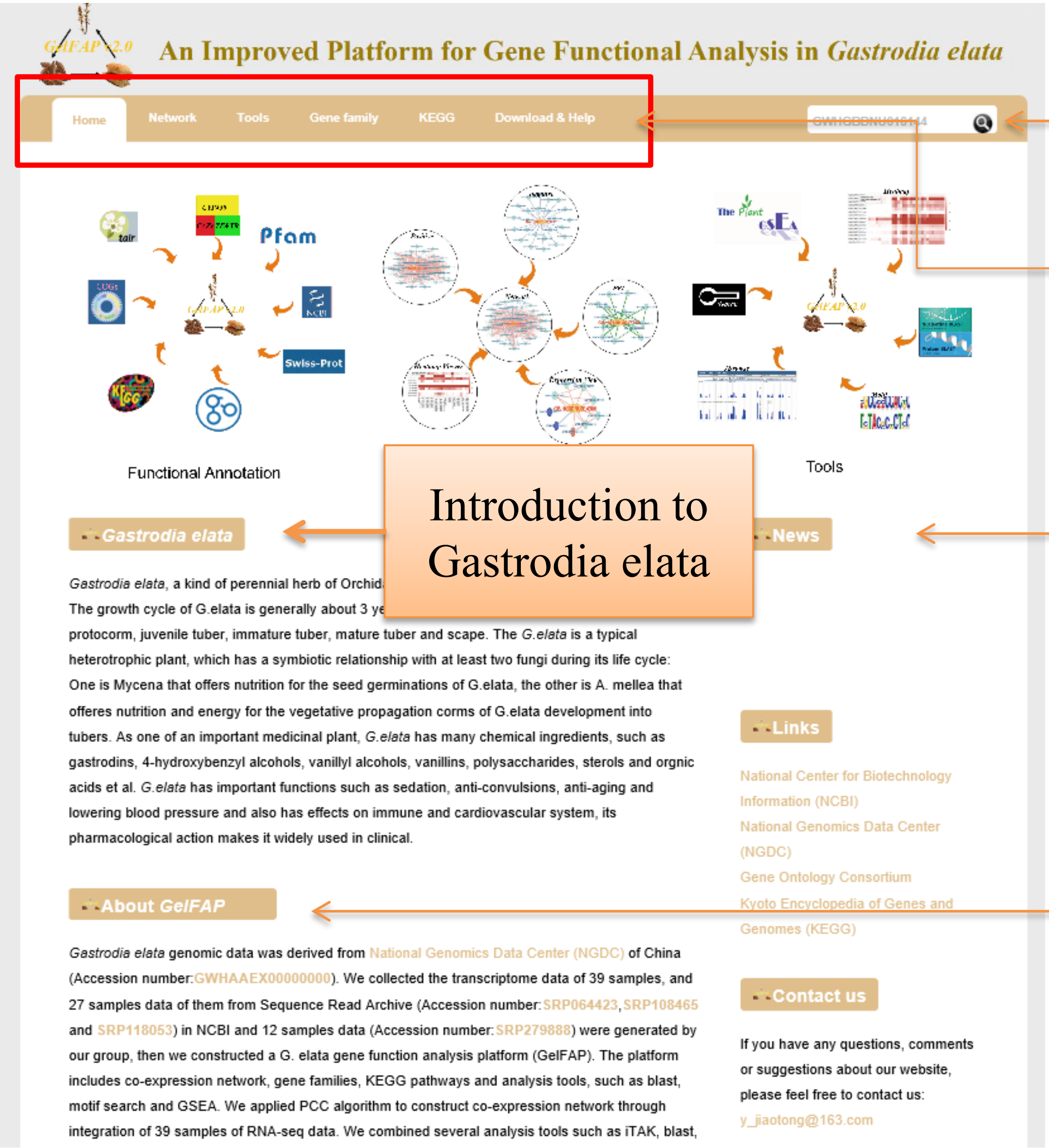
Manual for users

Home page



An Improved Platform for Gene Functional Analysis in *Gastrodia elata*

Gastrodia elata

Gastrodia elata, a kind of perennial herb of Orchid
The growth cycle of G.elata is generally about 3 ye
protocorm, juvenile tuber, immature tuber, mature tuber and scape. The *G.elata* is a typical heterotrophic plant, which has a symbiotic relationship with at least two fungi during its life cycle: One is Mycena that offers nutrition for the seed germinations of G.elata, the other is A. mellea that offeres nutrition and energy for the vegetative propagation corms of G.elata development into tubers. As one of an important medicinal plant, *G.elata* has many chemical ingredients, such as gastrodins, 4-hydroxybenzyl alcohols, vanillyl alcohols, vanillins, polysaccharides, sterols and orgnic acids et al. *G.elata* has important functions such as sedation, anti-convulsions, anti-aging and lowering blood pressure and also has effects on immune and cardiovascular system, its pharmacological action makes it widely used in clinical.

About GelFAP

Gastrodia elata genomic data was derived from National Genomics Data Center (NGDC) of China (Accession number:GWHAAEX00000000). We collected the transcriptome data of 39 samples, and 27 samples data of them from Sequence Read Archive (Accession number:SRP064423,SRP108465 and SRP118053) in NCBI and 12 samples data (Accession number:SRP279888) were generated by our group, then we constructed a G. elata gene function analysis platform (GelFAP). 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 39 samples of RNA-seq data. We combined several analysis tools such as iTAK, blast,

News

Links

National Center for Biotechnology Information (NCBI)
National Genomics Data Center (NGDC)
Gene Ontology Consortium
Kyoto Encyclopedia of Genes and Genomes (KEGG)

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

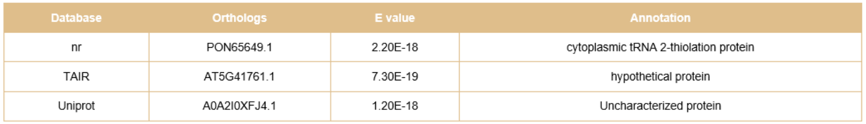
Introduction to Gastrodia elata

Update news

Introduction to GelFAP v2.o

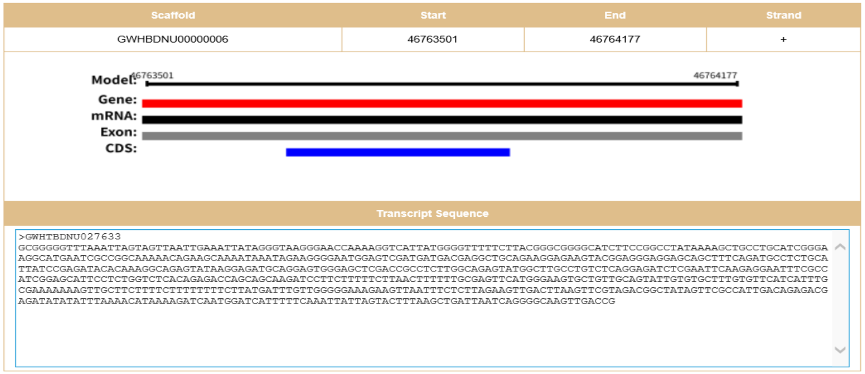
Gene Detail Information

Function annotation



Database	Orthologs	E value	Annotation
nr	PON65649.1	2.20E-18	cytoplasmic tRNA 2-thiolation protein
TAIR	AT5G41761.1	7.30E-19	hypothetical protein
Uniprot	A0A2I0XFJ4.1	1.20E-18	Uncharacterized protein

