

G03

小麦ERF类转录因子 生物信息学分析

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1月11

PCR引物设计及其分析

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引物设计时应注意的问题

- 1、引物长度（primer length） 15-30 bp不应大于38
- 2、引物序列在模板内应当没有相似性较高，尤其是3'端相似性较高的序列，否则容易导致错配引物3'端出现3个以上的连续碱基，如GGG或CCC，也会使错误引发机率增加
- 3、序列T_m值 (melting temperature)
如： $T_m = 4(G+C) + 2(A+T)$
- 4、G+C含量（composition） 40-60 %
- 5、引物二聚体及发夹结构（duplex formation and hairpin）
- 6、避免在引物的3'端使用碱基A

引物设计的软件

1

- Primer Primer5.0 (图形界面、自动搜索)

2

- Oligo 6.0 (图形界面、引物分析)

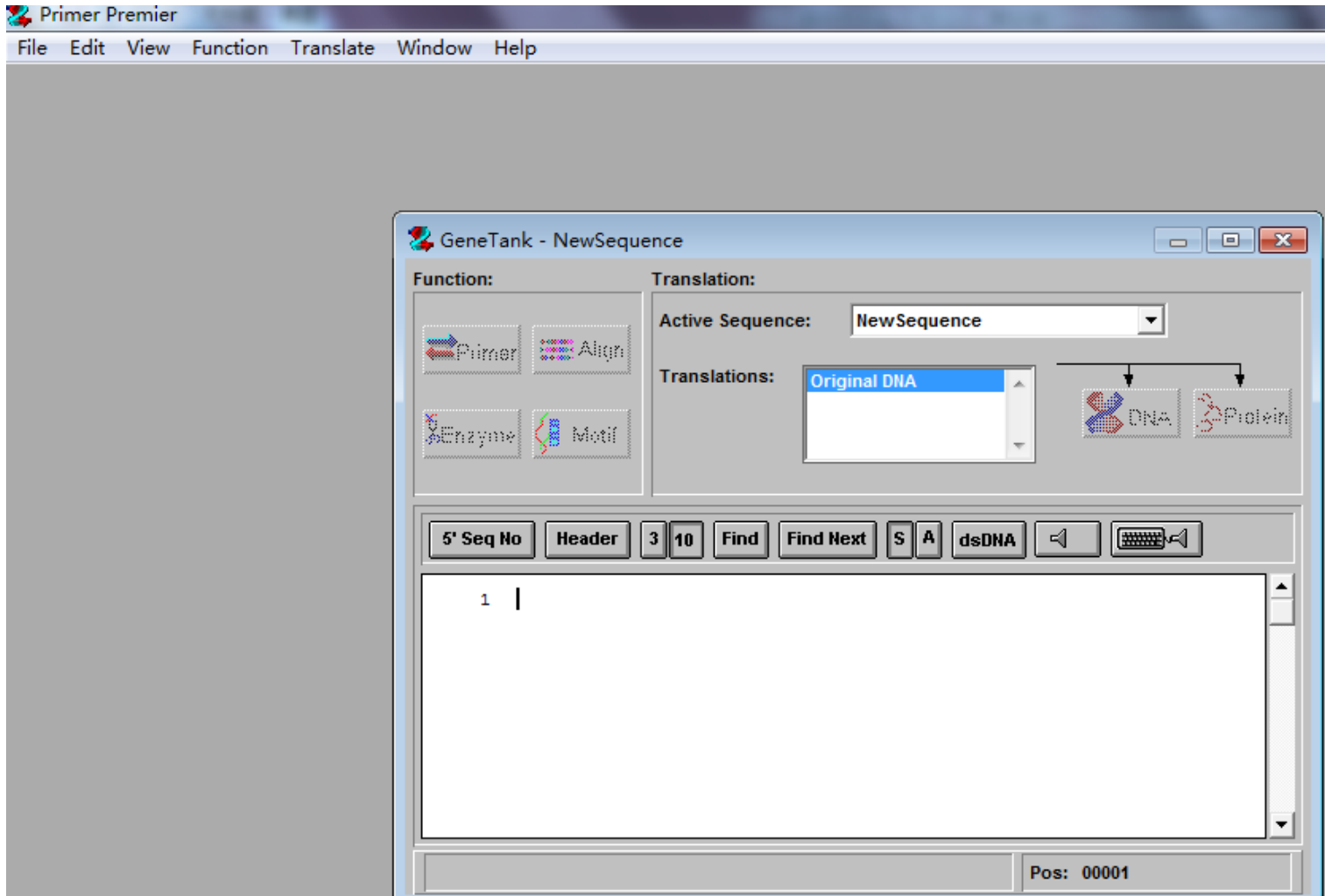
3

- Primer-Blast (同源序列分析)

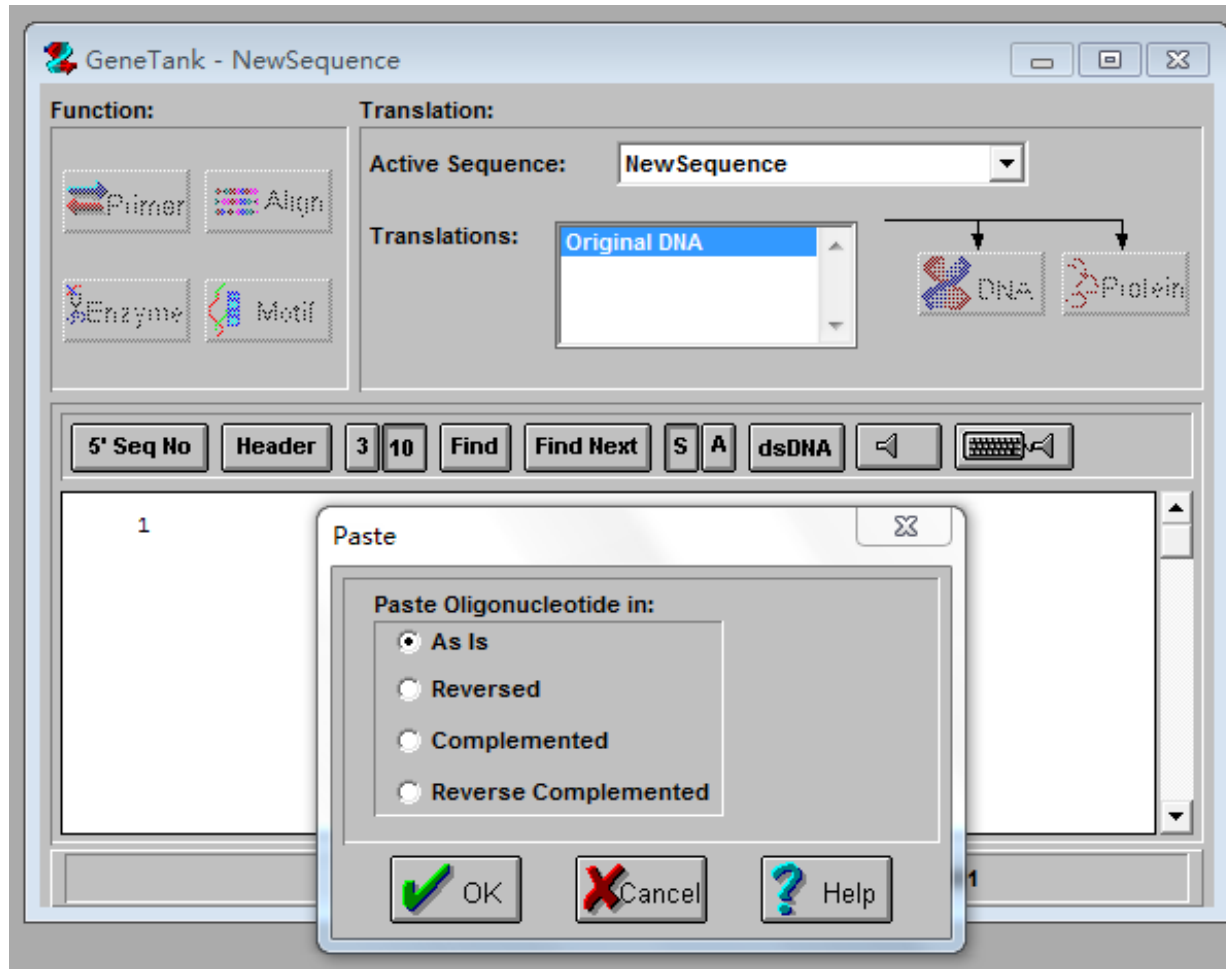
4

- Primer3 (引物分析、批量设计)

Primer Premier5.0-软件主界面



Primer Primer5.0-序列导入



序列分析

Primer Premier

Primer:

Direct Select:

3' TCGGGTGTCTCGTCTGGTTTCACGTT 5'

5' ATTGCATCACACATCAGTTAATTTAGTTCTCTTACGCCACAGCAGCACCAAAGTGCAAAACCTGCTATTGTTCTTTTATT 3'

I A S H I S - F S S P Y A T A A P K C K N L L L F F Y F

	Rating	Seq No	Length	Tm [°C]	GC%	ΔG [kcal/mol]	Activity [μg/OD]	Degeneracy	Ta Opt [°C]
Sense	65	1	25	56.8	28.0	-41.2	30.9	1	--
Anti-sense	60	59	25	74.4	56.0	-52.0	35.6	1	--
Product	23	--	59	78.5	42.4	--	--	--	47.0

	Hairpin	Dimer	False Priming	Cross Dimer
Sense	Found	Found	Found	Found
Anti-sense	Found	Found	Found	

Most Stable Hairpin: ΔG = 1.7 [kcal/mol] (3' Hairpin)

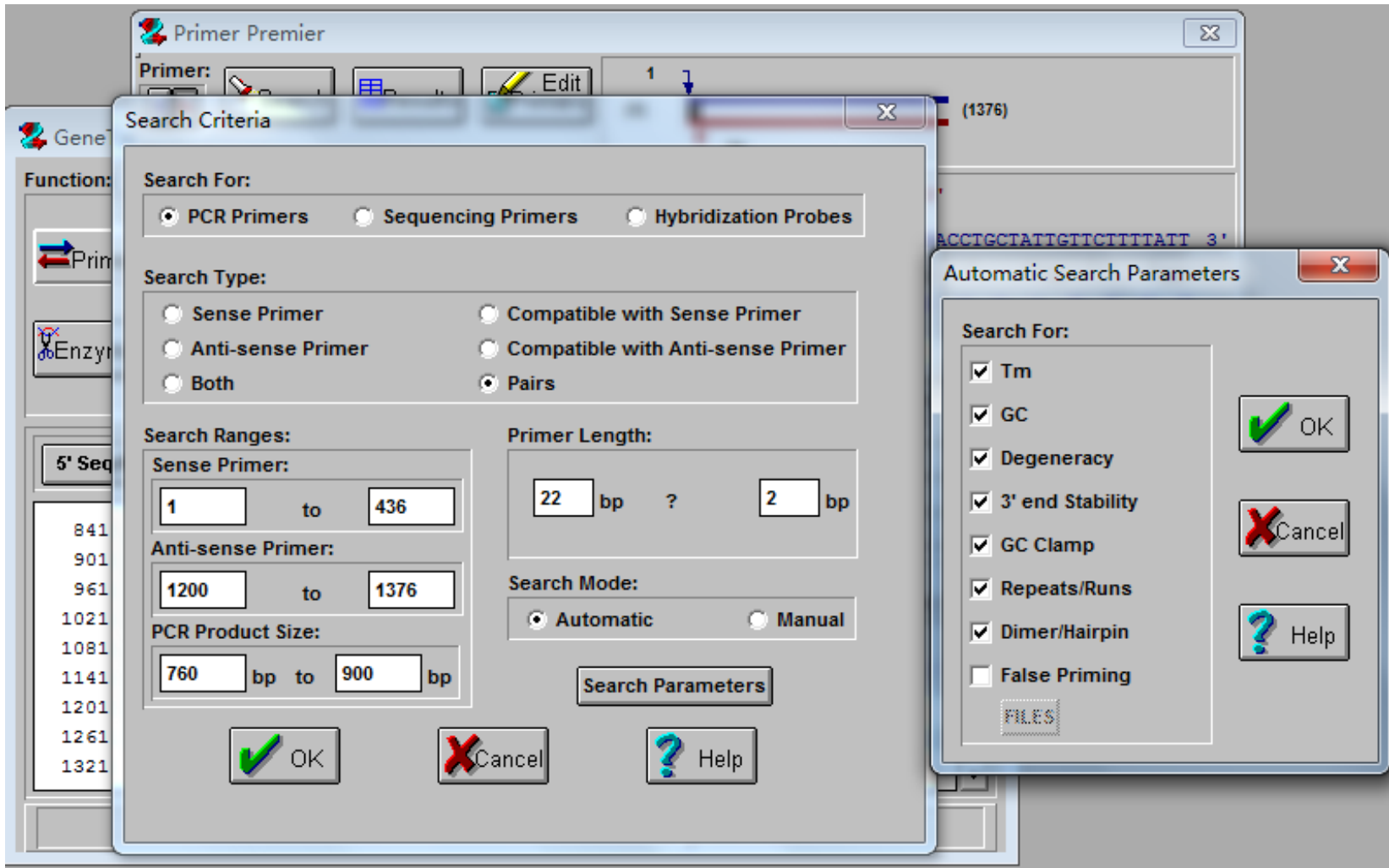
ACACTACGTTA 5'

