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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2021年5月11日

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背景

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背景

Background

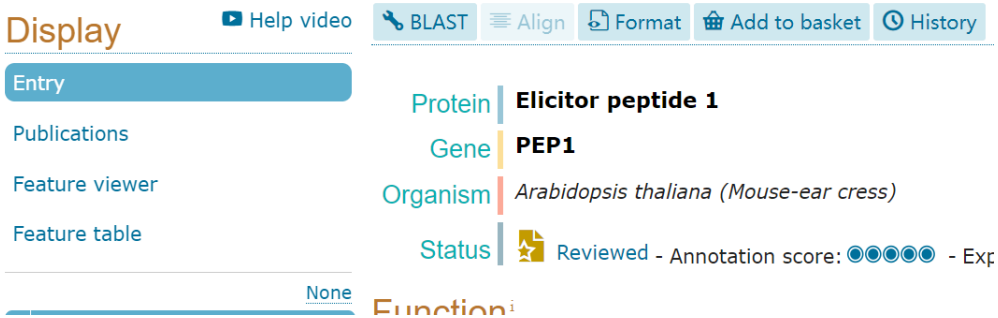
PEP1是在拟南芥中发现的参与植物先天免疫应答的多肽，属于十字花科激发子肽家族。当植物受到损伤，或者有茉莉酸甲酯或乙烯诱导时，该多肽会被诱导表达。PEP1含有92个氨基酸，可以激活防御基因防御素(PDF1.2)的转录并激活H2O2的合成，这两种基因都是先天免疫应答的组成部分。

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)

