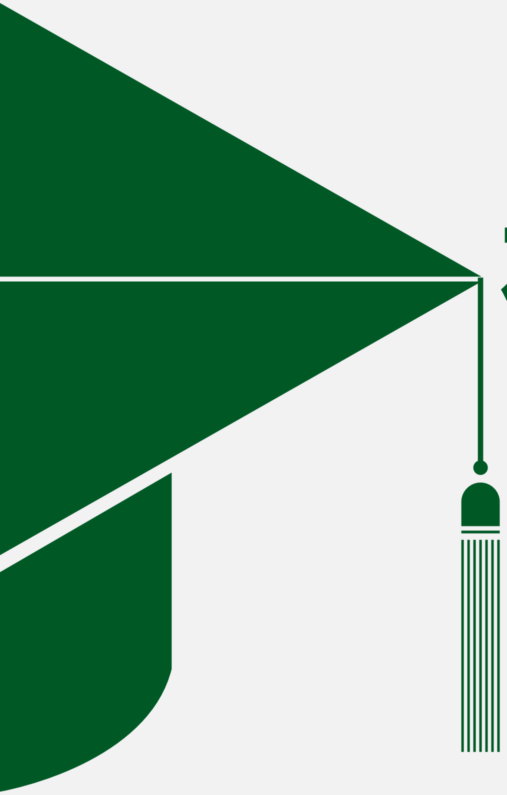
中国农业科学院
CHINESE ACADEMY OF AGRICULTURAL SCIENCES



水稻APO1-APO2模块的互作机制分析

Analysis of the Interaction Mechanism of the APO1-APO2 Module in Rice

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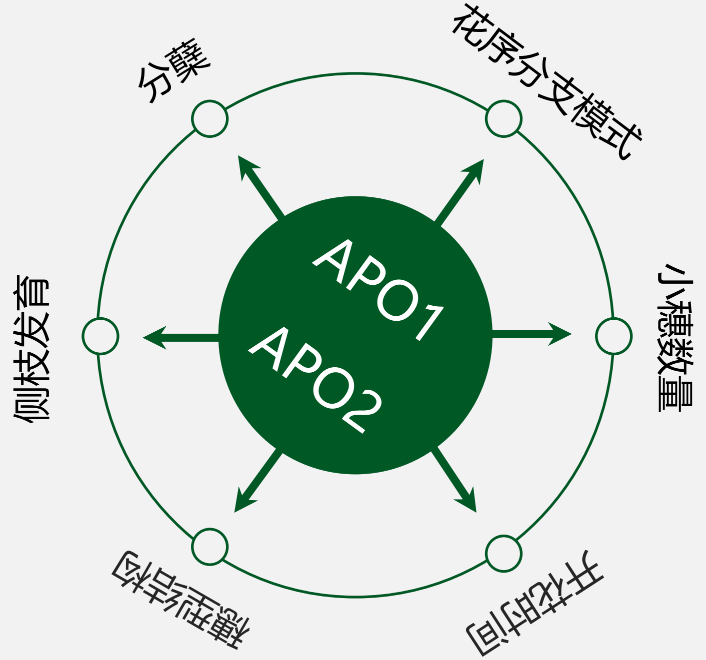
Part 1

