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CHINESE ACADEMY OF AGRICULTURAL SCIENCES

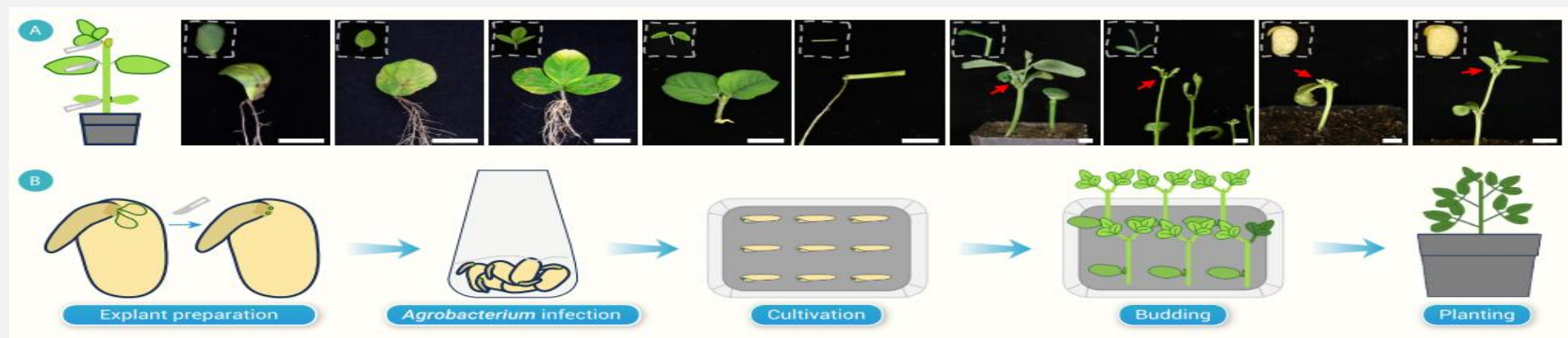
# 大豆异戊烯基转移酶基因家族 的生物信息学分析

G05成员：李文涛 郝文琦 谭剑英 田益康

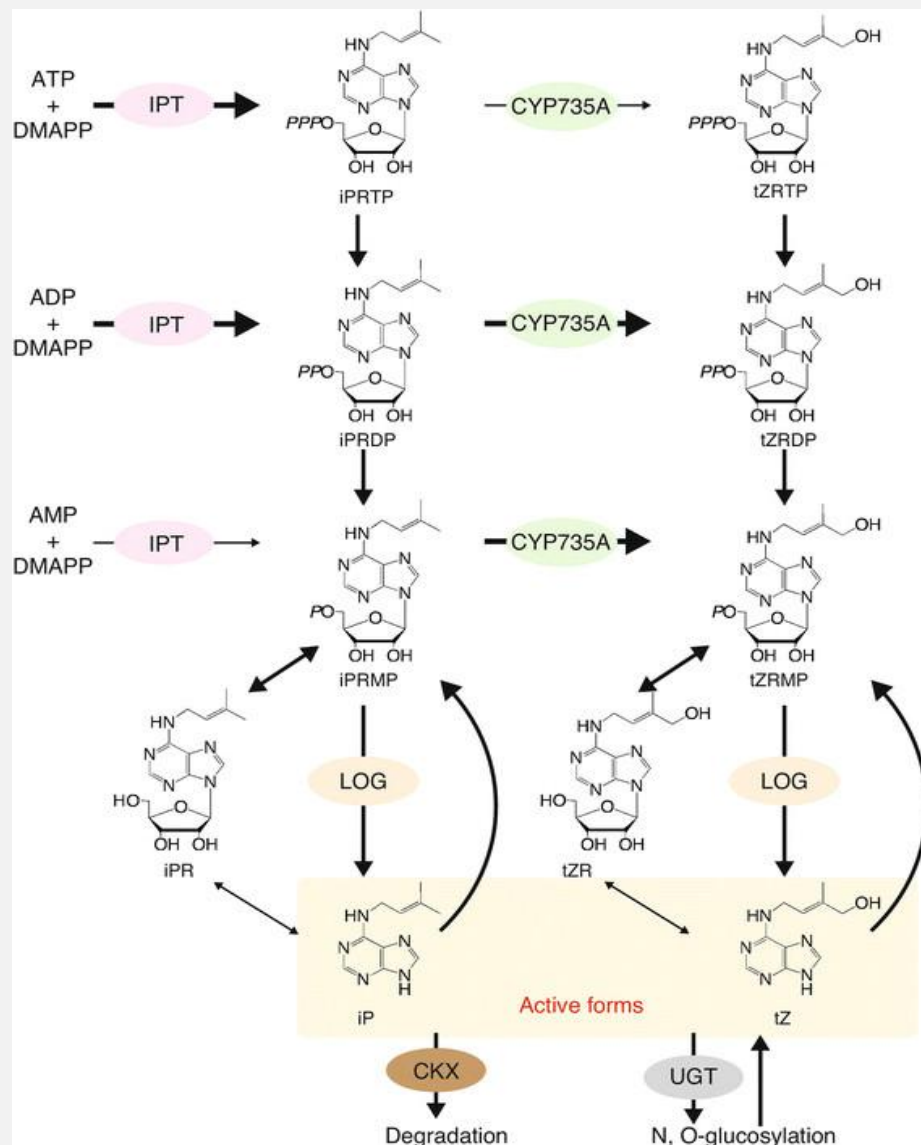
汇报人：田益康

日期：2025.1.10

- 大豆作为全球重要的油料和蛋白作物，遗传改良进程受制于基因型依赖且耗时费力的组织培养转化体系。
- 将在其它植物中建立的“剪切-浸染-出芽”（CDB）策略应用于大豆，建立了一套完全不依赖组织培养、操作极其简便且不依赖基因型的大豆遗传转化及基因编辑新体系。
- CDB策略可行，但初始效率较低（0.42%）。为了提升效率，研究团队引入了多种植物发育调节因子（DRs）。
- 在测试的多种DRs中，ipt（异戊烯基转移酶基因）表现最为出色，将转化效率提升至4.68%。



Reference: Cao, X.; Xie, H.; Wang, Z.; et al. 2025. An efficient tissue-culture-free soybean genetic transformation technology using the extremely simple cut-dip-budding strategy. *The Innovation*: 101221.



