

The Arabidopsis Information Resource (TAIR)

A Broad Overview

TAIR数据库在植物研究中的应用

Group 05

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The Arabidopsis Information Resource

The Arabidopsis Information Resource (TAIR) maintains a database of genetic and molecular biology data for the model higher plant *Arabidopsis thaliana*

TAIR全称是The Arabidopsis Information Resource拟南芥信息资源网站。

Data available from TAIR includes the complete genome sequence along with gene structure, gene product information, metabolism, gene expression, DNA and seed stocks, genome maps, genetic and physical markers, publications, and information about the Arabidopsis research community.

TAIR数据库可以为研究者提供完整的基因组序列、基因结构、基因产物、代谢过程、基因表达、DNA和种子库、遗传和物理标记、发表文献以及拟南芥研究的相关信息。



TAIR的特点(the features of TAIR):

- 信息全面** 涵盖基因组序列，基因结构、基因产物、DNA和突变体库、文献及拟南芥研究现状等多方面信息。
- 更新速度快** 基因产物功能每两周更新一次，基因结构信息每年更新1-2次。
- 数据量大** 从中可查阅拟南芥基因组中所有的29000个基因的最新功能信息
- 权威性高** 提供最权威的拟南芥基因组注释信息。
- 影响范围广** TAIR是从事模式植物拟南芥研究的国内外科研人员的最重要的参考网站，在业内具有广泛的影响。





Search

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Tools

Portals

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Gene Search

- Metabolic Pathways
- Textpresso full text
- Exact name search
- EST or BAC end
- Clone
- Person or lab
- Ecotype
- Gene**
- Germplasm
- Keyword
- Library
- Marker
- Polymorphisms
- Protein
- Seed stock
- DNA stock
- Vector

Home > Portals

FTP Directory: <ftp://ftp.arabidopsis.org/home/tair/>

[DIRUP]	Parent Directory		
[DIR]	ABRC	Jan 26 22:48	
[DIR]	ArDB	Aug 10 2006	
[DIR]	Data_Submission	Jan 04 2011	
[DIR]	Genes	Feb 15 23:00	
[DIR]	Images	Aug 23 2011	
[DIR]	Maps	May 14 18:38	
[DIR]	Microarrays	Dec 22 2010	
[DIR]	Ontologies	Aug 28 2006	
[DIR]	Pathways	Mar 13 23:52	
[DIR]	Polymorphisms	May 22 17:41	
[DIR]	Proteins	Sep 15 2011	
[DIR]	Protocols	Mar 25 2011	
[DIR]	Sequences	Aug 23 2011	
[DIR]	Software	Aug 16 2011	
[DIR]	User_Requests	Apr 04 01:15	
[DIR]	hide	Aug 23 2011	
[FILE]	hire	Aug 23 2011	66k [VIEW] [DOWNLOAD]
[DIR]	home	Aug 10 2006	
[DIR]	tmp	Dec 22 19:09	

Data Submission Overview

We encourage users of TAIR to share their data with their community. You can do this by submitting your data at one of these portals which will introduce you to resources.

Resources

About /

News Overview

This page provides news and events for the Arabidopsis research community.

Outr

Educational information about Arabidopsis, plant biology, genetics, genomics, methods in Arabidopsis research (protocols). Tools and tips for scientists, students and teachers.

Metabolomics Resources

Mutant and Mapping Resources

Nomenclature

Proteome Resources

ABRC Stocks Overview

The Arabidopsis Biological Resource Center (ABRC) at The Ohio State University provides the following services to the Arabidopsis community: 1) Collection, preservation and distribution of seeds; 2) Storage and distribution of DNA clones and libraries; and 3) Curation of data for stocks, orders and related information. Primary support of the ABRC is provided by a National Science Foundation grant.

intron lengths, alternative splicing and untranslated regions (UTRs), as well as on the function of



下面以PHYA为例
介绍TAIR的各种功能和应用
PHYA as an example to explain the
information and application in TAIR



1、gene information

Locus: AT1G09570

Date last modified 2012-04-17

TAIR Accession Locus:2012300

Representative Gene Model [AT1G09570.1](#)

