

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

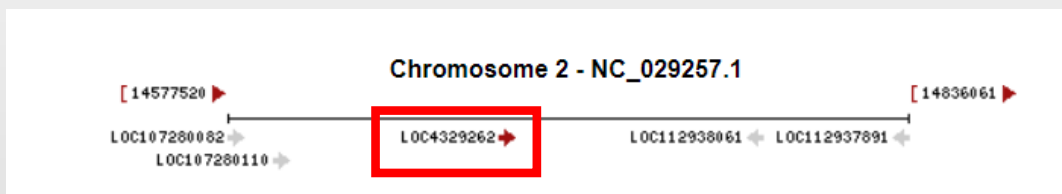
- 实验室前期发现OsSGD1基因在水稻株高和籽粒发育中有着重要作用。
- OsSGD1的突变体和敲除株系均表现出株高半矮化的表型，过表达材料表现出较野生型高的表型。
- OsSGD1可通过调控水稻分生组织细胞周期活动影响水稻的生长速度。
- 目前还没有对OsSGD1基因的报道。

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 predictedⁱ

Names & Taxonomyⁱ

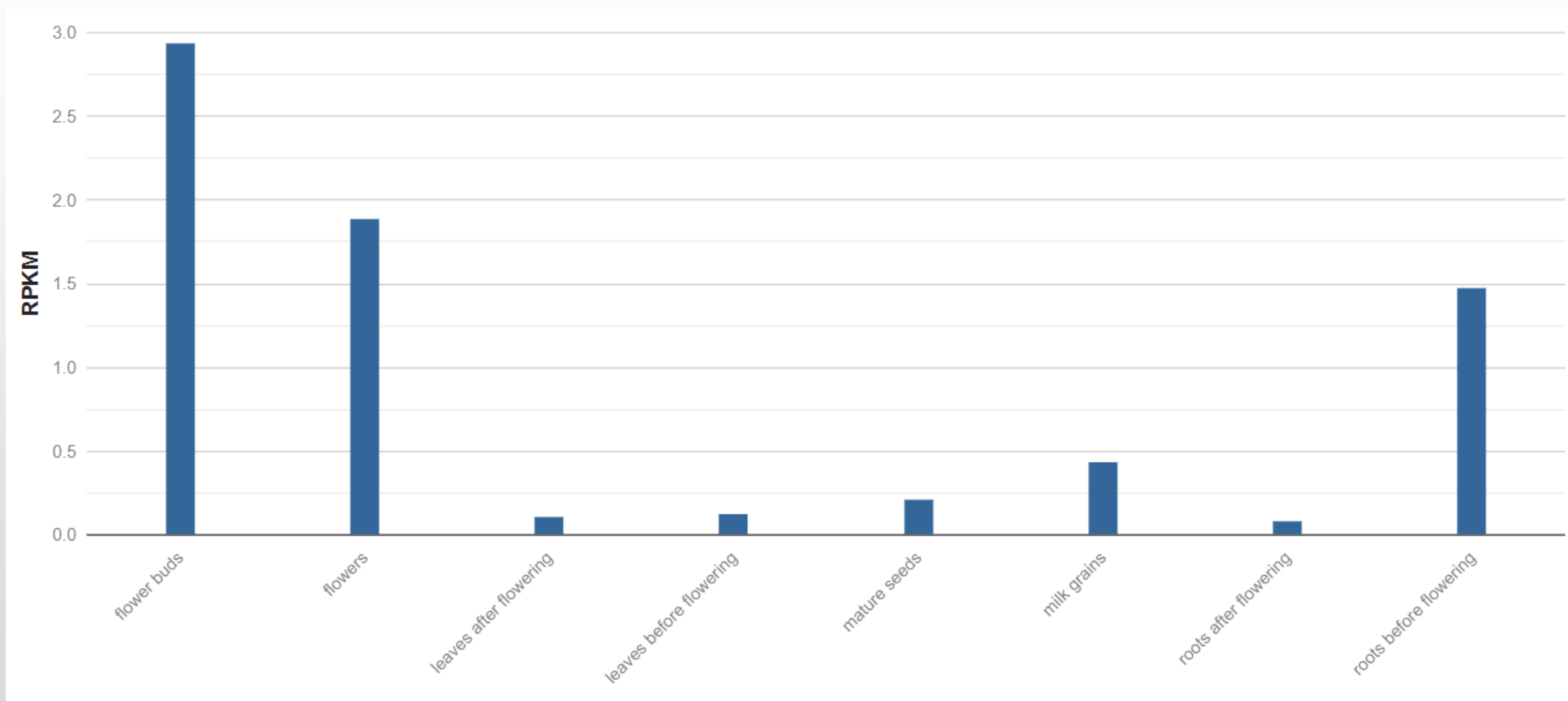
Protein names ⁱ	Submitted name: Os02g0450000 protein Imported
Gene names ⁱ	Ordered Locus Names:Os02g0450000 Imported ORF Names:OSNPB_020450000 Imported
Organism ⁱ	<i>Oryza sativa subsp. japonica (Rice)</i> Imported
Taxonomic	39947 [NCBI]

