

# 参与拟南芥先天免疫应答 的多肽PEP1的初步分析

Preliminary analysis of the peptide PEP1 involved  
in the innate immune response of Arabidopsis

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背景

Background



## 背景

Background

PEP1是在拟南芥中发现的参与植物**先天免疫应答**的多肽，属于**十字花科激发子肽家族**。当植物受到损伤，或者有茉莉酸甲酯或乙烯诱导时，该多肽会被诱导表达。PEP1含有92个氨基酸，可以激活防御基因防御素(PDF1.2)的转录并激活H<sub>2</sub>O<sub>2</sub>的合成，这两种基因都是先天免疫应答的组成部分。

另外研究发现，敲除拟南芥PEP1基因会延缓叶片的衰老，过表达则会促进叶片衰老；将一定浓度的PEP1喷施到烟草叶片表面，多次喷施后烟草叶片也出现提前落黄的现象。



# 初步分析

Initial Analysis



# UniProtKB - Q9LV87 (PEP1\_ARATH)

Display [Help video](#) [BLAST](#) [Align](#) [Format](#) [Add to basket](#) [History](#)

- Entry
- Publications
- Feature viewer
- Feature table

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[None](#)

Protein	<b>Elicitor peptide 1</b>
Gene	<b>PEP1</b>
Organism	<i>Arabidopsis thaliana</i> (Mouse-ear cress)
Status	Reviewed - Annotation score: ●●●●● - Exp

Function:

```
>sp|Q9LV87|PEP1_ARATH
Elicitor peptide 1
OS=Arabidopsis thaliana
OX=3702 GN=PEP1 PE=1 SV=1
MEKSDRRSEESH LWIPLQCLDQTLRAILK
CLGLFHQDSPTTSSPGTSKQPKEEKEDVT
MEKEEVVWTSRATKVKAKQRGKEKVSSGR
PGQHN
```



# Analyzed by NCBI

BLASTP programs search protein d

### Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s) [?](#) [Clear](#)

```
OX=3702 GN=PEP1 PE=1 SV=1
MEKSDRRSEESHLEWIPQLCLDQTLRAILKCLGLFHQDSPTTSSPGTSKQPK
EEKEDVTME
KEEVVTSRATKV/KAKQRGKEKVVSSGRPGQHN
```

Query subrange [?](#)

From

To

Or, upload file  未选择任何文件 [?](#)

Job Title

Enter a descriptive title for your BLAST search [?](#)

Align two or more sequences [?](#)

### Choose Search Set

Database  [?](#)

Organism Optional   exclude [Add organism](#)

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown. [?](#)

Exclude Optional  Models (XM/XP)  Non-redundant RefSeq proteins (WP)  Uncultured/environmental sample sequ

# Analyzed by NCBI



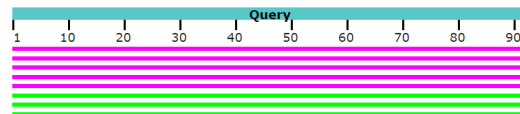
	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	precursor of peptide 1 [Arabidopsis thaliana]	Arabidopsis thaliana	152	152	100%	4e-50	100.00%	92	NP_569001.1
<input checked="" type="checkbox"/>	elicitor peptide 1 [Eutrema salsugineum]	Eutrema salsugineum	96.8	96.8	100%	2e-27	58.65%	127	XP_006394100.2
<input type="checkbox"/>	PREDICTED: elicitor peptide 1-like [Camelina sativa]	Camelina sativa	94.4	94.4	100%	2e-26	65.38%	103	XP_010444447.1
<input type="checkbox"/>	PREDICTED: elicitor peptide 1-like [Camelina sativa]	Camelina sativa	90.2	90.2	100%	8e-25	69.00%	98	XP_010484288.1
<input type="checkbox"/>	PREDICTED: elicitor peptide 1-like [Camelina sativa]	Camelina sativa	88.4	88.4	100%	5e-24	66.99%	102	XP_010462607.1
<input checked="" type="checkbox"/>	elicitor peptide 1 [Capsella rubella]	Capsella rubella	84.4	84.4	100%	2e-22	57.76%	116	XP_006281339.1
<input checked="" type="checkbox"/>	elicitor peptide 1 [Brassica rapa]	Brassica rapa	83.4	83.4	100%	5e-22	45.37%	108	XP_009150567.1
<input checked="" type="checkbox"/>	elicitor peptide 2 precursor [Arabidopsis thaliana]	Arabidopsis thaliana	80.5	80.5	100%	9e-21	54.17%	109	NP_569000.1
<input type="checkbox"/>	PREDICTED: elicitor peptide 1-like [Brassica oleracea var. oleracea]	Brassica oleracea var. oleracea	80.0	80.0	100%	1e-20	44.34%	106	XP_013626305.1
<input checked="" type="checkbox"/>	elicitor peptide 1-like [Brassica napus]	Brassica napus	79.4	79.4	100%	2e-20	42.59%	108	XP_013847069.1
<input type="checkbox"/>	PREDICTED: elicitor peptide 1-like [Raphanus sativus]	Raphanus sativus	78.6	78.6	100%	5e-20	44.44%	108	XP_018488921.1
<input type="checkbox"/>	PREDICTED: elicitor peptide 1-like [Raphanus sativus]	Raphanus sativus	78.1	78.1	100%	8e-20	50.48%	109	XP_018439357.1
<input type="checkbox"/>	PREDICTED: elicitor peptide 1-like [Brassica oleracea var. oleracea]	Brassica oleracea var. oleracea	77.3	77.3	100%	1e-19	43.40%	106	XP_013622601.1
<input type="checkbox"/>	PREDICTED: LOW QUALITY PROTEIN: elicitor peptide 2-like [Camelina sativa]	Camelina sativa	73.6	73.6	100%	6e-18	51.06%	114	XP_019094246.1
<input type="checkbox"/>	PREDICTED: elicitor peptide 2-like [Camelina sativa]	Camelina sativa	70.0	70.0	100%	2e-16	48.94%	113	XP_010444446.1
<input checked="" type="checkbox"/>	elicitor peptide 2 [Arabidopsis lyrata subsp. lyrata]	Arabidopsis lyrata subsp. lyrata	68.7	68.7	100%	6e-16	53.76%	112	XP_002866300.1
<input type="checkbox"/>	PREDICTED: uncharacterized protein LOC104763670 [Camelina sativa]	Camelina sativa	69.7	69.7	98%	1e-15	48.39%	233	XP_010485316.1
<input type="checkbox"/>	PREDICTED: elicitor peptide 1-like [Brassica oleracea var. oleracea]	Brassica oleracea var. oleracea	63.1	63.1	100%	1e-13	49.07%	112	XP_013819427.1
<input checked="" type="checkbox"/>	elicitor peptide 1-like [Brassica napus]	Brassica napus	61.6	61.6	100%	5e-13	49.07%	112	XP_013875421.1



