

Resource Summary Report

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CuGenDB

RRID:SCR_018401

Type: Tool

Proper Citation

CuGenDB (RRID:SCR_018401)

Resource Information

URL: <http://cucurbitgenomics.org/>

Proper Citation: CuGenDB (RRID:SCR_018401)

Description: Database to facilitate genomic and genetic data distribution, analysis, mining and integration for cucurbits. To store, mine, analyze, integrate and disseminate Cucurbitaceae family datasets and to provide central portal for cucurbit research and breeding community. Central portal for comparative and functional genomics of cucurbit crops.

Abbreviations: CuGenDB

Synonyms: Cucurbit Genomics Database, Cucurbitaceae family Genomics Database

Resource Type: data or information resource, topical portal, portal, database

Defining Citation: [PMID:30321383](#)

Keywords: Genomic data, genetic data, cucurbit, data distribution, data analysis, data mining, data integration, dataset, comparative genomics, functional genomics, cucurbit crop, FASEB list

Funding: USDA National Institute of Food and Agriculture Specialty Crop Research Initiative ;
US-Israel Binational Agricultural Research and Development Fund ;
USDA Agricultural Research Service ;
International Cucurbit Genomics Initiative

Availability: Free, Freely available

Resource Name: CuGenDB

Resource ID: SCR_018401

Record Creation Time: 20220129T080340+0000

Record Last Update: 20260811T043625+0000

Ratings and Alerts

No rating or validation information has been found for CuGenDB.

No alerts have been found for CuGenDB.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 285 mentions in open access literature.

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

Zhang S, et al. (2026) Comprehensive Genomic Analysis and Expression Profiling of the C2H2-Type Zinc Finger Protein Family Under Abiotic Stresses in Watermelon. *Genes*, 17(5).

Wang X, et al. (2026) Comprehensive analysis of the GeBP gene family in cucumber highlights functional divergence in fruit development and stress tolerance. *BMC plant biology*, 26(1).

Li S, et al. (2026) Genome-Wide Identification and Expression Analysis of the GDPD Gene Family in Cucumber (*Cucumis sativus* L.). *Current issues in molecular biology*, 48(6).

Guo WL, et al. (2026) Genome-wide analysis of WRKY gene family in *Cucurbita moschata* and involvement of CmWRKY22/63/84 in powdery mildew resistance. *BMC genomics*, 27(1), 23.

Bi W, et al. (2026) Genome-Wide Identification of the ZF-HD Gene Family in Melon and Functional Characterization of CmZHD8 in Salt Stress Tolerance. *Plants (Basel, Switzerland)*, 15(4).

Zhang Z, et al. (2026) Soil acidification dismantles a citrulline-mediated microbe-metabolite-host defense axis in watermelon, exacerbating *Fusarium* wilt. *NPJ biofilms and microbiomes*, 12(1).

Liu S, et al. (2026) Comprehensive genome-wide identification, structural analysis, and cold-responsive expression profiling of double B-box (DBB) transcription factors in melon (*Cucumis melo* L.). *BMC plant biology*, 26(1).

Tan J, et al. (2026) Photosystem Perturbation by Staygreen Mutations Confers Allele-Dependent Defences Against Infections of Pathogens With Different Lifestyles and Abiotic

Stress Tolerance. *Plant, cell & environment*, 49(1), 585.

Li M, et al. (2026) The Microtubule-Associated Protein CsTON2 Interacts With CsTRM5 and CsSUN to Regulate Fruit Shape Development in Cucumber. *Plant biotechnology journal*, 24(4), 2725.

Bao R, et al. (2026) Transcriptomic analysis identifies key regulatory genes for blossom-end scar size and GA3 regulation in melon (*Cucumis melo* L.). *BMC genomics*, 27(1).

Liang H, et al. (2026) Jasmonate regulates male sterility in cucumber. *aBIOTECH*, 7(2), 100041.

Wei HT, et al. (2026) Two pear phyto cytokines PbePep4 and PdrPep6 interfamilyally elicit broad-spectrum immunity against various pathogens in crops. *Horticulture research*, 13(5), uhag027.

Lan G, et al. (2026) Genome-Wide Identification and Expression Profiling of the PYL Gene Family in Watermelon Under Abiotic Stresses. *Genes*, 17(4).

Zhang X, et al. (2026) Evolutionary and Functional Characterization of an Auxin Methyltransferase (CsIAMT) in Cucumber Reveals Its Role in Stress Adaptation and Development. *Ecology and evolution*, 16(3), e73178.

Muthusamy B, et al. (2026) Functional Validation of the Melon Fom-1 Gene, Controlling Resistance to *Fusarium oxysporum* Races 0 and 2, by CRISPR/Cas9 Mutagenesis. *Molecular plant pathology*, 27(4), e70258.

Liu Y, et al. (2026) Whole genome identification and operational analysis of the bHLH gene family in longan and the role of DlbHLH8 in flowering regulation. *Frontiers in plant science*, 17, 1824280.

Han J, et al. (2026) A comprehensive analysis of two Chinese cucumber genomes and a mutant population as resources for precision breeding. *Horticulture research*, 13(2), uhaf284.

Yang M, et al. (2026) Genome-wide analysis of the SOS2 gene family in melon (*Cucumis melo* L.) and functional characterization of MELO3C010334 in response to salt stress. *BMC plant biology*, 26(1).

Lai J, et al. (2026) Genome-wide identification of the ABCB gene family in melon (*Cucumis melo* L.) and their expression during axillary bud development. *Frontiers in plant science*, 17, 1770152.

Liu P, et al. (2025) Comparative Transcriptome Analysis of Gene Responses of Salt-Tolerant and Salt-Sensitive Watermelon Cultivars' Roots to Salt Stress. *Plants (Basel, Switzerland)*, 14(7).