None

- 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

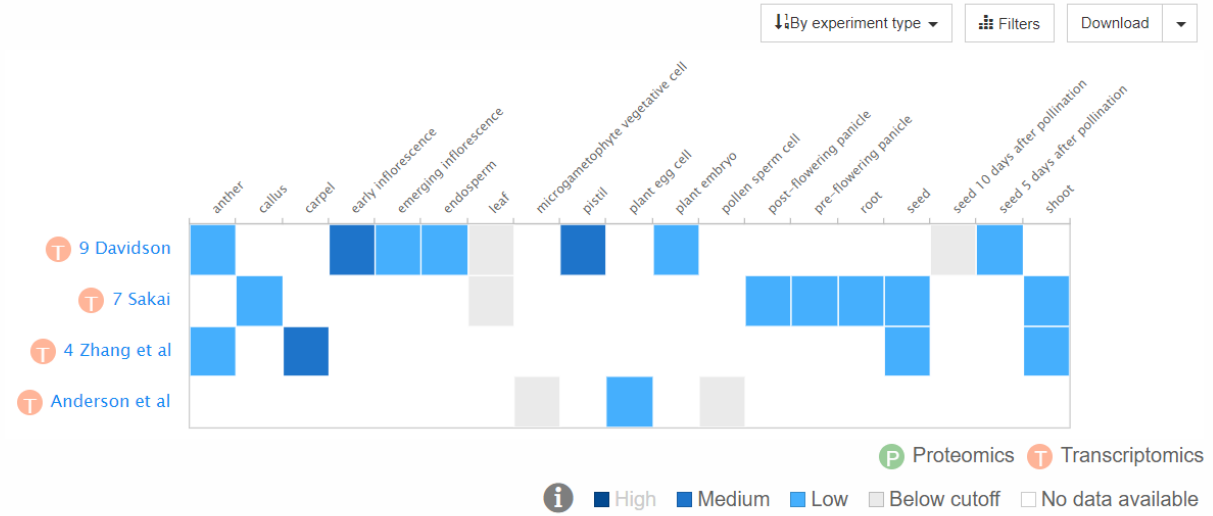
Cultivar

Fraction

Sampling site

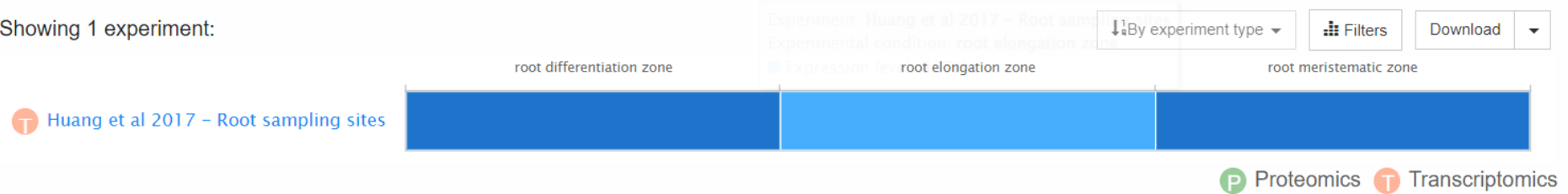
Organism part

Showing 4 experiments:



Sampling site

Showing 1 experiment:



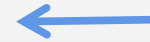
其在早花絮和雌蕊中表达量最高，且在分生区中大量表达。

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	XM_026023465.1
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	XM_026023464.1
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	XM_015767598.2
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	XM_015767595.2
<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	AP014958.1
<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	AP005648.2
<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	AK122096.1
<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	AK106956.1

在水稻中查询到的基因都是SGD1基因的不同剪接体。

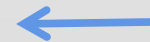


Job Title: Nucleotide Sequence
RID: YTAU1BAR013
Program: Citation
Database: nt
Query ID: Icl|Query_2289
Description: None
Molecule type: dna
Query Length: 2433
Other reports: 0

Filter Results
Percent Identity: [] to []
E value: [] to []
Query Coverage: [] to []
Buttons: Filter, Reset

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

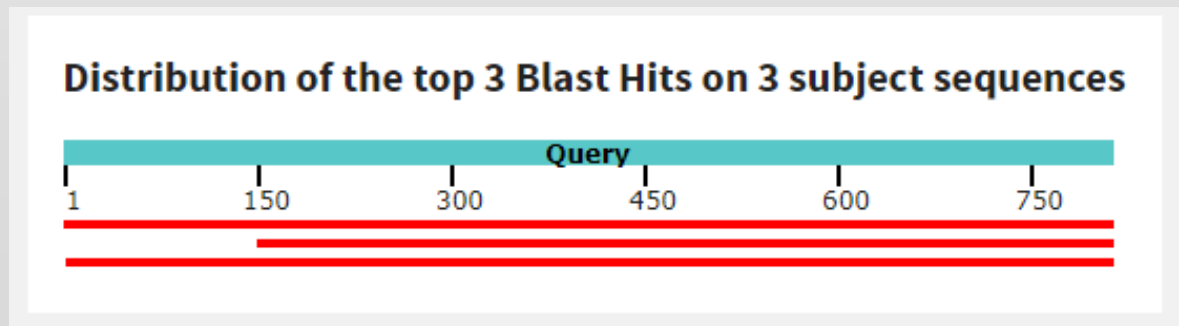
Sequences producing significant alignments [Download](#) [New](#) [Select columns](#) Show [?](#)

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

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

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 ?

