

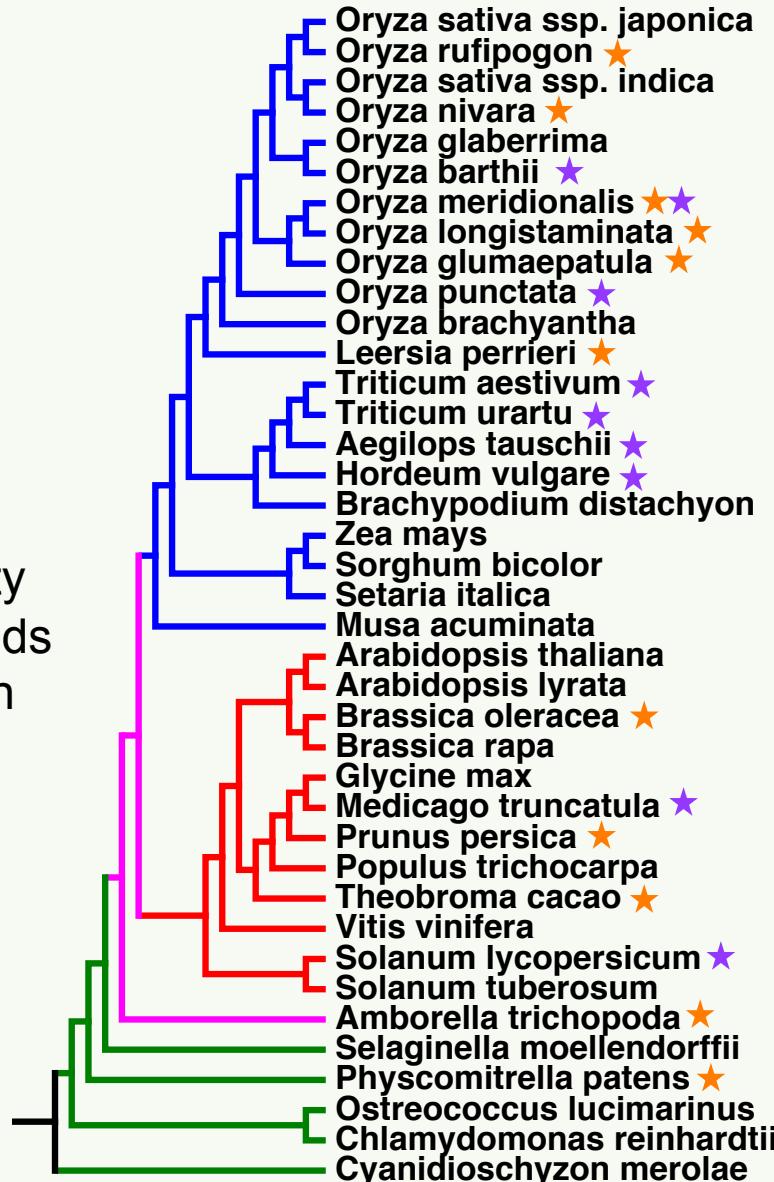


Webinar Oct 2015: BLAST

Sharon Wei

Driven by:

- Assembly quality
- Community needs
- Depth & breadth
- Project Support
- INSDC



★ = New (11)
★ = Updated (9)

Gramene Release 46

- 39 complete reference genomes
- 21 Monocots
- 12 Eudicots
- 1 basal angiosperm
- 5 Lower plants

Data served by Gramene browser



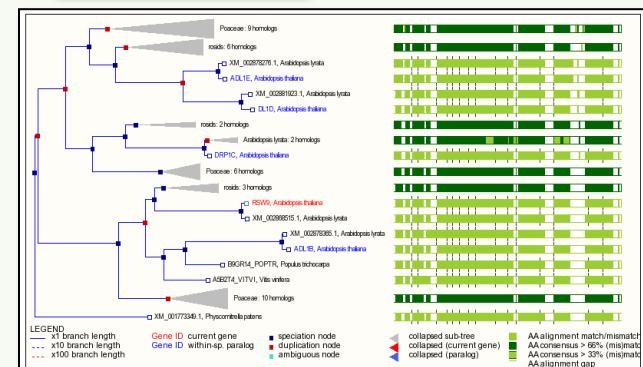
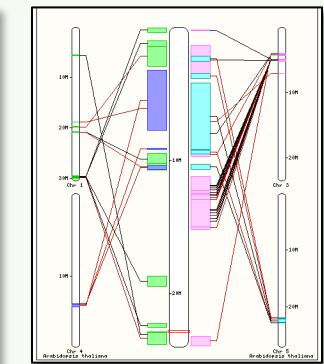
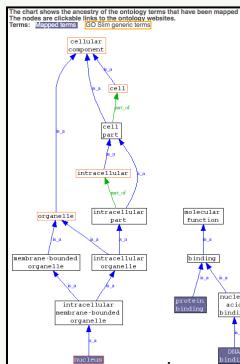
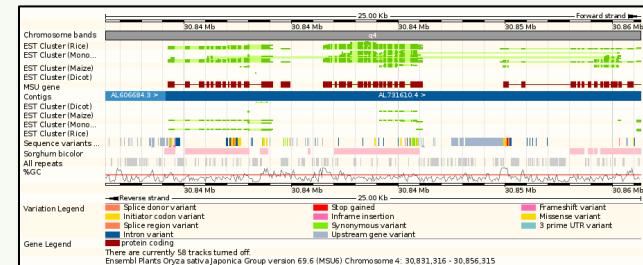
- ✓ Accessioned Genomes
- ✓ Community Annotation
- ✓ Expression
- ✓ Variation
- ✓ Epigenomics

