

谷子中真核生物翻译起始因子3 G亚基 (eIF3G) 分析

Group:01

成员：刘晓彤、王晖、李波、刘国祥



谷子 (*Setaria italica*) 是禾本科狗尾草属的一个二倍体 ($2n=18$) 栽培种，基因组大小约**515MB**，具有抗旱、耐贫瘠、营养价值高和种质资源丰富等多种优点，在基础研究和农业生产方面都有很大的发展潜力。



H124



Yu1



H124



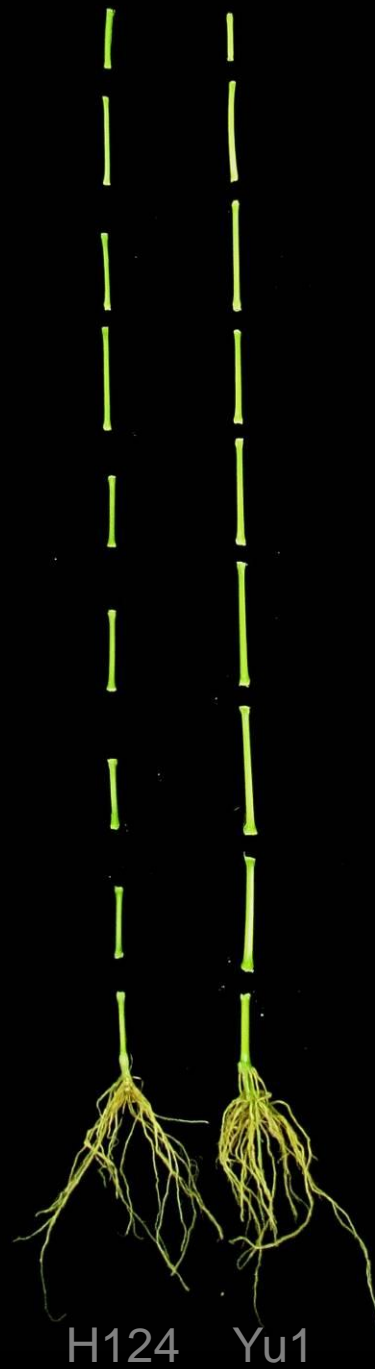
Yu1

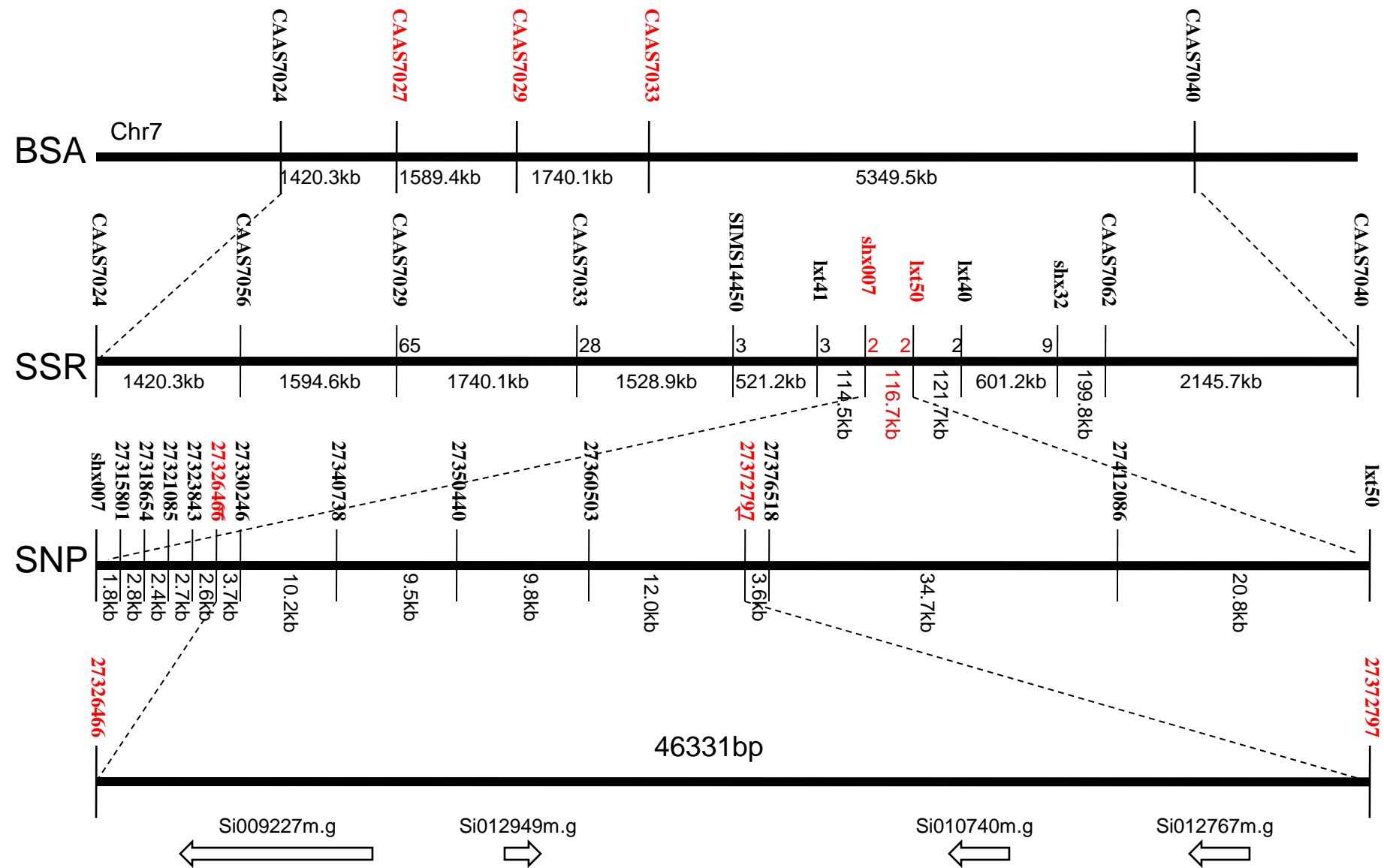


H124

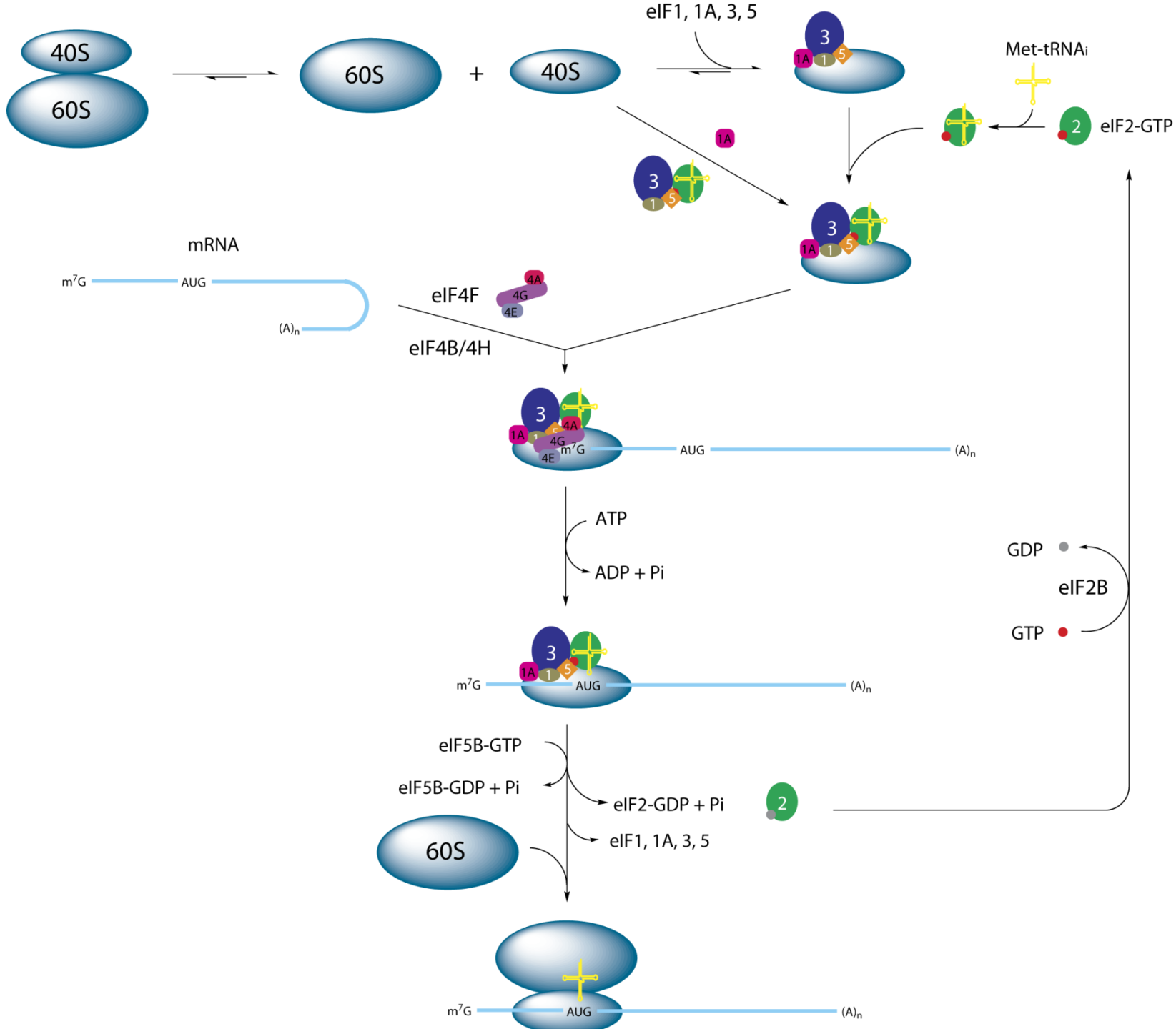


Yu1





Locus name	Location	Functional annotations
Si009227m.g	scaffold_7: 27330562 - 27339119	EUKARYOTIC TRANSLATION INITIATION FACTOR 2C
Si012949m.g	scaffold_7: 27340132 - 27340649	there are no functional annotations for this locus
Si010740m.g	scaffold_7: 27354499 - 27356216	EUKARYOTIC TRANSLATION INITIATION FACTOR 3
Si012767m.g	scaffold_7: 27365689 - 27367287	Protein of unknown function (DUF1618)