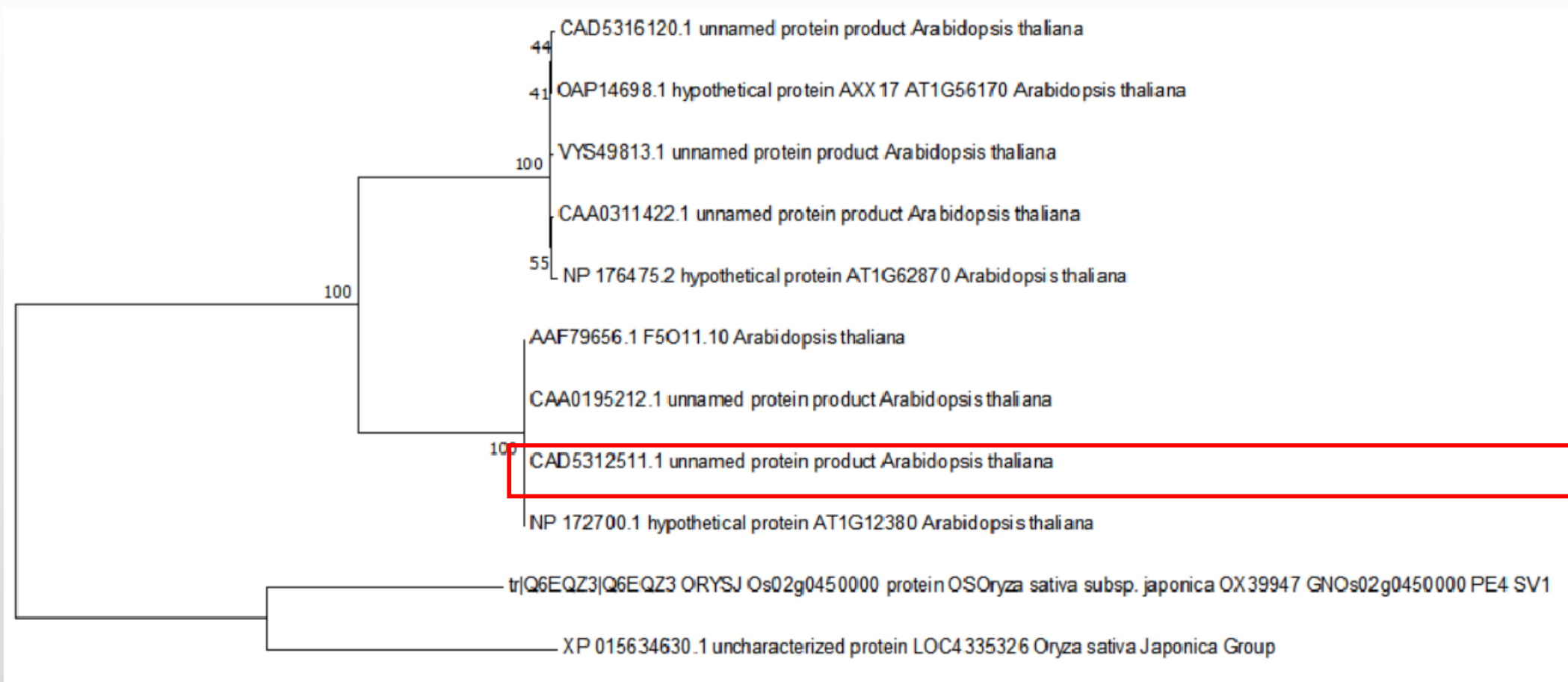
9 sequences selected ?

No putative conserved domains have been detected

Distribution of the top 9 Blast Hits on 9 subject sequences

Subject Sequence	Match Length (Query)
1	0 - 750
2	0 - 750
3	0 - 750
4	0 - 750
5	0 - 750
6	0 - 750
7	0 - 750
8	0 - 750
9	0 - 750