- 异戊烯基转移酶 (IPT) 是细胞分裂素生物合成的关键限速酶。
- 功能：催化异戊烯基从二甲基烯丙基二磷酸 (DMAPP) 向ATP、ADP和AMP的转移，形成异戊烯基腺苷磷酸。



**Gene Report: Glyma.17G017400**

**Genome:** [Glycine max Wm82.a4.v1](#) (Phytozome genome ID: 508 • NCBI taxonomy ID: [3847](#))  
**Gene Identifier:** [Glyma.17G017400](#) (PAC:41086196)  
**Transcripts:** [Glyma.17G017400.1](#) [Glyma.17G017400.2](#) [Glyma.17G017400.3](#)  
**Location:** [Gm17:1312212..1314182](#) forward  
**Alias:** [Glyma17g02080](#)  
**UniProt:** [Glyma.17G017400.1](#), [Glyma.17G017400.2](#): [A0A0R0F723](#)  
[Glyma.17G017400.1](#), [Glyma.17G017400.2](#): [A0A0R0F723\\_SOYBN](#)  
**Auto Define:** (1 of 1) [PF01715](#)//[PF01745](#) - IPP transferase (IPPT) // Isopentenyl transferase (IPT)  
**View:** [B](#)

# 蛋白序列的获取



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## A0A0R0F723 · A0A0R0F723\_SOYBN

Protein <sup>i</sup>	adenylate dimethylallyltransferase (ADP/ATP-dependent)	Amino acids	340 (go to sequence)
Gene <sup>i</sup>	LOC100778430	Protein existence <sup>i</sup>	Inferred from homology
Status <sup>i</sup>	■ UniProtKB unreviewed (TrEMBL)	Annotation score <sup>i</sup>	2/5
Organism <sup>i</sup>	Glycine max (Soybean) (Glycine hispida)		

数据来源: UniProt

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# 蛋白质理化性质分析



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Number of amino acids: 340  
Theoretical pI: 7.30  
Molecular weight: 37663.84

Amino acid composition: CSV format

Ala (A)	40	11.8%
Arg (R)	22	6.5%
Asn (N)	19	5.6%
Asp (D)	18	5.3%
Cys (C)	5	1.5%
Gln (Q)	9	2.6%
Glu (E)	20	5.9%
Gly (G)	17	5.0%
His (H)	17	5.0%
Ile (I)	14	4.1%
Leu (L)	30	8.8%
Lys (K)	16	4.7%
Met (M)	9	2.6%
Phe (F)	14	4.1%
Pro (P)	11	3.2%
Ser (S)	23	6.8%
Thr (T)	18	5.3%
Trp (W)	3	0.9%
Tyr (Y)	6	1.8%
Val (V)	29	8.5%
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): 38  
Total number of positively charged residues (Arg + Lys): 38

#### Atomic composition:

Carbon	C	1655
Hydrogen	H	2623
Nitrogen	N	487
Oxygen	O	492
Sulfur	S	14

Formula:  $C_{1655}H_{2623}N_{487}O_{492}S_{14}$

Total number of atoms: 5271

#### Extinction coefficients:

Extinction coefficients are in units of  $M^{-1} cm^{-1}$ , at 280 nm measured in water.

Ext. coefficient 25690

Abs 0.1% (=1 g/l) 0.682, assuming all pairs of Cys residues form cystines

Ext. coefficient 25440

Abs 0.1% (=1 g/l) 0.675, assuming all Cys residues are reduced

#### Estimated half-life:

The N-terminal of the sequence considered is M (Met).

The estimated half-life is: 30 hours (mammalian reticulocytes, in vitro).

>20 hours (yeast, in vivo).

>10 hours (Escherichia coli, in vivo).

#### Instability index:

The instability index (II) is computed to be 36.60

This classifies the protein as stable.

