



茶树谷氨酸受体序列预测分析

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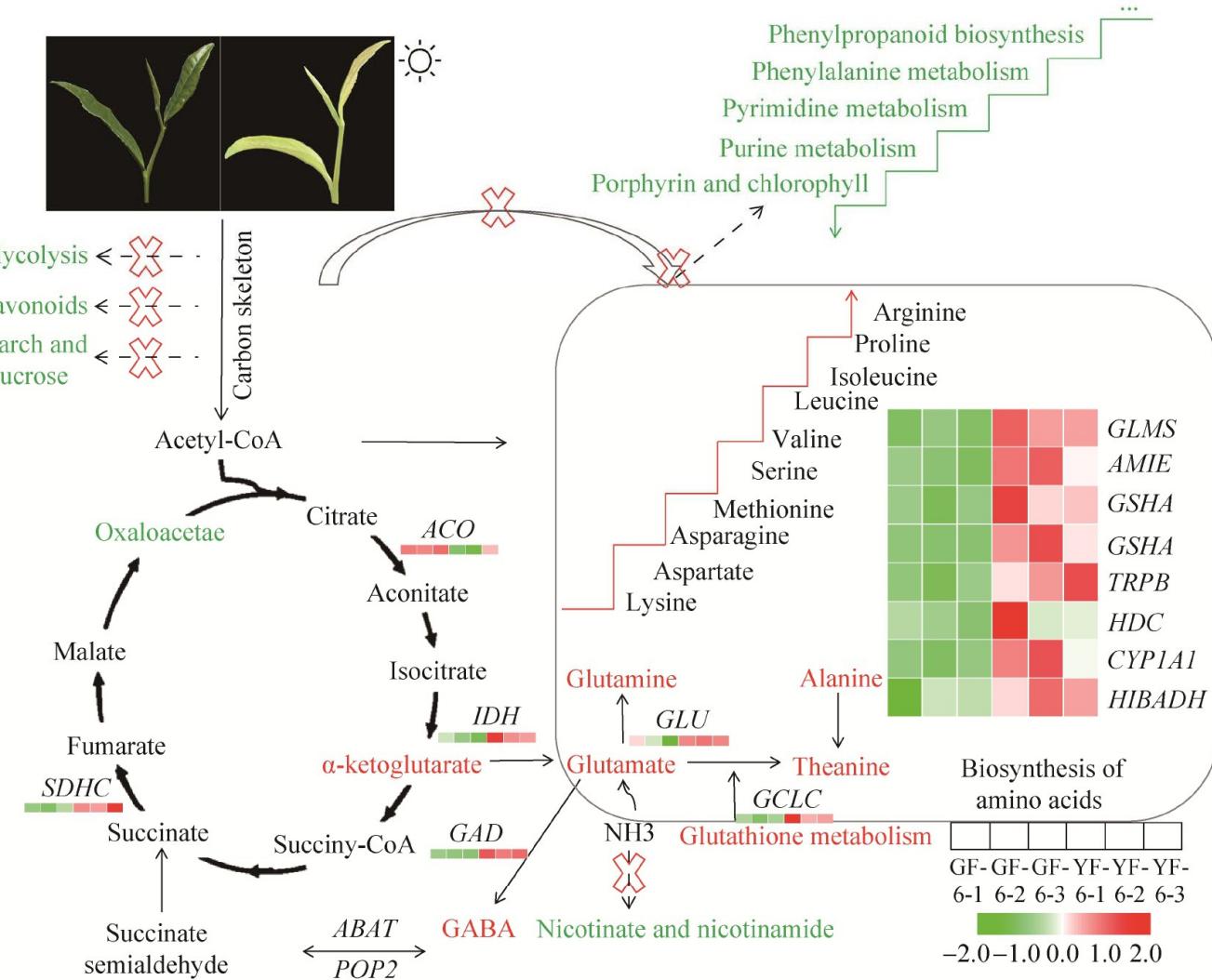
PART **04**

研究展望



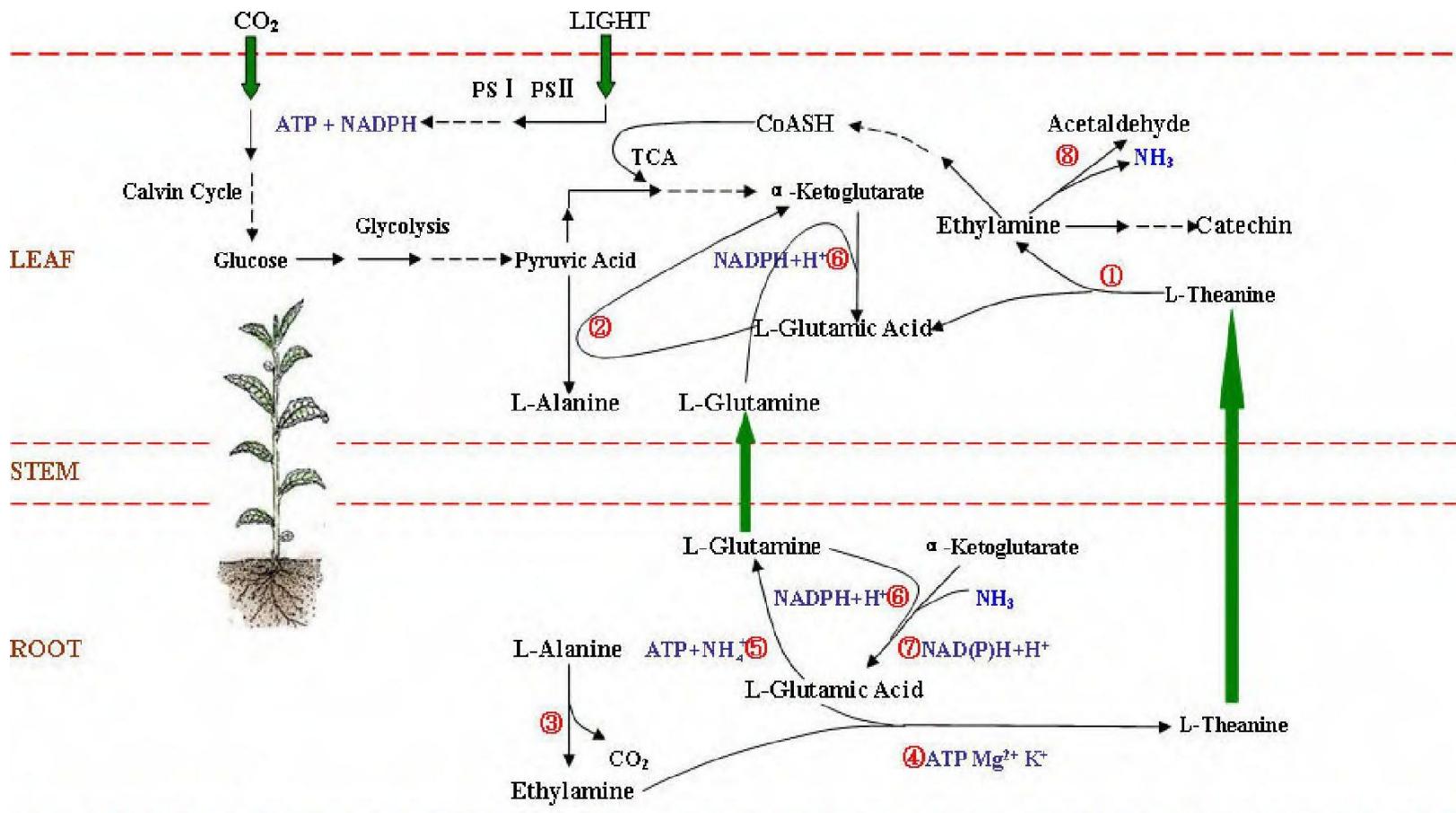
PART-01

研究背景



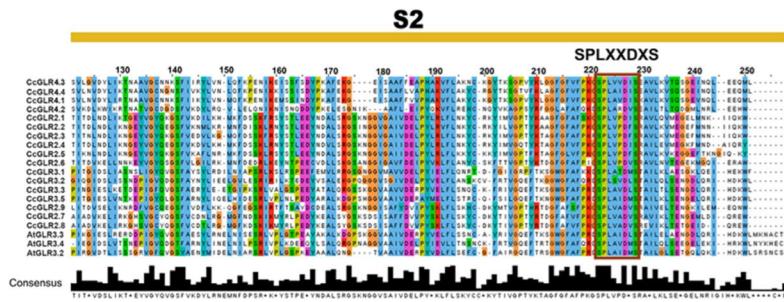
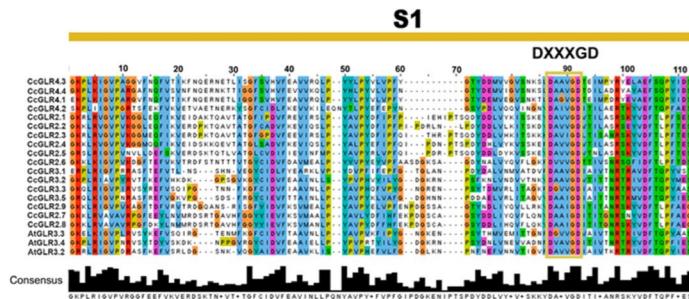
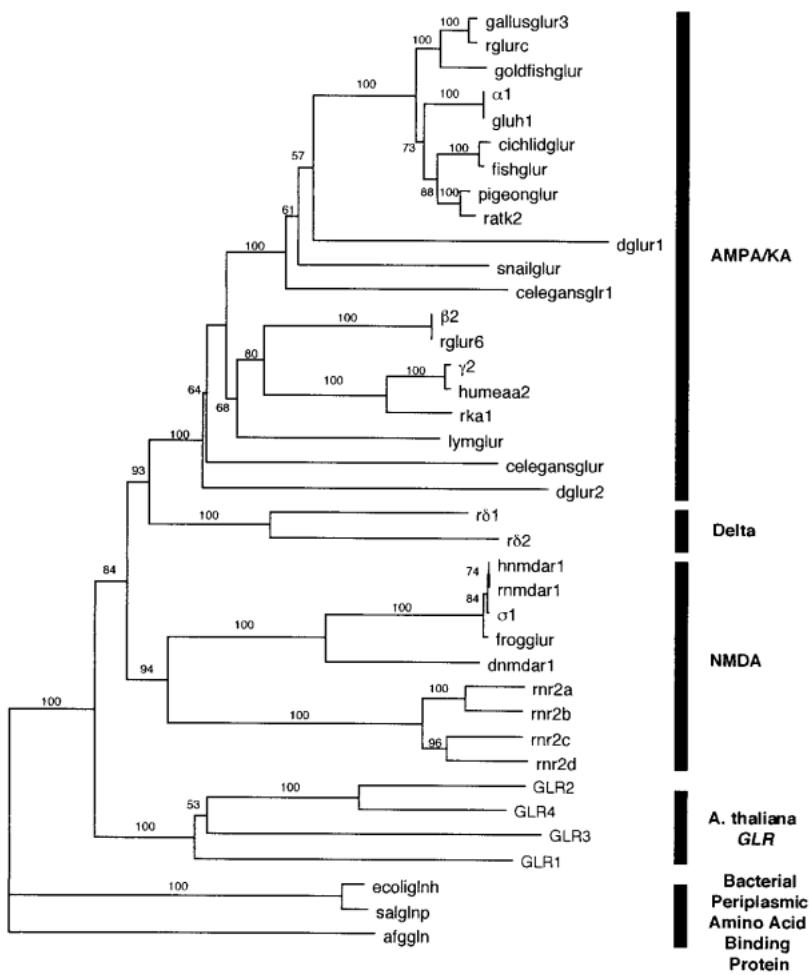
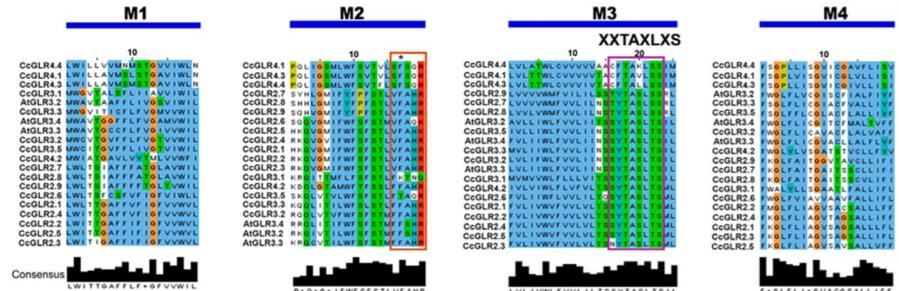
- 茶氨酸 (L-Theanine) 是茶叶特有一种氨基酸，化学式为 C₇H₁₄N₂O₃，在干茶中占重量的1%-2%。
- 茶氨酸含量与茶叶品质密切相关。新鲜嫩芽和嫩叶中的茶氨酸含量较高，因此特级绿茶、白茶和黄茶通常具有鲜爽和清新口感。
- 具有较高含量的茶氨酸以及其他多种游离氨基酸，其积累可能是氮资源、氨基在叶片中被更有效储存，使得氨基酸合成通路中的代谢物及相关基因表达上调，茶氨酸成为黄化叶中显著积累的含氮化合物。

