HpeNet manual for users

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About HpeNet

Paeonia lactiflora Pall., commonly known as the herbaceous peony, is an ornamental flowering plant known around the world. Its oil contains a high proportion of polyunsaturated fatty acids (PUFAs). We produced 40 in-house RNA-seq datasets from 10 different tissues and performed *de novo* transcriptome assembly to obtain a complete transcriptome. Moreover, we had constructed the co-expression network database, HpeNet, which contains transcriptome data, gene information, the co-expression network, and so forth. Furthermore some analytical tools, such as blast, gene expression profiling analysis and gene set enrichment analysis (GSEA), were supported for network analysis and functional annotation. We hope that the HpeNet database will be beneficial to future work on *Paeonia lactiflora* Pall.

Contact US

If you have any questions or suggestions, please contact us: shmh100@cau.edu.cn, zhangxiaodong@baafs.net.cn and zhensu@cau.edu.cn. If you want to know more about our work, please click here.

News

2019.6.15: The constructed co-expression network was available.

2019.5.05: The basic function of the platform was available!

2019.4.19: The detailed information of lipid-related pathways was available!

2019.3.05: Some analysis tools, such as

Visitor Tracking

update news

visitor tracking

Gene detail info

Detailed information for Cluster-55448.309693 [Network]

1. Annotation

fatty acid desaturase 2

Functional annotation

2. Top Hits Annotation

Species	Top Hits	E-value	Annotation
Arabidopsis thaliana	AT3G12120	1.90E-16	FAD2|fatty acid desaturase 2

Top hits in Arabidopsis

3. Sequence

Gene:

> Cluster-55448.309693

```
CATCCAACCCTTATTAGTAACCTCTCTCCAATACCTAAATAATATCTACTAAACTTTTTGAGCCTGTTTGGTCATTCCATAGCTTCTCAAGTCTCATTCATAATTTATTCTACATTCCAATGAACACTTGAATTCATCGGTACGTGTATAGAT
ATTTATTGAAGGCTACCATCTCATCAATTATTTGTATGGTCTCATTCAAATATAAGTAAATCATGAATAAGCCCACTCAAGTAACCAAACAGGCTTTTGAAAAGTCACTCGGGCCTTGCTGCCGAAAATGTATACGTG
GTAGTACACAACATCTCCAGTATCGTTAACGTAGTGGTCTTGATTGATGCTCCTTACTAGATTCTTGATCAAGTGAATTGGGAATGGCCCAGATTTTCTGGCACTCTGTAATATTTTCCAAGAATTGSCTTGGCCGCCTTTGCTGGCTGGTAT
CAAATGATAGTGTGGAATTTGAGGGAAGAGGTGATGTACAACATGGGTGCCAATGTCATGGTGGATGTTATTGAACCATCCGTAATCCCGATCAATTGTGGTAAGCCCTCCTCTAAGGTAACTCCA
```

DNA sequence

4. Gene family

Gene family	Subfamily
-	-

Gene family

5. Gene Ontology

GO term	Description	Category
GO:0006629	lipid metabolic process	Biological Process

Gene ontology

6. KEGG pathway

KO	Enzyme	Enzyme ID	Pathway
K10257	omega-3 fatty acid desaturase (delta-15 desaturase)	EC:1.14.19	Biosynthesis of unsaturated fatty acids
			Fatty acid metabolism