Sequence & Location



Scaffold	Start	End	Strand
GWHBDNU00000006	46763501	46764177	+

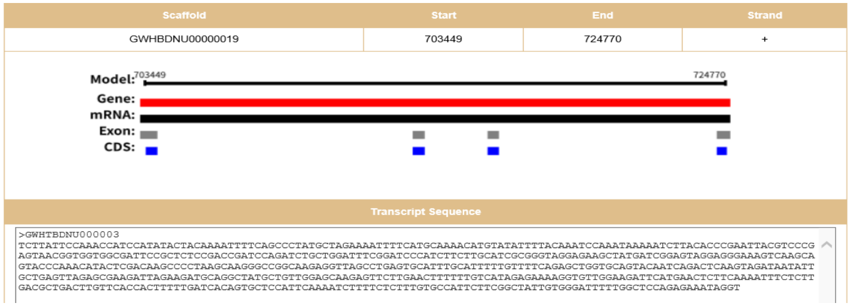
Transcript Sequence

```
>GWHTBDNU027633
GCGGGGGTTTAAATTAGTAGTTAATTGAAATTATAGGGTAAGGGAACCAAAAGGTCATTATGGGGTTTTTCTTACGGGCGGGGCATCTTCCGGCCTATAAAAGCTGCCTGCATCGGGA
AGGCATGAATCGCCGGCAAAAACAGAAGCAAAATAAATAGAAGGGGAATGGAGTCGATGATGACGAGGCTGCAGAAGGAGAAGTACGGAGGGAGGAGCAGCTTTCAGATGCCTCTGCA
TTATCCGAGATACACAAAGGCAGAGTATAAGGAGATGCAGGAGTGGGAGCTCGACCGCCTCTTGGCAGAGTATGGCTTGCCTGTCTCAGGAGATCTCGAATTCAAGAGGAATTTCGCC
ATCGGAGCATTCCTCTGGTCTCACAGAGACCAGCAGCAAGATCCTTCTTTTTCTTAACTTTTTTGCGAGTTCATGGGAAGTGCTGTTGCAGTATTGTGTGCTTTGTGTTCATCATTTG
CGAAAAAAAGTTGCTTCTTTTCTTTTTTTTCTTATGATTTGTTGGGGGAAAGAAGTTAATTTCTCTTAGAAGTTGACTTAAGTTCGTAGACGGCTATAGTTCGCCATTGACAGAGACG
AGATATATATTTAAAACATAAAAGATCAATGGATCATTTTTCAAATTATTAGTACTTTAAGCTGATTAATCAGGGGCAAGTTGACCG
```

Links for Network

Network category	Network	Top300 PCC genelist
Coexpression Positive	Network	Top300 PCC genelist
Coexpression Negative	Network	Top300 PCC genelist

Protein Structure



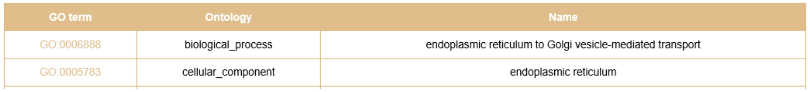
Scaffold	Start	End	Strand
GWHBDNU00000019	703449	724770	+

Transcript Sequence

```
>GWHTBDNU000003
TCTTATTCCAAACCATCCATATACTACAAAATTTTCAGCCCTATGCTAGAAAATTTTCATGCAAAACATGTATATTTTACAAATCCAAATAAAAATCTTACACCCGAATTACGTCCCG
AGTAACGGTGGTGGCGATTCCGCTCTCCGACCGATCCAGATCTGCTGGATTTCGGATCCCATCTTCTTGCATCGCGGGTAGGAGAAGCTATGATCGGAGTAGGAGGGAAAGTCAAGCA
GTACCCAAACATACTCGACAAGCCCCTAAGCAAGGGCCGGCAAGAGGTTAGCCTGAGTGCATTTGCATTTTTGTTTTCAGAGCTGGTGCAGTACAATCAGACTCAAGTAGATAATATT
GCTGAGTTAGAGCGAAGATTAGAAGATGCAGGCTATGCTGTTGGAGCAAGAGTTCTTGAACTTTTTTGTCATAGAGAAAAGGTGTTGGAAGATTCATGAACTCTTCAAAATTTCTCTT
GACGCTGACTTGTTCACCACTTTTTGATCACAGTGCTCCATTCAAAATCTTTTCTCTTTGTGCCATTCTTCGGCTATTGTGGGATTTTTGGCTCCAGAGAAATAGGT
```

GO Annotation

Gene Ontology



GO term	Ontology	Name
GO:0006888	biological_process	endoplasmic reticulum to Golgi vesicle-mediated transport
GO:0005783	cellular_component	endoplasmic reticulum

