Various organizations provide legume information resources as subsets within larger information resources. For example, TIGR provides annotated EST information on three legume species within their larger Gene Indices information resource. In an effort to organize dozens of legume information resources we have summarized them as multi-species information resources and species-specific information resources.

The multi-species information resources are presented in the following format:

**Name of the information resource** (URL),
- Species,
- Types of Information and
- Services

**Multi-Species Information Resources**
A note of caution: The summary should not be interpreted as a complete matrix. For example, the Legume Information System has data and information from a dozen species, but for most species the information consists of only linkage maps, QTL and mapped genetic markers. Only a few species, e.g., Medicago and Soybean have all data and information types in the LIS.

**Legumes.org** ([http://www.legumes.org/](http://www.legumes.org/))
- portal to other legume resources

- Medicago, Lotus, Soybean, Peanut, Lentil, Alfalfa, Pea, Phaseolus beans, Chickpea, Cowpea, [Arabidopsis]
- Linkage maps, QTL, Physical maps, ESTs, EST clusters, Consensus EST contigs, Assembled Genomic Contigs, Annotations (GO, Interpro, Blocks+), Pathways, Whole Plant Phenotypes
- BLAST, motif analyses, ESTs by library, Placement of EST Consensus contigs on Assembled Genomic Contigs, Gene Predictions, Comparative views of functional annotations, Comparative Sequence Viewer, Comparative linkage and physical maps, portal to most legume resources

- All species with sequence data
- Primarily data. EST, GSS and Trace data (where available); genomic clone and WGS sequence assemblies; STS and other sequence-based marker data; protein sequences (predicted and experimental), protein structure and domains; Unigene
clusters for highly-represented species; limited SAGE expression data (only Medicago); limited genetic map data. (only Soybean)

- Wide variety of BLAST-based services; ePCR; similarity-based annotation of Unigene sequences, per-library analysis and Digital Differential Display of Unigene representation; mRNA-to-genomic alignment (Spidey); integrated map viewer; precomputed sequence similarities; third-party annotation

**PlantGDB** ([http://www.plantgdb.org/](http://www.plantgdb.org/))

- Medicago, Soybean, Alfalfa, Pea, Peanut, Phaseolus beans, Lupine, [Arabidopsis and many other plant species]
- Assembled EST contigs, Genomic Contigs
- BLAST, Placement of EST Consensus contigs on Assembled Genomic Contigs and GeneSeqer gene prediction

**The TIGR Plant Repeat Databases** ([http://www.tigr.org/tdb/e2k1/plant.repeats/index.shtml](http://www.tigr.org/tdb/e2k1/plant.repeats/index.shtml))

- Medicago, Lotus, Soybean, [Arabidopsis and other plant species]
- Compilation and identification of repeat sequences in Medicago


- Medicago, Lotus, Soybean, [Arabidopsis and many more plant species]
- ESTs, EST clusters, Consensus EST contigs (TC), Assembled Genomic Contigs, Annotation of TC (TOGs-tentative ortholog assignment, GO annotations, tentative annotation) Pathways, Whole Plant Phenotypes
- BLAST, ESTs by library, Placement of EST Consensus contigs on Assembled Genomic Contigs and in KEGG Pathway maps via putative EC functions, Identification of ORFs, Identification of unique oligos, identification of alternative splice sites.

**openSputnik** comparative genomics platform ([http://sputnik.btk.fi/ests](http://sputnik.btk.fi/ests))

- Medicago, Lotus, Soybean, Phaseolus coccineus (other plant species)
- ESTs, clusters and consensus sequences
- EST distribution reports by library property and functional assignment; consensus and predicted peptide functional annotation; SNP mining; BLAST services

The species-specific information resources are presented in the following format:
**Name of the information resource** (URL),

- Types of Information and
- Services

**Alfalfa**

**AlfaGenes** ([http://ukcrop.net/perl/ace/search/AlfaGenes](http://ukcrop.net/perl/ace/search/AlfaGenes))

- genetic maps, molecular markers, ESTs, pathways, molecular markers, enzymes, metabolites, phenotypes, germplasm

**Chickpea and Lentil**

**CoolGenes** ([http://ukcrop.net/perl/ace/search/CoolGenes](http://ukcrop.net/perl/ace/search/CoolGenes))

- genetic maps data for Chickpea and Lentil
Lotus

Kazusa *Lotus japonicus*  (http://www.kazusa.or.jp/lotus/)
- Linkage maps, Annotated clustered ESTs, Annotated genomic clones, seed stocks, RI lines
- BLAST against TAC/BAC end sequences

The *Lotus japonicus* Website (http://www.lotusjaponicus.org/)
- Mutant stocks,
- Tilling service

EU Project LOTUS (http://www.mpimp-golm.mpg.de/lotus/)
- EU Research Project overview

The Lotus Newsletter Home Page (http://dmz.inia.org.sitios/lnl/)

Medicago

MENS - Medicago EST Navigation System (http://medicago.toulouse.inra.fr/Mt/EST/)
- Annotated and Assembled ESTs, cluster and library expression patterns, maps to KEGG pathways
- BLAST and pattern scan services

MtDB (http://www.medicago.org/)
- EST clusters, linkage maps, BAC overlaps, BAC registry, genomic clone marker associations, annotated repetitive elements
- ORF prediction, cluster comparison to TIGR TCs, BLAST services, alignment against unigenes from various species, genome-to-genome comparisons against Arabidopsis

