data repository, database, organism-related portal, portal, production service resource, service resource, storage service resource, topical portal

Defining Citation: [PMID:21624896](#), [PMID:18769488](#), [PMID:15888678](#), [PMID:14681441](#)

Keywords: ze mays, corn, model organism, genome, locus, metabolic pathway, genetics, genomics, sequence, gene product, function, literature reference, phenotype, trait, pest, gel pattern, mutant, blast, gene, image, corn, genotype-environment interaction, gene mapping, plant genome mapping, plant genome, gold standard, bio.tools, FASEB list

Funding: National Corn Growers Association ;
NSF ;
USDA/ARS ;
USDA

Availability: Free, Freely available, Acknowledgement requested, The community can contribute to this resource

Resource Name: MaizeGDB

Resource ID: SCR_006600

Alternate IDs: OMICS_01655, biotools:MaizeDIG, nif-0000-03096, r3d100010795

Alternate URLs: <https://bio.tools/MaizeDIG>, <https://doi.org/10.17616/R3V32B>

Record Creation Time: 20220129T080237+0000

Record Last Update: 20260821T193813+0000

Ratings and Alerts

No rating or validation information has been found for MaizeGDB.

No alerts have been found for MaizeGDB.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1047 mentions in open access literature.

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

Wang J, et al. (2026) Integrated experimental and computational workflows for single-cell transcriptomics in plants. Plant methods, 22(1), 12.

Wang S, et al. (2026) Predicted protein 3D structures provide essential insights into the genetic architecture underlying phenotypic diversity in maize. Genome research, 36(1), 214.

Chen M, et al. (2026) Genome-wide association study identifies key loci and candidate genes for maize grain yield-related traits. BMC plant biology, 26(1).

Zhang X, et al. (2026) Genome-wide identification and characterization of the RPA gene family in maize. BMC plant biology, 26(1).

Abdolmaleki A, et al. (2026) Transcriptomic and physiological effects of superabsorbent polymer seed coating on maize under drought stress. Frontiers in plant science, 17, 1736004.

Sun J, et al. (2026) An integrated QTL-GWAS approach fine-maps a major locus (qMWS3 - 2) for stable resistance to maize white spot in tropical germplasm. BMC plant biology, 26(1).

- Wang S, et al. (2026) QTL mapping, validation, and candidate gene predicting for maize plant architecture traits via bulked segregant analysis plus linkage analysis with F₂ population. *BMC plant biology*, 26(1).
- Yang Z, et al. (2026) Identification and Expression Analysis of the Goji Haploid-Inducible Gene DMP. *International journal of molecular sciences*, 27(6).
- Sun S, et al. (2026) Integrating BSA-Seq and RNA-Seq to Identify Major QTLs and Candidate Genes Conferring Resistance to Fusarium Ear Rot in Maize. *Plants (Basel, Switzerland)*, 15(6).
- Fattel L, et al. (2026) Go Big or go home: a new gene ontology subset that improves plant gene function prediction. *Plant methods*, 22(1).
- Meng F, et al. (2026) Structural, Evolutionary, and Regulatory Divergence of FAH12 from FAD2 Reveals Recurrent Independent Neofunctionalization Underlying Ricinoleic Acid Biosynthesis in *Ricinus communis*. *Plants (Basel, Switzerland)*, 15(10).
- Guo C, et al. (2026) Coupling photosynthetic physiology and C₄ enzyme regulation enhances grain yield in no-tillage intercropped maize in an irrigated oasis region. *Frontiers in plant science*, 17, 1780528.
- Gee M, et al. (2026) Yield impact of source-sink-regulated senescence in hybrid maize and genetic architecture in exPVP inbreds. *TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik*, 139(5).
- Cui N, et al. (2026) Genome-wide-association-analysis-based identification of genetic loci and candidate genes associated with seedling emergence rate in super-sweet corn (*Zea mays* L.). *BMC plant biology*, 26(1).
- Zhu T, et al. (2026) NUT1-Exo70A1 Regulates Xylem Vessel Development and Influences Water Use Efficiency in Maize. *Nature communications*, 17(1).
- Xu T, et al. (2026) Genome-Wide Identification of Binding Motifs and Drought-Responsive Target Genes by the Transcription Factor ZmNAC20 in Maize. *Plants (Basel, Switzerland)*, 15(3).
- Li L, et al. (2026) Genome-Wide Analysis of YABBY Gene Family Reveals ZmYABBY8 as a Central Regulator Involved in Drought and Heat Stress Tolerance in Maize. *Plants (Basel, Switzerland)*, 15(5).
- Shi J, et al. (2026) ZmMYB127 controls maize endosperm filling via dual-transcriptional regulation to improve grain yield and quality. *Nature plants*, 12(3), 617.
- Sun J, et al. (2026) ZmWAKL21 is a maize wall-associated kinase-like protein that interacts with AvrRppC and contributes to southern corn rust resistance. *Cellular & molecular biology letters*, 31(1).
- Li X, et al. (2026) Genetic Mapping Identifies Stable QTL and Candidate Genes Regulating Internode Proportion for Maize Plant Architecture Improvement. *Genes*, 17(2).