<http://www.phytozome.net/genePage.php?crown&method=2304&search=1&searchText=clusterid%3A28133979&detail=1>

Species > Tools > Info > Help Contact Us **phytozome**

Setaria italica gene Si010740m.g

About this gene **?** Sequences Protein Homologs Gene Ancestry Get Data

Info:

Locus name	Si010740m.g
Transcript name	Si010740m
Description	
Links to external DBs	

Functional annotations for this locus:

Pfam:12353	Eukaryotic translation initiation factor 3 subunit G
Pfam:00076	RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
Panther:10352	EUKARYOTIC TRANSLATION INITIATION FACTOR 3
KOG:0122	Translation initiation factor 3, subunit g (eIF-3g)
GO:0003676	nucleic acid binding

Protein domain view:

1 ————— 292

Family: *eIF3g* (PF12353)



Summary

Domain organisation

Clan

Alignments

HMM logo

Trees

Curation & model

Species

Interactions

Structures

Jump to...

enter ID/acc Go

Summary: Eukaryotic translation initiation factor 3 subunit G

Pfam includes annotations and additional family information from a range of different sources. These sources can be accessed via the tabs below.

No Wikipedia article **Pfam** Interpro

This tab holds the annotation information that is stored in the Pfam database. As we move to using Wikipedia as our main source of annotation, the contents of this tab will be gradually replaced by the Wikipedia tab.

Eukaryotic translation initiation factor 3 subunit G [Add annotation](#)

This domain family is found in eukaryotes, and is approximately 130 amino acids in length. The family is found in association with [PF00076](#). This family is subunit G of the eukaryotic translation initiation factor 3. Subunit G is required for eIF3 integrity.

Literature references

1. Masutani M, Sonenberg N, Yokoyama S, Imataka H; EMBO J. 2007;26:3373-3383.: Reconstitution reveals the functional core of mammalian eIF3. [PUBMED:17581632](#)

External database links

PANDIT:	PF12353
Pseudofam:	PF12353
SYSTEMS:	eIF3g

相关文献: [Masutani M, Sonenberg N, Yokoyama S, Imataka H; EMBO J. 2007;26:3373-3383.: Reconstitution reveals the functional core of mammalian eIF3.](#)

Family: *RRM_1* (PF00076)

610 architectures 31837 sequences 5 interactions 1039 species 197 structures  收集本页

Summary

Domain organisation

Clan

Alignments

HMM logo

Trees

Curation & model

Species

Interactions

Structures

Jump to...

enter ID/accession

Summary: RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)

Pfam includes annotations and additional family information from a range of different sources. These sources can be accessed via the tabs below.

Wikipedia: RNA recognition motif

This tab holds the annotation information that is stored in the Pfam database. As we move to using Wikipedia as our main source of annotation, the contents of this tab will be gradually replaced by the Wikipedia tab.

RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)

The RRM motif is probably diagnostic of an RNA binding protein. RRM motifs are found in a variety of RNA binding proteins, including various hnRNP proteins, proteins implicated in regulation of alternative splicing, and protein components of snRNPs. The motif also appears in a few single stranded DNA binding proteins. The RRM structure consists of four strands and two helices arranged in an alpha/beta sandwich, with a third helix present during RNA binding in some cases. The C-terminal beta strand (4th strand) and final helix are hard to align and have been omitted in the SEED alignment. The LA proteins ([P05455](#)) have an N terminal rrm which is included in the seed. There is a second region towards the C terminus that has some features characteristic of a rrm but does not appear to have the important structural core of a rrm. The LA proteins ([P05455](#)) are one of the main autoantigens in Systemic lupus erythematosus (SLE), an autoimmune disease.

Literature references

1. Birney E., Kumar S., Krainer A.R., Nucleic Acid Res 1993;21:5803-5816.: Analysis of the RNA-recognition motif and RS and RGG domains: conservation in metazoan pre-mRNA splicing factors. [PubMed:8290338](#)

Clan

This family is a member of clan [RRM \(CL0221\)](#), which has a total of **14** members.



Example structure

POB entry 2VON: CRYSTAL STRUCTURE OF N-TERMINAL DOMAINS OF HUMAN LA PROTEIN COMPLEXED WITH RNA OLIGOMER AUAAUUU

[View a different structure:](#)

2VON

[相关文献: Birney E., Kumar S., Krainer A.R., Nucleic Acid Res 1993;21:5803-5816.: Analysis of the RNA-recognition motif and RS and RGG domains: conservation in metazoan pre-mRNA splicing factors.](#)

基因序列分析

Species > Tools > Info > Help Contact Us phytozome

Setaria italica gene Si010740m.g

About this gene Sequences ? Protein Homologs Gene Ancestry Get Data

Genomic sequence Transcript sequence CDS sequence Protein sequence Show all key: 5' UTR CDS 3' UTR