CATCAGTTAATTTA 3'

1321 GTCTTGGA CCTTCAGTG GATATATTTA TTAATATTGA TAGTTGCAG GTCTG

Pos: 01377

引物搜索设置



结果显示

Primer Premier

Primer: **S** **A** Search Results Edit Primers

Direct Select:

5' CGCTCATCTTCACTGACTACTT 3'
 3' TACGACGAAAAGAAGAAGAGCGCGAGTAGAAGTGACTGATGAAGAGAGAGACGTTAAAGGTAACAACCTTCTTCTCTCTCCAA 5'

340 350 360 370 380 390 400 410
 C C F L L L A L I F T D Y F S L C N F H C - R R R E V

	Rating	Seq No	Length	Tm [°C]	GC%	ΔG [kcal/mol]	Activity [μg/OD]	Degeneracy	Ta Opt [°C]
Sense	82	356	22	54.1	45.5	-37.3	34.6	1	--
Anti-sense	100	1237	22	55.7	45.5	-39.2	31.0	1	--
Product	81	--	882	88.4	47.1	--	--	--	53.1

Hairpin: None Dimer: None False Priming: Found Cross Dimer: Found

Most Stable Site:
 ΔG = -11.7 [kcal/mol]; Product = 0
 3' TTCATCAGTCACCTTCTACTCGC 5'
 5' (990) TACTGGATGAAGAAGATGACGA (1011)

1201 TTGAGAAGTG GGTTCAGTCCF CACCCCTTGT AACIAAATCA TGTTGGACGI CTAACCTTGT
 1261 AGTGGCTTAG GCTTCCTTTG TCATGCCATG ATGGTGTGGA ATATGTATTC AGTACTTTGG
 1321 GTCTTGTGAA CCTTTCAGTG GATATATTTA TTAATATTTA TAGTTTGCAG GTTCTG

Renumbers the bases of the sequence starting from 5' end Pos: 01377

Search Results

Sense Anti-sense Pairs

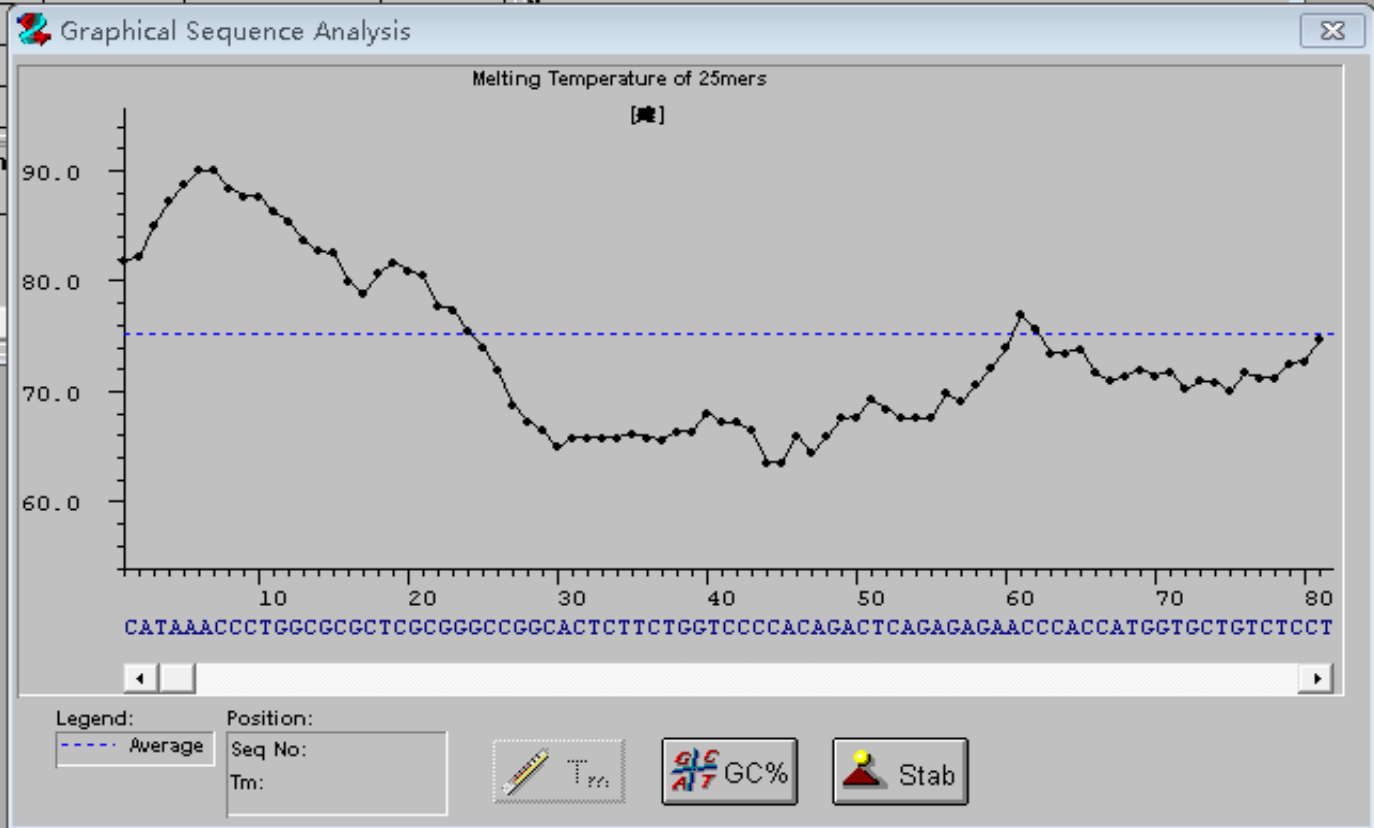
100 pairs found.

#	Rating	Tm [°C]	Product Size	Ta Opt [°C]	Mark
1	81	54.1 55.7	882	53.1	<input type="checkbox"/>
2	76	58.7 57.7	900	54.2	<input type="checkbox"/>
3	75	54.1 53.7	886	53.0	<input type="checkbox"/>
4	74	54.7 57.6	898	53.3	<input type="checkbox"/>
5	74	57.1 55.7	852	53.6	<input type="checkbox"/>

Tm [°C]	GC%	ΔG [kcal/mol]	Activity [μg/OD]	Degeneracy	Ta Opt [°C]
5.8	64.7	-35.4			
6.6	61.1	-36.7			
4.9	65.3	--			

Cross Dimer:

No Hairpin:



结果的保存

The screenshot displays the Primer Premier software interface. The main window shows a DNA sequence with primers (1) at positions 356 and 1237. The Search Results window indicates 100 pairs found. The Primer Database window is open, showing a list of primers and their properties.

Primer Database Table:

#	Name	Seq No	Sequence
1	PHD2-AS	1237	3' CAGGAGTGGGGAACATTGATT 5'
2	PHD2-S	356	5' CGCTCATCTTCACTGACTACT 3'

Search Results Table:

Tm [°C]	Product Size	Ta Opt [°C]	Mark
54.1 55.7	882	53.1	<input type="checkbox"/>
58.7 57.7	900	54.2	<input type="checkbox"/>
54.1 53.7	886	53.0	<input type="checkbox"/>
54.7 57.6	898	53.3	<input type="checkbox"/>
57.1 55.7	852	53.6	<input type="checkbox"/>

Current Primer Pair Table:

#	Seq No	Primer Sequence
1	356	5' CGCTCATCTTCACTGACTACT 3'
2	1237	5' TTAGTTACAAGGGGTGAGGAC 3'

Synthesis Order Form

Synthesis Order Form

Shipping Address:

Phone:

Fax:

E-mail:

Billing Address:

Phone:

Fax:

E-mail:

P.O.#:

Oligonucleotides:

#	Oligo Name	Oligo Sequence	Oligo Length	Purification	Scale(µm)	Modification
1.	PHD2-S	5' CGCTCATCTTCACTGACTACT T 3'	22	None	15	5' None 3' None

Special Instructions:

Primer-BLAST



A tool for finding specific primers

► [NCBI/ Primer-BLAST: Finding primers specific to your PCR template \(using Primer3 and BLAST\).](#) [more...](#) [Tips for finding specific primers](#)

PCR Template [Reset page](#) [Save search parameters](#) [Retrieve recent results](#)

Enter accession, gi, or FASTA sequence (A refseq record is preferred)

[Clear](#)

```
>GmWRKY5
GTTCTGCATCTTACACAACGAGCCATCTTAGCATGAGCTTCAACATGAGAA
ACAGTTCAACTATGGGTCAACATGGAACAAGGAGGAAGAGAGAACTACTCT
GACCACTCTTCCAACAAAAGCAAACCACGTGCCTCTCTTCAATCTCCACAA
GCATATTTCAAGTGCACATGGGGGTGAGACGGTTCTTGTTCATCTGCTTCTCT
```

Or, upload FASTA file

Range

	From	To	
Forward primer	<input type="text" value="1"/>	<input type="text" value="36"/>	Clear
Reverse primer	<input type="text" value="1400"/>	<input type="text" value="1805"/>	

Primer Parameters

Use my own forward primer (5' → 3' on plus strand) [Clear](#)

Use my own reverse primer (5' → 3' on minus strand) [Clear](#)

PCR product size

Min	<input type="text" value="600"/>	Max	<input type="text" value="2000"/>
-----	----------------------------------	-----	-----------------------------------

of primers to return

Primer melting temperatures (T_m)

Min	<input type="text" value="57.0"/>	Opt	<input type="text" value="60.0"/>	Max	<input type="text" value="63.0"/>	Max T _m difference	<input type="text" value="3"/>
-----	-----------------------------------	-----	-----------------------------------	-----	-----------------------------------	-------------------------------	--------------------------------

Exon/intron selection [A refseq mRNA sequence as PCR template input is required for options in the section](#)

参数设定

▼ **Advanced parameters** Note: Parameter values that differ from the default are highlighted

Primer Pair Specificity Checking Parameters

Blast max number of hit sequences: 50000

Blast expect (E) value: 30000

Blast word size: 7

Max primer pairs to screen: 1000

Primer Parameters

PCR Product Tm	Min	Opt: 60	Max
Primer Size	Min: 20	Opt: 22	Max: 24
Primer GC content (%)	Min: 45	Max: 55	
GC clamp	0		
Max Poly-X	5		
Max self complementarity:	8.00		
Max 3' end complementarity:	3.00		
SNP handling	<input type="checkbox"/> Primer binding site may not contain known SNP		
Repeat filter	Automatic		

Avoid repeat region for primer selection by filtering with repeat database

结果显示

Input PCR template
Range
Specificity of primers

GmWRKY5
1 - 1805

Primer pairs are specific to input template as no other targets were found in selected database: NCBI Transcript Reference Sequences (Organism limit Homo sapiens)

► [Graphical view of primer pairs](#)

▼ [Detailed primer reports](#)

Primer pair 1

	Sequence (5' -> 3')	Strand on template	Length	Start	Stop	Tm	GC%
Forward primer	CCTGCATCTTACACAAGTGGCC	Plus	24	4	27	57.18	50.00%
Reverse primer	ACAATGCCCAACTCTTGTGAAGCT	Minus	24	1729	1706	57.26	45.83%
Product length	1726						

Primer pair 2

	Sequence (5' -> 3')	Strand on template	Length	Start	Stop	Tm	GC%
Forward primer	TCCTGCATCTTACACAAGTGGCC	Plus	25	3	27	58.17	48.00%
Reverse primer	ACAATGCCCAACTCTTGTGAAGCT	Minus	25	1729	1705	57.60	44.00%
Product length	1727						

