Manual for users

Home page

Functional Analysis Platform For Medicinal Plant *Glycyrrhiza uralensis*

Glycyrrhiza uralensis

Glycyrrhiza uralensis, also known as Chinese liquorice, is a pe outer skin and light yellow inside. Licorice usually grows in arid hills. Licorice is a kind of tonic Chinese herbal medicine with medicinal roots and rhizomes and has the effects of clearing away heat and detoxifying and relieving cough.

About *GurFAP*

The platform includes co-expression network, gene families, KEGG pathways and analysis tools, such as blast, motif search and GSEA. We applied PCC algorithm to construct co-expression network through integration of 35 samples of RNA-seq data. We combined several analysis tools such as iTAK, blast, HMM, interProScan, Pfam to classify the proteins into different families: cytochrome P450 families, transcription regulators, kinase proteins, ubiquitin proteasome system, carbohydrate-active enzymes and EAR motif-containing proteins. In addition,GO terms were collected from AgriGOv2. Enzymes and metabolism pathways were annotated by KOALA from KEGG database.

In *GurFAP*, co-expression networks of genes can be browsed from gene families or metabolism pathways and functional annotation. Moreover, Blast, cis-element enrichment and Gene Sets analysis tools were provided to explore potential function of group genes.

News

2019.9.20: The gene detail pages was available

Links

Wikipedia
Glycyrrhiza uralensis genome database

Contact us

If you have any questions, comments or suggestions about our website, please feel free to contact us: y_jiaotong@163.com

Gene Search

Navigation Bar

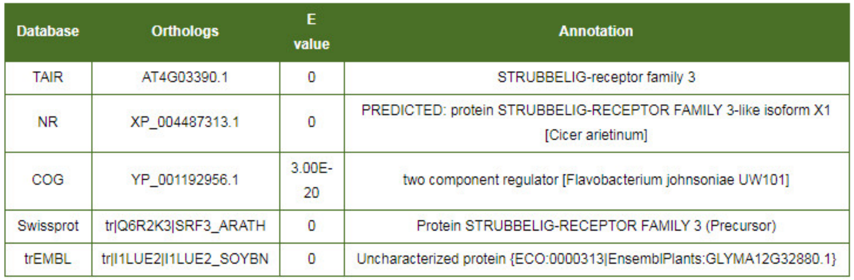
Introduction to glycyrrhiza uralensis

Update news

Introduction to GurFAP

Gene Detail Information

Function annotation



Database	Orthologs	E value	Annotation
TAIR	AT4G03390.1	0	STRUBBELIG-receptor family 3
NR	XP_004487313.1	0	PREDICTED: protein STRUBBELIG-RECEPTOR FAMILY 3-like isoform X1 [Cicer arietinum]
COG	YP_001192956.1	3.00E-20	two component regulator [Flavobacterium johnsoniae UW101]
Swissprot	tr|Q6R2K3|SRF3_ARATH	0	Protein STRUBBELIG-RECEPTOR FAMILY 3 (Precursor)
trEMBL	tr|I1LUE2|I1LUE2_SOYBN	0	Uncharacterized protein {ECO:0000313|EnsemblPlants:GLYMA12G32880.1}