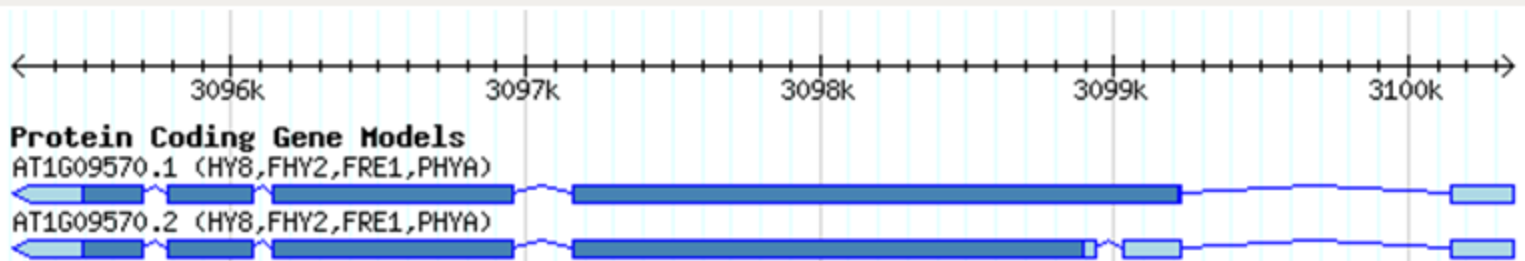
Gene Model Type protein_coding

Other names: ELONGATED HYPOCOTYL 8, FAR RED ELONGATED 1, FAR RED ELONGATED HYPOCOTYL 2, FHY2, FRE1, HY8, PHYA, PHYTOCHROME A

Description Light-labile cytoplasmic red/far-red light photoreceptor involved in the regulation of photomorphogenesis. It exists in two interconvertible forms: Pr and Pfr (active) and functions as a dimer. The N terminus carries a single tetrapyrrole chromophore, and the C terminus is involved in dimerization. It is the sole photoreceptor mediating the FR high irradiance response (HIR). Major regulator in red-light induction of phototropic enhancement. Involved in the regulation of de-etiolation. Involved in gravitropism and phototropism. Requires FHY1 for nuclear accumulation.

Other Gene Models [AT1G09570.2](#) (splice variant)

Map Detail Image





2、生物学功能(biological function)

Annotations ?	category	relationship type ?	keyword ?
	GO Biological Process	involved in	G-protein coupled receptor signaling pathway, detection of visible light, gravitropism, photomorphogenesis, phototropism, protein phosphorylation, red light signaling pathway, red, far-red light phototransduction, regulation of transcription, DNA-dependent, response to arsenic-containing substance, response to continuous far red light stimulus by the high-irradiance response system, response to very low fluence red light stimulus, signal transduction
	GO Biological Process	related to	response to far red light
	GO Cellular Component	located in	cytoplasm, nuclear body, nucleus
	GO Molecular Function	functions in	protein binding
	GO Molecular Function	has	G-protein coupled photoreceptor activity, far-red light photoreceptor activity, identical protein binding, protein binding, protein histidine kinase activity, red or far-red light photoreceptor activity, signal transducer activity
	Growth and Developmental Stages	expressed during	4 anthesis, 4 leaf senescence stage, C globular stage, D bilateral stage, E expanded cotyledon stage, F mature embryo stage, LP.02 two leaves visible, LP.04 four leaves visible, LP.06 six leaves visible, LP.08 eight leaves visible, LP.10 ten leaves visible, LP.12 twelve leaves visible, 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, pollen, root, seed, sepal, shoot apex, shoot system, stamen, stem, vascular leaf

Annotation Detail





3、芯片数据 (RNA Data)

RNA Data

Two-channel Arrays

array element name ⓘ	avg. log ratio (std. error)	avg. intensity (std. error)	expression viewer	spot history (SMD)
134J14	-0.036 (0.036)	4619.948 (198.865)	Viewer	138910
H10D1	-0.081 (0.046)	10045.494 (585.234)	Viewer	138742
157P15	-0.0010 (0.028)	9050.073 (371.03)	Viewer	140064
PHYA-3'	-0.127 (0.058)	2975.772 (158.413)	Viewer	415639
H6E7	-0.316 (0.08)	4278.746 (367.023)	Viewer	227347
M24C4	0.056 (0.034)	4640.704 (256.144)	Viewer	371701
G7B7	0.043 (0.048)	4990.146 (272.192)	Viewer	374383
91A19	-0.014 (0.021)	5241.245 (155.183)	Viewer	139767

One-channel Arrays

array element name ⓘ	avg. signal intensity (std. error)	avg. signal percentile (std. error)
14623_G_AT	290.169 (15.029)	76.805 (1.218)
264508_AT	459.366 (11.879)	80.976 (0.334)
14622_AT	1146.06 (46.29)	92.724 (0.405)





4、序列信息 (Sequence)

Nucleotide
Sequence ?