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

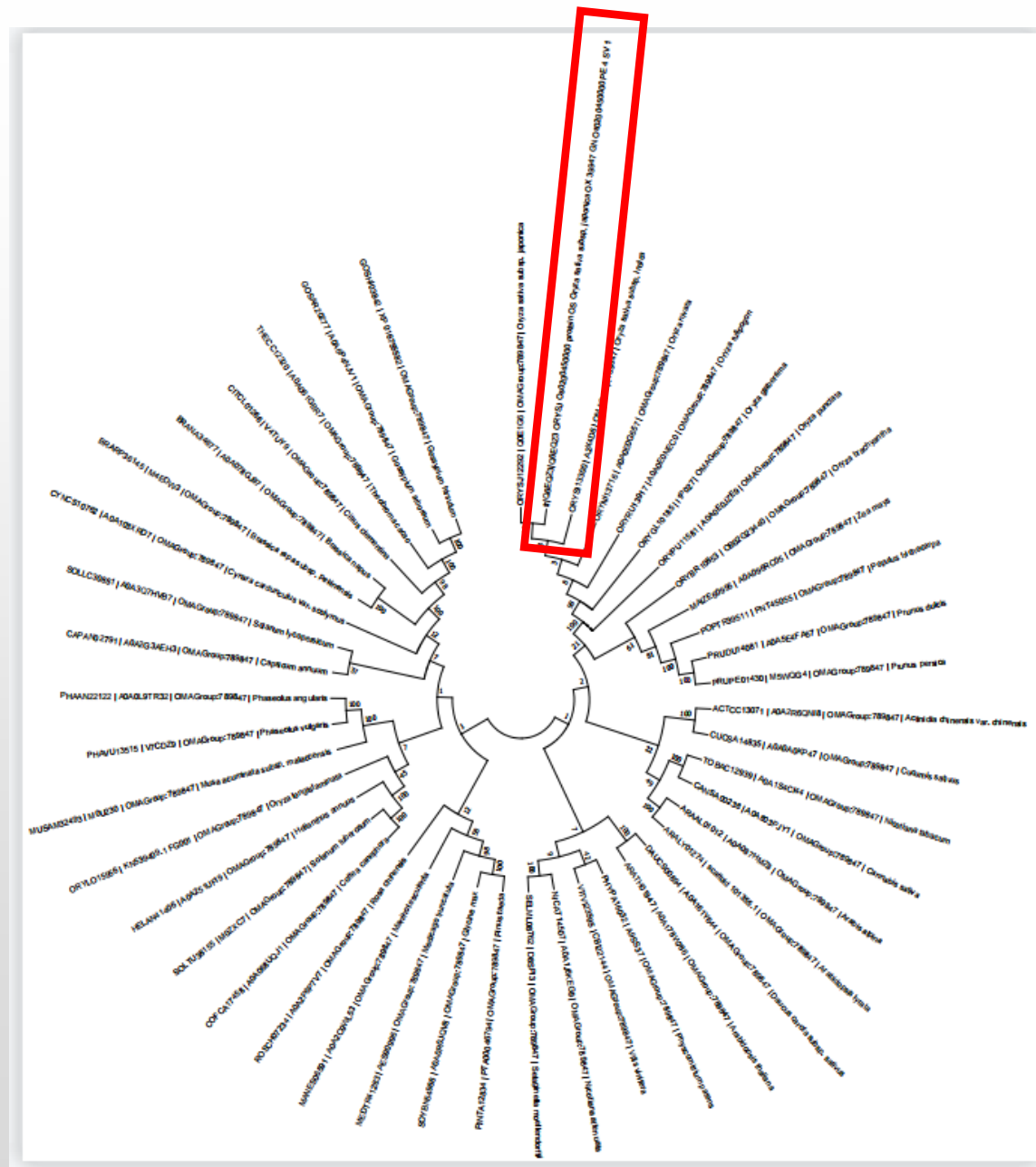
FILTER BY TAXONOMY:

- All Taxa
- Eukaryota
- Viridiplantae
- Fungi
- Metazoa

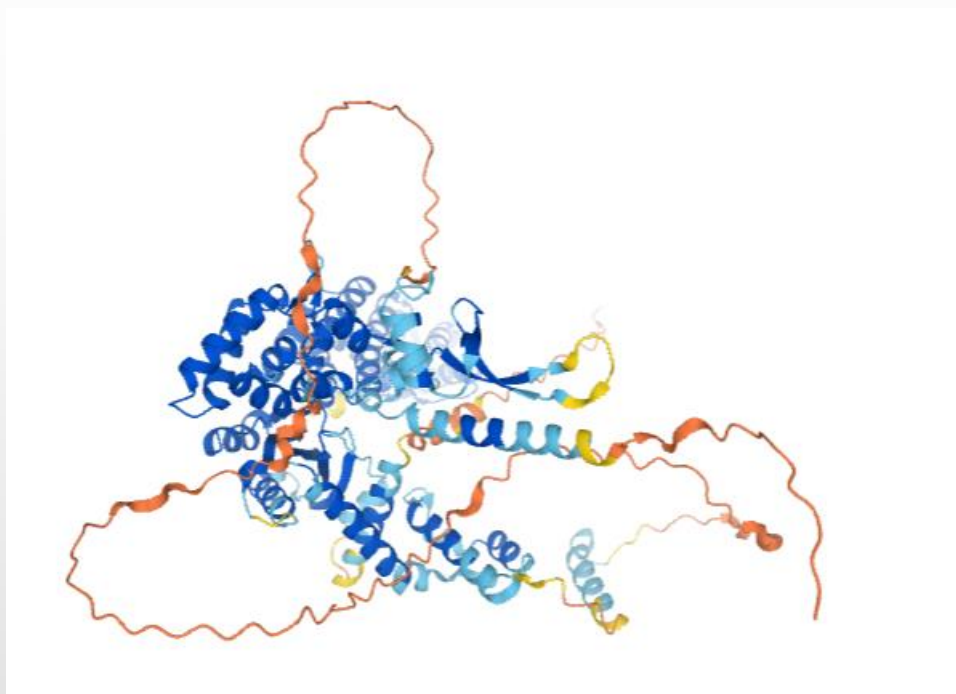
Domains	Taxon	Protein ID
	Volvox carteri	VOLCA14307
	Physcomitrium patens	PHYPA16032
	Pinus taeda	PINTA12834
	Oryza brachyantha	ORYBR10853

