

# OsSGD1调控水稻幼苗生长发育的功能和机理

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# 一、研究背景：

- 随着社会发展，劳动力向城市汇集，土地集中管理、农业机械化程度升高，轻简化栽培方式正在大规模兴起。其中最具有代表性的是水稻直播技术。
- 水稻直播种植是指在水稻栽培过程中省去育秧和移栽作业，在本田里直接播种、培育水稻的技术。
- 水稻直播技术，具有巨大的优势，省工省力，节约成本，生育期缩短等。也存在较多的问题，比如出苗较难、出苗不齐、抗倒伏能力较差等。
- 在一定深度播种能使水稻更好的吸收土壤养分，还可以保护幼苗免受低温伤害，同时水稻需要应对水淹缺氧等问题，因此研究水稻种子萌发及发育调控机理具有重要的意义。

# 研究背景

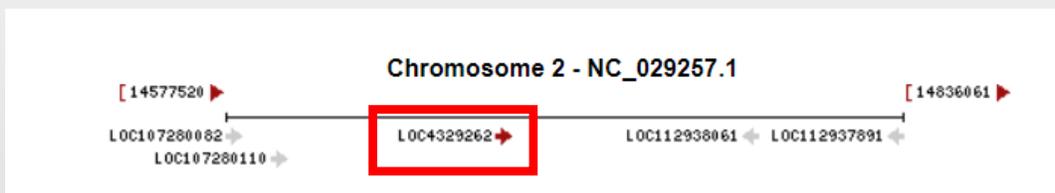
- 实验室前期发现OsSGD1基因在水稻株高和籽粒发育中有着重要作用。
- OsSGD1的突变体和敲除株系均表现出株高半矮化的表型，过表达材料表现出较野生型高的表型。
- OsSGD1可通过调控水稻分生组织细胞周期活动影响水稻的生长速度。
- 目前还没有对OsSGD1基因的报道。

## 二、OsSGD1基本信息

登录号: Os02g0450000

登录号: LOC4329262

染色体位置:



BETA THE NEW UNIPROT WEBSITE IS

### UniProtKB - Q6EQZ3 (Q6EQZ3\_ORYSJ)

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

**Entry**

Protein Submitted name: **Os02g0450000 protein**

Gene **Os02g0450000**

Organism *Oryza sativa subsp. japonica (Rice)*

Status [Unreviewed](#) - Annotation score: ●○○○○ - Protein predicted<sup>i</sup>

**Names & Taxonomy<sup>i</sup>**

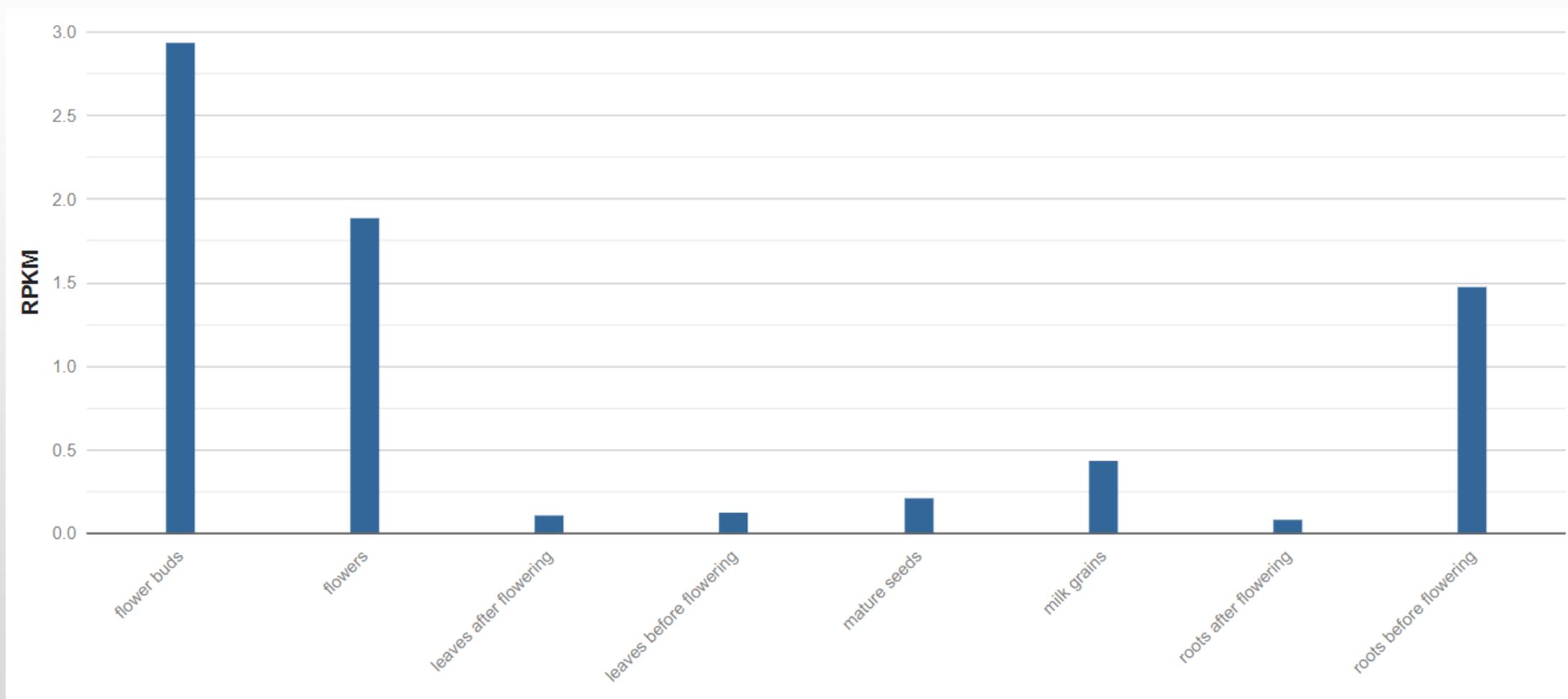
Protein names <sup>i</sup>	Submitted name: Os02g0450000 protein <a href="#">Imported</a>
Gene names <sup>i</sup>	Ordered Locus Names: Os02g0450000 <a href="#">Imported</a> ORF Names: OSNPB_020450000 <a href="#">Imported</a>
Organism <sup>i</sup>	<i>Oryza sativa subsp. japonica (Rice)</i> <a href="#">Imported</a>
Taxonomic	39947 [NCBI]