Sequence

Transcript Sequence

```
>Glyur000009s00001422.1
GTAATTTTTAATTTTTAATCACACTCATTATTATTTTTATTCTATTATTCTATTCTATGCCAAAAGCTCAGCAATGCTTACGTTTTCCACTCCCACTACTGTTTTTTCAGTTCTG
AATCTTAGCCGTTAAGTTTATTTATATTTACACACACTTCACAAACCTTTTCTAGTTTTCTTTCCTTTTTTTTTCCTCCTTTCCCCGGCTCTGTTTTCGTAAAGATATTTCCAGC
ATTATCTCCCAAACTTGTTCCCTTTCTAANGTCCTTGCTGGCGATTTTTCAGCTGGGAGGGAGAAGGGTTTGGTGACAGGGTTCAACGGAGAGGAACAAGCTGAAGATTAAGGTT
GAACTAGGGAATCAATGGGTGAGGTGAGATCTGCTTCACAGTACAAGAGAGTGAGAATCCATATACAAGTTCTATTGGGATTTATGTTGATCTGTGCAGTCCAGTTTTCGCTTGC
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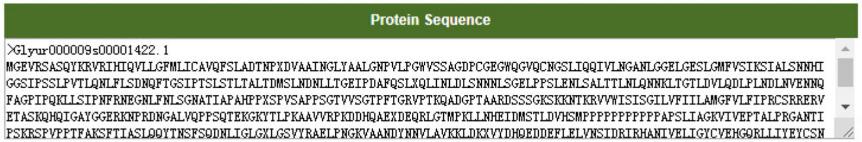
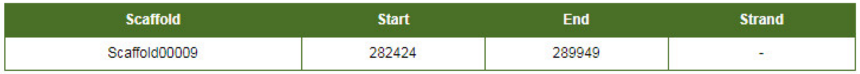


Protein Sequence

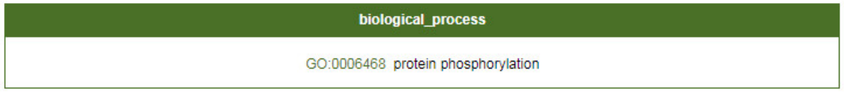
```
>Glyur000009s00001422.1
MGEVRSASQYKRVRIHIQVLLGFMLICAVQFSLADTNPXDVAAINGLYAALGNPVLPGWVSSAGDPCGEGWQGVQCNGSLIQQIVLNGANLGGELGESLGMFVSIKSIALSNNHI
GGSIPSSLPVTLQNLFLSDNQFTGSIPTSLSTLTALTDMSLNDNLLTGEIPDAFQSLXQLINLDLSNNNLSGELPPSLENLSALTTLNLQNNKLTGTLDVLQDLPLNDLNVENNQ
FAGPIPQKLLSIPNFRNEGNLFNLSGNATIAPAHPPXSPVSAPPSGTVVSGTPFTGRVPTKQADGPTAARDSSSGKSKKNTKRVVWISISGILVFIILAMGFVLFIPRCSRRERV
ETASKQHQIGAYGGERKNPRDNGALVQPPSQTEKGKYTLPKAAVVRPKDDHQAEXDEQRLGTMPKLLNHEIDMSTLDVHSMPPPPPPPPPPPAPSLIAGKVIVEPTALPRGANTI
PSKRSPVPPTFAKSFTIASLQQYTNSFSQDNLIGLGXLGSVYRAELPNGKVAANDYNNVLAVKKLDKXVYDHQEDDEFLELVNSIDRIRHANIVELIGYCVEHGQRLLIYEYCSN
```

Location



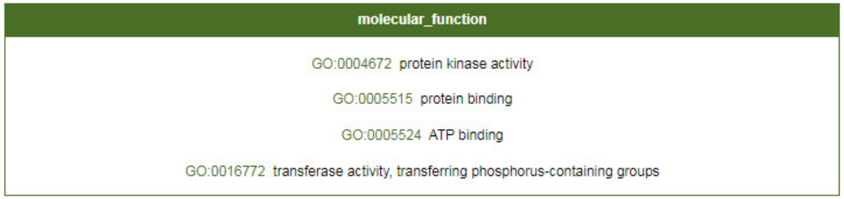
Scaffold	Start	End	Strand
Scaffold00009	282424	289949	-

GO annotation



biological_process

GO:0006468 protein phosphorylation



molecular_function

GO:0004672 protein kinase activity

GO:0005515 protein binding

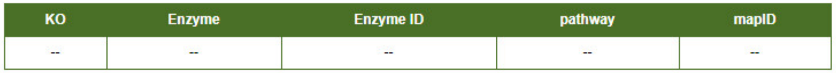
GO:0005524 ATP binding

GO:0016772 transferase activity, transferring phosphorus-containing groups

Gene Family

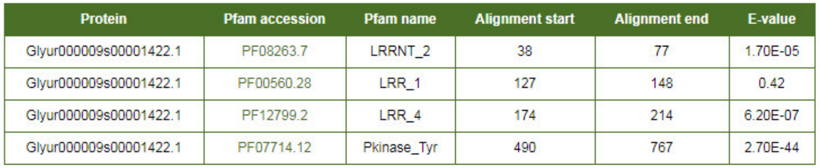
Gene family	subfamily
Protein Kinases Family	PPC:1.1.1

KEGG orthology



KO	Enzyme	Enzyme ID	pathway	mapID
--	--	--	--	--

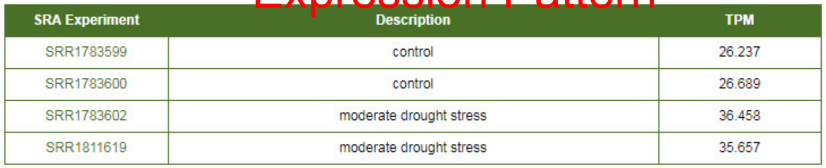
Pfam Domain



Protein	Pfam accession	Pfam name	Alignment start	Alignment end	E-value
Glyur000009s00001422.1	PF08263.7	LRRNT_2	38	77	1.70E-05
Glyur000009s00001422.1	PF00560.28	LRR_1	127	148	0.42
Glyur000009s00001422.1	PF12799.2	LRR_4	174	214	6.20E-07
Glyur000009s00001422.1	PF07714.12	Pkinase_Tyr	490	767	2.70E-44

Expression Pattern

SRP053019

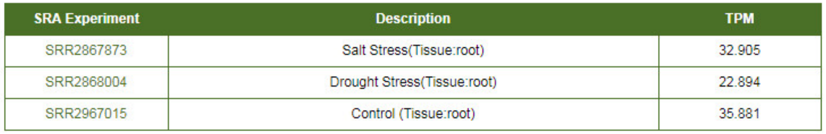


SRA Experiment	Description	TPM
SRR1783599	control	26.237
SRR1783600	control	26.689
SRR1783602	moderate drought stress	36.458
SRR1811619	moderate drought stress	35.657

DRP000996

SRA Experiment	Description	TPM
DRR006519	Root Summer glycyrrhizin high producing strain	19.237
DRR006520	Root Summer glycyrrhizin high producing strain	18.952
DRR006521	Root Winter glycyrrhizin high producing strain	78.485
DRR006522	Root Winter glycyrrhizin high producing strain	76.109
DRR006523	Root Summer glycyrrhizin low producing strain	21.590
DRR006524	Root Summer glycyrrhizin low producing strain	21.173
DRR006525	Leaf Summer glycyrrhizin high producing strain	6.768
DRR006526	Leaf Summer glycyrrhizin high producing strain	6.762

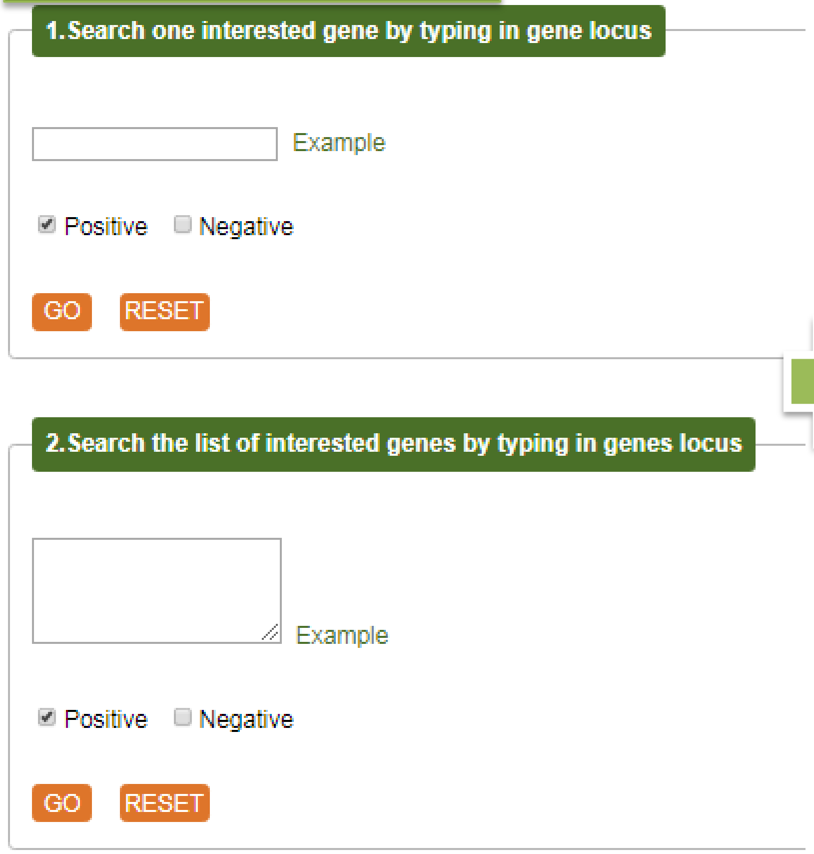
SRP065514



SRA Experiment	Description	TPM
SRR2867873	Salt Stress(Tissue:root)	32.905
SRR2868004	Drought Stress(Tissue:root)	22.894
SRR2967015	Control (Tissue:root)	35.881

Network

Network Search Page



1.Search one interested gene by typing in gene locus

Example

☑ Positive ☐ Negative

GO RESET

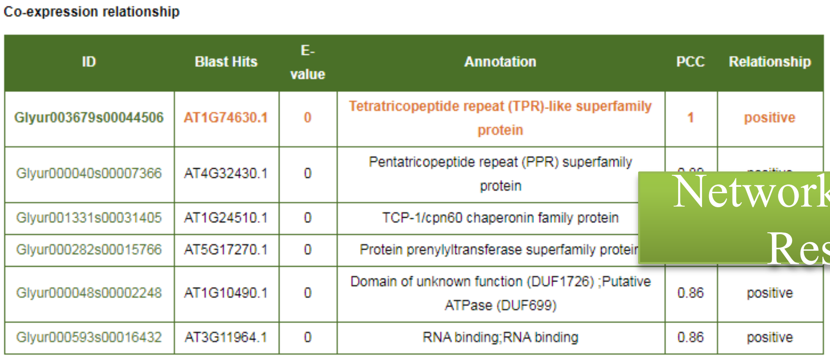
