



InterMine is a powerful open source data warehouse system, created specifically for integrating and analyzing complex biological data. Benefiting from over a decade of data warehousing experience and input from a wide range of research collaborators, InterMine is still in active development. InterMine features include:

- Sophisticated data integration facilities
- Fast, flexible querying
- User-friendly web interface and analysis tools
- Extensive set of APIs and web tools
- Highly developed and extensible system

# LegFed InterMines



JCVI and NCGR have been developing mines for LegFed:

**MedicMine**     *Medicago truncatula* (developed along with ThaleMine)

**BeanMine**     *Phaseolus vulgaris*, from LIS chado

**SoyMine**     *Glycine max*, from SoyBase+

**PeanutMine**     *Arachis duranensis* + *Arachis ipaensis*, from PeanutBase+

**LegumeMine** combines above

**CowpeaMine** soon: with genetics from UC-Riverside

These mines are all cross-linked via the “friendly mine” interface.

# MedicMine enhancements 1



**MedicMine** *Medicago truncatula* genome database  
Updated on Sep-16-2016 (v1.2.0, [Mt4.0v2](#) Release 08/2014)

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Search:

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Gene : **Medtr2g036650** *M. truncatula*

DB Identifier	<b>Medtr2g036650</b>	Secondary Identifier	<b>MTR_2g036650</b>
Brief Description	<b>plasma membrane H<sup>+</sup>-ATPase</b>	Probeset Identifier	<b>Mtr.44243.1.S1_at</b>

[SHARE](#)

MedicMine hosts the latest Mt4.0 genome and Mt4.0v2 annotation along with supporting datasets from NCBI, UniProt, GO Consortium, InterPro and KEGG.

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**Genome feature**

Region:	<b>gene</b>	Length:	7998 <a href="#">FASTA...</a>
Location:	<b>chr2:15863690-15871687</b>		

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**1 Organism**

**Genomics**

Gene models - **Medtr2g036650** **Medtr2g036650**

Gene models

[Transcripts](#): 1 [Exons](#): 17 [Introns](#): 16 [CDSs](#): 1

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**Genome Browser**

Center on **Medtr2g036650** [Full-screen view](#)

15,865,000 15,867,500 15,870,000 15,872,500

Gene

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**Lists**

This Gene isn't in any lists. Upload a list.

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**Links to other Mines**

**BeanMine**

*P. vulgaris*

- [Phvul.009G239000](#)
- [Phvul.001G058900](#)
- [Phvul.009G208000](#)
- [Phvul.005G180700](#)
- [Phvul.010G159400](#)
- [Phvul.003G159200](#)
- [Phvul.009G100900](#)
- [Phvul.003G143800](#)

**SoyMine**

*G. max*

- [Glyma.15G004300](#)
- [Glyma.06G076100](#)

# MedicMine enhancements 2



## LIS Gene Families

Data Source: [LegumeMine](#)

☐ Manage Columns

☐ Manage Filters


☐ Manage Relationships

☐ Generate Python code

☐ Export

MedicMine uses LegumeMine web services to acquire gene family info and orthologs without hosting the data locally.

Showing rows 1 to 1 of 1

   Gene Family Name	   Gene Family Description	   Genes DB identifier
<a href="#">phytozome_10_2.59279443</a>	plasma membrane H <sup>+</sup> -ATPase IPR001757 (Cation-transporting P-type ATPase), IPR023214 (HAD-like domain), IPR023298 (P-type ATPase, transmembrane domain) GO:0000166 (nucleotide binding), GO:0006200 (ATP ...	 74 Gene DB identifiers

# NCGR mine enhancements



- Chado data importers (for LIS data)
- **Genetic** data extensions (markers, QTLs, genetic maps, etc.)
- Genetic data visualization (linkage group diagrams, genotyping)
- Shared motif search (e.g. upstream gene flanking regions)
- Expression heat maps

Note: core InterMine does not contain genetic data.