Aliphatic index: 86.97

Grand average of hydropathicity (GRAVY): -0.215

数据来源: ExPASy-ProtParam

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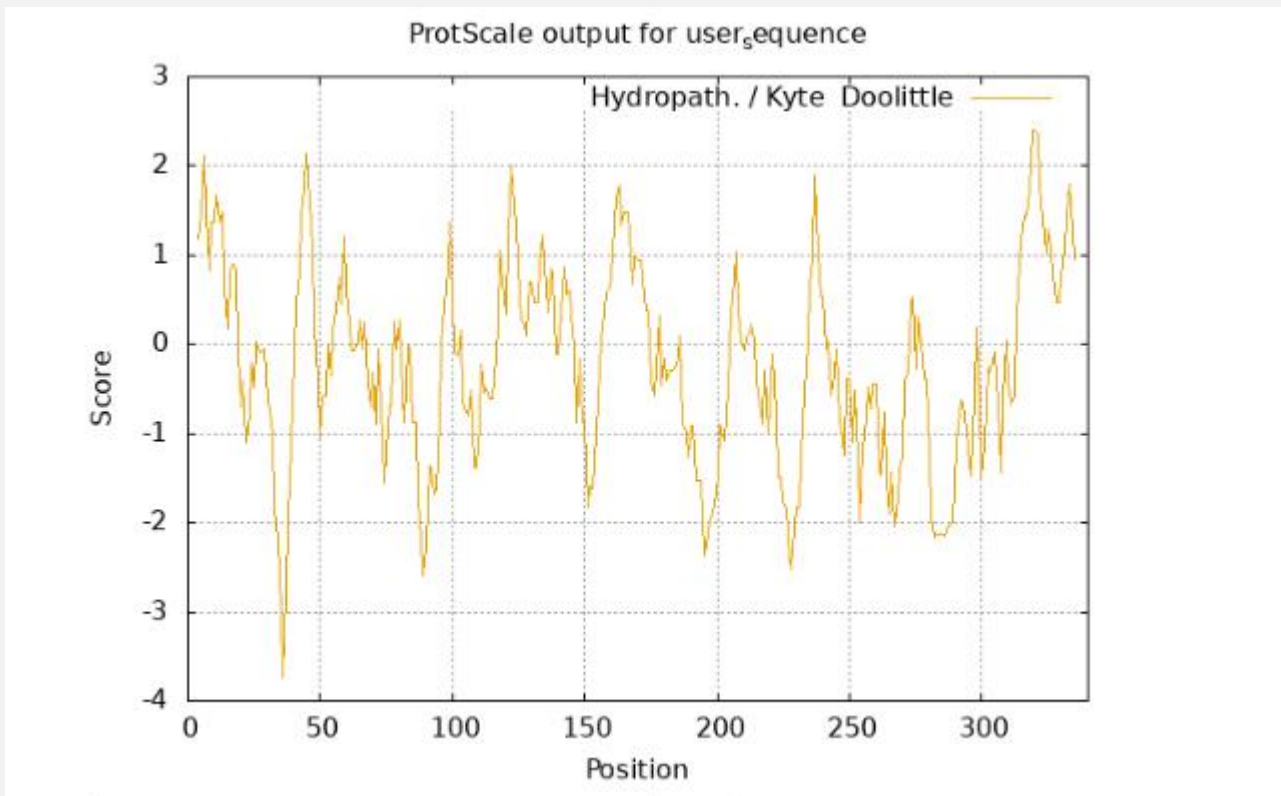
# 蛋白质理化性质分析



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## 亲疏水性分析



MIN: -3.744, MAX: 2.400

Sequence:

```
MNMVSVSAAVCKPVVASFNPASLRNMDLSLFRHHRNNKEKV  
YGMWKRNMHRLDATEVFLKNATRQEEAEEAWEDHVLSKSRRI
```

Scale: **Hydropathicity.**

Window size: 9

Scale not normalized.

Relative weight for window edges: 100 %

Weight variation model: linear

数据来源: ExPASy-ProtScale

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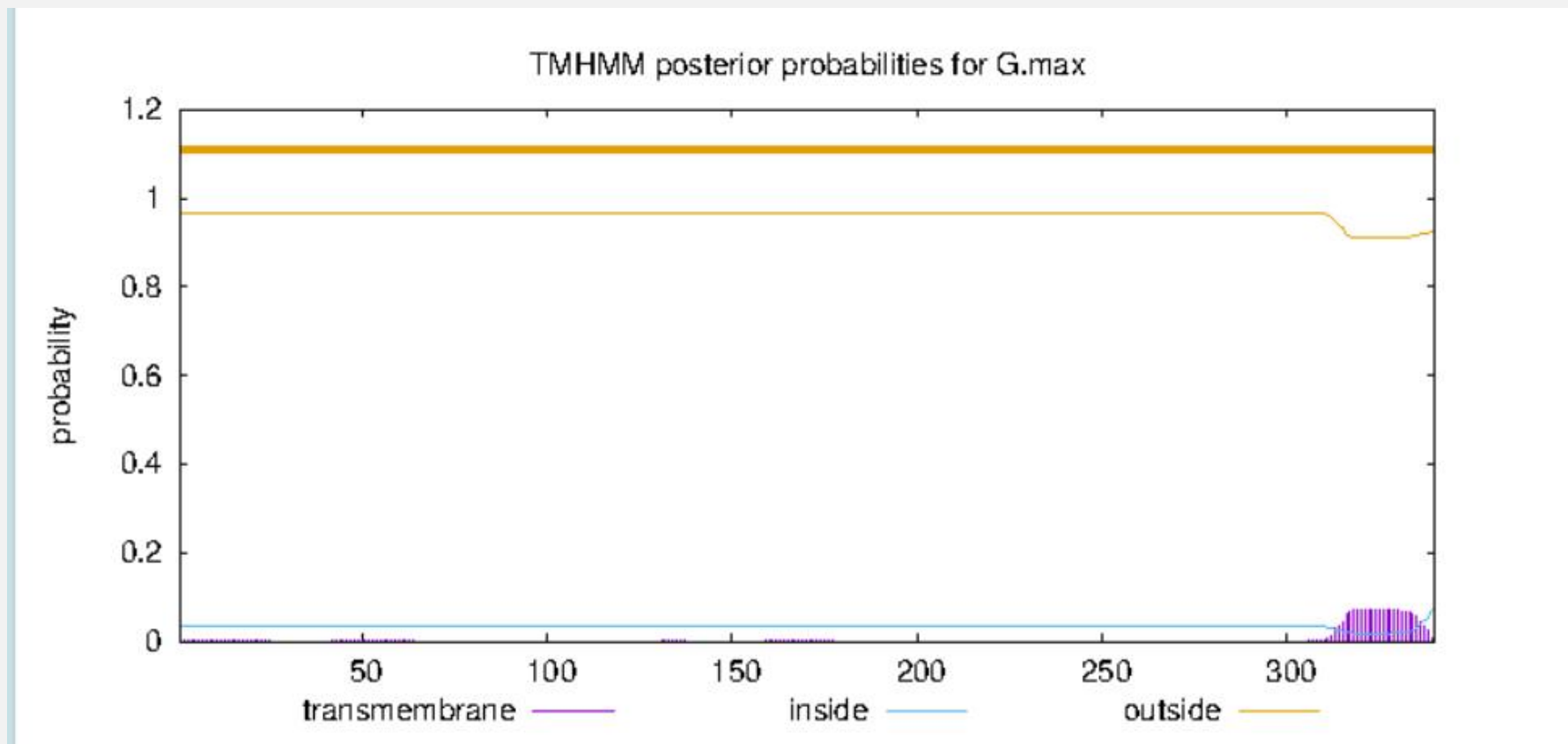
# 蛋白质理化性质分析



