

# GelFAP manual for users

# Homepage

**Gene Functional Analysis Platform For *Gastrodia elata***

Home Network Tools Gene family KEGG Download & Help GWHGAAEX017506

、体用平天  
痲麻子肝  
痲木頭、  
抽、痛息  
插小眩風  
兒暈、  
驚、止  
風肢痛

Network Gene Family Pathway Domain  
GO Slim Blast GSEA Cis-element

**Gastrodia elata**

*Gastrodia elata*, a kind of perennial herb of Orchidaceae, is traditional Chinese herbal medicine. The growth cycle of *G.elata* is generally about 3 years, including development stages of seed, 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 offers 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 organic 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**

The platform includes co-expression network, gene families, KEGG pathways and analysis tools, such as blast, motif search and GSEA. We applied PCC and MR algorithm to construct co-expression network through integration of 39 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 predicted by interProScan. Enzymes and metabolism pathways were annotated by KOALA from KEGG database.

In GelfAP, 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**

2020.4.29: The website is online now.

**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

Search One Gene  
Detail

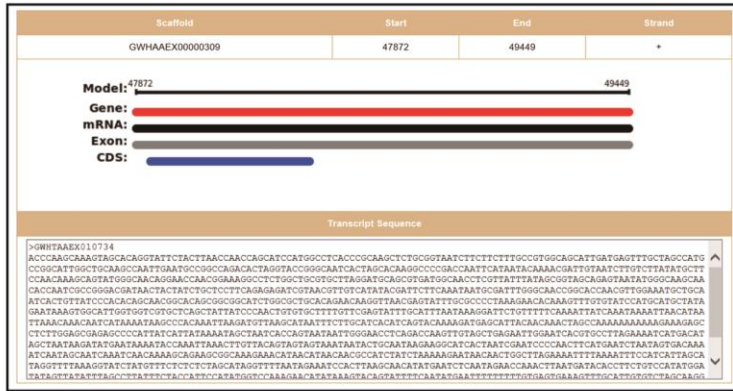
Update News

Introduction to  
*Gastrodia elata*

Introduction to  
GelfAP

# Gene detail information

## Location And Transcript Sequence



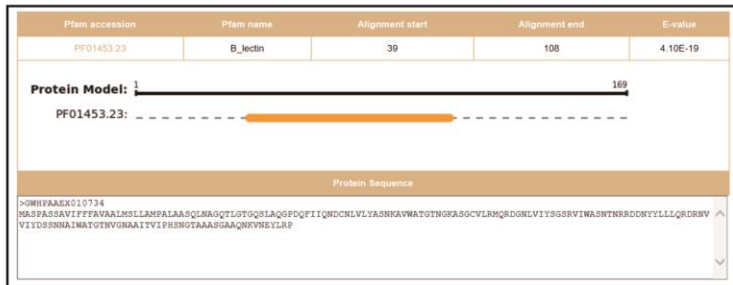
## Network

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

## Functional Module

Module ID	Function Annotation
module_8242	<p>GlycosylTransferases 14 GlycosylTransferases 14 GO:0008375 acetylglucosaminyltransferase activity GOslim:molecular_function GO:0008460 dTDP-glucose 4,6-dehydratase activity GOslim:molecular_function GO:0009225 nucleotide-sugar metabolic process GOslim:biological_process map00520 Amino sugar and nucleotide sugar metabolism map03008 Ribosome biogenesis in eukaryotes</p>
module_0763	<p>GO:0001522 pseudouridine synthesis GOslim:biological_process GO:0006364 rRNA processing GOslim:biological_process GO:0008168 methyltransferase activity GOslim:molecular_function GO:0008757 S-adenosylmethionine-dependent methyltransferase activity GOslim:molecular_function GO:0042254 ribosome biogenesis GOslim:biological_process GO:0045454 cell redox homeostasis GOslim:biological_process GO:0051726 regulation of cell cycle GOslim:biological_process map04110 Cell cycle map04218 Cellular senescence map04350 TGF-beta signaling pathway Transcription factor RB Family Transcription factor RB Family</p>