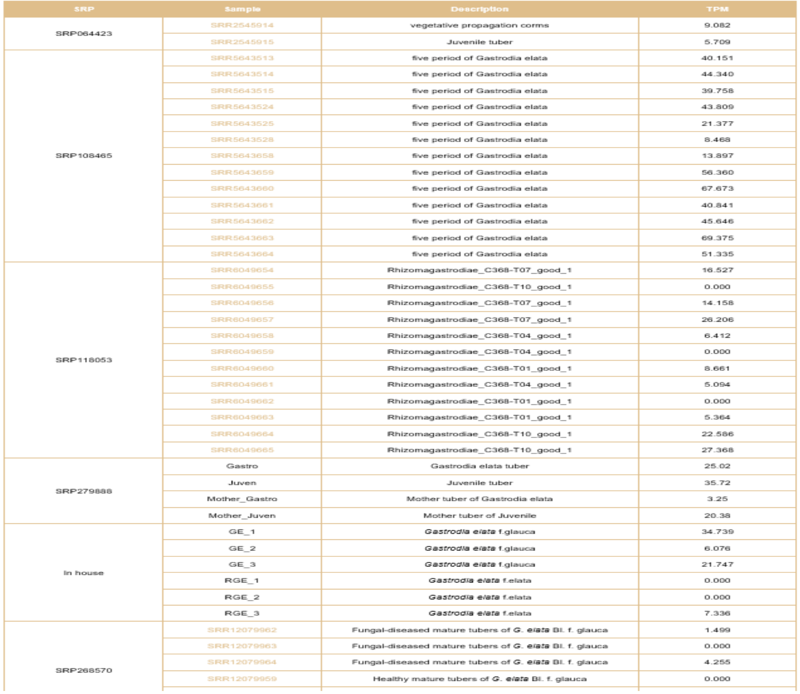
Gene Family

Gene family	subfamily
--	--

KEGG orthology

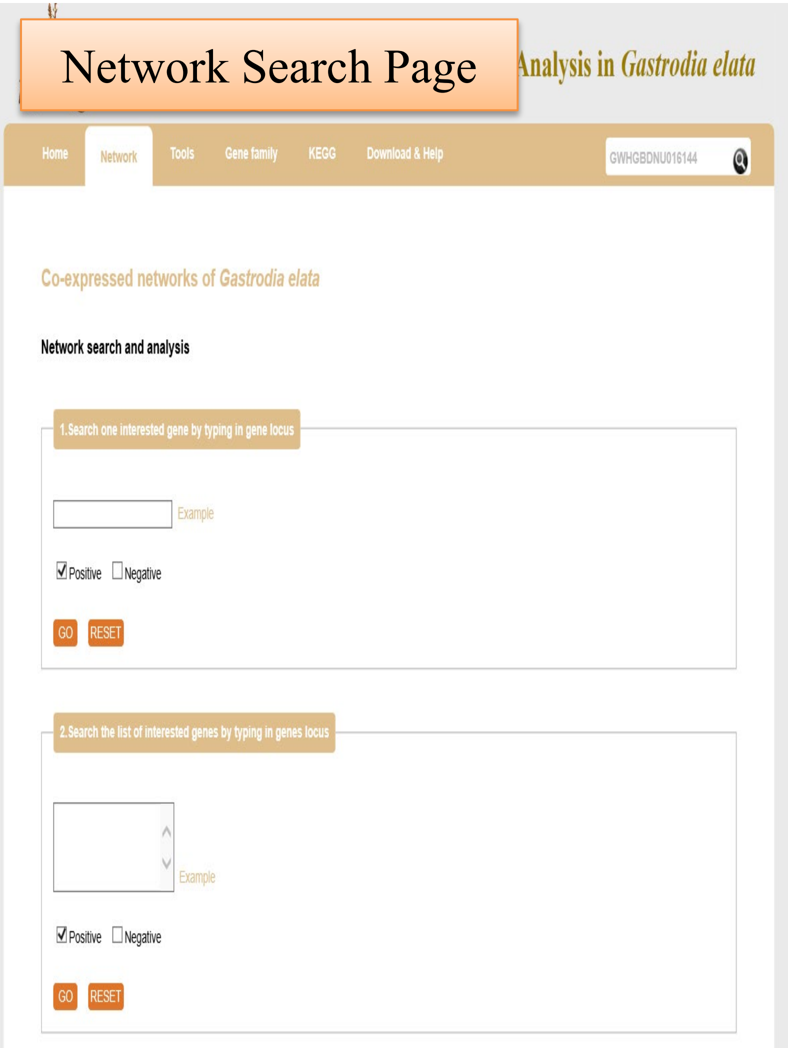
KO	Enzyme	pathway	mapID
--	--	--	--

Expression Pattern



SRP	Sample	Description	TPM
SRP064423	SRR2545914	vegetative propagation corms	9.082
	SRR2545915	Juvenile tuber	5.709
SRP108465	SRR5643513	five period of Gastrodia elata	40.151
	SRR5643514	five period of Gastrodia elata	44.340
	SRR5643515	five period of Gastrodia elata	39.758
	SRR5643524	five period of Gastrodia elata	43.809
	SRR5643525	five period of Gastrodia elata	21.377
	SRR5643528	five period of Gastrodia elata	8.468
	SRR5643658	five period of Gastrodia elata	13.897
	SRR5643659	five period of Gastrodia elata	56.360
	SRR5643660	five period of Gastrodia elata	67.673
	SRR5643661	five period of Gastrodia elata	40.841
	SRR5643662	five period of Gastrodia elata	45.646
	SRR5643663	five period of Gastrodia elata	69.375
	SRR5643664	five period of Gastrodia elata	51.335
SRP118053	SRR6049654	Rhizomagastrodiae_C368-T07_good_1	16.527
	SRR6049655	Rhizomagastrodiae_C368-T10_good_1	0.000
	SRR6049656	Rhizomagastrodiae_C368-T07_good_1	14.158
	SRR6049657	Rhizomagastrodiae_C368-T07_good_1	26.206
	SRR6049658	Rhizomagastrodiae_C368-T04_good_1	6.412
	SRR6049659	Rhizomagastrodiae_C368-T04_good_1	0.000
	SRR6049660	Rhizomagastrodiae_C368-T01_good_1	8.661
	SRR6049661	Rhizomagastrodiae_C368-T04_good_1	5.094
	SRR6049662	Rhizomagastrodiae_C368-T01_good_1	0.000
	SRR6049663	Rhizomagastrodiae_C368-T01_good_1	5.364
	SRR6049664	Rhizomagastrodiae_C368-T10_good_1	22.586
	SRR6049665	Rhizomagastrodiae_C368-T10_good_1	27.368
SRP279888	Gastro	Gastrodia elata tuber	25.02
	Juven	Juvenile tuber	35.72
	Mother_Gastro	Mother tuber of Gastrodia elata	3.25
	Mother_Juven	Mother tuber of Juvenile	20.38
In house	GE_1	*Gastrodia elata* f.glauca	34.739
	GE_2	*Gastrodia elata* f.glauca	6.076
	GE_3	*Gastrodia elata* f.glauca	21.747
	RGE_1	*Gastrodia elata* f.elata	0.000
	RGE_2	*Gastrodia elata* f.elata	0.000
	RGE_3	*Gastrodia elata* f.elata	7.336
SRP268570	SRR12079962	Fungal-diseased mature tubers of *G. elata* Bl. f. glauca	1.499
	SRR12079963	Fungal-diseased mature tubers of *G. elata* Bl. f. glauca	0.000
	SRR12079964	Fungal-diseased mature tubers of *G. elata* Bl. f. glauca	4.255
	SRR12079959	Healthy mature tubers of *G. elata* Bl. f. glauca	0.000

Network



Network Search Page

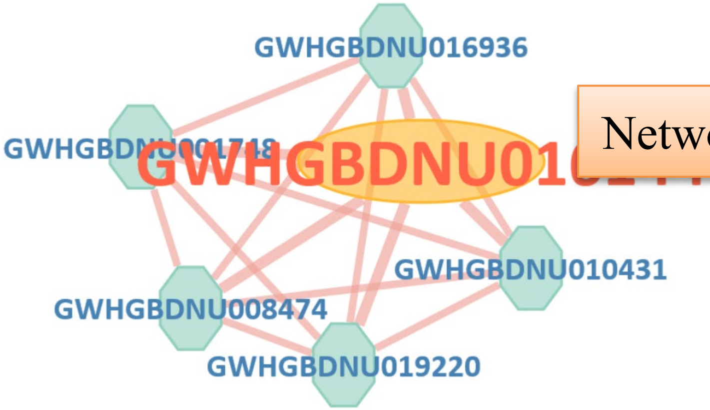
Analysis in *Gastrodia elata*

Co-expressed networks of *Gastrodia elata*

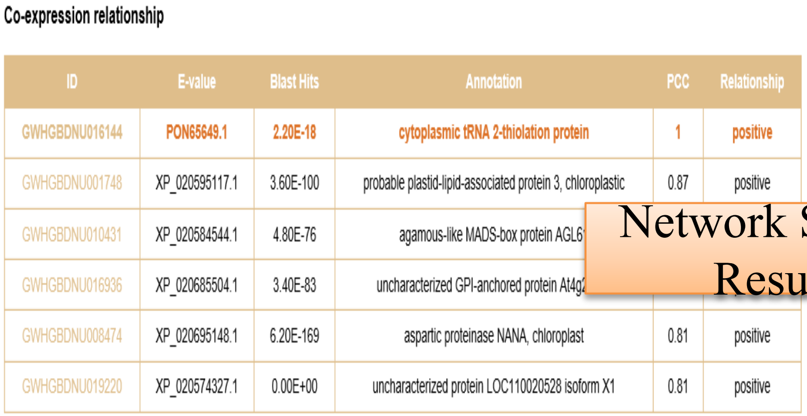
Network search and analysis

1.Search one interested gene by typing in gene locus

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



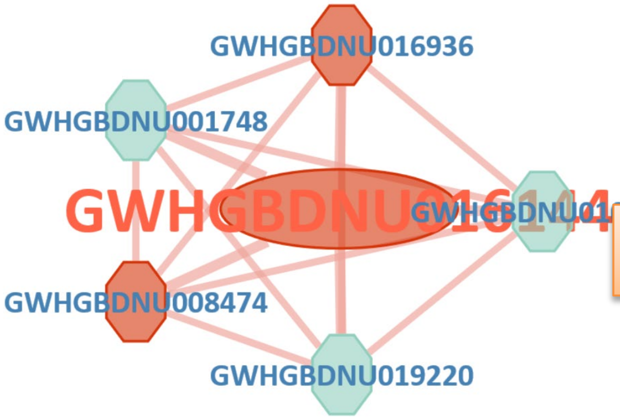
Network Display



Co-expression relationship

ID	E-value	Blast Hits	Annotation	PCC	Relationship
GWHGBDNU016144	PON65649.1	2.20E-18	cytoplasmic tRNA 2-thiolation protein	1	positive
GWHGBDNU001748	XP_020595117.1	3.60E-100	probable plastid-lipid-associated protein 3, chloroplastic	0.87	positive
GWHGBDNU010431	XP_020584544.1	4.80E-76	agamous-like MADS-box protein AGL6		
GWHGBDNU016936	XP_020685504.1	3.40E-83	uncharacterized GPI-anchored protein At4g2		
GWHGBDNU008474	XP_020695148.1	6.20E-169	aspartic proteinase NANA, chloroplast	0.81	positive
GWHGBDNU019220	XP_020574327.1	0.00E+00	uncharacterized protein LOC110020528 isoform X1	0.81	positive

