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: A 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: production service resource, data analysis service, service resource, analysis service resource, 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

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USDA 58-1907-0-041;
USDA 1907-21000-030;
NSF 0321685;
NSF 0703908;
NSF 0851652

Availability: Acknowledgement required, Open unspecified license

Resource Name: Gramene

Resource ID: SCR_002829

Alternate IDs: SCR_000532, nif-0000-02926, nlx_65829, biotools:gramene

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

Record Creation Time: 20220129T080215+0000

Record Last Update: 20250428T053014+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 756 mentions in open access literature.

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

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.

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

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

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).

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

Rajendran S, et al. (2024) Functional characterization of plant specific Indeterminate Domain (IDD) transcription factors in tomato (Solanum lycopersicum L.). Scientific reports, 14(1), 8015.

Kumar KP, et al. (2024) Enhancing stress resilience in rice (Oryza sativa L.) through profiling early-stage morpho-physiological and molecular responses to multiple abiotic stress tolerance. Frontiers in plant science, 15, 1342441.

Catlin NS, et al. (2024) Structural variants contribute to phenotypic variation in maize. bioRxiv : the preprint server for biology.

Kazemzadeh S, et al. (2024) Genome-wide association study and genotypic variation for the major tocopherol content in rice grain. Frontiers in plant science, 15, 1426321.

Das AK, et al. (2024) Genome-wide characterization of nitric oxide-induced NBS-LRR genes from Arabidopsis thaliana and their association in monocots and dicots. BMC plant biology, 24(1), 934.

Sowadan O, et al. (2024) Genome-Wide Association Analysis Unravels New Quantitative Trait Loci (QTLs) for Eight Lodging Resistance Constituent Traits in Rice (Oryza sativa L.). Genes, 15(1).

Ferrero-Serrano Á, et al. (2024) Oryza CLIMtools: A genome-environment association resource reveals adaptive roles for heterotrimeric G proteins in the regulation of rice agronomic traits. Plant communications, 5(4), 100813.

Sachdeva S, et al. (2024) New insights into QTNs and potential candidate genes governing rice yield via a multi-model genome-wide association study. BMC plant biology, 24(1), 124.

Zhu M, et al. (2024) The ZmCPK39-ZmDi19-ZmPR10 immune module regulates quantitative resistance to multiple foliar diseases in maize. Nature genetics, 56(12), 2815.

Li N, et al. (2024) Comparative transcriptome analysis and meta-QTLs mapping reveal the regulatory mechanism of cold tolerance in rice at the budding stage. Heliyon, 10(18), e37933.

Zeng R, et al. (2024) Genetic variation in the aquaporin TONOPLAST INTRINSIC PROTEIN 4;3 modulates maize cold tolerance. Plant biotechnology journal, 22(11), 3037.

Kasule F, et al. (2024) Genetic diversity, population structure, and a genome-wide association study of sorghum lines assembled for breeding in Uganda. Frontiers in plant science, 15, 1458179.

Mizutani M, et al. (2024) Identification of An7 as a positive awn regulator from two wild rice species. Breeding science, 74(3), 247.

Guo J, et al. (2024) Genome-wide association study reveals novel QTLs and candidate genes for panicle number in rice. Frontiers in genetics, 15, 1470294.

Espinosa-Vellarino FL, et al. (2024) Enzymes Involved in Antioxidant and Detoxification Processes Present Changes in the Expression Levels of Their Coding Genes under the Stress Caused by the Presence of Antimony in Tomato. Plants (Basel, Switzerland), 13(5).