## Protein Structure



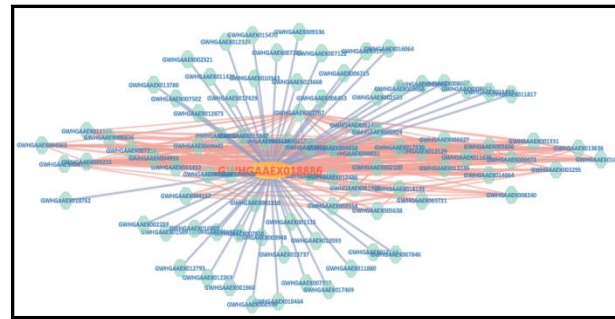
## Functional Annotation

Database	Orthologs	E value	Annotation
COG	gi 407486868 orf YF_006812445.1	4.00E-15	hypothetical protein O3I_037620 [Nocardia brasiliensis ATCC 700358]
nr	gi 73486959 gb AAZ76593.1	5.88E-116	antifungal protein precursor [Gastrodia elata]
Swissprot	tr P30617 LECGALNI	2.00E-33	Mannose-specific lectin (Precursor)
trEMBL	tr Q3YFJ3 Q3YFJ3_BASPA	2.00E-116	Antifungal protein [ECO:0000313]EMBL:AAZ76593.1 (Precursor)

## Expression pattern

SRP	Sample	Description	FPKM
SRP064423	SRR2545914	vegetative propagation coms	1031.750
	SRR2545915	Juvenile tuber	836.010
	SRR5643513	five period of Gastrodia elata	1425.820
	SRR5643514	five period of Gastrodia elata	2002.810
	SRR5643515	five period of Gastrodia elata	1919.810
SRP108465	SRR5643524	five period of Gastrodia elata	3287.270
	SRR5643525	five period of Gastrodia elata	3775.880
	SRR5643528	five period of Gastrodia elata	2953.840
	SRR5643658	five period of Gastrodia elata	563.140
	SRR5643659	five period of Gastrodia elata	630.900
	SRR5643660	five period of Gastrodia elata	325.100
	SRR5643661	five period of Gastrodia elata	284.030
	SRR5643662	five period of Gastrodia elata	157.760
	SRR5643663	five period of Gastrodia elata	190.880
	SRR5643664	five period of Gastrodia elata	139.810
SRP118053	SRR6049654	Rhizomagastrodiae_C368-T07_good_1	353.890
	SRR6049655	Rhizomagastrodiae_C368-T10_good_1	1290.080
	SRR6049656	Rhizomagastrodiae_C368-T07_good_1	675.940
	SRR6049657	Rhizomagastrodiae_C368-T07_good_1	395.130
	SRR6049658	Rhizomagastrodiae_C368-T04_good_1	700.160
	SRR6049659	Rhizomagastrodiae_C368-T04_good_1	782.740
	SRR6049660	Rhizomagastrodiae_C368-T01_good_1	581.390
	SRR6049661	Rhizomagastrodiae_C368-T04_good_1	797.040
	SRR6049662	Rhizomagastrodiae_C368-T01_good_1	684.550
	SRR6049663	Rhizomagastrodiae_C368-T01_good_1	646.430
In house	SRR6049664	Rhizomagastrodiae_C368-T10_good_1	646.430
	SRR6049665	Rhizomagastrodiae_C368-T10_good_1	646.430
	Gastro_1	Gastrodia elata tuber	659.750
	Gastro_2	Gastrodia elata tuber	659.750
	Gastro_3	Gastrodia elata tuber	515.690
	Juven_1	Juvenile tuber	63.670
	Juven_2	Juvenile tuber	168.080
	Juven_3	Juvenile tuber	223.830
	Mother_Gastro_1	Mother tuber of Gastrodia elata	224.660
	Mother_Gastro_2	Mother tuber of Gastrodia elata	219.120
Mother_Gastro_3	Mother tuber of Gastrodia elata	7809.680	
Mother_Juven_1	Mother tuber of Juvenile	3999.540	
Mother_Juven_2	Mother tuber of Juvenile	7359.510	
Mother_Juven_3	Mother tuber of Juvenile	3540.560	