在植物中有45个SGD1家族，并将他们做成进化树分析。

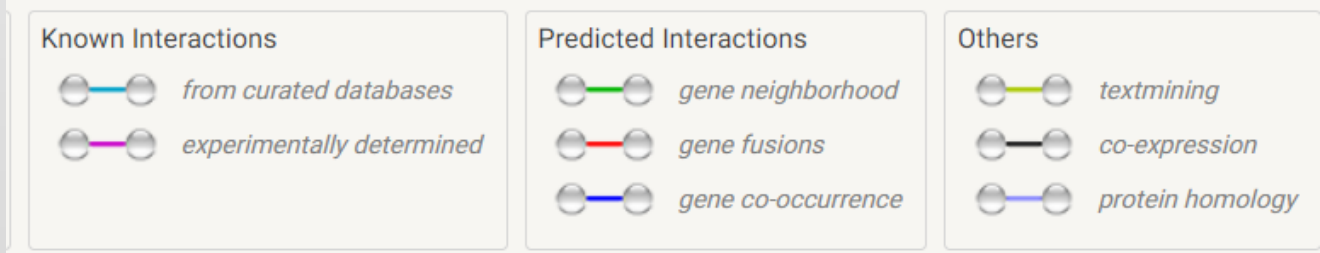
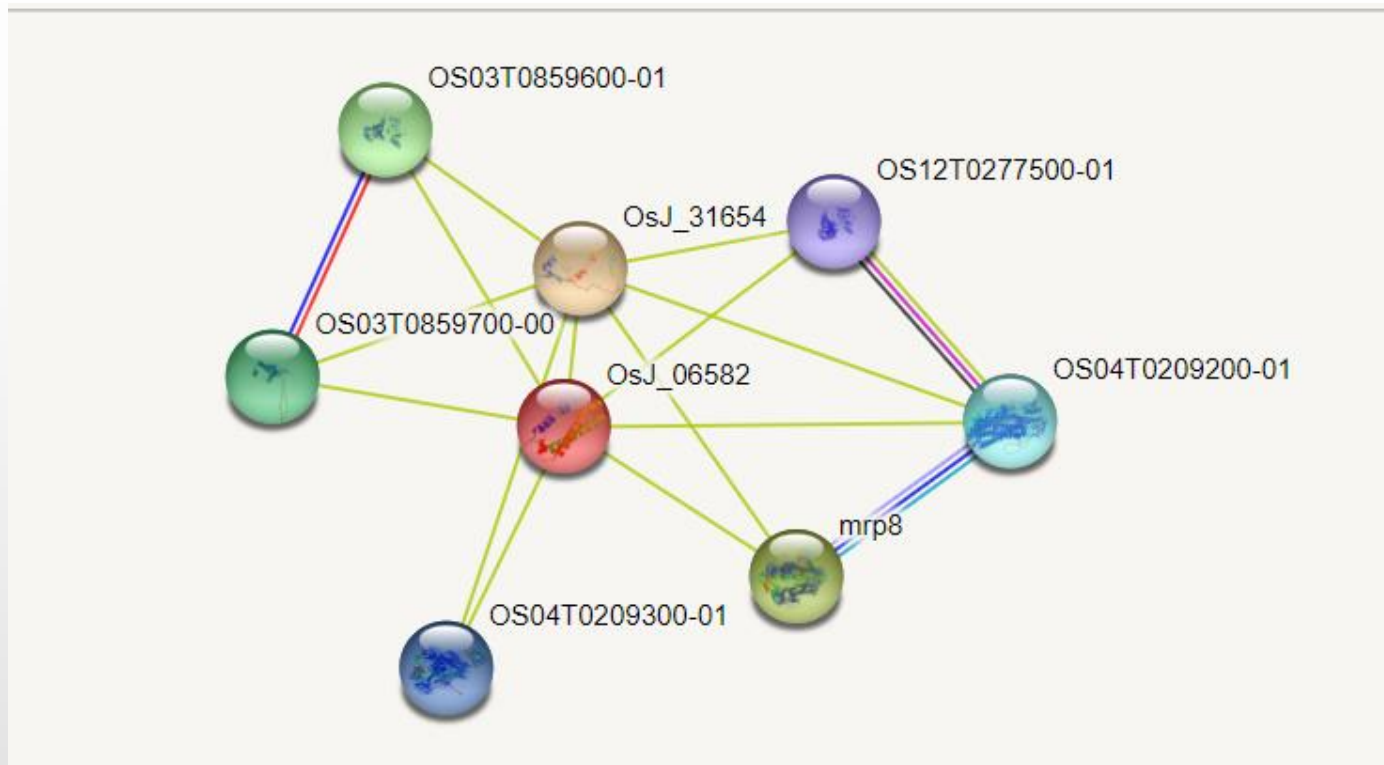
其与水稻中的QOE1G6蛋白同源性最高。



