

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 [dkNET](#) .

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.