2.Search the list of interested genes by typing in genes locus

Example

☑ Positive ☐ Negative

GO RESET

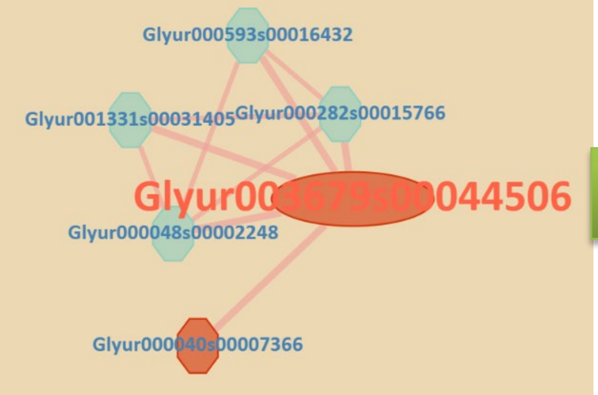
Network Display



Co-expression relationship

ID	Blast Hits	E-value	Annotation	PCC	Relationship
Glyur003679s00044506	AT1G74630.1	0	Tetratricopeptide repeat (TPR)-like superfamily protein	1	positive
Glyur000040s00007366	AT4G32430.1	0	Pentatricopeptide repeat (PPR) superfamily protein	[illegible]	[illegible]
Glyur001331s00031405	AT1G24510.1	0	TCP-1/cpn60 chaperonin family protein	[illegible]	[illegible]
Glyur000282s00015766	AT5G17270.1	0	Protein prenylyltransferase superfamily protei	[illegible]	[illegible]
Glyur000048s00002248	AT1G10490.1	0	Domain of unknown function (DUF1726) ;Putative ATPase (DUF699)	0.86	positive
Glyur000593s00016432	AT3G11964.1	0	RNA binding;RNA binding	0.86	positive

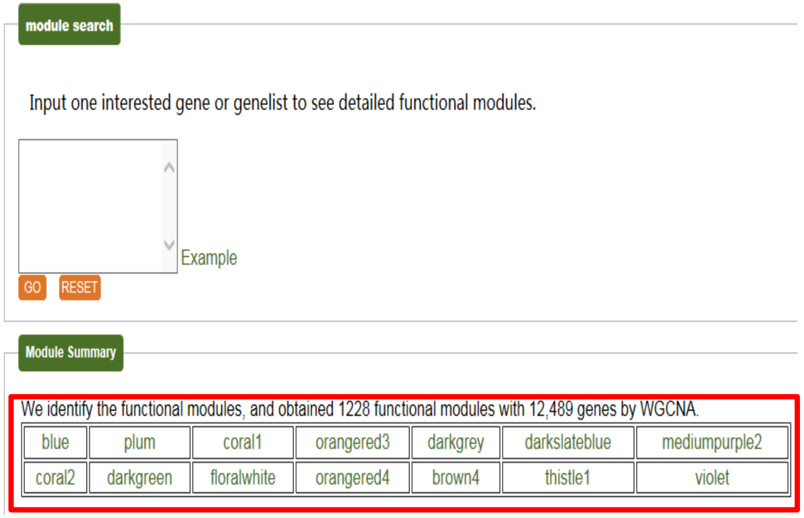
Network Search Result



Network with expression view

Functional Modules

Module Search Page



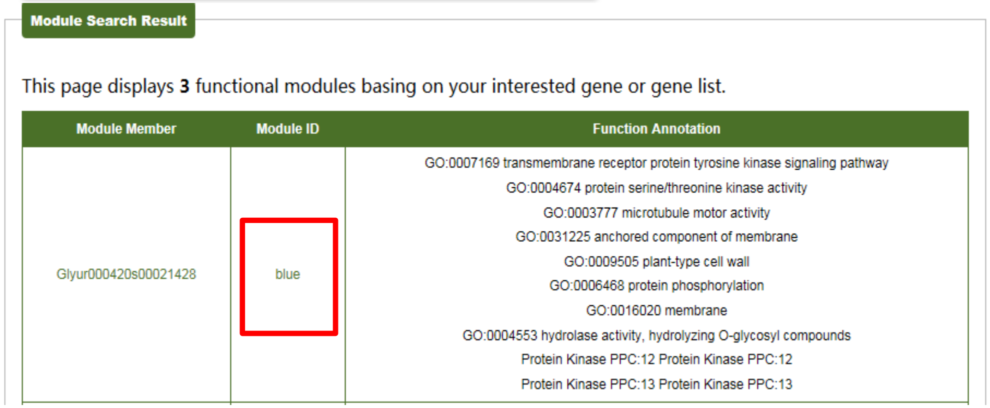
Input one interested gene or genelist to see detailed functional modules.

We identify the functional modules, and obtained 1228 functional modules with 12,489 genes by WGCNA.

blue	plum	coral1	orangered3	darkgrey	darkslateblue	mediumpurple2
coral2	darkgreen	floralwhite	orangered4	brown4	thistle1	violet

All functional modules are displayed here.

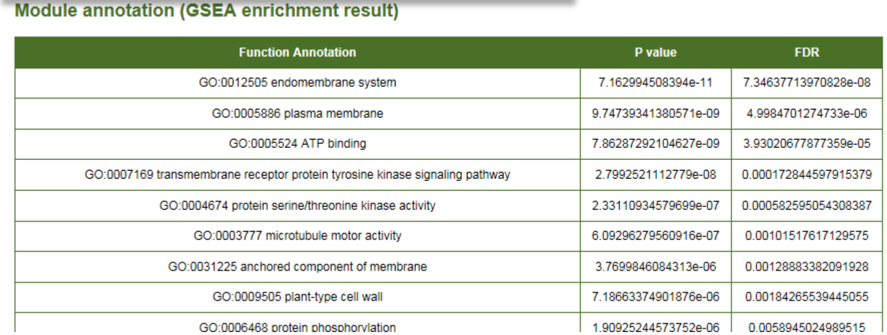
Module Search Result Page



This page displays **3** functional modules basing on your interested gene or gene list.

Module Member	Module ID	Function Annotation
Glyur000420s00021428	blue	GO:0007169 transmembrane receptor protein tyrosine kinase signaling pathway GO:0004674 protein serine/threonine kinase activity GO:0003777 microtubule motor activity GO:0031225 anchored component of membrane GO:0009505 plant-type cell wall GO:0006468 protein phosphorylation GO:0016020 membrane GO:0004553 hydrolase activity, hydrolyzing O-glycosyl compounds Protein Kinase PPC:12 Protein Kinase PPC:12 Protein Kinase PPC:13 Protein Kinase PPC:13

Module Detail Annotation

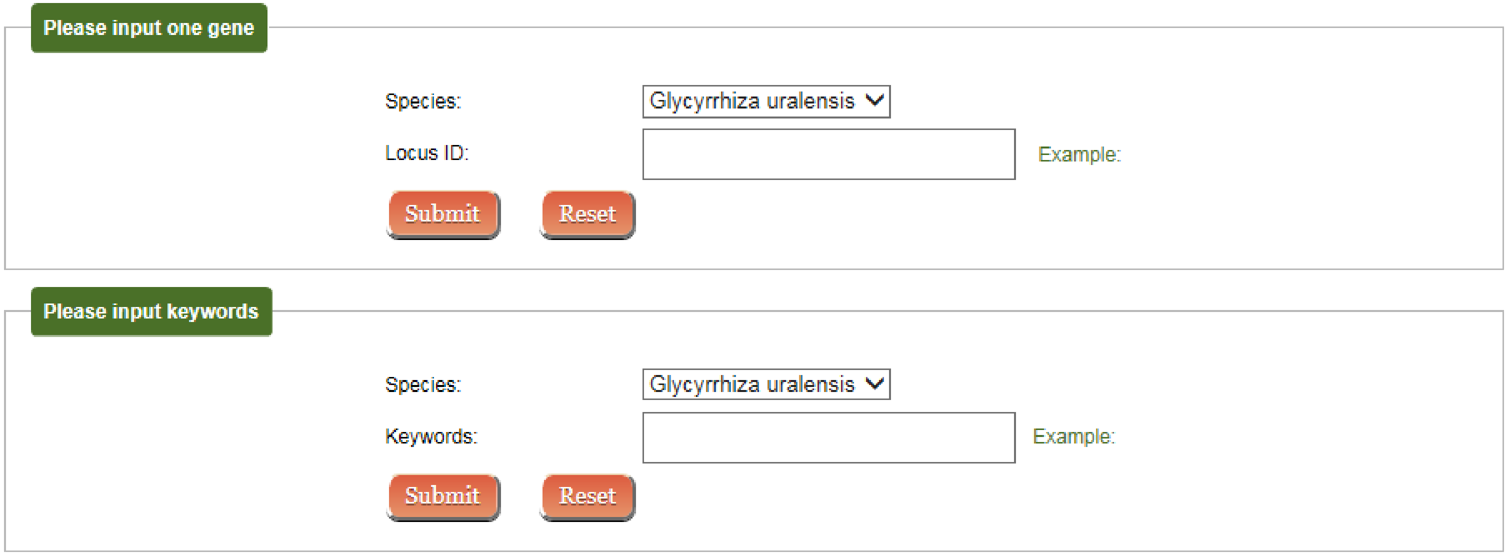


Module annotation (GSEA enrichment result)

Function Annotation	P value	FDR
GO:0012505 endomembrane system	7.162994508394e-11	7.34637713970828e-08
GO:0005886 plasma membrane	9.74739341380571e-09	4.9984701274733e-06
GO:0005524 ATP binding	7.86287292104627e-09	3.93020677877359e-05
GO:0007169 transmembrane receptor protein tyrosine kinase signaling pathway	2.7992521112779e-08	0.000172844597915379
GO:0004674 protein serine/threonine kinase activity	2.33110934579699e-07	0.000582595054308387
GO:0003777 microtubule motor activity	6.09296279560916e-07	0.00101517617129575
GO:0031225 anchored component of membrane	3.7699846084313e-06	0.00128883382091928
GO:0009505 plant-type cell wall	7.18663374901876e-06	0.00184265539445055
GO:0006468 protein phosphorylation	1.90925244573752e-06	0.0058945024989515

Tools:Search

Users can enter the Locus ID or keywords in corresponding text box, and click submit to search.



Please input one gene

Species: Glycyrrhiza uralensis

Locus ID:

Example:

Please input keywords

Species: Glycyrrhiza uralensis

Keywords:

Example:

Tools:Blast

Users can enter the nucleic acid or protein sequence in the text box, and click Blast for sequence similarity search.

Blast Search page

Program: Blastp ▼ Database: G.uralensis.protein ▼

Enter sequence below in **FASTA** format