# Network



Co-expression/PPI network

## Network search and analysis

1. Search one interested gene by typing in gene locus

Example

Positive  Negative  Predicted PPI

GO RESET

Search One

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

Example

Positive  Negative

GO RESET

Search Gene List

Co-expression relationship

ID	Ortholog in Arabidopsis	Annotation	PCC	Relationship
QWVHGAEX018886	AT2G47620	SWITCH/sucrose nonfermenting 3A	1	positive
QWVHGAEX007787	--	--	0.902851108	positive
QWVHGAEX007214	AT2G38010	Neutral/alkaline non-lysosomal ceramidase	0.889015134	positive
QWVHGAEX011448	AT3G26340	N-terminal nucleophile aminohydrolases (Nth hydrolases) superfamily protein	0.883886686	positive
QWVHGAEX005215	--	--	0.882155096	positive
QWVHGAEX004471	AT3G08530	Clastrin, heavy chain	0.879837507	positive
QWVHGAEX006827	AT4G14000	Putative methyltransferase family protein	0.876584885	positive
QWVHGAEX015432	AT5G57870	MIF40 domain-containing protein / MA3 domain-containing protein	0.863529647	positive
QWVHGAEX004563	AT3G18165	modifier of snct1.4	0.86344895	positive
QWVHGAEX000072	--	--	0.86151747	positive
QWVHGAEX001958	AT1G052620	Pentatricopeptide repeat (PPR) superfamily protein	0.856540771	positive
QWVHGAEX011676	AT5G17070	--	0.855408552	positive
QWVHGAEX014886	AT1G72830	nuclear factor Y, subunit A3	0.852319701	positive
QWVHGAEX011189	--	--	0.850359657	positive
QWVHGAEX002100	AT5G03800	Pentatricopeptide repeat (PPR) superfamily protein	0.848008287	positive
QWVHGAEX011216	--	--	0.847164053	positive
QWVHGAEX017530	AT1G64570	Homeodomain-like superfamily protein	0.846692739	positive
QWVHGAEX009941	AT5G053000	2A phosphatase associated protein of 48 kD	0.846660139	positive
QWVHGAEX003606	AT5G20240	K-box region and MAD9-box transcription factor family protein	0.846611307	positive
QWVHGAEX014084	--	--	0.843156476	positive
QWVHGAEX004855	AT3G11670	UDP-Glycosyltransferase superfamily protein	0.84271942	positive
QWVHGAEX000031	AT1G05120	Helicase protein with RINGU-box domain	0.840294287	positive
QWVHGAEX012129	--	--	0.840221227	positive
QWVHGAEX016394	AT4G01220	Nucleotide-diphospho-sugar transferase family protein	0.837773334	positive
QWVHGAEX001131	AT4G35230	BR-signaling kinase 1	0.837238345	positive
QWVHGAEX013636	AT4G33950	Protein kinase superfamily protein	0.832493001	positive
QWVHGAEX013133	AT3G13440	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	0.830203941	positive
QWVHGAEX004157	AT5G50340	ATP-dependent peptidases,nucleotide binding,serine-type endopeptidases,DNA helicases,ATP binding,damaged DNA binding,nucleoside-triphosphatases	0.829604841	positive
QWVHGAEX018133	--	--	0.828513015	positive
QWVHGAEX002554	AT1G11660	heat shock protein 70 (Hsp 70) family protein	0.828399455	positive
QWVHGAEX005924	AT3G62940	Cysteine proteinases superfamily protein	0.828320887	positive
QWVHGAEX016503	AT5G22370	P-loop containing nucleoside triphosphate hydrolases superfamily protein	0.8177644	positive
QWVHGAEX008240	AT5G19580	glyoxal oxidase-related protein	0.816988545	positive
QWVHGAEX000836	AT5G19960	RNA-binding (RRM/RDR/RNP motifs) family protein	0.815389589	positive
QWVHGAEX003295	AT3G03380	DegP protease 7	0.813120726	positive
QWVHGAEX004458	AT5G13520	peptidase M1 family protein	0.812071136	positive
QWVHGAEX011115	AT5G57170	Tautomerase/MIF superfamily protein	0.806482592	positive
QWVHGAEX005721	AT3G09970	Calcineurin-like metallo-phosphoesterase superfamily protein	0.805339404	positive
QWVHGAEX005636	AT1G05150	RNA-binding (RRM/RDR/RNP motifs) family protein	0.796575788	positive
QWVHGAEX002485	--	--	0.791623673	positive
QWVHGAEX006888	AT1G73320	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	0.790842793	positive
QWVHGAEX001310	AT4G15010	Mitochondrial substrate carrier family protein	0.756740727	positive
QWVHGAEX017623	--	--	-0.853873508	negative
QWVHGAEX011880	AT2G20360	NAD(P)+binding Rossmann-fold superfamily protein	-0.827759569	negative