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Elicitor peptide 1
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OX=3702 GN=PEP1 PE=1 SV=1
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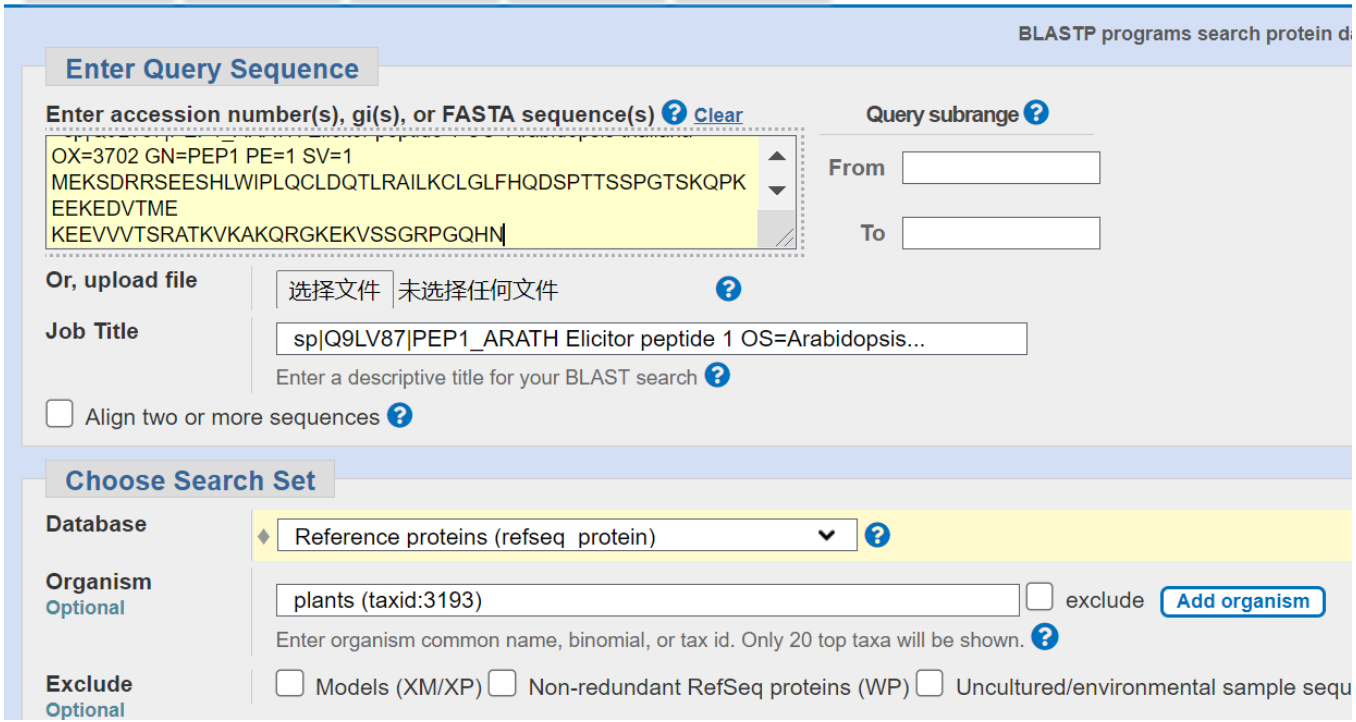
MEKEEVVVTSRATKVKAKQRGKEKVSSGR
PGQHN
```

Analyzed by NCBI



Analyzed by NCBI

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	precursor of peptide 1 [Arabidopsis thaliana]	Arabidopsis thaliana	152	152	100%	4e-50	100.00%	92	NP_569001.1
☑	elicitor peptide 1 [Eutrema salsugineum]	Eutrema salsugineum	96.8	96.8	100%	2e-27	58.65%	127	XP_006394100.2
☐	PREDICTED: elicitor peptide 1-like [Camelina sativa]	Camelina sativa	94.4	94.4	100%	2e-26	65.38%	103	XP_010444447.1
☐	PREDICTED: elicitor peptide 1-like [Camelina sativa]	Camelina sativa	90.2	90.2	100%	8e-25	69.00%	98	XP_010484288.1
☐	PREDICTED: elicitor peptide 1-like [Camelina sativa]	Camelina sativa	88.4	88.4	100%	5e-24	66.99%	102	XP_010462607.1
