Resource Summary Report

Generated by dkNET on May 6, 2025

MaizeGDB

RRID:SCR_006600

Type: Tool

Proper Citation

MaizeGDB (RRID:SCR_006600)

Resource Information

URL: http://www.maizegdb.org

Proper Citation: MaizeGDB (RRID:SCR_006600)

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

Defining Citation: PMID:21624896, PMID:18769488, PMID:15888678, PMID:14681441

Keywords: zea 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: USDA; USDA/ARS;

NSF;

National Corn Growers Association

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

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

Record Creation Time: 20220129T080237+0000

Record Last Update: 20250506T060707+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 736 mentions in open access literature.

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

Mishra SJ, et al. (2025) Unraveling the interactive effect of opaque2 and waxy1 genes on kernel nutritional qualities and physical properties in maize (Zea mays L.). Scientific reports, 15(1), 3425.

Wang X, et al. (2025) Genome-wide identification and functional roles relating to anthocyanin biosynthesis analysis in maize. BMC plant biology, 25(1), 57.

Farid B, et al. (2025) Expression divergence of BAG gene family in maize under heat stress. BMC plant biology, 25(1), 16.

Sullivan A, et al. (2025) 20 years of the Bio-Analytic Resource for Plant Biology. Nucleic acids research, 53(D1), D1576.

Casatejada-Anchel R, et al. (2025) Metabolic engineering of the serine/glycine network as a means to improve the nitrogen content of crops. Plant biotechnology journal, 23(1), 268.

Yang X, et al. (2025) Novel candidate genes and genetic basis analysis of kernel starch content in tropical maize. BMC plant biology, 25(1), 105.

Feng H, et al. (2025) Cross-species single-nucleus analysis reveals the potential role of whole-genome duplication in the evolution of maize flower development. BMC genomics, 26(1), 3.

Zhou Y, et al. (2025) Maize-Tripsacum-Teosinte allopolyploid (MTP), a novel dwarf mutant inducer tool in maize. Plant biotechnology journal, 23(1), 112.

Gupta M, et al. (2025) Meta-QTL analysis for mining of candidate genes and constitutive gene network development for viral disease resistance in maize (Zea mays L.). Heliyon, 11(1), e40984.

Yang M, et al. (2025) Identification of the arl1 locus controlling leaf rolling and its application in maize breeding. Molecular breeding: new strategies in plant improvement, 45(1), 9.

Urrutia M, et al. (2024) Identification of metabolic and protein markers representative of the impact of mild nitrogen deficit on agronomic performance of maize hybrids. Metabolomics: Official journal of the Metabolomic Society, 20(6), 128.

Luo B, et al. (2024) SPX family response to low phosphorus stress and the involvement of ZmSPX1 in phosphorus homeostasis in maize. Frontiers in plant science, 15, 1385977.

Gupta P, et al. (2024) Plant Reactome Knowledgebase: empowering plant pathway exploration and OMICS data analysis. Nucleic acids research, 52(D1), D1538.

Mendieta JP, et al. (2024) Investigating the cis-Regulatory Basis of C3 and C4 Photosynthesis in Grasses at Single-Cell Resolution. bioRxiv: the preprint server for biology.

Wu Q, et al. (2024) Transcription factor ZmEREB97 regulates nitrate uptake in maize (Zea mays) roots. Plant physiology, 196(1), 535.

Sidhu JS, et al. (2024) Cortical parenchyma wall width regulates root metabolic cost and maize performance under suboptimal water availability. Journal of experimental botany, 75(18), 5750.

Kawa D, et al. (2024) The soil microbiome modulates the sorghum root metabolome and cellular traits with a concomitant reduction of Striga infection. Cell reports, 43(4), 113971.

Vladeji? J, et al. (2024) Zeocin-induced DNA damage response in barley and its dependence on ATR. Scientific reports, 14(1), 3119.

LaPorte MF, et al. (2024) Investigating genomic prediction strategies for grain carotenoid traits in a tropical/subtropical maize panel. G3 (Bethesda, Md.), 14(5).

Wang Z, et al. (2024) Natural polymorphisms in ZMET2 encoding a DNA methyltransferase modulate the number of husk layers in maize. Plant physiology, 195(3), 2129.