KEGG pathway

7. KOG

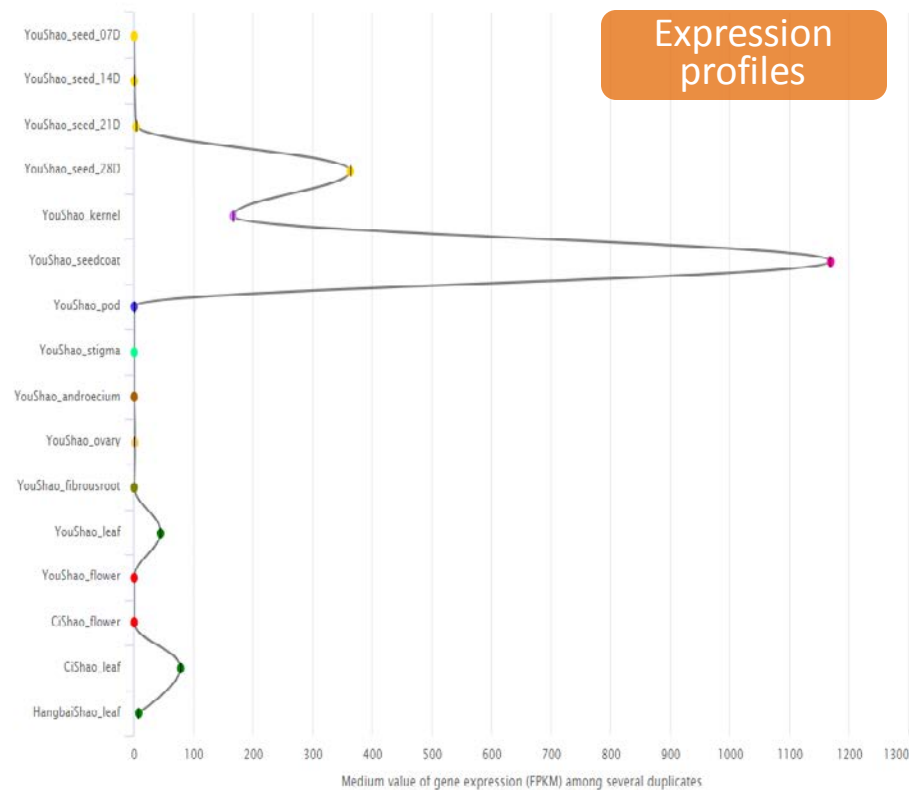| KOG ID	Description
-	-

KOG annotation

8. Pfam Domain

Pfam accession	Description
PF00487	Fatty acid desaturase

Pfam domain

Expression profiles

Expression trends for Cluster-55448.309693 in all RNA-seq samples.

Expression profiles

Medium value of gene expression (FPKM) among several duplicates

Highcharts.com

Gene function and orthologous search

gene function search

Input your interested function to get the related genes.

Interested function: [fatty acid]   Example

[Submit] [RESET]

Gene function Search Results

We find **319** records based on your search.

Gene	Annotation	Ortholog in *Arabidopsis* (E-value)	Annotation in *Arabidopsis*
Cluster-55448.324051	Fatty acid hydroxylase superfamily	AT5G57800 (2.20E-65)	CER3|ECERIFERUM 3; FLP1|FACELESS POLLEN 1
Cluster-139.0	Fatty acid hydroxylase superfamily	AT2G37700 (0.0000032)	Fatty acid hydroxylase superfamily
Cluster-55448.144168	fatty acid desaturase 2	AT3G12120 (1.50E-15)	FAD2|fatty acid desaturase 2
Cluster-55448.180243	fatty acid amide hydrolase	AT5G64440 (7.50E-31)	AtFAAH|fatty acid amide hydrolase
Cluster-55448.28514	fatty acid desaturase 8	AT5G05580 (1.00E-11)	FAD8|fatty acid desaturase 8
Cluster-55448.220736	fatty acid reductase 6	AT3G56700 (0.000000013)	FAR6|fatty acid reductase 6

Orthologous search

Input your interested gene list in *Arabidopsis thaliana* to get their ortho

Gene list:
```
AT3G12120
AT2G29980
AT4G30950
AT1G43800
AT2G43710
AT3G02610
```
Example

[Submit] [RESET]

Orthologous gene search results

Basing on your search, we found **147** records which included **147** genes in *Herbaceous*

Gene ID	Annotation	Top hits in *Arabidopsis* (E-value)	Annotation in *Arabidopsis*
Cluster-55448.144168	fatty acid desaturase 2	AT3G12120 (1.50E-15)	FAD2|fatty acid desaturase 2
Cluster-63748.0	fatty acid desaturase 2	AT3G12120 (1.60E-10)	FAD2|fatty acid desaturase 2
Cluster-55448.79835	fatty acid desaturase 2	AT3G12120 (0.000000033)	FAD2|fatty acid desaturase 2
Cluster-55448.279495	fatty acid desaturase 2	AT3G12120 (2.80E-09)	FAD2|fatty acid desaturase 2
Cluster-55448.336059	fatty acid desaturase 2	AT3G12120 (6.80E-17)	FAD2|fatty acid desaturase 2
Cluster-55448.309692	fatty acid desaturase 2	AT3G12120 (0.0000014)	FAD2|fatty acid desaturase 2
Cluster-55448.309693	fatty acid desaturase 2	AT3G12120 (1.90E-16)	FAD2|fatty acid desaturase 2
Cluster-55448.293086	fatty acid desaturase 2	AT3G12120 (3.30E-10)	FAD2|fatty acid desaturase 2