Co-expression Gene List

# Tools: blast

## Blast search

Program:  Database:

Program

Enter sequence below in FASTA format

Input Sequence

Input Sequence

Or upload file (max filesize 5MB)

## Parameter Options

Expect  Matrix   Perform ungapped align

Parameter

Graphical Overview Descriptions  Alignments

Blast Results

## Blast result

Query id	Subject id	alignment length	mismatches	query start	query end	subject start	subject end	% identity	e-value	bit score
GWHPAAEX017506	GWHPAAEX017506	755	0	1	755	1	755	100.00	0.0	1535
GWHPAAEX017506	GWHPAAEX011535	732	243	26	749	37	765	65.30	0.0	858
GWHPAAEX017506	GWHPAAEX010494	756	313	2	750	26	778	57.28	0.0	810
GWHPAAEX017506	GWHPAAEX004567	715	374	39	735	43	752	44.48	2e-150	529
GWHPAAEX017506	GWHPAAEX010268	78	44	25	102	28	105	43.59	2e-13	73.6
GWHPAAEX017506	GWHPAAEX010269	57	29	116	172	2	58	49.12	3e-08	56.6
GWHPAAEX017506	GWHPAAEX006435	55	31	574	628	273	322	34.55	0.32	33.5
GWHPAAEX017506	GWHPAAEX016638	249	136	307	536	309	515	20.88	0.78	32.0
GWHPAAEX017506	GWHPAAEX005339	127	83	24	150	1077	1186	21.26	1.5	31.2

# Tools: motif analysis

## Motif analysis of *Gastrodia elata*

Combining text-mining technology with data sources from [plantCARE](#), [PLACE](#), [AthMap](#) etc. We collected 930 motifs with published annotations. With these identified motifs and published annotations, we predicted TF/TR-binding regions. In addition to scanning for motif sequences, we offer a Z-score method that calculates the significance enrichment of motifs.

1. Sequence Scan

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

Example

GO
RESET

Sequence Scan

2. Name Scan

Please input a list of *Gastrodia elata* gene names, and we'll compute the significant motifs local. show each motif and its frequency, users can also significantly analyze these motifs, and a job

Example

GO
RESET

Motif Enrichment analysis

Or submit your previous job ID

GO
RESET

Search By Job ID

## Motif Search Results

Motif name	Motif sequence	Count	Bg 1K	Bg 2K	Bg 3K
S00new15	AAC	31	28.57	58.62	88.37
S000028	CAAT	16	12.04	24.57	36.87
S000198	GRWAAW	15	7.91	15.60	23.12
plantCARE000350	TATA	14	22.95	41.53	59.24
Snnzh000094	NGAC	14	6.19	13.01	20.03
S000449	YACT	13	12.64	26.46	40.83
S000265	AAAG	12	12.12	24.70	37.25
Snnzh000102	RGATY	12	4.26	8.97	13.89