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

Query seq. | H E K S D A R S E E S H L W I P L Q C L Q O T L R A I L K V C L G L F H D S P I T T S S P Q T S K O P K E E K E D V T H E K E E V V V T S R A T K V K A K O R G E K V S S O R P O H N  
 Specific hits | DUF5306  
 Superfamilies | DUF5306 superfamily

Distribution of the top 8 Blast Hits on subject sequences





# Analyzed by MEGA



M7: Sequence Data Explorer

Data Display Search Groups Highlight Statistics Help

MEGA XL CSV [Icons] UUC [Icons] C V Pi S 0 2 4 Special [Icons]

Name	Sequence
1. NP 569001.1 precursor of peptide 1 Arabidopsis thaliana	- M E K S D R R S E E S - H L W I - P L Q C L D Q T L R A I L K C L G
2. XP 006394100.2 elicitor peptide 1 Eutrema salsgineum	S M E K L D K R S E E E T Y L W V - P F Q F L D Q T L R A I F R C L G
3. XP 006281339.1 elicitor peptide 1 Capsella rubella	- M E K S D R Q S E E A T Y L W I - P L Q Y L D Q T L K A I L R C L G
4. XP 009150567.1 elicitor peptide 1 Brassica rapa	- M E K V E R Q S E E A S Y L W L - P F H F L N Q T I K A I L R C L G
5. NP 569000.1 elicitor peptide 2 precursor Arabidopsis thaliana	- M E K L D K R R E E E T Y L W I - P V Q F L D Q A L I A V L K C I G
6. XP 013647069.1 elicitor peptide 1-like Brassica napus	- M E K V E R Q S E E A S Y L W L - P F H F L N Q T I K A I L R C L G
7. XP 002866300.1 elicitor peptide 2 Arabidopsis lyrata subsp. lyrata	- M E K L D R R S E E E T Y L W I - S F Q F L D Q T L I A I F K C L G
8. XP 013675421.1 elicitor peptide 1-like Brassica napus	- M E K Y E R L S E E E T Y W W M I P F K F L D Q T L K A I F K C L G

1/161 Conserved: 25/161 Data

M7: Sequence Data Explorer

Data Display Search Groups Highlight Statistics Help

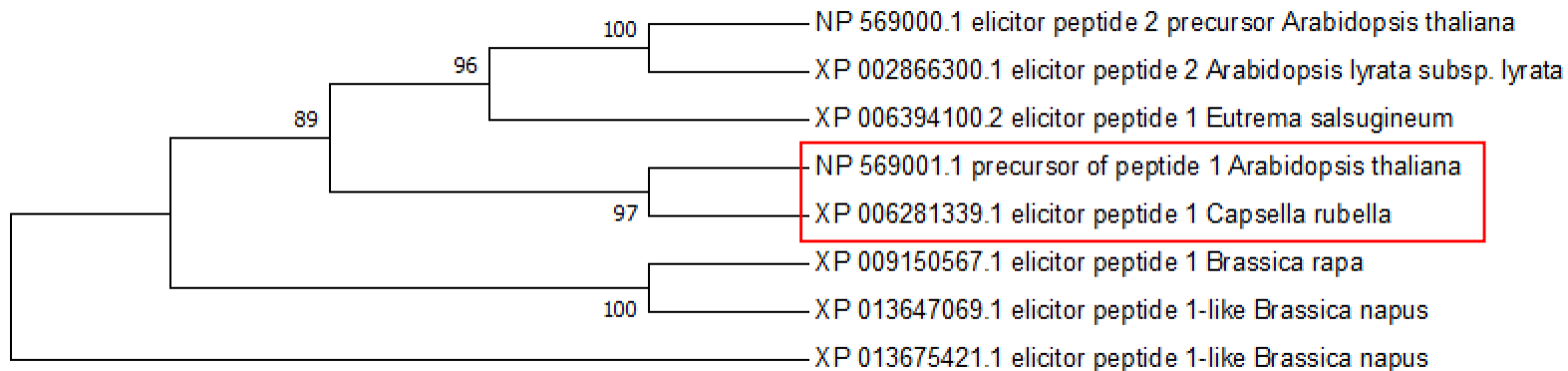
MEGA XL CSV [Icons] UUC [Icons] C V Pi S 0 2 4 Special [Icons]