Co-expression network

Co-expressed network analysis

1. Please input your interested one gene or gene list

```
Cluster-55448.309693
Cluster-55448.309691
Cluster-55448.32905
```

Example (Limit:6)

2. Please select MR cut-off values

- ● MR ≤ 30   ○ MR ≤ 50

3. Please select one or more co-expression relationships

☑ Positive ☑ Negative

Submit   RESET

Network search

Network nodes info

Information about network nodes

ID	Annotation	Ortholog (E-value)	Annotation in *Arabidopsis*	PCC	Relationship
Cluster-55448.309693	fatty acid desaturase 2	AT3G12120 (1.90E-16)	FAD2|fatty acid desaturase 2	1	positive
Cluster-55448.309945	BURP domain-containing protein	AT1G23760 (3.70E-22)	PG3|POLYGALACTURONASE 3	0.9940	positive
Cluster-5892.0				0.9939	positive
Cluster-55448.312567	Glycosyl hydrolase family 35 protein	AT5G01075 (0.0000084)	Glycosyl hydrolase family 35 protein	0.9917	positive
Cluster-55448.30585	nodulin MtN21 /EamA-like transporter family protein	AT4G08290 (3.90E-51)	UMAMIT20|Usually multiple acids move in and out Transporters 20	0.9895	positive
Cluster-55448.314667				0.9880	positive
Cluster-55448.47726	AGAMOUS-like 20	AT2G45660 (3.30E-19)	AGL20|AGAMOUS-like 20; ATSOC1|SUPPRESSOR OF OVEREXPRESSION OF CO 1	0.9877	positive

Co-expression network (MR30)

Query genes: Cluster-55448.309693   Cluster-55448.309691   Cluster-55448.32905

Detailed info: Network edges

Network analysis: Gene expression analysis   Gene set enrichment analysis   Get gene sequence

Further analysis for network members
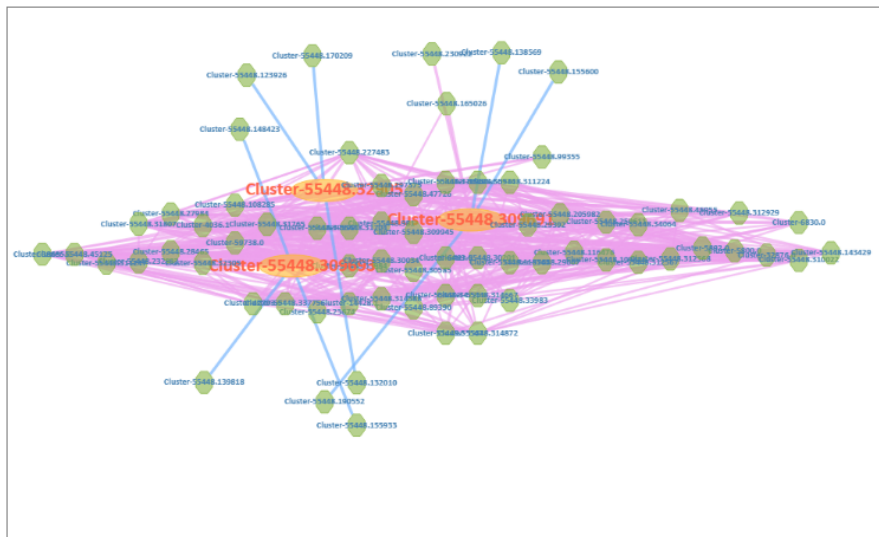
Gene:
Yellow--query gene
Green--co-expressed genes
Gray--Genes without expression profile

Interaction line:
Pink--Genes positive co-expression relationship with target genes
Blue--Genes negative co-expression relationship with target genes
Gray--Genes without expression profile

Tissue preferential analysis

○ Fibrous root ○ Seed coat ○ Seed ○ Androecium ○ Stigma ○ Ovary ○ Kernel ○ Pod ○ Leaf ○ Flower

Submit   RESET

Tissue preferential analysis

Comparative analysis between different cultivars

Tissue:: [Leaf ▾]

Cultivar:: [Shaoyou17C VS ChiShao ▾]

Submit   RESET   [?]