Primer pair 3

	Sequence (5' -> 3')	Strand on template	Length	Start	Stop	Tm	GC%
Forward primer	TTCCTGCATCTTACACAAGTGGCC	Plus	25	2	26	57.29	48.00%
Reverse primer	AACAATGCCCAACTCTTGTGAAGCT	Minus	25	1730	1706	57.60	44.00%
Product length	1729						

example

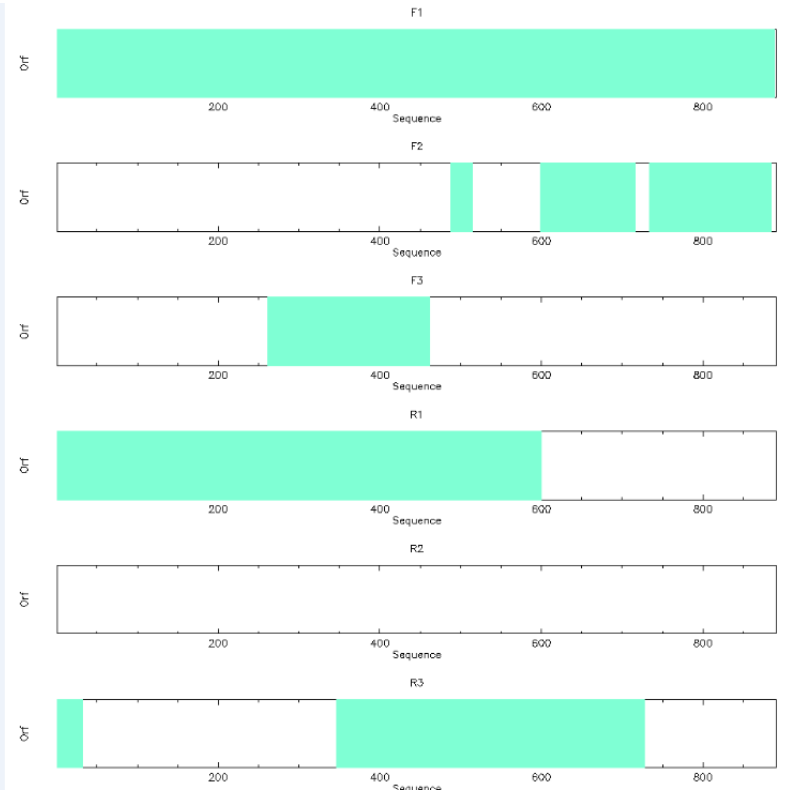
- >Homo sapiens hemoglobin

```
CATAAACCCCTGGCGCGCTCGCGGGCCGGCACTCTTCTGGTCCCCACAGACTCAGAGAGAACCCACCATGG
TGCTGTCTCCTGCCGACAAGACCAACGTCAAGGCCGCCTGGGGTAAGGTCGGCGCGCACGCTGGCGAGTA
TGGTGCGGAGGCCCTGGAGAGGATGTTCTGTCCTTCCCCACCACCAAGACCTACTTCCCGCACTTCGAC
CTGAGCCACGGCTCTGCCAGGTTAAGGGCCACGGCAAGAAGGTGGCCGACGCGCTGACCAACGCCGTGG
CGCACGTGGACGACATGCCCAACGCGCTGTCCGCCCTGAGCGACCTGCACGCGCACAAAGCTTCGGGTGGA
CCCGGTCAACTTCAAGCTCCTAAGCCACTGCCTGCTGGTGACCCTGGCCGCCACCTCCCCGCCGAGTTC
ACCCCTGCGGTGCACGCCTCCCTGGACAAGTTCCTGGCTTCTGTGAGCACCGTGCTGACCTCCAAATACC
GTTAAGCTGGAGCCTCGGTAGCCGTTCTCCTGCCCGCTGGGCCTCCCAACGGGCCCTCCTCCCCTCCTT
GCACCGGCCCTTCTGGTCTTTGAATAAAGTCTGAGTGGGCAGCAAAAAAAAAAAAAAAAAAAAAA
```


研究背景

- ERF（乙烯响应因子）转录因子在植物响应非生物胁迫以及激素和病原菌应答中发挥重要作用,以ERF转录因子W17为诱饵,筛选小麦干旱处理的cDNA文库,得到三株阳性克隆:STPK、Hsp90、PPR,利用基因克隆技术得到三个基因全长,对这三个基因实时定量分析,推测受多种非生物胁迫和生物胁迫诱导表达的基因,这三个基因表达的蛋白可能是W17互作蛋白,利用酵母双杂交、BIFC（荧光双分子互补）PULL-DOWN方法进一步验证W17与STPK、Hsp90、PPR之间的互作关系。根据STPK、Hsp90、PPR亚细胞定位,蛋白保守域,已经报道的文献,推测它们之间可能的互作关系,互作方式及互作位点,在分别对STPK、Hsp90、PPR这三个基因进行筛选小麦干旱处理的cDNA文库,找到互作蛋白,推测W17转录因子可能参与的信号通路

具体操作：利用Jemboss软件克隆到的基因分析其ORF





Plant Transcription Factor Database

v2.0

Center for Bioinformatics, Peking University, China

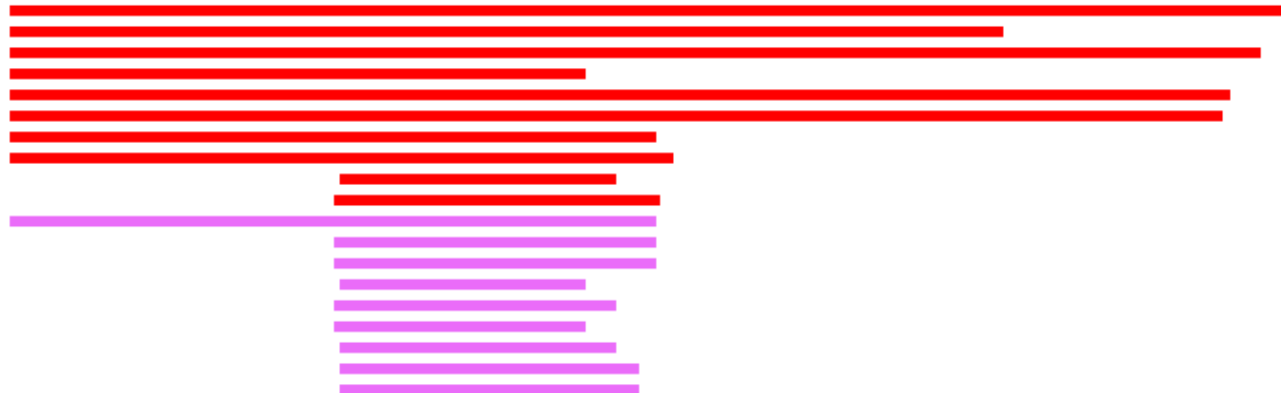
[Previous version](#)

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(eg: SPL2)

Blast Result

Color key for alignment score



Query:

Tae005772
Tae004922
Tae004677
Tae015561
Tae004885
Tae004880
Tae003967
Tae013225
Tae017743
Tae004315
Tae003831
Tae003691
Tae009861
Tae012979
Tae007054
Tae006839
Tae007976
Tae008935
TaeAAAA1A

- 克隆到一个基因，分析可能是ERF类转录因子，BLAST分析与小麦Tae005772相似度最高



Plant Transcription Factor Database

v2.0

Center for Bioinformatics, Peking University, China

[Previous version](#)

[Home](#) | [Blast](#) | [Search](#) | [Download](#) | [WebService](#) | [Help](#) | [About](#) | [Links](#)

(eg: SPL2)

Transcription Factor Information

[Basic Information](#) | [Signature Domain](#) | [Sequence](#)
[Protein Features](#) | [Gene Ontology](#) | [3D Structure](#) | [Expression](#) |

Basic Information

[? help](#)

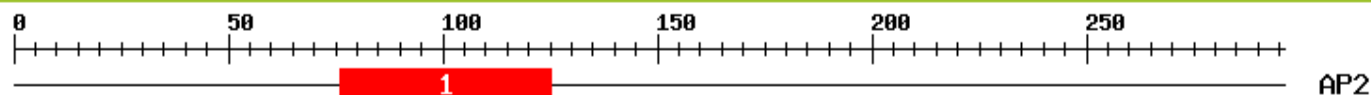
[Back to Top](#)

Species	<i>Triticum aestivum</i>			
TF ID	Tae005772			
Family	ERF			
Protein Properties	Length: 296aa MW: 31791 Da PI: 4.2632			
Gene Model	Gene Model ID	Type	Source	Coding Sequence
	gnl UG Ta#S29895629	PU_ref	Unigene	View CDS

Signature Domain

[? help](#)

[Back to Top](#)



No.	Domain	Score	E-value	Start	End	HMM Start	HMM End
1	AP2	54.6	2.7e-17	76	125	2	54

Tae005772基因NCBI比对及进化树分析

Home Recent Results Help [\[Sign In\]](#)

[Phylogenetic Tree](#) [Edit and Resubmit](#) [Back to Blast Results](#) [Download](#)

Download alignment

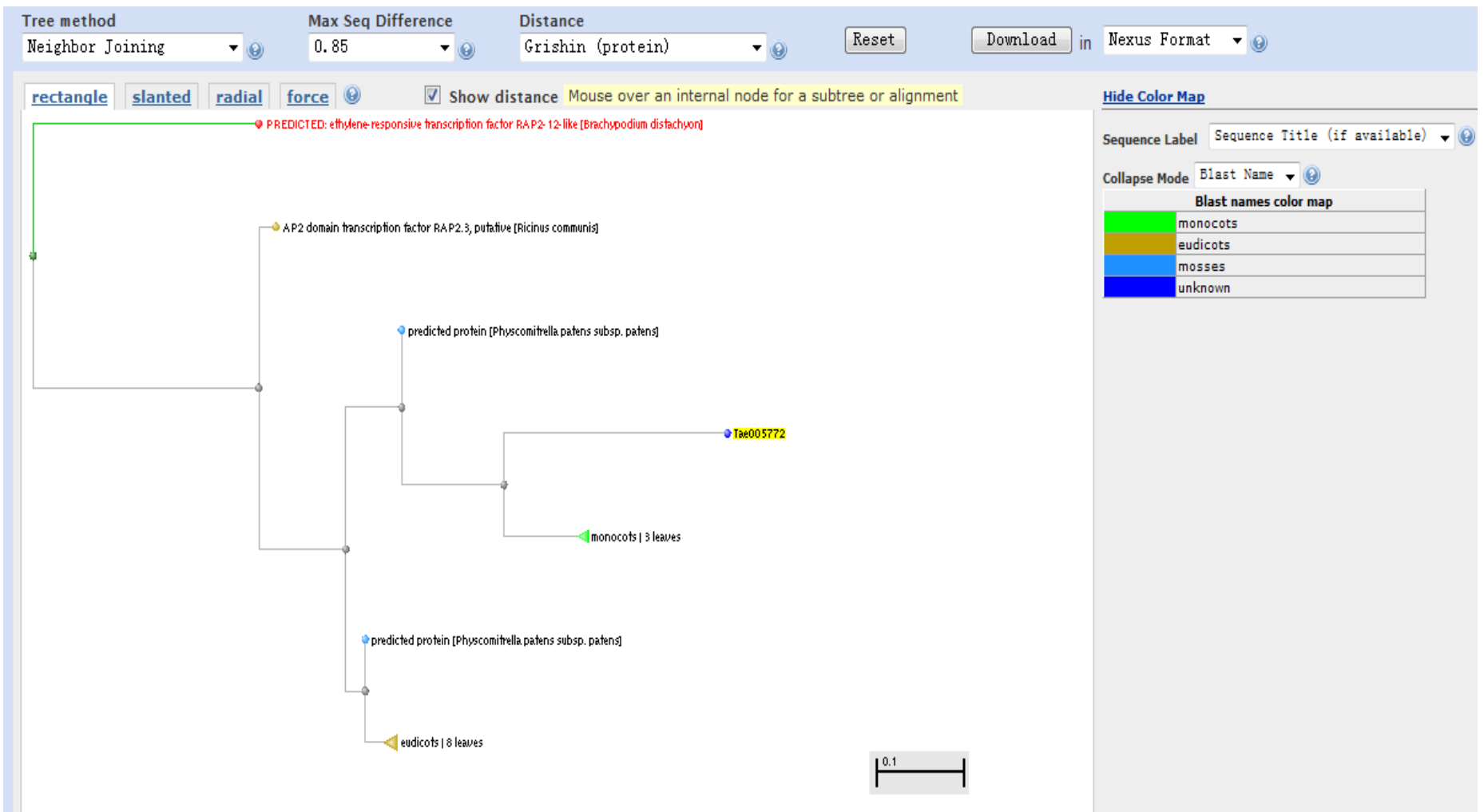
[Fasta plus gaps](#) [Clustal](#) [Phylip](#) [Nexus](#) [ASN.1](#)

Multiple Alignment Results - Tae005772 - Cobalt RID DSRK80J1212 (8 seqs)

Descriptions Select All [Re-align](#) [Alignment parameters](#)