☑	elicitor peptide 1 [Capsella rubella]	Capsella rubella	84.4	84.4	100%	2e-22	57.76%	116	XP_006281339.1
☑	elicitor peptide 1 [Brassica rapa]	Brassica rapa	83.4	83.4	100%	5e-22	45.37%	108	XP_009150567.1
☑	elicitor peptide 2 precursor [Arabidopsis thaliana]	Arabidopsis thaliana	80.5	80.5	100%	9e-21	54.17%	109	NP_569000.1
☐	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
☑	elicitor peptide 1-like [Brassica napus]	Brassica napus	79.4	79.4	100%	2e-20	42.59%	108	XP_013647069.1
☐	PREDICTED: elicitor peptide 1-like [Raphanus sativus]	Raphanus sativus	78.6	78.6	100%	5e-20	44.44%	108	XP_018488921.1
☐	PREDICTED: elicitor peptide 1-like [Raphanus sativus]	Raphanus sativus	78.1	78.1	100%	8e-20	50.48%	109	XP_018439357.1
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☐	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
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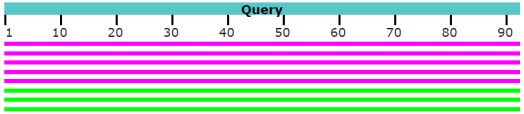
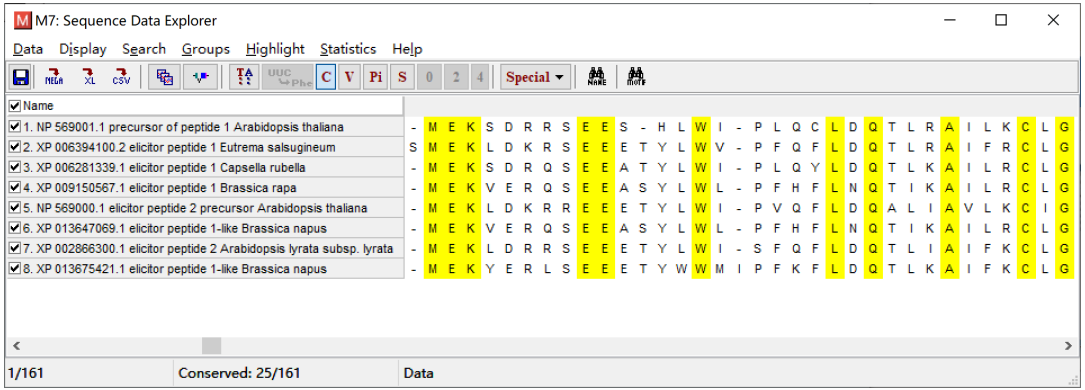
☑	elicitor peptide 2 [Arabidopsis lyrata subsp. lyrata]	Arabidopsis lyrata subsp. lyrata	68.7	68.7	100%	6e-16	53.76%	112	XP_002866300.1