**Feature table**

- Function
- Names & Taxonomy
- Subcellular location
- Pathology & Biotech
- PTM / Processing

在Uniprot数据库中功能及细胞定位没有相关信息。

### 三、水稻不同发育阶段各器官转录组学分析



Show anatomograms

Filter your results

Oryza sativa

Organism part

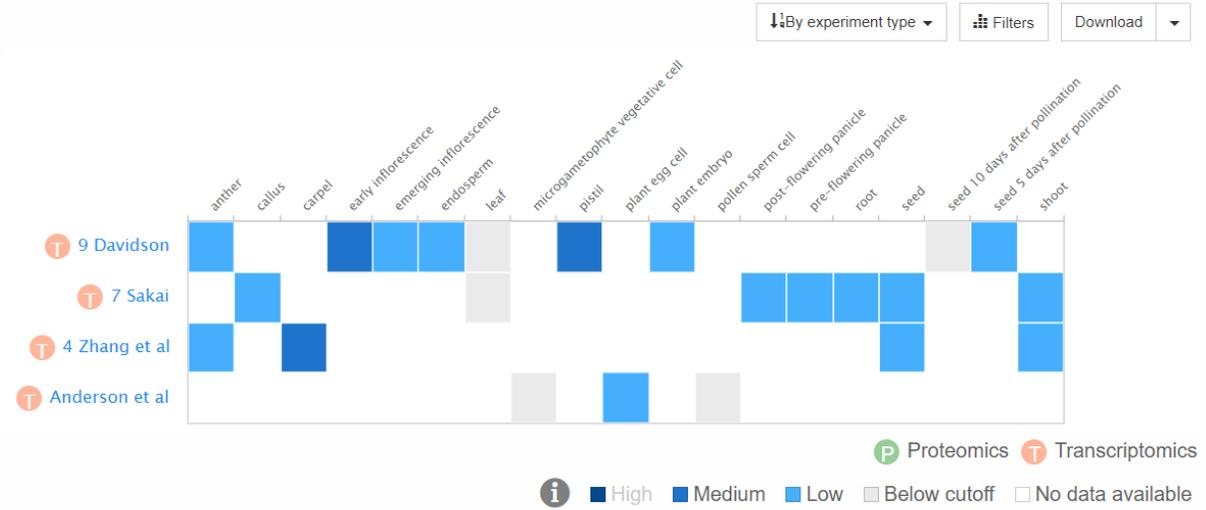
Cultivar

Fraction

Sampling site

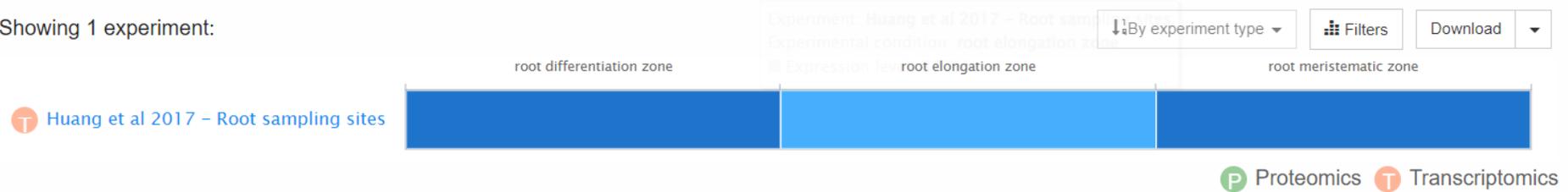
Organism part

Showing 4 experiments:



Sampling site

Showing 1 experiment:



其在早花絮和雌蕊中表达量最高，且在分生区中大量表达。

# 四、OsSGD1序列分析

## 1、在NCBI中用SGD1DNA序列进行序列比对

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
PREDICTED: <i>Oryza sativa</i> Japonica Group uncharacterized LOC4329262 (LOC4329262) .transcript va...	<i>Oryza sativa</i> Ja...	4494	4494	100%	0.0	100.00%	5543	<a href="#">XM_026023465.1</a>
PREDICTED: <i>Oryza sativa</i> Japonica Group uncharacterized LOC4329262 (LOC4329262) .transcript va...	<i>Oryza sativa</i> Ja...	4494	4494	100%	0.0	100.00%	5550	<a href="#">XM_026023464.1</a>
PREDICTED: <i>Oryza sativa</i> Japonica Group uncharacterized LOC4329262 (LOC4329262) .transcript va...	<i>Oryza sativa</i> Ja...	4494	4494	100%	0.0	100.00%	5566	<a href="#">XM_015767598.2</a>
PREDICTED: <i>Oryza sativa</i> Japonica Group uncharacterized LOC4329262 (LOC4329262) .transcript va...	<i>Oryza sativa</i> Ja...	4494	4494	100%	0.0	100.00%	5571	<a href="#">XM_015767595.2</a>
<i>Oryza sativa</i> Japonica Group DNA .chromosome 2 .cultivar .Nipponbare .complete sequence	<i>Oryza sativa</i> Ja...	4494	4494	100%	0.0	100.00%	35937250	<a href="#">AP014958.1</a>
<i>Oryza sativa</i> Japonica Group genomic DNA .chromosome 2 .BAC clone:OSJNBa0055I13	<i>Oryza sativa</i> Ja...	4494	4494	100%	0.0	100.00%	169486	<a href="#">AP005648.2</a>
<i>Oryza sativa</i> Japonica Group cDNA clone J033125D04 .full insert sequence	<i>Oryza sativa</i> Ja...	4453	4453	100%	0.0	99.67%	3733	<a href="#">AK122096.1</a>
<i>Oryza sativa</i> Japonica Group cDNA clone.002-119-E09 .full insert sequence	<i>Oryza sativa</i> Ja...	3672	3672	81%	0.0	100.00%	2381	<a href="#">AK106956.1</a>

在水稻中查询到的基因都是SGD1基因的不同剪接体。



Job Title: **Nucleotide Sequence**

RID: [YTAU1BAR013](#) Search expires on 01-24 08:11 am [Download All](#)

Program: [Citation](#)

Database: nt [See details](#)

