

Resource Summary Report

Generated by [RRID](#) on Aug 10, 2026

[BnTIR](#)

RRID:SCR_023021

Type: Tool

Proper Citation

BnTIR (RRID:SCR_023021)

Resource Information

URL: <http://yanglab.hzau.edu.cn/BnTIR>

Proper Citation: BnTIR (RRID:SCR_023021)

Description: Searchable database of Brassiceae genomic data hosted on the website.

Synonyms: Brassica napus Transcriptome Information Resource

Resource Type: database, data or information resource

Keywords: Brassica napus, transcriptome information, Brassiceae genomic data

Funding: National Key Research and Development Plan of China

Availability: Free, Freely available

Resource Name: BnTIR

Resource ID: SCR_023021

Record Creation Time: 20221130T050154+0000

Record Last Update: 20260808T190445+0000

Ratings and Alerts

No rating or validation information has been found for BnTIR.

No alerts have been found for BnTIR.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 23 mentions in open access literature.

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

Hu Y, et al. (2026) Genome-Wide Identification of Sigma Factors in Brassica napus and Role of BnSIG5A in Response to Cold Stress. International journal of molecular sciences, 27(7).

Hu Y, et al. (2026) Profiling the transcriptional regulatory network reveals putative shared regulatory elements within homoeologs in polyploid Brassica napus. Genome biology, 27(1).

Luo W, et al. (2026) Genome-wide identification and expression analysis of the expansin gene family in Brassica napus L. Scientific reports, 16(1).

Hui W, et al. (2025) BnaC04.bZIP16 can be phosphorylated and inhibited by BnaA06.SnRK2 and negatively regulates the accumulation of fatty acids in Brassica napus. The Plant journal : for cell and molecular biology, 124(1), e70506.

Chen X, et al. (2025) The Root Development Genes (RDGs) Network in Brassica napus and the Role of BnaSHR-6 in Response to Low Nitrogen. Plants (Basel, Switzerland), 14(12).

Qian X, et al. (2025) The Potassium Utilization Gene Network in Brassica napus and Functional Validation of BnaZSHAK5.2 Gene in Response to Potassium Deficiency. International journal of molecular sciences, 26(2).

Chen X, et al. (2025) Identification and expression analysis of N6-methyltransferase and demethylase in rapeseed (Brassica napus L.). BMC genomics, 26(1), 526.

Li H, et al. (2024) Targeted mutagenesis of flavonoid biosynthesis pathway genes reveals functional divergence in seed coat colour, oil content and fatty acid composition in Brassica napus L. Plant biotechnology journal, 22(2), 445.

Gu J, et al. (2024) The story of a decade: Genomics, functional genomics, and molecular breeding in Brassica napus. Plant communications, 5(4), 100884.

Wu Z, et al. (2024) Genome-Wide Characterization of Alfin-like Genes in Brassica napus and Functional Analyses of BnaAL02 and BnaAL28 in Response to Nitrogen and Phosphorus Deficiency. Plants (Basel, Switzerland), 13(17).

Li Y, et al. (2023) New Insights into the TIFY Gene Family of Brassica napus and Its Involvement in the Regulation of Shoot Branching. International journal of molecular sciences, 24(23).

Li L, et al. (2023) Characterization of novel loci controlling seed oil content in Brassica napus by marker metabolite-based multi-omics analysis. Genome biology, 24(1), 141.

Yu K, et al. (2023) Targeted mutagenesis of BnaSTM leads to abnormal shoot apex development and cotyledon petiole fusion at the seedling stage in Brassica napus L.

Frontiers in plant science, 14, 1042430.

Liu D, et al. (2023) Comparative transcriptome profiling reveals the multiple levels of crosstalk in phytohormone networks in *Brassica napus*. *Plant biotechnology journal*, 21(8), 1611.

Zhang K, et al. (2022) BnaA03.MKK5-BnaA06.MPK3/BnaC03.MPK3 Module Positively Contributes to *Sclerotinia sclerotiorum* Resistance in *Brassica napus*. *Plants (Basel, Switzerland)*, 11(5).

Fan S, et al. (2022) BnGF14-2c Positively Regulates Flowering via the Vernalization Pathway in Semi-Winter Rapeseed. *Plants (Basel, Switzerland)*, 11(17).

Liu Y, et al. (2022) CRISPR/Cas9-Targeted Mutagenesis of BnaFAE1 Genes Confers Low-Erucic Acid in *Brassica napus*. *Frontiers in plant science*, 13, 848723.

Cheng X, et al. (2022) The genome wide analysis of Tryptophan Aminotransferase Related gene family, and their relationship with related agronomic traits in *Brassica napus*. *Frontiers in plant science*, 13, 1098820.

Ahmad N, et al. (2022) Quantitative trait loci mapping reveals important genomic regions controlling root architecture and shoot biomass under nitrogen, phosphorus, and potassium stress in rapeseed (*Brassica napus* L.). *Frontiers in plant science*, 13, 994666.

Zhou E, et al. (2022) Identification and Characterization of the MIKC-Type MADS-Box Gene Family in *Brassica napus* and Its Role in Floral Transition. *International journal of molecular sciences*, 23(8).