Name	Sequence
1. NP 569001.1 precursor of peptide 1 Arabidopsis thaliana	- - - - V V V T S R A T K V K A K Q R G K E K V S S G R P G Q H N -
2. XP 006394100.2 elicitor peptide 1 Eutrema salsgineum	G G K D G V V V S S R G I K V R A K K K G K E R V S S G R P G Q H H -
3. XP 006281339.1 elicitor peptide 1 Capsella rubella	G L N R G V V V K S R A T K V Q A K S R G K E T V S R G R R G Q H H -
4. XP 009150567.1 elicitor peptide 1 Brassica rapa	G S K N G I I I T S R G T K V N A K R K E K A K V S S G R P G K H H -
5. NP 569000.1 elicitor peptide 2 precursor Arabidopsis thaliana	- - - - V V V L L R D N K A K S K K R D K E K P S S G R P G Q T N S -
6. XP 013647069.1 elicitor peptide 1-like Brassica napus	A I K N G I I I T S R G T K V N A K R K E K A K V S S G R P G K H H -
7. XP 002866300.1 elicitor peptide 2 Arabidopsis lyrata subsp. lyrata	- - - - V V L S T R G K K P K A K K R D K E N T S K G R P G Q T N K
8. XP 013675421.1 elicitor peptide 1-like Brassica napus	G S K - - T L A T S R G - - V K A K T K K K E Q K S S G R P G Q H H K

1/161 Conserved: 25/161 Data



# Analyzed by MEGA



# Analyzed by NEBcutter



## NEBcutter V2.0



This tool will take a DNA sequence and find the large, non-overlapping open reading frames using the E.coli genetic code and the sites for all Type II and commercially available Type III restriction enzymes that cut the sequence just once. By default, only enzymes available from NEB are used, but other sets may be chosen. Just enter your sequence and "submit". Further options will appear with the output. **The maximum size of the input file is 1 MByte, and the maximum sequence length is 300 Kbases.**

[What's new in V2.0](#) [Citing NEBcutter](#)

Local sequence file:  未选择任何文件

GenBank number:  [\[Browse GenBank\]](#)

or paste in your DNA sequence: *(plain or FASTA format)*

Standard sequences:  
# Plasmid vectors ▾  
# Viral + phage ▾

The sequence is:  Linear  Circular

Enzymes to use:  
 NEB enzymes  
 All commercially available specificities  
 All specificities  
 All + defined oligonucleotide sequences  
 Only defined oligonucleotide sequences  
[\[define oligos\]](#)

Minimum ORF length to display:  a.a.

Name of sequence:  *(optional)*

**Earlier projects:**

*Note: Your earlier projects will be deleted 2 days after they were last accessed. You need to have cookies enabled in your browser for this feature to work.*

Disable NEBcutter cookies

# Analyzed by NEBcutter



```
>NC_003076.8:25937078-25938176 PROPEP1 [organism=Arabidopsis thaliana]
[GeneID=836613] [chromosome=5]
GATTTATGAAAATGTAATTTTATAGTAATAAAGAGTCACACCCCAATACCGAGTTAGCCCACTATAAAAAGGC+
AAAGATGTCTCTCTGCGCAATCCTCACATATAAAAAACAGCTTCACCTCTCACCAAAATAATCAGA+
TTAATAAAAAGTTTTCTCTGTCTTATCAGATCTCAATGGAGAAAATCAGATAGACGAAAGCGAAGAAAAGTCA+
CCTATGGATTCCCTCTCAGTGCCTCGACCAAAACCCCTCAGAGCTATCTTGAATGCTTGGTCTTTTTTCAT+
CAAGATCTCCGACAACGCTCTCCTCCGGAACTTCGAAACAGCCGGTAAGCTTTGCAAGAGTATATTTTG+
GACTAATATGAGATTATTAATTTATGTCTGTTCTGTATACACTATAAAAGCGGTTATGCATGGAAATTTTA+
AAAATGGAAATAATTTAATCTCTTATTTGAACACCAAAAAAATGAAAAAGATGTTAAAGATTTGGTAGT+
AACAAATTTATAAATGAACGTTTGTATATAAATATATTTTCCAATACTTTTGGAGTTAGCTAGGATATGAT+
CAAAAGTATTAGCTATTTTACTTTTGAGTTAATCCTGTTAAAAATATCAAATACGTTTAGATGAGAATA+
AGAATCAGGTAATTAATTTTGGTTTTAAAAAGTCATTAGCAATGTTTTAGGAATATTATATAACATGAAT+
CCAACAGATATGTACATGTGTTTATAATTGCAGAAGGAGGAAAAAGAACGCTTACCATGAAAAGGAGG+
AGTCTGTTGTGACAGTAGAGCCACAAGGTCAAGGCAAGCAAGGGGGAAGGAGAAAGTTAGCTCAGG+
CCGCTCTGGCCAACATAATTAGGCACCTTAAAGTTACATGTTTAGTCTAATTTATTGACGTGAAAATGTG+
TTAATTTAATATCACTGTTTACTTTTTTATTATATCAACAATCTACAGACAAAACAAAATTCATTAAGT+
TCTTGTTCACATACGAGTTTTTCTCTTTTATTTTCATGCAATTTTTTTTTCCCGTATTTGATGTGATAT+
TTGGGTTGAACAAAAGTAAATATGTTTCGACCATCATAAGTTCATAACCA+
```

**Gene:** PROPEP1  
**RNA title:** mRNA-precursor of peptide 1  
**Protein title:** precursor of peptide 1  
**Protein comment:** precursor of peptide 1 (PROPEP1); BEST Arabidopsis thaliana protein match is: elicitor peptide 2 precursor (TAIR:AT5G64890.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).  
**Merged features:** NM\_125888.4 and NP\_569001.1  
**Location:** 25,937,078..25,938,176  
[Length]  
**Span on NC\_003076.8:** 1,099 nt  
**Aligned length:** 691 nt  
**CDS length:** 279 nt  
**Protein length:** 92 aa  
[NM\_125888.4]  
**Intron:** 1 of 1  
**mRNA sequence:** AACTTCGAAACAGCCG[...]AAGGAGGAAAAAGA  
[NP\_569001.1]  
**Protein sequence:** HQDSPTTSSPGTSKQP[...]KEEKEDVTMEKEEV