```
>case1
MDVVDGNKFLNTVLLLVATTVVAKLISAFIIPKSRKRLPPVMKGWPIIGGLPRFLKGPIFMLREEYPKLGGVFTLKLFHKNI
TFLIGPEVSAHFFKAPESDLSQQEVYQFNVPTFGPGVVFDVDYSVRQEQFRFFTEALRVNKLKGYVNQMVAEAEDYFSKWGS
SGEVDLKYELEHLIILTASRCLLGREVRDKLFDDVSALFHDLDNGMLPISVLFPYLPIPAHRRRDQARKKLAEIFASIIASR
KSASNSEDDMLQCFIDSKYKDGRPTTEAEVTGLLIAALFAGQXTSSITSTWTGAYLLCNNQYLSAVVEEQKKLMEKHGEKVD
HDVLAEMDVLYRCIKEALRLHPPLIMLLRSSHSDFSVKTREGKEYDIPKGHIVATSPAFANRLPHIFKDPDRYDPDRFAVGR
EEDKAAGAFSYISFGGGRHGCLGEPFAYLQIKAIWSHLLRNFELELLSPFPEIDWNAMVVGVKGKVMVRYKRRELSVNQ
```

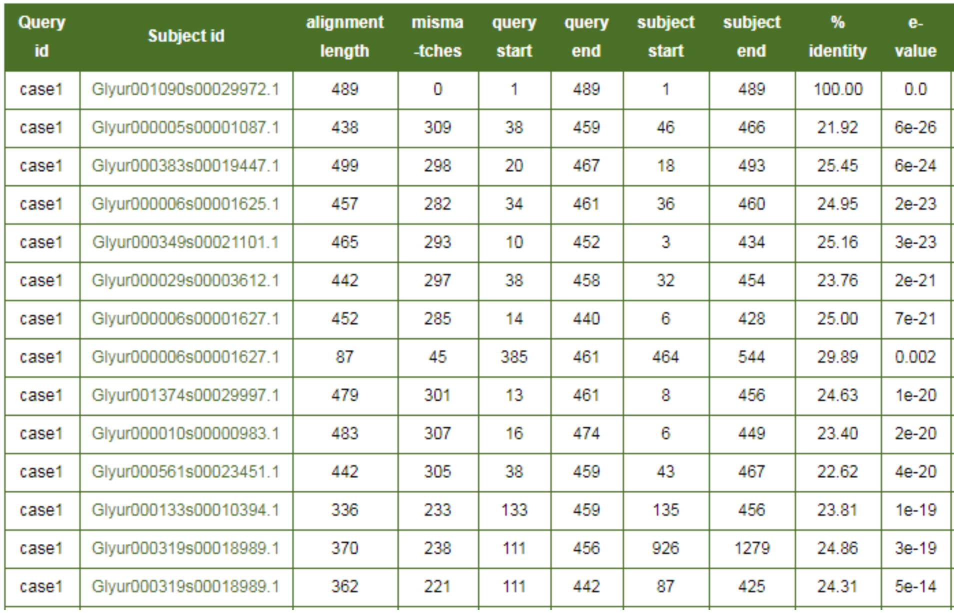
Or upload file (max filesize 5MB) 选择文件 未选择任何文件

Parameter Options

Expect 10 ▼ Matrix BLOSUM62 ▼ ☐ Perform ungapped alignment

☐ Graphical Overview Descriptions 100 ▼ Alignments 50 ▼

Blast Search Results

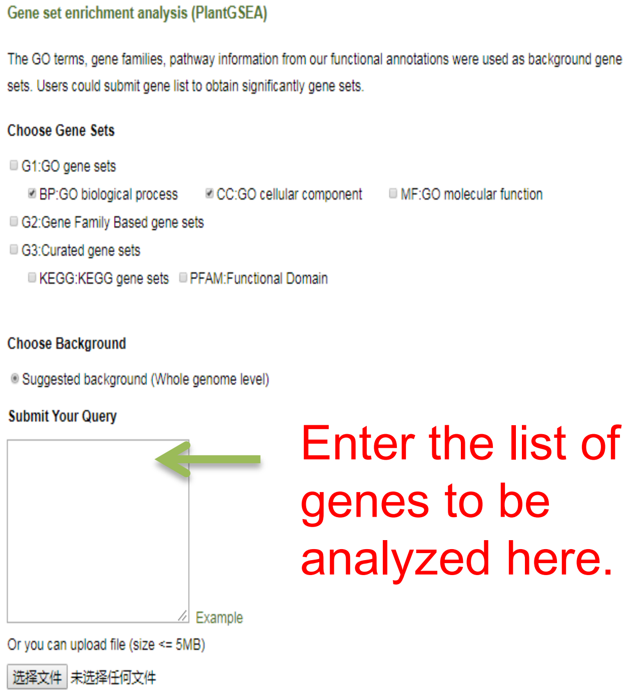


Query id	Subject id	alignment length	misma -tches	query start	query end	subject start	subject end	% identity	e-value
case1	Glyur001090s00029972.1	489	0	1	489	1	489	100.00	0.0
case1	Glyur000005s00001087.1	438	309	38	459	46	466	21.92	6e-26
case1	Glyur000383s00019447.1	499	298	20	467	18	493	25.45	6e-24
case1	Glyur000006s00001625.1	457	282	34	461	36	460	24.95	2e-23
case1	Glyur000349s00021101.1	465	293	10	452	3	434	25.16	3e-23
case1	Glyur000029s00003612.1	442	297	38	458	32	454	23.76	2e-21
case1	Glyur000006s00001627.1	452	285	14	440	6	428	25.00	7e-21
case1	Glyur000006s00001627.1	87	45	385	461	464	544	29.89	0.002
case1	Glyur001374s00029997.1	479	301	13	461	8	456	24.63	1e-20
case1	Glyur000010s00000983.1	483	307	16	474	6	449	23.40	2e-20
case1	Glyur000561s00023451.1	442	305	38	459	43	467	22.62	4e-20
case1	Glyur000133s00010394.1	336	233	133	459	135	456	23.81	1e-19
case1	Glyur000319s00018989.1	370	238	111	456	926	1279	24.86	3e-19
case1	Glyur000319s00018989.1	362	221	111	442	87	425	24.31	5e-14

Tools:GSEA

GSEA is a tool for functional enrichment analysis of gene sets

GSEA page



Gene set enrichment analysis (PlantGSEA)

The GO terms, gene families, pathway information from our functional annotations were used as background gene sets. Users could submit gene list to obtain significantly gene sets.

Choose Gene Sets

☐ G1:GO gene sets
  ☑ BP:GO biological process ☑ CC:GO cellular component ☐ MF:GO molecular function
☐ G2:Gene Family Based gene sets
☐ G3:Curated gene sets
  ☐ KEGG:KEGG gene sets ☐ PFAM:Functional Domain

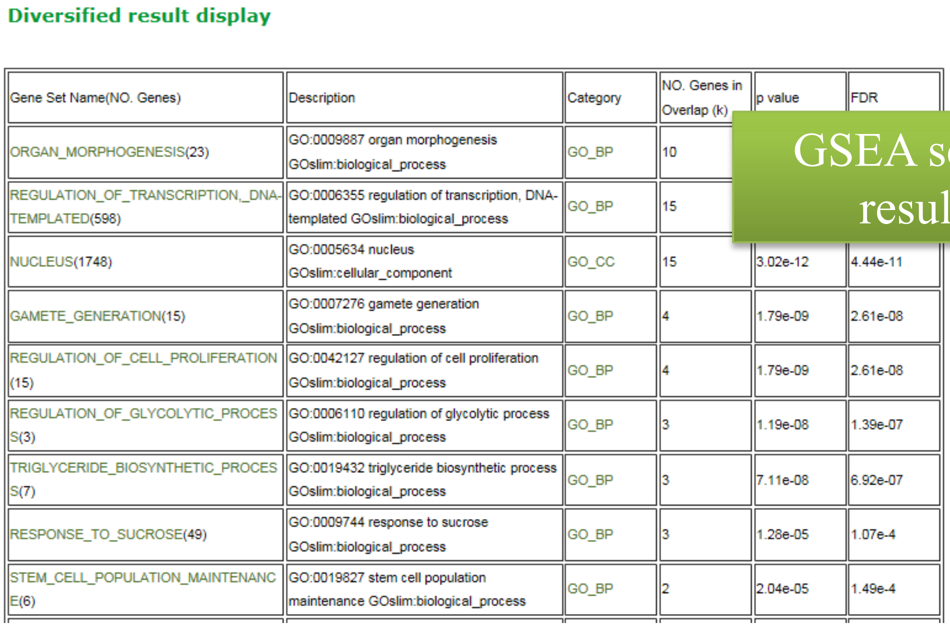