[full length CDS](#) [unknown_sequence](#) [full length genomic](#) [full length cDNA](#)

Protein Data ?

name	length (aa)	molecular weight	isoelectric point	domains(# of domains)
AT1G09570.1	1122	124499.8	6.2786	ATPase-like, ATP-binding domain:IPR003594(4) GAF:IPR003018(2) PAS:IPR000014(5) Phytochrome chromophore attachment domain:IPR016132(1) PAS fold-2:IPR013654(1) Phytochrome:IPR001294(10) Phytochrome, central region:IPR013515(1) Phytochrome chromophore binding site:IPR013516(1) PAS fold:IPR013767(2) Signal transduction histidine kinase, core:IPR005467(1) Phytochrome A/B/C/D/E:IPR012129(1) Signal transduction histidine kinase, subgroup 1, dimerisation/phosphoacceptor domain:IPR003661(2)



blastn results for 1 sequence searched against: TAIR10 Transcripts (-introns, +UTRs) (DNA) [New search](#)

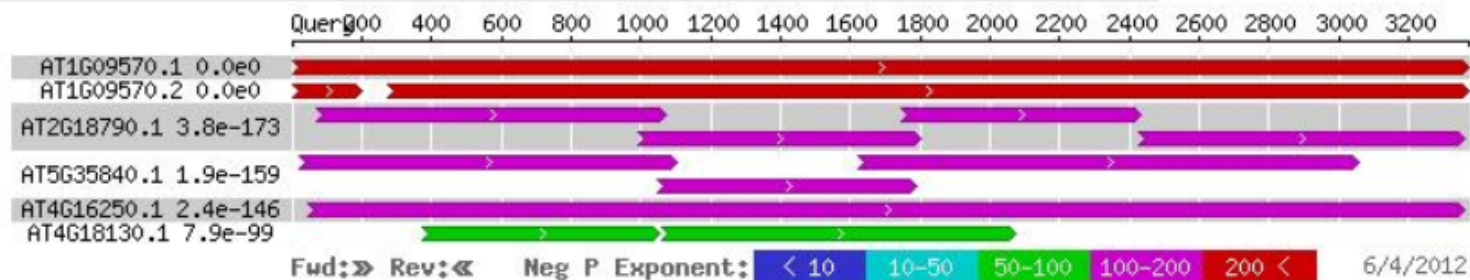
Title: optional, will be added to output for your use

>

Summary of BLAST Results [Help](#)

All hits shown.

Mouse-overs require JavaScript



WU-BLAST 2.0 query on *Arabidopsis* sequences

Query performed by TAIR ; for full BLAST options and parameters, refer to the [BLAST Documentation at NCBI](#)

Or upload a file

TCCTTTTGATCCCATTCCTGTGACATGAGGACTTCGTGAAAG ...

浏览...





5、基因定位 (gene location)

Map Locations							
	chrom	map	map type	coordinates	orientation	attrib	
	1	AGI	nuc_sequence	3095256 - 3100357 bp	reverse	details	
	1	F14.I9	assembly_unit	76859 - 81960 bp	reverse		
Map Links							
	Map Viewer	Sequence Viewer	GBrowse				
Genetic Markers							
	name	type	alias	chromosome	position	mapViewer	seqViewer
	PHYA	visible	FHY2, FRE1, HY8	1	16.0-16.0 cM	Map Viewer	
	SGCSNP107	hyb_based	SNP107	1	3097937-3097977 bp	Map Viewer	Sequence Viewer
				1	11.86-11.86 cM		
	PHYA	CAPS		1	3097740-3099087 bp	Map Viewer	Sequence Viewer
				1	11.35-11.35 cM		





SeqViewer Close-up View

[SeqViewer Home](#) | [Release Note](#) | [Print Version](#)