研究背景

研究背景

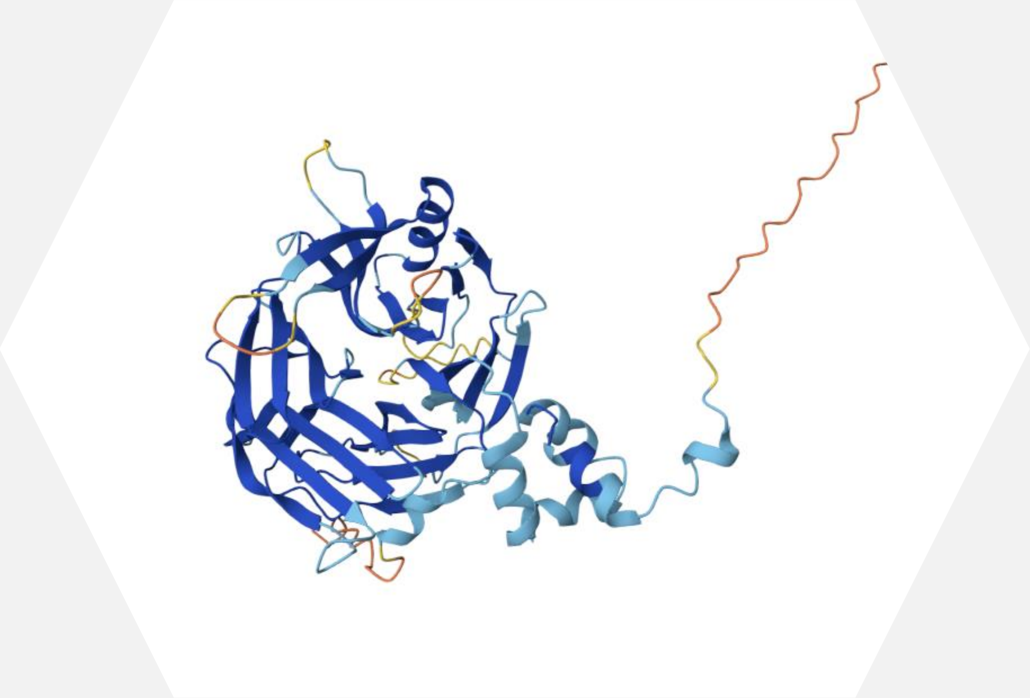
APO1和APO2基因

APO1和APO2基因是调控水稻（*Oryza sativa*）生殖发育的重要遗传因子，特别是在调控分蘖、穗型结构、开花时间以及产量相关性状方面具有核心功能。APO1和APO2基因的突变会导致显著的形态学改变，从而影响最终的籽粒产量。因此，厘清APO1和APO2基因互作的机制能够深化对水稻花序发育分子机制的理解，也为高产育种提供了重要的候选基因资源。



研究背景

APO1（ABERRANT PANICLE ORGANIZATION 1)是一个F-box蛋白编码基因，主要通过控制分生组织中细胞增殖来调节水稻穗部结构。F-box蛋白是一类在真核生物中广泛存在的关键调控蛋白，是E3泛素连接酶复合物的核心识别亚基，主要是在蛋白质降解、信号转导、细胞周期调控及发育过程中发挥重要作用。在野生型水稻中，主轴分生组织通常会形成10-12个初级枝梗，而在*apo1*突变体中，该分生组织提前转变为小穗分生组织，导致初级枝梗数量显著减少，进而降低每穗粒数和总产量。