图1 ‘福云6号’和‘福黄2号’光合作用通路分析 (林馨颖等, 2022)



- ①L-Theanine Hydrolase; ②Alanine transaminase; ③L-Alanine Decarboxylase; ④L-Theanine Synthetase; ⑤Glutamine Synthetase;
⑥Glutamine-2-Oxoglutamate-Aminotransferase; ⑦Glutamate Dehydrogenase; ⑧Amine Oxidase.

图3 茶氨酸代谢途径①L-谷氨酸水解酶、②丙氨酸转氨酶、③L-丙氨酸脱羧酶、④L-茶氨酸合酶、⑤谷氨酰胺合酶、⑥谷氨酰胺合成酶/谷氨酰胺-α-酮戊二酸氨基转移酶、⑦谷氨酸脱氢酶、⑧胺氧化酶
(陈林等, 2009)

A**B****C**

植物 GLR 序列与
其动物对应物之间的
同源区域跨越所有重
要结构域，包括形成
激动剂结合结构域的
四个跨膜片段（M1-
M4）和 S1 和 S2 区域。

系统发育分析表明，动物 iGluR 和 AtGLRs 的分化发生在不同动物 iGluR 类别（N-甲基-D-天冬氨酸受体（NMDA）、(S)- α 氨基-3-羟基-5-甲基异恶唑-4-丙酸酯受体（AMPA）、Delta-红藻氨酸受体）分化之前。在 iGluR/GLR 家族进化历史的早期，在植物和动物分化之前，发生了一次重组事件，将祖先 iGluR/GLR 的 LIVBP 结构域与 GPCR 的七个跨膜结构域融合，从而产生了祖先家族 C GPCR（G 蛋白偶联受体的 C 家族）（Turano 等人，2001 年）。

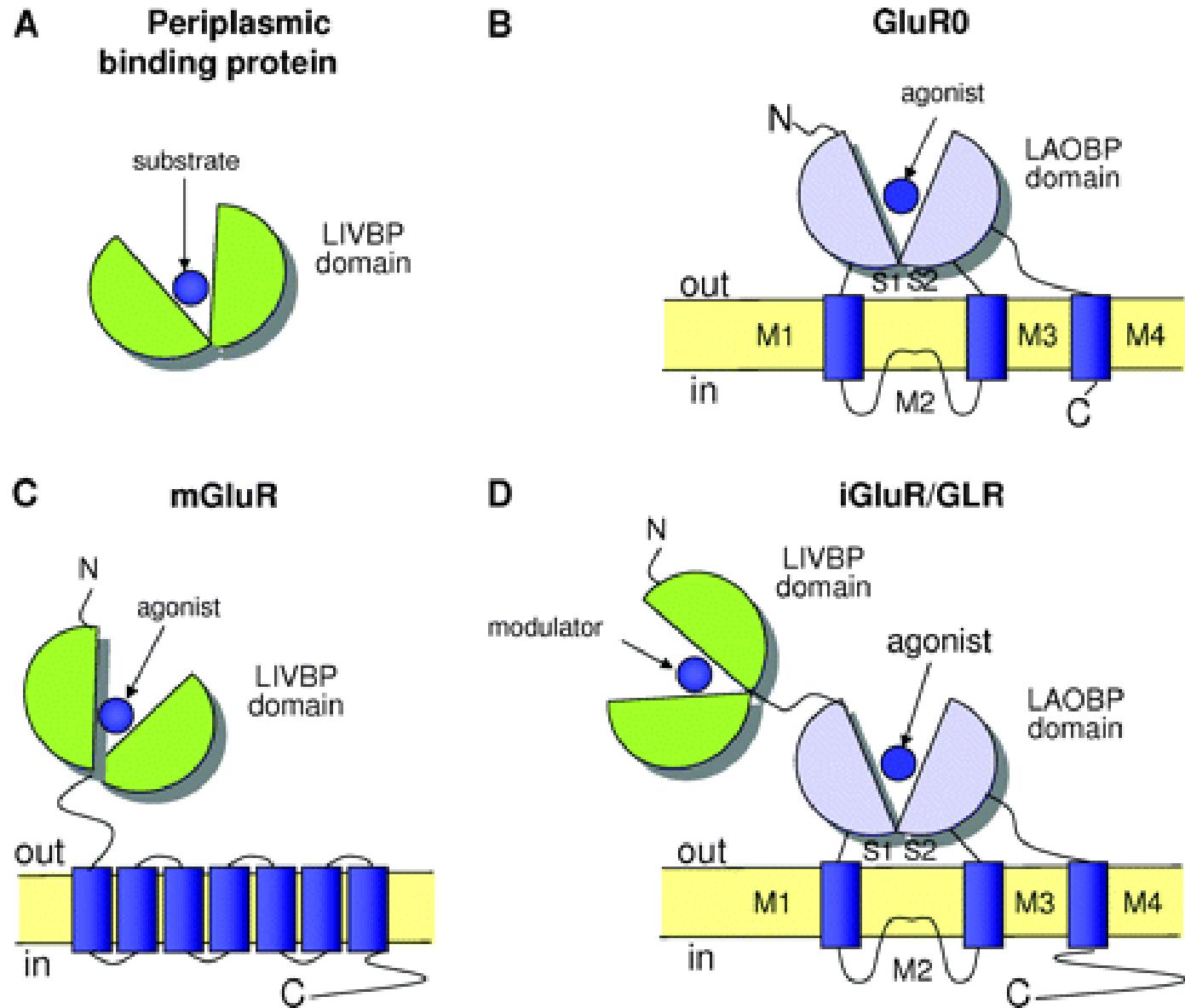


图 2. 真核谷氨酸受体的 3D 结构示意图以及与之共享同源结构域的细菌蛋白。两种类型的维纳斯捕蝇器 (Venus fly trap, VFT) 结构域出现在 iGluR/GLR 家族的成员中：激动剂结合的 LAOBP 结构域（由一级序列的 S1 和 S2 区域形成）和延伸 N 末端区域的 LIVBP 结构域，它可以充当变构调节结构域。细菌谷氨酸受体 (GluR0) 缺乏 C 端和 LIVBP 结构域。M1-M4 是指 GluR0/iGluR/GLR 家族中的跨膜结构域（修改自 Acher 和 Bertrand, 2004）。哺乳动物离子型谷氨酸受体 (iGluR)，代谢型谷氨酸受体 (mGluR)。（Brian G. Forde. et al, 2007）



PART-02

序 列 分 析

Status

 Unreviewed (TrEMBL) (37)

Taxonomy

4442

Filter by taxonomy

Group by

Taxonomy

Keywords

Gene Ontolog

Enzyme Class

Proteins with

Chain (20)

Compositional bias (11)

Disulfide bond (14)

UniProtKB 37 results

or expand search to "4442" to include lower taxonomic ranks or restrict to reference proteome

UP000593564

Tools ▾ Download (37) Add View: Cards ○ Table ○ Customize columns Share ▾

Entry ▲	Entry Name ▲	Protein Names ▲	Gene Names ▲	Organism ▲	Length ▼
<input type="checkbox"/> A0A7J7G6I6	■ A0A7J7G6I6_CAMSI	Ionotropic glutamate receptor C-terminal domain-containing protein	HYC85_027491	Camellia sinensis (Tea plant) (Thea sinensis)	1,013 AA
<input type="checkbox"/> A0A7J7G3D8	■ A0A7J7G3D8_CAMSI	Glutamate receptor	HYC85_026369	Camellia sinensis (Tea plant) (Thea sinensis)	944 AA
<input type="checkbox"/> A0A7J7HMI0	■ A0A7J7HMI0_CAMSI	Glutamate receptor	HYC85_011100	Camellia sinensis (Tea plant) (Thea sinensis)	932 AA

Overview

Trees

Percent Identity Matrix

Text Output

Input Parameters

API Request

Advanced | List

Search



Help

Cladogram

- tr|**A0A7J7HMI0**|A0A7J7HMI0_CAMSI
 - tr|**A0A7J7HKT2**|A0A7J7HKT2_CAMSI
 - tr|**A0A7J7HEH3**|A0A7J7HEH3_CAMSI
 - tr|**A0A7J7G3D8**|A0A7J7G3D8_CAMSI
 - tr|**A0A7J7FSX1**|A0A7J7FSX1_CAMSI
 - tr|**A0A7J7HAW1**|A0A7J7HAW1_CAMSI
 - tr|**A0A7J7HWC6**|A0A7J7HWC6_CAMSI
 - tr|**A0A7J7HTR6**|A0A7J7HTR6_CAMSI
 - tr|**A0A7J7HWB2**|A0A7J7HWB2_CAMSI
 - tr|**A0A7J7HF35**|A0A7J7HF35_CAMSI
 - tr|**A0A7J7H9J3**|A0A7J7H9J3_CAMSI
 - tr|**A0A7J7HVJ8**|A0A7J7HVJ8_CAMSI
 - tr|**A0A7J7GTH5**|A0A7J7GTH5_CAMSI
 - tr|**A0A7J7I7F7**|A0A7J7I7F7_CAMSI
 - tr|**A0A7J7HEV6**|A0A7J7HEV6_CAMSI

