

Resource Summary Report

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BGI-RISe - Beijing Genomics Institute Rice Information System

RRID:SCR_013446

Type: Tool

Proper Citation

BGI-RISe - Beijing Genomics Institute Rice Information System (RRID:SCR_013446)

Resource Information

URL: <http://rise.genomics.org.cn/>

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Description: Integrated information resource for rice genomes as well as a workbench for comparative genomic analysis among cereal crops. Sequence contigs of Beijing indica and Syngenta japonica have been further assembled and anchored onto the rice chromosomes. The rice genomes have been annotated for gene content, repetitive elements, and SNPs. Sequence polymorphisms between different rice subspecies have also been identified. Designed as a basic platform for rice study, the sequenced genomes and related information is presented in systematic and graphical ways for the convenience of in-depth comparative studies. In addition to the comprehensive data of *Oryza sativa* L. ssp. indica sequenced, BGI-RIS will host carefully curated genome information of *Oryza sativa* L. ssp. japonica.

Synonyms: BGI-RIS

Resource Type: data or information resource, database

Keywords: cereal, crop, oryza sativa, rice, rice chromosome, rice genome, software

Resource Name: BGI-RISe - Beijing Genomics Institute Rice Information System

Resource ID: SCR_013446

Alternate IDs: nif-0000-02601

Record Creation Time: 20220129T080316+0000

Record Last Update: 20260821T194001+0000

Ratings and Alerts

No rating or validation information has been found for BGI-RIS - Beijing Genomics Institute Rice Information System.

No alerts have been found for BGI-RIS - Beijing Genomics Institute Rice Information System.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Zhang Y, et al. (2019) LMM24 Encodes Receptor-Like Cytoplasmic Kinase 109, Which Regulates Cell Death and Defense Responses in Rice. *International journal of molecular sciences*, 20(13).

Zhu X, et al. (2016) The Multivesicular Bodies (MVBs)-Localized AAA ATPase LRD6-6 Inhibits Immunity and Cell Death Likely through Regulating MVBs-Mediated Vesicular Trafficking in Rice. *PLoS genetics*, 12(9), e1006311.

Wang Y, et al. (2015) Map-based cloning and characterization of BPH29, a B3 domain-containing recessive gene conferring brown planthopper resistance in rice. *Journal of experimental botany*, 66(19), 6035.

Wei L, et al. (2008) Bioinformatics in China: a personal perspective. *PLoS computational biology*, 4(4), e1000020.

Du L, et al. (2007) The two-component signal system in rice (*Oryza sativa* L.): a genome-wide study of cytokinin signal perception and transduction. *Genomics*, 89(6), 697.

Zhang Z, et al. (2007) A genome-wide microsatellite polymorphism database for the indica and japonica rice. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 14(1), 37.

Zhao H, et al. (2005) Neighboring-nucleotide effects on the mutation patterns of the rice genome. *Genomics, proteomics & bioinformatics*, 3(3), 158.

Yu J, et al. (2005) The Genomes of *Oryza sativa*: a history of duplications. *PLoS biology*, 3(2), e38.

Galperin MY, et al. (2005) The Molecular Biology Database Collection: 2005 update. *Nucleic acids research*, 33(Database issue), D5.