

实用生物信息技术课程期末 汇报



CAAS 2017_G11

组长：战徊旭

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汇报人：赵洁

时间：2017.12.13

战徇旭—绞股蓝核糖体失活蛋白RIP

- ✧ 绞股蓝，葫芦科、绞股蓝属草质攀援植物。绞股蓝俗称超人参、遍地生根等，为多年生草质藤木。绞股蓝有着提高免疫力、降血脂、双向调节血压、降血糖等功效。林毅在预实验中分离到一种新的核糖体失活蛋白(RIP)，它具有很高的抗TMV活性。其分子量约为27kDa。
- ✧ 本课题打算构建相应载体，经农杆菌介导转入烟草，获得转基因植株，并探索叶绿体表达蛋白可能性。
- ✧ 由于RIP具有抗肿瘤，抗病毒等效果，希望凭借烟草生物量巨大的优势，利用烟草表达抗病毒蛋白，提高RIP产量，提纯后作为生物药剂开发。同时，还可以研究表达RIP蛋白的转基因烟草的病毒抗性。

战徊旭—绞股蓝核糖体失活蛋白RIP

- ✧ 方法：氨基酸和蛋白的序列比对，系统发育树构建，蛋白检索，蛋白结构预测，引物设计
- ✧ 工具：Blast, MEGA7.0, DNAMAN, ExPASy 上的ProtScale 工具, ExPASy 中ProtScale 工具, TMpred, DAS-TMfilter ,
- ✧ 数据库：NCBI, UniProt, Phyre2, PubMed, EMBOSS, Predict Protein

孔令磊—棉花腺体相关基因的精细定位与克隆

棉花是我国重要的经济作物，棉籽中富含蛋白质和脂肪，是重要的植物油料和蛋白资源。



因此，选育棉籽中无棉酚，植株中有棉酚的品种成为当务之急，既保持了植株对病虫害的**抗性**又能使棉花蛋白和油脂得到**充分利用**。

孔令磊—棉花腺体相关基因的精细定位与克隆

1. 引物设计: Primer 5
2. 遗传图谱构建: JionMap 4.0
3. 基因预测: FGENESH
4. 基因结构分析: GENSCAN、PromoterScan
5. 序列比对: BLAST
6. 系统发育树构建: MEGA7.0
7. 蛋白序列分析、功能预测: PredictProtein
8. 蛋白质结构预测: Phyre2

袁高鹏、高源—抗病转录因子

- ✧ 分析方法可能涉及GO功能分析、KEGG富集、系统进化树构建等。
- ✧ 工具可能包括：BLAST、MEGA7.0、EMBOSS软件包中的序列比对程序Needle等。
- ✧ 数据库：NCBI BLAST 数据库、Ref-seq、PlantTFDB等。

调控大豆多叶基因*Lf1*基因的生物信息学分析

Bioinformatics Analysis of the *Lf1* gene that controls leaflet number in soybean



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- ✧ Background
- ✧ Analysis
- ✧ Acknowledgement