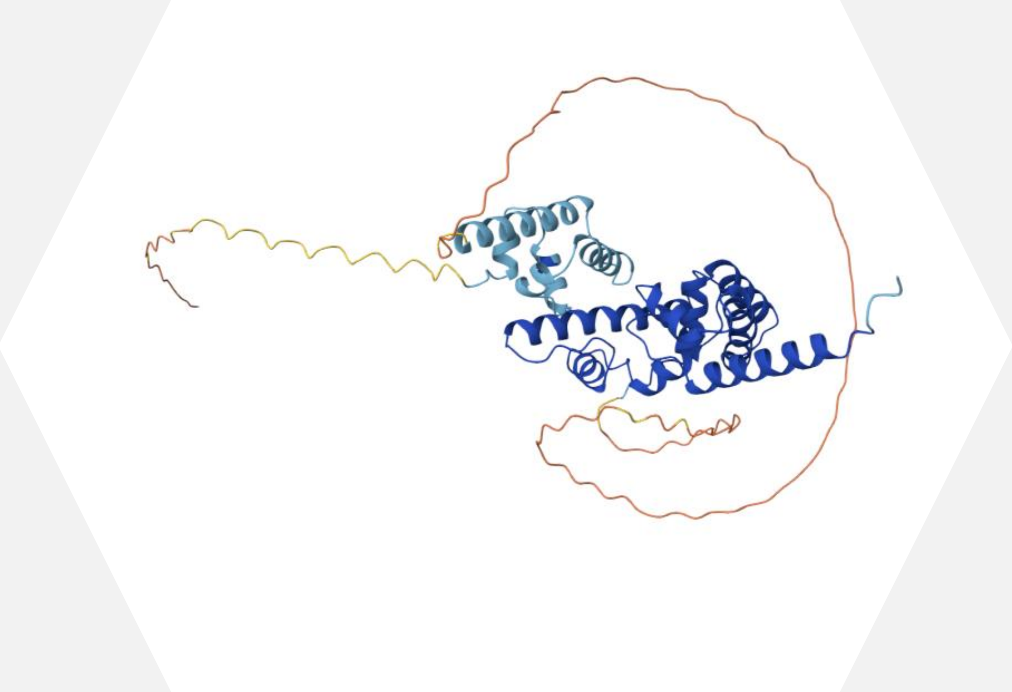


APO1

陈水福.水稻形态建成关键基因RFL的功能研究[D].华南农业大学,2019.

研究背景

APO2（ABERRANT PANICLE ORGANIZATION 2)也称为RFL基因，在调控水稻从营养生长向生殖生长转变的过程中发挥重要作用。该基因的主要功能包括抑制花序分生组织向花分生组织的过早转化，并参与多个阶段的穗形成过程。研究表明，*apo2*突变体会表现出小型化穗部结构，初级枝梗数量减少，且由于小穗分生组织提前形成而导致穗粒数下降。此外，APO2还影响节间伸长速率和开花时间，*apo2*突变体通常表现为晚花表型。



APO1

万书.水稻穗发育基因APO2/RFL及其互作蛋白的功能分析[D].南京农业大学,2019.

