

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: analysis service resource, controlled vocabulary, data analysis service, data or information resource, data repository, database, ontology, production service resource, service resource, storage 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: 20260905T132958+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 830 mentions in open access literature.

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

Tang J, et al. (2026) Editing a gibberellin receptor gene improves yield and nitrogen fixation in soybean. *Journal of integrative plant biology*, 68(1), 75.

Chowdhury S, et al. (2026) Genome-Wide Identification of Candidate Loci Associated with the Regulation of the Protein, Oil, and Carbohydrate Content in Soybean. *Plants (Basel, Switzerland)*, 15(6).

Sileshi Y, et al. (2026) Multilocus genome-wide association study reveals genomic regions associated with resistance to red leaf blotch in soybean. *BMC plant biology*, 26(1).

Moon K, et al. (2026) Transcriptomic and Metabolic Insight Into Flavonoid Biosynthesis Underlying Black and Yellow Seed Coat Color Variation in Soybean (*Glycine max*). *Plant direct*, 10(2), e70153.

Cho H, et al. (2026) Genome-wide association study on soybean canopy wilting under drought stress conditions in a rainout-shelter greenhouse. *Frontiers in plant science*, 17, 1840313.

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.

- Liu C, et al. (2026) QTL/Segment Mapping and Candidate Gene Analysis for Oil Content Using a Wild Soybean Chromosome Segment Substitution Line Population. *Plants (Basel, Switzerland)*, 15(2).
- Zhang Z, et al. (2026) Genome-wide identification and characterization of the Groucho/Tup1-like corepressor family identifies a potential role in the epigenetic regulation of abiotic stress responses in soybean. *Frontiers in plant science*, 17, 1825108.
- Lian M, et al. (2026) Genome-Scale Identification, Phylogeny, Expression Profiling, and Functional Analysis of Sugarcane DUF4228 Family Involved in Drought Stress. *Plants (Basel, Switzerland)*, 15(11).
- Li Y, et al. (2026) Identification of genetic loci and domestication gene GmZFP1 associated with soybean hypocotyl elongation in seedling stage by genome-wide association study. *BMC plant biology*, 26(1), 215.
- Yoo YH, et al. (2026) Unravelling mechanisms of drought tolerance in a soybean cultivar (Daewonkong roots): insights into integrative transcriptomic and metabolite analyses. *BMC plant biology*, 26(1), 274.
- Bruggink J, et al. (2026) Conserved regulatory modules and hub genes linking leaf transcriptomes to soybean seed weight. *BMC plant biology*, 26(1).
- Song Q, et al. (2026) Development of user-selectable diverse sets of cultivated and wild soybean germplasm for genetic and breeding applications. *The plant genome*, 19(1), e70216.
- Han Y, et al. (2026) Glycine max Jumonji C domain-containing proteins JMJ19/20 exhibit endopeptidase activity and interact with LUXs to mediate flowering time. *Nucleic acids research*, 54(5).
- Kassem MA, et al. (2026) Mining Two Decades of Soybean Genomics Literature Using Rule-Based Text Mining: Chromosome-Resolved Patterns of Glyma Gene Mentions. *International journal of molecular sciences*, 27(8).
- Yuan M, et al. (2026) Genome wide association analysis for saline-alkaline stress tolerance during the soybean germination stage. *Frontiers in plant science*, 17, 1827987.
- Xu B, et al. (2026) Genome-wide identification of CAD and CCoAOMT gene families in soybean and analysis of expression patterns under *Peronospora manshurica* (P. manshurica) infection. *Frontiers in plant science*, 17, 1834683.
- Li A, et al. (2026) Signaling Pathway Analysis and Downstream Genes Associated with Disease Resistance Mediated by GmSRC7. *Plants (Basel, Switzerland)*, 15(2).
- Hao X, et al. (2026) Constitution and function of intergenic genome regions in cultivated versus annual wild soybean in China. *Journal of integrative plant biology*, 68(7), 2105.
- Pierson S, et al. (2026) Exploring salicylic acid biosynthesis in *Trichoderma* spp. using an enhanced transformation approach. *Fungal biology and biotechnology*, 13(1).