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## 跨膜结构域预测



数据来源: TMHMM

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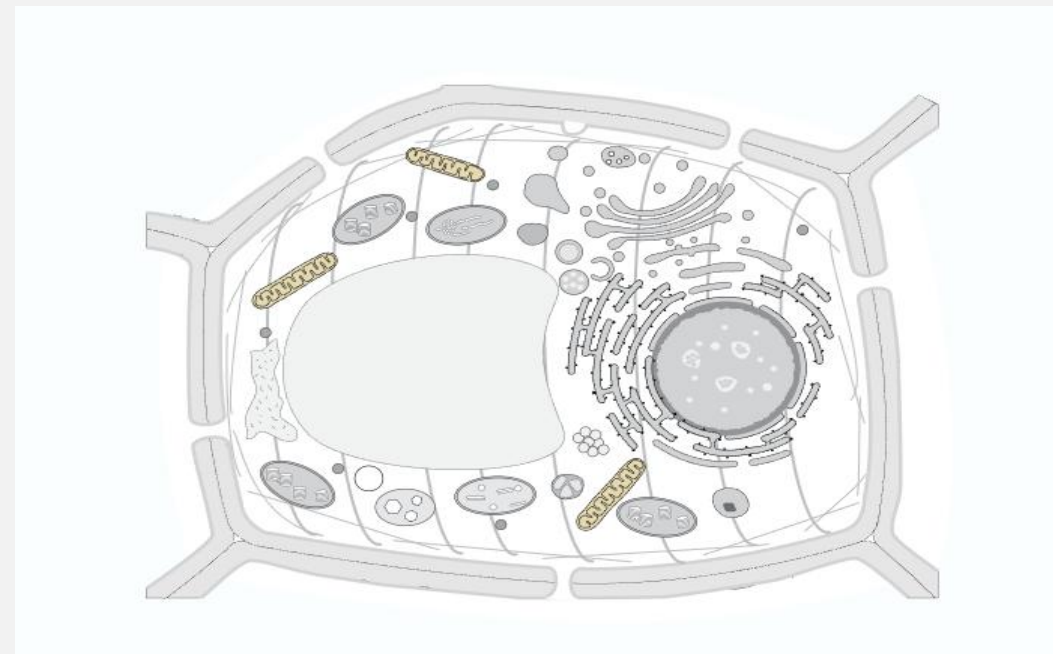
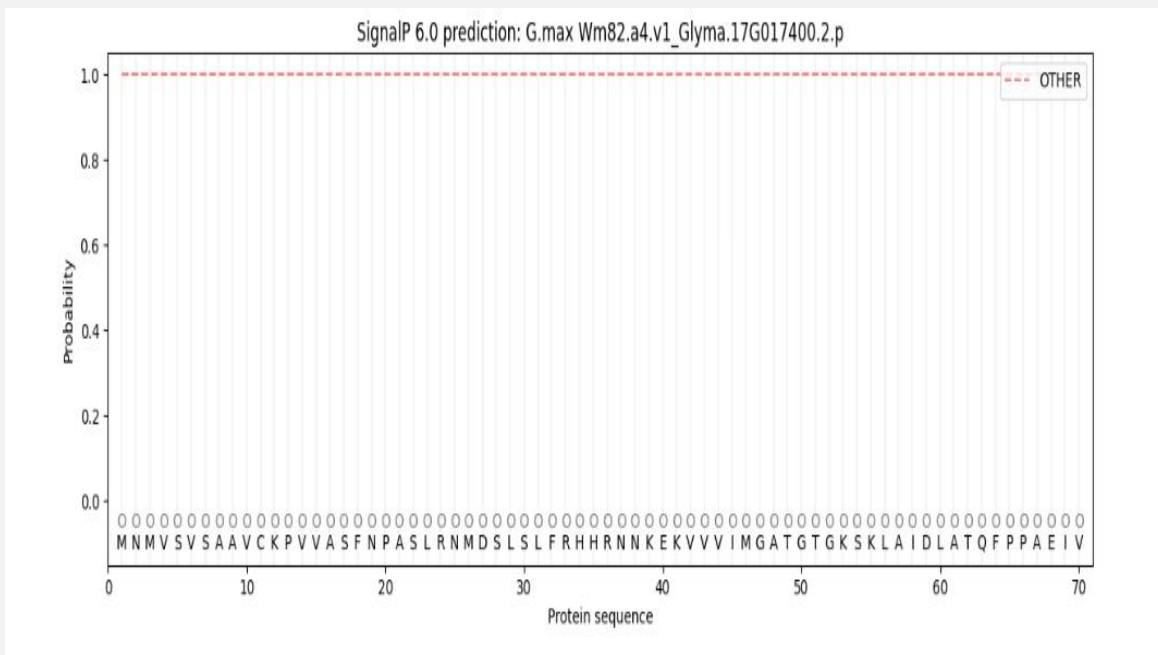
# 蛋白质理化性质分析