 Markers

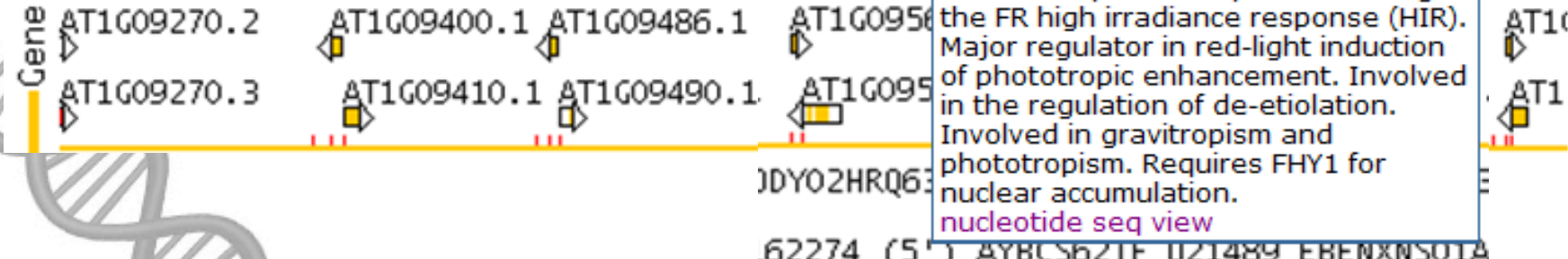
 Polymorphisms



```

ataatccatattatTTTTTgttcaaagttgactaaagacaggtgaagaagtcgaggttgatctaactctaaaagcttcaaaacaggtgaagctaatTTatct v A
gacttttcagataaaataatcaacttgagagactcttaacgatgggtctaataaaactgattacttaattaacatgataacttattttttacttcacac T
acatgtgcttcttctaacagaaaactaagtgtacttcatatggccagctaataagatctctgttaagttcgaagaactatgtttgcttcttcatggagtt 1
gagccaaagctaattgttgaaaccaagacttcttgcaacatagtcacgaatcatgcattaccttaataaccttaaaagaaggagattatatgaaactag G
atagaatatttgttgagtttctgccattatgataaaccatggaccgtaaacattagctcatttctcctatattacttattttgaatgatacatcatgaa 0
acaaaacactcaggaggagattagatagtcacatatttcacagcttcagaaaagagttcaacagaagatgtaaattggatggatatttcatcgttactg 9
aaatttgaaaacgaaaacaaaagcgataaggaagttacaagcaagaacaaccagtgactttttatatcaagccagacccttttcttttggggaCTA 5
CTGTGTTGCTGCGAGCGAGTTCGCGAGTGATAATGAAACTTGATTTCCAGCTTGTCTCAAGTACTGAACATCTCCATTTCATCAGCTTCACCAGTTCCGG 6
CTAACCATTAAGCTCAATCCTTCTTCTGACACATCTTCCTCAGTCCCAAACATTTGGTTTAGTAAAAACTCAGGTATCCCAGCTCCGGTATGCGTTAACc 0
tgttttcataatcccaatatectcaatgcactgtttttaacatcatattatgcattctgattatgaatataatctatTTTtactGATCTCTAGATTAGCAA .
GATGCACAGAACGCCCGAGCTGATCCTTCCCTCAGGGAAGCTGAAACAGTTAGCTGACCTCCGGATGGTGTAAAGTTTACAGCCATCAGCATGAAATCTGC 1
CAAGACTTGTGGAAGCCTAATACTGTCTCCATACAAAGTGTCCAGACATTACTTCTTCTCCGGTCTCATTGTTATCCGAACACTCTTCCGGTACTCTTC | 7
ATCATTACTTGTGGAAGCAGTCAACACTTCATTTAAGGTGAATTCTTTTCAATCCAAATCCAAGCATctgcacagtcaaattccaacataagaac | 0
acagataaaccatattttaaatggactttcattctagcatacCCTTCAATGATGCTTTCAAGATCCGAATCATCGAGGATCTTGCTTAGTTGCTTCTGAC | .
ATAACCGCGTAGTTTGCAAAATCCGCTCTTTGCTCTGGTCCTAATTCAGTACCCTCTATCATTTCCTTGTAAACATGATCCCAGATAGCGGATTCTGAT | 1
CTGTCTTTTTATGTATGCTAGAGCCTTTAGTCTCTTCACTGCGGTTCCGTCAGCTAAACGTTGAACATGGAGCGCTTGTGTCAGCTCATGGCTGGCAAGT |
TGCAGGAACAGAAAGACACCTGTCCACTACACCTTCCCTGTCCAGTTTCTTACTCACACACAAGACACTCCACATACTTGCACCTCTTGTAAAGAAAG |
CAAACGATACCTTCTCTGGATCTTGTGCTGGTTCACAGCATTGTTTCAGCAACAATCCCAAGGTTTACAAAGGCTTCTTGATTCTTTAGACGACAACATGACTT |
CTGCGTCCCAAATACTTCTCTTCTAAGAGCATTGTTGTCATCACTTCTCTCGCTTCAAAACCGGTTAACTTTGACATTGCTGGATTCCACTCTGTGCACCAT |
  