Comparative analysis

KEGG pathway

Lipid-related Pathway

Lipid-related pathway

Lipid-related Pathway >>> Fatty Acid Synthesis (FAS)

Plant fatty acids are synthesized mainly in leaf mesophyll cells, seeds, and oil-accumulating fruits. The process occurs mainly in plastids, although mitochondria are also capable of synthesizing fatty acids. The plastidial pyruvate dehydrogenase complex generates acetyl-coenzyme A that is used as a building block for fatty acid production. Fatty acids are grown by sequential condensation of two-carbon units by enzymes of the fatty acid synthase complex. During each cycle four reactions occur: condensation, reduction, dehydration and reduction. Acyl carrier protein is a cofactor in all reactions. Synthesis of a C16 fatty acid requires that the cycle be repeated seven times. During the first turn of the cycle, the condensation reaction is catalyzed by ketoacyl-ACP synthase (KAS) III. For the next six turns of the cycle, the condensation reaction is catalyzed by isoform I of KAS. Finally, KAS II is used during the conversion of 16:0 to 18:0.

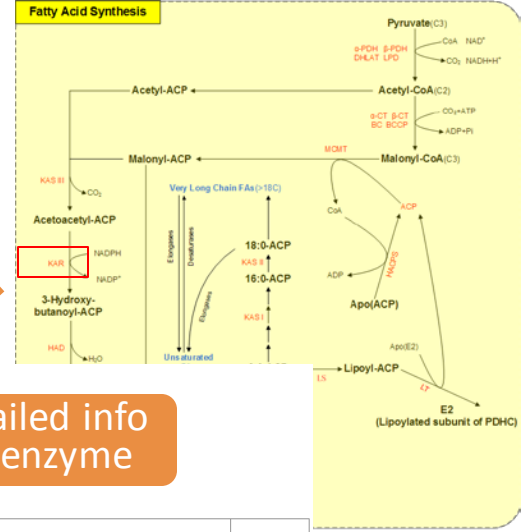Expand all | Close all

Lipid Pathway Tree
- Fatty acid and TAG metabolism
  - Fatty acid Synthesis
  - Fatty acid Elongation, Desaturation and Export from Plastid
  - Triacylglycerol Biosynthesis
  - Triacylglycerol and Fatty acid Degradation
- Galactolipid, Phospholipid, Sphingolipid, Sulfolipid Metabolism
  - Eukaryotic Galactolipid and Sulfolipid Synthesis
  - Prokaryotic Galactolipid, Sulfolipid, Phospholipid Synthesis
  - Eukaryotic Phospholipid Metabolism
  - Mitochondrial Phospholipid Metabolism
  - Sphingolipid Synthesis and Transport
- Other metabolism pathways
  - Mitochondrial Lipoic Acid Synthesis
  - Wax Synthesis and Transport
  - Cutin Synthesis and Transport
  - Suberin Synthesis and Transport
  - Oxylipin Metabolism
  - Choline Synthesis

The detailed info of KAR enzyme

Lipid-related Pathway: Fatty Acid Synthesis (FAS)

Enzyme name: KAR
Full description: Ketoacyl-ACP Reductase

Detailed information about the enzyme

Gene ID	Annotation	Ortholog in *Arabidopsis* (E-value)	Annotation in *Arabidopsis*	Network
Cluster-55448.86471	NAD(P)-binding Rossmann-fold superfamily protein	AT1G24360 (4.70E-17)	NAD(P)-binding Rossmann-fold superfamily protein	network
Cluster-55448.86473	NAD(P)-binding Rossmann-fold superfamily protein	AT1G24360 (4.80E-17)	NAD(P)-binding Rossmann-fold superfamily protein	network
Cluster-55448.86472	NAD(P)-binding Rossmann-fold superfamily protein	AT1G24360 (4.20E-17)	NAD(P)-binding Rossmann-fold superfamily protein	network
Cluster-1089.0	NAD(P)-binding Rossmann-fold superfamily protein	AT1G24360 (0.00000069)	NAD(P)-binding Rossmann-fold superfamily protein	network
Cluster-55448.258927	NAD(P)-binding Rossmann-fold superfamily protein	AT1G24360 (1.70E-20)	NAD(P)-binding Rossmann-fold superfamily protein	network
Cluster-55448.33611	NAD(P)-binding Rossmann-fold superfamily protein	AT1G24360 (3.50E-16)	NAD(P)-binding Rossmann-fold superfamily protein	network