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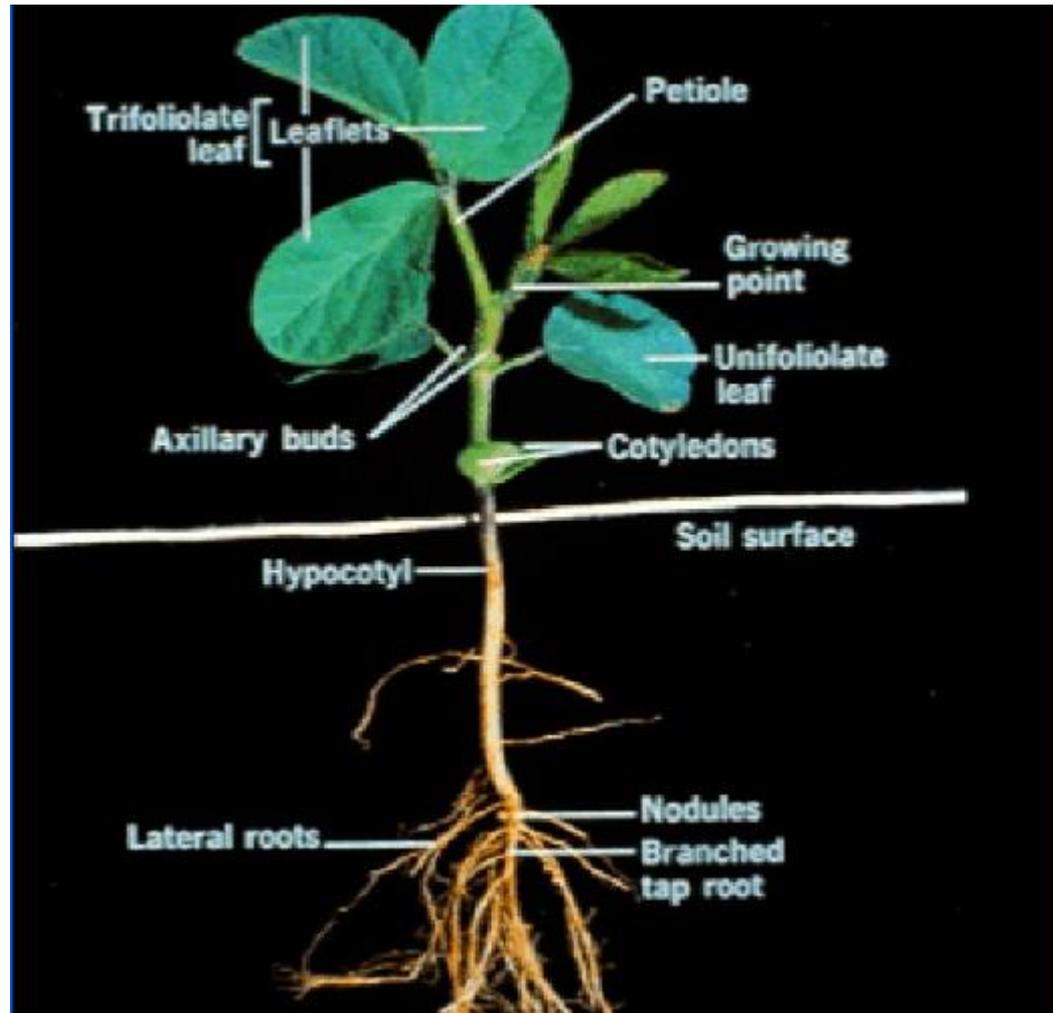


Background

- 大豆是世界上重要的粮油兼用作物，也是人类优质蛋白的主要来源。既是我国主要作物之一，也是我国进口量最大的农产品。大豆是关系国际民生的重要基础性、战略性物资，又是最具经济效益的作物，其延长的产业链和价值链具有很大发展潜力，在农产品贸易领域扮演着举足轻重的角色。



Backound



Backound



Backound

由于叶子是植物的光合作用工厂，所以作物的叶片发育对于作物的产量是至关重要的。叶是开花植物茎尖分生组织侧翼连续发育的侧生器官。许多研究表明，叶发育常常与来自花和相关组织的其他侧生器官（例如花和豆荚或果实）的发育共享关键的调控基因。因此，研究叶子的发育对于提高产量也是至关重要的。



Contents



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↪ Analysis

↪ Acknowledgement



文献检索

- [Confirmation of the pleiotropic control of **leaflet** shape and **number** of seeds per pod by the *Ln* gene in induced **soybean** mutants.](#)
 1. Sayama T, Tanabata T, Saruta M, Yamada T, Anai T, Kaga A, Ishimoto M. *Breed Sci.* 2017 Sep;67(4):363-369. doi: 10.1270/jsbbs.16201. Epub 2017 Jul 28. PMID: 29085246 [Free PMC Article](#)
[Similar articles](#)

- [Genetic analysis of the Lf1 gene that controls **leaflet number** in **soybean**.](#)
 2. Jeong SC, Kim JH, Bae DN. *Theor Appl Genet.* 2017 Aug;130(8):1685-1692. doi: 10.1007/s00122-017-2918-0. Epub 2017 May 17. PMID: 28516383
[Similar articles](#)

- [Ln is a key regulator of **leaflet** shape and **number** of seeds per pod in **soybean**.](#)
 3. Jeong N, Suh SJ, Kim MH, Lee S, Moon JK, Kim HS, Jeong SC. *Plant Cell.* 2012 Dec;24(12):4807-18. doi: 10.1105/tpc.112.104968. Epub 2012 Dec 14. PMID: 23243125 [Free PMC Article](#)
[Similar articles](#)

UniProt information

UniProtKB - K7L9F6 (K7L9F6_SOYBN)