Feedback

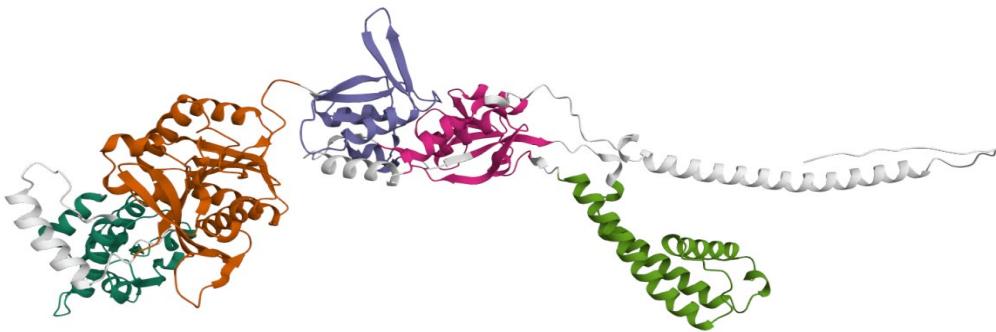
Help

	Overview	Trees	Percent Identity Matrix	Text Output		Input Parameters		API Request													
Percent Identity Matrix																					
<input type="checkbox"/> tr A0A7J7HAW1 A0A7J7HAW1_CAMSI	100.00%	37.93%	38.35%	38.60%	30.07%	30.03%	31.06%	31.70%	31.44%	30.95%	35.12%	35.23%	37.61%	37.61%	37.61%	37.61%	37.61%	37.61%	37.61%	37.61%	37.61%
<input checked="" type="checkbox"/> tr A0A7J7HWC6 A0A7J7HWC6_CAMSI	37.93%	100.00%	92.85%	90.93%	29.80%	30.30%	30.38%	32.12%	30.64%	29.81%	29.26%	30.12%	30.12%	30.12%	30.12%	30.12%	30.12%	30.12%	30.12%	30.12%	30.12%
<input checked="" type="checkbox"/> tr A0A7J7HWB2 A0A7J7HWB2_CAMSI	38.35%	92.85%	100.00%	94.68%	29.96%	30.30%	29.71%	31.48%	30.76%	29.40%	29.15%	29.81%	29.81%	29.81%	29.81%	29.81%	29.81%	29.81%	29.81%	29.81%	29.81%
<input checked="" type="checkbox"/> tr A0A7J7HTR6 A0A7J7HTR6_CAMSI	38.60%	90.93%	94.68%	100.00%	30.38%	30.85%	29.34%	31.54%	30.94%	29.69%	29.17%	29.57%	29.57%	29.57%	29.57%	29.57%	29.57%	29.57%	29.57%	29.57%	29.57%
<input type="checkbox"/> tr A0A7J7HF35 A0A7J7HF35_CAMSI	30.07%	29.80%	29.96%	30.38%	100.00%	76.00%	56.65%	56.15%	56.71%	53.62%	31.44%	29.90%	33.11%	33.11%	33.11%	33.11%	33.11%	33.11%	33.11%	33.11%	33.11%
<input type="checkbox"/> tr A0A7J7H9J3 A0A7J7H9J3_CAMSI	30.03%	30.30%	30.30%	30.85%	76.00%	100.00%	55.98%	54.67%	56.00%	53.77%	31.02%	29.06%	32.71%	32.71%	32.71%	32.71%	32.71%	32.71%	32.71%	32.71%	32.71%

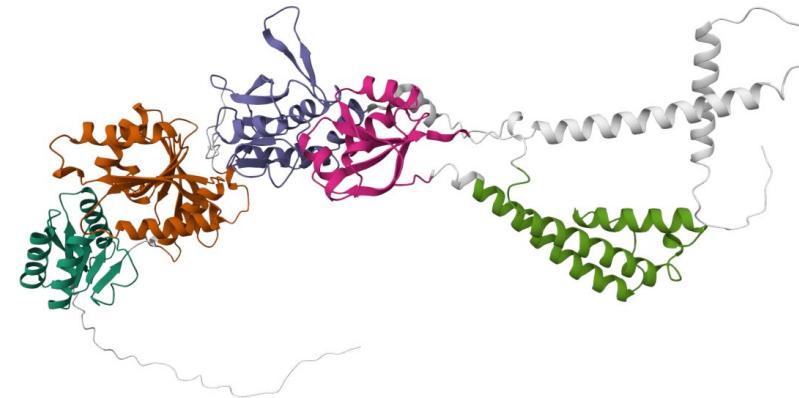
Feedback

Help

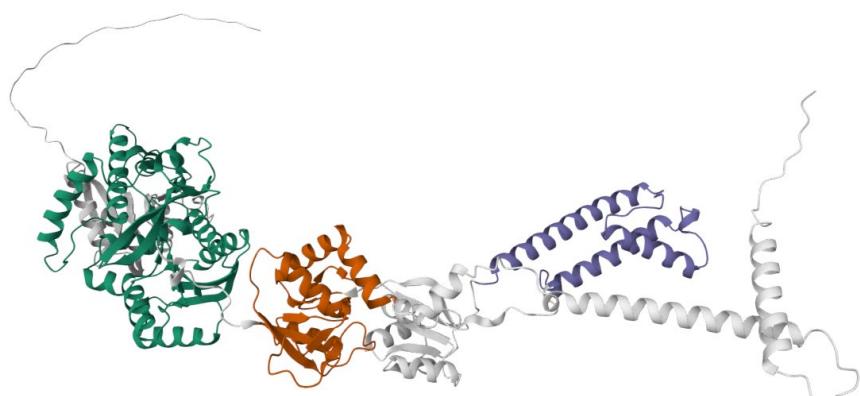
AOA7J7HAW1



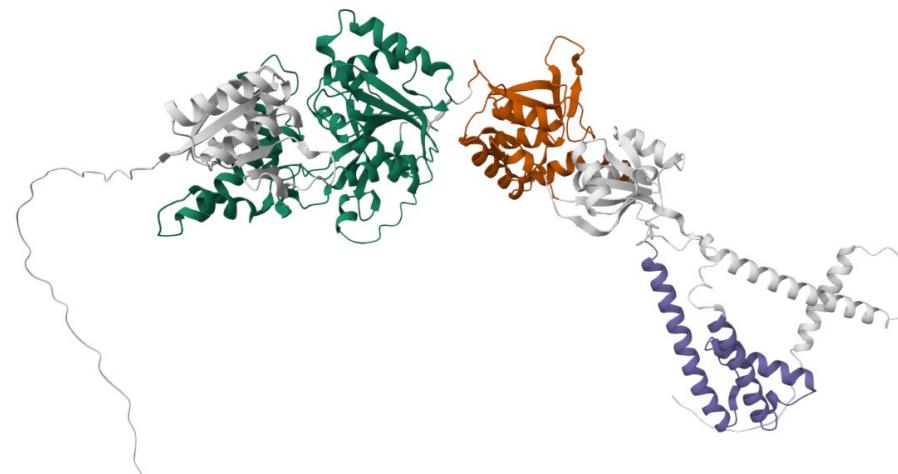
AOA7J7HWC6



AOA7J7HTR6



AOA7J7HWB2



数据来源：AlphaFold 产
生介于 0 和 100 之
间的每残差模型置信度分
数 (pLDDT)

- 非常高 ($p\text{LDDT} > 90$)
- 高 ($90 > p\text{LDDT} > 70$)
- 低 ($70 > p\text{LDDT} > 50$)
- 非常低 ($p\text{LDDT} < 50$)