## 信号肽和亚细胞定位



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根据以上理化性质分析结果，该蛋白质无跨膜结构，无信号肽且为亲水性，与亚细胞定位显示该蛋白只定位于线粒体中结果相符。

数据来源: SignalP-6.0 UniProt

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# 蛋白质结构预测

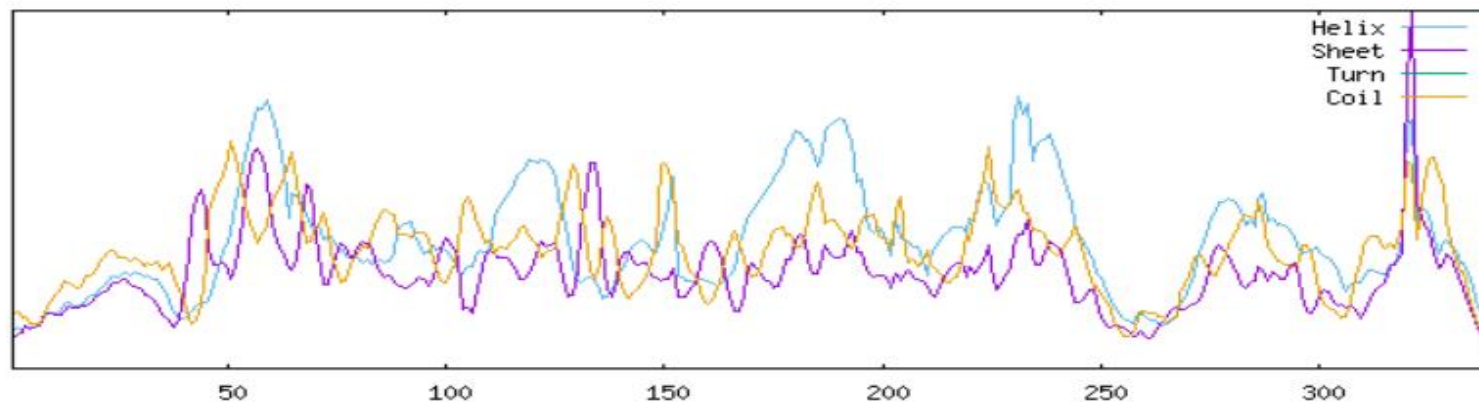
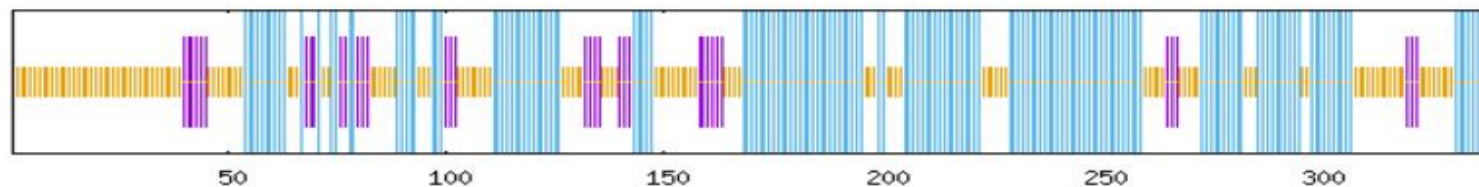
## 二级结构