五、蛋白结构分析

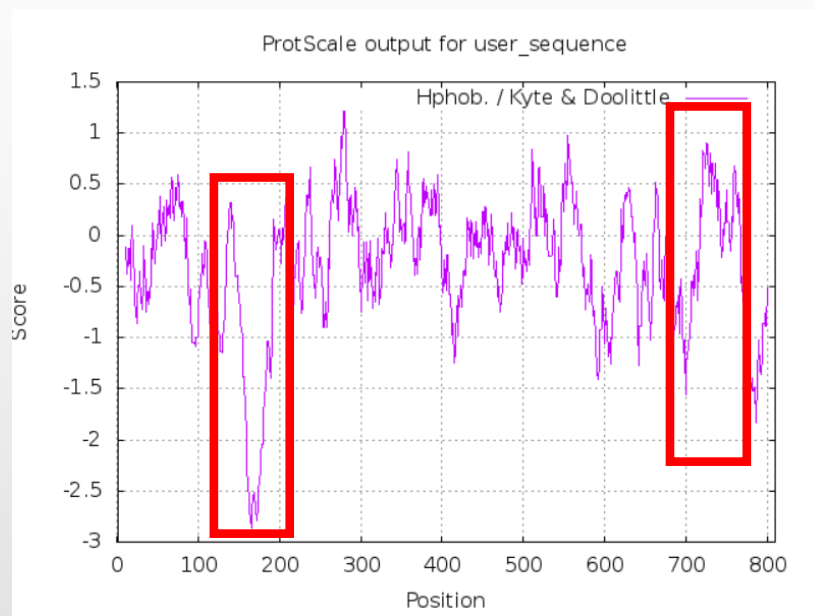


Uniprot数据库中的蛋白结构

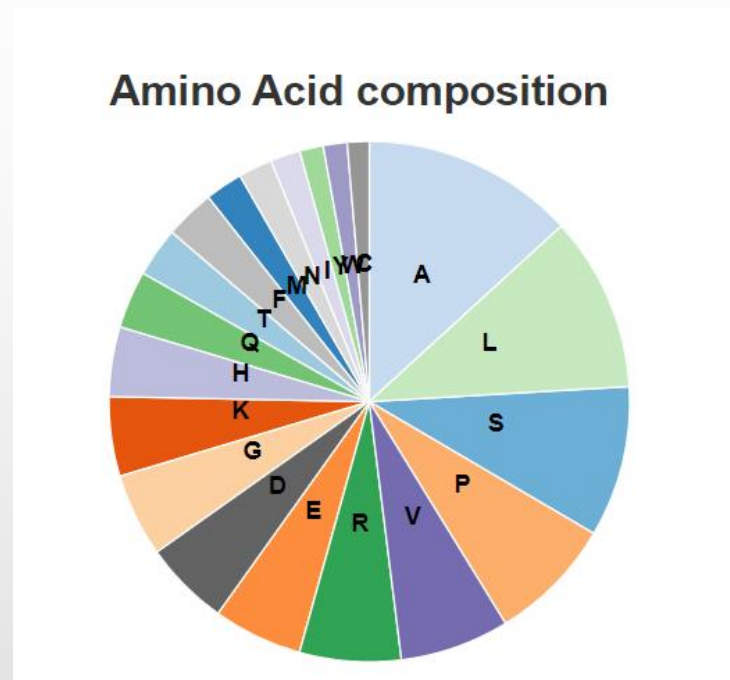


蛋白互动情况

1、一级结构分析



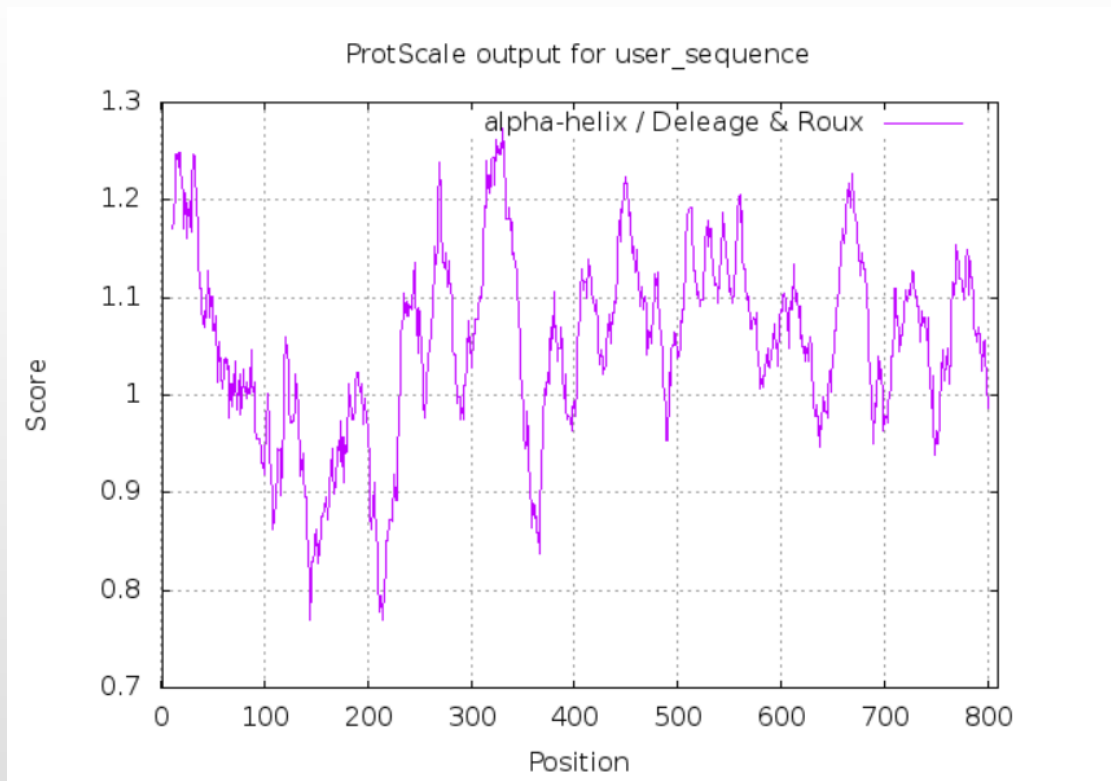
亲疏水性



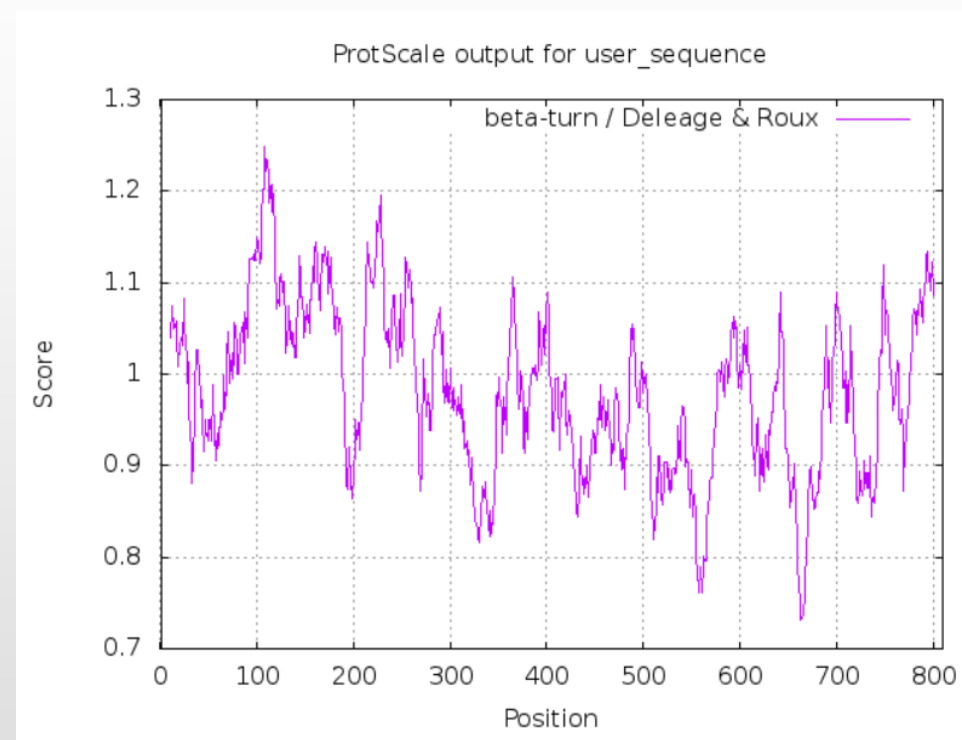
氨基酸组成