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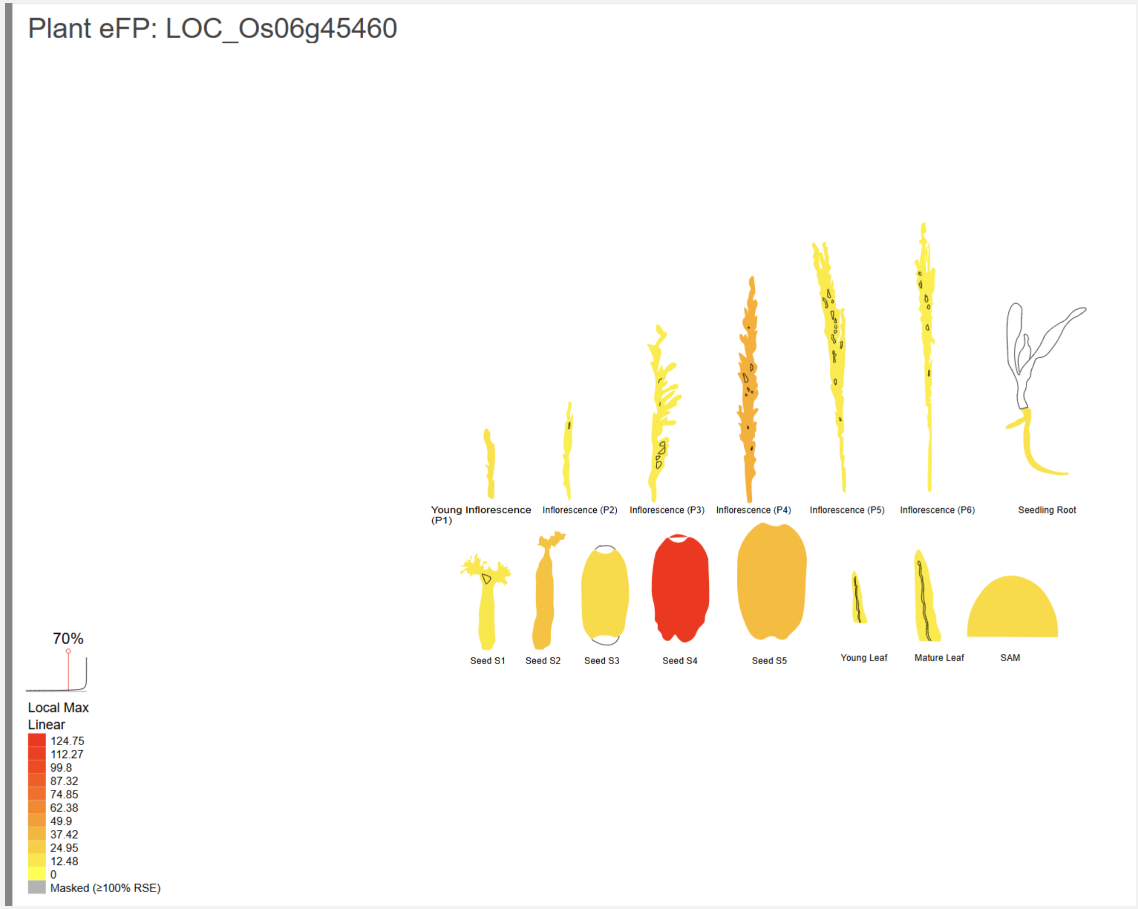
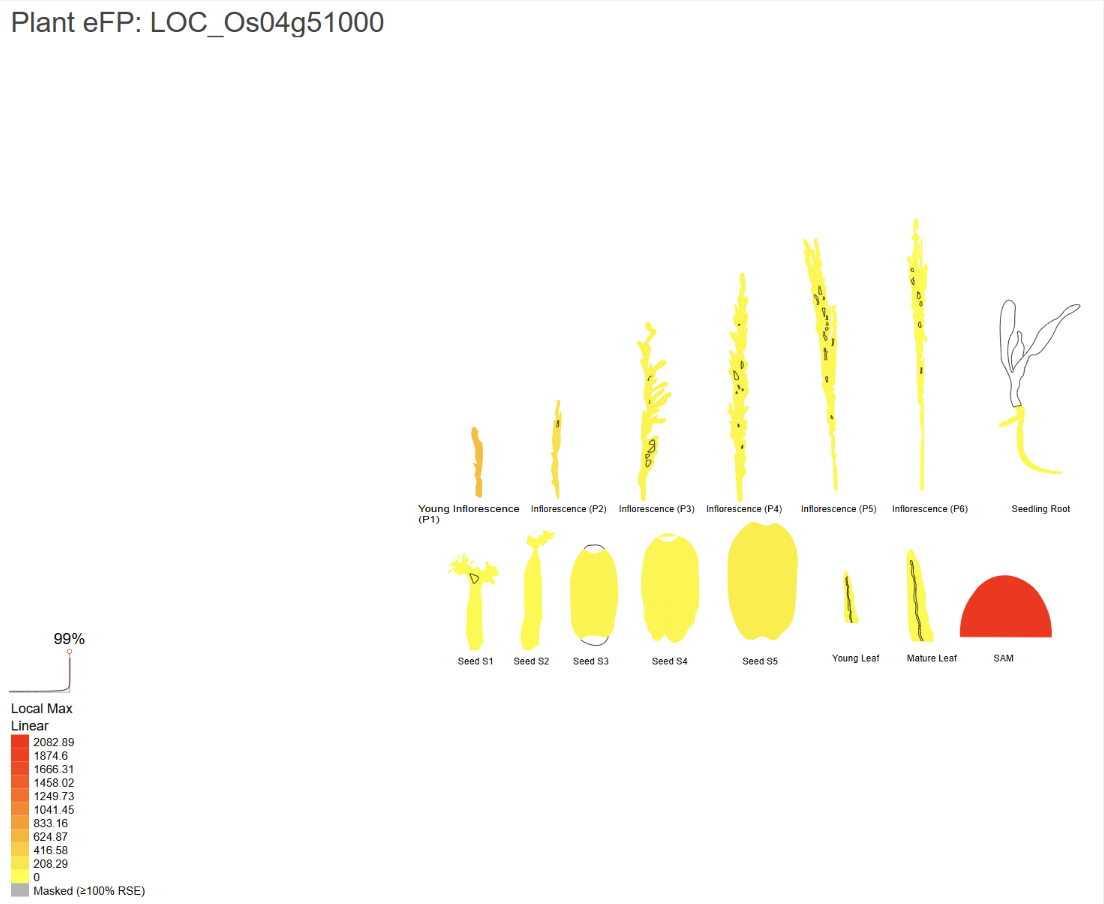
Part 2