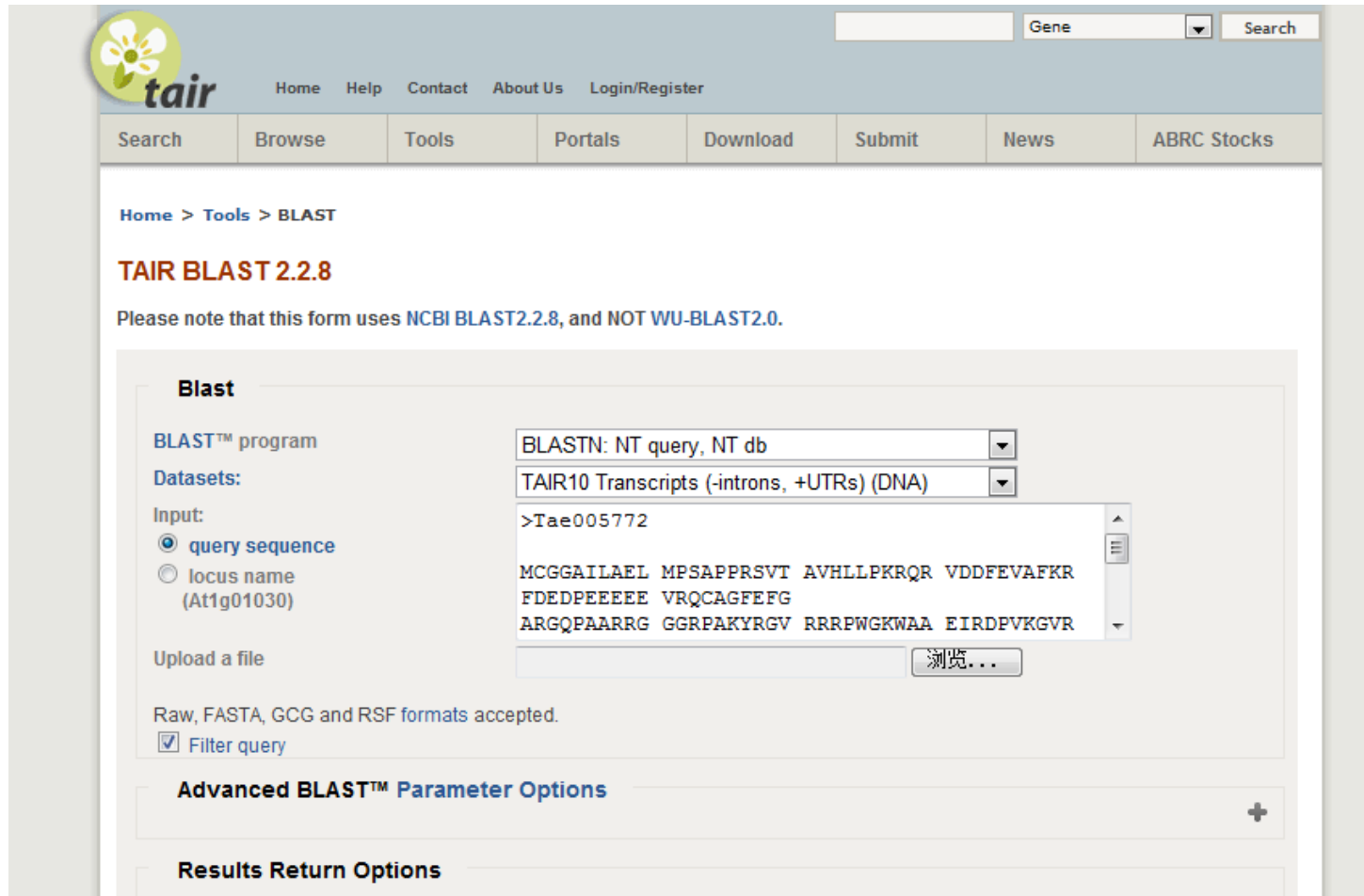
Legend for links to other resources: [U](#) UniGene [E](#) GEO [G](#) Gene [S](#) Structure [M](#) Map Viewer

Accession	Description	Links
<input checked="" type="checkbox"/> XP_003558659.1	PREDICTED: ethylene-responsive transcription factor RAP2-12-like [Brachypodium distachyon]	G
<input checked="" type="checkbox"/> NP_001147529.1	ethylene-responsive element binding protein 2 [Zea mays] >gb ACG27833.1 ethylene-responsive element binding	UG
<input checked="" type="checkbox"/> XP_003591474.1	Ethylene responsive transcription factor 2b [Medicago truncatula] >gb AES61725.1 Ethylene responsive transcripti	UG
<input checked="" type="checkbox"/> NP_001243393.1	ethylene-responsive transcription factor RAP2-3-like [Glycine max] >gb AEQ55265.1 ethylene-responsive transcrip	UG
<input checked="" type="checkbox"/> XP_003627419.1	Ethylene-responsive transcription factor [Medicago truncatula] >gb AET01895.1 Ethylene-responsive transcription 1	UG
<input checked="" type="checkbox"/> NP_188299.1	ethylene-responsive transcription factor RAP2-3 [Arabidopsis thaliana] >sp P42736.2 RAP23_ARATH RecName: F1	UGM
<input checked="" type="checkbox"/> NP_001117587.1	ethylene-responsive transcription factor ERF073 [Arabidopsis thaliana] >gb AEE35312.1 ethylene-responsive tran	GM
<input checked="" type="checkbox"/> XP_002320996.1	AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gb EEE99311.1 AP2/ERF domain-containi	UGM



扩大范围比对，结果显示Tae005772基因与单子叶植物亲缘关系最近，来源于相同的祖先，有相同的起源

拟南芥基因BLAST结果显示



The image shows the TAIR BLAST 2.2.8 web interface. At the top, there is a navigation bar with the TAIR logo and links for Home, Help, Contact, About Us, and Login/Register. Below this is a search bar with a dropdown menu set to 'Gene' and a 'Search' button. A secondary navigation bar contains buttons for Search, Browse, Tools, Portals, Download, Submit, News, and ABRC Stocks.

The main content area shows the breadcrumb path: Home > Tools > BLAST. The title is 'TAIR BLAST 2.2.8'. A note states: 'Please note that this form uses NCBI BLAST2.2.8, and NOT WU-BLAST2.0.'

The 'Blast' section contains the following fields and options:

- BLAST™ program:** A dropdown menu set to 'BLASTN: NT query, NT db'.
- Datasets:** A dropdown menu set to 'TAIR10 Transcripts (-introns, +UTRs) (DNA)'.
- Input:** Radio buttons for 'query sequence' (selected) and 'locus name (At1g01030)'. The text area contains the query sequence: '>Tae005772' followed by three lines of amino acid sequences: 'MCGGAILAEL MPSAPPRSVT AVHLLPKRQR VDDFEVAFKR', 'FDEDPEEEEE VRQCAGFEFG', and 'ARGQPAARRG GGRPAKYRGV RRRPWGKWA EIRDPVKGVR'.
- Upload a file:** A text input field with a '浏览...' (Browse...) button.
- Raw, FASTA, GCG and RSF formats accepted.**
- Filter query**

Below the main form are two expandable sections: 'Advanced BLAST™ Parameter Options' and 'Results Return Options', both currently collapsed.



Locus: AT3G16770

Date last modified 2010-08-30

TAIR Accession Locus:2089368

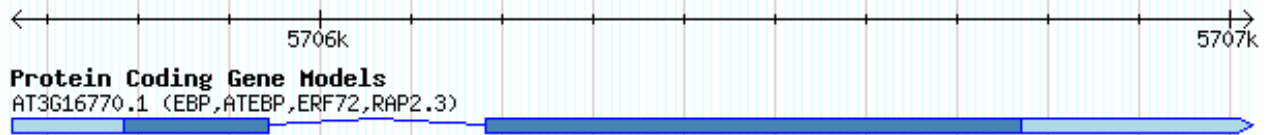
Representative Gene Model [AT3G16770.1](#)

Gene Model Type protein_coding

Other names: ATEBP, EBP, ERF72, ETHYLENE RESPONSE FACTOR 72, ETHYLENE-RESPONSIVE ELEMENT BINDING PROTEIN, RAP2.3, RELATED TO AP2.3

Description [?](#) Encodes a member of the ERF (ethylene response factor) subfamily B-2 of the plant specific ERF/AP2 transcription factor family (RAP2.3). The protein contains one AP2 domain. There are 5 members in this subfamily including RAP2.2 AND RAP2.12. It is localized to the nucleus and acts as a transcriptional activator through the GCC-box. It has been identified as a suppressor of Bax-induced cell death by functional screening in yeast and can also suppress Bax-induced cell death in tobacco plants. Overexpression of this gene in tobacco BY-2 cells confers resistance to H₂O₂ and heat stresses. Overexpression in Arabidopsis causes upregulation of PDF1.2 and GST6. It is part of the ethylene signaling pathway and is predicted to act downstream of EIN2 and CTR1, but not under EIN3.

Map Detail Image



Annotations [?](#)

category	relationship type ?	keyword ?
GO Biological Process	involved in	cell death, ethylene mediated signaling pathway, positive regulation of transcription, DNA-dependent, regulation of transcription, DNA-dependent, response to cytokinin stimulus, response to ethylene stimulus, response to jasmonic acid stimulus, response to other organism, response to stress

与拟南芥中的AT3G16770相似度最高，通过了解此基因能初步分析亚细胞定位

Arabidopsis eFP Browser



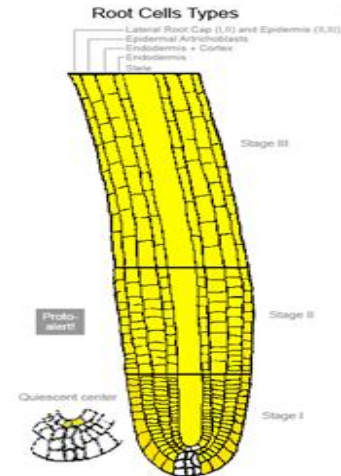
Arabidopsis eFP Browser

- For ATH1 data, this probe set reaches its maximum expression level (expression potential) of 16572.8 in the Root data source.

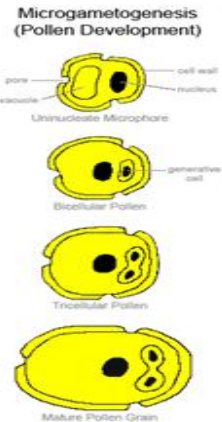


Arabidopsis eFP Browser at bar.utoronto.ca
 Winter et al., 2007, PLoS One 2(8): e718

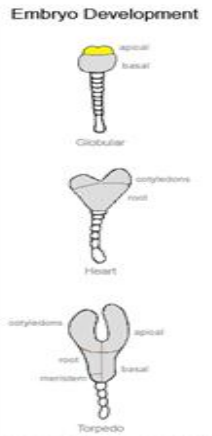
At3g16770.258434_at ATH16770



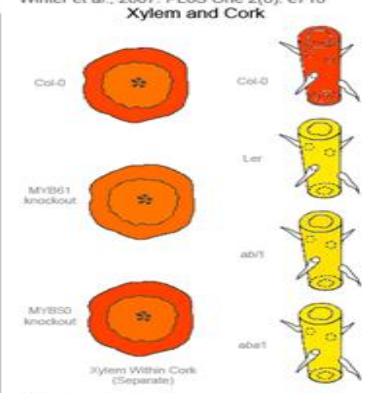
- Material from the roots of 6 day old wild-type Col-0 Arabidopsis thaliana plants was analyzed
 - Plants grown under 16/8 hour light/dark conditions on MS + 4.5% sucrose media
 - Root cell types were isolated by protoplasting and fluorescence-activated cell sorting. RNA was extracted from protoplasts and hybridized to ATH1 GeneChips
 - The data were normalized by GCOS normalization, TGT 100. Triplicate measurements were made.
 Results from Benabou et al. (2003) Science 302:1956 and Nawy et al. (2005) Plant Cell 17:1905.



- Plant material from the pollen of S.10 growth stage wild-type Arabidopsis thaliana plants of Ler-0 ecotype was analyzed
 - Plants grown under 16/8 hour light/dark conditions at 21°C
 - All measurements were taken in triplicates - the average of which is shown
 - RNA was isolated and hybridized to the ATH1 GeneChip
 - The data were normalized by GCOS normalization, TGT 100
 Horys & Twell (2004) Genom. Biol. 5:R85

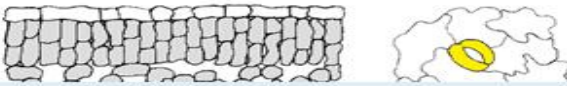


- Plant material from embryos of wild-type Col-0 Arabidopsis thaliana plants of was isolated by laser capture microdissection
 - Plants grown under 16/8 hour light/dark conditions
 - RNA was amplified and hybridized to the ATH1 GeneChip. Note: 3' bias!
 - All measurements were taken in triplicates - the average is shown
 - Results can be highly variable - standard deviation filtering advisable!
 - The data were normalized by GCOS normalization, TGT 100
 Casson et al. (2005) Plant J. 42:111



- Plant material from the xylem and cork of Arabidopsis thaliana plants of Columbia-0 ecotype was analyzed
 - Secondary thickened hypocotyl was induced by continual removal of the inflorescence stem for 10 weeks
 - Plants grown in growth room under continuous light conditions at 22°C
 - All measurements were taken in triplicates - the average of which is shown
 - RNA was isolated and hybridized to the ATH1 GeneChip
 - The data were normalized by GCOS normalization, TGT 100
 Results provided by the Campbell Lab

Guard and Mesophyll Cells
 Water Spray for 4 hours



- Plant material from the leaves of 5 week old Arabidopsis thaliana plants of Columbia-0 ecotype was analyzed
 - Mesophyll and guard cell protoplasts were used
 - Plants grown in growth room under 16/8 hour light/dark conditions at 22°C
 - Measurements were taken in triplicates - the average of which is shown. Actinomycin and...

