

Resource Summary Report

Generated by [dkNET](#) on Jul 29, 2026

RiceGAAS

RRID:SCR_007896

Type: Tool

Proper Citation

RiceGAAS (RRID:SCR_007896)

Resource Information

URL: <http://RiceGAAS.dna.affrc.go.jp/>

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Description: A rice genome automated annotation system. This system integrates programs for prediction and analysis of protein-coding gene structure. Integrated softwares are coding region prediction programs (GENSCAN, RiceHMM, FGENESH, MZEF), splice site prediction programs (SplicePredictor), homology search analysis programs (Blast, HMMER, ProfileScan, MOTIF), tRNA gene prediction program (tRNAscan-SE), repetitive DNA analysis programs (RepeatMasker, Printrepeats), signal scan search program (Signal Scan), protein localization site prediction program (PSORT), and program of classification and secondary structure prediction of membrane proteins (SOSUI). Blast against full-length cDNA sequences of japonica rice is integrated. The full-length rice cDNA sequence is provided by KOME database. Interpretation of the coding region is fully automated and gene prediction is accomplished without manual evaluation and modification. Therefore some differences exist between the predicted genes by the system and the manually predicted genes included in the GenBank entries. Please see "comparison table of gene prediction", http://RiceGAAS.dna.affrc.go.jp/rga-bin/col_accur.pl in detail. Further, a unique function is automatically assigned for predicted gene by GFSelector based on the protein homology of the gene. Additionally, the keyword search from the functions predicted by GFSelector is provided.

Synonyms: RiceGAAS

Resource Type: data or information resource, database

Resource Name: RiceGAAS

Resource ID: SCR_007896

Record Creation Time: 20220129T080244+0000

Record Last Update: 20260729T044214+0000

Ratings and Alerts

No rating or validation information has been found for RiceGAAS.

No alerts have been found for RiceGAAS.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 24 mentions in open access literature.

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

Fang N, et al. (2019) Fine mapping of a panicle blast resistance gene Pb-bd1 in Japonica landrace Bodao and its application in rice breeding. Rice (New York, N.Y.), 12(1), 18.

Shimada T, et al. (2018) MITE insertion-dependent expression of CitRKD1 with a RWP-RK domain regulates somatic embryogenesis in citrus nucellar tissues. BMC plant biology, 18(1), 166.

Xu Y, et al. (2017) OSCNGC13 promotes seed-setting rate by facilitating pollen tube growth in stylar tissues. PLoS genetics, 13(7), e1006906.

Liu L, et al. (2017) Fine Mapping and Candidate Gene Analysis of the Tiller Suppression Gene ts1 in Rice. PloS one, 12(1), e0170574.

Sun L, et al. (2017) Isolation and characterization of a spotted leaf 32 mutant with early leaf senescence and enhanced defense response in rice. Scientific reports, 7, 41846.

Ma J, et al. (2016) Phosphatidylserine Synthase Controls Cell Elongation Especially in the Uppermost Internode in Rice by Regulation of Exocytosis. PloS one, 11(4), e0153119.

Liang Z, et al. (2016) A New Recessive Gene Conferring Resistance Against Rice Blast. Rice (New York, N.Y.), 9(1), 47.

Marzin S, et al. (2016) Are PECTIN ESTERASE INHIBITOR Genes Involved in Mediating Resistance to Rhynchosporium commune in Barley? PloS one, 11(3), e0150485.

Yeo FK, et al. (2016) Haplotype divergence and multiple candidate genes at Rphq2, a partial resistance QTL of barley to Puccinia hordei. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 129(2), 289.

Sato K, et al. (2016) Alanine aminotransferase controls seed dormancy in barley. Nature communications, 7, 11625.

Li YY, et al. (2016) Overexpression of OsHox32 Results in Pleiotropic Effects on Plant Type Architecture and Leaf Development in Rice. Rice (New York, N.Y.), 9(1), 46.

Lv W, et al. (2014) BAC and RNA sequencing reveal the brown planthopper resistance gene BPH15 in a recombination cold spot that mediates a unique defense mechanism. BMC genomics, 15(1), 674.

Cheng X, et al. (2013) A rice lectin receptor-like kinase that is involved in innate immune responses also contributes to seed germination. The Plant journal : for cell and molecular biology, 76(4), 687.

Leroy P, et al. (2012) TriAnnot: A Versatile and High Performance Pipeline for the Automated Annotation of Plant Genomes. Frontiers in plant science, 3, 5.

Fukuoka S, et al. (2012) A multiple gene complex on rice chromosome 4 is involved in durable resistance to rice blast. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 125(3), 551.

Feuillet C, et al. (2012) Integrating cereal genomics to support innovation in the Triticeae. Functional & integrative genomics, 12(4), 573.

Jiang N, et al. (2012) Molecular mapping of the Pi2/9 allelic gene Pi2-2 conferring broad-spectrum resistance to Magnaporthe oryzae in the rice cultivar Jefferson. Rice (New York, N.Y.), 5(1), 29.

Bulgarelli D, et al. (2010) The CC-NB-LRR-type Rdg2a resistance gene confers immunity to the seed-borne barley leaf stripe pathogen in the absence of hypersensitive cell death. PloS one, 5(9).

Pietsch C, et al. (2009) Linkage mapping of putative regulator genes of barley grain development characterized by expression profiling. BMC plant biology, 9, 4.

Bourgis F, et al. (2008) Characterization of the major fragrance gene from an aromatic japonica rice and analysis of its diversity in Asian cultivated rice. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 117(3), 353.