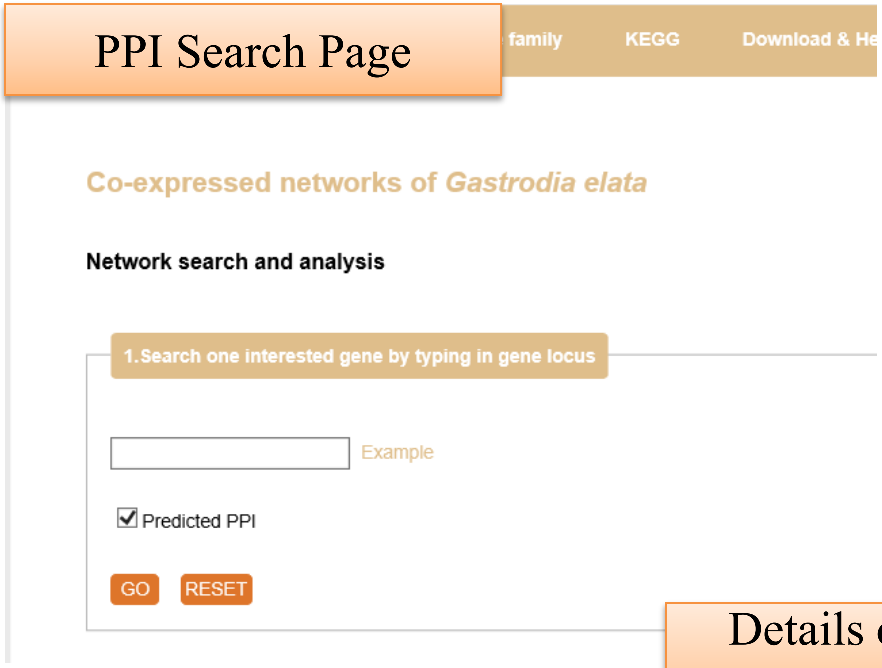
Network Search Result



Network with expression view

PPI Search

PPI Search Page



Co-expressed networks of *Gastrodia elata*

Network search and analysis

1.Search one interested gene by typing in gene locus

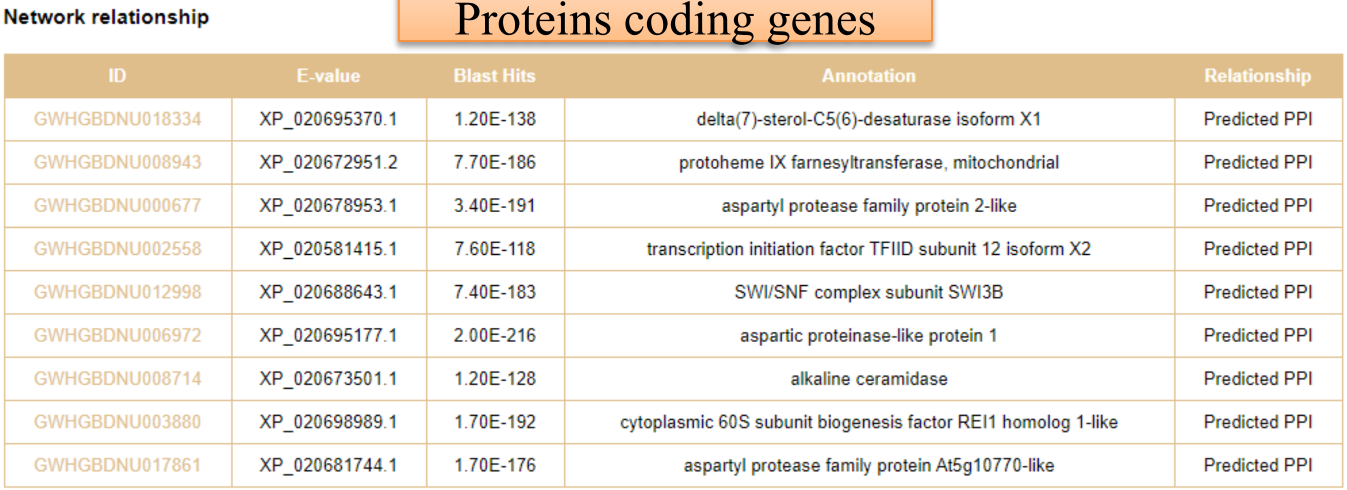
Example

☑ Predicted PPI

GO RESET

Network Display

Details of Interaction Proteins coding genes



Network relationship

ID	E-value	Blast Hits	Annotation	Relationship
GWHGBDNU018334	XP_020695370.1	1.20E-138	delta(7)-sterol-C5(6)-desaturase isoform X1	Predicted PPI
GWHGBDNU008943	XP_020672951.2	7.70E-186	protoheme IX farnesyltransferase, mitochondrial	Predicted PPI
GWHGBDNU000677	XP_020678953.1	3.40E-191	aspartyl protease family protein 2-like	Predicted PPI
GWHGBDNU002558	XP_020581415.1	7.60E-118	transcription initiation factor TFIID subunit 12 isoform X2	Predicted PPI
GWHGBDNU012998	XP_020688643.1	7.40E-183	SWI/SNF complex subunit SWI3B	Predicted PPI
GWHGBDNU006972	XP_020695177.1	2.00E-216	aspartic proteinase-like protein 1	Predicted PPI
GWHGBDNU008714	XP_020673501.1	1.20E-128	alkaline ceramidase	Predicted PPI
GWHGBDNU003880	XP_020698989.1	1.70E-192	cytoplasmic 60S subunit biogenesis factor REI1 homolog 1-like	Predicted PPI
GWHGBDNU017861	XP_020681744.1	1.70E-176	aspartyl protease family protein At5g10770-like	Predicted PPI

Tools:Search

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

Please input one gene

Species: Gastrodia elata

Locus ID:

Example:

Please input keywords

Species: Gastrodia elata

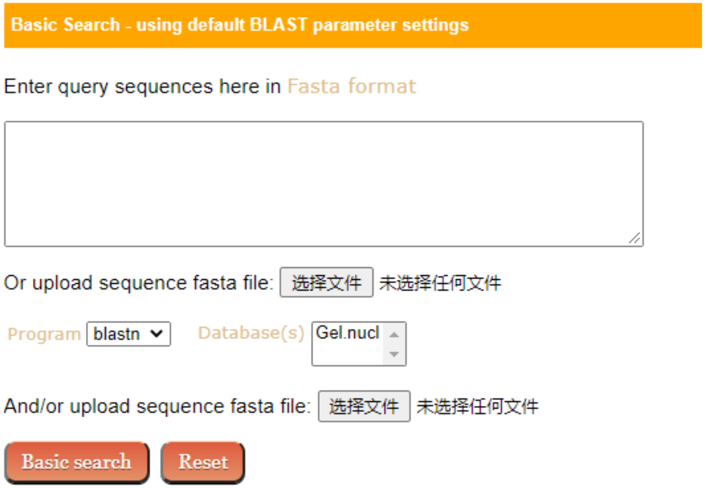
Keywords:

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



Basic Search - using default BLAST parameter settings

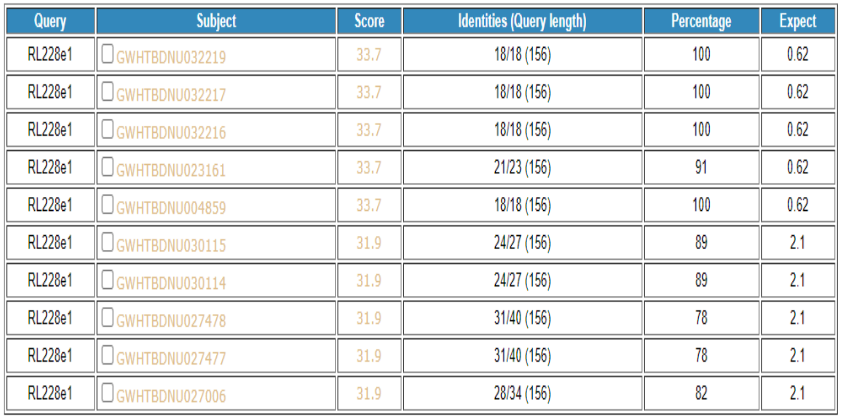
Enter query sequences here in Fasta format

Or upload sequence fasta file: 选择文件 未选择任何文件

Program: blastn Database(s): Gel.nucl

And/or upload sequence fasta file: 选择文件 未选择任何文件

Blast Search Results

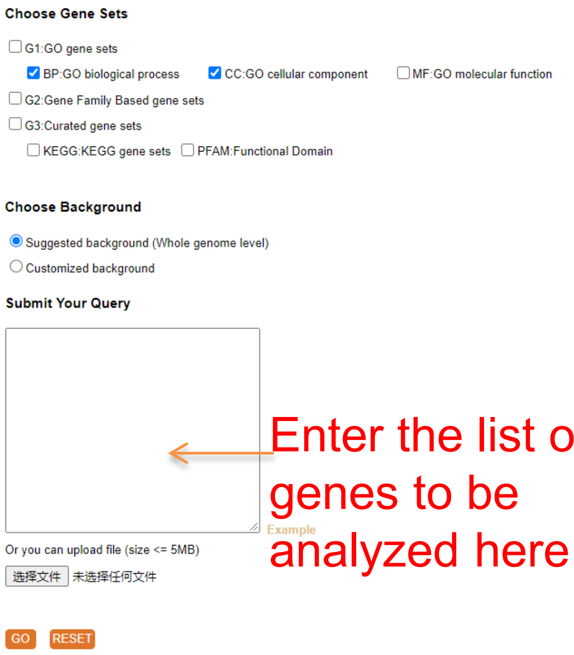


Query	Subject	Score	Identities (Query length)	Percentage	Expect
RL228e1	☐ GWHTBDNU032219	33.7	18/18 (156)	100	0.62
RL228e1	☐ GWHTBDNU032217	33.7	18/18 (156)	100	0.62
RL228e1	☐ GWHTBDNU032216	33.7	18/18 (156)	100	0.62
RL228e1	☐ GWHTBDNU023161	33.7	21/23 (156)	91	0.62
RL228e1	☐ GWHTBDNU004859	33.7	18/18 (156)	100	0.62
RL228e1	☐ GWHTBDNU030115	31.9	24/27 (156)	89	2.1
RL228e1	☐ GWHTBDNU030114	31.9	24/27 (156)	89	2.1
RL228e1	☐ GWHTBDNU027478	31.9	31/40 (156)	78	2.1
RL228e1	☐ GWHTBDNU027477	31.9	31/40 (156)	78	2.1
RL228e1	☐ GWHTBDNU027006	31.9	28/34 (156)	82	2.1

Tools:GSEA

GSEA is a tool for functional enrichment analysis of gene sets

GSEA page



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)