Protein | Submitted name: **AP2 domain-containing protein**

Gene | **Glyma.08g281900**

Organism | *Glycine max (Soybean) (Glycine hispida)*

Status |  Unreviewed - Annotation score: ●○○○○○ - Protein predictedⁱ

Names & Taxonomy¹

Protein names ⁱ	Submitted name: AP2 domain-containing protein  Imported ▾
Gene names ⁱ	ORF Names: Glyma.08g281900  Imported ▾, GLYMA_08G281900  Imported ▾
Organism ⁱ	<i>Glycine max (Soybean) (Glycine hispida)</i>  Imported ▾
Taxonomic identifier ⁱ	3847 [NCBI]
Taxonomic lineage ⁱ	Eukaryota > Viridiplantae > Streptophyta > Embryophyta > Tracheophyta > Spermatophyta > Magnoliophyta > eudicotyledons > Gunneridae > Pentapetalae > rosids > fabids > Fabales > Fabaceae > Papilionoideae > Phaseoleae > Glycine > Soja 
Proteomes ⁱ	UP000008827 Component ⁱ : Chromosome 8

UniProt information

Functionⁱ

Regions

Feature key	Position(s)	Description	Actions	Graphical view	Length
DNA binding ⁱ	47 - 104	AP2/ERF PROSITE-ProRule annotation	Add BLAST		58

GO - Molecular functionⁱ

- DNA binding [Source: UniProtKB-UniRule](#)
- transcription factor activity, sequence-specific DNA binding [Source: InterPro](#)

[View the complete GO annotation on QuickGO ...](#)

GO - Biological processⁱ

- transcription, DNA-templated [Source: UniProtKB-UniRule](#)

Inferred from electronic annotation

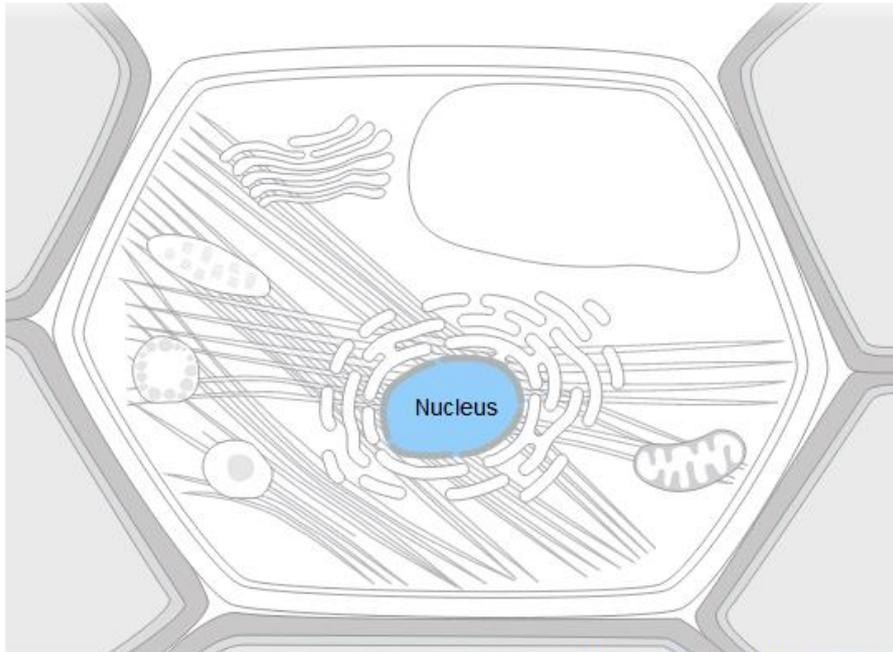
[View the complete GO annotation on QuickGO ...](#)

Keywordsⁱ

Molecular function	DNA-binding PROSITE-ProRule annotation SAAS annotation
Biological process	Transcription, Transcription regulation PROSITE-ProRule annotation SAAS annotation

Subcellular Localization

UniProt information



Graphics by Christian Stolte; Source: [WIKIPEARTMENTS](#)

Predict Protein



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

Subcellular localization

TargetP 程序

```
### targetp v1.1 prediction results #####  
Number of query sequences: 1  
Cleavage site predictions not included.  
Using PLANT networks.
```

