

Resource Summary Report

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Gramene

RRID:SCR_002829

Type: Tool

Proper Citation

Gramene (RRID:SCR_002829)

Resource Information

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

Proper Citation: Gramene (RRID:SCR_002829)

Description: Curated, open-source, integrated data resource for comparative functional genomics in crops and model plant species to facilitate the study of cross-species comparisons using information generated from projects supported by public funds. It currently hosts annotated whole genomes in over two dozen plant species and partial assemblies for almost a dozen wild rice species in the Ensembl browser, genetic and physical maps with genes, ESTs and QTLs locations, genetic diversity data sets, structure-function analysis of proteins, plant pathways databases (BioCyc and Plant Reactome platforms), and descriptions of phenotypic traits and mutations. The web-based displays for phenotypes include the Genes and Quantitative Trait Loci (QTL) modules. Sequence based relationships are displayed in the Genomes module using the genome browser adapted from Ensembl, in the Maps module using the comparative map viewer (CMap) from GMOD, and in the Proteins module displays. BLAST is used to search for similar sequences. Literature supporting all the above data is organized in the Literature database. In addition, Gramene now hosts a variety of web services including a Distributed Annotation Server (DAS), BLAST and a public MySQL database. Twice a year, Gramene releases a major build of the database and makes interim releases to correct errors or to make important updates to software and/or data. Additionally you can access Gramene through an FTP site.

Abbreviations: GR

Synonyms: GR PROTEIN, RiceGenes, GR REF, GR GENE, Gramene: A Resource for Comparative Grass Genomics, GR QTL

Resource Type: database, data or information resource

Defining Citation: [PMID:21076153](#), [PMID:17984077](#), [PMID:16381966](#)

Keywords: crop, plant genome, genetic, blast, gene, genome, genetic diversity, pathway, protein, marker, quantitative trait locus, comparative map, phenotype, genomics, physiology, comparative, grain, expressed sequence tag, trait, mutation, environment, taxonomy, web service, bio.tools, FASEB list

Funding: USDA IFAFS 00-52100-9622;
USDA 58-1907-0-041;
USDA 1907-21000-030;
NSF 0321685;
NSF 0703908;
NSF 0851652

Availability: Free, Freely available

Resource Name: Gramene

Resource ID: SCR_002829

Alternate IDs: r3d100010856, nif-0000-02926, nlx_65829, biotools:gramene

Alternate URLs: <https://bio.tools/gramene>, <https://doi.org/10.17616/R3GG7M>

License: Open unspecified license

Record Creation Time: 20220129T080215+0000

Record Last Update: 20260805T044045+0000

Ratings and Alerts

No rating or validation information has been found for Gramene.

No alerts have been found for Gramene.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 778 mentions in open access literature.

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

Yang D, et al. (2026) GNA regulates rice spikelet formation via DEP1-enhanced repression of OsCKX2 and cytokinin modulation. Plant signaling & behavior, 21(1), 2604856.

Wu S, et al. (2025) OsLC1, a transaldolase, regulates cell patterning and leaf morphology through modulation of secondary metabolism. Plant biotechnology

journal, 23(5), 1751.

Ji S, et al. (2025) Pan-WD40ome analysis of 26 diverse inbred lines reveals the structural and functional diversity of WD40 proteins in maize. *BMC genomics*, 26(1), 181.

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.

Concepcion JCT, et al. (2025) Metabolite Quantitative Trait Loci Mapping for Fragrance and Fatty Acid Composition in Rice (*Oryza Sativa* L.). *Rice* (New York, N.Y.), 18(1), 96.

Ardie SW, et al. (2025) Foxtail millet research in supporting climate change resilience efforts: Bibliometric analysis and focused literature review. *Heliyon*, 11(3), e42348.

Wu H, et al. (2025) Multiplexed transcriptomic analyzes of the plant embryonic hourglass. *Nature communications*, 16(1), 802.

Wang F, et al. (2025) A telomere-to-telomere genome assembly of Chinese grain sorghum 654. *Scientific data*, 12(1), 460.

Yu Z, et al. (2025) Genetic dissection of QTL for important agronomic traits and fine-mapping of *qGL4* and *qGW6* based on a short-width grain rice CSSL-Z691. *Frontiers in plant science*, 16, 1539625.

Kumar B, et al. (2025) Dissecting the genetic architecture of polygenic nutritional traits in maize through meta-QTL analysis. *Food chemistry. Molecular sciences*, 10, 100256.

Kazemzadeh S, et al. (2025) Genome-wide association mapping and transcriptional analysis uncover genetic determinants of minor tocopherols in rice seeds. *Scientific reports*, 15(1), 28530.

Huang K, et al. (2025) *OsMYBR1*, a 1R-MYB Family Transcription Factor Regulates Starch Biosynthesis in Rice Endosperm. *Life* (Basel, Switzerland), 15(6).

Yang Y, et al. (2025) Identification and Genetic Analysis of Collinearity Loci for Interspecific Hybrid Sterility in Genus *Oryza*. *Rice* (New York, N.Y.), 18(1), 43.

Liu H, et al. (2025) Maize big embryo 6 reveals roles of plastidial and cytosolic prephenate aminotransferases in seed and plant development. *The Plant cell*, 37(6).

Basmenj ER, et al. (2025) Computational epitope-based vaccine design with bioinformatics approach; a review. *Heliyon*, 11(1), e41714.

Mu X, et al. (2025) Whole-genome identification of HSF family genes in *Cerasus humilis* and expression analysis under high-temperature stress. *Frontiers in plant science*, 16, 1553187.

Jin X, et al. (2025) *OsPRMT6b* balances plant growth and high temperature stress by feedback inhibition of abscisic acid signaling. *Nature communications*, 16(1), 5173.

Lv D, et al. (2025) Analysis of candidate genes identified via genome-wide association analysis of sugar-related traits in maize kernels. *The plant genome*, 18(3), e70101.

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

Steele K, et al. (2025) Thousands of trait-specific KASP markers designed for diverse breeding applications in rice (*Oryza sativa*). *G3 (Bethesda, Md.)*, 15(1).