```

3



is the sole photoreceptor mediating the FR high irradiance response (HIR). Major regulator in red-light induction of phototropic enhancement. Involved in the regulation of de-etiolation. Involved in gravitropism and phototropism. Requires FHY1 for nuclear accumulation.

[nucleotide seq view](#)



6、突变体概述 (polymorphism):

Polymorphism ?	name ?	type ?	polymorphism site	allele type ?
Showing 15 of 45 entries (see all)	ars4	insertion	intron	unknown
	eid4	substitution	unknown	hypermorphic
	GK-437D07-018192	insertion	promoter	unknown
	GK-483H11-019729	insertion	intron	unknown
	GK-508F06-019540	insertion	intron	unknown
	ossowski_1129689	insertion	intron	unknown
	ossowski_16555	substitution	intron	unknown
	ossowski_16556	substitution	intron	unknown
	ossowski_16557	substitution	promoter	unknown
	ossowski_16558	substitution	promoter	unknown
	PERL0019826	substitution	5'UTR	unknown
	PERL0019827	substitution	5'UTR	unknown
	PERL0019828	substitution	coding_region	unknown
	PERL0019830	substitution	coding_region	unknown
PERL0019834	substitution	coding_region	unknown	



突变体具体信息(germplasm)

Germplasm	name	polymorphisms	background	stock name	select
Showing 15 of 26 entries (see all)	CS6223	phyA-211		CS6223	<input type="checkbox"/>
images None available					
phenotypes ⓘ <ul style="list-style-type: none"> • Arsenic accumulation appeared slightly decreased in the mutants, but it did not differ significantly from that of wild type. Sung, Dong-Yul, Lee, David, Harris, Hugh, Raab, Andrea, Feldmann, Jörg, Meharg, Andrew, Kumabe, Brya(2007) • Mutant showed no light dependence of arsenic tolerance, whereas wild-type seedlings showed an increased arsenate tolerance when grown in the dark compared with WT seedlings grown in the light. Sung, Dong-Yul, Lee, David, Harris, Hugh, Raab, Andrea, Feldmann, Jörg, Meharg, Andrew, Kumabe, Brya(2007) • When grown under constant light, mutant seeds showed a significantly higher rate of survival than WT seeds in the presence of arsenate. Sung, Dong-Yul, Lee, David, Harris, Hugh, Raab, Andrea, Feldmann, Jörg, Meharg, Andrew, Kumabe, Brya(2007) • Whereas, in WT seeds, germination could be promoted by a single red or far-red pulse given after 48 h but not after 3 h (matching the time of highest phyA abundance), the germination was no longer promoted in the mutant in either treatment. Rösler, Jutta, Klein, Ilse, Zeidler, Mathias(2007) • strong allele; long hypocotyl and unexpanded cotyledons in far-red light; hypocotyl elongation not affected in white or red light; reduced ability to de-etiolate after growth in the dark compared to wild type; mature plants grown under continuous white light have similar phenotype and flowering time to wild type Phenotype curated by ABRC. 					

CS6224	phyA-201; phyB-5	CS6224	<input type="checkbox"/>
--------	------------------	--------	--------------------------

images



phenotypes

 ⓘ

- double mutant; slightly longer hypocotyl than the phy B single mutant in white light; longer hypocotyl than the phyB single mutant in red light and same length as that of the phyA mutant in far-red light; poorly developed cotyledons in red light unlike the single mutants, reduced red-light induction of CAB gene expression and reduced chlorophyll induction. Phenotype curated by ABRC.