Query ID: Icl|Query\_2289

Description: None

Molecule type: dna

Query Length: 2433

Other reports: [?](#)

**Filter Results**

Percent Identity:  to

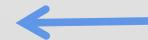
E value:  to

Query Coverage:  to

[Filter](#) [Reset](#)

**Warning:** No significant similarity found. For reasons why, [click here](#).

在模式生物拟南芥中



## 2、SGD1蛋白序列分析

### 在水稻中进行序列比对

Other reports [Distance tree of results](#) [Multiple alignment](#) [MSA viewer](#) [Filter](#) [Reset](#)

**Descriptions** Graphic Summary Alignments Taxonomy

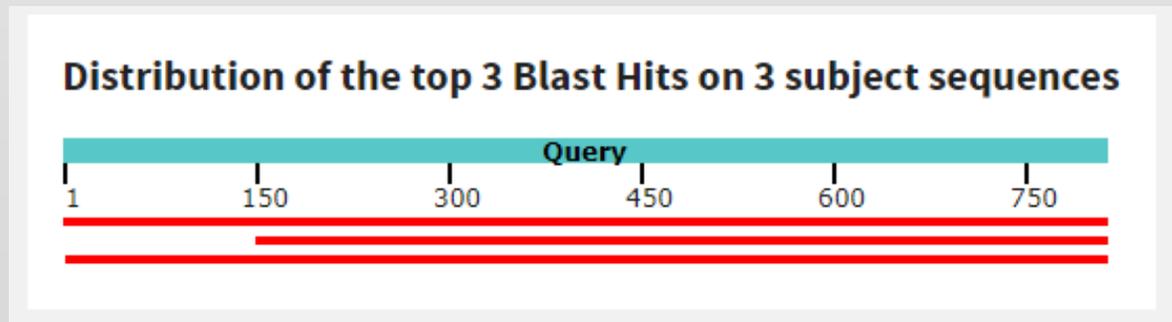
Sequences producing significant alignments [Download](#) [New](#) [Select columns](#) Show 100 [?](#)

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
<input checked="" type="checkbox"/>	<a href="#">uncharacterized protein LOC4329262 [Oryza sativa Japonica Group]</a>	<a href="#">Oryza sativa Japonica Group</a>	1113	1113	100%	0.0	100.00%	810	<a href="#">XP_015623081.1</a>
<input checked="" type="checkbox"/>	<a href="#">Os02g0450000 [Oryza sativa Japonica Group]</a>	<a href="#">Oryza sativa Japonica Group</a>	936	936	81%	0.0	100.00%	661	<a href="#">BAS78502.1</a>
<input checked="" type="checkbox"/>	<a href="#">uncharacterized protein LOC4335326 [Oryza sativa Japonica Group]</a>	<a href="#">Oryza sativa Japonica Group</a>	843	843	99%	0.0	68.84%	770	<a href="#">XP_015634630.1</a>

同一个基因

在水稻中就只有一条序列与其同源



# 在模式生物拟南芥中进行序列比对

Descriptions Graphic Summary Alignments Taxonomy

Sequences producing significant alignments Download New Select columns Show 100 ?

select all 9 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="#">F5O11.10 [Arabidopsis thaliana]</a>	<a href="#">Arabidopsis thaliana</a>	713	713	96%	0.0	50.74%	856	<a href="#">AAF79656.1</a>
<input checked="" type="checkbox"/>	<a href="#">hypothetical protein AT1G12380 [Arabidopsis thaliana]</a>	<a href="#">Arabidopsis thaliana</a>	713	713	96%	0.0	50.74%	793	<a href="#">NP_172700.1</a>
<input checked="" type="checkbox"/>	<a href="#">unnamed protein product [Arabidopsis thaliana]</a>	<a href="#">Arabidopsis thaliana</a>	712	712	96%	0.0	50.68%	794	<a href="#">CAA0195212.1</a>
<input checked="" type="checkbox"/>	<a href="#">unnamed protein product [Arabidopsis thaliana]</a>	<a href="#">Arabidopsis thaliana</a>	686	686	96%	0.0	49.32%	765	<a href="#">CAD5312511.1</a>
<input checked="" type="checkbox"/>	<a href="#">hypothetical protein AT1G62870 [Arabidopsis thaliana]</a>	<a href="#">Arabidopsis thaliana</a>	708	708	96%	0.0	52.28%	762	<a href="#">NP_176475.2</a>
<input checked="" type="checkbox"/>	<a href="#">unnamed protein product [Arabidopsis thaliana]</a>	<a href="#">Arabidopsis thaliana</a>	708	708	96%	0.0	52.15%	760	<a href="#">VYS49813.1</a>
<input checked="" type="checkbox"/>	<a href="#">hypothetical protein AXX17_AT1G56170 [Arabidopsis thaliana]</a>	<a href="#">Arabidopsis thaliana</a>	708	708	96%	0.0	52.53%	760	<a href="#">OAP14698.1</a>
<input checked="" type="checkbox"/>	<a href="#">unnamed protein product [Arabidopsis thaliana]</a>	<a href="#">Arabidopsis thaliana</a>	705	705	96%	0.0	52.03%	760	<a href="#">CAA0311422.1</a>
<input checked="" type="checkbox"/>	<a href="#">unnamed protein product [Arabidopsis thaliana]</a>	<a href="#">Arabidopsis thaliana</a>	689	689	94%	0.0	51.81%	720	<a href="#">CAD5316120.1</a>

Other reports [Distance tree of results](#) [Multiple alignment](#) [MSA viewer](#)

Descriptions **Graphic Summary** Alignments Taxonomy

[hover to see the title](#) [click to show alignments](#)  Show Conserved Domains Alignment Scores ■ < 40 ■ 40 - 50 ■ 50 - 80 ■ 80 - 200 ■ >= 200 ?