In the Xylem and cork express the highest amount

Abiotic stress



Can endure high temperature

生物信息学分析Tae005772基因

PDB entry 1gcc



SOLUTION NMR STRUCTURE OF THE COMPLEX OF GCC-BOX BINDING DOMAIN OF ATERF1 AND GCC-BOX DNA, MINIMIZED AVERAGE STRUCTURE

Download PDB file

View in 3D

Similar structures

Quaternary structure

The structure was published by Allen, M.D., Yamasaki, K., Ohme-Takagi, M., Tateno, M., and Suzuki, M., in 1998 in a paper entitled "A novel mode of DNA recognition by a beta-sheet revealed by the solution structure of the GCC-box binding domain in complex with DNA." ([abstract](#)).

The structure was determined using NMR spectroscopy and deposited in 1998.

The [experimental data](#) on which the structure is based was also deposited.

This PDB entry contains a complex of 3 biomacromolecules, namely DNA (5'-D(*TP*AP*GP*CP*CP*GP*CP*CP*AP*GP*C)-3), DNA (5'-D(*GP*CP*TP*GP*GP*CP*GP*GP*CP*TP*A)-3), and ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 1.

The molecule most likely forms heterotrimer.

The following tables show cross-reference information to other databases (to obtain a list of all PDB entries sharing the same property or classification, click on the magnifying glass icon):

Chain	Name	UniProt	Name of source organism	% of UniProt sequence present in the sample	Residues in the sample molecules	% of residues observed
A	ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 1	Q80337 (146-208) (EF100_ARATH)	Arabidopsis thaliana	< 90%	63	100%

This entry contains 1 unique UniProt protein:

UniProt accession	Name	Organism	PDB
Q80337 (146 - 208)	ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 1	Arabidopsis thaliana	Related PDB sequences UniProt coverage

1gcc

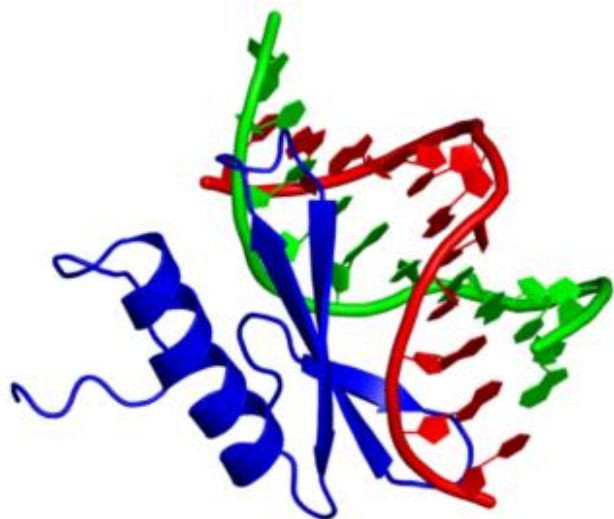
CATH domains

- 1 copy of domain [3.30.730.10](#) (GCC-box Binding Domain) is shown in **green** ([Explore](#) all PDB entries with this CATH domain).
- [Search](#) for PDB entries with similar 3D structure.

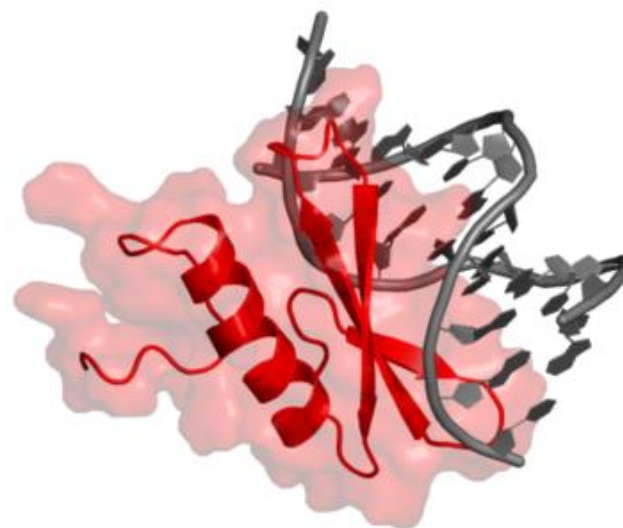
蛋白与拟南芥中的Ethylene Responsive Element Binding Factor 1相似

拟南芥 Ethylene Responsive Element Binding Factor 1 的3D结构

1gcc



1gcc



PDB

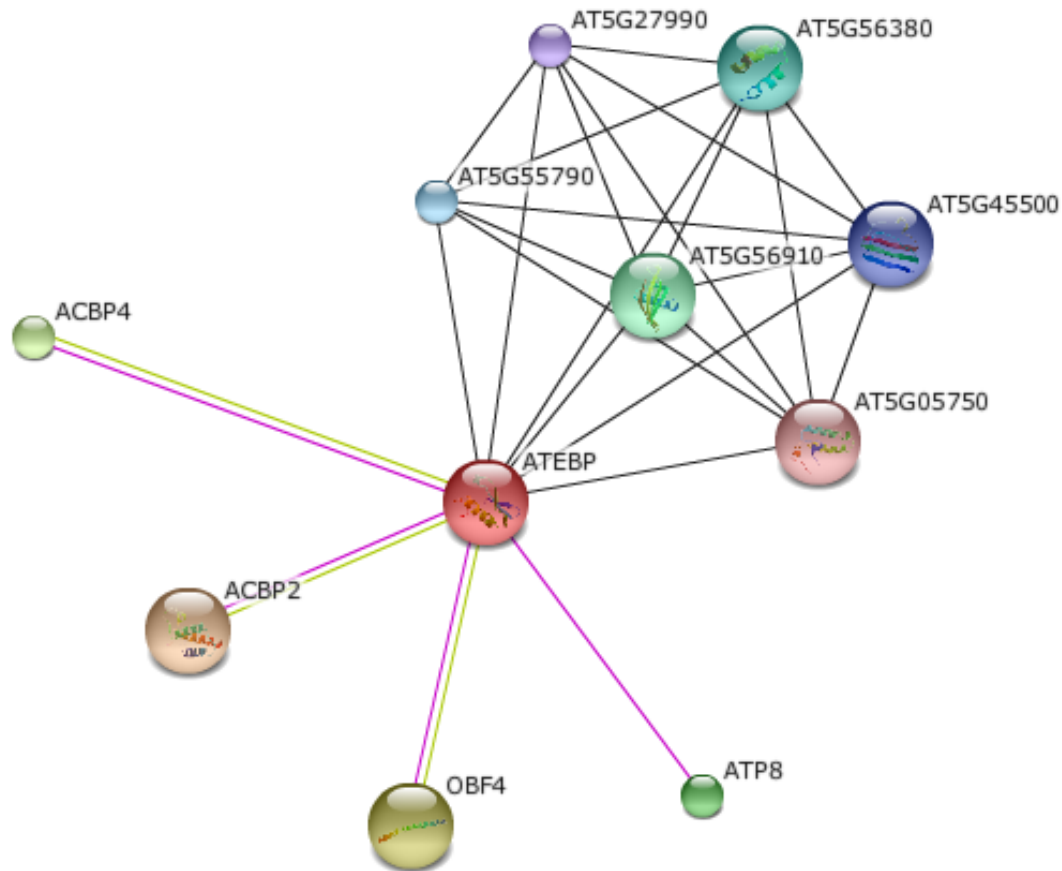
PDB

1gcc

PDB

Protein Interaction

Help/Info



Your Input:

- ATEBP** ATEBP (ETHYLENE-RESPONSIVE ELEMENT BINDING PROTEIN); DNA binding / protein binding / transcription activator/ transcription factor; Encodes a member of the ERF (ethylene response factor) subfamily B-2 of the plant specific ERF/AP2 transcription factor family (RAP2.3). The protein contains one AP2 domain. There are 5 members in this subfamily including RAP2.2 AND RAP2.12.It is localized to the nucleus and acts as a transcriptional activator through the GCC-box. It has been identified as a suppressor of Bax-induced cell death by functional screening in yeast and can also suppress Bax-ind [...] (248 aa)
(*Arabidopsis thaliana*)

Predicted Functional Partners:

		Neighborhood	Gene Fusion	Cooccurrence	Coexpression	Experiments	Databases	Textmining	[Homology]	Score
ACBP2	ACBP2 (ACYL-COA BINDING PROTEIN ACBP 2); acyl-CoA binding / lead ion binding; Encodes acyl-CoA- [...] (354 aa)					•		•		0.987
OBF4	TGA4 (TGACG MOTIF-BINDING FACTOR 4); DNA binding / calmodulin binding / transcription factor; E [...] (364 aa)					•		•		0.918
ACBP4	ACBP4 (ACYL-COA BINDING PROTEIN 4); acyl-CoA binding; Acyl-CoA binding protein with high affini [...] (669 aa)					•		•		0.916
ATP8	RCD1 (RADICAL-INDUCED CELL DEATH1); protein binding; Encodes a protein belonging to the (ADP-ri [...] (589 aa)					•				0.863
AT5G56910	unknown protein; INVOLVED IN- biological_process unknown; EXPRESSED IN- 22 plant structures; EX [...] (224 aa)					•				0.837
AT5G56380	F-box family protein; F-box family protein; FUNCTIONS IN- molecular_function unknown; INVOLVED [...] (439 aa)					•				0.837
AT5G55790	unknown protein; unknown protein; FUNCTIONS IN- molecular_function unknown; INVOLVED IN- biolog [...] (191 aa)					•				0.837
AT5G45500	unknown protein; unknown protein; FUNCTIONS IN- molecular_function unknown; INVOLVED IN- biolog [...] (771 aa)					•				0.837
AT5G27990	unknown protein; unknown protein; FUNCTIONS IN- molecular_function unknown; INVOLVED IN- biolog [...] (184 aa)					•				0.837
AT5G05750	DNAJ heat shock N-terminal domain-containing protein; DNAJ heat shock N-terminal domain-contain [...] (294 aa)					•				0.837

Views:

Neighborhood



Fusion



Occurrence



Coexpression



Experiments



Database

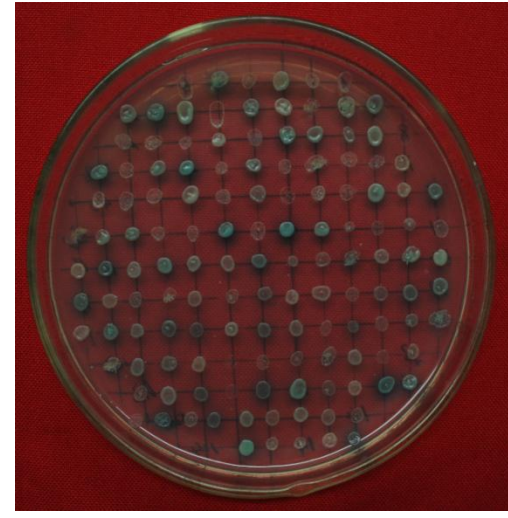
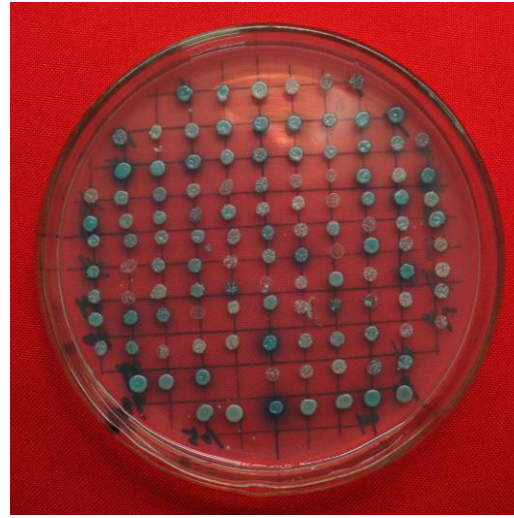
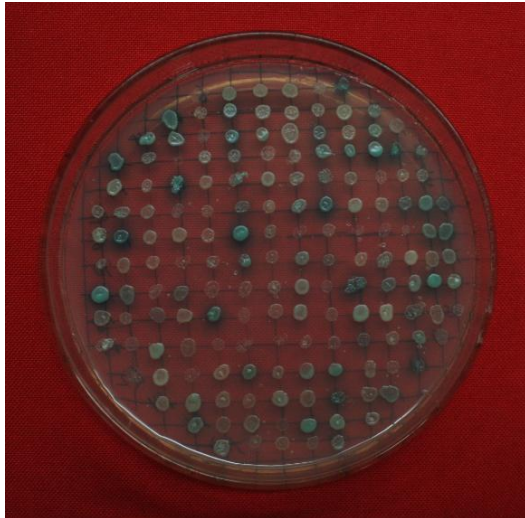
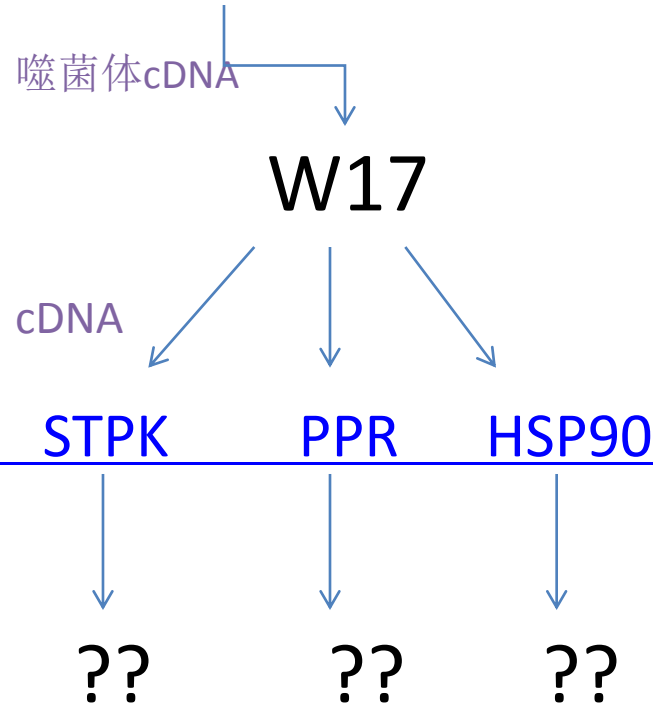


Textmining



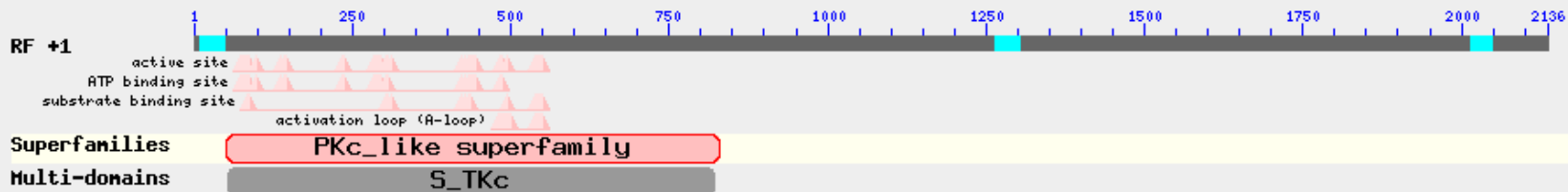
Summary Network

AP2保守域



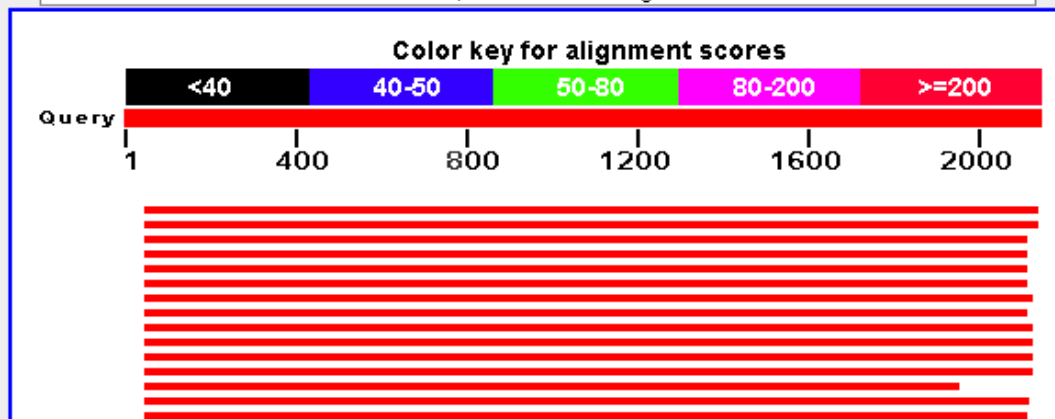
STPK基因NCBI BLAST结果

Putative conserved domains have been detected, click on the image below for detailed results.



Distribution of 109 Blast Hits on the Query Sequence

Mouse-over to show define and scores, click to show alignments



S_TKc

0 100 200 300 400 500 600 700

STPK 比对拟南芥数据库



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Locus: AT2G37840

Update History AT2G37840 replaces AT2G37850 on 2003-10-24

Date last modified 2003-05-02

TAIR Accession Locus:2065680

Representative Gene Model [AT2G37840.1](#)

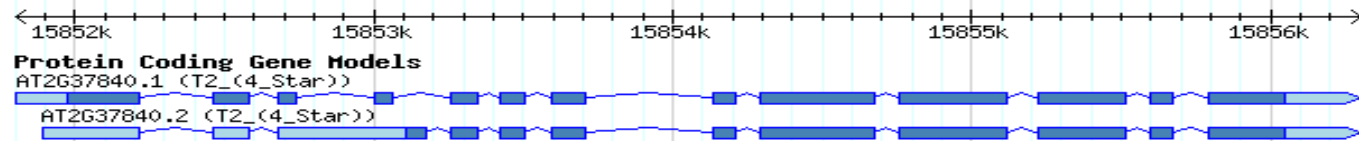
Gene Model Type protein_coding

Other names:

Description Protein kinase superfamily protein; FUNCTIONS IN: protein serine/threonine kinase activity, protein kinase activity, kinase activity, ATP binding; INVOLVED IN: protein amino acid phosphorylation; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Protein kinase, ATP binding site (InterPro:IPR017441), Serine/threonine-protein kinase domain (InterPro:IPR002290), Serine/threonine-protein kinase, putative (InterPro:IPR020655), Serine/threonine-protein kinase-like domain (InterPro:IPR017442), Serine/threonine-protein kinase, active site (InterPro:IPR008271), Protein kinase-like domain (InterPro:IPR011009), Protein kinase, catalytic domain (InterPro:IPR000719), Tyrosine-protein kinase, catalytic domain (InterPro:IPR020635), Calcium/calmodulin-dependent protein kinase-like (InterPro:IPR020636); BEST Arabidopsis thaliana protein match is: Protein kinase superfamily protein (TAIR:AT3G53930.2); Has 132594 Blast hits to 129738 proteins in 4259 species: Archae - 150; Bacteria - 15212; Metazoa - 48728; Fungi - 13428; Plants - 32505; Viruses - 540; Other Eukaryotes - 22031 (source: NCBI BLink).

Other Gene Models [AT2G37840.2](#) (splice variant)

Map Detail Image



Annotations

category	relationship type	keyword
GO Biological Process	involved in	glucuronoxylan metabolic process, plant-type cell wall biogenesis, protein phosphorylation, xylan biosynthetic process
GO Cellular Component	located in	cytoplasm

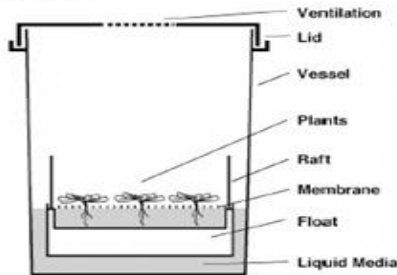
Arabidopsis eFP Browser

Data Source: Abiotic Stress At-TAX
 Mode: Absolute
 Primary Gene ID: AT2G37840
 Secondary Gene ID: At3g27340
 Signal Threshold: 141.27
 Go

- For ATH1 data, this probe set reaches its maximum expression level (expression potential) of 1058.6 in the Root data source.
- For ATH1 data, note the maximum signal value has decreased to 141.27 from 304.58. Use the [Signal Threshold option to keep it constant at 304.58](#), or enter a value in the Signal Threshold box, such as [1058.6](#). The same colour scheme will then be applied across all views.



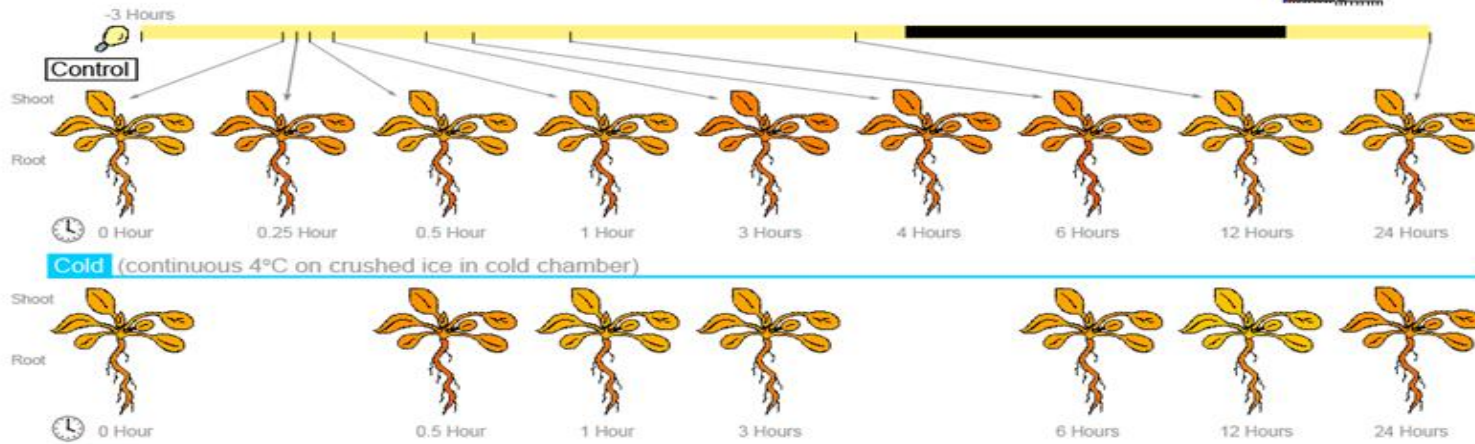
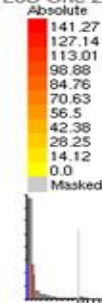
At2g37840 266080_at




- Plant material from 18 day old wild-type *Arabidopsis thaliana* plants of Columbia-0 ecotype was analyzed
- The seeds were sown on rafts in Magenta boxes containing MS-Agar-media. After 2 days in the cold room (4°C, dark), the boxes were transferred to a long day chamber. At day 11, the rafts were transferred in Magenta boxes containing MS-liquid-media.
- The plants were grown under long day conditions with 16/8 hrs light/dark, 24°C, 50% humidity and 150 µEinstein/cm² sec light intensity
- All measurements were taken in duplicates - the average of which is shown
- RNA was isolated and hybridized to the ATH1 GeneChip
- The data were normalized by GCOS normalization, TGT 100
- This study is part of the AtGenExpress project, funded by the DFG

Figure and data from Kilian et al. (2007, Plant Journal 50:347-63)

Arabidopsis eFP Browser at bar.utoronto.ca
Winter et al., 2007. PLoS One 2(8): e718



PPR



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Locus: AT2G17033

Date last modified 2007-04-17

TAIR Accession Locus:505006249

Representative Gene Model [AT2G17033.2](#)

Gene Model Type protein_coding

Other names:

Description pentatricopeptide (PPR) repeat-containing protein; CONTAINS InterPro DOMAIN/s: Pentatricopeptide repeat (InterPro:IPR002885), Smr protein/MutS2 C-terminal (InterPro:IPR002625); BEST Arabidopsis thaliana protein match is: Pentatricopeptide repeat (PPR) superfamily protein (TAIR:AT5G48730.1); Has 2363 Blast hits to 1770 proteins in 90 species: Archae - 0; Bacteria - 0; Metazoa - 2; Fungi - 0; Plants - 2346; Viruses - 0; Other Eukaryotes - 15 (source: NCBI BLINK).