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```
SOPMA :  
Alpha helix      (Hh) : 163 is 47.94%  
310 helix      (Gg) : 0 is 0.00%  
Pi helix        (Ii) : 0 is 0.00%  
Beta bridge     (Bb) : 0 is 0.00%  
Extended strand (Ee) : 36 is 10.59%  
Beta turn       (Tt) : 0 is 0.00%  
Bend region     (Se) : 0 is 0.00%  
Random coil     (Cc) : 141 is 41.47%  
Ambiguous states (?) : 0 is 0.00%  
Other states    : 0 is 0.00%
```



数据来源: SOPMA

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# 蛋白质结构预测

## 三级结构



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Structure Assessment

Compare

Download files Display files

Oligo-State: Monomer GMQE: 0.85

Template: A0A0R0F723.1.A adenylate dimethylallyltransferase (ADP/ATP-dependent) Seq Identity: 100.00% Coverage:

AlphaFold DB model of A0A0R0F723\_SOYBN (gene: LOC100778430, organism: Glycine max (Soybean) (Glycine hispida))

Biounit Oligo State: Monomer

QSQE: -

Method: AlphaFold v2

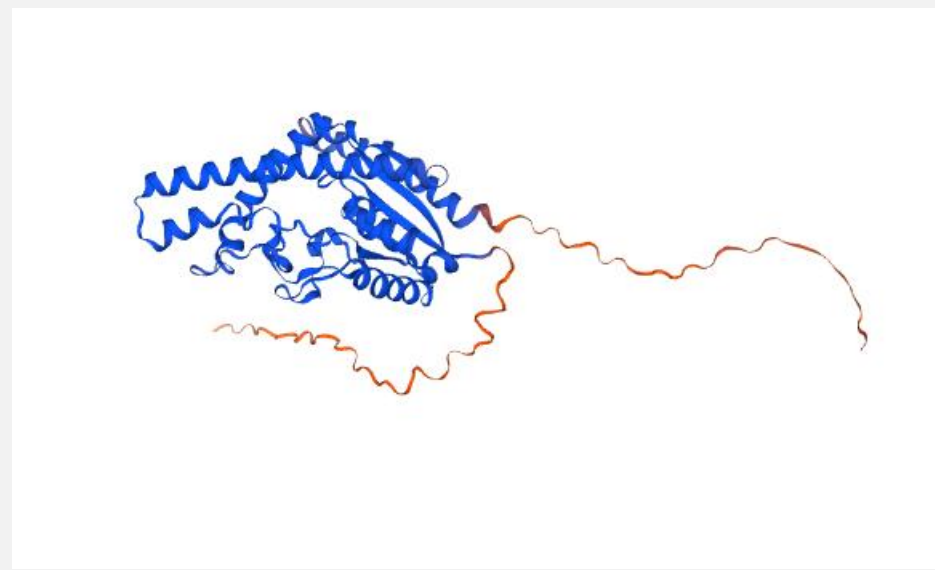
Seq Similarity: 0.61

Coverage: 1.00

Range: 1-340

Model-Template Alignment

Model_01	MNMVSVSAAYCKPVVASFNPASLRNMDLSL	30
A0A0R0F723.1.A	MNMVSVSAAYCKPVVASFNPASLRNMDLSL	30
Model_01	LFRHHRNNKEKVVVYDCAATGIGKSKLAIDL	60
A0A0R0F723.1.A	LFRHHRNNKEKVVVYDCAATGIGKSKLAIDL	60
Model_01	ATQFPFAEIVYSDKMQVDEGLDITITNKVTE	90
A0A0R0F723.1.A	ATQFPFAEIVYSDKMQVDEGLDITITNKVTE	90
Model_01	EEERGVLHMLLGTDPNPNNTNFTAQDFCDHAT	120
A0A0R0F723.1.A	EEERGVLHMLLGTDPNPNNTNFTAQDFCDHAT	120
