

Resource Summary Report

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Shanghai Rapeseed Database

RRID:SCR_007923

Type: Tool

Proper Citation

Shanghai Rapeseed Database (RRID:SCR_007923)

Resource Information

URL: <http://rapeseed.plantsignal.cn>

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Description: The Shanghai Rapeseed Database contains genomic information about the Rapeseed plant. Resources available through the website include BLAST search functions, cDNA library construction, microarray hybridization, SAGE, and ethylmethanesulfonate (EMS) induced mutant population data. Multiple high-throughput genomic approaches were performed to study the gene expression profiles during *Brassica napus* (huyou-15) seed development and fatty acid (FA) metabolism, as well as the relevant regulation. Serial Analysis of Gene Expression (SAGE) using seed materials obtained a total of 68,716 tags, of which 23,895 were unique and 503 tags were functionally identified, and further revealed the transcriptome of approximately 35,000 transcripts in *B. napus* developing seeds. Further, ~22,000 independent ESTs were obtained by large-scale sequencing using immature embryos at different stages. 8462 uni-ESTs and 3526 full-length cDNAs were identified respectively, resulting in the systemic identification of *B. napus* FA biosynthesis-related genes. Gene expression profiles were further studied employing cDNA chip hybridization to reveal the global regulatory network of FA metabolism in developing seeds.

Synonyms: Shanghai Rapeseed Database

Resource Type: data or information resource, database

Resource Name: Shanghai Rapeseed Database

Resource ID: SCR_007923

Record Creation Time: 20220129T080244+0000

Record Last Update: 20260815T182903+0000

Ratings and Alerts

No rating or validation information has been found for Shanghai Rapeseed Database.

No alerts have been found for Shanghai Rapeseed Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Raza A, et al. (2021) Omics: The way forward to enhance abiotic stress tolerance in Brassica napus L. GM crops & food, 12(1), 251.

Chandna R, et al. (2012) Evaluation of candidate reference genes for gene expression normalization in Brassica juncea using real time quantitative RT-PCR. PloS one, 7(5), e36918.

Yang B, et al. (2009) Identification and expression analysis of WRKY transcription factor genes in canola (Brassica napus L.) in response to fungal pathogens and hormone treatments. BMC plant biology, 9, 68.

Niu Y, et al. (2009) Global analysis of gene expression profiles in Brassica napus developing seeds reveals a conserved lipid metabolism regulation with Arabidopsis thaliana. Molecular plant, 2(5), 1107.