**Download FASTA:** [NP\\_569001.1](#)  
[NM\\_125888.4](#)  
[NM\\_125888.4 exons](#)



# Analyzed by NEBcutter

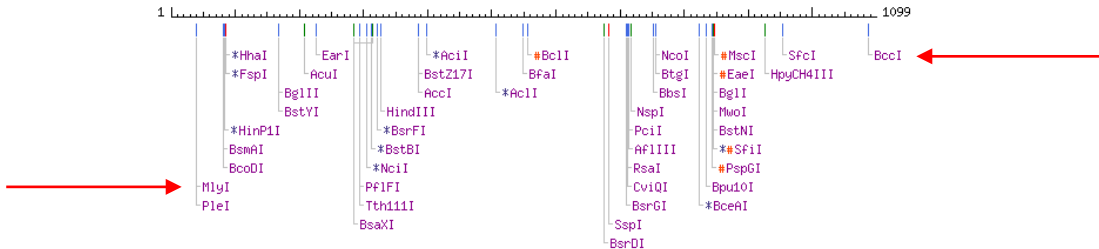


[Help](#) [Comments](#)

**Display:** - NEB single cutter restriction enzymes  
- Main non-overlapping, min. 100 aa ORFs

GC=33%, AT=67%

Cleavage code	Enzyme name code
⌵   blunt end cut	Available from NEB
⌵   5' extension	Has other supplier
⌵   3' extension	Not commercially available
⌵   cuts 1 strand	*: cleavage affected by CpG meth.
	#: cleavage affected by other meth.
	(enz.name): ambiguous site



**Main options**

- New DNA
- Custom digest
- View sequence
- ORF summary
- Save project
- Print

**Availability**

- All commercial
- All

**Display**

- 2 cutters
- 3 cutters

**Zoom**

- Zoom in
- More...

Minimum ORF length to display:  aa

**List**

- 0 cutters
- 1 cutters
- All sites
- Save all sites
- Flanking enzymes



# Analyzed by Primer Premier



Primer Premier

Primer: Search Results Edit Primers

Direct Select:

3' CTAATACTTTTACATAAATATCA 5'  
|||||  
5' GATTTTATGAAAATGATTTTATAGTATAAAGAGTCAACCCCAATACCGAGTTAGCCCACTATAAAAAGGCAAGATGCTCT 3'

D L - K C I L - - - R V T P N T E L A H Y K R Q R C L S

	Rating	Seq No	Length	Tm [°C]	GC%	ΔG [kcal/mol]	Activity [μg/OD]	Degeneracy	Ta Opt [°C]
Sense	66	1	25	48.5	16.0	-38.1	30.2	1	--
Anti-sense	67	25	25	48.5	16.0	-38.1	29.8	1	--
Product	15	--	25	55.7	16.0	--	--	--	28.5

Most Stable Hairpin:  
ΔG = -1.3 [kcal/mol]

Sense Found Found Found Found  
Anti-sense Found Found Found

AGAATA AGAATCAGGT  
ATTATA TAACATGAAT  
AGAAGA CGTTACCATG

781 GACGAGTAGA GCCACAAAGG TCAAGGCRAA GCAAAAGGGG  
841 CCGTCTGGC CAACATAATT AGGCACITTA AGTTACATTG  
901 TCGAAATGTG TTAATTTAAT ATCACTGTIT TACTITTTTA  
961 CAACAAAAT TGCATTAAGT TCTGTGTGAC TATAGAGTIT  
1021 ATTTTTTTTT TCCCGTAITT GATGTGATAT TTGGGTGAA CAAAAGTAAA TATGTTCGAC  
1081 CATCATAAGT TCATAACCA

Search Criteria

Search For:  
 PCR Primers  Sequencing Primers  Hybridization Probes

Search Type:  
 Sense Primer  Compatible with Sense Primer  
 Anti-sense Primer  Compatible with Anti-sense Primer  
 Both  Pairs

Search Ranges:  
Sense Primer: 1 to 691  
Anti-sense Primer: 692 to 1099  
PCR Product Size: 100 bp to 500 bp

Primer Length: 23 bp ? 2 bp

Search Mode:  
 Automatic  Manual

Search Parameters

OK Cancel Help



# Analyzed by Primer Premier

The screenshot shows the Primer Premier software interface. The main window displays the analysis of a primer pair. The primer sequences are:

Direct Select:  
5' AGAGTCACACCCRATACCGAG 3'  
3' TAICATAITTTCTCAGTGTGGGTTATGGGCTCAATCGGGTGATATTTTCGGTTTCTACAGAGAGACGGGTTAGTGAGTGTATA 5'

The analysis table shows the following results:

	Rating	Seq No	Length	Tm [°C]	GC%	ΔG (kcal/mol)	Activity [μg/100]	Degeneracy	Ta Opt [°C]
Sense	100	31	21	56.5	62.4	-37.9	30.4	1	...
Anti-sense	100	834	21	56.5	47.6	-40.1	37.0	1	...
Product	94	...	804	83.1	34.2	...	...	...	50.1

Below the table, there are sections for 'Hairpin', 'Dimer', 'False Priming', and 'Cross Dimer'. The 'Cross Dimer' section shows 'Found'.