7、相关链接 external links

链接种类	功能
AtGDB View	植物基因组学数据库，基因比对到基因组上，基因注释
AceView	链接到NCBI,非冗余序列基因全面信息
Agrisera (antibody)	商业化抗体
AtGenExpress Visualization Tool	基因表达量（表达时期，不同处理）
AtProteome	蛋白表达信息（培养条件，不同组织）
ATTED-II	基因表达调控网站
BioGRID	蛋白质相互作用
e-FP Browser	基因表达量（不同部位，处理等）
Genevestigator Expression Data	基因表达量
InParanoid Ortholog Groups	在真核生物里面的同源基因
IntAct (Protein Interaction Database at EBI)	蛋白相互作用
MIPS	慕尼黑蛋白序列信息中心

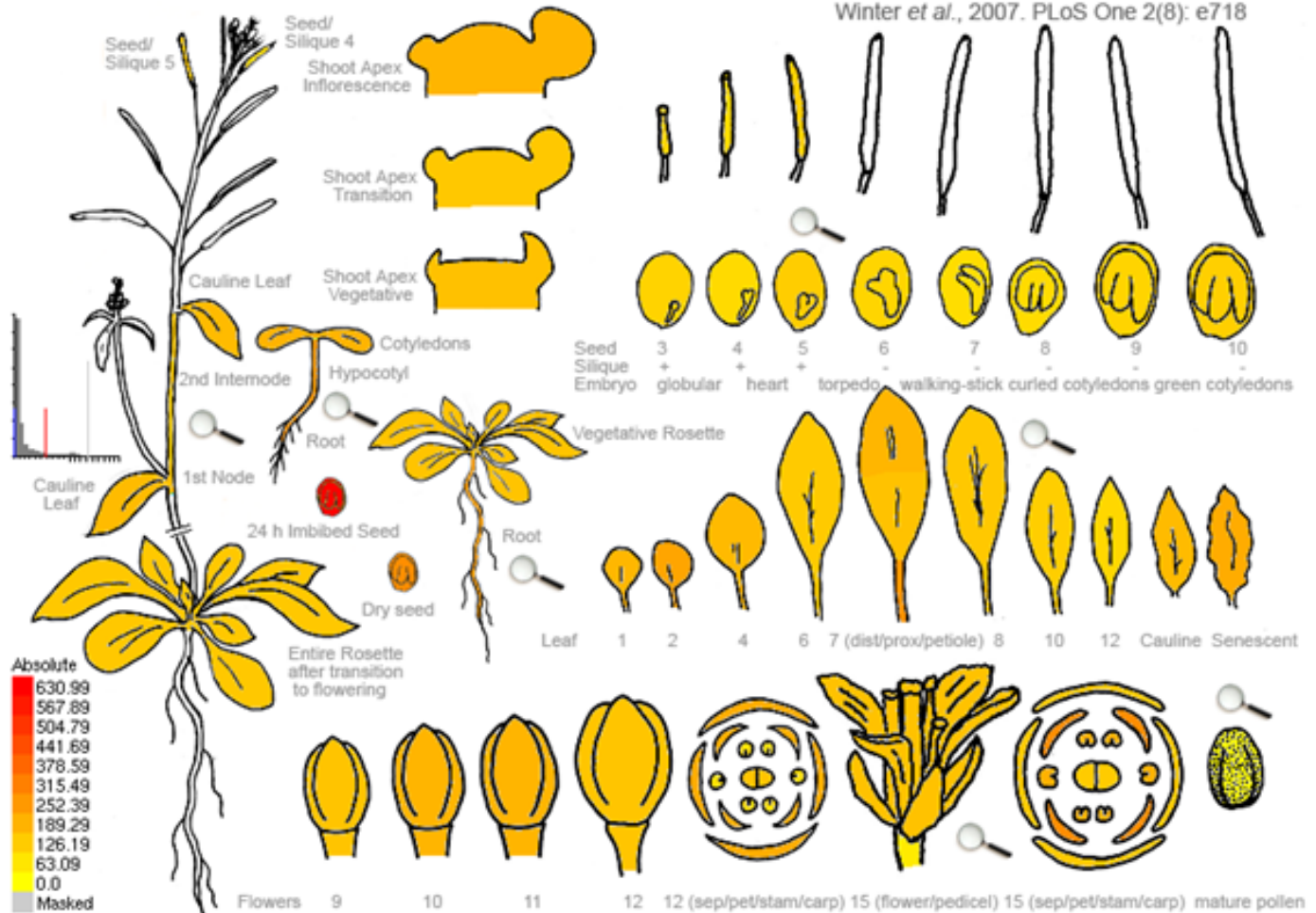


7、相关链接

链接种类	功能
NASCArrays Digital Northern	NASC芯片数据库
NASCArrays Spot History	基因表达芯片数据
NCBI-Entrez Gene	NCBI数据库中的基因全面信息
PGDD duplications and orthologs	植物基因组重复数据库
Phytozome Plant Gene Families	同源基因数据库
Plant Proteome Database	蛋白质组学数据库（蛋白信息预测，相关基因，组学数据等）
Plaza	比较基因组学（比较全面的基因信息）
Salk SNP Viewer	SNP位点
T-DNA Express	T-DNA插入基因图谱
The Subcellular Location of Proteins in Arabidopsis Database (SUBA)	蛋白的亚细胞定位
UDelaware Small RNA/PARE/Methylation	基因分析(small RNA 和mRNA)
View Aracyc reaction 2.7.13.3-RXN (2.7.13.3)	基因编码的蛋白所参与的反应

At1g09570 264508_at *flr2*

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



eFP Browser by B. Vinegar, drawn by J. Alls and N. Provart. Data from Gene Expression Map of Arabidopsis Development: Schmid et al., 2005, Nat. Gen. 37:501, and the Nambara lab for the imbibed and dry seed stages. Data are normalized by the GCOS method, TGT value of 100. Most tissues were sampled in triplicate.



NCBI-Entrez Gene

http://www.ncbi.nlm.nih.gov/sites/entrez?

db=gene&cmd=Retrieve&dopt=full_report&list_uids=837483

Display Settings: Full Report

[Send to:](#)

PHYA phytochrome A [*Arabidopsis thaliana*]

Gene ID: 837483, updated on 8-May-2012

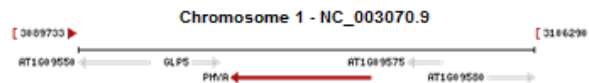
Summary

Gene symbol PHYA
Gene description phytochrome A
Primary source [TAIR:AT1G09570](#)
Locus tag AT1G09570
Gene type protein coding
RefSeq status REVIEWED
Organism [Arabidopsis thaliana \(ecotype: Columbia\)](#)