- Genomic sequence [1718 nucleotides]
- Transcript sequence [937 nucleotides]
- CDS sequence [879 nucleotides]
- Protein sequence [292 residues]

BLAST this sequence: Phytozome NCBI

BLAST this sequence: Phytozome NCBI

BLAST this sequence: Phytozome NCBI

BLAST this sequence: Phytozome NCBI

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WILDTYPE
H124-6T

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MAGA 5.0

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wildtype	G	T	C	T	C	C	A	C	C	G	A	A	G	A	G	G	T	C	C	T	C	C	T	C	G	A	G	C	G	C	C	C	A	C	T	T
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蛋白分析

Species > Tools > Info > Help Contact Us phytozome

Setaria italica gene Si010740m.g

About this gene Sequences Protein Homologs ? Gene Ancestry Get Data

- Align sequences in JalView
- Get data for selected genes
- Filter homologs

<input type="checkbox"/>	Org	Defline	MRSF Score	Similarity	1	this gene	292
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<input type="checkbox"/>	<input type="checkbox"/> <i>Pvi</i> Pavir00022198m		GRA 1215	77.7%			
<input type="checkbox"/>	<input type="checkbox"/> <i>Osa</i> LOC_Os02g54700.2: RNA recognition motif containing protein, puta		969	64.4%			
<input type="checkbox"/>	<input type="checkbox"/> <i>Gra</i> Grai_003G128700.1		914	61.6%			

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蛋白分析

<http://www.uniprot.org/uniprot/?query=eif3G+AND+taxonomy%3APoaceae&sort=score>

Search in

Query

Protein Knowledgebase (UniProtKB)

eif3G AND taxonomy:Poaceae

Entry	Entry name	Status	Protein names	Gene names	Organism	Length
<input checked="" type="checkbox"/>	I1IDB7	I1IDB7_BRADI	★ Eukaryotic translation initiation factor 3 subunit G	BRADI3G53710	Brachypodium distachyon (Purple false brome) (Trachynia distachya)	287
<input type="checkbox"/>	C5YE20	C5YE20_SORBI	★ Putative uncharacterized protein Sb06g025590	Sb06g025590 SORBIDRAFT_06g025590	Sorghum bicolor (Sorghum) (Sorghum vulgare)	217
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<input checked="" type="checkbox"/>	J3LHU5	J3LHU5_ORYBR	★ Eukaryotic translation initiation factor 3 su...	OB02G42120	Oryza brachyantha	290
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<input checked="" type="checkbox"/>	Q6K4P2	Q6K4P2_ORYSJ	★ Eukaryotic translation initiation factor 3 su...	OSJNBa0054K20.21 Os02g0788300 OsJ_08662	Oryza sativa subsp. japonica (Rice)	289
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<http://www.uniprot.org/align/2012122771P1D5XO2C>

Sequences (in FASTA format) or UniProt identifiers

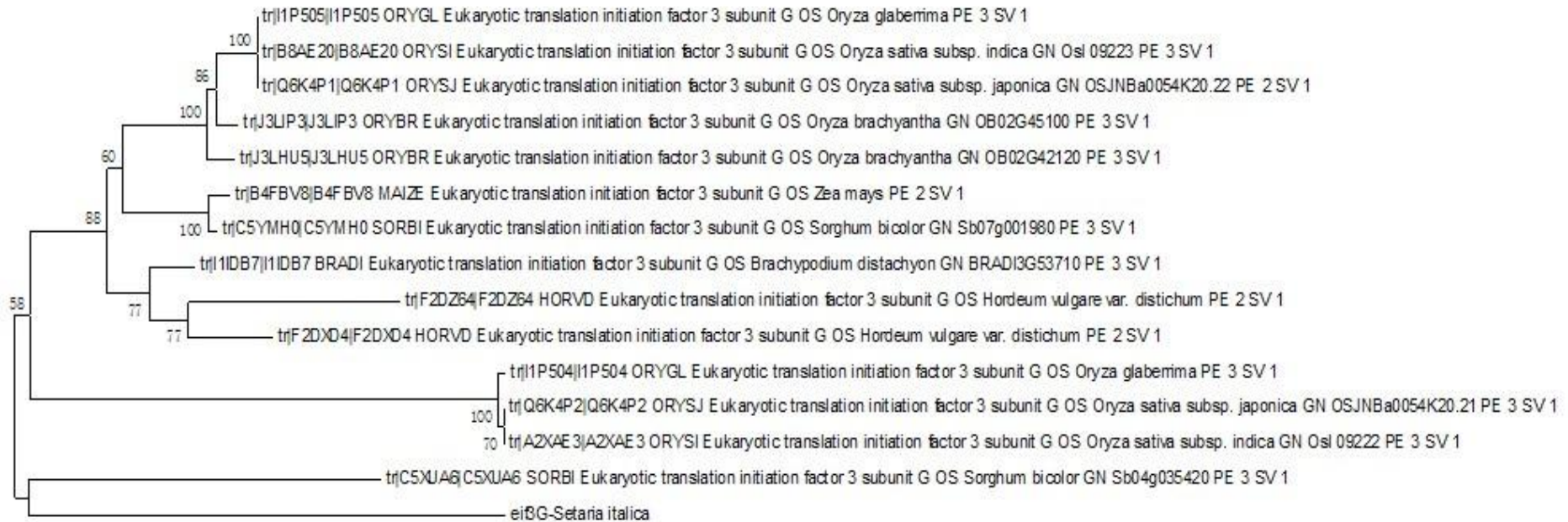
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Align
Clear