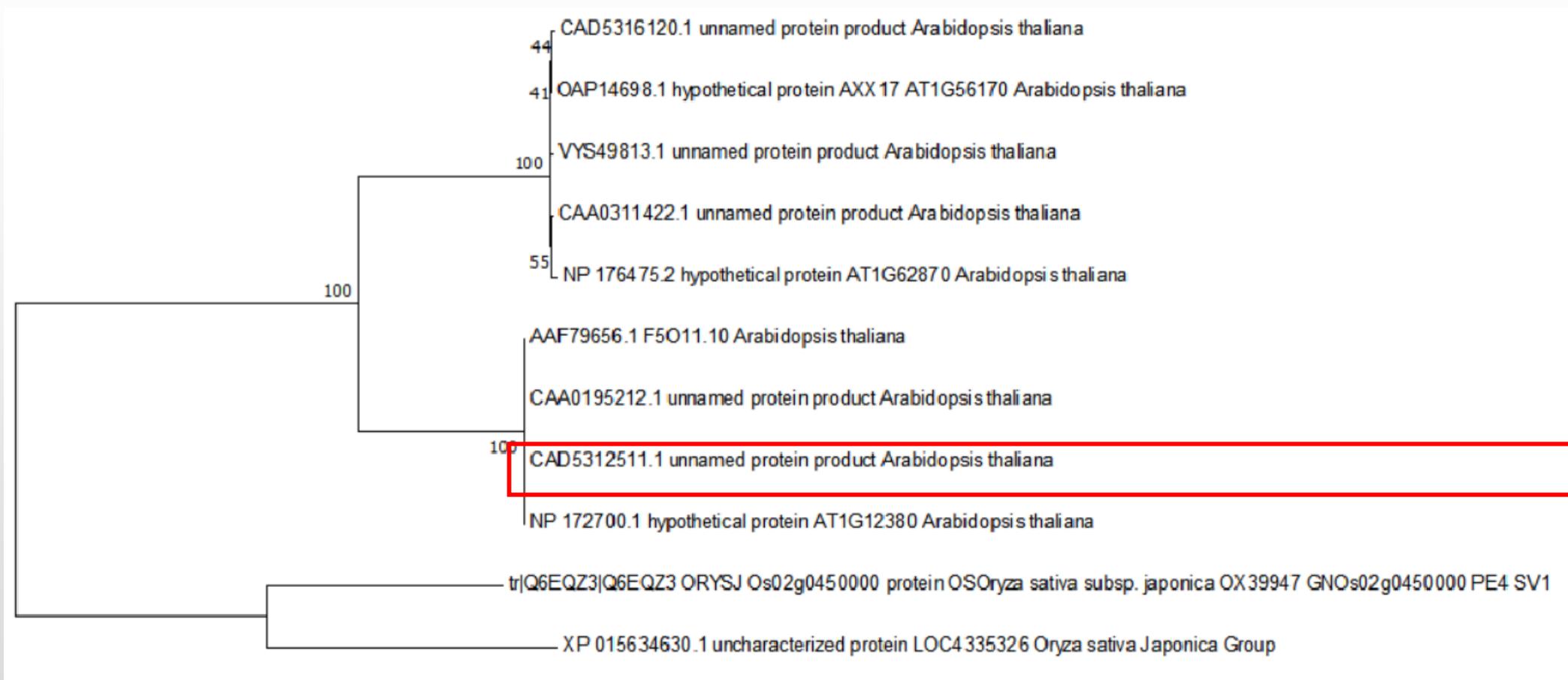
9 sequences selected ?

**No putative conserved domains have been detected**

**Distribution of the top 9 Blast Hits on 9 subject sequences**

Subject Sequence	Query Coverage
1	100%
2	100%
3	100%
4	100%
5	100%
6	100%
7	100%
8	100%
9	100%

### 3、SGD1同源蛋白进行进化树分析



## OMA GROUP 789847 with 45 members.

Fingerprint: KPRVGQC | Uncharacterized protein

Sequences (fasta)

Members 45

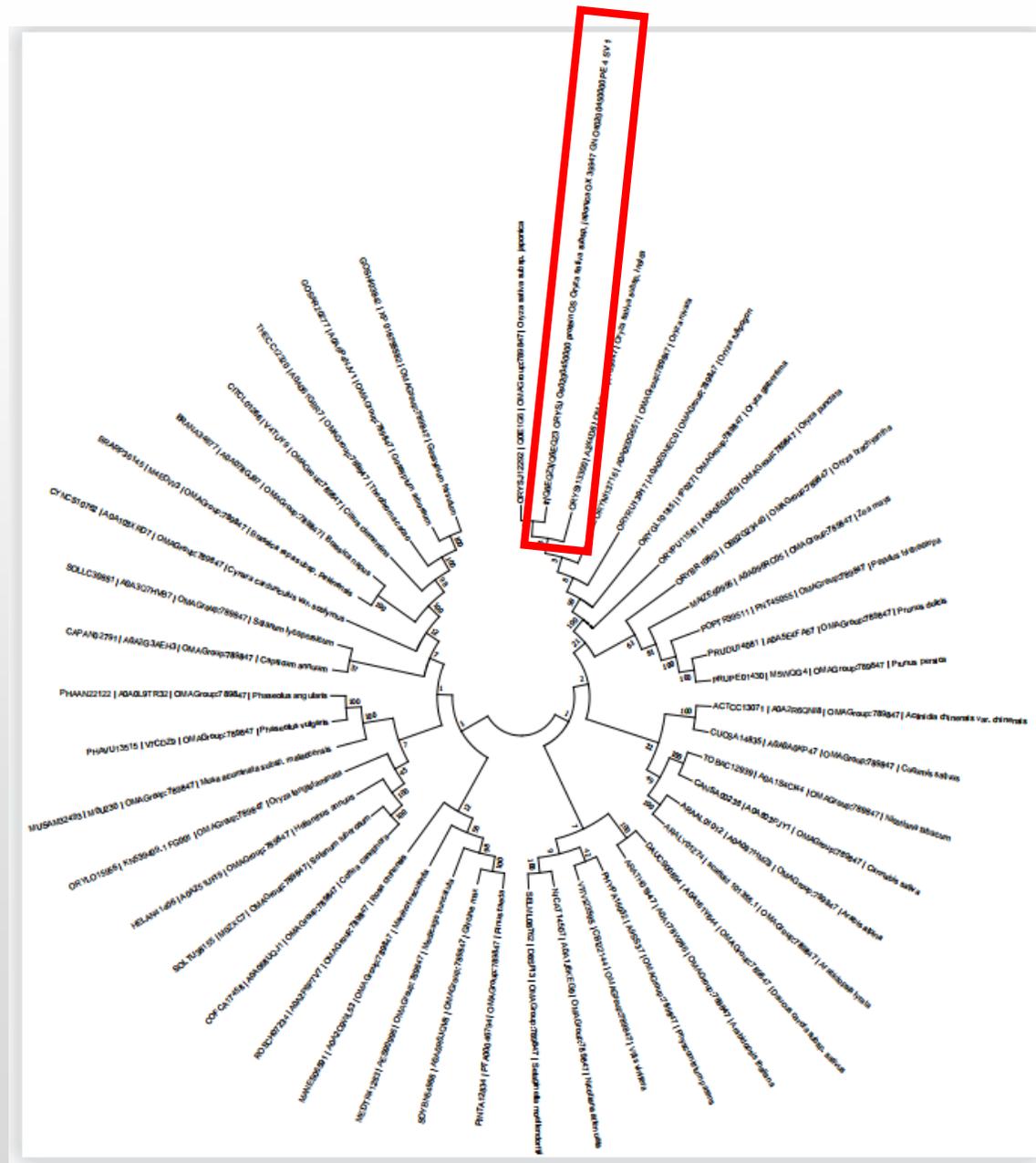
FILTER BY TAXONOMY:

- All Taxa
- Eukaryota
- Viridiplantae
- Fungi
- Metazoa

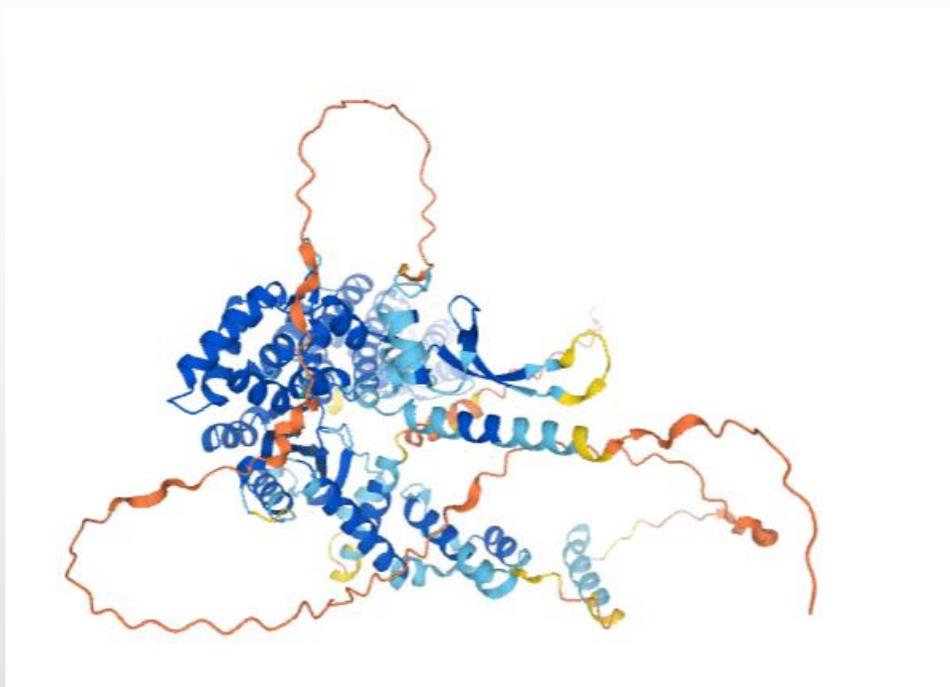
Domains	Taxon	Protein ID
	Volvox carteri	<a href="#">VOLCA14307</a>
	Physcomitrium patens	<a href="#">PHYPA16032</a>
	Pinus taeda	<a href="#">PINTA12834</a>
	Oryza brachyantha	<a href="#">ORYBR10853</a>

在植物中有45个SGD1家族，并将他们做成进化树分析。

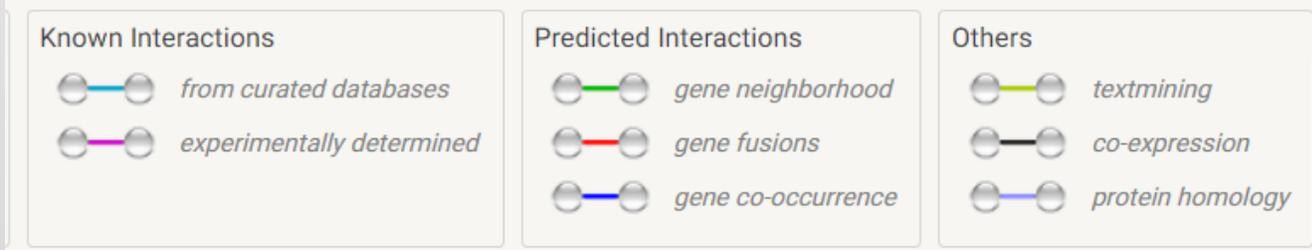
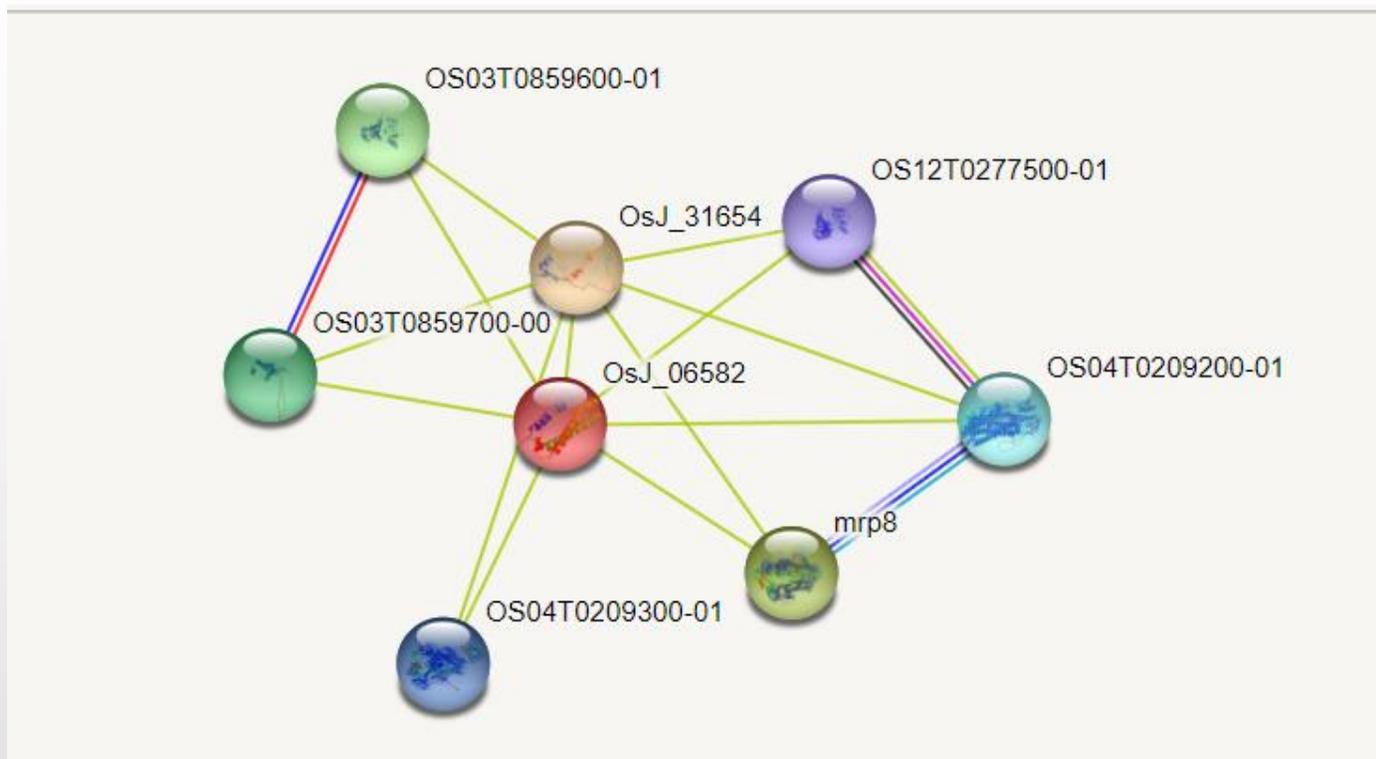
其与水稻中的QOE1G6蛋白同源性最高。