Name	Len	cTP	mTP	SP	other	Loc	RC
tr_K7L9F6_K7L9F6_SOY	354	0.326	0.060	0.025	0.866	_	3
cutoff		0.000	0.000	0.000	0.000		

cTP: 叶绿体转运肽 mTP: 线粒体靶向肽 sp: 信号肽

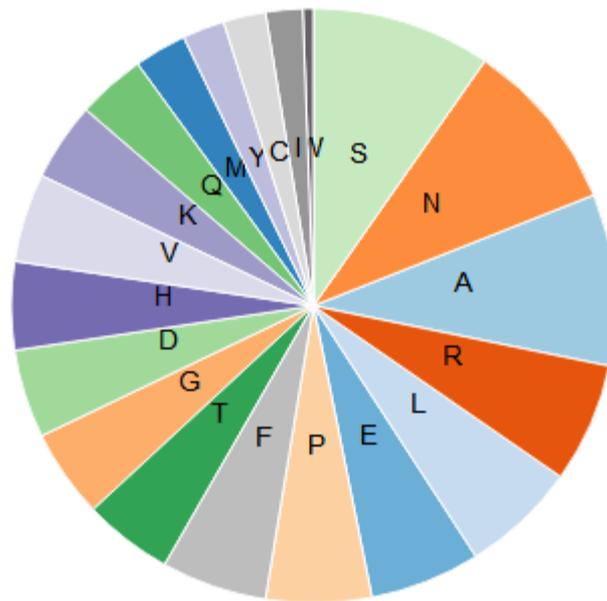
氨基酸序列分析

Predict Protein检索结果

Summary

Sequence Length	354
Number of Aligned Proteins	40

Amino Acid composition



氨基酸序列分析

ExPASy 上的 ProtParam 工具分析结果如下:

Amino acid composition:

Ala (A)	33	9.3%
Arg (R)	23	6.5%
Asn (N)	33	9.3%
Asp (D)	17	4.8%
Cys (C)	8	2.3%
Gln (Q)	13	3.7%
Glu (E)	21	5.9%
Gly (G)	17	4.8%
His (H)	17	4.8%
Ile (I)	7	2.0%
Leu (L)	22	6.2%
Lys (K)	15	4.2%
Met (M)	10	2.8%
Phe (F)	20	5.6%
Pro (P)	20	5.6%
Ser (S)	34	9.6%
Thr (T)	17	4.8%
Trp (W)	2	0.6%
Tyr (Y)	8	2.3%
Val (V)	17	4.8%
Pyl (O)	0	0.0%
Sec (U)	0	0.0%