Domain 1

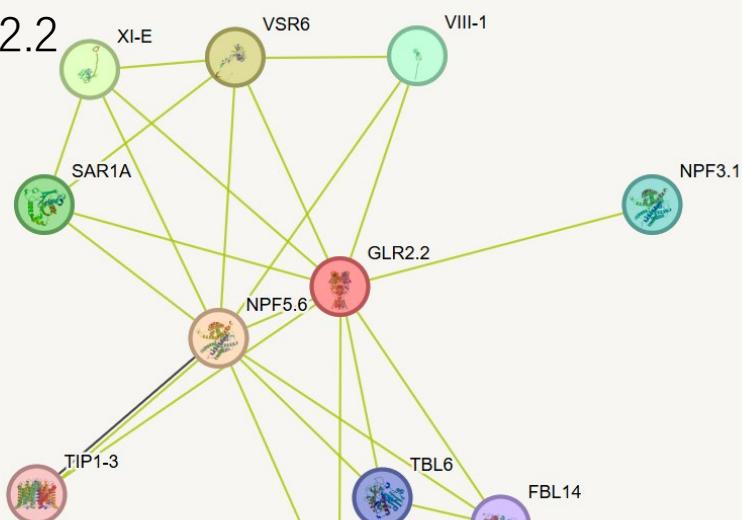
Domain 2

Domain 3

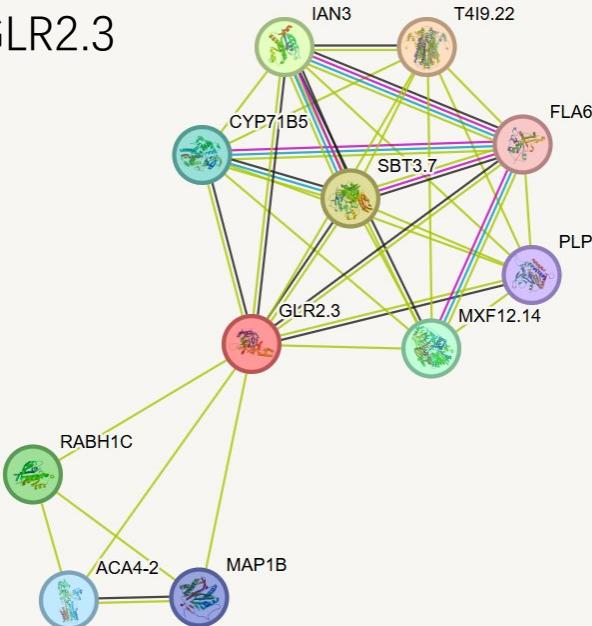
Domain 4

Domain 5

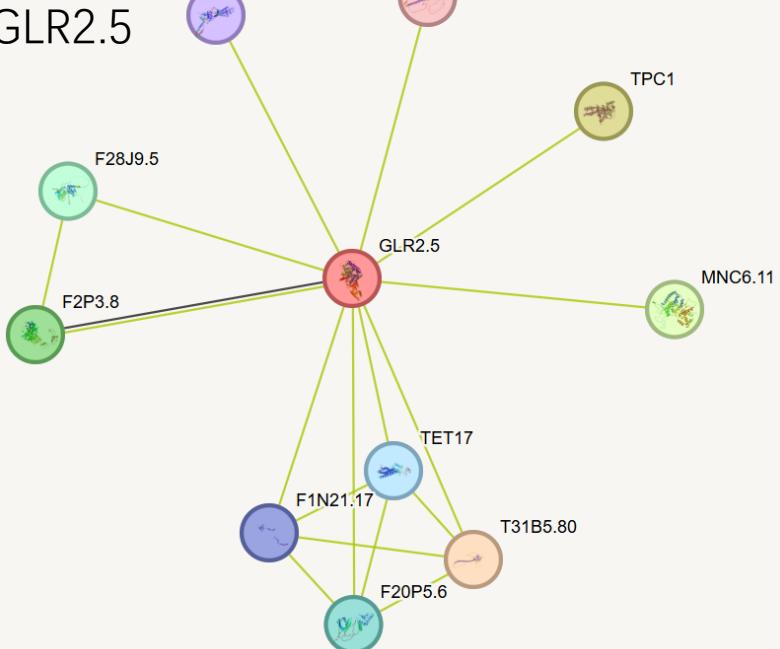
GLR2.2



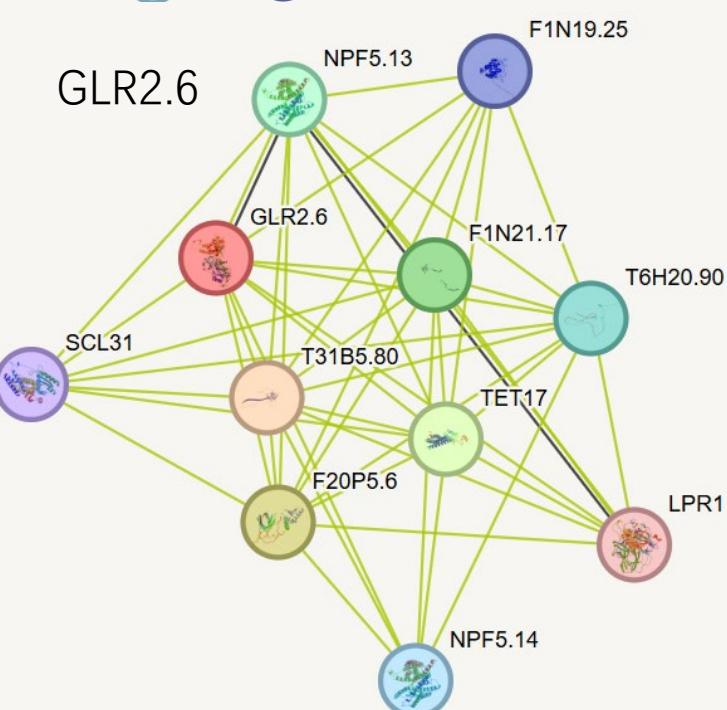
GLR2.3



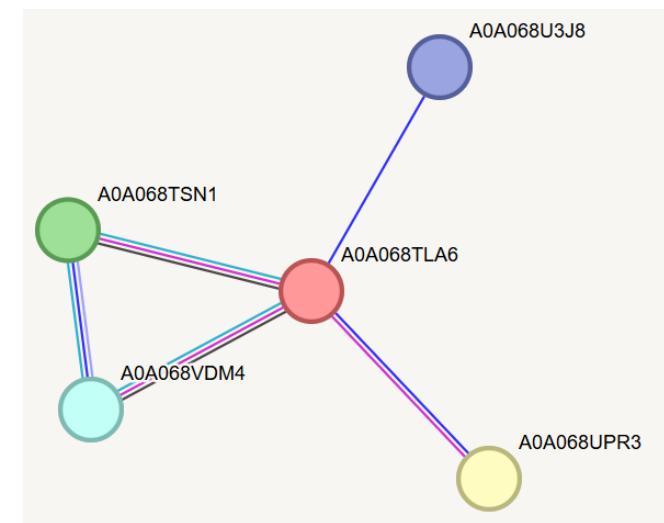
GLR2.5



GLR2.6



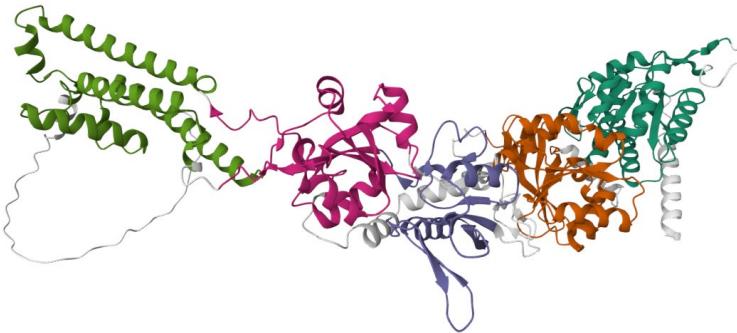
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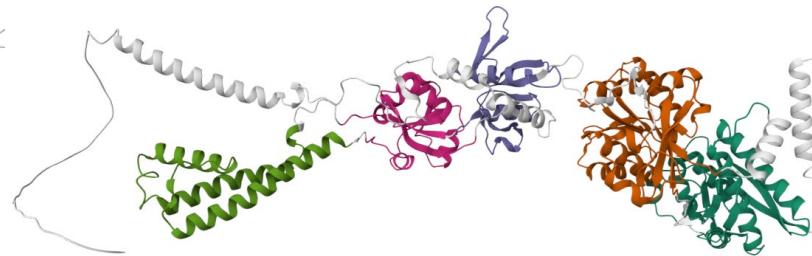
STRING: AlphaFold 产生介于 0 和 100 之间的每残差模型置信度分数 (pLDDT)

- 非常高 (pLDDT > 90)
- 高 (90 > pLDDT > 70)
- 低 (70 > pLDDT > 50)
- 非常低 (pLDDT < 50)

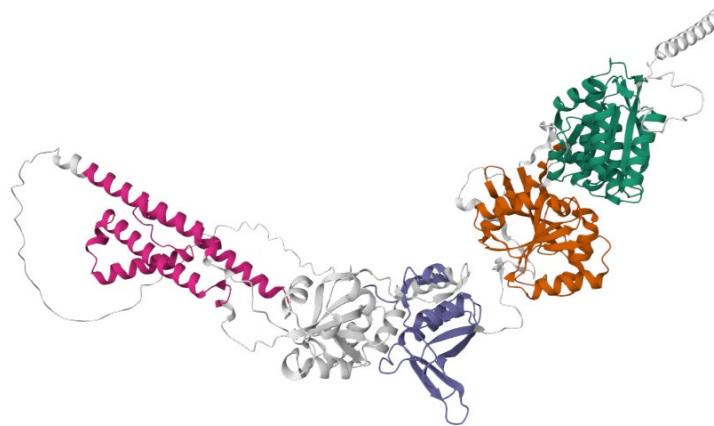
GLR2.2



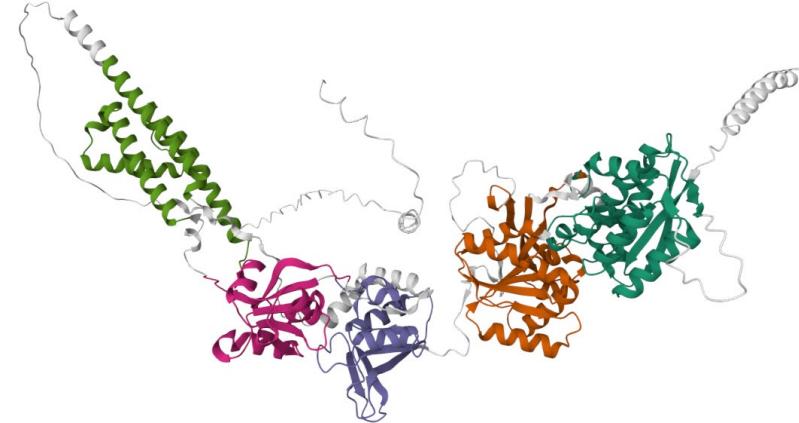
GLR2.3



GLR2.5



GLR2.6



Domain 1

Domain 2

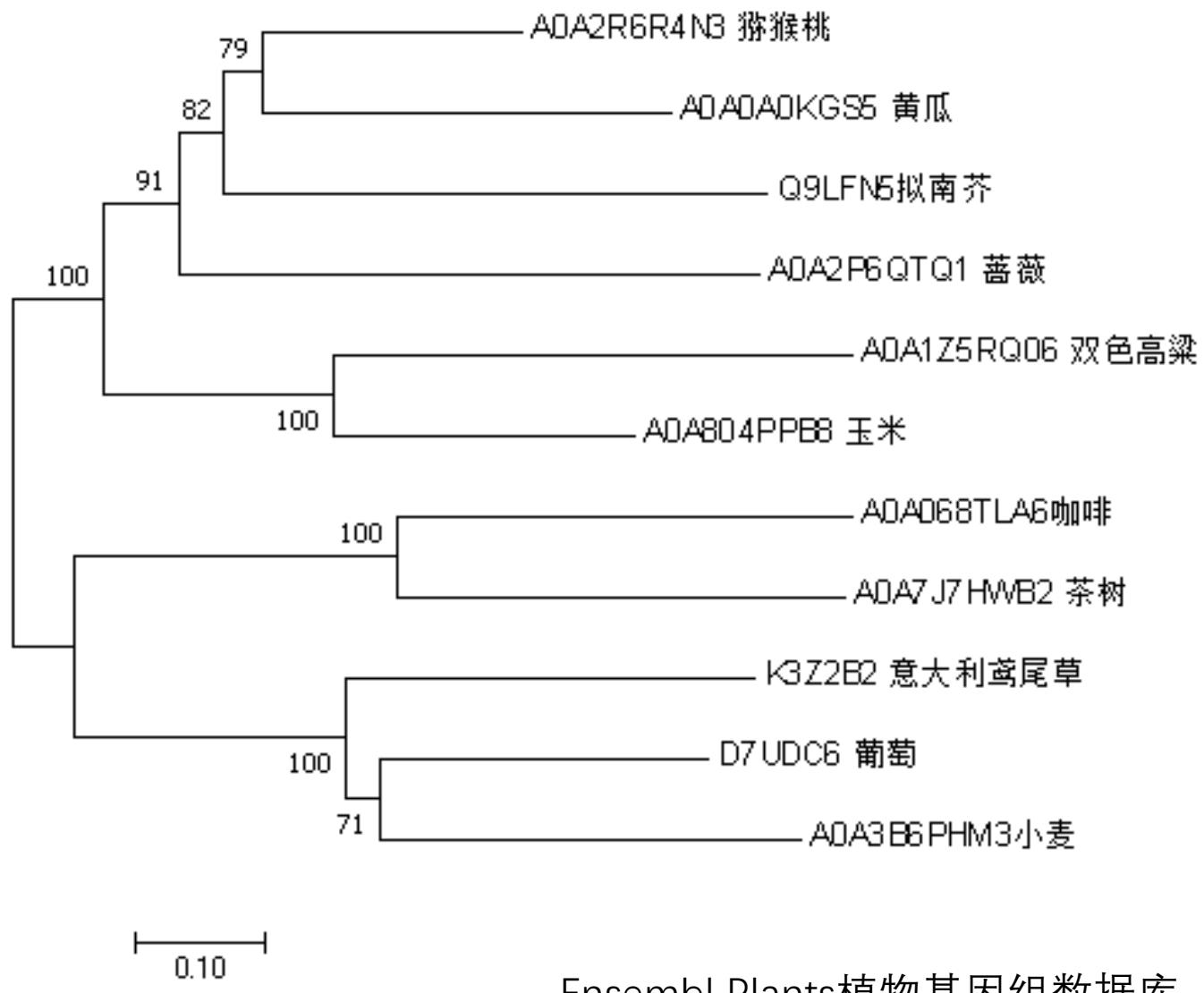
Domain 3

Domain 4

Domain 5

数据来源：AlphaFold 产
生介于 0 和 100 之
间的每残差模型置信度分
数 (pLDDT)