# 五、蛋白结构分析

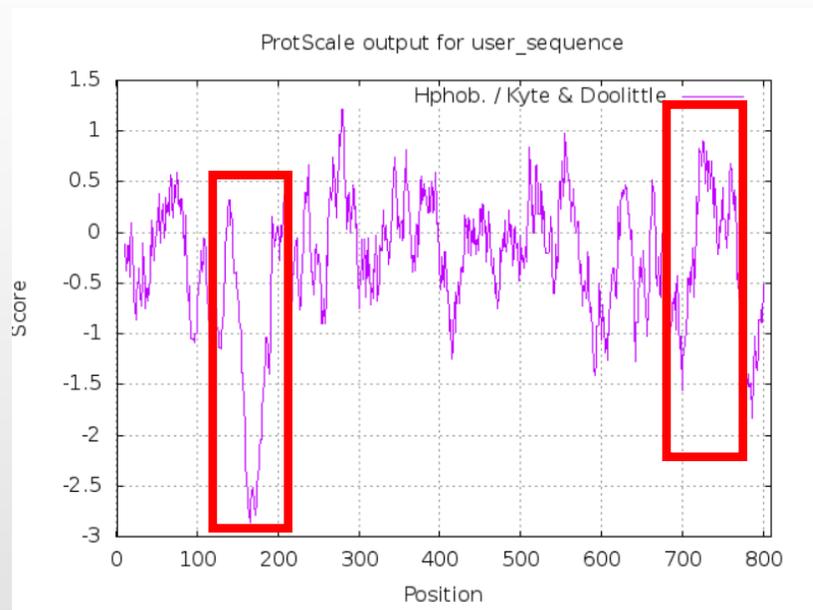


Uniprot数据库中的蛋白结构

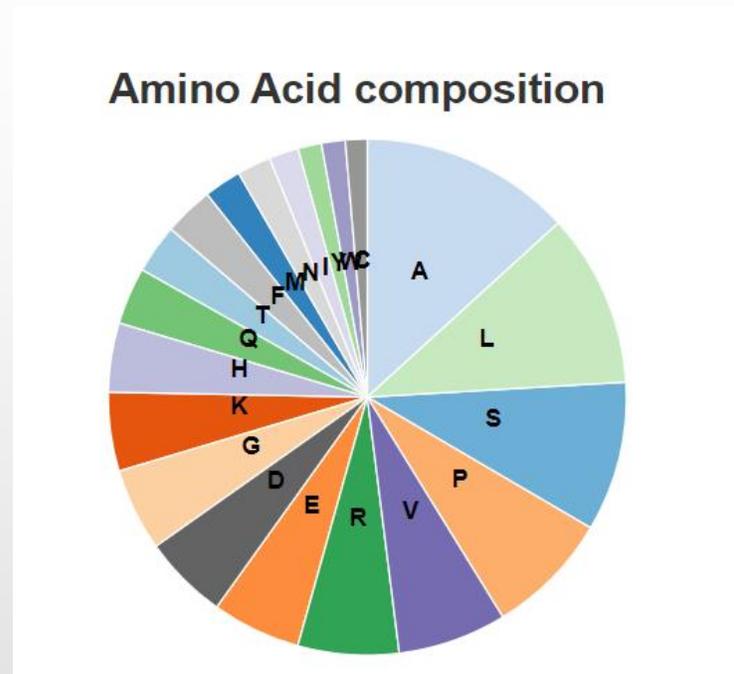


蛋白互动情况

# 1、一级结构分析



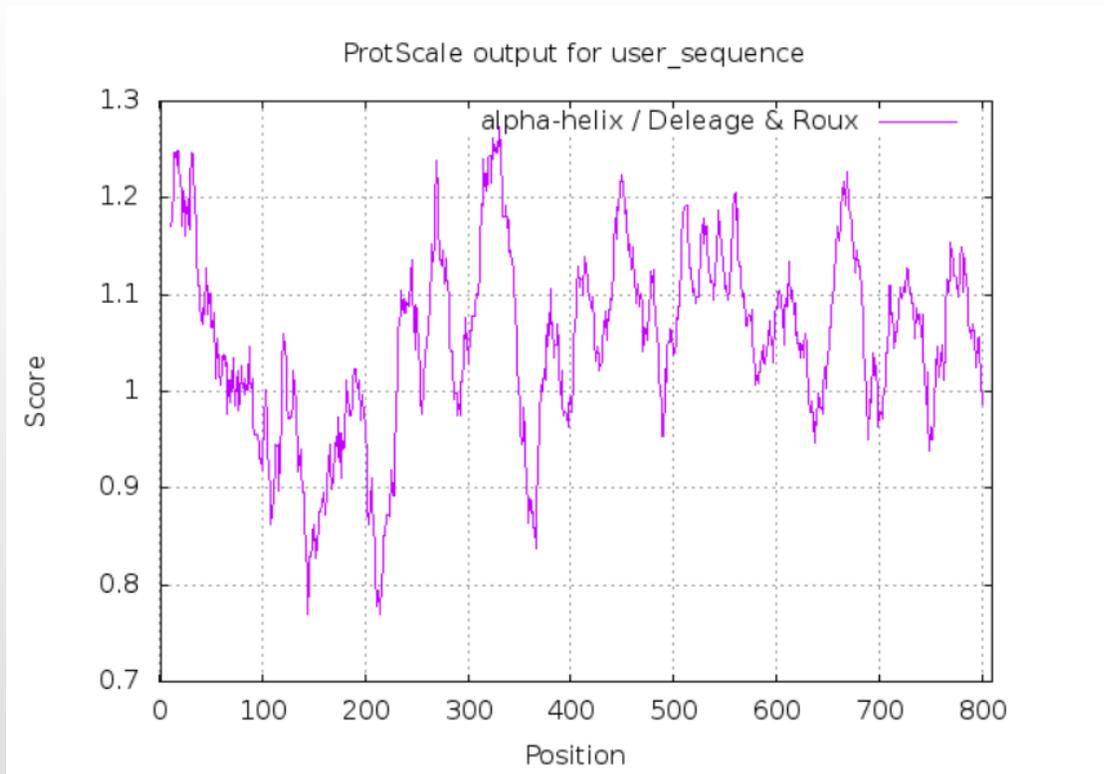
亲疏水性



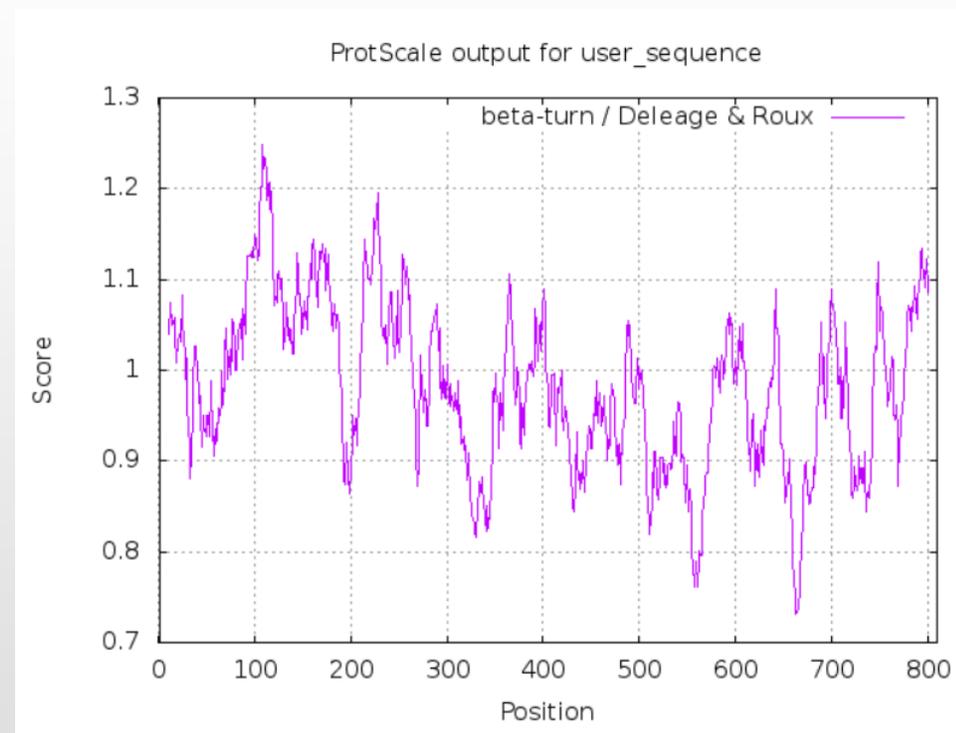
氨基酸组成

丙氨酸: 13.21%  
亮氨酸: 10.86%  
丝氨酸: 9.38%

## 2、二级结构分析



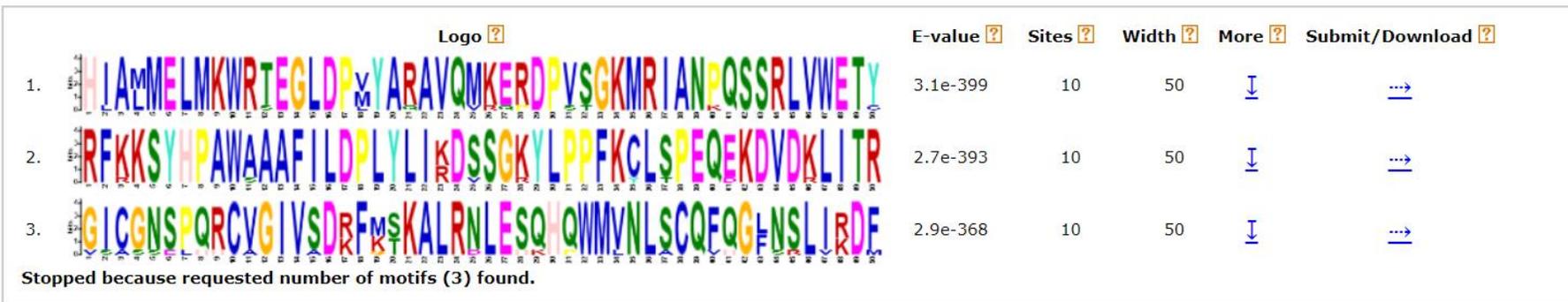
