

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>

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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: data or information resource, database

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: 20260811T043150+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 863 mentions in open access literature.

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

Tan K, et al. (2026) Near-complete genome assembly of a transformation-efficient elite inbred line LH244 and its comparison with B73. Journal of integrative plant biology, 68(2), 366.

Zhang J, et al. (2026) Transcriptional Regulation of Starch Biosynthesis in Sorghum Grain by a MIKC-Type MADS-Box Transcription Factor: An In Vitro Analysis. Plants (Basel,

Switzerland), 15(7).

Ni J, et al. (2026) A rice ceRNA module suppresses *Rhizoctonia solani*-induced cross-kingdom RNAi to reduce fungal pathogenicity. *Nature communications*, 17(1).

Yuan S, et al. (2026) The receptor-like pseudokinase LENG stimulates chilling tolerance in rice by inhibiting the activity of the OsCRPK1-OsGF14d module. *Journal of integrative plant biology*, 68(5), 1333.

Zhong T, et al. (2026) The maize mitogen-activated protein kinase kinase gene *ZmMAPKKK45* is associated with multiple disease resistance. *The New phytologist*, 249(6), 3003.

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.

Sandhu N, et al. (2026) GWAS reveals genetic interplay between root architecture and nitrogen uptake in *Aegilops tauschii*. *BMC plant biology*, 26(1).

Liang C, et al. (2026) QTL mapping for different resistant starch subtypes identified a superior haplotype balancing high RS content and relatively good eating and cooking qualities in rice. *Frontiers in plant science*, 17, 1763165.

de Araujo AT, et al. (2026) KitBase Expanded: An Integrated Genomic and Phenotypic Resource for 3,268 Fast-Neutron-Irradiated Rice Mutants. *Database : the journal of biological databases and curation*, 2026.

Feng X, et al. (2026) A new plant SUMO ligase, MPEL1, synergizes with MAPK16 to regulate resistance against *Fusarium* pathogens. *The EMBO journal*, 45(13), 4670.

Park JR, et al. (2026) Integrating image-based phenotyping and QTL mapping to enhance genetic resistance and accelerate breeding for bacterial grain rot resistance in rice. *TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik*, 139(4).

Cheng S, et al. (2026) Redundant Glycerol-3-Phosphate Acyltransferases Regulate Thermo-Sensitive Genic Male Sterility in Rice. *Plant biotechnology journal*, 24(7), 4689.

Liu B, et al. (2026) Perturbation of Anion/Cation Transport Leads to Apical Panicle Abortion in Rice by Disrupting Ca²⁺ Homeostasis. *Plant biotechnology journal*, 24(3), 1503.

Mohamadiaza M, et al. (2026) Analysis of Genetic Variation of Rice Straw Characteristics and Its Influence on Biomass. *Plant direct*, 10(1), e70134.

Reddy Challa VK, et al. (2026) qAG2.1 Is Associated with Anaerobic Germination Tolerance in Rice Seeds: Evidence from Haplotype Analysis and Marker-Assisted Breeding. *Plants (Basel, Switzerland)*, 15(5).

Hou H, et al. (2026) Genome-wide characterization of cytochrome P450 genes in *Solanum tuberosum* and StCYP481 role in salt tolerance. *BMC plant biology*, 26(1).

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).

Darmagaru S, et al. (2026) Genome-wide association studies for identifying SNPs and candidate genes associated with grain quality traits in rice (*Oryza sativa* L.). *The plant genome*, 19(2), e70190.

Tello-Ruiz MK, et al. (2026) Adoption of Standard Reference SNP Identifiers in Agricultural Genomics for Interoperability and Data Reuse. *Scientific data*, 13(1).

Das S, et al. (2026) Genome-wide association analysis to identify QTLs and candidate genes associated with grain yield and its related traits under low light conditions in rice (*Oryza sativa* L.). *The plant genome*, 19(1), e70191.