Choose Background

● Suggested background (Whole genome level)

Submit Your Query

Or you can upload file (size <= 5MB)

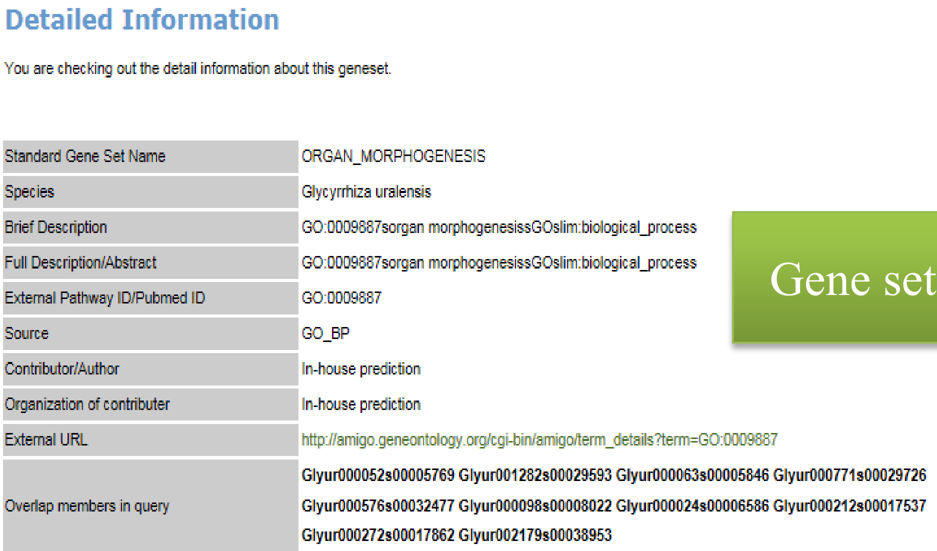
Enter the list of genes to be analyzed here.



Diversified result display

Gene Set Name(NO. Genes)	Description	Category	NO. Genes in Overlap (k)	p value	FDR
ORGAN_MORPHOGENESIS(23)	GO:0009887 organ morphogenesis GOslim:biological_process	GO_BP	10		
REGULATION_OF_TRANSCRIPTION,_DNA-TEMPLATED(598)	GO:0006355 regulation of transcription, DNA-templated GOslim:biological_process	GO_BP	15		
NUCLEUS(1748)	GO:0005634 nucleus GOslim:cellular_component	GO_CC	15	3.02e-12	4.44e-11
GAMETE_GENERATION(15)	GO:0007276 gamete generation GOslim:biological_process	GO_BP	4	1.79e-09	2.61e-08
REGULATION_OF_CELL_PROLIFERATION (15)	GO:0042127 regulation of cell proliferation GOslim:biological_process	GO_BP	4	1.79e-09	2.61e-08
REGULATION_OF_GLYCOLYTIC_PROCESS(3)	GO:0006110 regulation of glycolytic process GOslim:biological_process	GO_BP	3	1.19e-08	1.39e-07
TRIGLYCERIDE_BIOSYNTHETIC_PROCESS(7)	GO:0019432 triglyceride biosynthetic process GOslim:biological_process	GO_BP	3	7.11e-08	6.92e-07
RESPONSE_TO_SUCROSE(49)	GO:0009744 response to sucrose GOslim:biological_process	GO_BP	3	1.28e-05	1.07e-4
STEM_CELL_POPULATION_MAINTENANCE(6)	GO:0019827 stem cell population maintenance GOslim:biological_process	GO_BP	2	2.04e-05	1.49e-4

GSEA search results



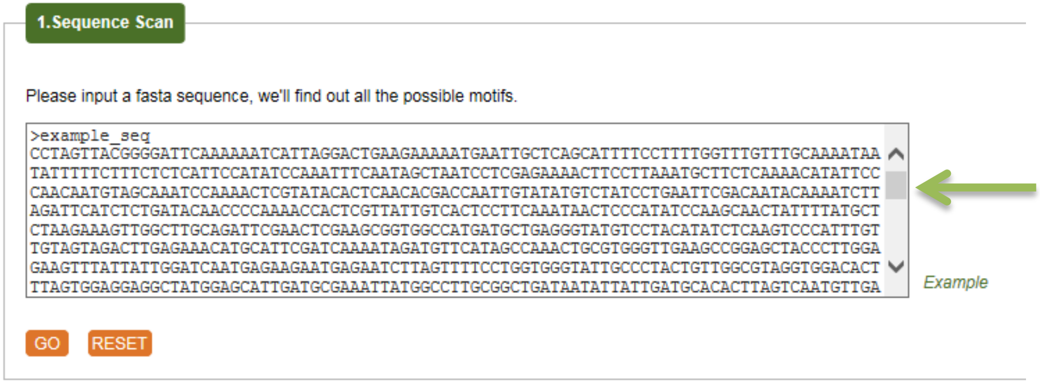
Detailed Information

You are checking out the detail information about this geneset.

Standard Gene Set Name	ORGAN_MORPHOGENESIS
Species	Glycyrrhiza uralensis
Brief Description	GO:0009887sorgan morphogenesissGOslim:biological_process
Full Description/Abstract	GO:0009887sorgan morphogenesissGOslim:biological_process
External Pathway ID/Pubmed ID	GO:0009887
Source	GO_BP
Contributor/Author	In-house prediction
Organization of contributer	In-house prediction
External URL	http://amigo.geneontology.org/cgi-bin/amigo/term_details?term=GO:0009887
Overlap members in query	**Glyur000052s00005769 Glyur001282s00029593 Glyur000063s00005846 Glyur000771s00029726 Glyur000576s00032477 Glyur000098s00008022 Glyur000024s00006586 Glyur000212s00017537 Glyur000272s00017862 Glyur002179s00038953**

Gene sets detail

Tools:Motif

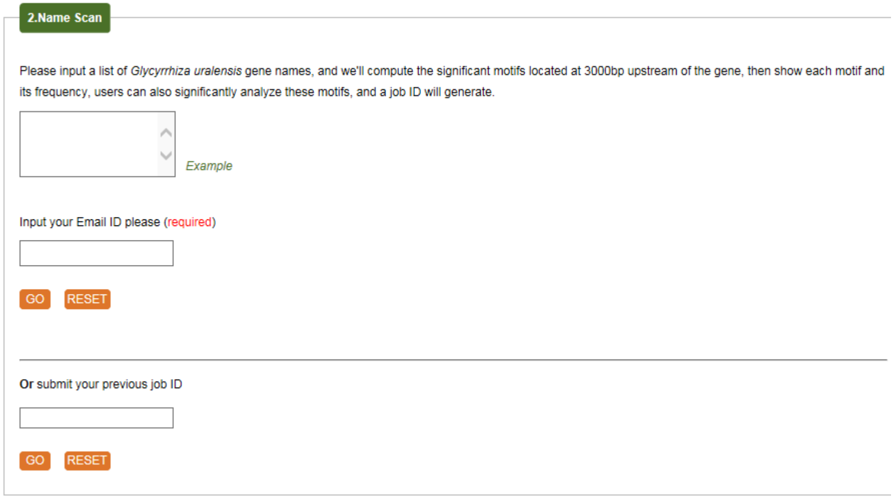


1.Sequence Scan

Please input a fasta sequence, we'll find out all the possible motifs.