Tools: blast

Blast alignments

Blast alignment results

Blast search

Program: [BLASTN ▾]   Database: [Hpe_DNA ▾]
- BLASTN
- TBLASTN

Enter seq[ ] FASTA format

```
>Cluster-55448.309693
GATGCAACCCTTATTAGTAACCTCTCTCCAATACCTAAATAATATCTACT
AAACTTTTTGAGCCTGTTTGGTCATTCCATAGCTTCTGAAGTCTCATTCAT
AATTTATTCTACATTCGAATGAACACTTGAATTGATGAGATGAGTTATAG
AAATATAAGTAAATCATGAATAAGCCCACTCAAGTAACCAAACAGGCTT
TTGAAAAGTCACTCGGCCTTGCTGCGCGAAAATGTATAGAGCTCATGGT
CGGTCTTTGTAGTACACAACATCTCCAGTATCGTTAACGTAGTGGTCTTG
ATTGATGCTCCTTACTAGATTCTTGATCAAGTGAATTGGGAATGGCCCA
GATTTTTCTGGCACTCTGTAATATTTTCCAAGAATTGGCTTGGCCGCCTT
TGTCGCTTCTATCAAATGATAGTGTGGAATTTGAGGGAAGAGGTGATGT
```
Example

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

[Submit] [RESET]

Parameter Options

Expect [10 ▾]   Matrix [BLOSUM62 ▾]   ☐ Perform ungapped alignment
☐ Graphical Overview   Descriptions [100 ▾]   Alignments [50 ▾]

Blast result

Query id	Subject id	alignment length	mismatches	query start	query end	subject start	subject end	% identity	e-value	bit score
Cluster-55448.309693	Cluster-55448.309693	585	0	1	585	1	585	100.00	0.0	1160
Cluster-55448.309693	Cluster-55448.32905	181	2	405	585	1432	1252	98.90	9e-93	343
Cluster-55448.309693	Cluster-55448.308922	181	2	405	585	1199	1019	98.90	9e-93	343
Cluster-55448.309693	Cluster-55448.309691	181	2	405	585	1516	1336	98.90	9e-93	343
Cluster-55448.309693	Cluster-55448.672	181	10	405	585	605	425	94.48	1e-73	280
Cluster-55448.309693	Cluster-55448.50890	274	37	297	570	390	117	86.50	1e-64	250
Cluster-55448.309693	Cluster-55448.63700	274	37	297	570	1419	1146	86.50	1e-64	250
Cluster-55448.309693	Cluster-55448.63699	274	37	297	570	2091	1818	86.50	1e-64	250
Cluster-55448.309693	Cluster-55448.565	289	43	297	585	713	425	85.12	2e-59	232
Cluster-55448.309693	Cluster-55448.2335	289	43	297	585	1112	824	85.12	2e-59	232

Tools: gene set enrichment analysis

Gene set enrichment analysis (PlantGSEA)

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

Choose gene set and input your gene list

Choose Gene Sets
☑ **G1**: Gene ontology gene sets
  ☑ BP: GO biological process   ☑ CC: GO cellular component   ☑ MF: GO molecular function
☑ **G2**: Transcription factor Based gene sets
☑ **G3**: Curated gene sets
  ☑ KEGG: KEGG gene sets sets

Choose Background
◉ Suggested background (Whole genome level)
○ Customized background

Submit Your Query

```
Cluster-55448.204822
Cluster-43356.0
Cluster-47026.0
Cluster-42890.0
Cluster-55448.272818
Cluster-29930.0
Cluster-55448.222823
Cluster-55448.129011
Cluster-45560.0
Cluster-49628.0
Cluster-55448.156817
Cluster-55448.163721
Cluster-44918.0
Cluster-51201.0
```
Example

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

选择文件 | 未选择任何文件

[Submit] [RESET]