Lineage Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; malvids; Brassicales; Brassicaceae; Camelineae; Arabidopsis
Also known as ELONGATED HYPOCOTYL 8; F14J9.23; F14J9_23; FAR RED ELONGATED 1; FAR RED ELONGATED HYPOCOTYL 2; FHY2; FRE1; HY8; PHYA; phytochrome A
Summary Light-labile cytoplasmic red/far-red light photoreceptor involved in the regulation of photomorphogenesis. It exists in two inter-convertible forms: Pr and Pfr (active) and functions as a dimer. The N terminus carries a single tetrapyrrole chromophore, and the C terminus is involved in dimerization. It is the sole photoreceptor mediating the FR high irradiance response (HIR). Major regulator in red-light induction of phototropic enhancement. Involved in the regulation of de-etiolation. Involved in gravitropism and phototropism. Requires FHY1 for nuclear accumulation.

Genomic context

Location: chromosome: 1
Sequence: Chromosome: 1; NC_003070.9 (3095256..3100357, complement)

See PHYA in [MapViewer](#)



Genomic regions, transcripts, and products

Genomic Sequence

Go to [reference sequence details](#)

Go to [nucleotide](#) [Graphics](#) [FASTA](#) [GenBank](#)

The Subcellular Location of Proteins in Arabidopsis Database (SUBA):
<http://suba.plantenergy.uwa.edu.au/flatfile.php?id=AT1G09570>

Subcellular Localization	GFP	MS/MS	Annotators	Predictors
	cytosol : 21169346 cytosol : 20739301 cytosol : 16333572 cytosol : 15155879 cytosol : 12119373 nucleus : 21169346 nucleus : 16333572 nucleus : 12119377 nucleus : 12119373	no data	no data	iPSORT : mitochondrion LOCtree : no data MitoPred : no data Mitoprot 2 : no data MultiLoc : mitochondrion Peroxp : no data Predotar : no data SubLoc : cytosol TargetP : mitochondrion WoLFPSORT : plastid





[IntAct \(Protein Interaction Database at EBI\):](http://www.ebi.ac.uk/intact/pages/interactions/interactions.xhtml;jsessionid=1ayh1osuehax31pc11u7v743zz?conversationContext=1)