☐	PREDICTED: uncharacterized protein LOC104763670 [Camelina sativa]	Camelina sativa	69.7	69.7	98%	1e-15	48.39%	233	XP_010485316.1
☐	PREDICTED: elicitor peptide 1-like [Brassica oleracea var. oleracea]	Brassica oleracea var. oleracea	63.1	63.1	100%	1e-13	49.07%	112	XP_013619427.1
☑	elicitor peptide 1-like [Brassica napus]	Brassica napus	61.6	61.6	100%	5e-13	49.07%	112	XP_013675421.1

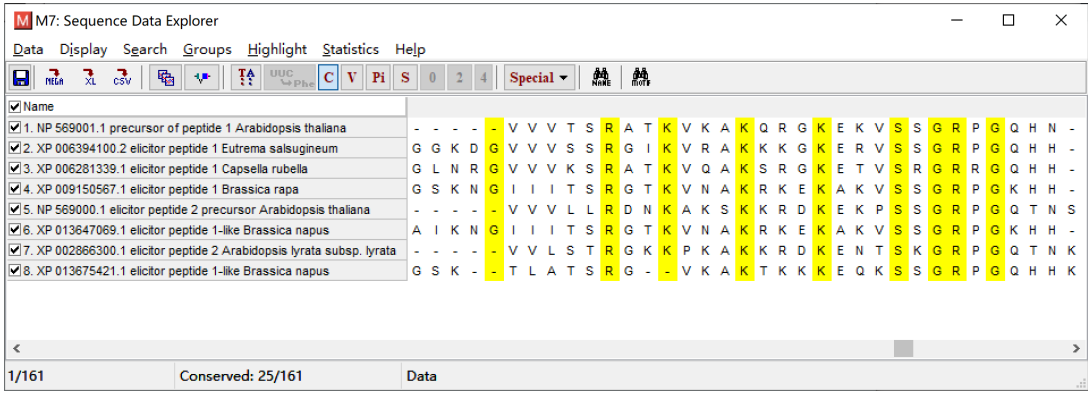
Putative conserved domains have been detected, click on the image below for detailed results.

Distribution of the top 8 Blast Hits on subject sequences



Analyzed by MEGA





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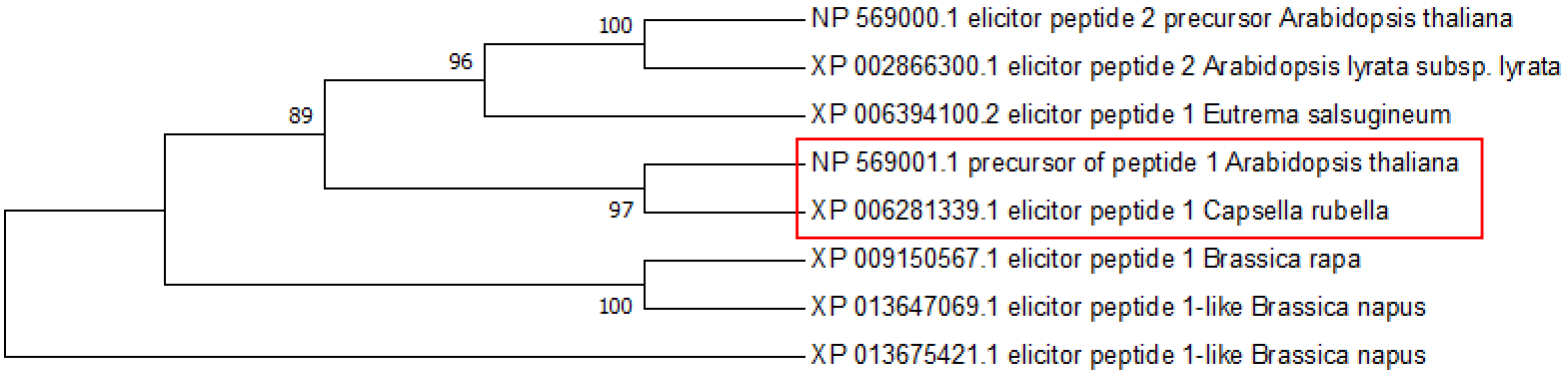

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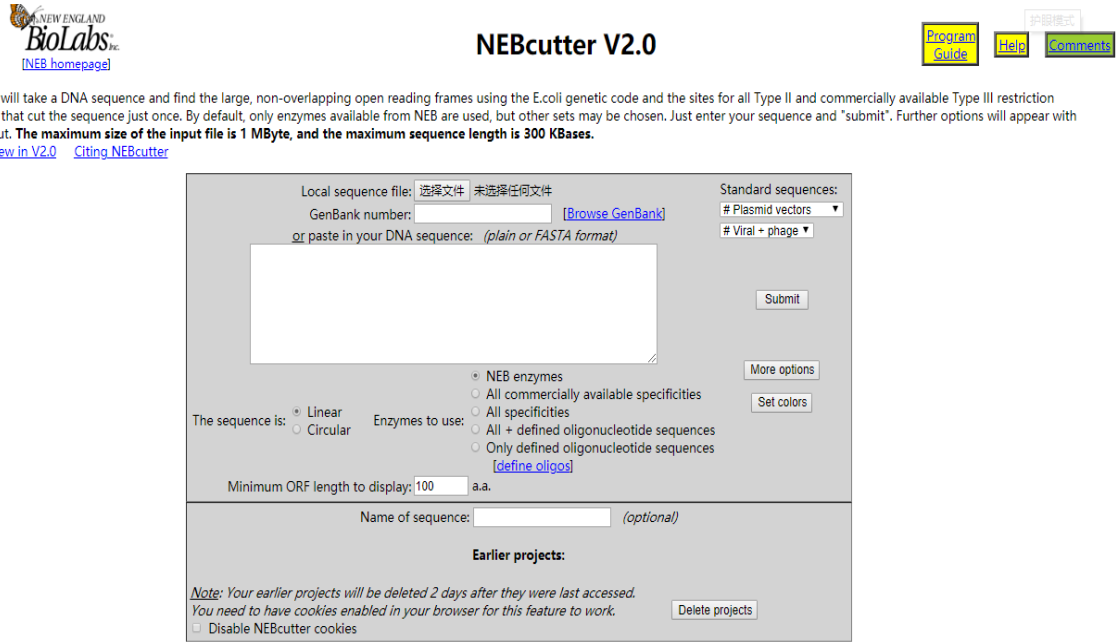

Analyzed by NEBcutter

>NC_003076.8:25937078-25938176 PROPEP1 [organism=Arabidopsis thaliana] [GeneID=836613] [chromosome=5]