互作位点分析

APO1与APO2表达部位预测


Plant eFP: LOC_Os06g45460

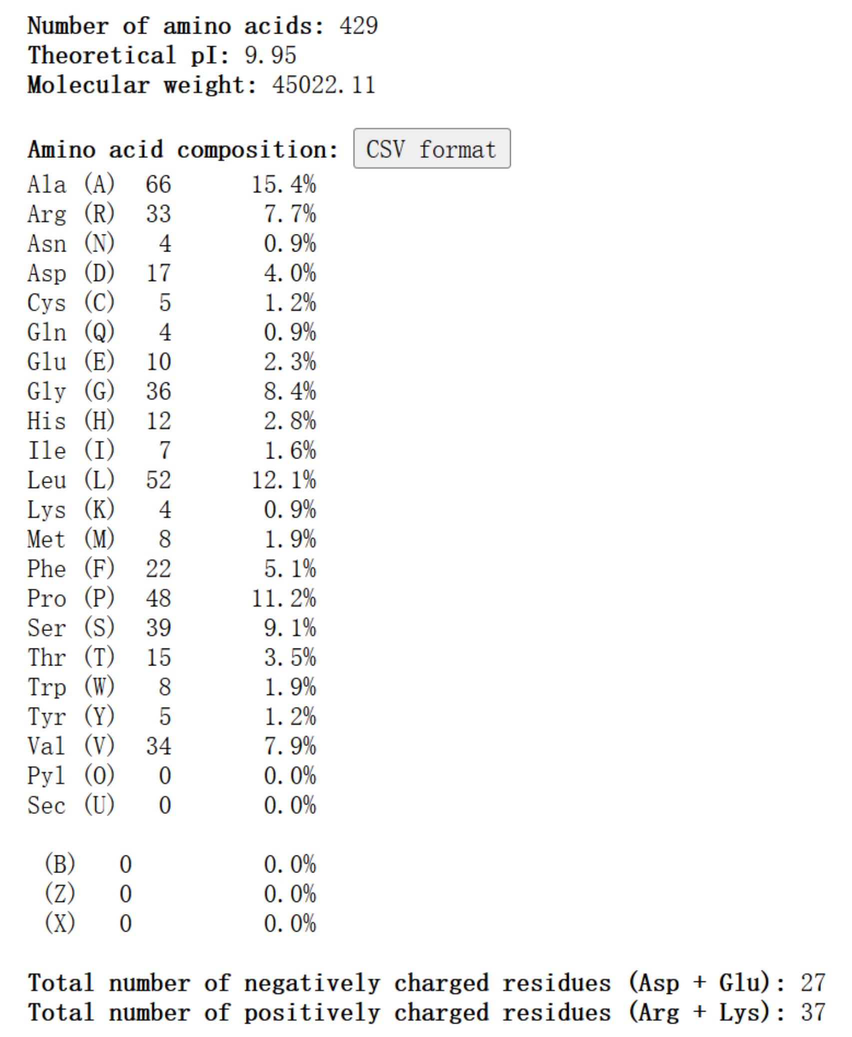
APO1


Plant eFP: LOC_Os04g51000

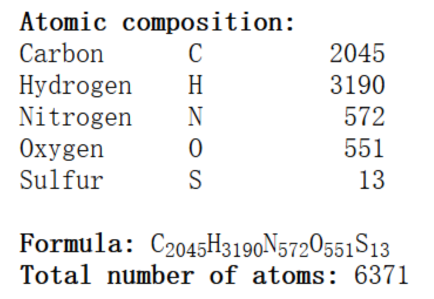
APO2

https://bar.utoronto.ca/eplant_rice/

APO1理化性质的预测分析

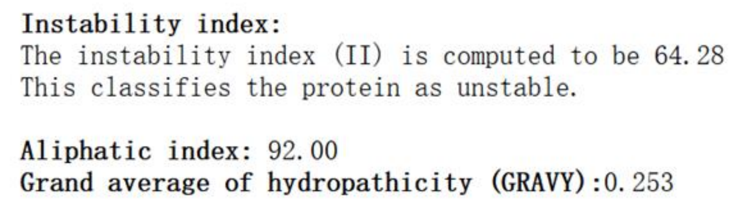


```
Number of amino acids: 429
Theoretical pI: 9.95
Molecular weight: 45022.11

Amino acid composition:  CSV format
Ala (A)  66      15.4%
Arg (R)  33       7.7%
Asn (N)   4       0.9%
Asp (D)  17       4.0%
Cys (C)   5       1.2%
Gln (Q)   4       0.9%
Glu (E)  10       2.3%
Gly (G)  36       8.4%
His (H)  12       2.8%
Ile (I)   7       1.6%
Leu (L)  52      12.1%
Lys (K)   4       0.9%
Met (M)   8       1.9%