Sequencing *Medicago truncatula* at the University of Oklahoma (http://www.genome.ou.edu/medicago.html)
- Annotated BACs from WGS assembly, BAC Clone Descriptions
- BLAST

Medicago Genome Project at UC Davis (http://mtgenome.ucdavis.edu/)
- Physical map and linkage map, BAC end sequences, SSR, molecular markers
- Contig viewer, BLAST

TIGR Medicago *truncatula* Database (http://www.tigr.org/tdb/e2k1/mta1/)
- Annotated and Assembled genomic contigs,
- BLAST, Gene prediction, Assigned gene ontologies

Medicago genome database UrMeLDB (http://mips.gsf.de/proj/plant/jsf/medi/index.jsp)
- Annotated and Assembled genomic contigs,

*Medicago truncatula* functional genomics and bioinformatics (http://medicago.vbi.vt.edu/)
- Genes, Proteins, Metabolites

The Samuel Roberts Noble Foundation 2D-PAGE Protein Database (http://www.noble.org/2DPage/Search.asp)
- 2D-PAGE gel archives
• Browse and search based on multiple criteria including species, genotype/treatment, tissue source, subcellular fraction and date of analysis

**Australian National University - 2D-PAGE Database** ([http://semele.anu.edu.au/](http://semele.anu.edu.au/))
- 2D-PAGE gel images
- Browse and search for 2D images from Medicago

- Proteome analysis of Medicago truncatula roots in interaction either with the mycorrhizal fungus Glomus mosseae or the bacterium Sinorhizobium meliloti;
- online images of gel results

**Phaseolus Beans**

**Phaseomics: Phaseolus genome initiative** ([http://www.phaseolus.net/](http://www.phaseolus.net/))
- Overview of initiative
- Portal to bean related resources

**BeanGenes** ([http://beangenes.cws.ndsu.nodak.edu/](http://beangenes.cws.ndsu.nodak.edu/))
- genetic maps, molecular markers, gene classification, phenotypes, pathogens, germplasm

**Soybean**

**Soybase** ([http://soybase.org/](http://soybase.org/))
- genetic and QTL maps, molecular markers, ESTs, pathways, germplasm, phenotypes
- soybean bulletin boards

**SIU Soybean Genome** ([http://soybeangenome.siu.edu/](http://soybeangenome.siu.edu/))
- Soybean Forrest Physical Map; FPC contigs anchored to genetic map along with QTL, EST and marker data

**Soybean Genomics Initiative** ([http://soybean.ccgb.umn.edu/](http://soybean.ccgb.umn.edu/))
- cDNA and BAC library info, SAGE tag data, EST clusters,
- BLAST

- ESTs

- Microarray project overview and results

**Soybean Genomics and Microarray Database** ([http://psi081.ba.ars.usda.gov/SGMD/Default.htm](http://psi081.ba.ars.usda.gov/SGMD/Default.htm))
- EST and analyzed microarray data

**The Public Soybean EST Project at WUSTL** ([http://genome.wustl.edu/est/index.php?soybean=1](http://genome.wustl.edu/est/index.php?soybean=1))
- EST and Trace Data

**TAMU Soybean Genome** ([http://hbz7.tamu.edu/homelinks/phymap/soybean/soy_home.htm](http://hbz7.tamu.edu/homelinks/phymap/soybean/soy_home.htm))
• BAC/BIBAC-based physical map of the soybean genome from five complementary BAC and BIBAC libraries of 3Glycine max cvs.

Symbionts

Molecular Basics of Mycorrhizal Symbioses ([http://www.genetik.uni-bielefeld.de/MolMyk/](http://www.genetik.uni-bielefeld.de/MolMyk/))
  • Project status, macro/microarrays, Annotated EST clusters

RhizoBase- the Genome database for Rhizobia ([http://www.kazusa.or.jp/rhizobase/](http://www.kazusa.or.jp/rhizobase/))
  • Genes, maps, Annotated genome, Annotated KEGG pathways,
  • Gene finding (FrameD), BLAST, PatScan

  • Physical map, Sequence and annotation of Rhizobium meliloti

  • regulatory signals of transcription initiation, promoters, regulatory binding sites and terminators, as well as information on genes clustered in operons.

Other web-enabled Legume Information Resources

Noble - Center for Medicago Genomics
Medicago Genomics Group - Wageningen University Plant Sciences
Integrated structural, functional and comparative genomics of the model legume Medicago truncatula
Medicago truncatula Gene Nomenclature
Medicago Genetics Group at the Institute of Genetics Biological Research Center, SoyCAP: Soybean Coordinated Agricultural Project
Soybean Genomics and Improvement Laboratory (SGIL), National Center for Soybean Biotechnology
Soybean Genetics Newsletter: Home Page
Agricultural Network Information Center (AgNic)Soybean Information
Soybean Genetics - Keim genetics lab
Hymowitz's Soybean Genetics Lab University of Illinois at Urbana-Champaign
North Central Soybean Research Program
UW Soybean Research and Extension
Soybean Sudden Death Syndrome and Cyst Nematode Research
Agriculture and Agri-Food Canada Research Program - Soybean Genomics
Agricultural Network Information Center (AgNic)Soybean Information
United Soybean Board
Soybean/Maize Germplasm, Pathology, and Genetics Research Unit
NSRL : National Soybean Research Laboratory
The Shoemaker Lab
International Consortium to Sequence the Soybean Genome
Comparative Analysis of Legume Genome Evolution
USDA ARS Rhizobium Germplasm Resource Center