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48	DGNKVFITTTIVKRLARRSKSAIERRSNKFGDAAE---DAGSRITVSTEEVLEFR	106	B4FBV8	B4FBV8_MAIZE	214	SEDTREPDLLERLRTTGVSRVYVAVDQQTSSRGGFGFVNFVREDAAASLNGYGYD	273	B4FBV8	B4FBV8_MAIZE
51	DGNKVFITTTIVKRLARRSKSAIERRSNKFGDAAE---DAGSRITVSTEEVLEFR	109	J3LIP3	J3LIP3_ORYBR	218	SEDTREPDLLERLRTTGVSRVYVAVDQQTSSRGGFGFVNFVREDAAASLNGYGYD	277	J3LIP3	J3LIP3_ORYBR
52	DGNKVFITTTIVKRLARRSKSAIERRSNKFGDAAE---DAGSRITVSTEEVLEFR	110	J3LHU5	J3LHU5_ORYBR	217	SEDTREPDLLERLRTTGVSRVYVAVDQQTSSRGGFGFVNFVREDAAASLNGYGYD	276	J3LHU5	J3LHU5_ORYBR
59	DGNKVFITTTIVKRLARRSKSAIERRSNKFGDAAE---DAGSRITVSTEEVLEFR	118	I1P504	I1P504_ORYGL	216	SEDTREPDLLERLRTTGVSRVYVAVDQQTSSRGGFGFVNFVREDAAASLNGYGYD	275	I1P504	I1P504_ORYGL
51	DGNKVFITTTIVKRLARRSKSAIERRSNKFGDAAE---DAGSRITVSTEEVLEFR	109	I1P505	I1P505_ORYGL	216	SEDTREPDLLERLRTTGVSRVYVAVDQQTSSRGGFGFVNFVREDAAASLNGYGYD	275	I1P505	I1P505_ORYGL
50	DGNKVFITTTIVKRLARRSKSAIERRSNKFGDAAE---DAGSRITVSTEEVLEFR	109	F2DZ64	F2DZ64_HORVD	214	SEDTREPDLLERLRTTGVSRVYVAVDQQTSSRGGFGFVNFVREDAAASLNGYGYD	273	F2DZ64	F2DZ64_HORVD
48	DGNKVFITTTIVKRLARRSKSAIERRSNKFGDAAE---DAGSRITVSTEEVLEFR	107	F2DXD4	F2DXD4_HORVD	216	SEDTREPDLLERLRTTGVSRVYVAVDQQTSSRGGFGFVNFVREDAAASLNGYGYD	275	F2DXD4	F2DXD4_HORVD
59	DGNKVFITTTIVKRLARRSKSAIERRSNKFGDAAE---DAGSRITVSTEEVLEFR	118	Q6K4P2	Q6K4P2_ORYSJ	216	SEDTREPDLLERLRTTGVSRVYVAVDQQTSSRGGFGFVNFVREDAAASLNGYGYD	275	Q6K4P2	Q6K4P2_ORYSJ
51	DGNKVFITTTIVKRLARRSKSAIERRSNKFGDAAE---DAGSRITVSTEEVLEFR	109	B8AE20	B8AE20_ORYSI	216	SEDTREPDLLERLRTTGVSRVYVAVDQQTSSRGGFGFVNFVREDAAASLNGYGYD	275	B8AE20	B8AE20_ORYSI
59	DGNKVFITTTIVKRLARRSKSAIERRSNKFGDAAE---DAGSRITVSTEEVLEFR	118	A2XAE3	A2XAE3_ORYSI	216	SEDTREPDLLERLRTTGVSRVYVAVDQQTSSRGGFGFVNFVREDAAASLNGYGYD	275	A2XAE3	A2XAE3_ORYSI
51	DGNKVFITTTIVKRLARRSKSAIERRSNKFGDAAE---DAGSRITVSTEEVLEFR	109	Q6K4P1	Q6K4P1_ORYSJ	216	SEDTREPDLLERLRTTGVSRVYVAVDQQTSSRGGFGFVNFVREDAAASLNGYGYD	275	Q6K4P1	Q6K4P1_ORYSJ
49	DGNKVFITTTIVKRLARRSKSAIERRSNKFGDAAE---DAGSRITVSTEEVLEFR	108	Setaria	Q6K4P1_ORYSJ	220	SEDTREPDLLERLRTTGVSRVYVAVDQQTSSRGGFGFVNFVREDAAASLNGYGYD	279	Setaria	Q6K4P1_ORYSJ
106	RAPGSK-----DESSSGDPLA---SFGGAVLMVCTICRGGGHTSKPYKDLAQ	158	I1IDB7	I1IDB7_BRADI	274	NLILRVEWATERREN--	287	I1IDB7	I1IDB7_BRADI
110	RAPGSK-----DESSSGDPLA---SFGGAVLMVCTICRGGGHTSKPYKDLAQ	162	C5YMHO	C5YMHO_SORBI	277	NLILRVEWATERREN--	290	C5YMHO	C5YMHO_SORBI
110	RAPGSK-----DESSSGDPLA---SFGGAVLMVCTICRGGGHTSKPYKDLAQ	167	C5XUA6	C5XUA6_SORBI	286	NLILRVEWATERREN--	299	C5XUA6	C5XUA6_SORBI
107	RAPGSK-----DESSSGDPLA---SFGGAVLMVCTICRGGGHTSKPYKDLAQ	159	B4FBV8	B4FBV8_MAIZE	274	NLILRVEWATERREN--	287	B4FBV8	B4FBV8_MAIZE
110	RAPGSK-----DESSSGDPLA---SFGGAVLMVCTICRGGGHTSKPYKDLAQ	160	J3LIP3	J3LIP3_ORYBR	278	NLILRVEWATERREN--	291	J3LIP3	J3LIP3_ORYBR
111	RAPGSK-----DESSSGDPLA---SFGGAVLMVCTICRGGGHTSKPYKDLAQ	161	J3LHU5	J3LHU5_ORYBR	277	NLILRVEWATERREN--	290	J3LHU5	J3LHU5_ORYBR
119	RAPGSK-----DESSSGDPLA---SFGGAVLMVCTICRGGGHTSKPYKDLAQ	165	I1P504	I1P504_ORYGL	276	NLILRVEWATERREN--	289	I1P504	I1P504_ORYGL
110	RAPGSK-----DESSSGDPLA---SFGGAVLMVCTICRGGGHTSKPYKDLAQ	160	I1P505	I1P505_ORYGL	276	NLILRVEWATERREN--	289	I1P505	I1P505_ORYGL
110	RAPGSK-----DESSSGDPLA---SFGGAVLMVCTICRGGGHTSKPYKDLAQ	160	F2DZ64	F2DZ64_HORVD	274	NLILRVEWATERREN--	288	F2DZ64	F2DZ64_HORVD
108	RAPGSK-----DESSSGDPLA---SFGGAVLMVCTICRGGGHTSKPYKDLAQ	160	F2DXD4	F2DXD4_HORVD	274	NLILRVEWATERREN--	288	F2DXD4	F2DXD4_HORVD
119	RAPGSK-----DESSSGDPLA---SFGGAVLMVCTICRGGGHTSKPYKDLAQ	165	Q6K4P2	Q6K4P2_ORYSJ	276	NLILRVEWATERREN--	289	Q6K4P2	Q6K4P2_ORYSJ
110	RAPGSK-----DESSSGDPLA---SFGGAVLMVCTICRGGGHTSKPYKDLAQ	160	B8AE20	B8AE20_ORYSI	276	NLILRVEWATERREN--	289	B8AE20	B8AE20_ORYSI
119	RAPGSK-----DESSSGDPLA---SFGGAVLMVCTICRGGGHTSKPYKDLAQ	165	A2XAE3	A2XAE3_ORYSI	276	NLILRVEWATERREN--	289	A2XAE3	A2XAE3_ORYSI
110	RAPGSK-----DESSSGDPLA---SFGGAVLMVCTICRGGGHTSKPYKDLAQ	160	Q6K4P1	Q6K4P1_ORYSJ	276	NLILRVEWATERREN--	289	A2XAE3	A2XAE3_ORYSI
109	RAPGSK-----DESSSGDPLA---SFGGAVLMVCTICRGGGHTSKPYKDLAQ	167	Setaria	Q6K4P1_ORYSJ	276	NLILRVEWATERREN--	289	Q6K4P1	Q6K4P1_ORYSJ
					280	NLILRVEWATERREN--	292	Setaria	Q6K4P1_ORYSJ

