

Resource Summary Report

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CNS Genoscope

RRID:SCR_023020

Type: Tool

Proper Citation

CNS Genoscope (RRID:SCR_023020)

Resource Information

URL: <https://www.genoscope.cns.fr/brassicanapus/>

Proper Citation: CNS Genoscope (RRID:SCR_023020)

Description: Web tool as Brassica napus genome browser.

Resource Type: web service, software resource, data access protocol

Keywords: Brassica napus, genome browser, Brassica napus genome browser

Availability: Free, Freely available

Resource Name: CNS Genoscope

Resource ID: SCR_023020

Record Creation Time: 20221130T050154+0000

Record Last Update: 20260812T044423+0000

Ratings and Alerts

No rating or validation information has been found for CNS Genoscope.

No alerts have been found for CNS Genoscope.

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](#) .

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.

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

Ding LN, et al. (2024) A GDSL motif-containing lipase modulates Sclerotinia sclerotiorum resistance in Brassica napus. Plant physiology, 196(4), 2973.

Li K, et al. (2024) Identification of genetic loci and candidate genes regulating photosynthesis and leaf morphology through genome-wide association study in Brassica napus L. Frontiers in plant science, 15, 1467927.

Zhou Z, et al. (2024) Transcriptome analysis to identify genes related to programmed cell death resulted from manipulating of BnaFAH ortholog by CRISPR/Cas9 in Brassica napus. Scientific reports, 14(1), 26389.

An H, et al. (2024) Gene expression bias between the subgenomes of allopolyploid hybrids is an emergent property of the kinetics of expression. PLoS computational biology, 20(1), e1011803.

Xu J, et al. (2024) Identification and expression profiling of GAPDH family genes involved in response to Sclerotinia sclerotiorum infection and phytohormones in Brassica napus. Frontiers in plant science, 15, 1360024.

Zhang W, et al. (2024) A systems genomics and genetics approach to identify the genetic regulatory network for lignin content in Brassica napus seeds. Frontiers in plant science, 15, 1393621.

Chen B, et al. (2023) Moderate Salinity Stress Increases the Seedling Biomass in Oilseed Rape (Brassica napus L.). Plants (Basel, Switzerland), 12(8).

Zhang C, et al. (2023) Integrated multi-locus genome-wide association studies and transcriptome analysis for seed yield and yield-related traits in Brassica napus. Frontiers in plant science, 14, 1153000.

Cui X, et al. (2023) BnaOmics: A comprehensive platform combining pan-genome and multi-omics data from Brassica napus. Plant communications, 4(5), 100609.

Gong W, et al. (2023) Glycerol-3-Phosphate Acyltransferase GPAT9 Enhanced Seed Oil Accumulation and Eukaryotic Galactolipid Synthesis in Brassica napus. International journal of molecular sciences, 24(22).

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.

Jia X, et al. (2022) Promising Novel Method of Acetylation Modification for Regulating Fatty Acid Metabolism in *Brassica napus* L. *Biology*, 11(4).

Wang L, et al. (2022) Genome Structures and Evolution Analysis of Hsp90 Gene Family in *Brassica napus* Reveal the Possible Roles of Members in Response to Salt Stress and the Infection of *Sclerotinia sclerotiorum*. *Frontiers in plant science*, 13, 854034.

Guo J, et al. (2022) CRISPR/Cas9-Mediated Targeted Mutagenesis of BnaCOL9 Advances the Flowering Time of *Brassica napus* L. *International journal of molecular sciences*, 23(23).

Yin X, et al. (2022) Genome-Wide Characterization of DGATs and Their Expression Diversity Analysis in Response to Abiotic Stresses in *Brassica napus*. *Plants (Basel, Switzerland)*, 11(9).

Xu J, et al. (2022) Genome-Wide Identification and Expression Analysis of SNARE Genes in *Brassica napus*. *Plants (Basel, Switzerland)*, 11(5).

Luo T, et al. (2022) Genome-wide identification and functional analysis of Dof transcription factor family in *Camelina sativa*. *BMC genomics*, 23(1), 812.

Hussain MA, et al. (2022) Genome-wide transcriptome profiling revealed biological macromolecules respond to low temperature stress in *Brassica napus* L. *Frontiers in plant science*, 13, 1050995.