

Resource Summary Report

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Legume Information System

RRID:SCR_007761

Type: Tool

Proper Citation

Legume Information System (RRID:SCR_007761)

Resource Information

URL: <http://www.comparative-legumes.org/>

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Description: LIS is a publicly accessible legume resource that integrates genetic and molecular data from multiple legume species and enables cross-species genomic, transcript and map comparisons. The intent of the LIS is to help researchers leverage data-rich model plants to fill knowledge gaps across crop plant species and provide the ability to traverse between interrelated data types. LIS, a component of the Model Plant Initiative (MPI), is being developed as part of a cooperative research agreement between the National Center for Genome Resources (NCGR) and the USDA Agricultural Research Service (ARS).

Synonyms: LIS

Resource Type: data or information resource, database

Keywords: FASEB list

Resource Name: Legume Information System

Resource ID: SCR_007761

Alternate IDs: nif-0000-03078

Record Creation Time: 20220129T080243+0000

Record Last Update: 20260811T043316+0000

Ratings and Alerts

No rating or validation information has been found for Legume Information System.

No alerts have been found for Legume Information System.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 32 mentions in open access literature.

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

Czy? KB, et al. (2020) A Tale of Two Families: Whole Genome and Segmental Duplications Underlie Glutamine Synthetase and Phosphoenolpyruvate Carboxylase Diversity in Narrow-Leafed Lupin (*Lupinus angustifolius* L.). *International journal of molecular sciences*, 21(7).

Menéndez AB, et al. (2019) Polyamines and Legumes: Joint Stories of Stress, Nitrogen Fixation and Environment. *Frontiers in plant science*, 10, 1415.

Ksi??kiewicz M, et al. (2016) Expansion of the phosphatidylethanolamine binding protein family in legumes: a case study of *Lupinus angustifolius* L. FLOWERING LOCUS T homologs, LanFTc1 and LanFTc2. *BMC genomics*, 17(1), 820.

Wyrwa K, et al. (2016) Integration of *Lupinus angustifolius* L. (narrow-leafed lupin) genome maps and comparative mapping within legumes. *Chromosome research : an international journal on the molecular, supramolecular and evolutionary aspects of chromosome biology*, 24(3), 355.

Pandey MK, et al. (2016) Emerging Genomic Tools for Legume Breeding: Current Status and Future Prospects. *Frontiers in plant science*, 7, 455.

Dash S, et al. (2016) Legume information system (LegumeInfo.org): a key component of a set of federated data resources for the legume family. *Nucleic acids research*, 44(D1), D1181.

Przysiecka ?, et al. (2015) Structure, expression profile and phylogenetic inference of chalcone isomerase-like genes from the narrow-leafed lupin (*Lupinus angustifolius* L.) genome. *Frontiers in plant science*, 6, 268.

Zhang C, et al. (2015) Genome-wide survey of the soybean GATA transcription factor gene family and expression analysis under low nitrogen stress. *PloS one*, 10(4), e0125174.

Bell A, et al. (2015) SGRL can regulate chlorophyll metabolism and contributes to normal plant growth and development in *Pisum sativum* L. *Plant molecular biology*, 89(6), 539.

Ksi??kiewicz M, et al. (2015) Remnants of the Legume Ancestral Genome Preserved in Gene-Rich Regions: Insights from *Lupinus angustifolius* Physical, Genetic, and Comparative Mapping. *Plant molecular biology reporter*, 33(1), 84.

Dhanapal AP, et al. (2015) Unlimited Thirst for Genome Sequencing, Data Interpretation, and Database Usage in Genomic Era: The Road towards Fast-Track Crop Plant

Improvement. Genetics research international, 2015, 684321.

Patil G, et al. (2015) Soybean (*Glycine max*) SWEET gene family: insights through comparative genomics, transcriptome profiling and whole genome re-sequence analysis. BMC genomics, 16(1), 520.

Meisrimler CN, et al. (2015) Pre-fractionation strategies to resolve pea (*Pisum sativum*) sub-proteomes. Frontiers in plant science, 6, 849.

Bohra A, et al. (2014) Genomics-assisted breeding in four major pulse crops of developing countries: present status and prospects. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 127(6), 1263.

Oldach KH, et al. (2014) Genetic analysis of tolerance to the root lesion nematode *Pratylenchus neglectus* in the legume *Medicago littoralis*. BMC plant biology, 14, 100.

Peng D, et al. (2014) Bayesian phylogeny of sucrose transporters: ancient origins, differential expansion and convergent evolution in monocots and dicots. Frontiers in plant science, 5, 615.

Trujillo DI, et al. (2014) Genomic characterization of the LEED..PEEDs, a gene family unique to the medicago lineage. G3 (Bethesda, Md.), 4(10), 2003.

Wang X, et al. (2014) A comprehensive analysis of the Cupin gene family in soybean (*Glycine max*). PloS one, 9(10), e110092.

Reinprecht Y, et al. (2013) In silico comparison of genomic regions containing genes coding for enzymes and transcription factors for the phenylpropanoid pathway in *Phaseolus vulgaris* L. and *Glycine max* L. Merr. Frontiers in plant science, 4, 317.

Guo Y, et al. (2013) Genome-wide analysis of the Dof transcription factor gene family reveals soybean-specific duplicable and functional characteristics. PloS one, 8(9), e76809.