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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

NEW ENGLAND BioLabs Inc. NEBcutter

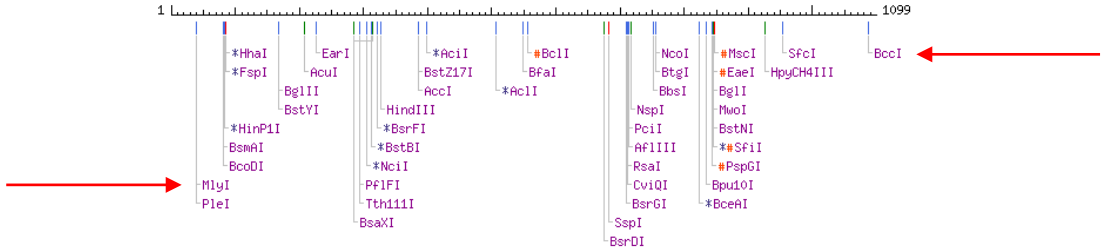
[redacted]

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	Availability	Display	Zoom	List
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Custom digest	All	3 cutters	More...	1 cutters
View sequence				All sites
ORF summary				Save all sites
Save project				Flanking enzymes
Print				

Minimum ORF length to display: 100 aa. OK

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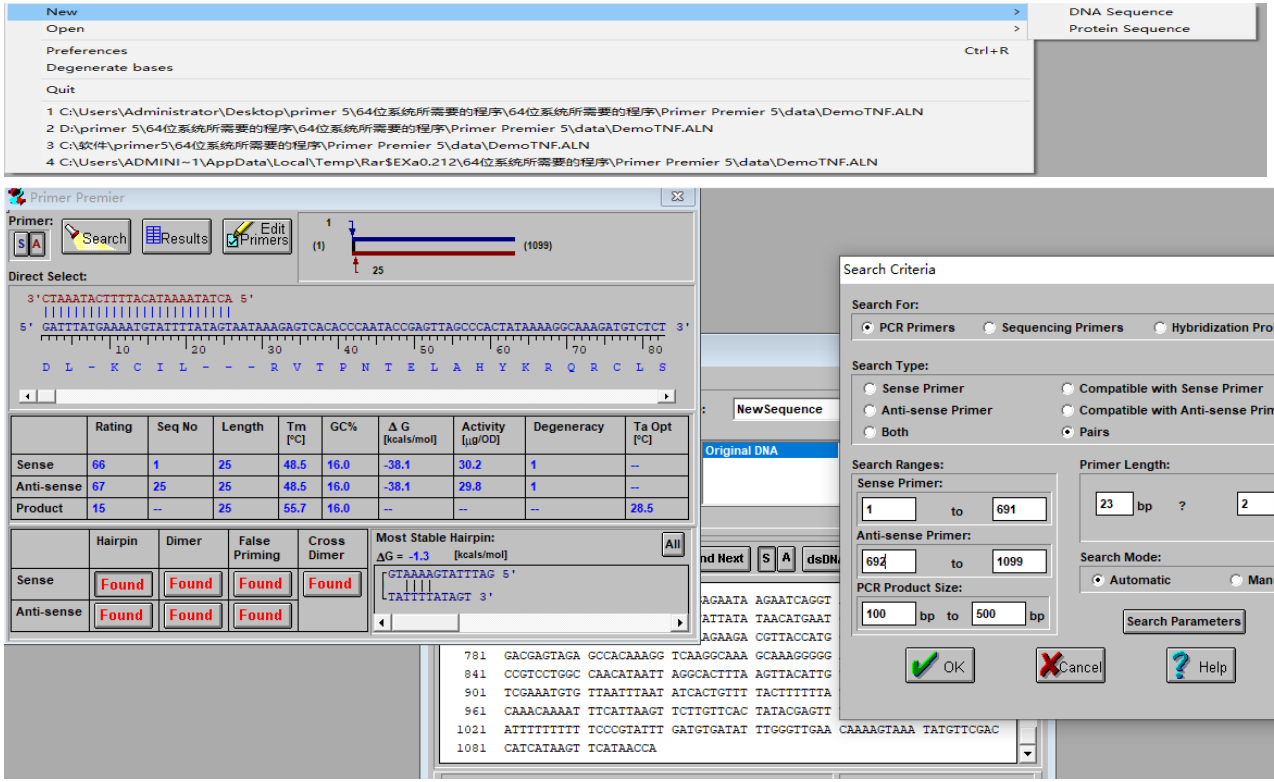

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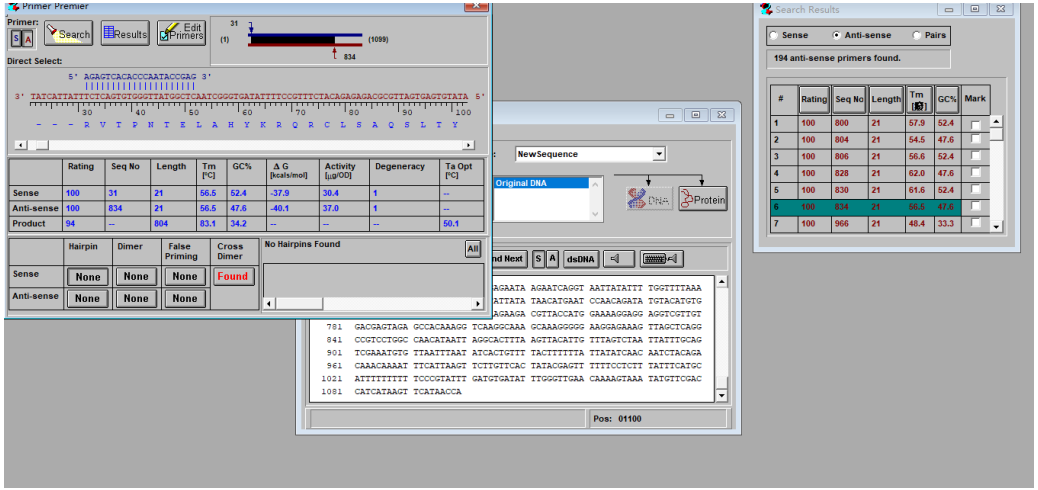

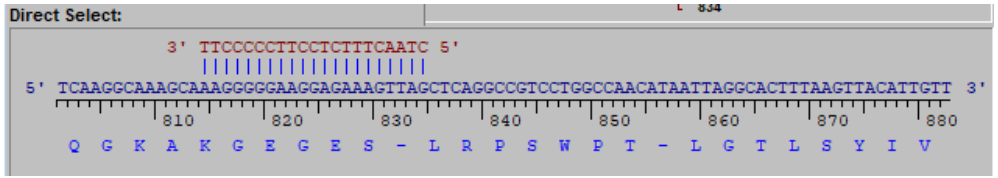

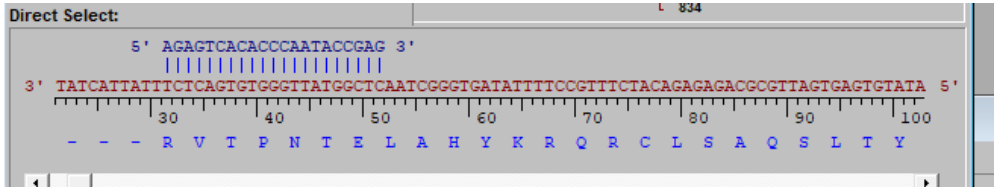

Analyzed by ProtParam

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:

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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
```
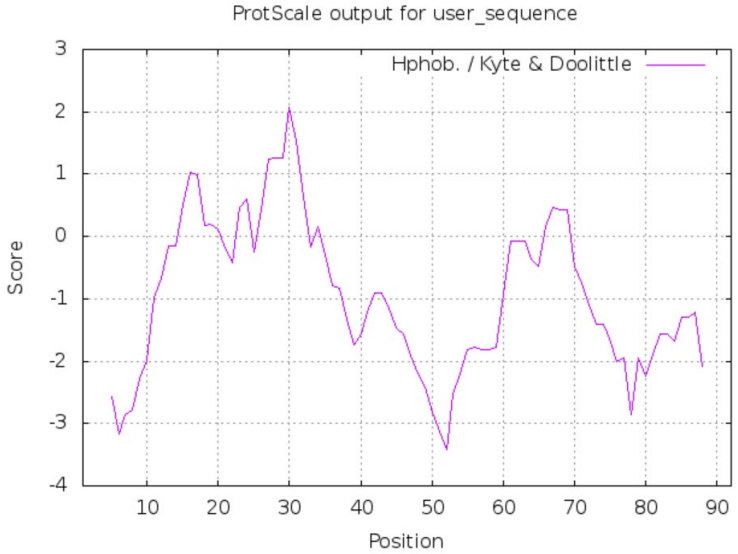