The 'Search Results' window shows 194 anti-sense primers found. The table below shows the top 7 results:

#	Rating	Seq No	Length	Tm [°C]	GC%	Mark
1	100	800	21	57.9	52.4	
2	100	804	21	54.5	47.6	
3	100	806	21	56.6	52.4	
4	100	828	21	62.0	47.6	
5	100	830	21	61.6	52.4	
6	100	834	21	56.5	47.6	
7	100	966	21	48.4	33.3	

Direct Select: 834

3' TTCCOCCCTTCCCTTTTCAATC 5'  
|||||

5' TCAAGGC AAAGCAAAGGGGGAGGAGAAAGTTAGCTCAGGCGCTCCTGGCCACATAATTAGGCACITTAAGTTACATTGTT 3'

810 820 830 840 850 860 870 880

Q G K A K G E G E S - L R P S W P T - L G T L S Y I V

Direct Select: 834

5' AGAGTCACACCCRATACCGAG 3'  
|||||

3' TAICATAITTTCTCAGTGTGGGTTATGGGCTCAATCGGGTGATATTTTCGGTTTCTACAGAGAGACGGGTTAGTGAGTGTATA 5'

30 40 50 60 70 80 90 100

- - - R V T P N T E L A H Y K R Q R C L S A Q S L T Y



# Analyzed by ProtParam

Number of amino acids: 92

Molecular weight: 10388.76

Theoretical pI: 9.00

Amino acid composition:

[CSV format](#)

Ala (A)	3	3.3%
Arg (R)	6	6.5%
Asn (N)	1	1.1%
Asp (D)	4	4.3%
Cys (C)	2	2.2%
Gln (Q)	6	6.5%
Glu (E)	10	10.9%
Gly (G)	5	5.4%
His (H)	3	3.3%
Ile (I)	2	2.2%
Leu (L)	7	7.6%
Lys (K)	11	12.0%
Met (M)	2	2.2%
Phe (F)	1	1.1%
Pro (P)	5	5.4%
Ser (S)	10	10.9%
Thr (T)	7	7.6%
Trp (W)	1	1.1%
Tyr (Y)	0	0.0%
Val (V)	6	6.5%
Pyl (O)	0	0.0%
Sec (U)	0	0.0%
(B)	0	0.0%
(Z)	0	0.0%
(X)	0	0.0%

Total number of negatively charged residues (Asp + Glu): 14

Total number of positively charged residues (Arg + Lys): 17

Atomic composition:

Carbon	C	442
Hydrogen	H	735
Nitrogen	N	135
Oxygen	O	145
Sulfur	S	4

Number of amino acids: 92

Molecular weight: 10388.76

Theoretical pI: 9.00



# Analyzed by ProtScale



SEQUENCE LENGTH: 92

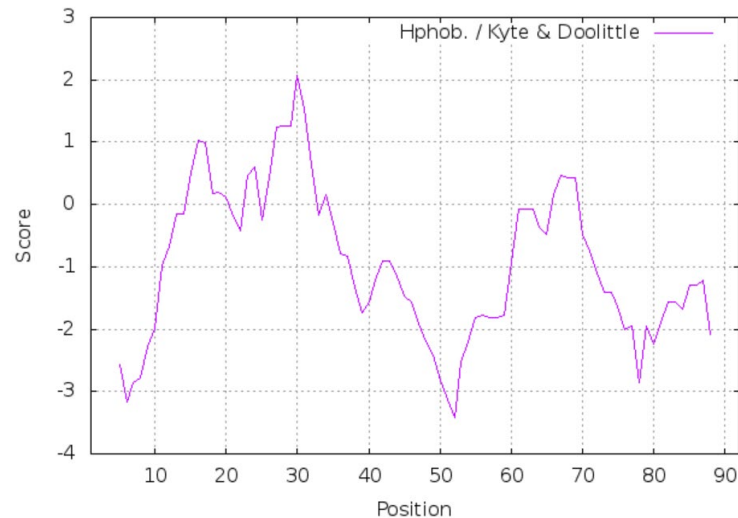
Using the scale **Hphob. / Kyte & Doolittle**, the individual values for the 20 amino acids are:

Ala: 1.800 Arg: -4.500 Asn: -3.500 Asp: -3.500 Cys: 2.500 Gln: -3.500  
Glu: -3.500 Gly: -0.400 His: -3.200 Ile: 4.500 Leu: 3.800 Lys: -3.900  
Met: 1.900 Phe: 2.800 Pro: -1.600 Ser: -0.800 Thr: -0.700 Trp: -0.900  
Tyr: -1.300 Val: 4.200 : -3.500 : -3.500 : -0.490

Weights for window positions 1,...,9, using **linear weight variation model**:

1	2	3	4	5	6	7	8	9
1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
edge				center				edge

ProtScale output for user\_sequence

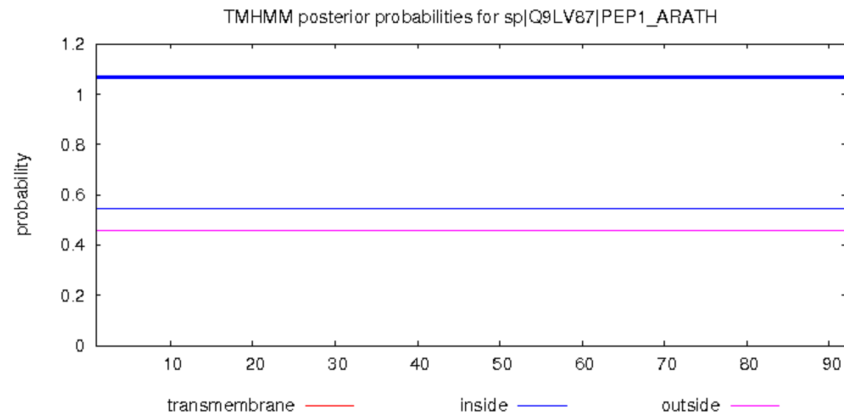


# Analyzed by TMHMM



---

```
# sp|Q9LV87|PEP1_ARATH Length: 92
# sp|Q9LV87|PEP1_ARATH Number of predicted TMHs: 0
# sp|Q9LV87|PEP1_ARATH Exp number of AAs in TMHs: 0.002
# sp|Q9LV87|PEP1_ARATH Exp number, first 60 AAs: 0.002
# sp|Q9LV87|PEP1_ARATH Total prob of N-in: 0.54285
sp|Q9LV87|PEP1_ARATH TMHMM2.0 inside 1 92
```