- 非常高 ($p\text{LDDT} > 90$)
- 高 ($90 > p\text{LDDT} > 70$)
- 低 ($70 > p\text{LDDT} > 50$)
- 非常低 ($p\text{LDDT} < 50$)



Ensembl Plants植物基因组数据库

M M7: Analysis Preferences

Options Summary	
Option	Selection
Analysis	Phylogeny Reconstruction
Scope	All Selected Taxa
Statistical Method	Neighbor-joining
Phylogeny Test	
Test of Phylogeny	Bootstrap method
No. of Bootstrap Replications	100
Substitution Model	
Substitutions Type	Amino acid
Model/Method	Poisson model
Rates and Patterns	
Rates among Sites	Uniform rates
Gamma Parameter	Not Applicable
Pattern among Lineages	Same (Homogeneous)
Data Subset to Use	
Gaps/Missing Data Treatment	Complete deletion
Site Coverage Cutoff (%)	Not Applicable

Buttons: Help, Compute (highlighted), Cancel

Name	p-value	Motif Locations
Q9LFN5_ARATH	2.24e-146	
D7UDC6_VITVI	7.56e-169	
A0A1Z5RQ06_SORBI	2.03e-96	
A0A068TLA6_COFC	4.74e-138	
K3Z2B2_SETIT	1.91e-165	
A0A804PPB8_MAIZE	1.37e-150	
A0A0A0KGS5_CUCSA	5.38e-125	
A0A2P6QTQ1_ROSCH	1.41e-135	
A0A2R6R4N3_ACTCC	4.70e-182	
A0A3B6PHM3_WHEAT	4.52e-164	
A0A7J7HWB2_CAMSI	2.14e-132	

Motif	Symbol	Motif Consensus
1.		RGPPKHQJGTIFWFSFSTLFFAHRE
2.		WLFVVLILTSYASLTSMLTQQL
3.		VVGDTIVANRSRYVDFTQPYTESG
4.		WPGDTTSVPKGWVFPSNGKKLKIGV
5.		TGFVVWILEHRINEEF
6.		WIFLKPLTLELWLATF
7.		ARKLGMMSEGYVWIAT
8.		GYCIDVFDALVLLPY
9.		GFAFPGRSPLAVDVSRAILNLTENG
10.		NGGVAFAFDEIPYLKLFLSTYC

11个物种谷氨酸受体基因家族，motif 1到motif10高度保守，在氨基酸序列上的分布及其位置基本一致。

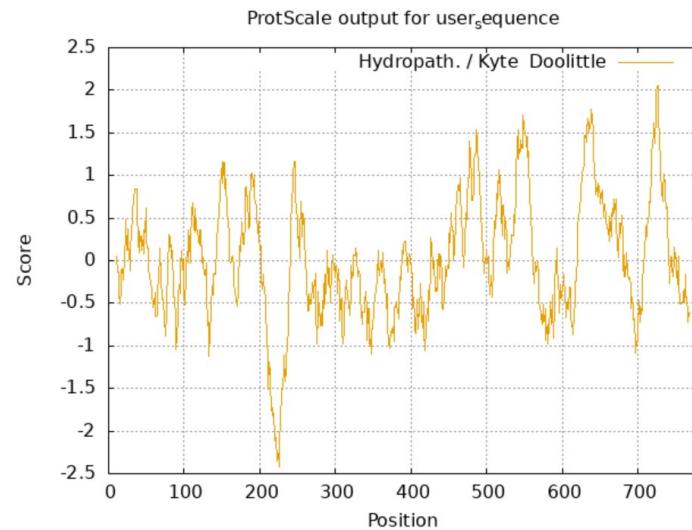


茶树谷氨酸受体蛋白理化性质

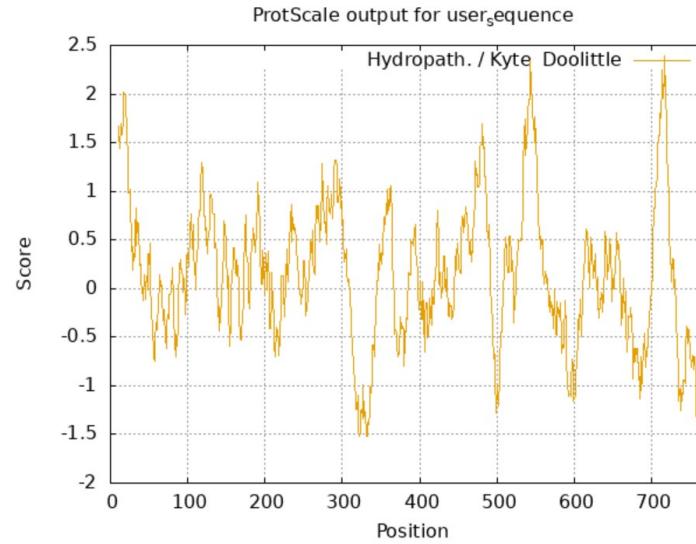
ID	氨基酸数目	相对分子质量	等电点	主要氨基酸	不稳定系数	脂肪系数	总平均亲水性
tA0A7J7HA W1	779	87115.6	8.41	Leu (L) 9.8%、 Ser (S) 8.1%、 Ala (A) 7.1% Val (V) 7.1%	37.17	89.61	0.019
A0A7J7HW C6	783	87787.18	6.23	Ser (S) 9.5%、 Leu (L) 9.3%、 Val (V) 9.1%	34.33	96.81	0.129
A0A7J7HT R6	865	97116.26	6.18	Ser (S) 9.8%、 Leu (L) 8.9%、 Val (V) 7.7%	36.27	90.81	-0.015
A0A7J7HW B2	876	98234.28	5.81	Ser (S) 10.0%、 Leu (L) 9.0%、 Val (V) 7.6%	34.87	90.45	-0.009

蛋白稳定，A0A7J7HWB2与A0A7J7HTR6为亲水性蛋白。疏水氨基酸：亮氨酸Leu、缬氨酸Val、丙氨酸Ala；亲水氨基酸：丝氨酸Ser。不稳定性指数指数大于40表示不稳定，小于40表示稳定。脂肪系数：反映蛋白质的疏水性。总平均亲水性（GRAVY）：负值表示亲水性好，正值表示疏水性强。

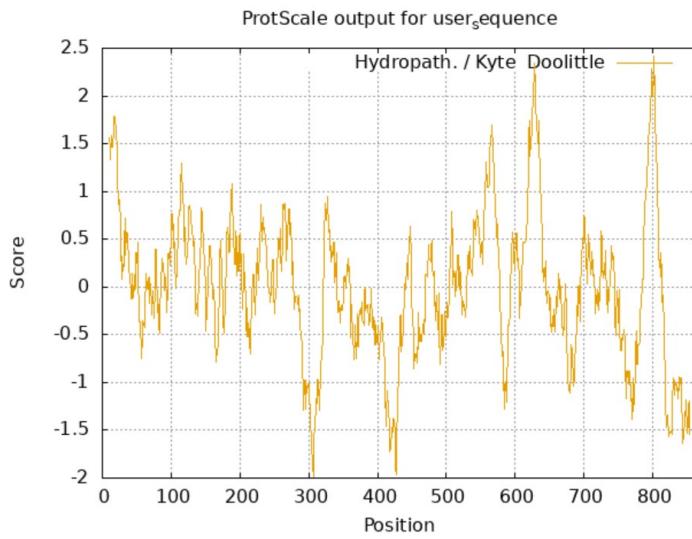
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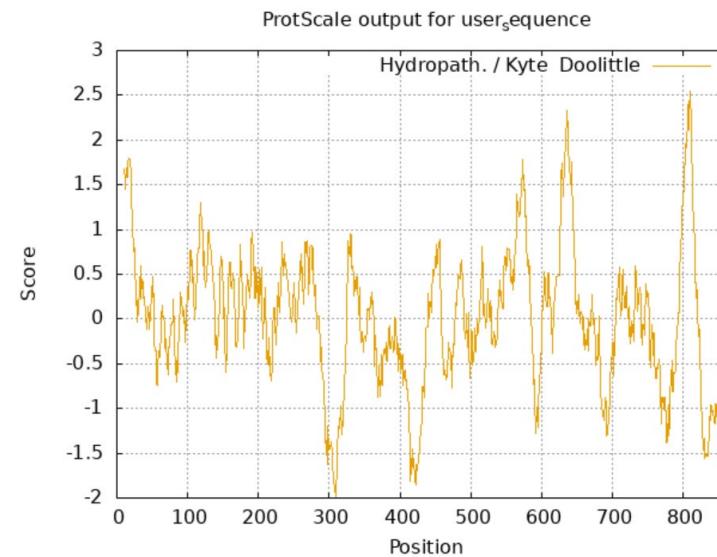
AOA7J7HWC6



