

Resource Summary Report

Generated by NIF on Aug 19, 2026

Germplasm Resources Information Network

RRID:SCR_006675

Type: Tool

Proper Citation

Germplasm Resources Information Network (RRID:SCR_006675)

Resource Information

URL: <http://www.ars-grin.gov/>

Proper Citation: Germplasm Resources Information Network (RRID:SCR_006675)

Description: Web server to provide germplasm information about plants, animals, microbes, invertebrates and access to databases that maintain passport, characterization, evaluation, inventory, and distribution data for the management and utilization of national germplasm collections. Under control of the U.S. Department of Agriculture's Agricultural Research Service to support the National Genetic Resources Program (NGRP). Operated by the Database Management Unit of the National Germplasm Resource Laboratory in Beltsville, Maryland.

Abbreviations: GRIN

Synonyms: GRIN, Germplasm Resources Information Network

Resource Type: data or information resource, database, department portal, organization portal, portal

Keywords: agriculture, food, germplasm, information, plant, animal, microbe, invertebrate, access, database, distribution, data, management, , FASEB list

Funding: the U.S. Department of Agriculture

Resource Name: Germplasm Resources Information Network

Resource ID: SCR_006675

Alternate IDs: SCR_016462, nlx_21883

Record Creation Time: 20220129T080237+0000

Record Last Update: 20260818T043254+0000

Ratings and Alerts

No rating or validation information has been found for Germplasm Resources Information Network.

No alerts have been found for Germplasm Resources Information Network.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 357 mentions in open access literature.

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

Behnken B, et al. (2026) Natural variation in expression of a plant immune receptor mediates elicitor sensitivity. PloS one, 21(4), e0343332.

Baumann U, et al. (2026) OzBarley: A genetic and phenotypic data resource capturing the Australian barley breeding history. Scientific data, 13(1).

Poudel M, et al. (2026) Genome-wide association study of exotic *Fragaria* germplasm accessions for resistance to *Phytophthora* crown rot in strawberry. BMC plant biology, 26(1), 324.

Ricks KD, et al. (2026) Signatures of local nitrogen adaptation in the *Brachypodium distachyon* root microbiome. The New phytologist, 249(1), 433.

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.

Bian J, et al. (2026) Telomere-to-telomere genome assemblies and population resequencing of diploid and allotetraploid peanut varieties. Nature genetics, 58(5), 1151.

Branham SE, et al. (2025) Extreme-phenotype genome-wide association study (XP-GWAS) of powdery mildew race 2??W tolerance in the USDA *Citrullus* germplasm collection. Scientific reports, 15(1), 4781.

Ohno S, et al. (2025) The medial prefrontal cortex encodes procedural rules as sequential neuronal activity dynamics. Molecular brain, 18(1), 56.

Ponciano G, et al. (2025) Characterization of Small Rubber Particle Protein 1 promoter from guayule (*Parthenium argentatum*). BMC research notes, 18(1), 380.

Han J, et al. (2025) 24-hour simultaneous mPFC's miniature 2-photon imaging, EEG-EMG, and video recording during natural behaviors. Scientific data, 12(1), 1226.

Chen H, et al. (2025) Dissecting the genetic architecture of key agronomic traits in lettuce using a MAGIC population. Genome biology, 26(1), 67.

Neupane A, et al. (2025) Genetic improvement of FHB and DON resistance by combining the Fhb1 gene with additional resistance QTL in winter wheat population. *The plant genome*, 18(3), e70084.

Behnken B, et al. (2025) Natural variation in expression of a plant immune receptor mediates elicitor sensitivity. *bioRxiv : the preprint server for biology*.

Pettit N, et al. (2025) Genetic and biochemical analyses identify a major locus, GH-PA1, underlying pollen carotenoid accumulation and pigmentation in upland cotton. *Journal of experimental botany*, 76(22), 6776.

Yeh PT, et al. (2025) Discrete photoentrainment of mammalian central clock is regulated by bi-stable dynamic network in the suprachiasmatic nucleus. *Nature communications*, 16(1), 3331.

Shrestha A, et al. (2025) Environmental pressures shape regional patterns of genetic diversity and ancestry in cotton landraces. *Frontiers in plant science*, 16, 1707011.

Daba SD, et al. (2025) Proteomics analysis of round and wrinkled pea (*Pisum sativum* L.) seeds during different development periods. *Proteomics*, 25(3), e2300363.

Pruthi R, et al. (2025) A comparative transcriptomic analysis provides insights into molecular mechanisms driving salt tolerance in soybean. *Scientific reports*, 15(1), 31869.

Frandsen PB, et al. (2025) A chromosome-scale genome assembly and annotation of the tetraploid herb "epazote" (*Dysphania ambrosioides*). *G3 (Bethesda, Md.)*, 15(11).

Lockett-Ruiz V, et al. (2025) Effect of gradient-index lenses on the optical performance of SyntEyes. *Journal of optometry*, 18(3), 100568.