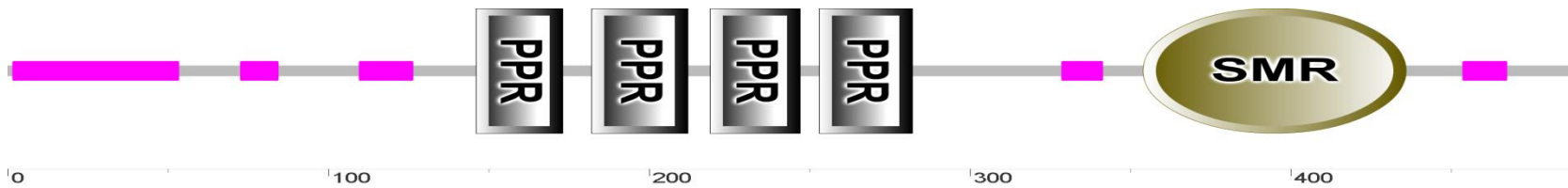
Other Gene Models [AT2G17033.1](#)

Map Detail Image

Annotations

category	relationship type	keyword
GO Biological Process	involved in	aromatic amino acid family biosynthetic process, iron-sulfur cluster assembly
GO Cellular Component	located in	mitochondrion
Growth and Developmental Stages	expressed during	4 anthesis stage, 4 leaf senescence stage, C globular stage, D bilateral stage, E expanded cotyledon stage, F mature embryo stage, L mature pollen stage, LP.02 two leaves visible stage, LP.04 four leaves visible stage, LP.06 six leaves visible stage, LP.08 eight leaves visible stage, LP.10 ten leaves visible stage, LP.12 twelve leaves visible stage, petal differentiation and expansion stage
Plant structure	expressed in	carpel, cauline leaf, collective leaf structure, cotyledon, flower, hypocotyl, inflorescence meristem, leaf apex, leaf lamina base, pedicel, petal, petiole, plant embryo, plant sperm cell, pollen, root, seed, sepal, shoot apex, shoot system, stamen, stem, vascular leaf

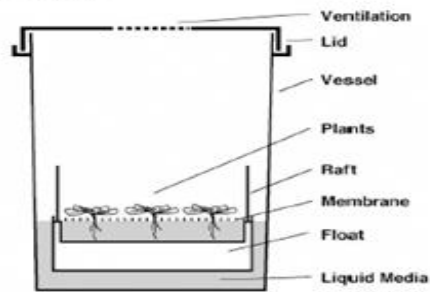
Annotation Detail



Data source: Abiotic Stress | Mode: Absolute | Primary gene ID: AT2G17033 | Secondary gene ID: At3g27340 | Signal Inresound: 186.84 | Go

- For ATH1 data, this probe set reaches its maximum expression level (expression potential) of 1219.92 in the Root data source.

At2g17033 263550_at

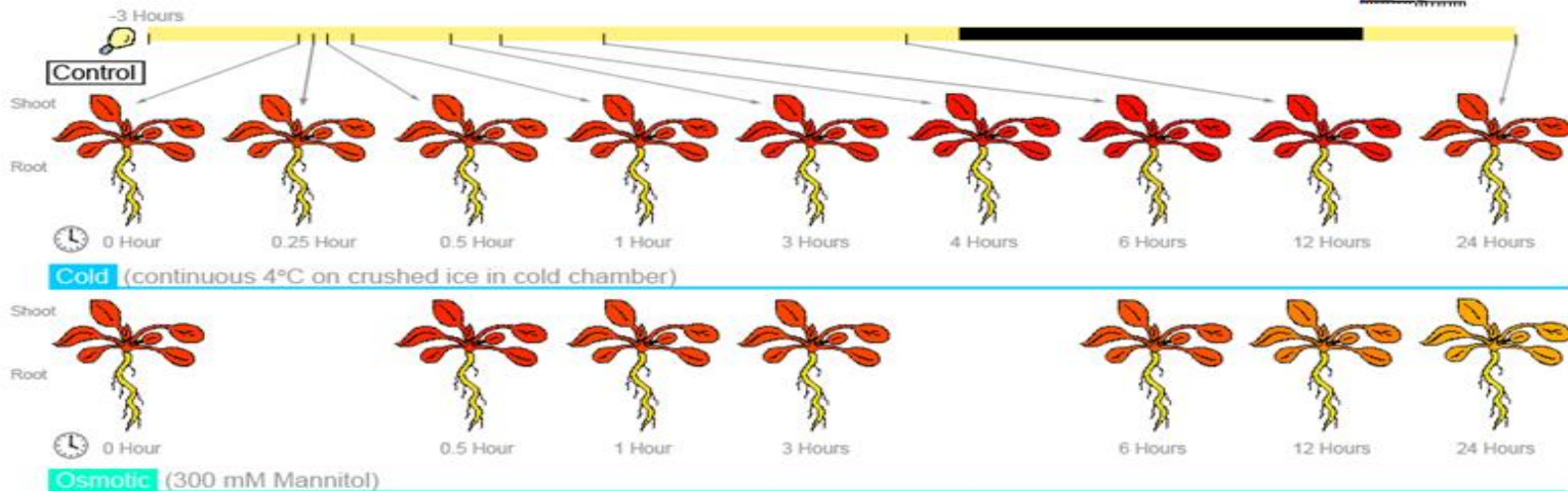
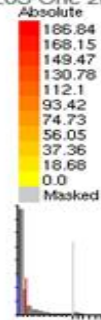


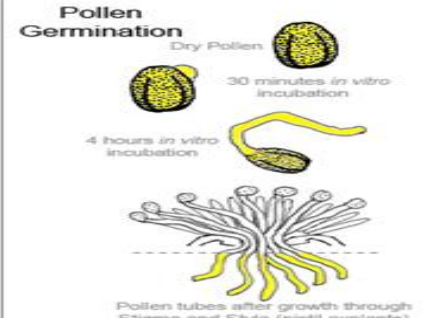
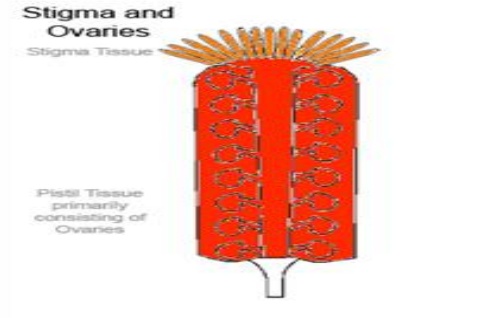
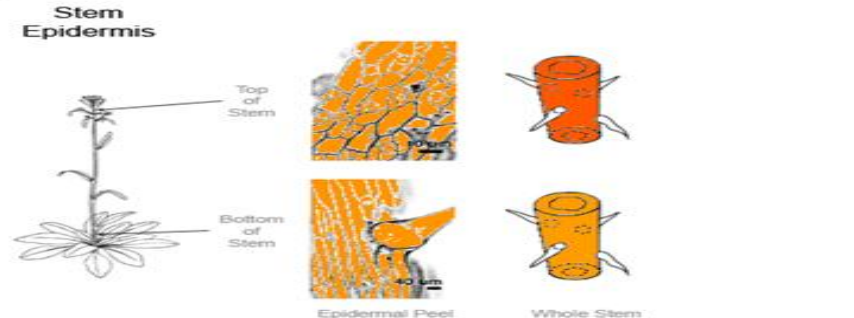
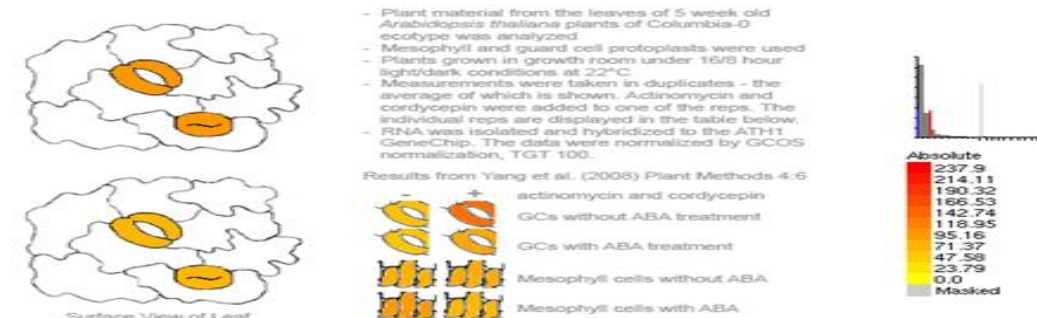
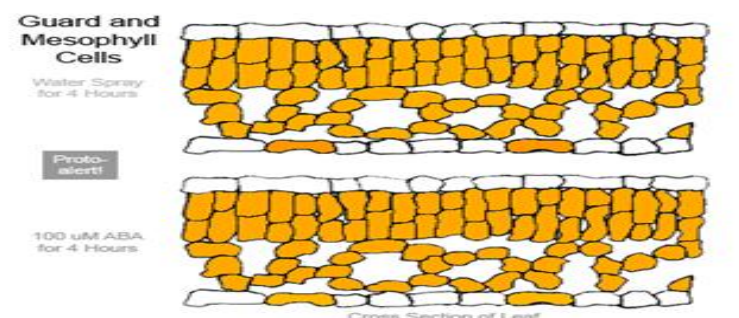
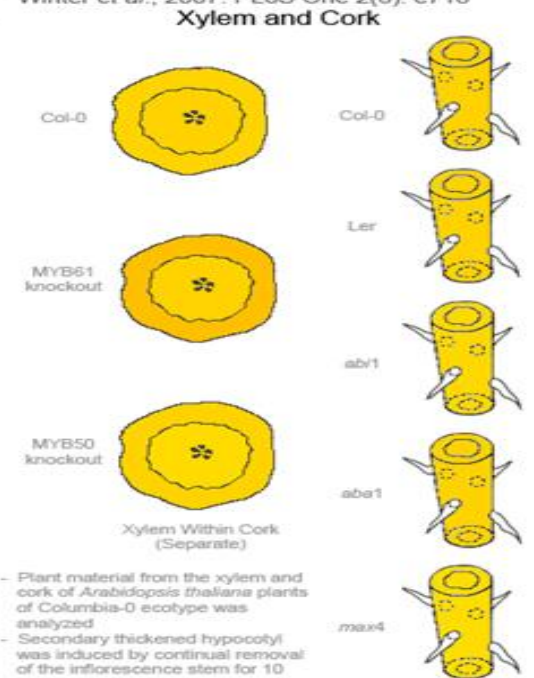
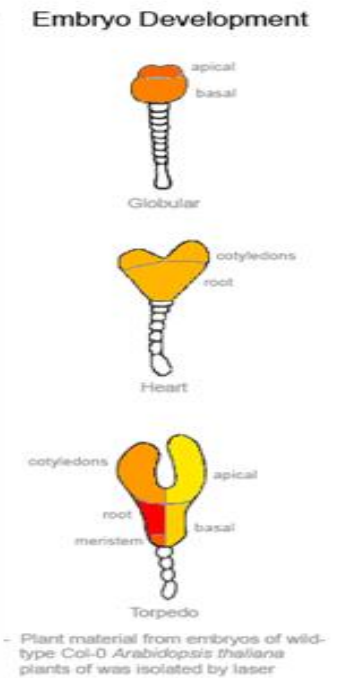
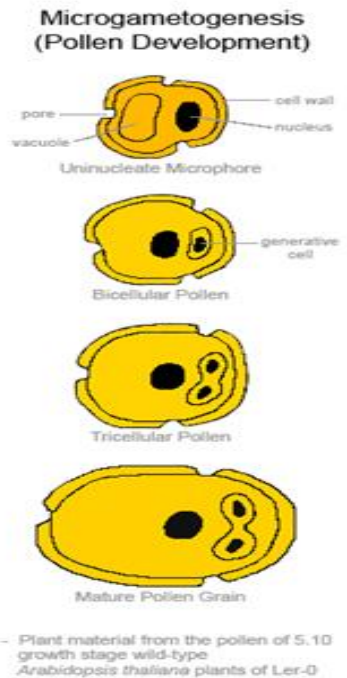
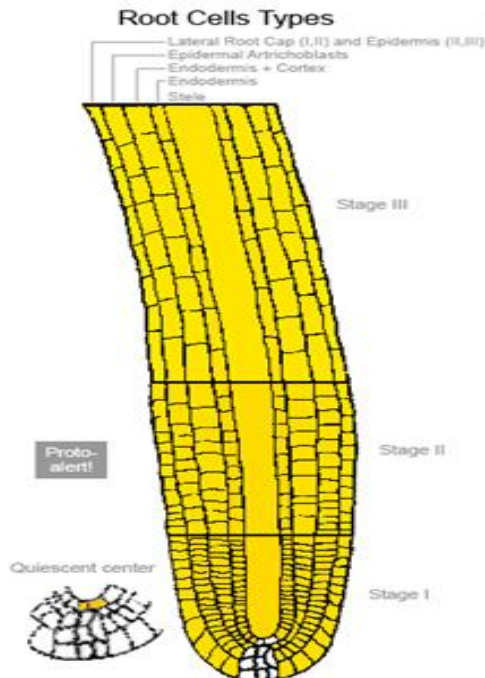
- Plant material from 18 day old wild-type *Arabidopsis thaliana* plants of Columbia-0 ecotype was analyzed
- The seeds were sown on rafts in Magenta boxes containing MS-Agar-media. After 2 days in the cold room (4°C, dark), the boxes were transferred to a long day chamber. At day 11, the rafts were transferred in Magenta boxes containing MS-liquid-media.
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Figure and data from Kilian et al. (2007, Plant Journal 50:347-63)