Model_01	LAVGSIDCRDGLPITAGCSNSFLDALVNH	150
A0A0R0F723.1.A	LAVGSIDCRDGLPITAGCSNSFLDALVNH	150
Model_01	TEFRLRYECCFLWYDVSPLPVLHSSLSARVD	180
A0A0R0F723.1.A	TEFRLRYECCFLWYDVSPLPVLHSSLSARVD	180
Model_01	RMIHAGQVHEVREKSFQYHNDYTVGLRDAI	210
A0A0R0F723.1.A	RMIHAGQVHEVREKSFQYHNDYTVGLRDAI	210
Model_01	GVPEFHDFFRAEADGADERTKQRLLEAAIA	240
A0A0R0F723.1.A	GVPEFHDFFRAEADGADERTKQRLLEAAIA	240
Model_01	SLKTNNCSLANRQVQKIHRLYGMWKRNMHR	270
A0A0R0F723.1.A	SLKTNNCSLANRQVQKIHRLYGMWKRNMHR	270
Model_01	LDATEVFLKNATRQEEAEEAWEDHVLSKSR	300
A0A0R0F723.1.A	LDATEVFLKNATRQEEAEEAWEDHVLSKSR	300
Model_01	RILNKFLYEDTHVAPAGIAASVVIASSPPA	330
A0A0R0F723.1.A	RILNKFLYEDTHVAPAGIAASVVIASSPPA	330
Model_01	MAAAAAATH	340
A0A0R0F723.1.A	MAAAAAATH	340



数据来源: SWISS-MODEL

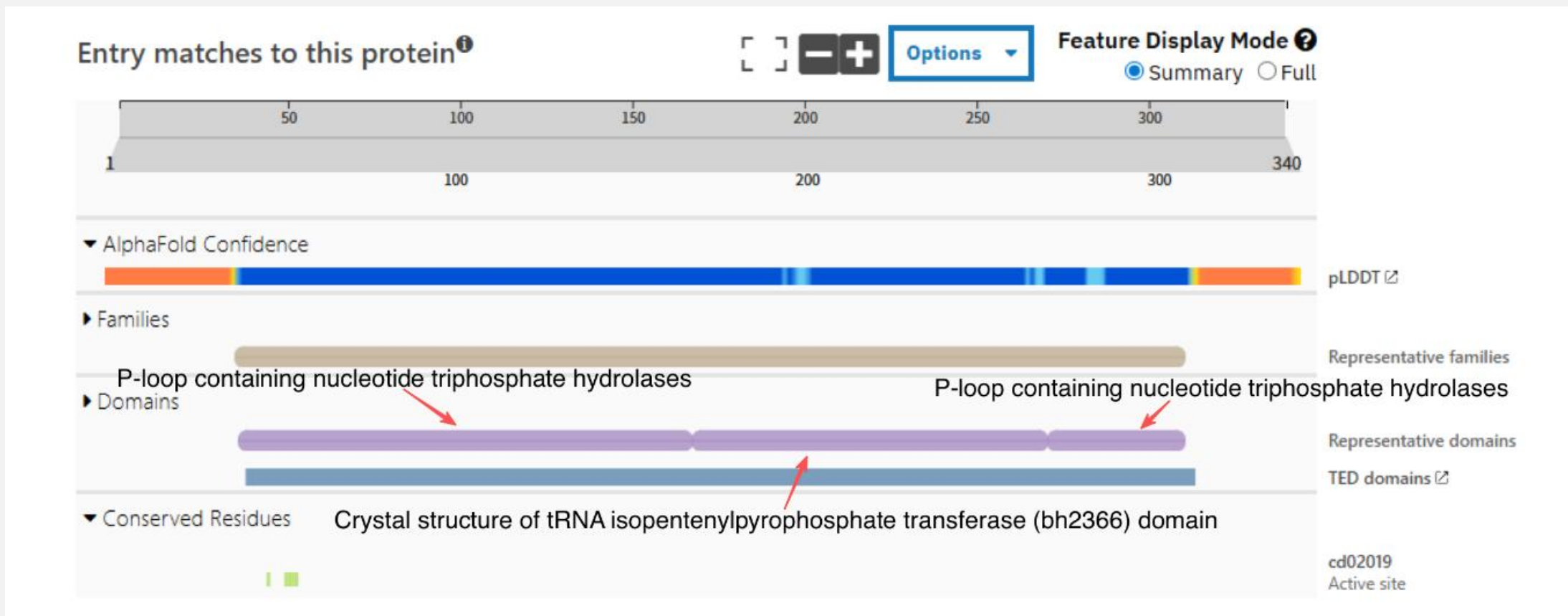
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# 蛋白质结构预测



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数据来源: InterPro

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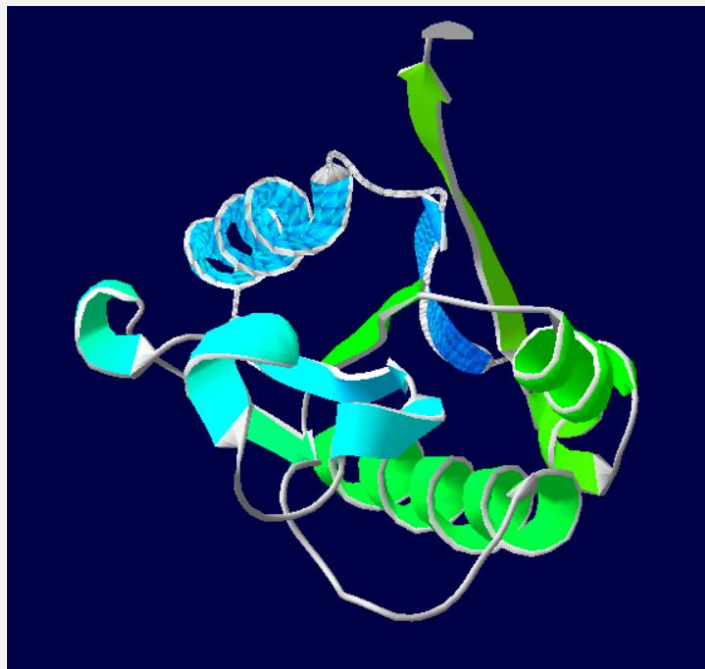
# 蛋白质结构预测

## 蛋白质各结构域结构



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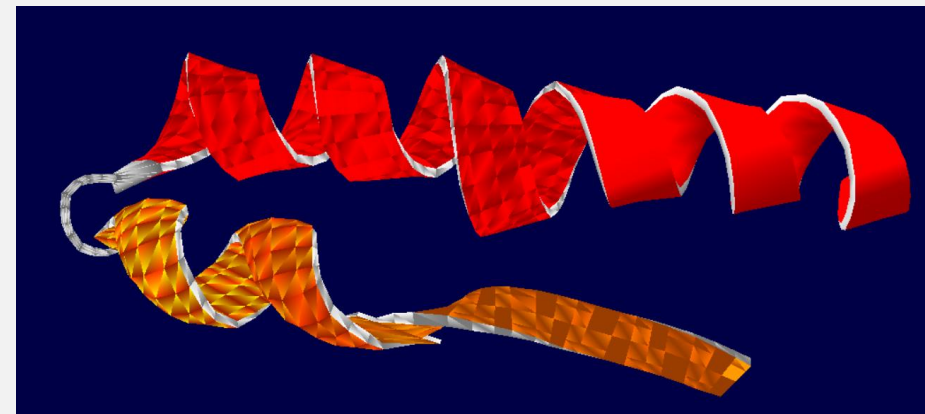
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P-loop containing nucleotide triphosphate hydrolases



Crystal structure of tRNA isopentenylpyrophosphate transferase (bh2366) domain



P-loop containing nucleotide triphosphate hydrolases

数据来源: Swiss PDB Viewer

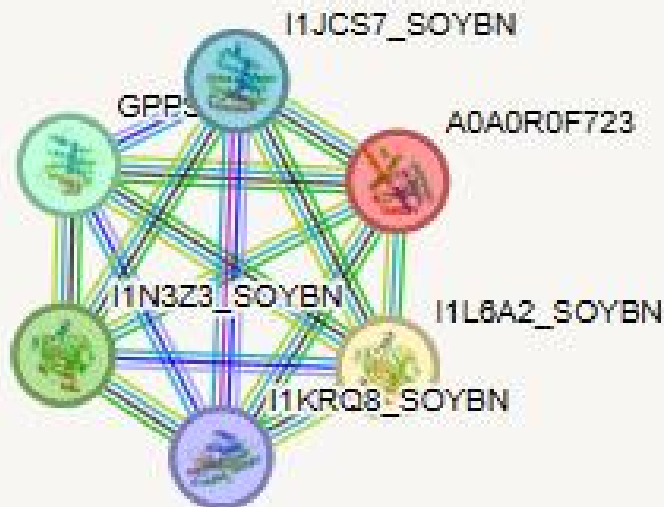
