Resource Summary Report

Generated by NIF on Apr 19, 2025

Gabi Primary Database

RRID:SCR_002755
Type: Tool

Proper Citation

Gabi Primary Database (RRID:SCR_002755)

Resource Information

URL: http://www.gabipd.org/

Proper Citation: Gabi Primary Database (RRID:SCR_002755)

Description: Database that collects, integrates and links all relevant primary information from the GABI plant genome research projects and makes them accessible via internet. Its purpose is to support plant genome research in Germany, to yield information about commercial important plant genomes, and to establish a scientific network within plant genomic research.
GreenCards is the main interface for text based retrieval of sequence, SNP, mapping data etc. Sharing and interchange of data among collaborating research groups, industry and the patent- and licensing agency are facilitated.
* GreenCards: Text based search for sequence, mapping, SNP data etc. * Maps: Visualization of genetic or physical maps. * BLAST: Secure BLAST search against different public databases or non-public sequence data stored in GabiPD. * Proteomics: View interactive 2D-gels and view or download information for identified protein spots. Registered users can submit data via secure file upload.

Abbreviations: GABI

Synonyms: GabiPD

Resource Type: data repository, data analysis service, analysis service resource, storage service resource, database, production service resource, service resource, data or information resource

Defining Citation: PMID:18812395

Keywords: molecular plant physiology, plant genome, genome, blast, sequence, snp,

mapping, proteomics, image collection

Funding: German Resource Center for Genome Research RZPD GmbH ;
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BMBF 0312272;
BMBF 0313112;
BMBF 0315046

Resource Name: Gabi Primary Database

Resource ID: SCR_002755

Alternate IDs: nif-0000-02866

Alternate URLs: http://gabi.rzpd.de/

Record Creation Time: 20220129T080215+0000

Record Last Update: 20250419T054900+0000

Ratings and Alerts

No rating or validation information has been found for Gabi Primary Database.

No alerts have been found for Gabi Primary Database.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 13 mentions in open access literature.

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

Yang Y, et al. (2021) Applications of Multi-Omics Technologies for Crop Improvement. Frontiers in plant science, 12, 563953.

Tomkowiak A, et al. (2019) Identification of Markers Associated with Yield Traits and Morphological Features in Maize (Zea mays L.). Plants (Basel, Switzerland), 8(9).

Zhang L, et al. (2018) Maize male sterile 33 encodes a putative glycerol-3-phosphate acyltransferase that mediates anther cuticle formation and microspore development. BMC plant biology, 18(1), 318.

Toueni M, et al. (2016) Quantitative Resistance to Verticillium Wilt in Medicago truncatula

Involves Eradication of the Fungus from Roots and Is Associated with Transcriptional Responses Related to Innate Immunity. Frontiers in plant science, 7, 1431.

Schönhals EM, et al. (2016) Identification and reproducibility of diagnostic DNA markers for tuber starch and yield optimization in a novel association mapping population of potato (Solanum tuberosum L.). TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 129(4), 767.

Obidiegwu JE, et al. (2015) Genomic architecture of potato resistance to Synchytrium endobioticum disentangled using SSR markers and the 8.3k SolCAP SNP genotyping array. BMC genetics, 16, 38.

Livaja M, et al. (2013) BSTA: a targeted approach combines bulked segregant analysis with next- generation sequencing and de novo transcriptome assembly for SNP discovery in sunflower. BMC genomics, 14, 628.

Draffehn AM, et al. (2013) Comparative transcript profiling by SuperSAGE identifies novel candidate genes for controlling potato quantitative resistance to late blight not compromised by late maturity. Frontiers in plant science, 4, 423.

Usadel B, et al. (2012) GabiPD - The GABI Primary Database integrates plant proteomic data with gene-centric information. Frontiers in plant science, 3, 154.

Haseneyer G, et al. (2011) From RNA-seq to large-scale genotyping - genomics resources for rye (Secale cereale L.). BMC plant biology, 11, 131.

Yang H, et al. (2010) Global characterization of the root transcriptome of a wild species of rice, Oryza longistaminata, by deep sequencing. BMC genomics, 11, 705.

Vizeacoumar FJ, et al. (2009) A picture is worth a thousand words: genomics to phenomics in the yeast Saccharomyces cerevisiae. FEBS letters, 583(11), 1656.

Pestsova E, et al. (2008) Transcript profiles uncover temporal and stress-induced changes of metabolic pathways in germinating sugar beet seeds. BMC plant biology, 8, 122.