## Motif Enrichment Analysis Results

Your job ID: **Job2020May03014854**

The following table deposited significant motifs (p-value <= 0.05) in promoters of these genes: [GWHGAAEX018886](#) [GWHGAAEX018877](#)

Motifname	Count	Z-score	P-value
ASF1MOTIFCAMV	10	2.62	0.004434
AUXREPSIAA4	1	2.22	0.013254
HEXMOTIFTAH3H4	3	2.17	0.015111
RYREPEATLEGUMINBOX	5	2.00	0.022961
RBCSCONSENSUS	6	2.63	0.004242
SPHCOREZMC1	1	5.17	0.000000
SURE2STPAT21	2	2.66	0.003899
LTRE1HVBLT49	4	2.02	0.021680
PALINDROMICCBBOXGM	2	4.03	0.000028
GGTCCCATGMSAUR	1	3.96	0.000038
E2FBNTRNR	1	3.67	0.000120

# Tools: GSEA

## Choose Gene Sets

- G1:GO gene sets
  - BP:GO biological process
  - CC:GO cellular component
- G2:Gene Family Based gene sets
- G3:Curated gene sets
  - KEGG:KEGG gene sets
  - MODULE:Functional module

Gene Sets

## Choose Background

- Suggested background (Whole genome level)
- Customized background

Background

## Submit Your Query

Example

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

浏览...

Gene list

Gene Sets Enrichment  
Analysis Results

## Information of Analysis Results

we show gene sets which has more significant FDR(<0.05) for page display.You can download related analysis result below.

### Basic computing summary

ID number of the Job: 523493061(Available in 3 months for retrieving).

Categories selected: BP CC

NO. query list after removing redundancy: 70

NO. redundant list in original query: 0

Computing Result in Table formatted :

### Diversified result display

Gene Set Name(NO. Genes)	Description	Category	NO. Genes in Overlap (k)	p value	FDR
GO_DNA_REPAIR(69)	GO:0006281 DNA repair GOSlim:biological_process	GO_BP	69	1.62e-155	9.45e-154
GO_BASE-EXCISION_REPAIR(16)	GO:0006284 base-excision repair GOSlim:biological_process	GO_BP	15	1.74e-29	5.1e-28
GO_DNA_RECOMBINATION(20)	GO:0006310 DNA recombination GOSlim:biological_process	GO_BP	14	2.71e-26	5.29e-25
GO_DNA_REPLICATION(45)	GO:0006260 DNA replication GOSlim:biological_process	GO_BP	9	3.36e-13	4.91e-12

# Tools:GO

## Gene Ontology enrichment analysis

The GO terms, gene families, pathway information from our functional annotations w  
list to obtain significantly gene sets.

Species:

Gastrodia elata ▼

Query list:

Gene list

Example:

reference:

gene ID (user defined) (eg.GWHGAAEX009339) ▼

Advanced options:

Submit

Reset

GO Enrichment Analysis Results

Detail information ⓘ

You can [ [Browse in tree traversing mode](#) ] [ [Browse all GO terms](#) ] [ [Download](#) ]

Or select from following significant terms to [ [Draw graphical results](#) ] [ [Create bar chart](#) ] [ [Scatter Plots analysis](#) ]

<input type="checkbox"/> GO term	Ontology	Description	Number in input list	Number in BG/Ref	p-value	FDR
<input type="checkbox"/> GO:0042743	P	hydrogen peroxide metabolic process	11	26	6.3e-09	1.2e-06
<input type="checkbox"/> GO:0042744	P	hydrogen peroxide catabolic process	11	26	6.3e-09	1.2e-06
<input type="checkbox"/> GO:0072593	P	reactive oxygen species metabolic process	12	32	3.8e-09	1.2e-06
<input type="checkbox"/> GO:0055114	P	oxidation-reduction process	47	667	2.2e-07	3e-05
<input type="checkbox"/> GO:0006979	P	response to oxidative stress	11	46	8e-07	8.7e-05
<input type="checkbox"/> GO:0071555	P	cell wall organization	9	60	0.0002	0.016