(B)	0	0.0%
(Z)	0	0.0%
(X)	0	0.0%

Number of amino acids: 354

Molecular weight: 39625.94

Theoretical pI: 7.28

Aliphatic index: 55.20

Grand average of hydropathicity (GRAVY): -0.733

Total number of negatively charged residues (Asp + Glu): 38

Total number of positively charged residues (Arg + Lys): 38

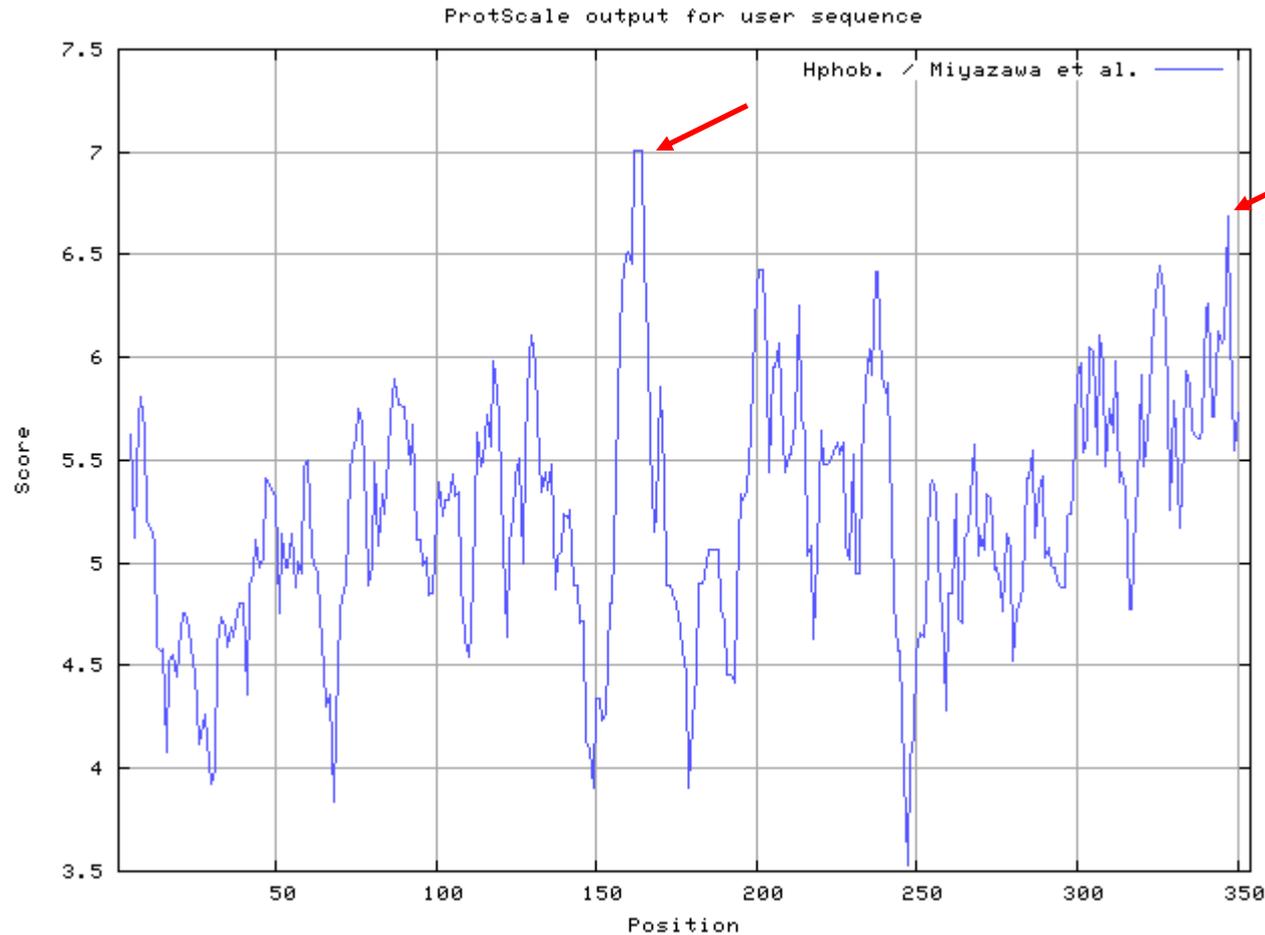
Instability index:

The instability index (II) is computed to be 46.28

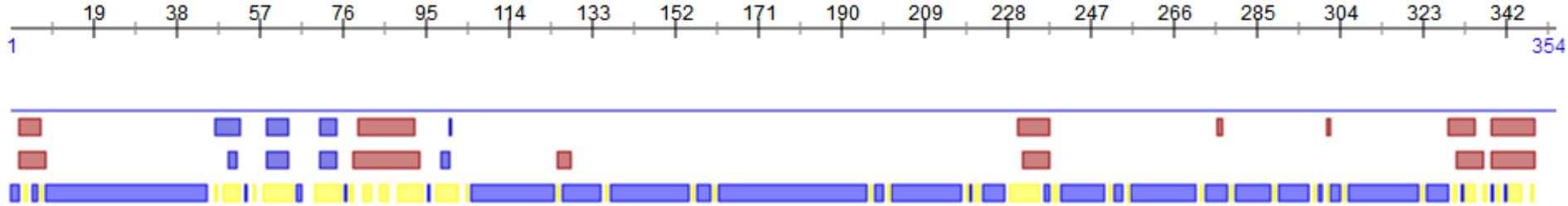
This classifies the protein as unstable.