AOA7J7HTR6



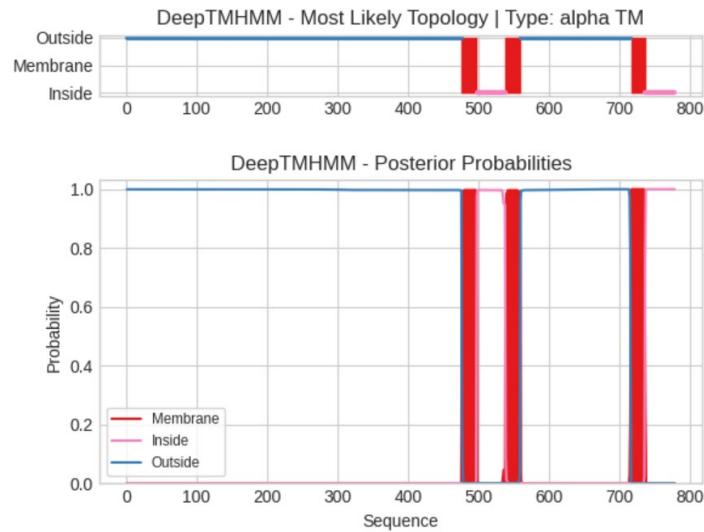
AOA7J7HWB2



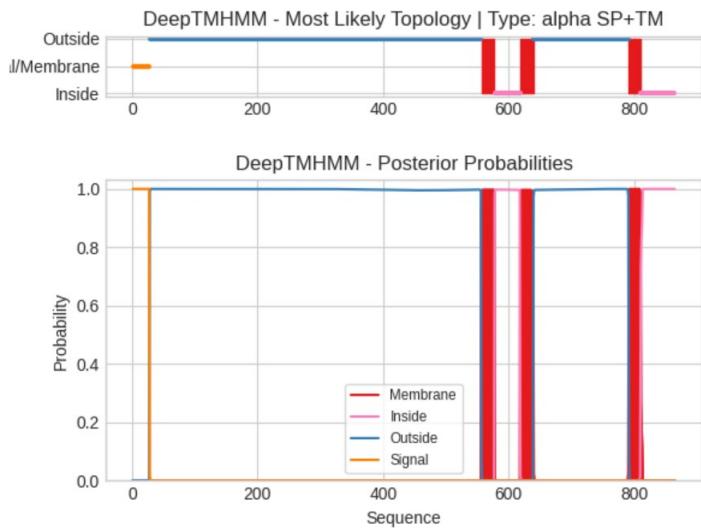
AOA7J7HTR6与AOA7J7HWB2
为亲水性蛋白。

图形的高峰值（正值）的区
域表示疏水的区域，而负值
的“低谷”区域是亲水区域。

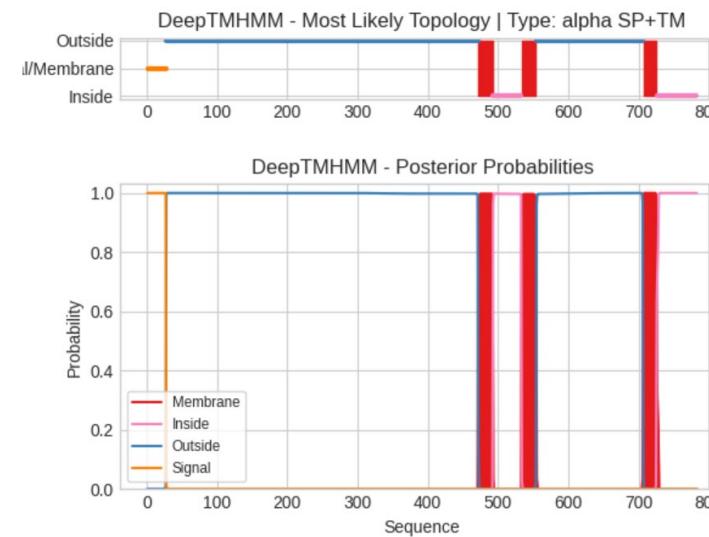
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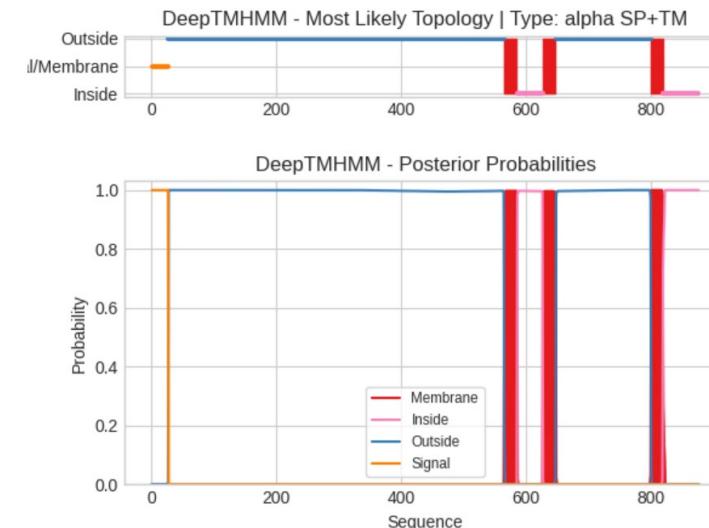
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AOA7J7HWC6



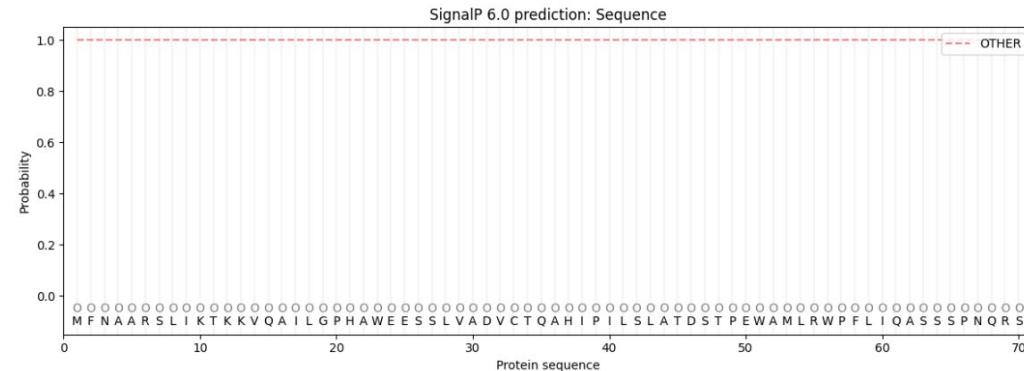
AOA7J7HWB2



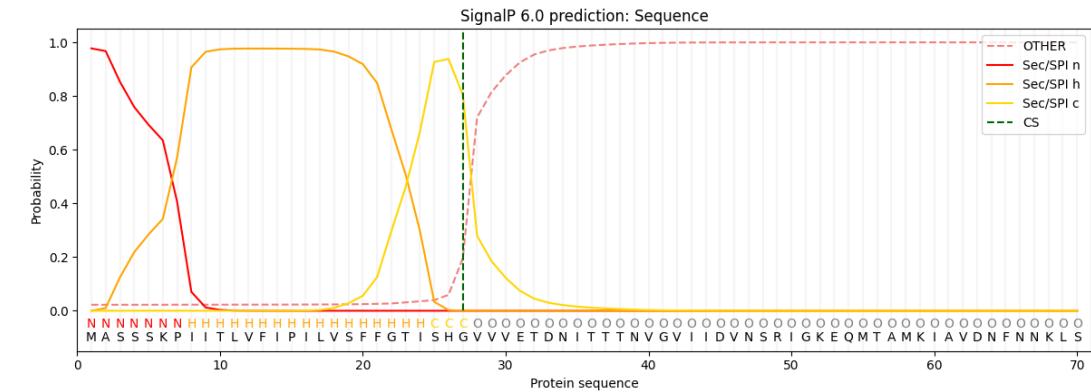
- 植物 GLR 序列与其动物对应物之间的同源区域跨越所有重要结构域，包括形成激动剂结合结构域的四个跨膜片段（M1-M4）和 S1 和 S2 区域。
- 在茶树中的预测蛋白序列中包含三个跨膜结构，跨膜蛋白。

AOA7J7HAW1

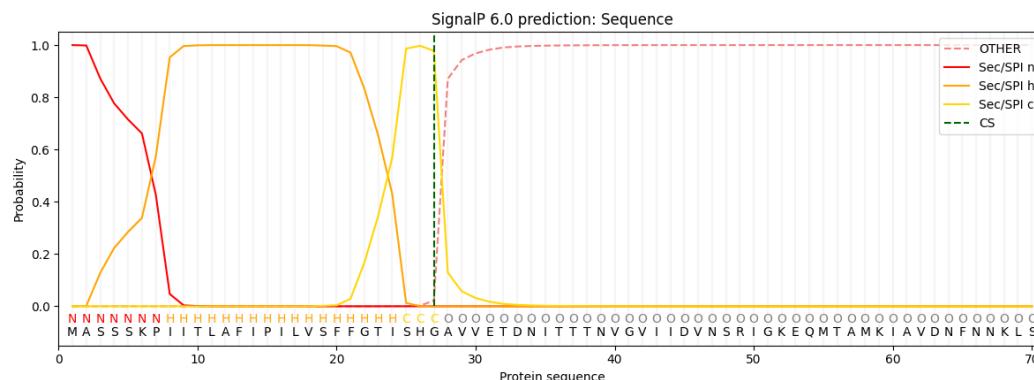
Download: [PNG](#) / [EPS](#) / [Tabular](#)



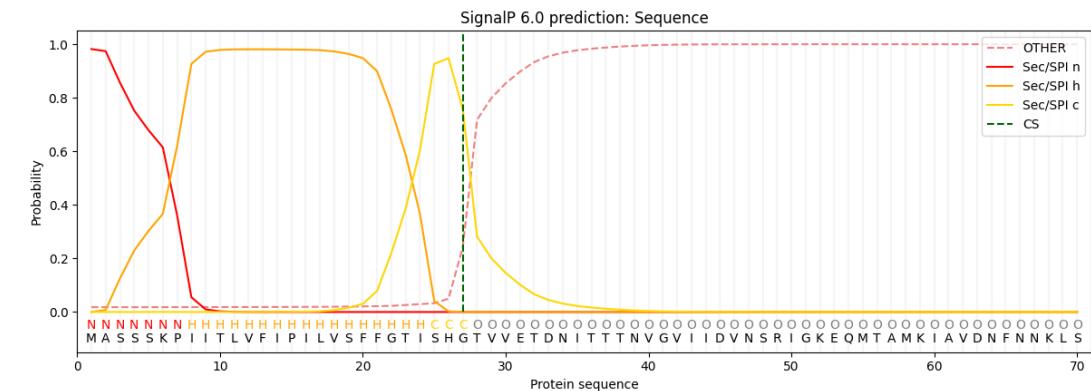
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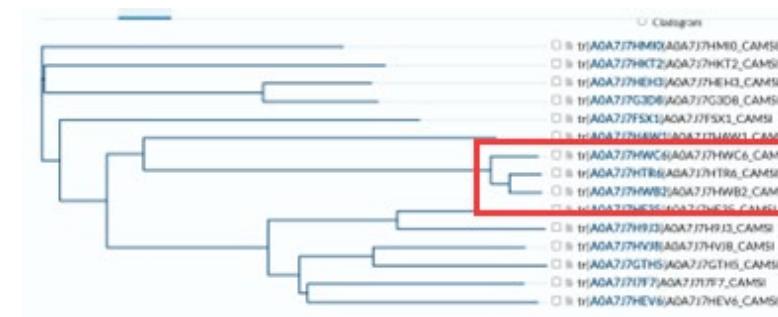
AOA7J7HTR6