○ Customized background

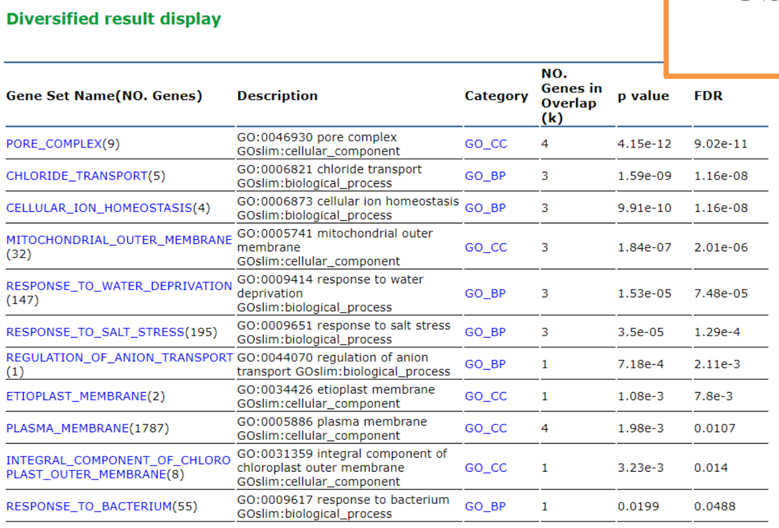
Submit Your Query

Example

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

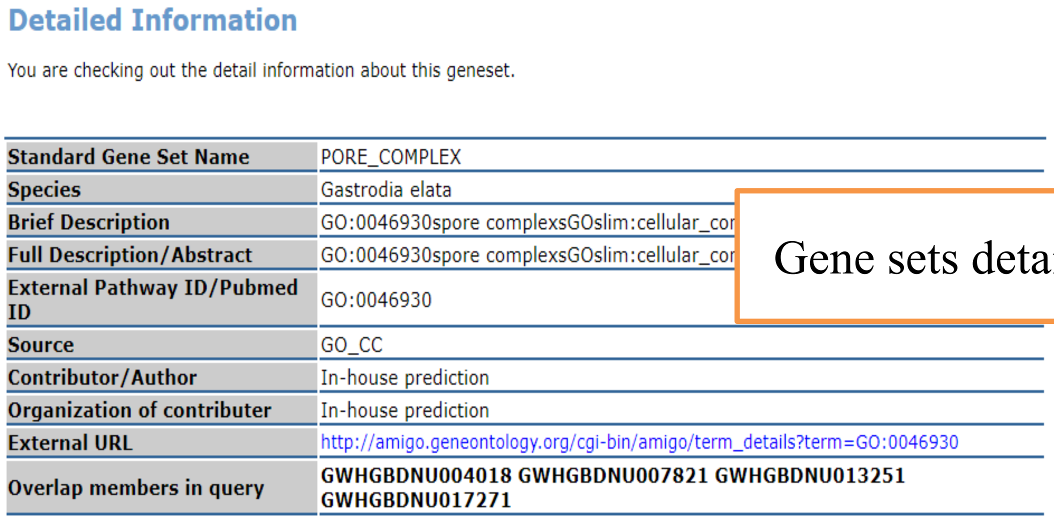
Enter the list of genes to be analyzed here.

GSEA search results



Diversified result display

Gene Set Name(NO. Genes)	Description	Category	NO. Genes in Overlap (k)	p value	FDR
PORE_COMPLEX(9)	GO:0046930 pore complex GOslim:cellular_component	GO_CC	4	4.15e-12	9.02e-11
CHLORIDE_TRANSPORT(5)	GO:0006821 chloride transport GOslim:biological_process	GO_BP	3	1.59e-09	1.16e-08
CELLULAR_ION_HOMEOSTASIS(4)	GO:0006873 cellular ion homeostasis GOslim:biological_process	GO_BP	3	9.91e-10	1.16e-08
MITOCHONDRIAL_OUTER_MEMBRANE (32)	GO:0005741 mitochondrial outer membrane GOslim:cellular_component	GO_CC	3	1.84e-07	2.01e-06
RESPONSE_TO_WATER_DEPRIVATION (147)	GO:0009414 response to water deprivation GOslim:biological_process	GO_BP	3	1.53e-05	7.48e-05
RESPONSE_TO_SALT_STRESS(195)	GO:0009651 response to salt stress GOslim:biological_process	GO_BP	3	3.5e-05	1.29e-4
REGULATION_OF_ANION_TRANSPORT (1)	GO:0044070 regulation of anion transport GOslim:biological_process	GO_BP	1	7.18e-4	2.11e-3
ETIOPLAST_MEMBRANE(2)	GO:0034426 etioplast membrane GOslim:cellular_component	GO_CC	1	1.08e-3	7.8e-3
PLASMA_MEMBRANE(1787)	GO:0005886 plasma membrane GOslim:cellular_component	GO_CC	4	1.98e-3	0.0107
INTEGRAL_COMPONENT_OF_CHLOROPLAST_OUTER_MEMBRANE(8)	GO:0031359 integral component of chloroplast outer membrane GOslim:cellular_component	GO_CC	1	3.23e-3	0.014
RESPONSE_TO_BACTERIUM(55)	GO:0009617 response to bacterium GOslim:biological_process	GO_BP	1	0.0199	0.0488



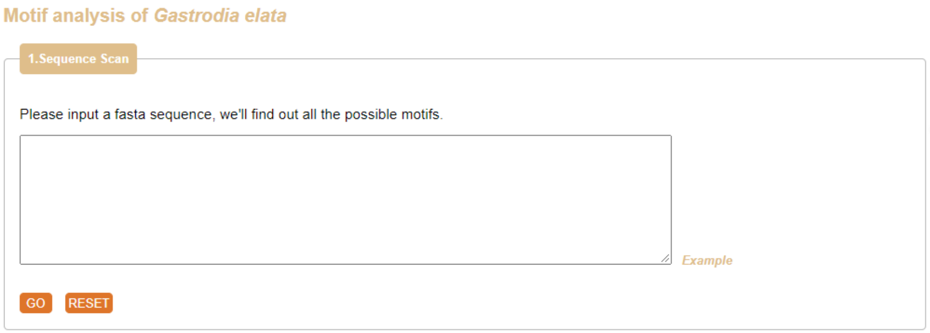
Detailed Information

You are checking out the detail information about this geneset.

Standard Gene Set Name	PORE_COMPLEX
Species	Gastrodia elata
Brief Description	GO:0046930spore complexsGOslim:cellular_cor
Full Description/Abstract	GO:0046930spore complexsGOslim:cellular_cor
External Pathway ID/Pubmed ID	GO:0046930
Source	GO_CC
Contributor/Author	In-house prediction
Organization of contributer	In-house prediction
External URL	http://amigo.geneontology.org/cgi-bin/amigo/term_details?term=GO:0046930
Overlap members in query	**GWHGBDNU004018 GWHGBDNU007821 GWHGBDNU013251 GWHGBDNU017271**