蛋白分析

MAGA 5.0



蛋白分析

MATAVATQQQHKFRWGDIA DTTATSASSSRRGSSSSGPTRPVIEYRFDDEGNKVKVTTTTTRTRSLARTRL
SRAVERRAWTKFGDAVKRDDAGSRLTMVSTEEVLLERPLAPVNSIVGKQAEESTPGDPLSMESMRG
GALLMLCRICKKKGDHWTSKCPYKDLAPQAAGFVDTPPSADGRAAPPGERAYVPPNKKEGADTRRAS
MMRRNDENSIRVNNLSEDTHEADLLELFRTFGPVTRAFVARDKWTRSSGGFGFVNFVRREDGEKAISK
LNGYGYDNLILRVEWSDRPN

WILDTYPE

H124-6T

MATAVATQQQHKFRWGDIA DTTATSASSSRRGSSSSGPTRPVIEYRFDDEGNKVKVTTTTTRTRSLARTRLS
RSAVERRAWTKFGDAVKRDDAGSRLTMVSTKKVLLERPLAPVNSIVGKQAEESTPGDPLSMESMRGG
ALLMLCRICKKKGDHWTSKCPYKDLAPQAAGFVDTPPSADGRAAPPGERAYVPPNKKEGADTRRASM
MRRNDENSIRVNNLSEDTHEADLLELFRTFGPVTRAFVARDKWTRSSGGFGFVNFVRREDGEKAISKLN
GYGYDNLILRVEWSDRPN