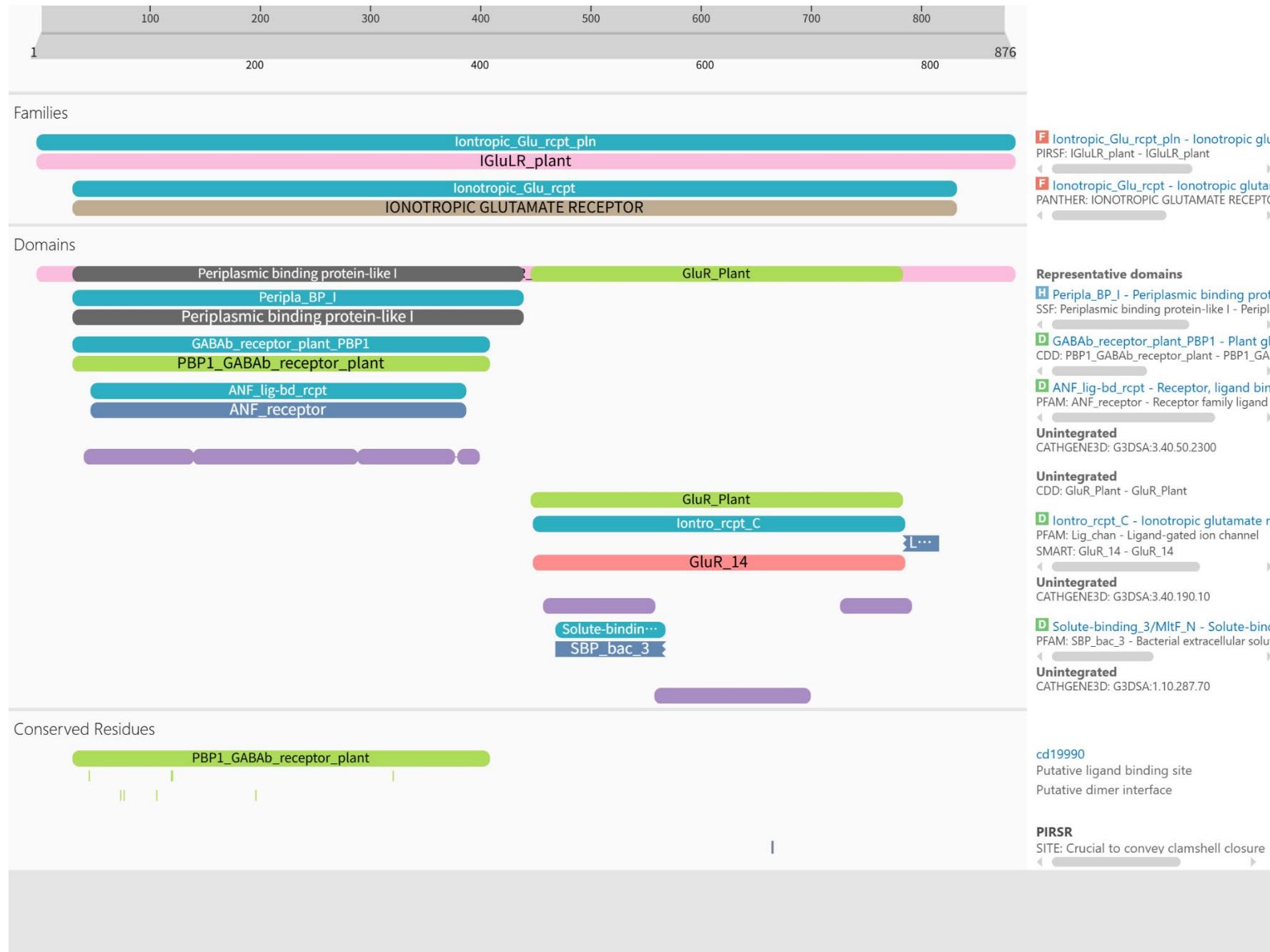


AOA7J7HWB2



➤ 在进化前, AOA7J7HAW1不含有信号肽。





Interpro

周质结合蛋白 (PBP)

由两个大裂片组成，它们闭合在结合的配体周围。这种结构在转录调节因子中得到重申，例如 lac 抑制因子。

在进化过程中，编码 PBP 的基因已经与整合膜蛋白的基因融合。因此，不同的哺乳动物受体包含与 PBP 同源的细胞外配体结合结构域；这些包括**谷氨酸/甘氨酸门控离子通道**，如 NMDA 受体、G 蛋白偶联受体，包括代谢型谷氨酸、GABA-B、钙感应和信息素受体，以及心房利钠肽-鸟苷酸环化酶受体。

TBtools



TPIA

There are 38 genes matched with glutamate receptor:

Locus Identifier	Putative Function
CSS0002452	PREDICTED: glutamate receptor 3.2 [Vitis vinifera]
CSS0002563	PREDICTED: LOW QUALITY PROTEIN: glutamate receptor 2.2-like [Vitis vinifera]
CSS0004371	PREDICTED: glutamate receptor 2.8-like [Pyrus x bretschneideri]
CSS0004579	PREDICTED: glutamate receptor 3.4 [Sesamum indicum]
CSS0006339	PREDICTED: glutamate receptor 2.7-like [Vitis vinifera]
CSS0006753	PREDICTED: glutamate receptor 3.3-like [Nicotiana tomentosiformis]
CSS0007573	Glutamate receptor 3.4 [Morus notabilis]
CSS0008433	PREDICTED: glutamate receptor 3.4 isoform X1 [Vitis vinifera]
CSS0008544	PREDICTED: glutamate receptor 3.4 isoform X1 [Vitis vinifera]
CSS0010180	PREDICTED: glutamate receptor 2.7-like [Vitis vinifera]
CSS0010837	PREDICTED: glutamate receptor 3.3 isoform X1 [Nicotiana sylvestris]
CSS0014467	Glutamate-gated kainate-type ion channel receptor subunit GluR5, putative [Theobroma cacao]
CSS0017047	PREDICTED: glutamate receptor 2.2-like [Sesamum indicum]
CSS0018199	PREDICTED: glutamate receptor 2.8-like [Nicotiana tomentosiformis]
CSS0019202	PREDICTED: glutamate receptor 3.4 isoform X1 [Vitis vinifera]
CSS0022589	PREDICTED: glutamate receptor 2.8-like [Nicotiana tomentosiformis]
CSS0022640	PREDICTED: glutamate receptor 3.7-like isoform X2 [Nelumbo nucifera]
CSS0023328	PREDICTED: glutamate receptor 3.4-like [Malus domestica]
CSS0025862	PREDICTED: glutamate receptor 3.7 [Vitis vinifera]
CSS0026840	PREDICTED: glutamate receptor 2.8-like [Nicotiana tomentosiformis]

PlantTFDB

Browse by Family

AP2 (4461)	ARF (4578)	ARR-B (2354)	B3 (10609)	BBR-BPC (1256)
BES1 (1549)	C2H2 (17740)	C3H (9693)	CAMTA (1343)	CO-like (2125)
CPP (1612)	DBB (1651)	Dof (5655)	E2F/DP (1781)	EIL (1234)
ERF (21129)	FAR1 (7527)	G2-like (9874)	GATA (5335)	GRAS (9304)
GRF (1876)	GeBP (1564)	HB-PHD (477)	HB-other (2277)	HD-ZIP (8602)
HRT-like (249)	HSF (4574)	LBD (7216)	LFY (253)	LSD (957)
M-type_MADS (7541)	MIKC_MADS (6918)	MYB (22032)	MYB_related (15369)	NAC (19997)
NF-X1 (403)	NF-YA (2461)	NF-YB (3099)	NF-YC (2446)	NZZ/SPL (109)
Nin-like (2766)	RAV (690)	S1Fa-like (359)	SAP (164)	SBP (4168)
SRS (1327)	STAT (214)	TALE (4433)	TCP (4187)	Trihelix (6256)
VOZ (635)	WOX (2358)	WRKY (14549)	Whirly (530)	YABBY (1719)
ZF-HD (2589)	bHLH (28698)	bZIP (15498)		

多数茶树谷氨酸受体蛋白含有7个外显子

Graphics ▾

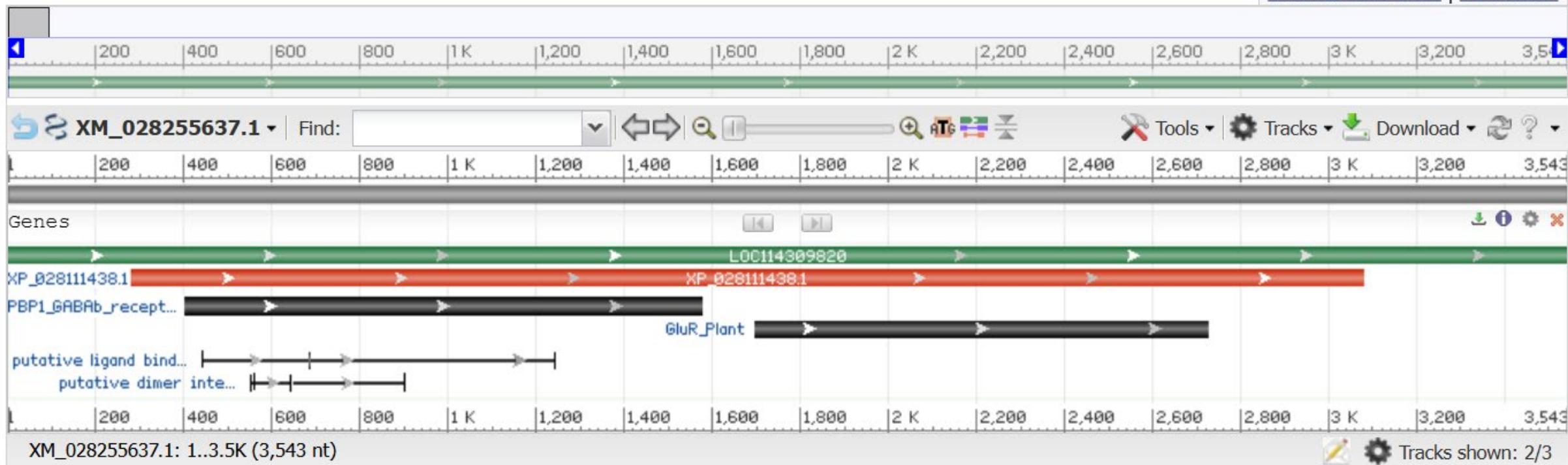
Send to: ▾

PREDICTED: Camellia sinensis glutamate receptor 3.4-like (LOC114309820), transcript variant X1, mRNA