```
>example_seq
CCTAGTTACGGGGATTCAAAAAATCATTAGGACTGAAGAAAAATGAATTGCTCAGCATTTTCCTTTTGGTTTGTTTGCAAAATAA
TATTTTTCTTTCTCTCATTCCATATCCAAATTTCAATAGCTAATCCTCGAGAAAACTTCCTTAAATGCTTCTCAAAACATATTCC
CAACAATGTAGCAAATCCAAAACTCGTATACACTCAACACGACCAATTGTATATGTCTATCCTGAATTCGACAATACAAAATCTT
AGATTCATCTCTGATACAACCCCAAAACCACTCGTTATTGTCACTCCTTCAAATAACTCCCATATCCAAGCAACTATTTTATGCT
CTAAGAAAGTTGGCTTGCAGATTCGAACTCGAAGCGGTGGCCATGATGCTGAGGGTATGTCCTACATATCTCAAGTCCCATTTGT
TGTAGTAGACTTGAGAAACATGCATTCGATCAAAATAGATGTTCATAGCCAAACTGCGTGGGTTGAAGCCGGAGCTACCCTTGGA
GAAGTTTATTATTGGATCAATGAGAAGAATGAGAATCTTAGTTTTCCTGGTGGGTATTGCCCTACTGTTGGCGTAGGTGGACACT
TTAGTGGAGGAGGCTATGGAGCATTGATGCGAAATTATGGCCTTGCGGCTGATAATATTATTGATGCACACTTAGTCAATGTTGA
```

The funtion can perform motif scanning on the nucleic acid sequence provided by the user and display the number of motifs.



2.Name Scan

Please input a list of *Glycyrrhiza uralensis* gene names, and we'll compute the significant motifs located at 3000bp upstream of the gene, then show each motif and its frequency, users can also significantly analyze these motifs, and a job ID will generate.

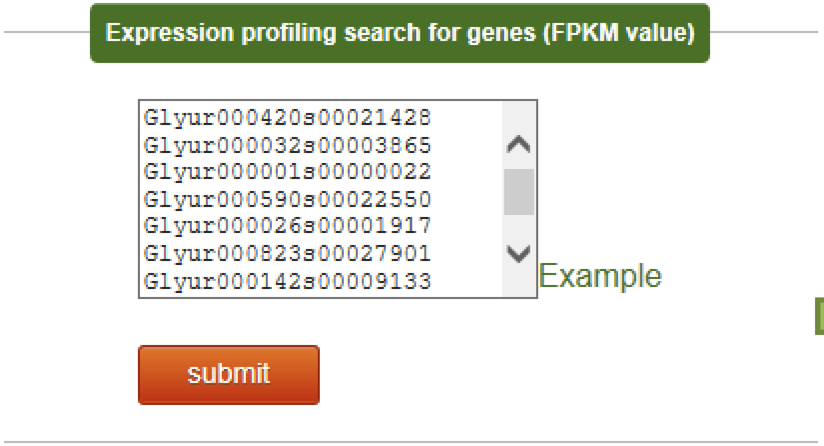
Input your Email ID please (required)

Or submit your previous job ID

This tool can scan the gene 3K promoter sequence provided by the user, and perform Motif enrichment analysis and result display.

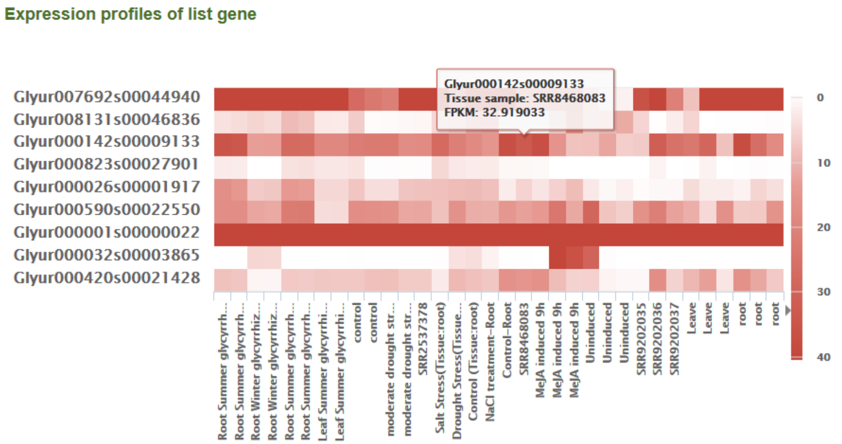
Tools:Heatmap

Users can enter gene IDs in the text box, and click submit to obtained heatmaps of gene expression.



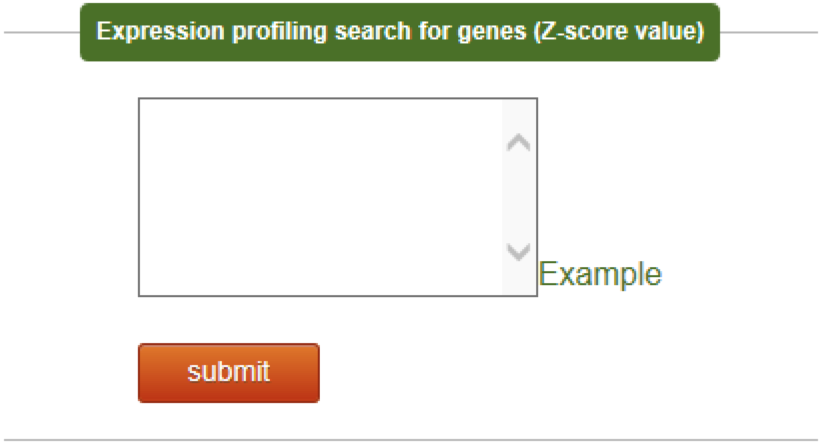
Expression profiling search for genes (FPKM value)