# Heat maps have K-means clustering



Date Created: 2016-10-24 13:37

## PvGEA: *Phaseolus vulgaris* Gene Expression Atlas

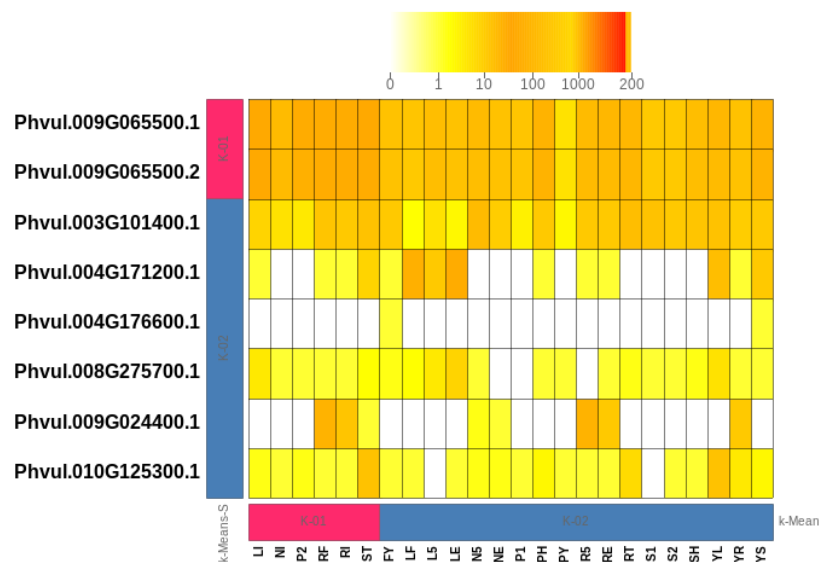
[View article on PubMed](#)

Heatmap visualization powered by [canvasXpress](#). Grab the edges with your mouse to resize the map. Zoom in/out on an area with your scroll wheel.

[Click to see/hide the expression map](#)