Weights for window positions 1,..,9, using **linear weight variation model**:

```
   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
```



Analyzed by TMHMM

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# 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
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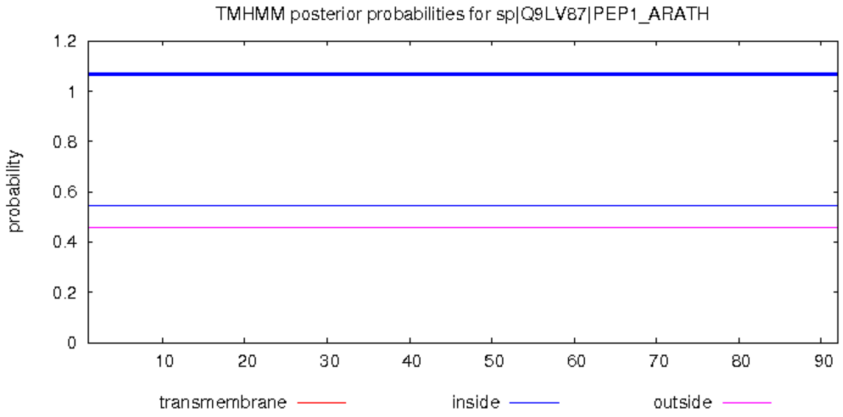


Analyzed by SOPMA

SOPMA SECONDARY STRUCTUR

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

Sequence name (optional) :

Paste a protein sequence below : help

MEKSDRRSEESHLWIPLQCLDQTLRAILKCLGLFHQDSPTTSSPGTSKQP
KEEKEDVTME KEEVVVTSRATKVKAKQRGKEKVSSGRPGQHN

Output width : 70

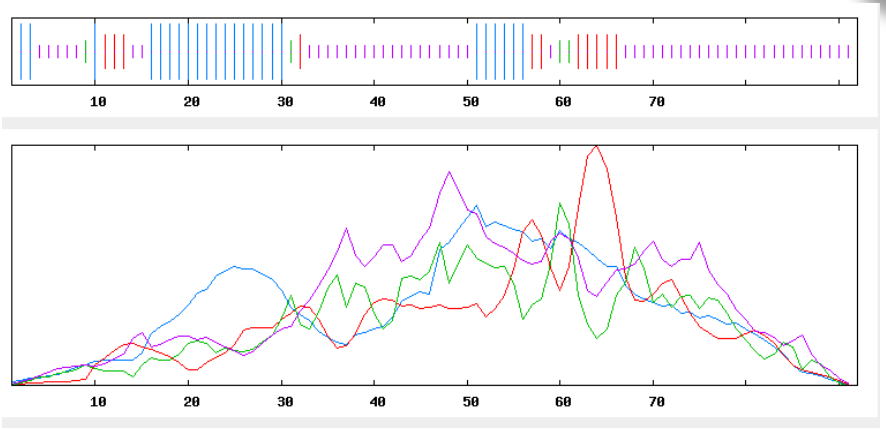
SUBMIT CLEAR

Parameters

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

Similarity threshold : 8

Window width : 17




```
         10        20        30        40        50        60        70
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TKVKAKQRGKEKVSSGRPGQHN
ccccccccccccccccccccc
```

```
SOPMA :
   Alpha helix      (Hh) :     26 is   28.26%
   3₁₀  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%
```

