

Resource Summary Report

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SoyBase

RRID:SCR_005096

Type: Tool

Proper Citation

SoyBase (RRID:SCR_005096)

Resource Information

URL: <http://soybase.org>

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Description: Professionally curated repository for genetics, genomics and related data resources for soybean that contains the most current genetic, physical and genomic sequence maps integrated with qualitative and quantitative traits. SoyBase includes annotated Williams 82 genomic sequence and associated data mining tools. The genetic and sequence views of the soybean chromosomes and the extensive data on traits and phenotypes are extensively interlinked. This allows entry to the database using almost any kind of available information, such as genetic map symbols, soybean gene names or phenotypic traits. The repository maintains controlled vocabularies for soybean growth, development, and traits that are linked to more general plant ontologies. Contributions to SoyBase or the Breeder's Toolbox are welcome.

Abbreviations: SoyBase

Synonyms: SoyBase and the Soybean Breeder's Toolbox, SoyBase and the Soybean Breeder's Toolbox: Integrating Genetics and Molecular Biology for Soybean Researchers

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

Defining Citation: [PMID:20008513](#)

Keywords: soybean, gene, genetic map, genome, data set, trait, phenotype, molecular biology, sequence, chromosome, quantitative trait locus, php, genetics, genomics, legume, bio.tools, FASEB list

Funding: USDA Agricultural Research Service

Availability: The community can contribute to this resource

Resource Name: SoyBase

Resource ID: SCR_005096

Alternate IDs: nif-0000-03483, r3d100010846, biotools:soybase

Alternate URLs: <https://bio.tools/soybase>, <https://doi.org/10.17616/R3S032>

Record Creation Time: 20220129T080228+0000

Record Last Update: 20260806T054410+0000

Ratings and Alerts

No rating or validation information has been found for SoyBase.

No alerts have been found for SoyBase.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 646 mentions in open access literature.

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

Niazian M, et al. (2026) CRISPR-induced knockouts reveal a dual role for the soybean NFR5?? gene in symbiotic nitrogen fixation and root hair development. The plant genome, 19(1), e70143.

Qu S, et al. (2025) Genome-wide association study and molecular marker development for resistance to soybean cyst nematode in soybean. The plant genome, 18(3), e70083.

Mugabe D, et al. (2025) Assessment of potential candidate genes for partial resistance to Sclerotinia stem rot caused by Sclerotinia sclerotiorum using real-time quantitative PCR. The plant genome, 18(1), e20561.

Silva ACD, et al. (2025) Genetic diversity, population structure in a historical panel of Brazilian soybean cultivars. PloS one, 20(1), e0313151.

Zhang Y, et al. (2025) Identification of superior haplotypes and candidate gene for seed size-related traits in soybean (Glycine max L.). Molecular breeding : new strategies in plant improvement, 45(1), 3.

Yamaguchi M, et al. (2025) LIPID RICH 1 modulates allocation of carbon between starch and triacylglycerol in Arabidopsis leaves. Journal of experimental botany, 76(8), 2144.

Burner N, et al. (2025) Identifying canopy wilting QTLs and evaluating remote sensing approaches for selecting drought-tolerant soybean. TAG. Theoretical and applied

genetics. Theoretische und angewandte Genetik, 138(11), 276.

He L, et al. (2025) The AP2/ERF transcription factor GmTINY mediates ethylene regulation of Rhg1-conferred resistance against soybean cyst nematode. Plant communications, 6(7), 101378.

Zhang C, et al. (2025) Natural allelic variation in SW14 determines seed weight and quality in soybean. Nature communications, 16(1), 8070.

Zatybekov A, et al. (2025) Uncovering the genetic landscape of soybean accessions from Kazakhstan in comparison with global germplasm using whole genome resequencing. BMC genomics, 26(1), 802.

Li C, et al. (2025) GmAP2 enhances plant tolerance to aluminum toxicity and phosphorus deficiency in Arabidopsis. Plant cell reports, 44(10), 231.

Zhang C, et al. (2025) QTL mapping for hundred-seed weight in soybean using high-density SLAF-seq technology. BMC plant biology, 25(1), 1748.

Liang X, et al. (2025) Genome-Wide Identification of GmPIF Family and Regulatory Pathway Analysis of GmPIF3g in Different Temperature Environments. International journal of molecular sciences, 26(2).

Zhu X, et al. (2025) GmERF13 mediates salt inhibition of nodulation through interacting with GmLBD16a in soybean. Nature communications, 16(1), 435.

Wood TD, et al. (2025) Chemical Informatics Combined with Kendrick Mass Analysis to Enhance Annotation and Identify Pathways in Soybean Metabolomics. Metabolites, 15(2).

Zhang K, et al. (2025) Integration of GWAS and transcriptome and haplotype analyses to identify QTNs and candidate genes controlling oil content in soybean seeds. Scientific reports, 15(1), 16803.

Sun R, et al. (2025) Chromosome-level genome assembly of a high-yield Chinese soybean variety Mengdou1137 unlocks genetic potential of disease and lodging resistance. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 138(6), 119.

Zhang C, et al. (2025) Comprehensively characterize the soybean CAM/CML gene family, as it provides resistance against both the soybean mosaic virus and Cercospora soja pathogens. Frontiers in plant science, 16, 1633325.

Wang X, et al. (2025) Transcriptome-Wide Association Uncovers LncRNAs Controlling Seed Weight in Soybean. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(41), e16794.

Zheng H, et al. (2025) GmSop20 Functions as a Key Coordinator of the Oil-To-Protein Ratio in Soybean Seeds. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(38), e05181.