Resource Summary Report

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LegumeIP

RRID:SCR_008906
Type: Tool

Proper Citation

LegumeIP (RRID:SCR_008906)

Resource Information

URL: http://plantgrn.noble.org/LegumeIP/

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Description: LegumeIP is an integrative database and bioinformatics platform for comparative genomics and transcriptomics to facilitate the study of gene function and genome evolution in legumes, and ultimately to generate molecular based breeding tools to improve quality of crop legumes. LegumeIP currently hosts large-scale genomics and transcriptomics data, including: * Genomic sequences of three model legumes, i.e. Medicago truncatula, Glycine max (soybean) and Lotus japonicus, including two reference plant species, Arabidopsis thaliana and Poplar trichocarpa, with the annotation based on UniProt TrEMBL, InterProScan, Gene Ontology and KEGG databases. LegumeIP covers a total 222,217 protein-coding gene sequences. * Large-scale gene expression data compiled from 104 array hybridizations from L. japonicas, 156 array hybridizations from M. truncatula gene atlas database, and 14 RNA-Seq-based gene expression profiles from G. max on different tissues including four common tissues: Nodule, Flower, Root and Leaf. * Systematic synteny analysis among M. truncatula, G. max, L. japonicus and A. thaliana. * Reconstruction of gene family and gene family-wide phylogenetic analysis across the five hosted species. LegumeIP features comprehensive search and visualization tools to enable the flexible query on gene annotation, gene family, synteny, relative abundance of gene expression.

Abbreviations: LegumeIP

Synonyms: LegumeIP: an integrative database for comparative genomics and transcriptomics of model legumes, LegumeIP - An Integrative Platform to Study Gene Function and Genome Evolution in Legumes

Resource Type: analysis service resource, data analysis service, data or information resource, database, production service resource, service resource

Defining Citation: PMID:22110036

Keywords: gene function, genome evolution, legume, gene, genome, plant, genomics, transcriptomic, gene annotation, gene family, synteny, gene expression, blast, genomic sequence, microarray, rna-seq, comparative genomics, bio.tools

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Resource Name: LegumeIP

Resource ID: SCR_008906

Alternate IDs: biotools:legumeip, nlx_151455

Alternate URLs: https://bio.tools/legumeip

Record Creation Time: 20220129T080250+0000

Record Last Update: 20260905T132630+0000

Ratings and Alerts

No rating or validation information has been found for LegumeIP.

No alerts have been found for LegumeIP.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 23 mentions in open access literature.

Listed below are recent publications. The full list is available at Kravitz .

Swain B, et al. (2026) Genome-wide identification and characterization of CaM and CML gene family in chickpea (Cicer arietinum L.). Scientific reports, 16(1).

Shao A, et al. (2023) Identification and evolution analysis of YUCCA genes of Medicago sativa and Medicago truncatula and their expression profiles under abiotic stress. Frontiers in plant science, 14, 1268027.

Saxena H, et al. (2023) LDRGDb - Legumes disease resistance genes database. Frontiers in plant science, 14, 1143111.

Vlk D, et al. (2022) Genes Associated with Biological Nitrogen Fixation Efficiency Identified Using RNA Sequencing in Red Clover (Trifolium pratense L.). Life (Basel, Switzerland), 12(12).

Singh RK, et al. (2022) Exploring Chickpea Germplasm Diversity for Broadening the Genetic Base Utilizing Genomic Resourses. Frontiers in genetics, 13, 905771.

Kataria R, et al. (2021) alfaNET: A Database of Alfalfa-Bacterial Stem Blight Protein-Protein Interactions Revealing the Molecular Features of the Disease-causing Bacteria. International journal of molecular sciences, 22(15).

Singer SD, et al. (2021) The CRISPR/Cas9-Mediated Modulation of SQUAMOSA PROMOTER-BINDING PROTEIN-LIKE 8 in Alfalfa Leads to Distinct Phenotypic Outcomes. Frontiers in plant science, 12, 774146.

Afzal M, et al. (2020) Legume genomics and transcriptomics: From classic breeding to modern technologies. Saudi journal of biological sciences, 27(1), 543.

Lorenzo CD, et al. (2020) Improvement of alfalfa forage quality and management through the down-regulation of MsFTa1. Plant biotechnology journal, 18(4), 944.

Sokolkova A, et al. (2020) Genomic Analysis of Vavilov's Historic Chickpea Landraces Reveals Footprints of Environmental and Human Selection. International journal of molecular sciences, 21(11).

Karikari B, et al. (2020) Identification of quantitative trait nucleotides and candidate genes for soybean seed weight by multiple models of genome-wide association study. BMC plant biology, 20(1), 404.

Tayade R, et al. (2019) Insight Into the Prospects for the Improvement of Seed Starch in Legume-A Review. Frontiers in plant science, 10, 1213.

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Sathyanarayana N, et al. (2017) Transcriptomic resources for the medicinal legume Mucuna pruriens: de novo transcriptome assembly, annotation, identification and validation of EST-SSR markers. BMC genomics, 18(1), 409.

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.

Li J, et al. (2016) LegumeIP 2.0--a platform for the study of gene function and genome evolution in legumes. Nucleic acids research, 44(D1), D1189.

Sallam A, et al. (2016) Identification and Verification of QTL Associated with Frost Tolerance Using Linkage Mapping and GWAS in Winter Faba Bean. Frontiers in plant science, 7, 1098.

Calzadilla PI, et al. (2016) Transcriptome Response Mediated by Cold Stress in Lotus japonicus. Frontiers in plant science, 7, 374.

Kavas M, et al. (2015) Genome-wide investigation and expression analysis of AP2-ERF gene family in salt tolerant common bean. EXCLI journal, 14, 1187.

Yu J, et al. (2014) SFGD: a comprehensive platform for mining functional information from soybean transcriptome data and its use in identifying acyl-lipid metabolism pathways. BMC genomics, 15, 271.