- Repeats/TE's
- Genes
- EST/cDNA features
- InterPro domain
- Gene Ontology (GO)
- Variants (Effect Predicted)

- ftp
- Public mysql server
- Ensembl API & RESTFUL interface
- Genome Browser

- Whole Genome Alignment
- Phylogenetic Gene Trees
- Ortholog/Paralog
- Synteny mapping

Browser Displays

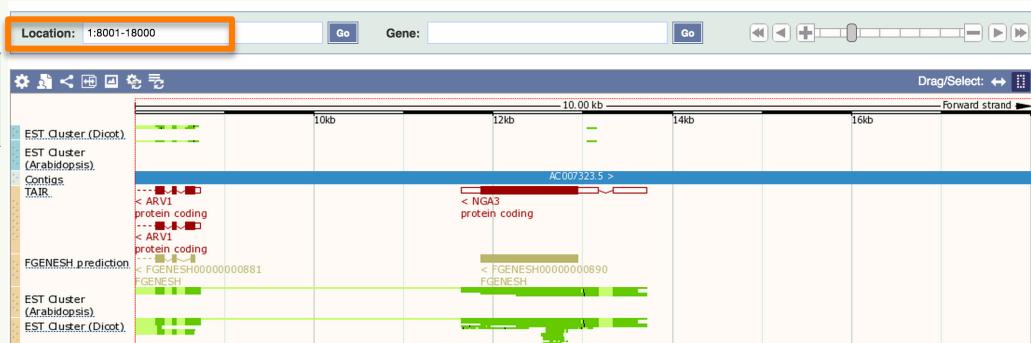


Where to start



- Species + Genomic Location

Location: 1:8001-18000



http://ensembl.gramene.org/Arabidopsis_thaliana/Location/View?r=1:8001-18000

Search results for 'bzip'
Showing 1-10 of 2897 Genes found in Ensembl Plants

Filter by species: Select a species...

SELMOORFAT_17885
Description: Putative leucine-zipper protein bZIP [Source:UniProtKB/TremBL Acc:D8EHEW]
Gene ID: SELMOORFAT_17885
Species: Selaginella moellendorffii
Location: GJ377816.36091..36078
Gene trees: EP01000000000002877 (Plant Compara) EGG37070000015833 (Pan-eukaryotic Compara)

AT1G66860
Description: basic leucine-zipper B [Source:TAIR Acc:AT1G66860]
Gene ID: AT1G66860
Species: Arabidopsis thaliana
Location: 1:2684207..2684901
Synonyms: BZIPP
Basic leucine zipper B
TBL
Gene trees: EP01000000000002877 (Plant Compara) EGG37070000015833 (Pan-eukaryotic Compara)

- Terms and IDs (Gene, Interpro, Variation, GO)

Search all species...

- Sequences (Protein, DNA)



Background on Basic Local Alignment Search Tool



Database Type	DNA databases	Protein databases
Query Type		
DNA	blastn , tblastx	blastx
Protein	tblastn	blastp

Basic BLAST

Choose a BLAST program to run.

[nucleotide blast](#)

Search a nucleotide database using a nucleotide query
Algorithms: **blastn**, **megablast**, **discontiguous megablast**

[protein blast](#)

Search protein database using a protein query
Algorithms: **blastp**, **psi-blast**, **phi-blast**

[blastx](#)

Search protein database using a translated nucleotide query

[tblastn](#)

Search translated nucleotide database using a protein query

[tblastx](#)

Search translated nucleotide database using a translated nucleotide query

Why Gramene Blast

- Gramene Blast is integrated with Gramene genome browser.
- Serve as entry point for Genome browsing
- Position a sequence to the genome
- Identify orthologs and paralogs, gene trees

Highlights

- Improved drastically since release 45 April 2015.
Better user interface and better efficiency.
- EBI NCBI-blast web services.
- Taxonomic tree of the target genomes
- Ticketing system. Automatic refreshing.
- Karyotype view of result hits
- Results can be downloaded and saved
- Hits lead to the location view of target region



Please see the Demo video at

[ftp://ftp.gramene.org/pub/gramene/outreach/
webinars/DemoFinal.zip](ftp://ftp.gramene.org/pub/gramene/outreach/webinars/DemoFinal.zip)