蛋白分析

Jemboss

1、由预测的二级结构来看，野生型的由99-110均为形成螺旋结构，H124-6T为97-102形成螺旋，103-107形成的是折叠

```
      . 60 . 70 . 80 . 90 . 100
      NKVKVTTTTTRTRSLARTRLSRSAVERRAWTKFGDAVKRDDAGSRLTMVST
helix          HHHHHHHH      HH      HH
sheet  EEEEE  EEEE          EEEE
turns  T      TTT  T      TTTT  TT
coil   CC      C  CCCCC      C  CCC  C
      . 110 . 120 . 130 . 140 . 150
      EEVLLERPLAPVNSIVGKQAEESTPGDPLSMESMRGGALLMLCRICKKK
helix HHHHHHHH          HHHHHHHHHHHHHHHH
sheet          EEEEE      EEE
turns          TT  T      TTT
coil          CC  CCCCC  C  CCCC
```

野生型

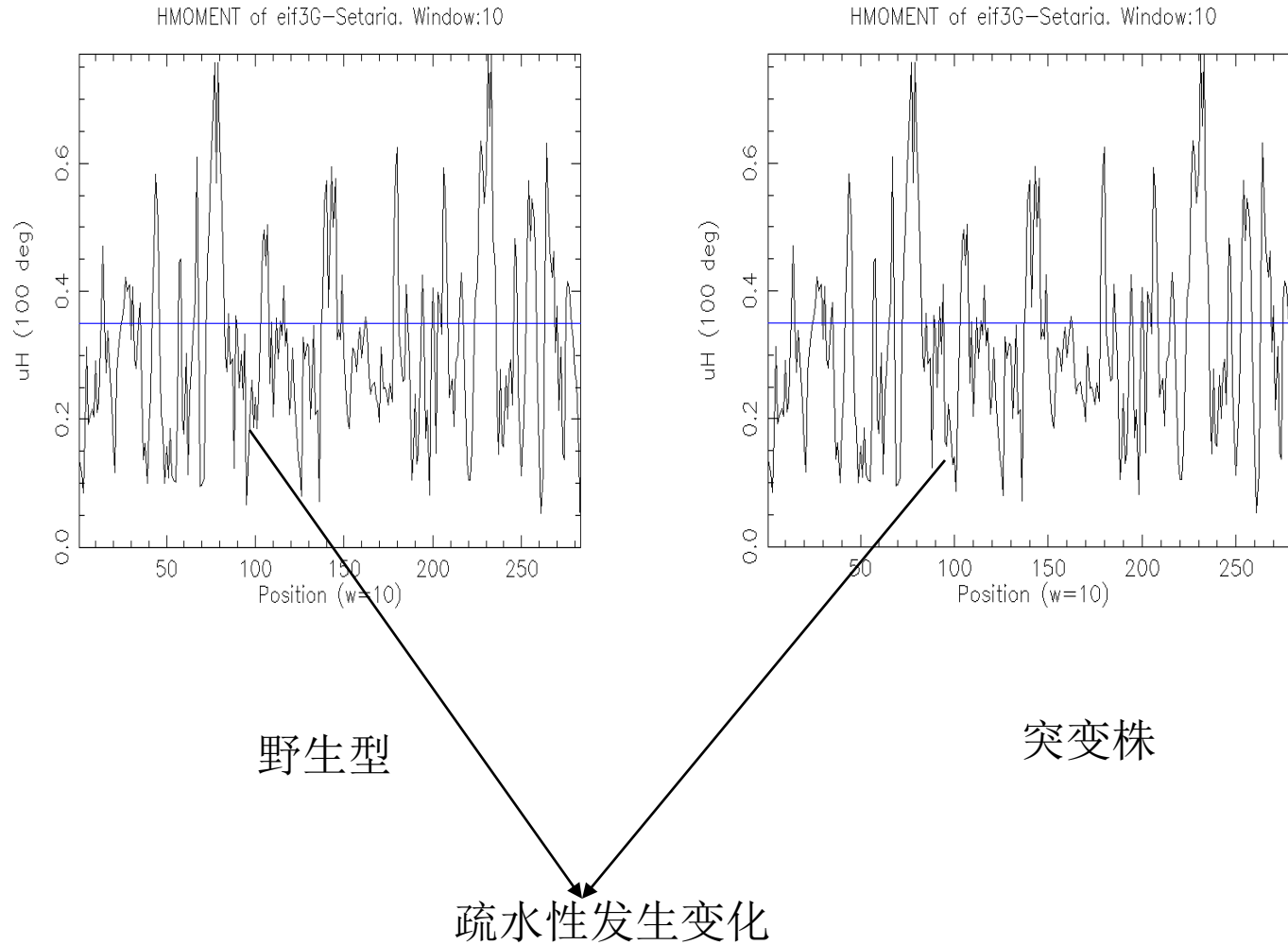
```
      . 60 . 70 . 80 . 90 . 100
      NKVKVTTTTTRTRSLARTRLSRSAVERRAWTKFGDAVKRDDAGSRLTMVST
helix          HHHHHHHH      HH      HH HH
sheet  EEEEE  EEEE          E
turns  T      TTT  T      TTTT  TT
coil   CC      C  CCCCC      C  CCC
      . 110 . 120 . 130 . 140 . 150
      KKVLLERPLAPVNSIVGKQAEESTPGDPLSMESMRGGALLMLCRICKKK
helix HH  H          HHHHHHHHHHHHHHHH
sheet  EEEEE  EEEEE          EEE
turns          TT  T      TTT
coil          CCC  CCCCC  C  CCCC
```