亲疏水性分析

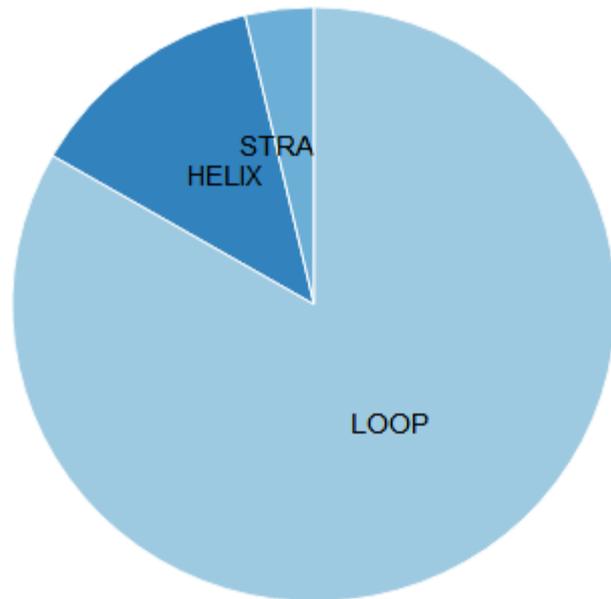
ExPASy 上的 ProtScale 工具分析结果如下：



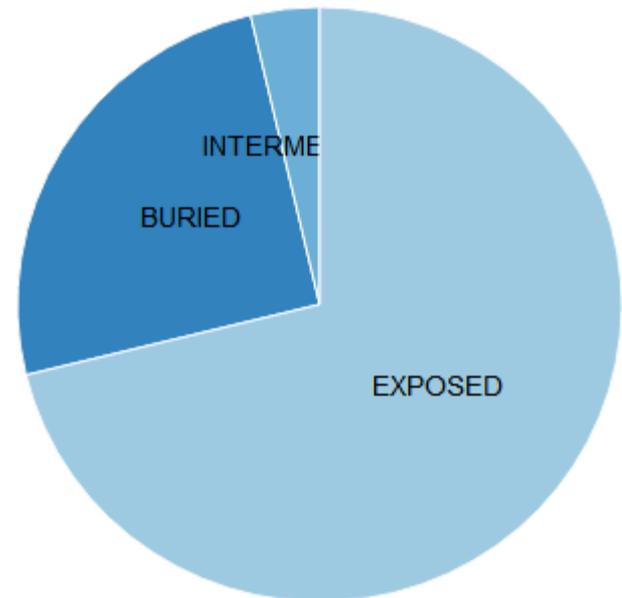
Secondary structure & Solvent accessibility