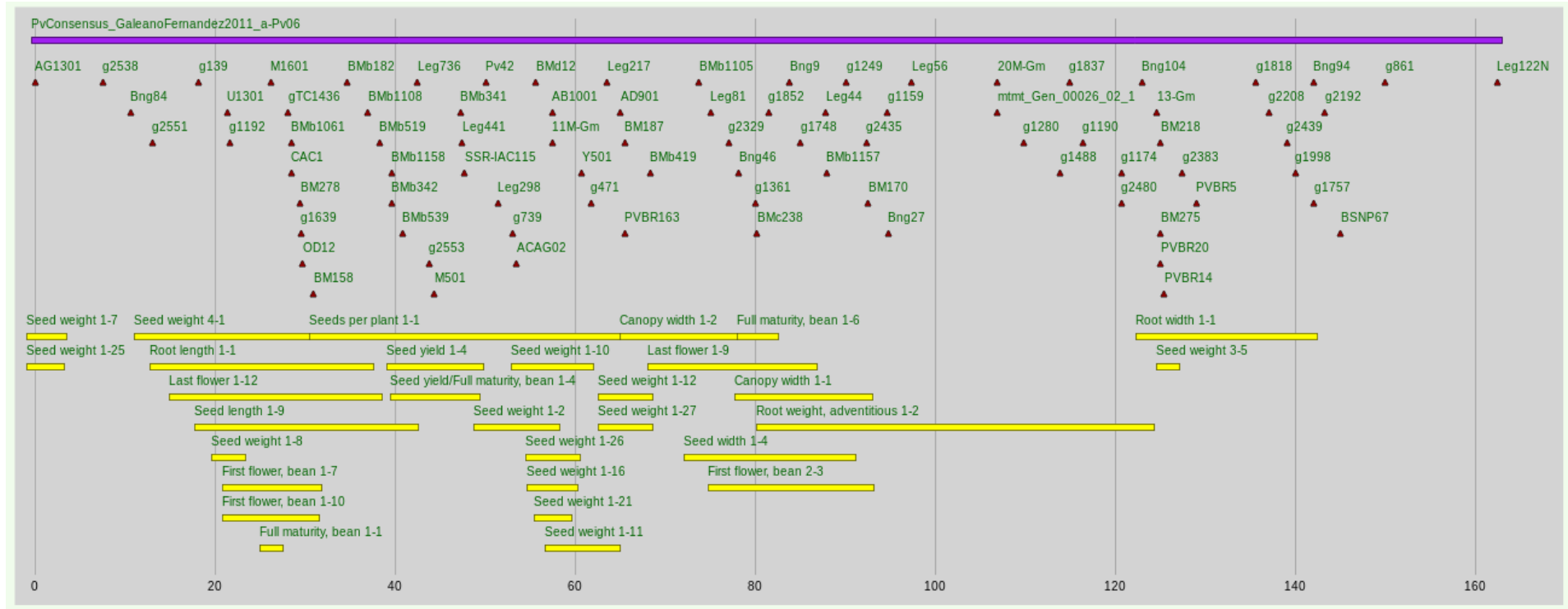
Expression K-means: 2 Tissue K-means: 2

mRNA RNA-seq expression (RPKM) : 8 transcripts



[More information](#)

# LG diagrams show markers and QTLs



**Leaf morphology in Cowpea [*Vigna unguiculata* (L.) Walp]: QTL analysis, physical mapping and identifying a candidate gene using synteny with model legume species.**

Reset

[illegible]

Next lines

A = Parent A, B = Parent B. Lower case: genotype calls reversed based on parental alleles.



# Shared motif search = realtime analysis



Date Created: 2016-10-24 13:39  
Click to toggle Shared Motif Search ▼

### Shared Motif Search

11 motifs close to top scorer:

**A TTTACATAAATGGAAA A**

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18

Show 10 entries

Motifs can be filtered: Search: CATAAATGGAAA

Motif	Length	Num	Score	Regions
TTACATAAATGGAAA*	15	5	3970	Phvul.004G171200 5.0kb upstream:1266-1280 Phvul.004G176600 5.0kb upstream:783-797 Phvul.009G024400 5.0kb upstream:1692-1706 Phvul.009G065500 5.0kb upstream:2044-2058 Phvul.010G125300 5.0kb upstream:3957-3971 <a href="#">List</a>
TACATAAATGGAAAA*	15	4	3176	Phvul.004G176600 5.0kb upstream:784-798 Phvul.008G275700 5.0kb upstream:3610-3624 Phvul.009G065500 5.0kb upstream:2045-2059 Phvul.010G125300 5.0kb upstream:3958-3972 <a href="#">List</a>
TTACATAAATGGAAAA*	16	3	2520	Phvul.004G176600 5.0kb upstream:783-798 Phvul.009G065500 5.0kb upstream:2044-2059 Phvul.010G125300 5.0kb upstream:3957-3972 <a href="#">List</a>
TACATAAATGGAAA*	14	3	2247	Phvul.004G171200 5.0kb upstream:1267-1280 Phvul.008G275700 5.0kb upstream:3610-3623 Phvul.009G024400 5.0kb upstream:1693-1706 <a href="#">List</a>
CATAAATGGAAAA	13	3	2109	Phvul.004G171200 5.0kb upstream:1315-1327 Phvul.008G275700 5.0kb upstream:3612-3624 Phvul.009G065500 5.0kb upstream:2047-2059 <a href="#">List</a>
ATTACATAAATGGAAAA*	18	2	1862	Phvul.009G065500 5.0kb upstream:2042-2059 Phvul.010G125300 5.0kb upstream:3955-3972 <a href="#">List</a>
ATTACATAAATGGAAAT*	17	2	1770	Phvul.004G171200 5.0kb upstream:1265-1281 Phvul.009G024400 5.0kb upstream:1691-1707 <a href="#">List</a>

Showing 1 to 7 of 7 entries (filtered from 101 total entries)

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