突变株

Different

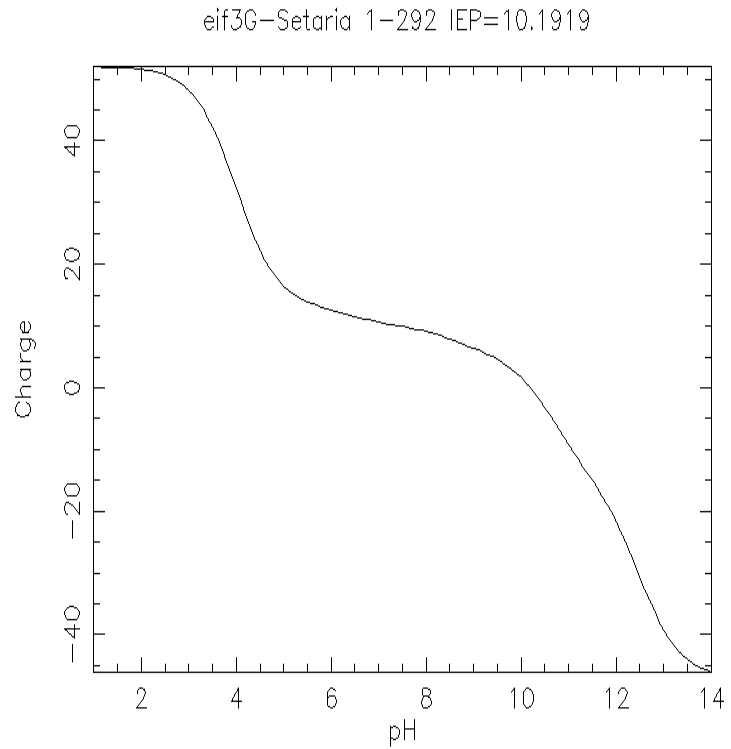
蛋白分析

由图中可以看出，突变株的疏水性略有增强

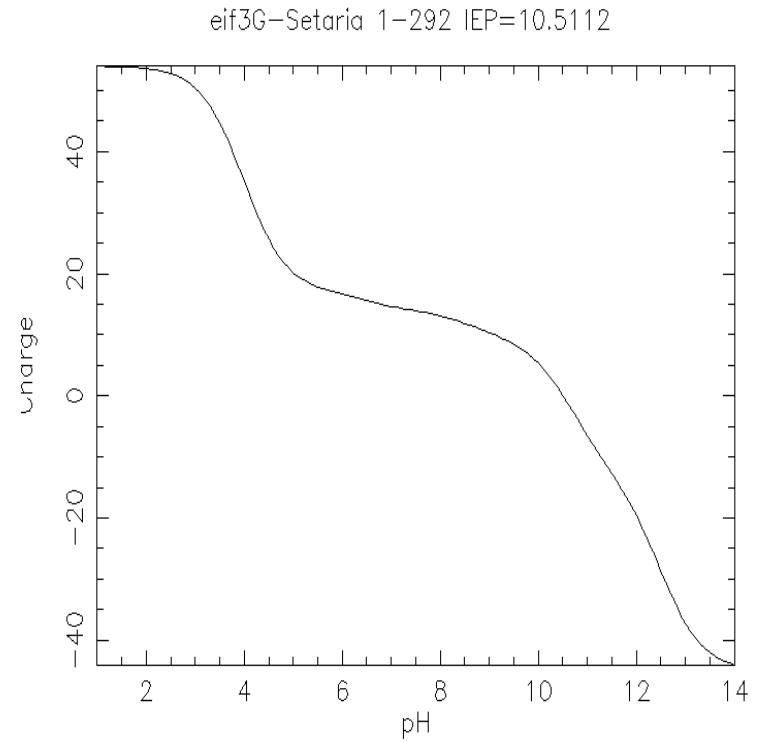


蛋白分析

野生型的等电点为10.1919；突变株的等电点为10.5112



野生型



突变株

通过上述分析，我们得知，突变体H124-6T **Si010740** 编码的蛋白质是一个翻译起始因子，此蛋白有两个结构域，分别为eIF3G和RRM，其中在编码eIF3G的序列中存在两个SNP，这两个碱基的改变使此基因编码的多肽101位点和102位点均由酸性的谷氨酸变为了碱性的赖氨酸。通过软件预测，这两个氨基酸的改变引起了编码蛋白质的结构上一系列改变。这些变化可能改变的该蛋白质的功能，从而引起了植株的突变表型。

THANK YOU