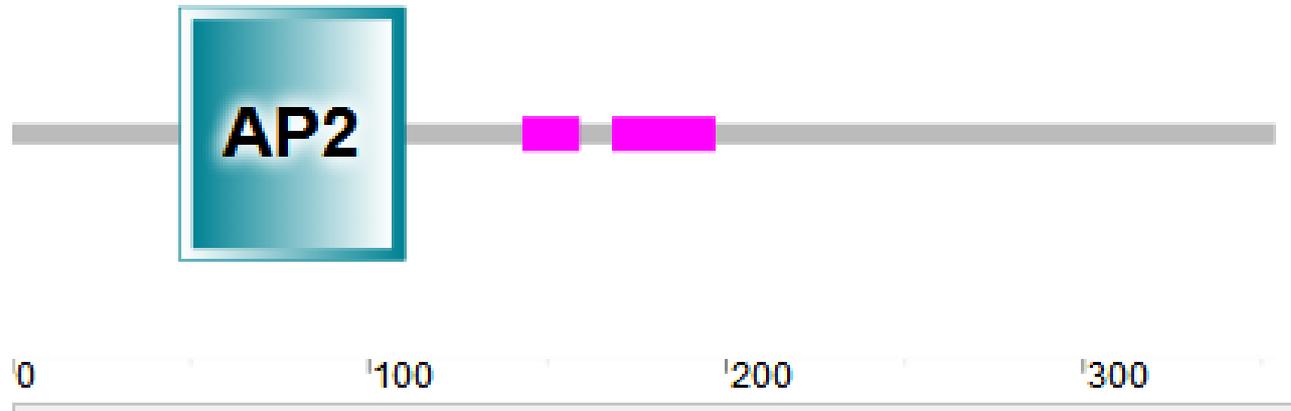
Secondary Structure Composition



Solvent Accessibility

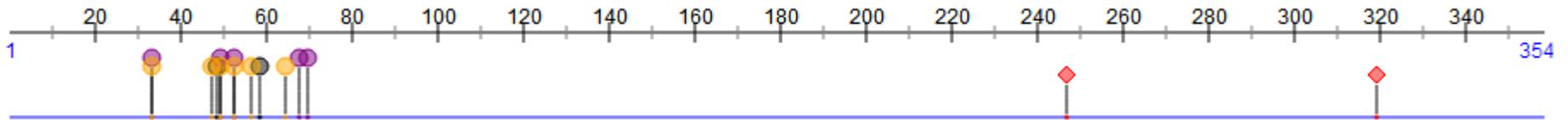


Smart



Binding Site

Predict Protein检索结果



○ DNA binding region

● Nucleotide binding region

○ RNA binding region

◇ Protein binding region

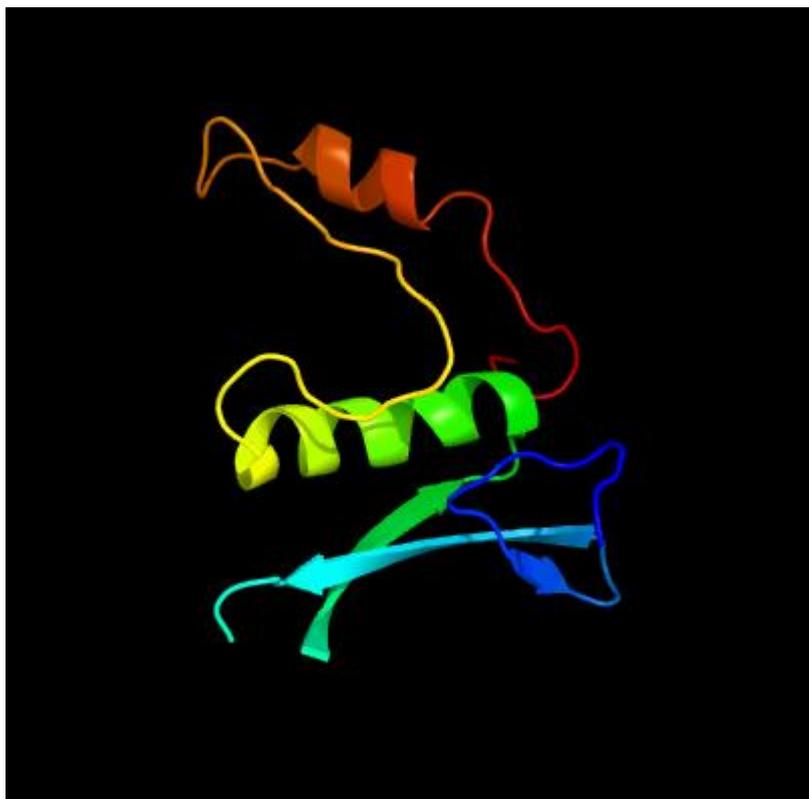
结构预测

www.sbg.bio.ic.ac.uk/phyre2/phyre2_output/dba0b4c61c461460/psi-blast.html

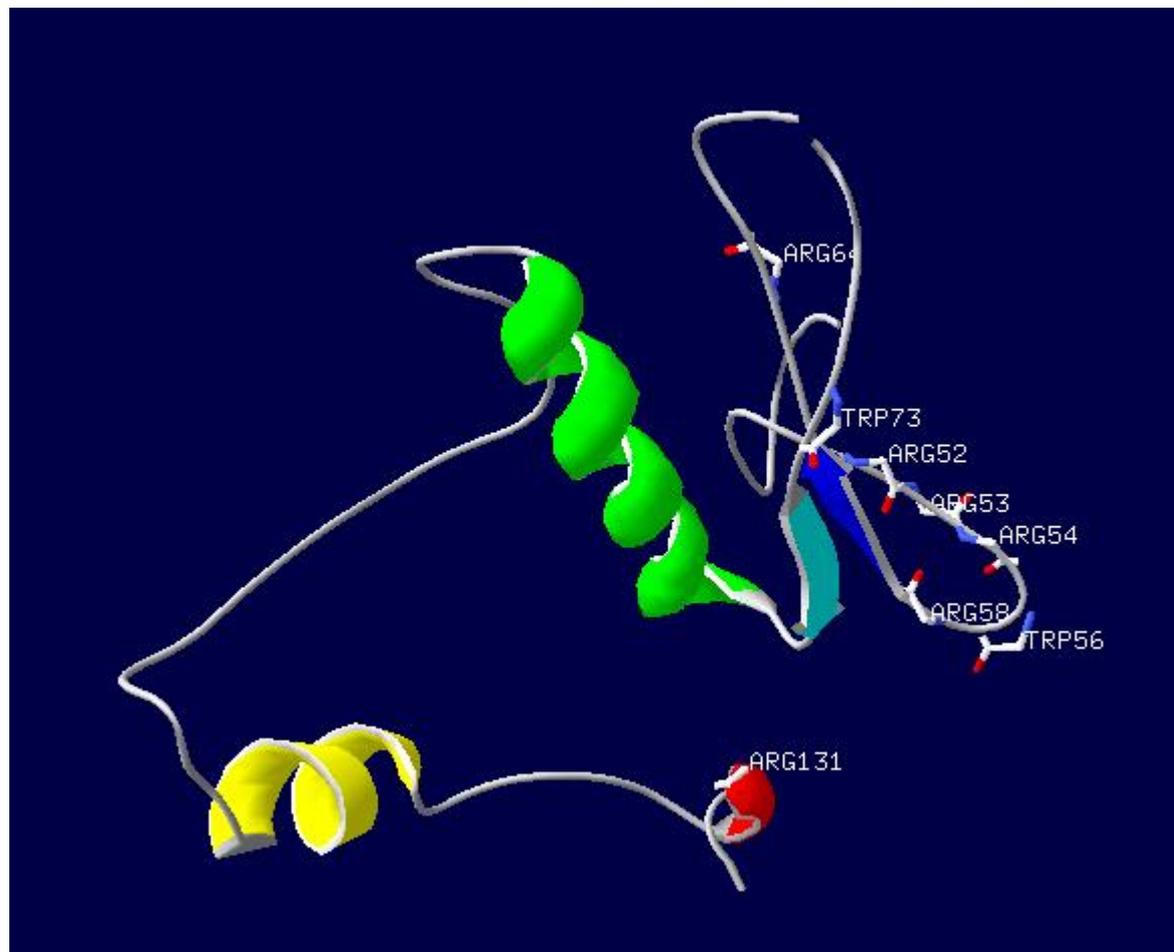
bits	E-value	N	100.0%	1:354	
171	3e-41	1	36.4%	1:354	1:417
164	5e-39	1	22.5%	24:316	79:366
162	2e-38	1	19.5%	1:339	91:417
158	3e-37	1	37.5%	47:350	2:348
155	3e-36	1	38.1%	1:354	1:438
150	7e-35	1	19.0%	35:349	123:395
149	1e-34	1	22.1%	10:317	40:325
149	2e-34	1	19.5%	1:256	33:288
146	1e-33	1	18.9%	11:322	41:310
144	5e-33	1	19.8%	3:245	133:382
143	9e-33	1	17.5%	1:315	18:327
143	1e-32	1	22.4%	27:227	3:191
141	5e-32	1	20.5%	34:316	119:391
140	7e-32	1	15.9%	15:309	62:326
139	2e-31	1	20.1%	1:278	22:289
139	2e-31	1	19.0%	12:322	40:306
138	3e-31	1	24.1%	1:224	33:256
137	5e-31	1	20.0%	29:313	55:317
137	6e-31	1	33.2%	1:316	1:291
136	9e-31	1	21.8%	16:322	22:326
136	1e-30	1	21.9%	1:279	32:315
136	1e-30	1	20.0%	3:247	125:376
136	1e-30	1	21.7%	31:316	95:347