```
Glyur000420s00021428
Glyur000032s00003865
Glyur000001s00000022
Glyur000590s00022550
Glyur000026s00001917
Glyur000823s00027901
Glyur000142s00009133
```

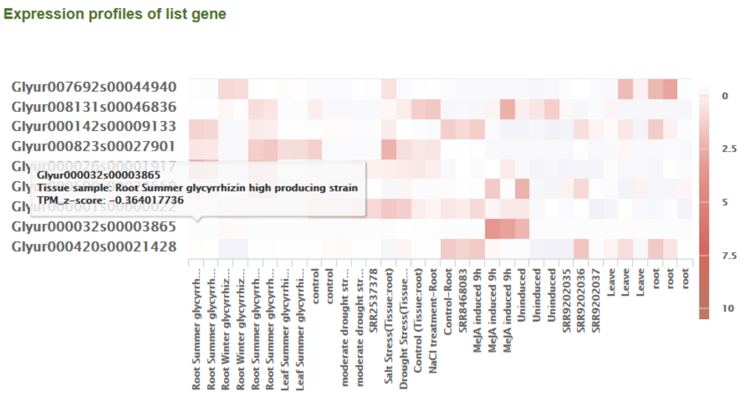


Expression profiles of list gene

Glyur000142s00009133
Tissue sample: SRR8468083
FPKM: 32.919033



Expression profiling search for genes (Z-score value)

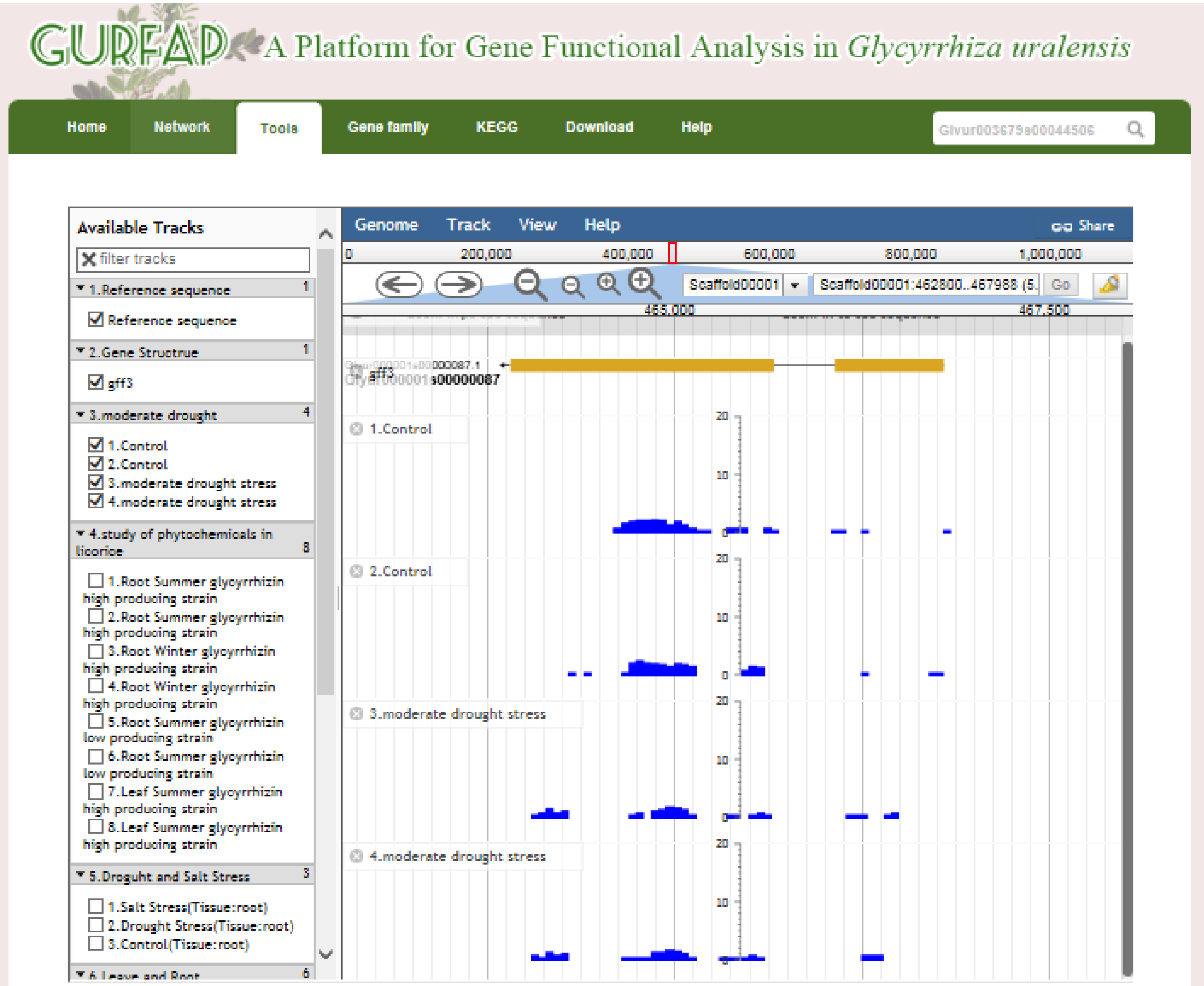


Expression profiles of list gene

Glyur000032s00003865
Tissue sample: Root Summer glycyrrhizin high producing strain
TPM_z-score: -0.364017736

Tools:JBrowse

JBrowse tool can provide users with the display of gene structure and transcriptome samples.



Available Tracks

filter tracks

1.Reference sequence 1
☑ Reference sequence

2.Gene Structrue 1
☑ gff3

3.moderate drought 4
☑ 1.Control
☑ 2.Control
☑ 3.moderate drought stress
☑ 4.moderate drought stress

4.study of phytochemicals in licorice 8
☐ 1.Root Summer glycyrrhizin high producing strain
☐ 2.Root Summer glycyrrhizin high producing strain
☐ 3.Root Winter glycyrrhizin high producing strain
☐ 4.Root Winter glycyrrhizin high producing strain
☐ 5.Root Summer glycyrrhizin low producing strain
☐ 6.Root Summer glycyrrhizin low producing strain
☐ 7.Leaf Summer glycyrrhizin high producing strain
☐ 8.Leaf Summer glycyrrhizin high producing strain

5.Droguht and Salt Stress 3
☐ 1.Salt Stress(Tissue:root)
☐ 2.Drought Stress(Tissue:root)
☐ 3.Control(Tissue:root)

6.Leave and Root 6

1.Control

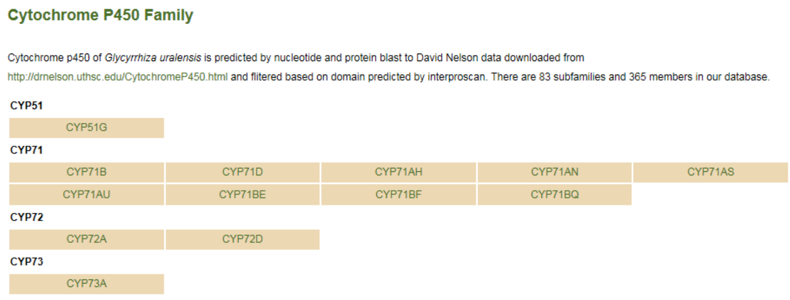
2.Control

3.moderate drought stress

4.moderate drought stress

Gene Family

Gene family section displayed predicted protein kinases (PKs), transcription regulators (TRs), and transcription factors (TFs) , ubiquitin proteins, CYP450 genes, carbohydrate-active enzymes and collected EAR motif-containing proteins.



Cytochrome P450 Family

Cytochrome p450 of *Glycyrrhiza uralensis* is predicted by nucleotide and protein blast to David Nelson data downloaded from http://drnelson.uthsc.edu/CytochromeP450.html and flitered based on domain predicted by interproscan. There are 83 subfamilies and 365 members in our database.

CYP51

CYP51G				

CYP71

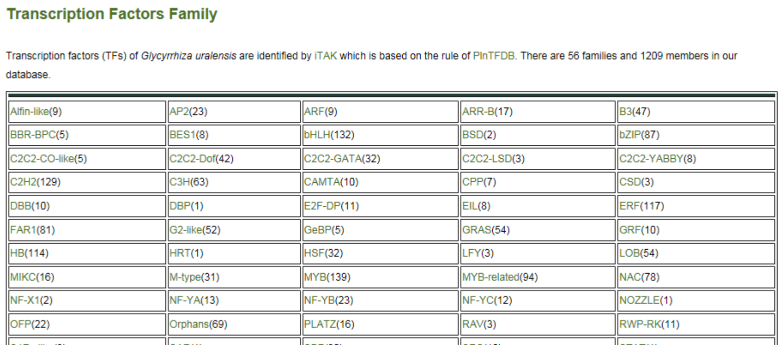
CYP71B	CYP71D	CYP71AH	CYP71AN	CYP71AS
CYP71AU	CYP71BE	CYP71BF	CYP71BQ	

CYP72

CYP72A	CYP72D			

CYP73

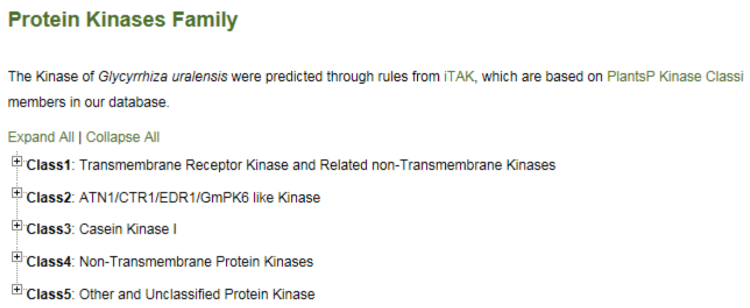
CYP73A				



Transcription Factors Family

Transcription factors (TFs) of *Glycyrrhiza uralensis* are identified by iTAK which is based on the rule of PlnTFDB. There are 56 families and 1209 members in our database.

Alfin-like(9)	AP2(23)	ARF(9)	ARR-B(17)	B3(47)
BBR-BPC(5)	BES1(8)	bHLH(132)	BSD(2)	bZIP(87)
C2C2-CO-like(5)	C2C2-Dof(42)	C2C2-GATA(32)	C2C2-LSD(3)	C2C2-YABBY(8)
C2H2(129)	C3H(63)	CAMTA(10)	CPP(7)	CSD(3)
DBB(10)	DBP(1)	E2F-DP(11)	EIL(8)	ERF(117)
FAR1(81)	G2-like(52)	GeBP(5)	GRAS(54)	GRF(10)
HB(114)	HRT(1)	HSF(32)	LFY(3)	LOB(54)
MIKC(16)	M-type(31)	MYB(139)	MYB-related(94)	NAC(78)
NF-X1(2)	NF-YA(13)	NF-YB(23)	NF-YC(12)	NOZZLE(1)
OFP(22)	Orphans(69)	PLATZ(16)	RAV(3)	RWP-RK(11)

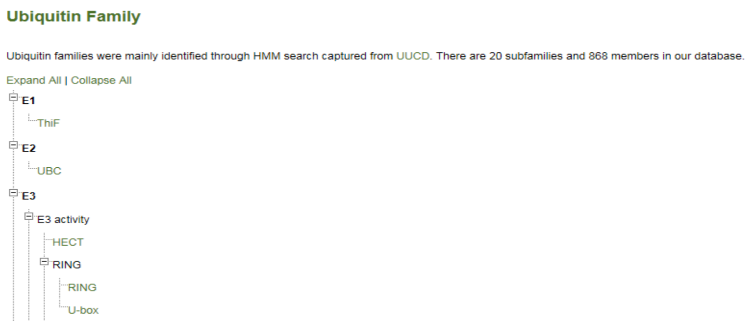


Protein Kinases Family

The Kinase of *Glycyrrhiza uralensis* were predicted through rules from iTAK, which are based on PlantsP Kinase Classi members in our database.

Expand All | Collapse All

- ⊞ **Class1**: Transmembrane Receptor Kinase and Related non-Transmembrane Kinases
- ⊞ **Class2**: ATN1/CTR1/EDR1/GmPK6 like Kinase
- ⊞ **Class3**: Casein Kinase I