Gene sets detail

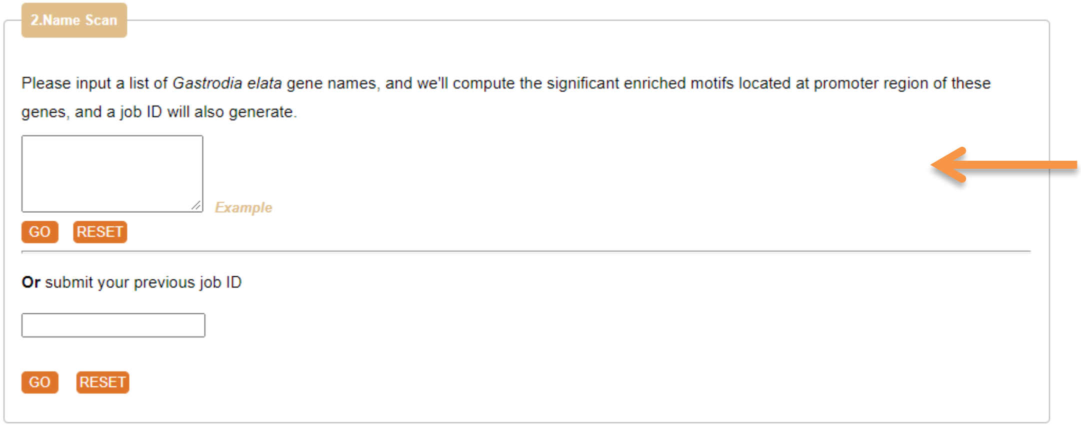
Tools:Motif


Motif analysis of *Gastrodia elata*

1.Sequence Scan

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

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


2.Name Scan

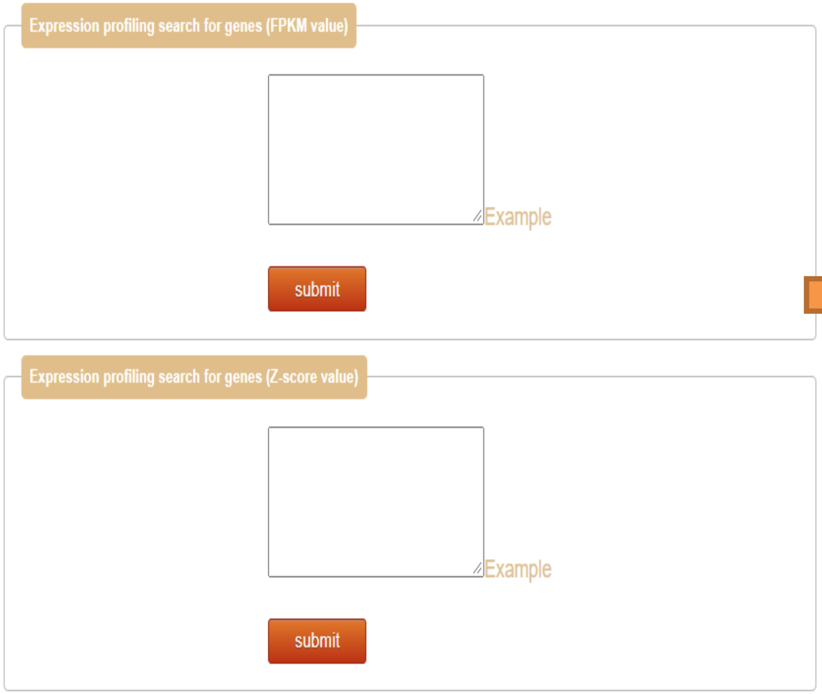
Please input a list of *Gastrodia elata* gene names, and we'll compute the significant enriched motifs located at promoter region of these genes, and a job ID will also generate.

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.

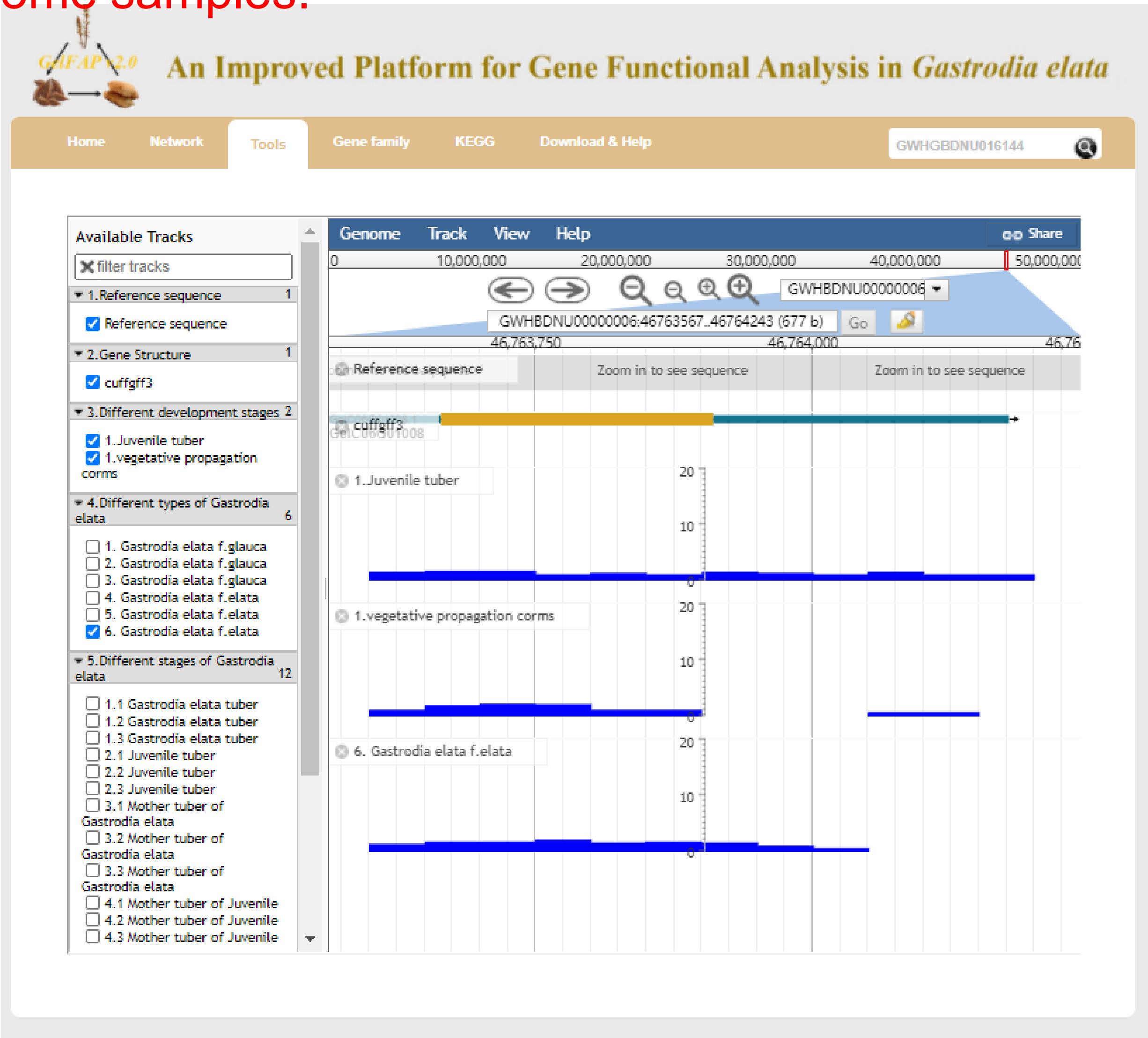


Heatmap Analysis

GWHGBDNU019456
Tissue sample: Juvenile tuber
FPKM: 0.033779

Tools:JBrowse

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



GWHBDNU00000006:46763567..46764243 (677 b)

Available Tracks

filter tracks

1.Reference sequence 1

☑ Reference sequence

2.Gene Structure 1

☑ cuffgff3

3.Different development stages 2

☑ 1.Juvenile tuber
☑ 1.vegetative propagation corms

4.Different types of Gastrodia elata 6

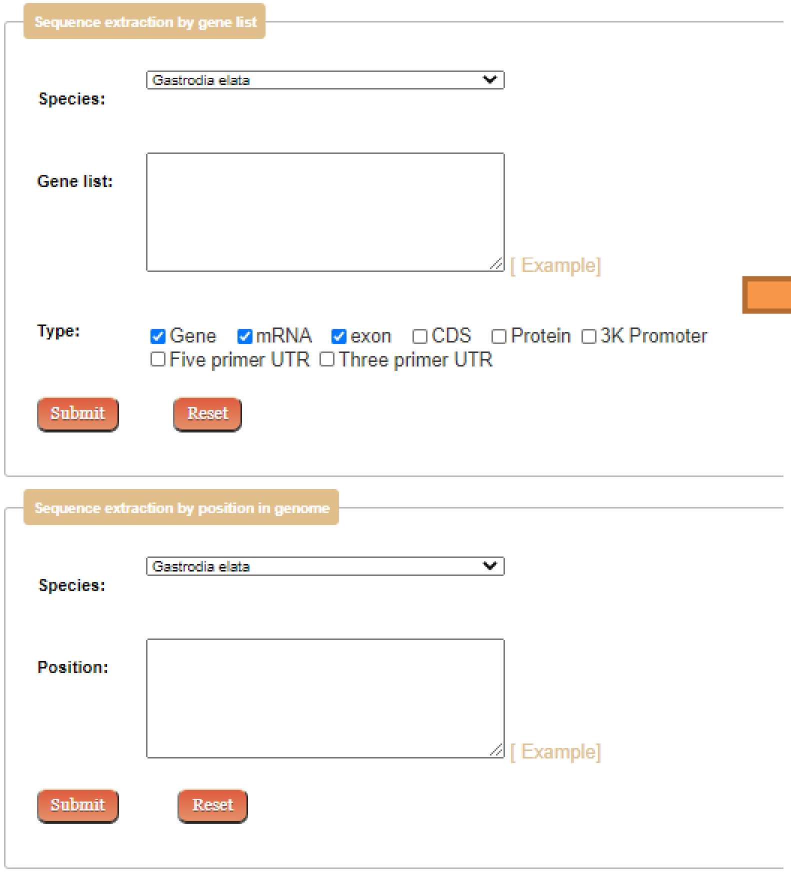
☐ 1. Gastrodia elata f.glauca
☐ 2. Gastrodia elata f.glauca
☐ 3. Gastrodia elata f.glauca
☐ 4. Gastrodia elata f.elata
☐ 5. Gastrodia elata f.elata
☑ 6. Gastrodia elata f.elata

5.Different stages of Gastrodia elata 12

☐ 1.1 Gastrodia elata tuber
☐ 1.2 Gastrodia elata tuber
☐ 1.3 Gastrodia elata tuber
☐ 2.1 Juvenile tuber
☐ 2.2 Juvenile tuber
☐ 2.3 Juvenile tuber
☐ 3.1 Mother tuber of Gastrodia elata
☐ 3.2 Mother tuber of Gastrodia elata
☐ 3.3 Mother tuber of Gastrodia elata
☐ 4.1 Mother tuber of Juvenile
☐ 4.2 Mother tuber of Juvenile
☐ 4.3 Mother tuber of Juvenile

Tools:Extraction Sequence

Users can obtain corresponding sequences according to gene number or location information.