丙氨酸: 13.21%
亮氨酸: 10.86%
丝氨酸: 9.38%

2、二级结构分析



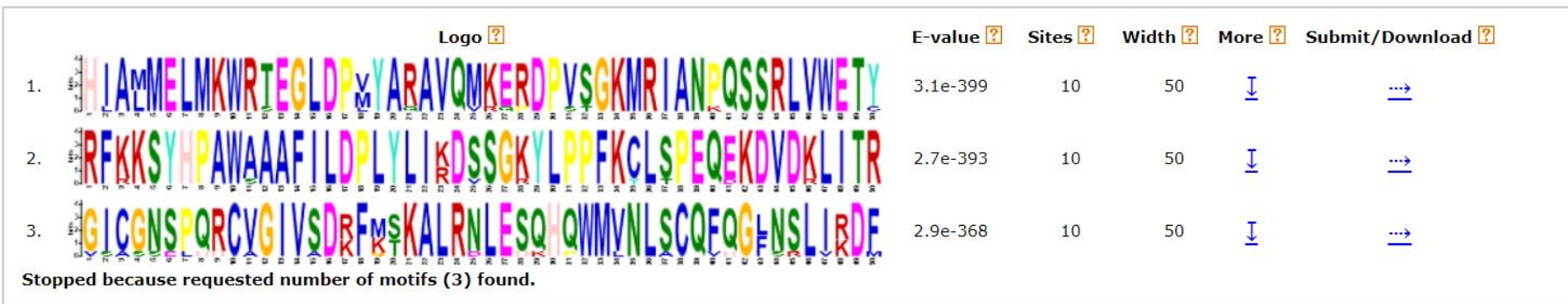
α -螺旋



β -折叠

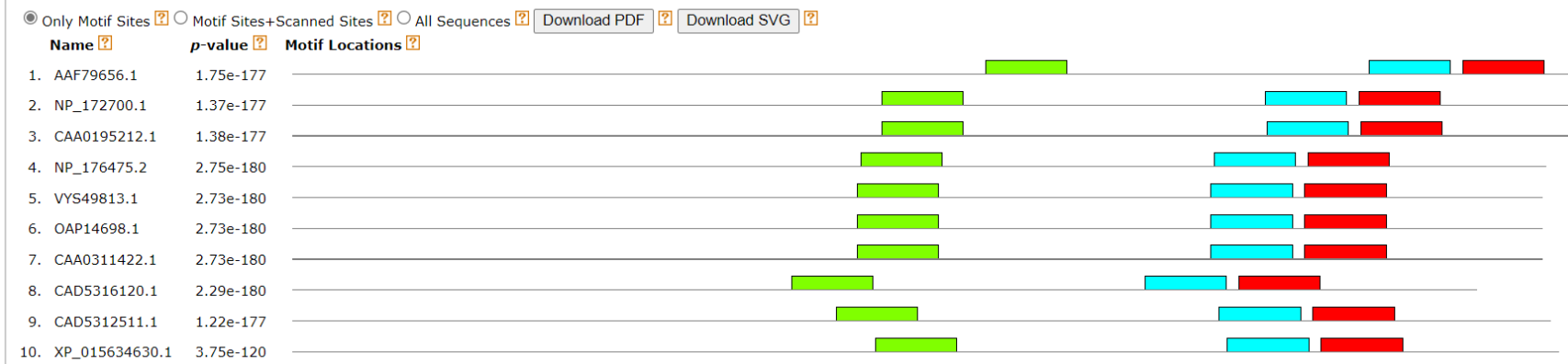
3、结构域预测

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