GSEA analysis results

Gene Set Name(NO. Genes)	Description	Category	NO. Genes in Overlap (k)	p value	FDR
GLYCEROPHOSPHOLIPID_METABOLISM(665)	Glycerophospholipid_metabolism	KEGG	49	3.3e-96	1.5e-94
FATTY_ACID_BIOSYNTHESIS(404)	Fatty_acid_biosynthesis	KEGG	35	9.94e-71	2.26e-69
FATTY_ACID_METABOLISM(827)	Fatty_acid_metabolism	KEGG	39	5.97e-69	9.05e-68
GLYCEROLIPID_METABOLISM(437)	Glycerolipid_metabolism	KEGG	33	8.62e-65	9.81e-64
ACYL-[ACYL-CARRIER-PROTEIN] DESATURASE ACTIVITY(86)	GO:0045300 acyl-[acyl-carrier-protein] desaturase activity, GOslim:molecular_function	GO_MF	17	2.29e-40	6.57e-38
BIOSYNTHESIS_OF_UNSATURATED_FATTY_ACIDS(481)	Biosynthesis_of_unsaturated_fatty_acids	KEGG	22	1e-38	9.12e-38
FATTY ACID METABOLIC PROCESS(411)	GO:0006631 fatty acid metabolic process, GOslim:biological_process	GO_BP	21	5.53e-38	1.94e-35
ETHER_LIPID_METABOLISM(214)	Ether_lipid_metabolism	KEGG	17	4.48e-34	3.4e-33
TRANSFERASE ACTIVITY, TRANSFERRING ACYL GROUPS(385)	GO:0016746 transferase activity, transferring acyl groups, GOslim:molecular_function	GO_MF	18	5.04e-32	7.22e-30
PHOSPHOTRANSFERASE ACTIVITY, FOR OTHER SUBSTITUTED PHOSPHATE GROUPS(27)	GO:0016780 phosphotransferase activity, for other substituted phosphate groups, GOslim:molecular_function	GO_MF	7	4.62e-18	4.41e-16
BIOTIN_METABOLISM(181)	Biotin_metabolism	KEGG	9	7.53e-17	4.9e-16
FATTY ACID BIOSYNTHETIC PROCESS(653)	GO:0006633 fatty acid biosynthetic process, GOslim:biological_process	GO_BP	11	2.75e-15	4.82e-13
PHOSPHOLIPID BIOSYNTHETIC PROCESS(140)	GO:0008654 phospholipid biosynthetic process, GOslim:biological_process	GO_BP	7	2.11e-13	2.46e-11
GLYCEROL-3-PHOSPHATE DEHYDROGENASE [NAD+] ACTIVITY(20)	GO:0004367 glycerol-3-phosphate dehydrogenase [NAD+] activity, GOslim:molecular_function	GO_MF	5	3.54e-13	2.54e-11
GLYCEROL-3-PHOSPHATE DEHYDROGENASE COMPLEX(20)	GO:0009331 glycerol-3-phosphate dehydrogenase complex, GOslim:cellular_component	GO_CC	5	3.54e-13	3.04e-11
GLYCEROL-3-PHOSPHATE METABOLIC PROCESS(20)	GO:0006072 glycerol-3-phosphate metabolic process, GOslim:biological_process	GO_BP	5	3.54e-13	3.1e-11
GLYCEROLIPID METABOLIC PROCESS(615)	GO:0046486 glycerolipid metabolic process, GOslim:biological_process	GO_BP	8	1.37e-10	9.56e-09
TRANSCRIPTION_FACTOR_SNF2(159)	Transcription_related, Transcription factor: SNF2	GFam	5	5.95e-09	1.78e-08
THIOLESTER HYDROLASE ACTIVITY(44)	GO:0016790 thiolester hydrolase activity, GOslim:molecular_function	GO_MF	4	3.55e-09	2.04e-07
CAROTENOID_BIOSYNTHESIS(407)	Carotenoid_biosynthesis	KEGG	5	5.73e-07	3.26e-06
PROPANOATE_METABOLISM(257)	Propanoate_metabolism	KEGG	4	3.24e-06	1.64e-05

Tools: get sequences

Get sequence Page

Batch gene search

Input your interested gene list to get corresponding DNA sequences.

Gene List:

```
Cluster-55448.228322
Cluster-55448.228320
Cluster-55448.228325
Cluster-55448.6945
```

Example

Submit   RESET

DNA Sequence:
>Cluster-55448.228322
GCTGAGAAGCAAATGGCAAGAGAGGTTTGTGTTGCGTTTAGGCAAGCGGTTTGTGGGTTTGATCTCTTGCGTTGCGACGGGCGCTCATACGTCTGTGATGTTAATGGATGGA
>Cluster-55448.228320
AAGAGTGGCTGCTGCTGCTTCTGCCGTAATTACTTGACCATATGCCTTCTTTTTTTTCTTCTTCTTTCTATTTTAGATATTTTGTACTATTAATATTTATGCAAGCTACACTCA
>Cluster-55448.228325
AAAAAAAAAAAAACTGTCAAATTTGTCTCTCACCTGCATATCAAATTAGCAATGCTTAACCAGTCAACGTCTTTATGAGATTCAATATCTTCATACACGTGTAGGATATTTCCAT
>Cluster-55448.6945
GGATAATGTTATCCTCAATTTCACTTTCTTTTTGAATTGTCGGGATTACTTTGATAAGTTATCTTCGATTATATTATAATATTATTGATTTCTAAATTCAAGAATAAGAGACTATTT