NCBI Reference Sequence: XM_028255637.1

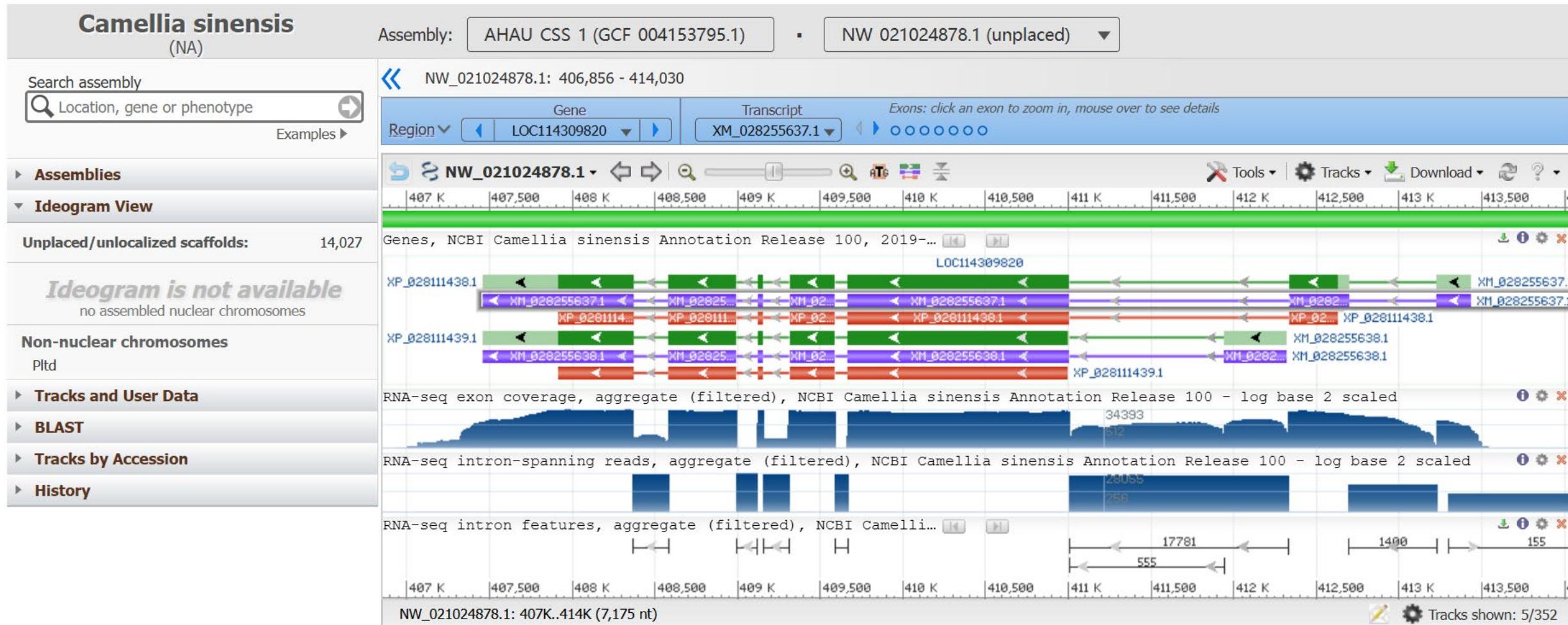
[GenBank](#) [FASTA](#)

[Link To This View](#) | [Feedback](#)



Standard databases (nr etc.): Core nucleotide database (core_nt)
暂无人工注释的序列

Genome Data Viewer



Saved Results

File Colour

18 Plain cmd

emboss_001.needle cmd

EMBOSS_001	51 GKEQMTAMKIAVDNFNNKLSLYFSSSGDPLQAAYAADQLIKEKQVQVII	100
A0A7J7HWB2_CA	51 GKEQMTAMKIAVDNFNNKLSLYFSSSGDPLQAAYAADQLIKEKQVQVII	100
EMBOSS_001	101 GMETWAETAI VAKIGKIGNQ AQVPVISLAAAIGATKTTQWPFLIQMVTNF	150
A0A7J7HWB2_CA	101 GMETWAETAI VA --K IGNQ AQVPVISLAAAIGATKTTQWPFLIQMVTNF	147
EMBOSS_001	151 SNQMDCTAALVHSFKWRRVIVVFEEDMFSGDSNMLAMLDALHNVGVIE	200
A0A7J7HWB2_CA	148 SNQMDCTAALVHSFKWRRVIVVFEEDMFSGDSNMLAMLDALHNVGVIE	197
EMBOSS_001	201 HHLVIPPFQSLSHPLEFVREELMKLNNIQPRAFIVLQSSLQFTSLLFSEA	250
A0A7J7HWB2_CA	198 HHLVIPPFQSLSHPLEFVREELMKLNNIQPRAFIVLQSSLQFTSLLFSEA	247
EMBOSS_001	251 RKMFIGKDSAWVITDTIASFLDSVNSSFISSMEGVFGIKIDYSENTTSF	300
A0A7J7HWB2_CA	248 RKMFIGKDSAWVITDTIASFLDSVNSSFISSMEGVFGIKIDYSENTTSF	297
EMBOSS_001	301 QDFKKQQSFRFYEPEEDNSNP GIYALRAYDSIATVIVAMMGAESTSS	350
A0A7J7HWB2_CA	298 QDFKKQQSFRFYEPEEDNSNP GIYALRAYDSIATVIVALERLTHSS	347
EMBOSS_001	351 TTSTRLLDTILSSNFGLSGEIHFEDERLSYKPIYRVINVNLTYNKEY	400
A0A7J7HWB2_CA	348 TTSTRLLDTILSSNFGLSGEIHFEDERLSYKPIYRVINVNLTYNKEY	397
EMBOSS_001	401 WSPEFGFLKSLDAAKSGNNGNGKDDWRKSLGNLKRVPKLWAMPSLEDPL	450
A0A7J7HWB2_CA	398 WSPEFGFLKSLDAAKSGNNGNGKDDWRKSLGNLKRVPKG WAMPSLEDPL	447
EMBOSS_001	451 IIGVPGRAAFDAFKITPSTKNTNETYDGFCISVFKEVLKILDYDLPYKF	500

NEEDLE

Needleman-Wunsch global alignment of two sequences

input section

Enter the sequence as:

file / database entry or paste or list of files

Sequence Cut and Paste

```
>EMBOSS_001
MASSKPIITLVFIPILVSFFGTISHGTWETDNITTNVGIIDVNSRIGKEQMTAMKI
AVDNFNNKLSLYFSSSGDPLQAAYAADQLIKEKQVQVIIGMETWAETALVAKIGKIGNQ
A0A7J7HWB2_CA
SNQMDCTAALVHSFKWRRVIVVFEEDMFSGDSNMLAMLDALHNVGVIE
HHLVIPPFQSLSHPLEFVREELMKLNNIQPRAFIVLQSSLQFTSLLFSEA
RKMFIGKDSAWVITDTIASFLDSVNSSFISSMEGVFGIKIDYSENTTSF
QDFKKQQSFRFYEPEEDNSNPGIYALRAYDSIATVIVAMMGAESTSS
TTSTRLLDTILSSNFGLSGEIHFEDERLSYKPIYRVINVNLTYNKEY
WSPEFGFLKSLDAAKSGNNGNGKDDWRKSLGNLKRVPKLWAMPSLEDPL
```

LOAD SEQUENCE ATTRIBUTES

Input Sequence Options **Reset**

required section

Number of times to perform the mutation operations (min:0 default:1)

Types of point mutations to perform (min:1 max:4 default:0)

- None
- Any of the following
- Insertions
- Deletions
- Changes

Types of block mutations to perform (min:1 max:4 default:0)

- None
- Any of the following
- Insertions
- Deletions
- Changes

Types of codon mutations to perform (min:1 max:4 default:0)

- None
- Any of the following
- Insertions
- Deletions
- Changes

output section

Brief identity and similarity

srspair Align format (srspair)

Execution mode: interactive **GO** Advanced Options

MSBAR

Mutate a sequence

LOAD SEQUENCE ATTRIBUTES

Enter the sequence as:

file / database entry or paste or list of files

Sequence Cut and Paste

```
TNNYCMKTYVIGSTYRFGGFVFQEQGSPMADDVSKAICQLSENGSCKRLEEEWLTPSS
CLDSQNTKVNDSLGEFSFWGLFLFSIVTSCICFLFVHLLRNRYHQSRIGDIHGSDES
VWNKTRKLARYLSNAEIKSQRKDPTTGQEVTGNSNS
```

Input Sequence Options **Reset**

LOAD SEQUENCE ATTRIBUTES

Output Sequence Name

Output Sequence Options

Execution mode: interactive **GO** Advanced Options



PART-03

讨 论 与 结 论

讨论与结论

分析了Uniprot、TPIA、NCBI数据库中茶树谷氨酸受体序列。系统发育分析在 iGluR/GLR 家族进化历史的早期，在植物和动物分化之前，发生了一次重组事件，将祖先 iGluR/GLR 的 LIVBP 结构域与 GPCR 的七个跨膜结构域融合，从而产生了祖先家族 C GPCR（G 蛋白偶联受体的C 家族）（Turano 等人，2001 年）。利用Ensembl Plant 数据库查找序列，MEGA7 构建系统进化树（Bootsrtap 设定为100）发现[茶树与咖啡](#)的谷氨酸受体基因亲缘关系较近，与祖先猕猴桃却截然相反。

蛋白理化性质分析与结构预测表明，茶树谷氨酸受体[氨基酸数目约为900AA](#)，在进化过程中，由疏水性蛋白演变为[亲水性蛋白](#)，并含有[信号肽](#)、[3个跨膜片段](#)（M1–M4）及 S1 和 S2 区域。已有研究表明，谷氨酸受体含有赖氨酸/精氨酸/鸟氨酸结合蛋白（LAOBP），亮氨酸/异亮氨酸/缬氨酸结合蛋白（LIVBP）保守结构域。[LIVBP 结构的配体结合特性](#)在单子叶植物和双子叶植物之间是保守的。[根尖 L-谷氨酸感应和信号转导的分子机制](#)是什么？是什么原因导致拟南芥生态型之间 L-谷氨酸敏感性的显著自然变化？L-谷氨酸引发的根结构变化是否构成适应性反应，也许是通过增强植物竞争有机氮局部斑块的能力？



PART-04

研究展望

研究不足与展望

- 以茶树谷氨酸受体基因为研究对象，分析其氨基酸序列特征及预测其蛋白功能。简要分析了茶树谷氨酸受体的基本性质，尚未研究启动子分析，转录因子调控、[基因家族进化分析](#)等内容。
- 后续除完善原有生物信息学分析内容外可对以下方面进一步研究:结合[茶氨酸含量](#)进行[关联分析](#)，研究茶树谷氨酸受体基因与茶树中茶氨酸代谢是否存在关联性；分析其不同茶树品种鲜叶的表达水平差异、具体含量测定、对茶汤滋味的贡献度、不同胁迫下谷氨酸受体在茶树[氮代谢的表达规律](#)等。

- [1] 陈林,张应根,陈键,等.茶树体内茶氨酸代谢及其酶学研究进展[J].茶叶科学技术,2009,(03):1-7.
- [2] 陈琪,孟祥宇,江雪梅,等.茶树茶氨酸代谢相关基因表达组织特异性分析[J].核农学报,2015,29(07):1285-1291.
- [3] 林馨颖,邵淑贤,王鹏杰,等.高茶氨酸茶树新品系‘福黄2号’黄化变异机理[J].生物工程学报,2022,38(10):3956-3972.
- [4] Brian G. Forde, Peter J. Lea, Glutamate in plants: metabolism, regulation, and signalling, Journal of Experimental Botany, Volume 58, Issue 9, July 2007, Pages 2339–2358,
- [5] Chiu J, DeSalle R, Lam HM, Meisel L, Coruzzi G. Molecular evolution of glutamate receptors: a primitive signaling mechanism that existed before plants and animals diverged. Mol Biol Evol. 1999 Jun;16(6):826-38. [6] García L F , Laynes G F , Tapia E G , et al. In Silico Analysis of Glutamate Receptors in Capsicum chinense : Structure, Evolution, and Molecular Interactions[J]. Plants, 2024, 13(6):
- [7] Simon A A , Barbosa-Caro J , Feijo J , et al. Molecular Evolution of Plant Glutamate Receptors[J]. Biophysical Journal, 2020, 118(3):586a-586a.



请老师和各位同学批评指正

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时间：2025年4月27日