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# 蛋白与蛋白互作分析

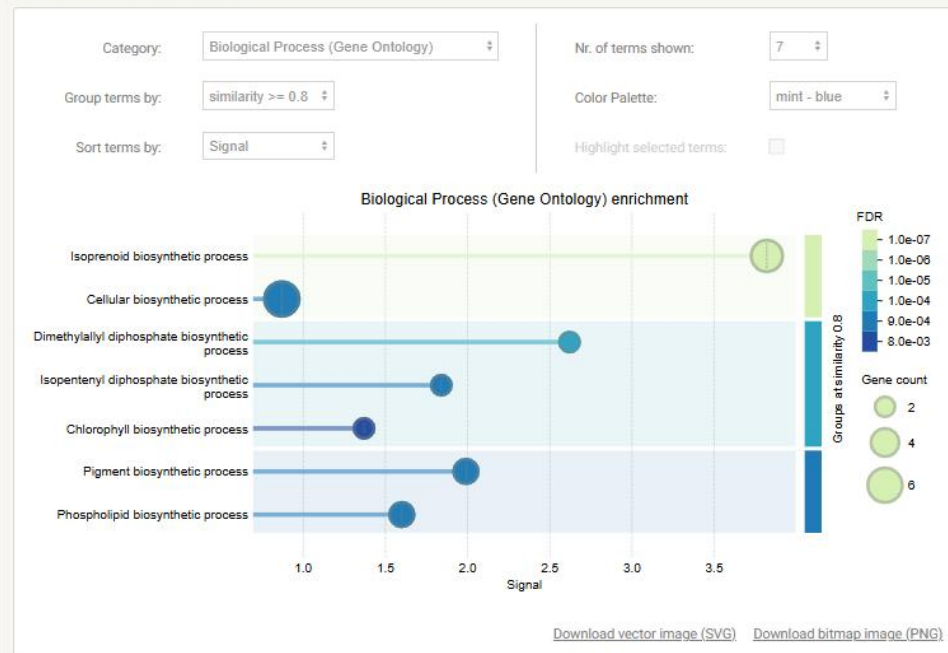


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Functional enrichment visualization



Your Input:

A0A0R0F723 Uncharacterized protein. (340 aa)

Predicted Functional Partners:

Partner	Description	Neighborhood	Gene Fusion	Cooccurrence	Coexpression	Experiments	Databases	Textmining	[Homology]	Score
I1L6A2_SOYBN	Nudix hydrolase domain-containing protein.									0.687
I1N3Z3_SOYBN	Nudix hydrolase domain-containing protein.									0.687
GPPS	Geranyl-diphosphate synthase.									0.674
I1JCS7_SOYBN	Uncharacterized protein; Belongs to the FPP/GGPP synthase family.									0.674
I1KRQ8_SOYBN	Uncharacterized protein; Belongs to the FPP/GGPP synthase family.									0.674

数据来源: STRING

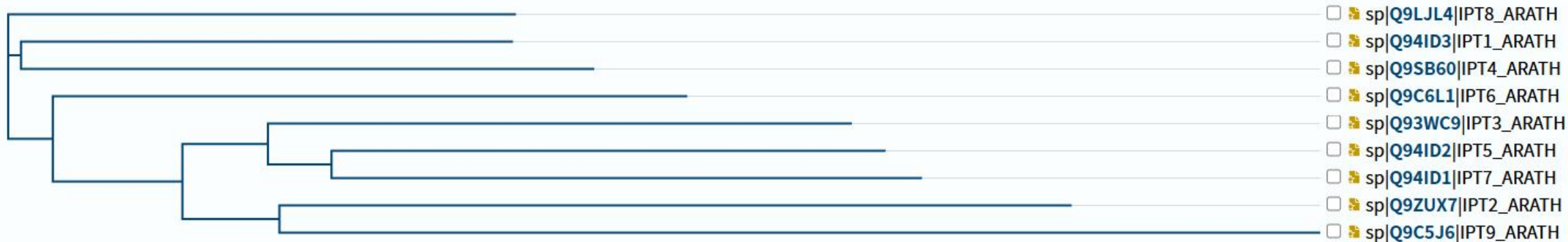
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# 蛋白质多序列比对



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拟南芥IPT家族基因

数据来源: UniProt

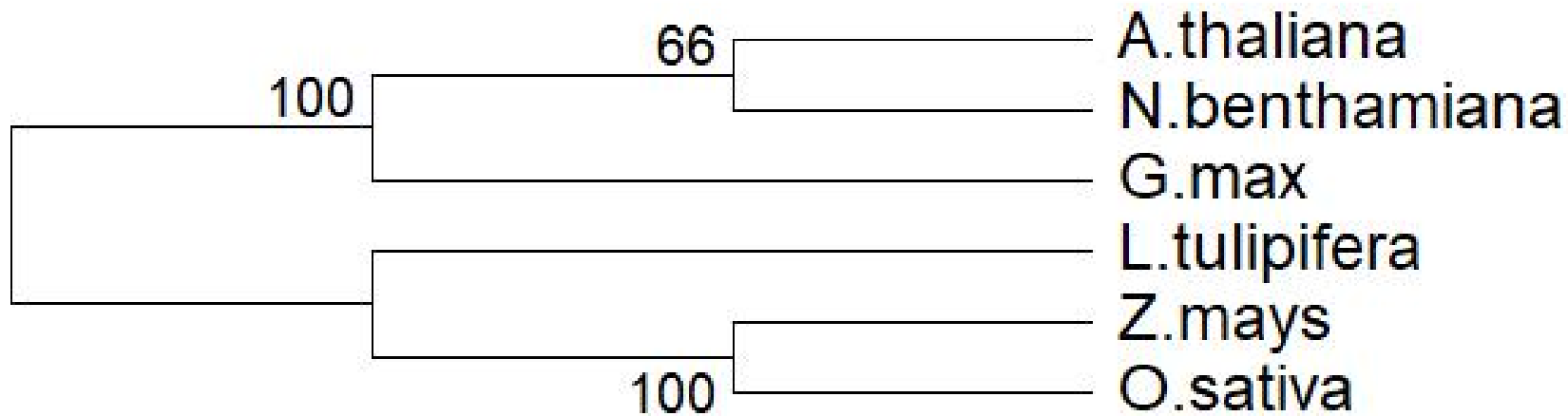
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# 系统发育分析



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不同物种中IPT基因

数据来源: MEGA

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# 总结



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了解异戊烯基转移酶蛋白的理化性质、结构等基本信息。

通过对拟南芥和其他物种的异戊烯基转移酶进行序列比对，了解它们之间的异同，为后续实验提供思路。

在接下来的研究中我们可以继续深入研究该蛋白质的作用机制，如何具体影响大豆遗传转化效率。





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请老师和同学们批评指正