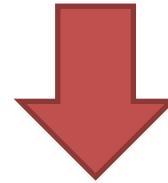
# Gene family

## Transcription Factors Family

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

Alfin-like(5)	AP2/ERF-ERF(57)	AP2/ERF-AP2(9)	AP2/ERF-RAV(2)	B3(21)
B3-ARF(13)	BBR-BPC(6)	BES1(5)	bHLH(67)	BSD(1)
bZIP(48)	C2C2-CO-like(3)	C2C2-YABBY(5)	C2C2-Dof(17)	C2C2-GATA(15)
C2C2-LSD(3)	C2H2(78)	C3H(45)	CAMTA(3)	CPP(5)
CSD(5)	DBE(1)	DBP(1)	DDT(6)	E2F-DP(8)
EIL(4)	FAR1(17)	GARP-G2-like(29)	GARP-ARR-E(6)	GeBP(7)
GRAS(43)	GRF(7)	HB-KNOX(4)	HB-BELL(10)	HB-PHD(1)
HB-HD-ZIP(22)	HB-other(10)	HB-WOX(8)	HRT(1)	HSF(14)

Gene Families



Family Members

### AP2/ERF-AP2's genelist

>>Gene Family>>TF family>>AP2/ERF-AP2

Order	Member	Pfam	Best_hit	Description
1	GWHGAAEX002539	PF00847.19	AT3G54320	Integrase-type DNA-binding superfamily protein
2	GWHGAAEX002785	PF00847.19	AT5G17430	Integrase-type DNA-binding superfamily protein
3	GWHGAAEX003056	PF00847.19	AT2G28550	related to AP2.7
4	GWHGAAEX003526	PF00847.19	AT4G37750	Integrase-type DNA-binding superfamily protein
5	GWHGAAEX003735	PF00847.19	AT4G37750	Integrase-type DNA-binding superfamily protein
6	GWHGAAEX007252	PF00847.19	AT4G36920	Integrase-type DNA-binding superfamily protein
7	GWHGAAEX007926	PF00847.19	AT5G67180	target of early activation tagged (EAT) 3
8	GWHGAAEX010251	PF00847.19	AT4G36920	Integrase-type DNA-binding superfamily protein
9	GWHGAAEX017898	PF00847.19	AT1G16060	ARIA-interacting double AP2 domain protein

# KEGG

Enzyme

Metabolic pathways

Genes	KO	Enzyme		Best Hit
GWHGAAEX007662	K00001	E1.1.1.1, adh	alcohol dehydrogenase [EC:1.1.1.1]	AT5G24760
GWHGAAEX009768	K00001	E1.1.1.1, adh	alcohol dehydrogenase [EC:1.1.1.1]	AT1G64710
GWHGAAEX005581	K00002	AKR1A1, adh	alcohol dehydrogenase (NADP+) [EC:1.1.1.2]	AT2G37790
GWHGAAEX012980	K00002	AKR1A1, adh	alcohol dehydrogenase (NADP+) [EC:1.1.1.2]	AT2G37790
GWHGAAEX017120	K00002	AKR1A1, adh	alcohol dehydrogenase (NADP+) [EC:1.1.1.2]	AT2G37770
GWHGAAEX003018	K00008	SORD, gutB	L-liditol 2-dehydrogenase [EC:1.1.1.14]	AT5G51970
GWHGAAEX003019	K00008	SORD, gutB	L-liditol 2-dehydrogenase [EC:1.1.1.14]	AT5G51970
GWHGAAEX003027	K00008	SORD, gutB	L-liditol 2-dehydrogenase [EC:1.1.1.14]	AT5G51970
GWHGAAEX008914	K00008	SORD, gutB	L-liditol 2-dehydrogenase [EC:1.1.1.14]	AT5G51970

## KEGG pathway

KEGG annotation was predicted by GhostKOALA. 4078 entries (20.7%) were annotated.

Expand All | Collapse All

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

Pathways



Pathway map