[http://www.ebi.ac.uk/intact/pages/interactions/](http://www.ebi.ac.uk/intact/pages/interactions/interactions.xhtml;jsessionid=1ayh1osuehax31pc11u7v743zz?conversationContext=1)

[interactions.xhtml;jsessionid=1ayh1osuehax31pc11u7v743zz?conversationContext=1](http://www.ebi.ac.uk/intact/pages/interactions/interactions.xhtml;jsessionid=1ayh1osuehax31pc11u7v743zz?conversationContext=1)

Home	Search	Interactions (31)	Browse	Lists	Interaction Details	Molecule View	Graph					
Browse by taxonomy , gene ontology .												
> 31 binary interactions were found in IntAct. 2 of them are originated from spoke expanded co-complexes and you may want to filter them.												
> No results in other databases.												
If the table below looks too crowded, you can switch to a Minimal or Basic table view.												
-- Select format to Download -- Download Show/hide columns <input checked="" type="checkbox"/> Show icons Table view												
#	Molecule 'A'	Links 'A'	Molecule 'B'	Links 'B'	Species 'A'	Species 'B'	Publication Identifier	Interaction Type	Interaction Detection Method	Interaction AC		
	1	PHYA iPR BA UN	UniProt Dasty2	PKS1 iPR FY UN	UniProt Dasty2	3702	3702	10348744	physical association	two hybrid	EBI-626207	ir
	2	iPR BA UN		iPR FY UN			10348744	physical association	two hybrid	EBI-626220	ir	
	3	iPR BA UN		iPR FY UN			10348744	physical association	pull down	EBI-626243	ir	
	4	PHYA iPR BA UN	UniProt Dasty2	CRY1 iPR FY UN	UniProt Dasty2	3702	3702	9651577	physical association	two hybrid	EBI-2315450	ir
	5	PHYA iPR BA UN	UniProt Dasty2	NDPK2 iPR FY UN	UniProt Dasty2	3702	3702	10524631	physical association	two hybrid	EBI-626459	ir
	6	iPR BA UN		iPR FY UN			10524631	physical association	two hybrid	EBI-626485	ir	
	7	iPR BA UN		iPR FY UN			10524631	physical association	two hybrid	EBI-626490	ir	



8、相关作者和文献(Authors and publications)

Attribution ⓘ				
type	name		date	
submitted_by	Joseph Ecker		06/24/2002	
submitted_by	SSP Consortium: Salk, Stanford, PGEC		06/24/2002	
Communication				
name	author name		date	
Functional Genomic Characterization Effort	Ecker/Davis/Theologis Salk/Stanford/PGEC Consortium		06/24/2002	
Functional Genomic Characterization Effort	Joseph R. Ecker		06/24/2002	
Publication ⓘ				
title	source	associated loci		date
A quadruple photoreceptor mutant still keeps track of time.	CURRENT BIOLOGY	AT1G04400 AT1G09570 AT2G18790 AT4G08920		2000
RSF1, an Arabidopsis Locus Implicated in Phytochrome A Signaling.	PLANT PHYSIOLOGY	AT1G02340 AT1G09570		2000
Light-induced stomatal movement of selected Arabidopsis thaliana mutants.	JOURNAL OF EXPERIMENTAL BOTANY	AT1G05180 AT1G08550 AT1G09570 AT2G26330		2000
Phytochrome A resets the circadian clock and delays tuber formation under long days in potato.	THE PLANT JOURNAL	AT1G09570 AT2G18790		2000
FIN219, an auxin-regulated gene, defines a link between phytochrome A and the downstream regulator COP1 in light control of Arabidopsis development.	GENES AND DEVELOPMENT	AT1G09570 AT2G32950 AT2G37678 AT2G46370		2000
Plant blue-light receptors.	TRENDS IN PLANT SCIENCE	AT1G04400 AT1G09570 AT4G08920		2000
Sustained but not transient phytochrome A signaling targets a region of an Lhcb1*2 promoter not necessary for phytochrome B action.	THE PLANT CELL	AT1G09570 AT2G18790		2000
Two photobiological pathways of phytochrome A activity, only one of which shows dominant negative suppression by phytochrome B.	PHOTOCHEMISTRY AND PHOTOBIOLOGY	AT1G09570 AT2G18790		2000

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