# Analyzed by SOPMA

## SOPMA SECONDARY STRUCTURE

[Abstract] [NPS@ help] [Original server]

Sequence name (optional):

Paste a protein sequence below: [help](#)

MEKSDRRSEESHVWIPQLCLDQTLRAILKCLGLFHQDSPITSSPGTSKQP  
KEEKEDVTME KEEVVVTSRATKVKAKQRGKEKVSSGRPGQHN

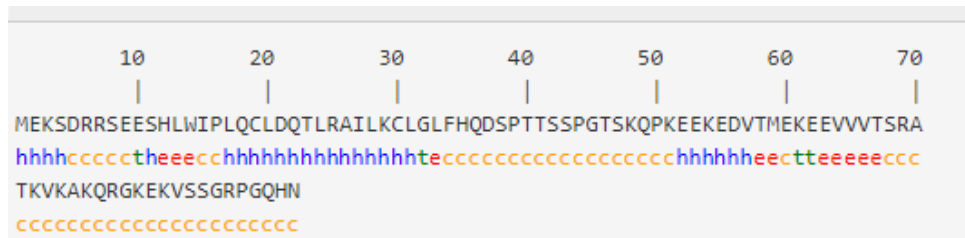
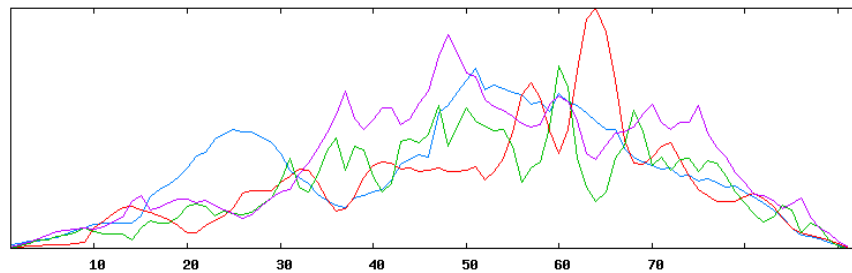
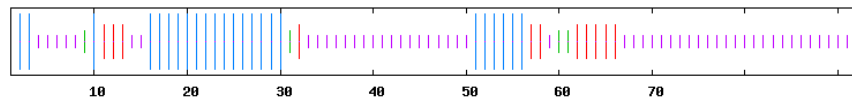
Output width:

### Parameters

Number of conformational states: 4 (Helix, Sheet, Turn, Coil) ▼

Similarity threshold:

Window width:



### SOPMA :

Alpha helix	(Hh) :	26 is	28.26%
3 <sub>10</sub> helix	(Gg) :	0 is	0.00%
Pi helix	(Ii) :	0 is	0.00%
Beta bridge	(Bb) :	0 is	0.00%
Extended strand	(Ee) :	11 is	11.96%
Beta turn	(Tt) :	4 is	4.35%
Bend region	(Ss) :	0 is	0.00%
Random coil	(Cc) :	51 is	55.43%
Ambiguous states (?)	:	0 is	0.00%
Other states	:	0 is	0.00%

# Analyzed by Predictprotein



Predicted localization for the Eukarya domain: Nucleus (GO term ID: [GO:0005634](#)) Prediction confidence 52



# 预测作用机理

Predictive Mechanism

# Analyzed by NCBI



## Search Set

UniProtKB/Swiss-Prot(swissprot) ?

plants (taxid:3193)  exclude [Add organism](#)

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown. ?

Models (XM/XP)  Non-redundant RefSeq proteins (WP)  Uncultured/environmental sample sequences

## Selection

blastp (protein-protein BLAST)

## Sequences producing significant alignments

Download  **New** Select columns  Show  ?

select all *3 sequences selected*

[GenPept](#) [Graphics](#) [Distance tree of results](#) [Multiple alignment](#) **New** [MSA Viewer](#)

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	<a href="#">RecName: Full=Elicitor peptide 1; Flags: Precursor [Arabidopsis thaliana]</a>	<a href="#">Arabidopsis thali...</a>	152	152	100%	2e-52	100.00%	92	<a href="#">Q9LV87.1</a>
<input checked="" type="checkbox"/>	<a href="#">RecName: Full=Elicitor peptide 2; Flags: Precursor [Arabidopsis thaliana]</a>	<a href="#">Arabidopsis thali...</a>	80.5	80.5	100%	6e-23	54.17%	109	<a href="#">Q9LV88.1</a>
<input checked="" type="checkbox"/>	<a href="#">RecName: Full=Mediator of RNA polymerase II transcription subunit 14; AltName: Full=Protein STRUWWELPETE... [Arabidopsis thali...</a>	<a href="#">Arabidopsis thali...</a>	31.6	31.6	25%	0.016	53.85%	1703	<a href="#">Q9SR02.1</a>