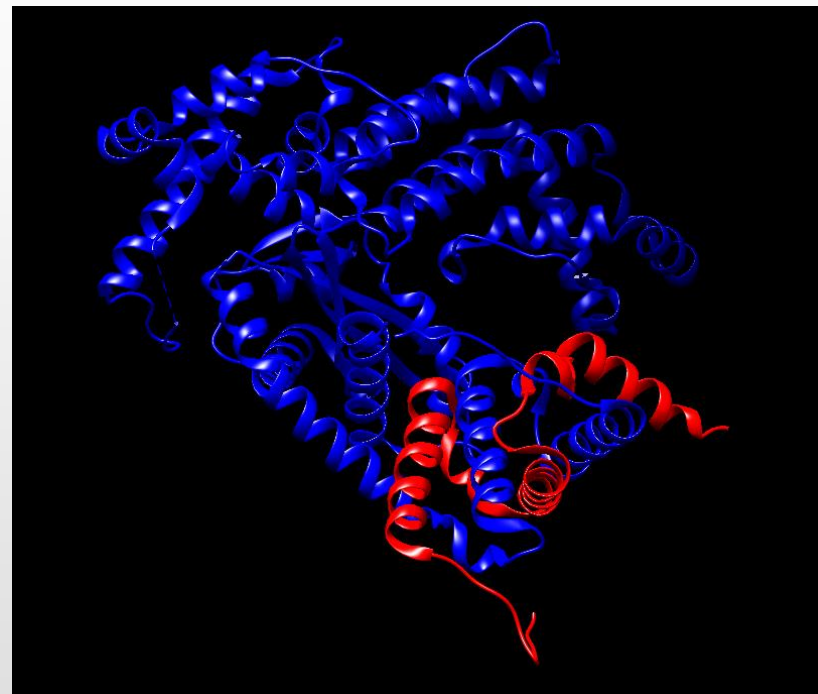
发现这些同源蛋白含有一些相同的保守结构位点。

4、SGD1三级结构

主要由 α 螺旋和 β 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

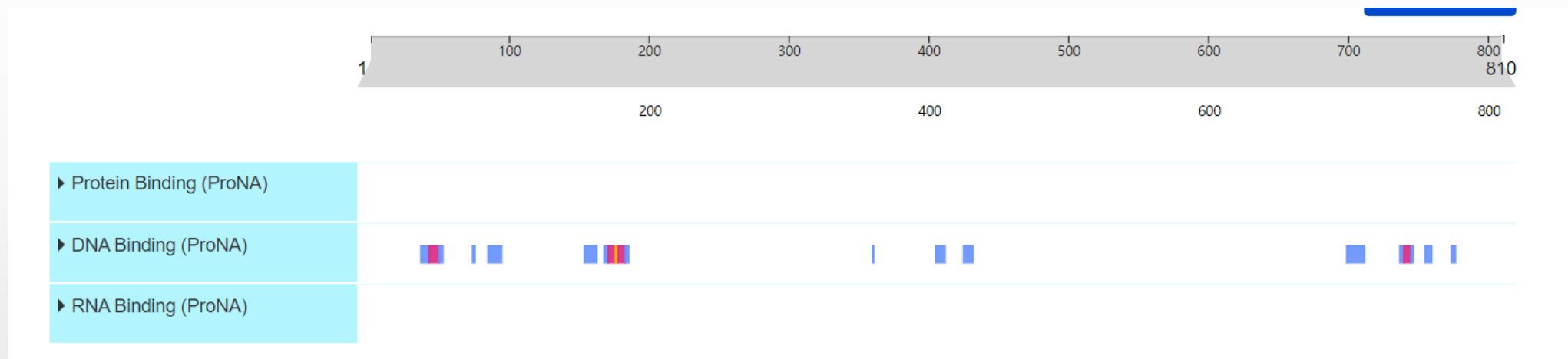
5、细胞亚定位预测



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！