$\alpha$ -螺旋



$\beta$ -折叠

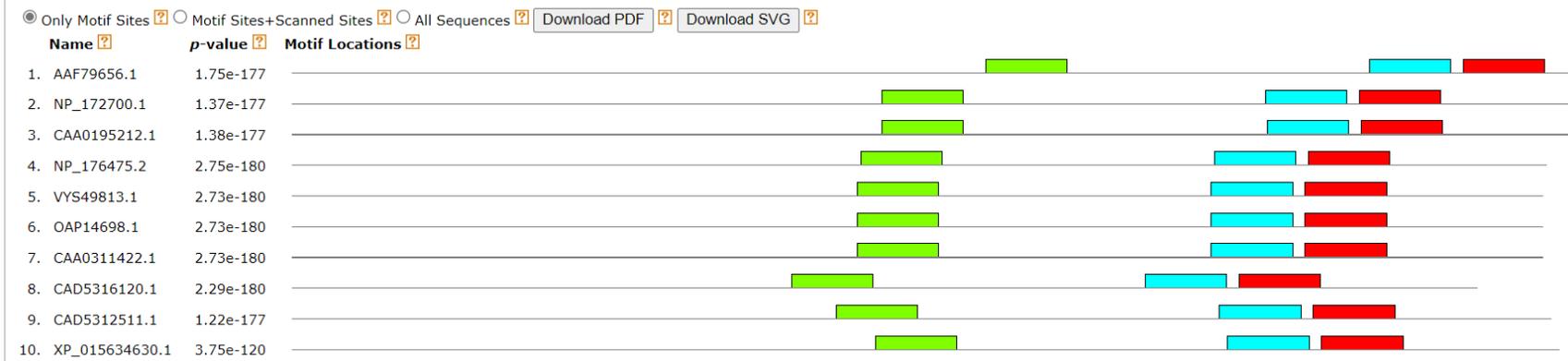
# 3、结构域预测

## DISCOVERED MOTIFS



通过MEME网站预测这10个同源蛋白的motif，发现存在相同的motif。

## MOTIF LOCATIONS



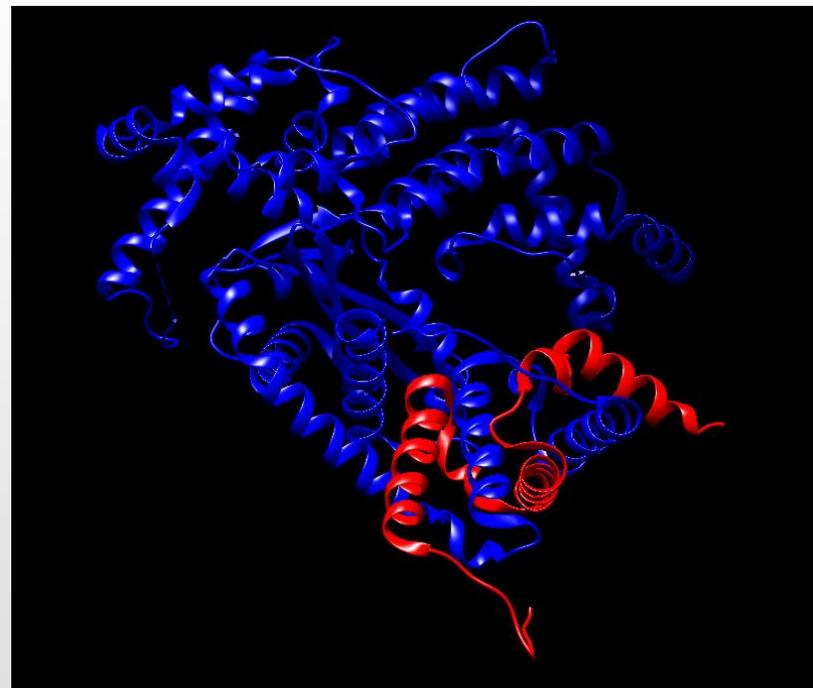
发现这些同源蛋白含有一些相同的保守结构位点。

## 4、SGD1三级结构

主要由 $\alpha$ 螺旋和 $\beta$ 折叠构成