Sequence extraction by gene list

Species: Gastrodia elata

Gene list:

[Example]

Type: ☑ Gene ☑ mRNA ☑ exon ☐ CDS ☐ Protein ☐ 3K Promoter ☐ Five primer UTR ☐ Three primer UTR

Sequence extraction by position in genome

Species: Gastrodia elata

Position:

[Example]

```
Gene Sequence:
>GWHGBDNU016144
GCGGGGGTTTAAATTAGTAGTTAATTGAAATTATAGGGTAAGGGAACCAAAAGGTCATTATGGGGTTTTTCTTACGGGCGGGGCATCTTCCGGCCTATAAAAGCTGCCTGCATCGGG
>GWHGBDNU001748
ATGTCCGGCCTCCTTGGTCCTTCGCCTCACTCATTCTGCTCCTATCTTCTTCCAACAACCACCCGCTTCACCTCCCCTCGCATCTTCTTCTCCCCTCCCAATTATTCCTCTCACCGGAACC
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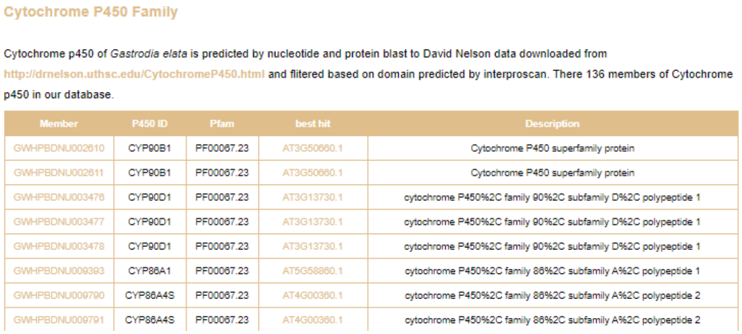
Gene Family

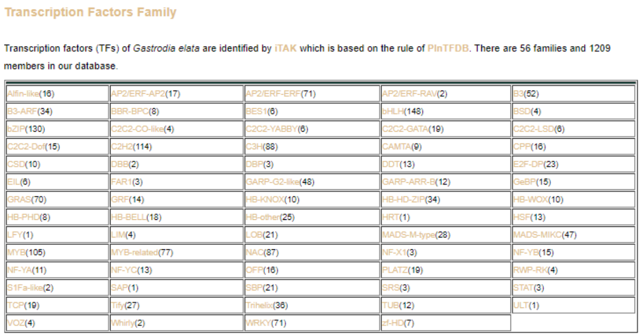
Gene family section displayed predicted protein kinases (PKs), transcription regulators (TRs), and transcription factors (TFs) , ubiquitin proteins, CYP450 genes, carbohydrate-active enzymes and collected EAR motif-containing proteins.



Cytochrome P450 Family

Cytochrome p450 of *Gastrodia elata* 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 136 members of Cytochrome p450 in our database.

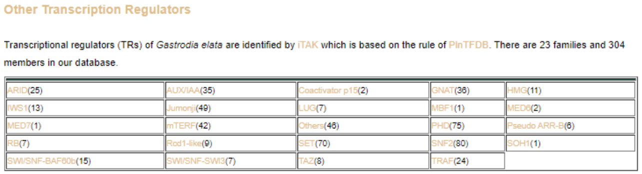
Member	P450 ID	Pfam	best hit	Description
GWHPBDNU002610	CYP90B1	PF00067.23	AT3G50660.1	Cytochrome P450 superfamily protein
GWHPBDNU002611	CYP90B1	PF00067.23	AT3G50660.1	Cytochrome P450 superfamily protein
GWHPBDNU003476	CYP90D1	PF00067.23	AT3G13730.1	cytochrome P450%2C family 90%2C subfamily D%2C polypeptide 1
GWHPBDNU003477	CYP90D1	PF00067.23	AT3G13730.1	cytochrome P450%2C family 90%2C subfamily D%2C polypeptide 1
GWHPBDNU003478	CYP90D1	PF00067.23	AT3G13730.1	cytochrome P450%2C family 90%2C subfamily D%2C polypeptide 1
GWHPBDNU009393	CYP86A1	PF00067.23	AT5G58860.1	cytochrome P450%2C family 86%2C subfamily A%2C polypeptide 1
GWHPBDNU009790	CYP86A4S	PF00067.23	AT4G00360.1	cytochrome P450%2C family 86%2C subfamily A%2C polypeptide 2
GWHPBDNU009791	CYP86A4S	PF00067.23	AT4G00360.1	cytochrome P450%2C family 86%2C subfamily A%2C polypeptide 2



Transcription Factors Family

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

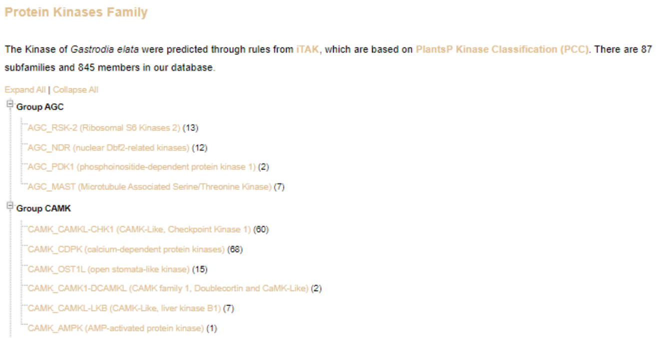
Alfin-like(16)	AP2/ERF-AP2(17)	AP2/ERF-ERF(71)	AP2/ERF-RAV(2)	B3(52)
B3-ARF(34)	BBR-BPC(8)	BES1(6)	bHLH(148)	BSD(4)
bZIP(130)	C2C2-CO-like(4)	C2C2-YABBY(6)	C2C2-GATA(19)	C2C2-LSD(6)
C2C2-Dof(15)	C2H2(114)	C3H(88)	CAMTA(9)	CPP(16)
CSD(10)	DBB(2)	DBP(3)	DDT(13)	E2F-DP(23)
EIL(6)	FAR1(3)	GARP-G2-like(48)	GARP-ARR-B(12)	GeBP(15)
GRAS(70)	GRF(14)	HB-KNOX(10)	HB-HD-ZIP(34)	HB-WOX(10)
HB-PHD(8)	HB-BELL(18)	HB-other(25)	HRT(1)	HSF(13)
LFY(1)	LIM(4)	LOB(21)	MADS-M-type(28)	MADS-MIKC(47)
MYB(105)	MYB-related(77)	NAC(87)	NF-X1(3)	NF-YB(15)
NF-YA(11)	NF-YC(13)	OFP(16)	PLATZ(19)	RWP-RK(4)
S1Fa-like(2)	SAP(1)	SBP(21)	SRS(3)	STAT(3)
TCP(19)	Tify(27)	Trihelix(36)	TUB(12)	ULT(1)
VOZ(4)	Whirly(2)	WRKY(71)	zf-HD(7)	



Other Transcription Regulators

Transcriptional regulators (TRs) of *Gastrodia elata* are identified by iTAK which is based on the rule of PlnTFDB. There are 23 families and 304 members in our database.

ARID(25)	AUX/IAA(35)	Coactivator p15(2)	GNAT(36)	HMG(11)
IWS1(13)	Jumonji(49)	LUG(7)	MBF1(1)	MED6(2)
MED7(1)	mTERF(42)	Others(46)	PHD(75)	Pseudo ARR-B(6)
RB(7)	Rcd1-like(9)	SET(70)	SNF2(80)	SOH1(1)
SWI/SNF-BAF60b(15)	SWI/SNF-SWI3(7)	TAZ(8)	TRAF(24)	

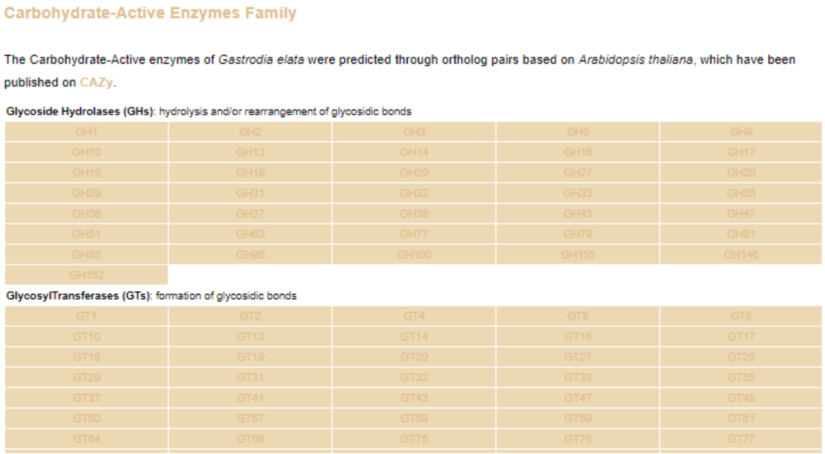


Protein Kinases Family

The Kinase of *Gastrodia elata* were predicted through rules from iTAK, which are based on PlantsP Kinase Classification (PCC). There are 87 subfamilies and 845 members in our database.

Expand All | Collapse All