135	2e-30	1	20.9%	27:313	65:336
135	3e-30	1	14.9%	1:335	30:376
134	5e-30	1	19.1%	1:256	44:300
134	7e-30	1	24.8%	29:338	31:301
133	8e-30	1	19.7%	5:324	41:329
131	1e-29	1	15.5%	3:312	196:495
132	1e-29	1	20.2%	5:262	138:394
132	1e-29	1	22.5%	9:270	181:448
132	1e-29	1	19.4%	16:293	2:272
132	3e-29	1	23.8%	15:241	89:319
131	4e-29	1	20.9%	29:349	109:432
130	6e-29	1	21.4%	8:222	12:222
130	7e-29	1	31.0%	1:303	1:290
130	9e-29	1	21.0%	12:349	94:422
130	1e-28	1	26.1%	13:188	63:238
130	1e-28	1	25.7%	10:223	139:355
129	1e-28	1	28.9%	1:142	30:170
129	1e-28	1	20.7%	3:190	194:388
129	2e-28	1	18.8%	1:340	31:368
129	2e-28	1	28.4%	23:307	18:286
129	2e-28	1	16.2%	3:330	31:383
129	2e-28	1	26.1%	25:222	87:295

Sequence alignment view showing amino acid sequences with color coding for conservation. The alignment is between a query sequence (top) and a reference sequence (bottom). The reference sequence is: **EEALRRNGMPTQDDITSDHHKKSATIKRGLRDTASSGTYRRCVRRVGRYAAERDQSKERRWLGTFDTBBAAQAYDCAARLRGAKRINEVYDAADHHHHFQYFNINKHCHVTRRVNQNADH**

结构预测



结构预测





Contents

- ↪ Background
- ↪ Analysis
- ↪ Acknowledgement



Acknowledgement



- ✧ Prof. Luo Jingchu
- ✧ My abc team members
- ✧ Whole abc classmates





THANKS
谢 谢 聆 听