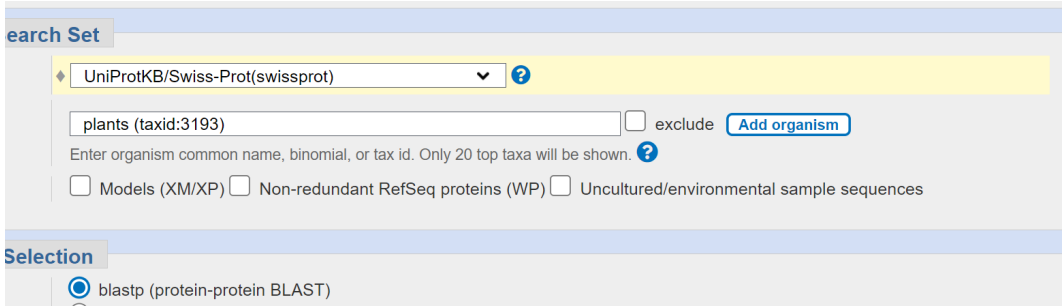
Analyzed by Predictprotein

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



Sequences producing significant alignments Download New Select columns Show 100

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
RecName: Full=Elicitor peptide 1; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thali…	152	152	100%	2e-52	100.00%	92	Q9LV87.1
RecName: Full=Elicitor peptide 2; Flags: Precursor [Arabidopsis thaliana]	Arabidopsis thali…	80.5	80.5	100%	6e-23	54.17%	109	Q9LV88.1
RecName: Full=Mediator of RNA polymerase II transcription subunit 14; AltName: Full=Protein STRUWWELPETE…	Arabidopsis thali…	31.6	31.6	25%	0.016	53.85%	1703	Q9SR02.1

Analyzed by NCBI

☑	precursor of peptide 1 [Arabidopsis thaliana]	Arabidopsis thaliana	152	152	100%	4e-50	100.00%	92	NP_569001.1
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☐	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
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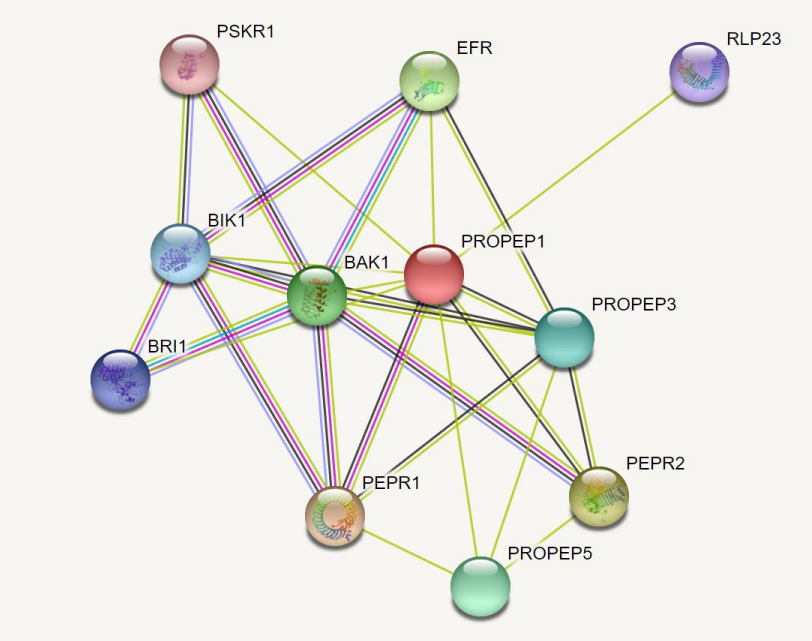
☐	PREDICTED: elicitor peptide 1-like [Brassica oleracea var. oleracea]	Brassica oleracea var. oleracea	63.1	63.1	100%	1e-13	49.07%	112	XP_013619427.1
☑	elicitor peptide 1-like [Brassica napus]	Brassica napus	61.6	61.6	100%	5e-13	49.07%	112	XP_013675421.1
☑	elicitor peptide 1-like [Brassica napus]	Brassica napus	61.3	61.3	100%	6e-13	46.79%	113	XP_013675440.1
☑	elicitor peptide 1-like [Brassica napus]	Brassica napus	60.0	60.0	100%	2e-12	42.45%	106	XP_013669821.1
☑	elicitor peptide 2 [Capsella rubella]	Capsella rubella	60.0	60.0	100%	2e-12	46.00%	114	XP_006281346.1
☑	elicitor peptide 2 [Arabidopsis lyrata subsp. lyrata]	Arabidopsis lyrata subsp. lyrata	55.3	55.3	100%	2e-10	54.64%	110	XP_002864928.1
☑	elicitor peptide 1 [Brassica rapa]	Brassica rapa	45.6	45.6	100%	1e-06	36.96%	78	XP_018511041.1
☑	elicitor peptide 1-like [Brassica napus]	Brassica napus	38.5	38.5	100%	8e-04	33.70%	78	XP_022549490.1
☑	elicitor peptide 1-like [Brassica napus]	Brassica napus	38.5	38.5	100%	8e-04	36.96%	78	XP_022548784.1
☐	PREDICTED: uncharacterized protein LOC104763670 [Camelina sativa]	Camelina sativa	69.7	69.7	98%	1e-15	48.39%	233	XP_010485316.1
☑	hypothetical protein AT5G09976 [Arabidopsis thaliana]	Arabidopsis thaliana	35.6	35.6	89%	0.011	35.37%	82	NP_001318523.1
☐	PREDICTED: elicitor peptide 1 [Raphanus sativus]	Raphanus sativus	46.1	46.1	88%	7e-07	35.80%	77	XP_018487962.1
☑	elicitor peptide 2 [Eutrema salsugineum]	Eutrema salsugineum	39.3	39.3	88%	4e-04	38.27%	81	XP_024012535.1
☐	PREDICTED: elicitor peptide 1-like [Tarenaya hassleriana]	Tarenaya hassleriana	39.8	39.8	84%	3e-04	30.38%	105	XP_010519955.1
☑	elicitor peptide 1-like [Brassica napus]	Brassica napus	45.8	45.8	83%	8e-07	35.06%	78	XP_022565499.1
☐	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