- **Group AGC**
  - AGC_RSK-2 (Ribosomal S6 Kinases 2) (13)
  - AGC_NDR (nuclear Dbf2-related kinases) (12)
  - AGC_PDK1 (phosphoinositide-dependent protein kinase 1) (2)
  - AGC_MAST (Microtubule Associated Serine/Threonine Kinase) (7)
- **Group CAMK**
  - CAMK_CAMKL-CHK1 (CAMK-Like, Checkpoint Kinase 1) (60)
  - CAMK_CDPK (calcium-dependent protein kinases) (68)
  - CAMK_OST1L (open stomata-like kinase) (15)
  - CAMK_CAMK1-DCAMKL (CAMK family 1, Doublecortin and CaMK-Like) (2)
  - CAMK_CAMKL-LKB (CAMK-Like, liver kinase B1) (7)
  - CAMK_AMPK (AMP-activated protein kinase) (1)



Carbohydrate-Active Enzymes Family

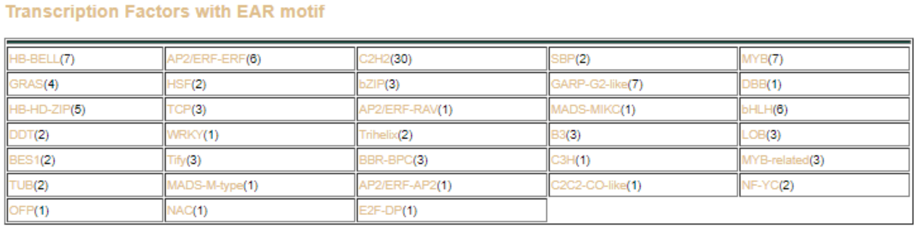
The Carbohydrate-Active enzymes of *Gastrodia elata* were predicted through ortholog pairs based on *Arabidopsis thaliana*, which have been published on CAZy.

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	GH95	GH100	GH116	GH146
GH152				

GlycosylTransferases (GTs): formation of glycosidic bonds

GT1	GT2	GT4	GT5	GT8
GT10	GT13	GT14	GT16	GT17
GT18	GT19	GT20	GT27	GT28
GT29	GT31	GT32	GT33	GT35
GT37	GT41	GT43	GT47	GT48
GT50	GT57	GT58	GT59	GT61
GT64	GT66	GT75	GT76	GT77

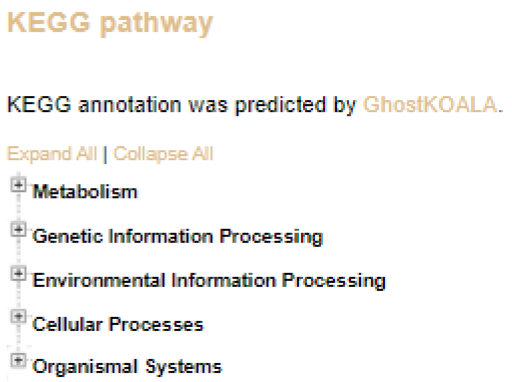


Transcription Factors with EAR motif

HB-BELL(7)	AP2/ERF-ERF(6)	C2H2(30)	SBP(2)	MYB(7)
GRAS(4)	HSF(2)	bZIP(3)	GARP-G2-like(7)	DBB(1)
HB-HD-ZIP(5)	TCP(3)	AP2/ERF-RAV(1)	MADS-MIKC(1)	bHLH(6)
DDT(2)	WRKY(1)	Trihelix(2)	B3(3)	LOB(3)
BES1(2)	Tify(3)	BBR-BPC(3)	C3H(1)	MYB-related(3)
TUB(2)	MADS-M-type(1)	AP2/ERF-AP2(1)	C2C2-CO-like(1)	NF-YC(2)
OFP(1)	NAC(1)	E2F-DP(1)		

Pathway

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



KEGG pathway

KEGG annotation was predicted by GhostKOALA.

Expand All | Collapse All

- ⊞ Metabolism
- ⊞ Genetic Information Processing
- ⊞ Environmental Information Processing
- ⊞ Cellular Processes
- ⊞ Organismal Systems

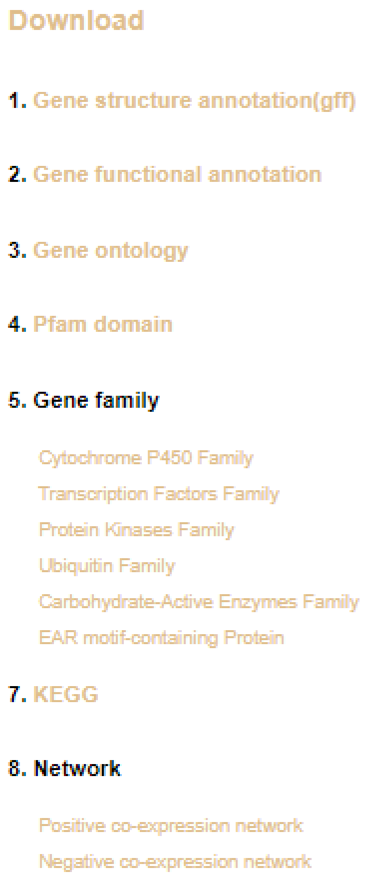
Enzyme information

Glycolysis / Gluconeogenesis

Genes	KO	Enzyme	Annotation	Best Hit
GWHPBDNU000389	K00927	PGK, pgk	phosphoglycerate kinase [EC:2.7.2.3]	AT3G12780.1
GWHPBDNU000393	K01803	TPI, tpiA	triosephosphate isomerase (TIM) [EC:5.3.1.1]	AT3G55440.1
GWHPBDNU000394	K01803	TPI, tpiA	triosephosphate isomerase (TIM) [EC:5.3.1.1]	AT3G55440.1
GWHPBDNU000395	K01803	TPI, tpiA	triosephosphate isomerase (TIM) [EC:5.3.1.1]	AT3G55440.1
GWHPBDNU000396	K01803	TPI, tpiA	triosephosphate isomerase (TIM) [EC:5.3.1.1]	AT3G55440.1
GWHPBDNU000756	K01623	ALDO	fructose-bisphosphate aldolase, class I [EC:4.1.2.13]	AT2G36460.1
GWHPBDNU002155	K01792	E5.1.3.15	glucose-6-phosphate 1-epimerase [EC:5.1.3.15]	AT5G66530.1
GWHPBDNU002156	K01792	E5.1.3.15	glucose-6-phosphate 1-epimerase [EC:5.1.3.15]	AT5G66530.1
GWHPBDNU002157	K01792	E5.1.3.15	glucose-6-phosphate 1-epimerase [EC:5.1.3.15]	AT5G66530.1
GWHPBDNU002158	K01792	E5.1.3.15	glucose-6-phosphate 1-epimerase [EC:5.1.3.15]	AT5G66530.1
GWHPBDNU002281	K01895	ACSS1_2, acs	acetyl-CoA synthetase [EC:6.2.1.1]	None
GWHPBDNU004267	K01895	ACSS1_2, acs	acetyl-CoA synthetase [EC:6.2.1.1]	AT5G36880.2
GWHPBDNU004271	K00873	PK, pyk	pyruvate kinase [EC:2.7.1.40]	AT3G52990.1

Download

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



Download

1. Gene structure annotation(gff)

2. Gene functional annotation

3. Gene ontology

4. Pfam domain

5. Gene family

   Cytochrome P450 Family
   Transcription Factors Family
   Protein Kinases Family
   Ubiquitin Family
   Carbohydrate-Active Enzymes Family
   EAR motif-containing Protein

7. KEGG

8. Network

   Positive co-expression network
   Negative co-expression network

Help

Shown this direction.