PBD号为: AF-Q6EQZ3-F1-model\_v2



预测的三级结构 PBD号为: 2BW3

大小为459氨基酸

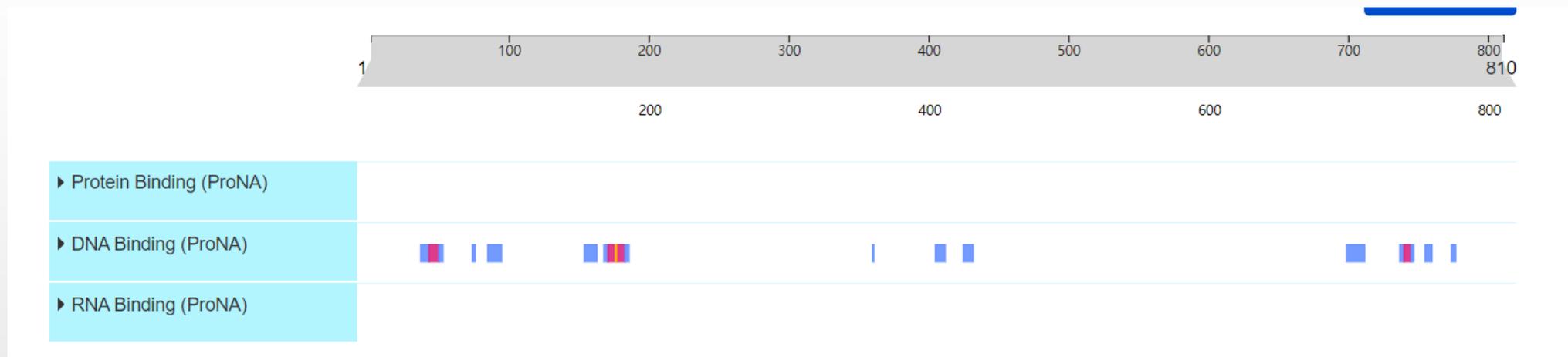
## 5、细胞亚定位预测



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

SGD1经预测定位于细胞核中

## 6、功能预测



总结：其定位与细胞核内，且具有多个与DNA结合的位点，且结合位点在亲水性强，猜测其功能类似于组蛋白，转录因子或者转运核酸的作用。

根据其不同器官转录组学分析发现其表达具有时空效应，具体的功能机制还需要实验继续验证。

感谢大家的聆听！