Arabidopsis eFP Browser at bar.utoronto.ca
Winter et al., 2007. PLoS One 2(8): e718





100

200

300

400

500

600


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[Search](#)[Browse](#)[Tools](#)[Portals](#)[Download](#)[Submit](#)[News](#)[ABRC
Stocks](#)**Locus: AT4G24190**

Date last modified 2012-09-17

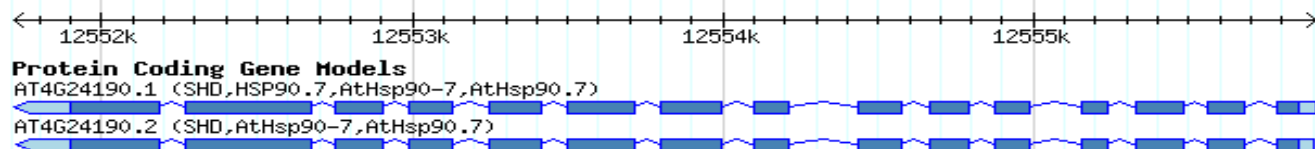
TAIR Accession Locus:2135887

Representative Gene Model [AT4G24190.1](#)

Gene Model Type protein_coding

Other names: ATHSP90-7, ATHSP90.7, HEAT SHOCK PROTEIN 90-7, HEAT SHOCK PROTEIN 90.7, HSP90.7, SHD, SHEPHERD

Description [?](#) encodes an ortholog of GRP94, an ER-resident HSP90-like protein and is involved in regulation of meristem size and organization. Single and double mutant analyses suggest that SHD may be required for the correct folding and/or complex formation of CLV proteins. Lines carrying recessive mutations in this locus exhibits expanded shoot meristems, disorganized root meristems, and defective pollen tube elongation. Transcript is detected in all tissues examined and is not induced by heat. Endoplasmic reticulum supports the protein secretory pathway and has a role in proliferating tissues.

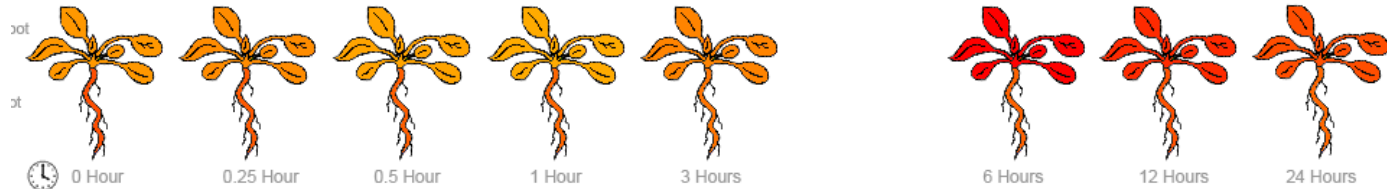
Other Gene Models [AT4G24190.2](#) (splice variant)**Map Detail Image****Annotations** [?](#)

category	relationship type	keyword
GO Biological Process	involved in	Golgi organization, N-terminal protein myristoylation, gluconeogenesis, glycolysis, hyperosmotic response, protein folding, protein secretion, regulation of meristem growth, regulation of meristem structural organization, response to cadmium ion, response to cold, response to endoplasmic reticulum stress, response to heat, response to high light intensity, response to hydrogen peroxide, response to salt stress, response to stress, response to temperature stimulus, response to water deprivation, water transport
GO Cellular Component	located in	apoplast, chloroplast, endoplasmic reticulum, membrane, mitochondrion, nucleus, plasma membrane, plasmodesma, vacuolar membrane, vacuole
GO Cellular Component	not located in	Golgi apparatus, cytosol

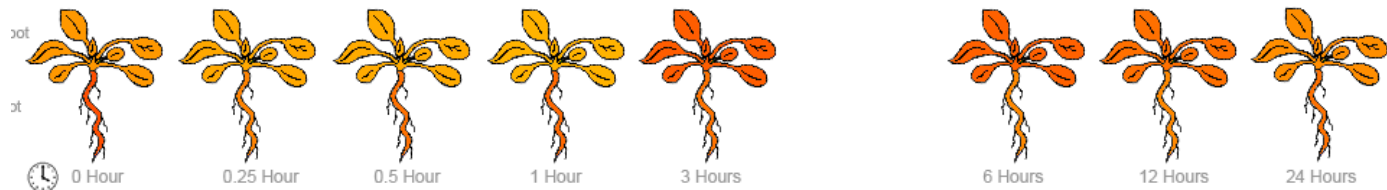
Oxidative (10 uM Methyl viologen)



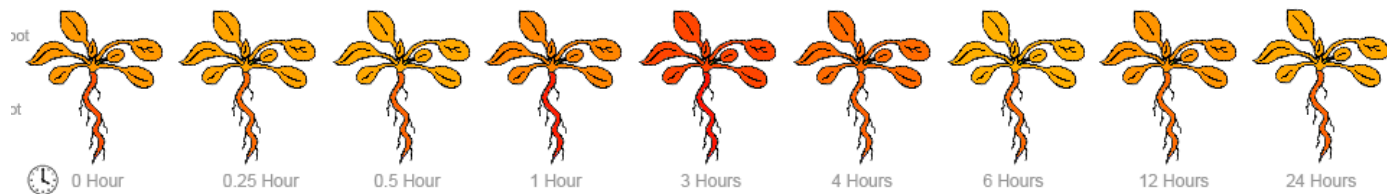
UV-B (15 minutes UV-B light field consisting of six fluorescent tubes filtered through transmission cutoff filters)



Wounding (punctuation of the leaves by 3 consecutive applications of a custom made pin-tool consisting of 16 needles)



Heat (3 hours at 38°C followed by recovery at 25°C)



Modelling

myWorkspace
Automated Mode
Alignment Mode
Project Mode

Tools

Template Identification
Domain Annotation
Structure Assessment
Template Library

Repository

Search by Sequence

SWISS-MODEL is a fully automated protein structure homology-modeling server, accessible via the ExPASy web server, or from the program DeepView (Swiss Pdb-Viewer). The purpose of this server is to make Protein Modelling accessible to all biochemists and molecular biologists worldwide.

What's new?

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- ... faster news on [Twitter](#)
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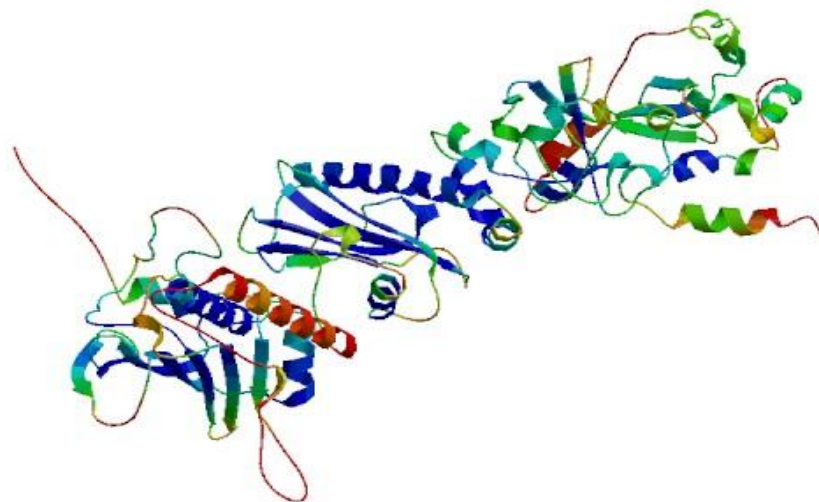
SWISS-MODEL Team

Torsten Schwede: Project Leader
Florian Kiefer: SWISS-MODEL Repository
Lorenza Bordoli: Method Development and user support
Konstantin Arnold: SWISS-MODEL Workspace

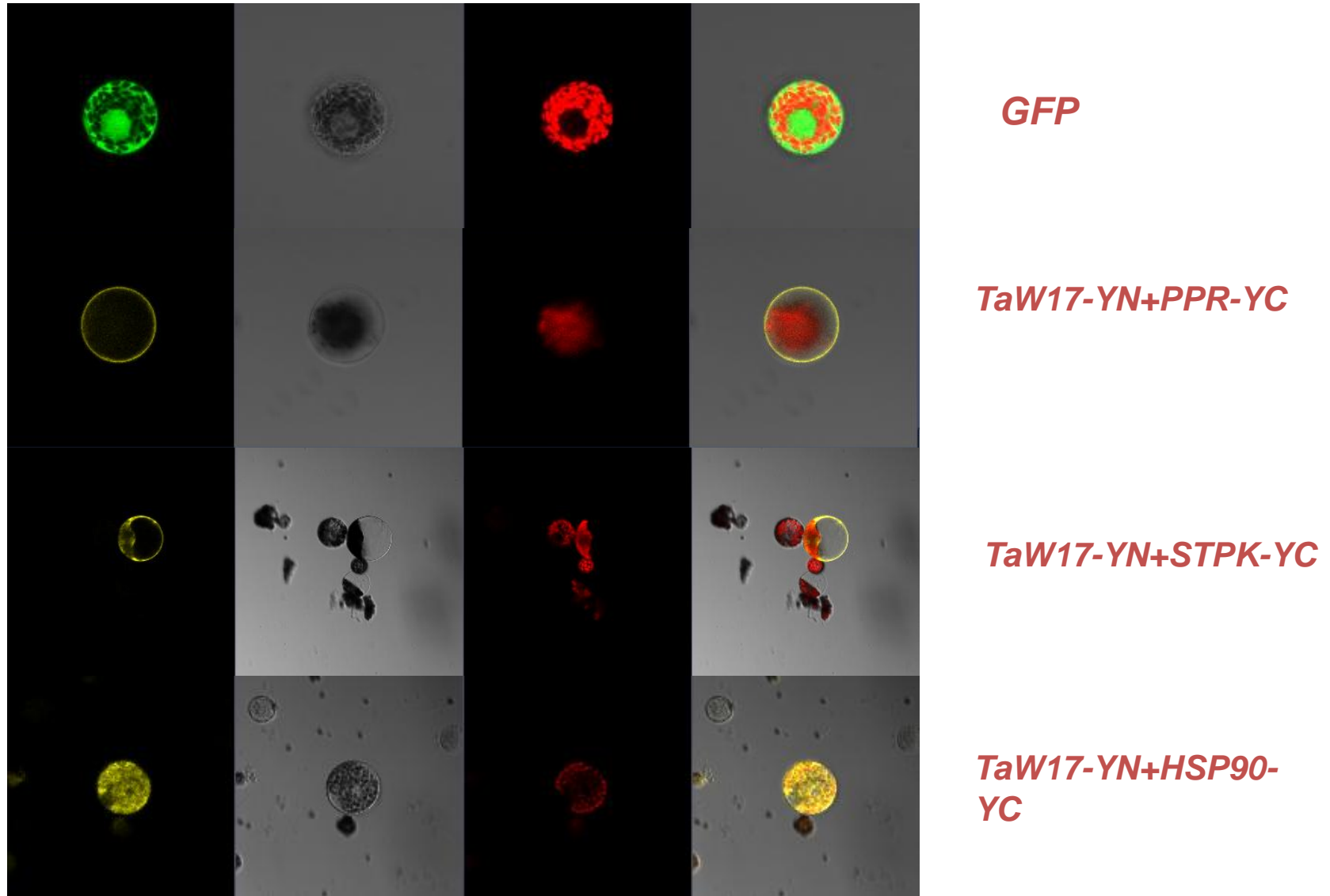
References:

When you publish or report results using SWISS-MODEL, please cite the relevant publications:

- Arnold K., Bordoli L., Kopp J., and Schwede T. (2006). The SWISS-MODEL Workspace: A web-based environment for protein structure homology modelling. *Bioinformatics*, 22,195-201.
- Kiefer F, Arnold K, Künzli M, Bordoli L, Schwede T (2009). The SWISS-MODEL Repository and associated resources. *Nucleic Acids Research*. 37, D387-D392.
- Brütsch, M. C. (1996). Protein modeling by E



W17+PPR W17+STPK W17+HSP90的 BIFC(双分子荧光互补)验证 (小麦原生质体)



- 目前已经初步验证互作，具体互作机制还不清楚，STPK、Hsp90、PPR已经筛选cDNA文库，下一步就是继续找到互作蛋白。

**Thank you for your
attention!**