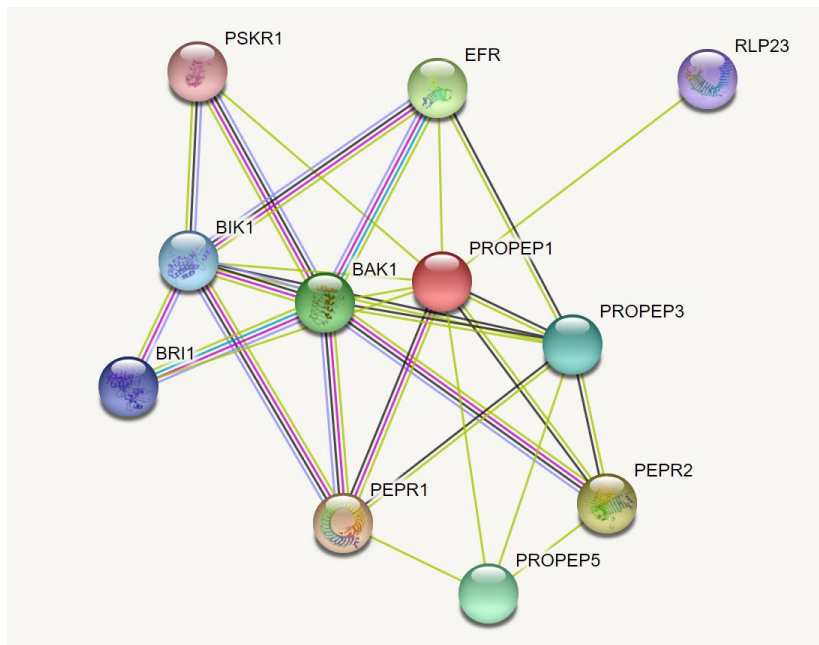
# Analyzed by NCBI

<input checked="" type="checkbox"/>	precursor of peptide 1 [Arabidopsis thaliana]	Arabidopsis thaliana	152	152	100%	4e-50	100.00%	92	NP_569001.1
<input checked="" type="checkbox"/>	elicitor peptide 1 [Eutrema salsugineum]	Eutrema salsugineum	96.8	96.8	100%	2e-27	58.65%	127	XP_006394100.2
<input type="checkbox"/>	PREDICTED: elicitor peptide 1-like [Camelina sativa]	Camelina sativa	94.4	94.4	100%	2e-26	65.38%	103	XP_010444447.1
<input type="checkbox"/>	PREDICTED: elicitor peptide 1-like [Camelina sativa]	Camelina sativa	90.2	90.2	100%	8e-25	69.00%	98	XP_010484288.1
<input type="checkbox"/>	PREDICTED: elicitor peptide 1-like [Camelina sativa]	Camelina sativa	88.4	88.4	100%	5e-24	66.99%	102	XP_010462607.1
<input checked="" type="checkbox"/>	elicitor peptide 1 [Capsella rubella]	Capsella rubella	84.4	84.4	100%	2e-22	57.76%	116	XP_006281339.1
<input checked="" type="checkbox"/>	elicitor peptide 1 [Brassica rapa]	Brassica rapa	83.4	83.4	100%	5e-22	45.37%	108	XP_009150567.1
<input checked="" type="checkbox"/>	elicitor peptide 2 precursor [Arabidopsis thaliana]	Arabidopsis thaliana	80.5	80.5	100%	9e-21	54.17%	109	NP_569000.1
<input type="checkbox"/>	PREDICTED: elicitor peptide 1-like [Brassica oleracea var. oleracea]	Brassica oleracea var. oleracea	80.0	80.0	100%	1e-20	44.34%	106	XP_013626305.1
<input checked="" type="checkbox"/>	elicitor peptide 1-like [Brassica napus]	Brassica napus	79.4	79.4	100%	2e-20	42.59%	108	XP_013647069.1
<input type="checkbox"/>	PREDICTED: elicitor peptide 1-like [Raphanus sativus]	Raphanus sativus	78.6	78.6	100%	5e-20	44.44%	108	XP_018488921.1
<input type="checkbox"/>	PREDICTED: elicitor peptide 1-like [Raphanus sativus]	Raphanus sativus	78.1	78.1	100%	8e-20	50.48%	109	XP_018439357.1
<input type="checkbox"/>	PREDICTED: elicitor peptide 1-like [Brassica oleracea var. oleracea]	Brassica oleracea var. oleracea	77.3	77.3	100%	1e-19	43.40%	106	XP_013622601.1
<input type="checkbox"/>	PREDICTED: LOW QUALITY PROTEIN: elicitor peptide 2-like [Camelina sativa]	Camelina sativa	73.6	73.6	100%	6e-18	51.06%	114	XP_019094246.1
<input type="checkbox"/>	PREDICTED: elicitor peptide 2-like [Camelina sativa]	Camelina sativa	70.0	70.0	100%	2e-16	48.94%	113	XP_010444446.1
<input checked="" type="checkbox"/>	elicitor peptide 2 [Arabidopsis lyrata subsp. lyrata]	Arabidopsis lyrata subsp. lyrata	68.7	68.7	100%	6e-16	53.76%	112	XP_002866300.1
<input type="checkbox"/>	PREDICTED: elicitor peptide 1-like [Brassica oleracea var. oleracea]	Brassica oleracea var. oleracea	63.1	63.1	100%	1e-13	49.07%	112	XP_013619427.1
<input checked="" type="checkbox"/>	elicitor peptide 1-like [Brassica napus]	Brassica napus	61.6	61.6	100%	5e-13	49.07%	112	XP_013675421.1
<input checked="" type="checkbox"/>	elicitor peptide 1-like [Brassica napus]	Brassica napus	61.3	61.3	100%	6e-13	46.79%	113	XP_013675440.1
<input checked="" type="checkbox"/>	elicitor peptide 1-like [Brassica napus]	Brassica napus	60.0	60.0	100%	2e-12	42.45%	106	XP_013669821.1
<input checked="" type="checkbox"/>	elicitor peptide 2 [Capsella rubella]	Capsella rubella	60.0	60.0	100%	2e-12	46.00%	114	XP_006281346.1
<input checked="" type="checkbox"/>	elicitor peptide 2 [Arabidopsis lyrata subsp. lyrata]	Arabidopsis lyrata subsp. lyrata	55.3	55.3	100%	2e-10	54.64%	110	XP_002864928.1
<input checked="" type="checkbox"/>	elicitor peptide 1 [Brassica rapa]	Brassica rapa	45.6	45.6	100%	1e-06	36.96%	78	XP_018511041.1
<input checked="" type="checkbox"/>	elicitor peptide 1-like [Brassica napus]	Brassica napus	38.5	38.5	100%	8e-04	33.70%	78	XP_022549490.1
<input checked="" type="checkbox"/>	elicitor peptide 1-like [Brassica napus]	Brassica napus	38.5	38.5	100%	8e-04	36.96%	78	XP_022548784.1
<input type="checkbox"/>	PREDICTED: uncharacterized protein LOC104763670 [Camelina sativa]	Camelina sativa	69.7	69.7	98%	1e-15	48.39%	233	XP_010485316.1
<input checked="" type="checkbox"/>	hypothetical protein AT5G09976 [Arabidopsis thaliana]	Arabidopsis thaliana	35.6	35.6	89%	0.011	35.37%	82	NP_001318523.1
<input type="checkbox"/>	PREDICTED: elicitor peptide 1 [Raphanus sativus]	Raphanus sativus	46.1	46.1	88%	7e-07	35.80%	77	XP_018487962.1
<input checked="" type="checkbox"/>	elicitor peptide 2 [Eutrema salsugineum]	Eutrema salsugineum	39.3	39.3	88%	4e-04	38.27%	81	XP_024012535.1
<input type="checkbox"/>	PREDICTED: elicitor peptide 1-like [Tarenaya hassleriana]	Tarenaya hassleriana	39.8	39.8	84%	3e-04	30.38%	105	XP_010519955.1
<input checked="" type="checkbox"/>	elicitor peptide 1-like [Brassica napus]	Brassica napus	45.8	45.8	83%	8e-07	35.06%	78	XP_022565499.1
<input type="checkbox"/>	PREDICTED: elicitor peptide 1-like [Tarenaya hassleriana]	Tarenaya hassleriana	42.7	42.7	81%	2e-05	29.33%	87	XP_010546386.1