- ⊞ **Class4**: Non-Transmembrane Protein Kinases
- ⊞ **Class5**: Other and Unclassified Protein Kinase

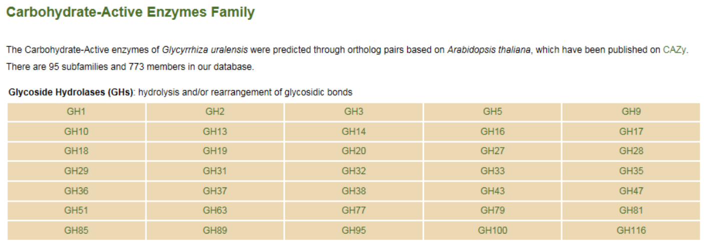


Ubiquitin Family

Ubiquitin families were mainly identified through HMM search captured from UUCD. There are 20 subfamilies and 868 members in our database.

Expand All | Collapse All

- ⊟ **E1**
  - ThiF
- ⊟ **E2**
  - UBC
- ⊟ **E3**
  - ⊟ E3 activity
    - HECT
    - ⊟ RING
      - RING
      - U-box

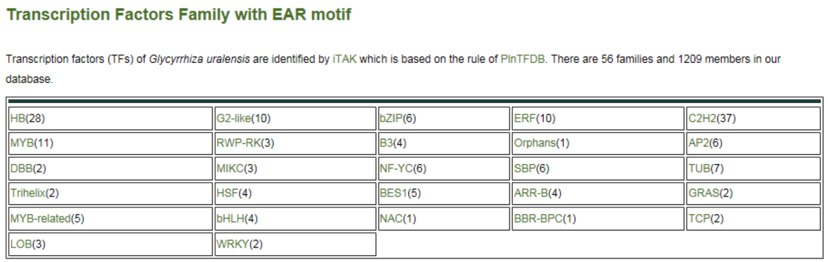


Carbohydrate-Active Enzymes Family

The Carbohydrate-Active enzymes of *Glycyrrhiza uralensis* were predicted through ortholog pairs based on *Arabidopsis thaliana*, which have been published on CAZy. There are 95 subfamilies and 773 members in our database.

Glycoside Hydrolases (GHs): hydrolysis and/or rearrangement of glycosidic bonds

GH1	GH2	GH3	GH5	GH9
GH10	GH13	GH14	GH16	GH17
GH18	GH19	GH20	GH27	GH28
GH29	GH31	GH32	GH33	GH35
GH36	GH37	GH38	GH43	GH47
GH51	GH63	GH77	GH79	GH81
GH85	GH89	GH95	GH100	GH116



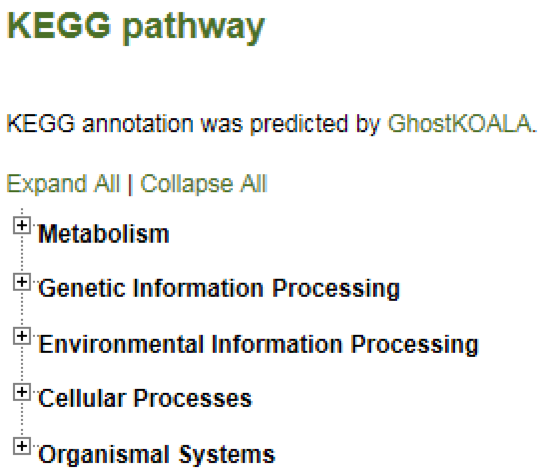
Transcription Factors Family with EAR motif

Transcription factors (TFs) of *Glycyrrhiza uralensis* are identified by iTAK which is based on the rule of PlnTFDB. There are 56 families and 1209 members in our database.

HB(28)	G2-like(10)	bZIP(6)	ERF(10)	C2H2(37)
MYB(11)	RWP-RK(3)	B3(4)	Orphans(1)	AP2(6)
DBB(2)	MIKC(3)	NF-YC(6)	SBP(6)	TUB(7)
Trihelix(2)	HSF(4)	BES1(5)	ARR-B(4)	GRAS(2)
MYB-related(5)	bHLH(4)	NAC(1)	BBR-BPC(1)	TCP(2)
LOB(3)	WRKY(2)			

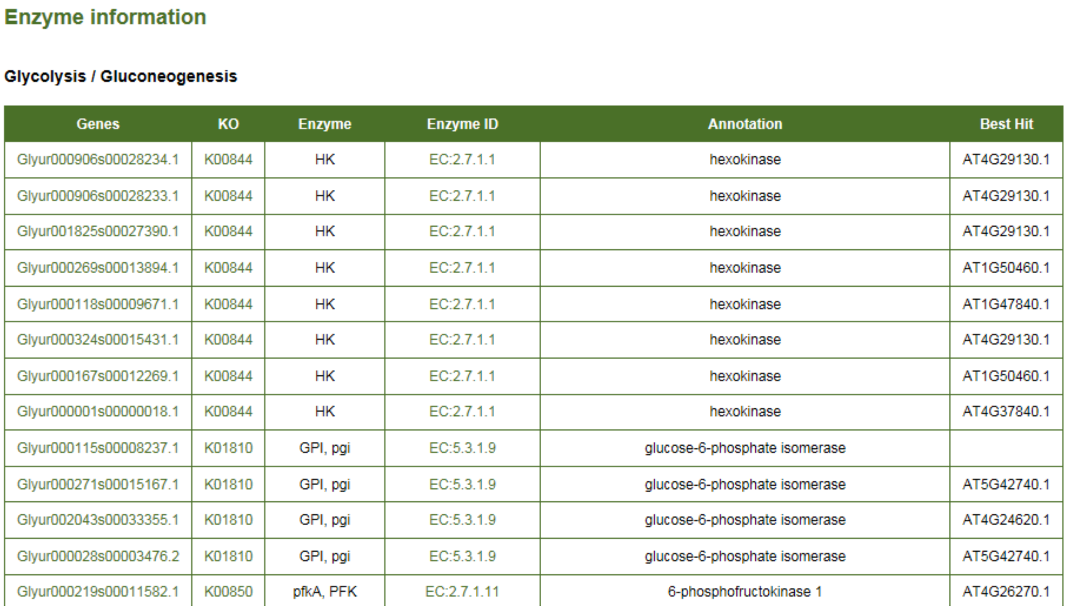
Pathway

This section contained KEGG annotation predicted by GhostKOALA.
This website can obtain Enzyme detailed information.



KEGG pathway

KEGG annotation was predicted by GhostKOALA.



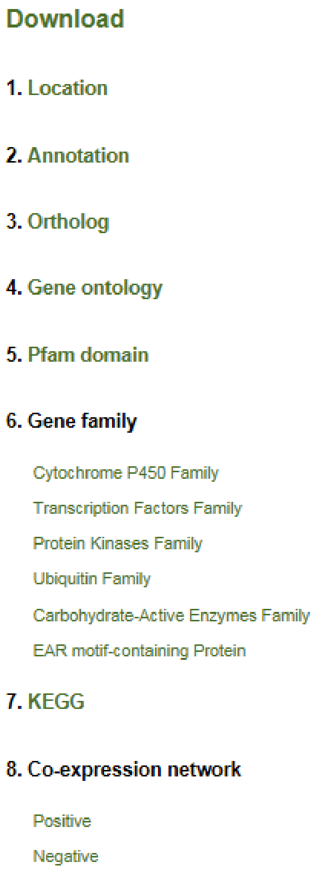
Enzyme information

Glycolysis / Gluconeogenesis

Genes	KO	Enzyme	Enzyme ID	Annotation	Best Hit
Glyur000906s00028234.1	K00844	HK	EC:2.7.1.1	hexokinase	AT4G29130.1
Glyur000906s00028233.1	K00844	HK	EC:2.7.1.1	hexokinase	AT4G29130.1
Glyur001825s00027390.1	K00844	HK	EC:2.7.1.1	hexokinase	AT4G29130.1
Glyur000269s00013894.1	K00844	HK	EC:2.7.1.1	hexokinase	AT1G50460.1
Glyur000118s00009671.1	K00844	HK	EC:2.7.1.1	hexokinase	AT1G47840.1
Glyur000324s00015431.1	K00844	HK	EC:2.7.1.1	hexokinase	AT4G29130.1
Glyur000167s00012269.1	K00844	HK	EC:2.7.1.1	hexokinase	AT1G50460.1
Glyur000001s00000018.1	K00844	HK	EC:2.7.1.1	hexokinase	AT4G37840.1
Glyur000115s00008237.1	K01810	GPI, pgi	EC:5.3.1.9	glucose-6-phosphate isomerase	
Glyur000271s00015167.1	K01810	GPI, pgi	EC:5.3.1.9	glucose-6-phosphate isomerase	AT5G42740.1
Glyur002043s00033355.1	K01810	GPI, pgi	EC:5.3.1.9	glucose-6-phosphate isomerase	AT4G24620.1
Glyur000028s00003476.2	K01810	GPI, pgi	EC:5.3.1.9	glucose-6-phosphate isomerase	AT5G42740.1
Glyur000219s00011582.1	K00850	pfkA, PFK	EC:2.7.1.11	6-phosphofructokinase 1	AT4G26270.1

Download

This section contain download gene location, gene annotation, orthologs, Gene Ontology, Pfam domain, Gene Family, KEGG annotation and co-expression network.



Download

1. Location
2. Annotation
3. Ortholog
4. Gene ontology
5. Pfam domain
6. Gene family
    - Cytochrome P450 Family
    - Transcription Factors Family
    - Protein Kinases Family
    - Ubiquitin Family
    - Carbohydrate-Active Enzymes Family
    - EAR motif-containing Protein
7. KEGG
8. Co-expression network
    - Positive
    - Negative

Help

Shown this direction.