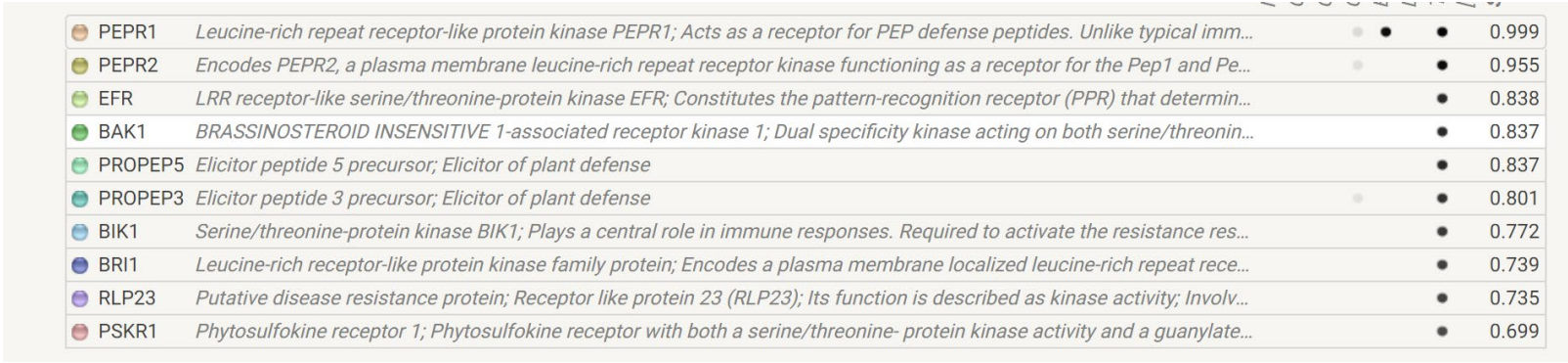


Known Interactions
- *from curated databases*
- *experimentally determined*

Predicted Interactions
- *gene neighborhood*
- *gene fusions*
- *gene co-occurrence*

Others
- *textmining*
- *co-expression*
- *protein homology*

Analyzed by STRING



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

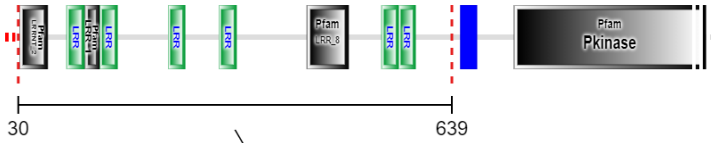
PSKR1

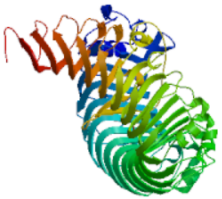
Information
Phytosulfokine receptor 1; Phytosulfokine receptor with both a serine/threonine- protein kinase activity and a guanylate cyclase activity. Regulates, in response to phytosulfokine binding, a signaling cascade involved in plant cell differentiation, organogenesis, somatic embryogenesis, cellular 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

e! KEGG RefSeq tair UniProt

- 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