Reference proteins  
(refseq protein)



# Analyzed by STRING



## Known Interactions

- from curated databases
- experimentally determined

## Predicted Interactions

- gene neighborhood
- gene fusions
- gene co-occurrence

## Others

- textmining
- co-expression
- protein homology





# Analyzed by STRING

1 2 3 4 5 6 7 8 9

● PEPR1	Leucine-rich repeat receptor-like protein kinase PEPR1; Acts as a receptor for PEP defense peptides. Unlike typical imm...	● ● ●	0.999
● PEPR2	Encodes PEPR2, a plasma membrane leucine-rich repeat receptor kinase functioning as a receptor for the Pep1 and Pe...	● ●	0.955
● EFR	LRR receptor-like serine/threonine-protein kinase EFR; Constitutes the pattern-recognition receptor (PPR) that determin...	●	0.838
● BAK1	BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1; Dual specificity kinase acting on both serine/threonin...	●	0.837
● PROPEP5	Elicitor peptide 5 precursor; Elicitor of plant defense	●	0.837
● PROPEP3	Elicitor peptide 3 precursor; Elicitor of plant defense	● ●	0.801
● BIK1	Serine/threonine-protein kinase BIK1; Plays a central role in immune responses. Required to activate the resistance res...	●	0.772
● BRI1	Leucine-rich receptor-like protein kinase family protein; Encodes a plasma membrane localized leucine-rich repeat rece...	●	0.739
● RLP23	Putative disease resistance protein; Receptor like protein 23 (RLP23); Its function is described as kinase activity; Involv...	●	0.735
● PSKR1	Phytosulfokine receptor 1; Phytosulfokine receptor with both a serine/threonine- protein kinase activity and a guanylate...	●	0.699



# Analyzed by STRING

PSKR1

## Information

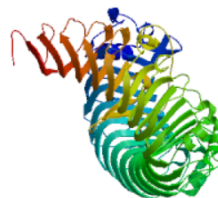
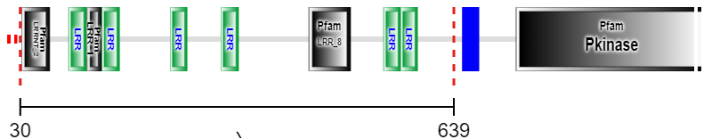
Phytosulfokine receptor 1; Phytosulfokine receptor with both a serine/threonine- protein kinase activity and a guanylate cyclase activity. Regulates, in response to phytosulfokine binding, a signaling cascade involved in plant cell differentiation, organogenesis, somatic embryogenesis, cellular proliferation and plant growth. Involved in plant immunity, with antagonistic effects on bacterial and fungal resistances. Not involved in PSY perception. CNGC17 and AHAs form a functional cation-translocating unit that is activated by PSKR1/BAK1 and possibly other BAK1/RLK complexes

Identifier: AT2G02220.1, PSKR1

Organism: Arabidopsis thaliana



- show protein sequence
- homologs among STRING organisms



◀ 1 of 2 ▶  
homology model (Q9ZVR7 / 4z63A)  
identity: 100%



# 结论

Conclusion



## 结论

Conclusion

- PEP1包含92个氨基酸、相对分子量为分子量10388.76，等电点为9.0
- PEP1没有跨膜结构，亚细胞定位在细胞核
- PEP1与PSKR1互作可能是影响叶片衰老的原因



感谢老师批评指正  
THANK YOU FOR WATCHING

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