

Resource Summary Report

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Brassicaceae Database

RRID:SCR_023019

Type: Tool

Proper Citation

Brassicaceae Database (RRID:SCR_023019)

Resource Information

URL: <http://brassicadb.cn>

Proper Citation: Brassicaceae Database (RRID:SCR_023019)

Description: Database includes newly released genome sequences of Brassicaceae species and published genomic data of most other Brassicaceae species. Data can be browsed in JBrowse or searched in BLAST. Offers service of searching for syntenic genes, which are generated based on their syntenic relationships to genes in Arabidopsis thaliana. Regularly updated with newly released reference genomes.

Abbreviations: BRAD

Resource Type: data or information resource, database

Defining Citation: [DOI:10.1093/nar/gkab1057](https://doi.org/10.1093/nar/gkab1057)

Keywords: genome sequences, Brassicaceae species, published genomic data, syntenic genes,

Funding: National Program on Key Research Project ;
National Natural Science Foundation of China

Availability: Free, Freely available

Resource Name: Brassicaceae Database

Resource ID: SCR_023019

Record Creation Time: 20221130T050154+0000

Record Last Update: 20260729T044545+0000

Ratings and Alerts

No rating or validation information has been found for Brassicaceae Database.

No alerts have been found for Brassicaceae Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 291 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Wang ?? C, et al. (2025) PSIA: A Comprehensive Knowledgebase of Plant Self-incompatibility. Genomics, proteomics & bioinformatics, 23(3).

Yan C, et al. (2025) Transcriptional activation of BoBCAT4 genes enhanced aliphatic glucosinolate accumulation in cabbage. Frontiers in plant science, 16, 1548003.

Zhao D, et al. (2025) The Function of Two Brassica napus γ -Ketoacyl-CoA Synthases on the Fatty Acid Composition. Plants (Basel, Switzerland), 14(2).

Garg P, et al. (2025) Insights into early generation synthetic amphidiploid Brassica juncea: a strategy to harness maximum parental genomic diversity for improving Indian mustard. Frontiers in plant science, 16, 1493618.

Bi Y, et al. (2025) Transcriptome Analysis Revealed Hub Genes Related to Tipburn Resistance in Chinese Cabbage (Brassica rapa L. ssp. pekinensis). Plants (Basel, Switzerland), 14(4).

Zhang J, et al. (2025) Evolution of HD-ZIP transcription factors and their function in cabbage leafy head formation. Frontiers in plant science, 16, 1583110.

Tian T, et al. (2025) ARGOS homolog evolution in brassicaceae and the role of BnaC6.ARGOS in conferring drought tolerance via expression-responsive localization and reduced seed porosity in rapeseed. BMC plant biology, 25(1), 1254.

Jia J, et al. (2025) Transcriptomic Analysis Reveals That the Photosynthesis and Carotenoid Metabolism Pathway Is Involved in the Salinity Stress Response in Brassica rapa L. ssp. Pekinensis. Plants (Basel, Switzerland), 14(4).

Kumar P, et al. (2025) High-level production of health-beneficial glucoraphanin by multiplex editing of AOP2 gene family in mustard. Plant biotechnology journal, 23(10), 4668.

Zhang Q, et al. (2025) Transcriptomic and metabolomic analyses reveal novel R2R3-MYB transcription factors control anthocyanin biosynthesis in broccoli. BMC plant biology, 25(1), 1354.

Cai Z, et al. (2025) Tuber mustard BjuFIP gene negatively regulates plant sensitivity to abscisic acid. *Scientific reports*, 15(1), 44770.

Zhang Z, et al. (2025) Origin, evolution and diversification of plant caleosins. *BMC plant biology*, 25(1), 433.

Guo X, et al. (2025) Developmental landscape and asymmetric gene expression in the leaf vasculature of *Brassica rapa* revealed by single-cell transcriptome. *Horticulture research*, 12(6), uhaf060.

Zhang D, et al. (2025) The Epigenetic Regulation of Agronomic Traits and Environmental Adaptability in Brassicas. *Plant, cell & environment*, 48(12), 8915.

Abdul Sattar G, et al. (2025) Genome-wide identification and characterization of germin-like protein family in *Brassica juncea* reveals their role against biotic stress. *BMC plant biology*, 26(1), 1.

Li J, et al. (2025) Genome-Wide Identification and Expression Analysis of bHLH-MYC Family Genes from Mustard That May Be Important in Trichome Formation. *Plants (Basel, Switzerland)*, 14(2).

Xue M, et al. (2025) Fine mapping and expression characteristics analysis of male-sterile gene BrRNR1 in Chinese cabbage (*Brassica rapa* L. ssp. *pekinensis*). *BMC plant biology*, 25(1), 49.

Wang K, et al. (2025) Genome wide identification and characterization of EPFL genes and its potential association with male sterility in *Brassica rapa*. *Scientific reports*, 15(1), 24033.

Ma M, et al. (2025) Regulation of transcriptional homeostasis by DNA methylation upon genome duplication in pak choi. *Molecular horticulture*, 5(1), 22.

Jiang H, et al. (2024) Genome-wide identification of SIMILAR to RCD ONE (SRO) gene family in rapeseed (*Brassica napus* L.) reveals their role in drought stress response. *Plant signaling & behavior*, 19(1), 2379128.