Phe (F)  22       5.1%
Pro (P)  48      11.2%
Ser (S)  39       9.1%
Thr (T)  15       3.5%
Trp (W)   8       1.9%
Tyr (Y)   5       1.2%
Val (V)  34       7.9%
Pyl (O)   0       0.0%
Sec (U)   0       0.0%

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

Total number of negatively charged residues (Asp + Glu): 27
Total number of positively charged residues (Arg + Lys): 37
```

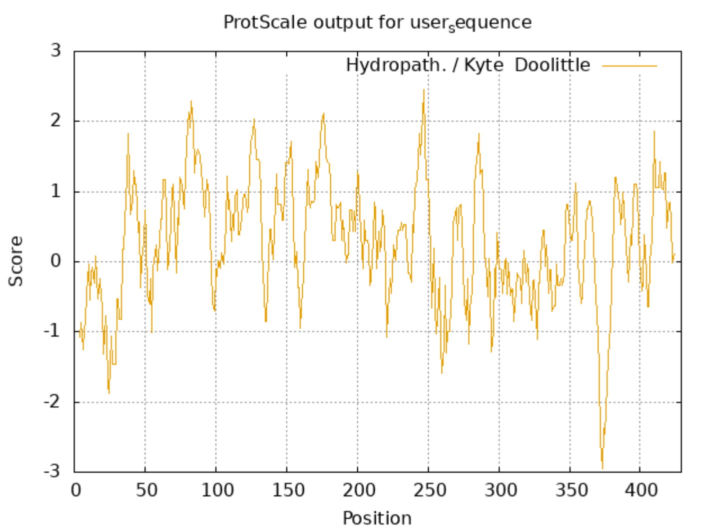


```
Atomic composition:
Carbon      C         2045
Hydrogen    H         3190
Nitrogen    N          572
Oxygen      O          551
Sulfur      S           13
```

Formula: $C_{2045}H_{3190}N_{572}O_{551}S_{13}$
Total number of atoms: 6371



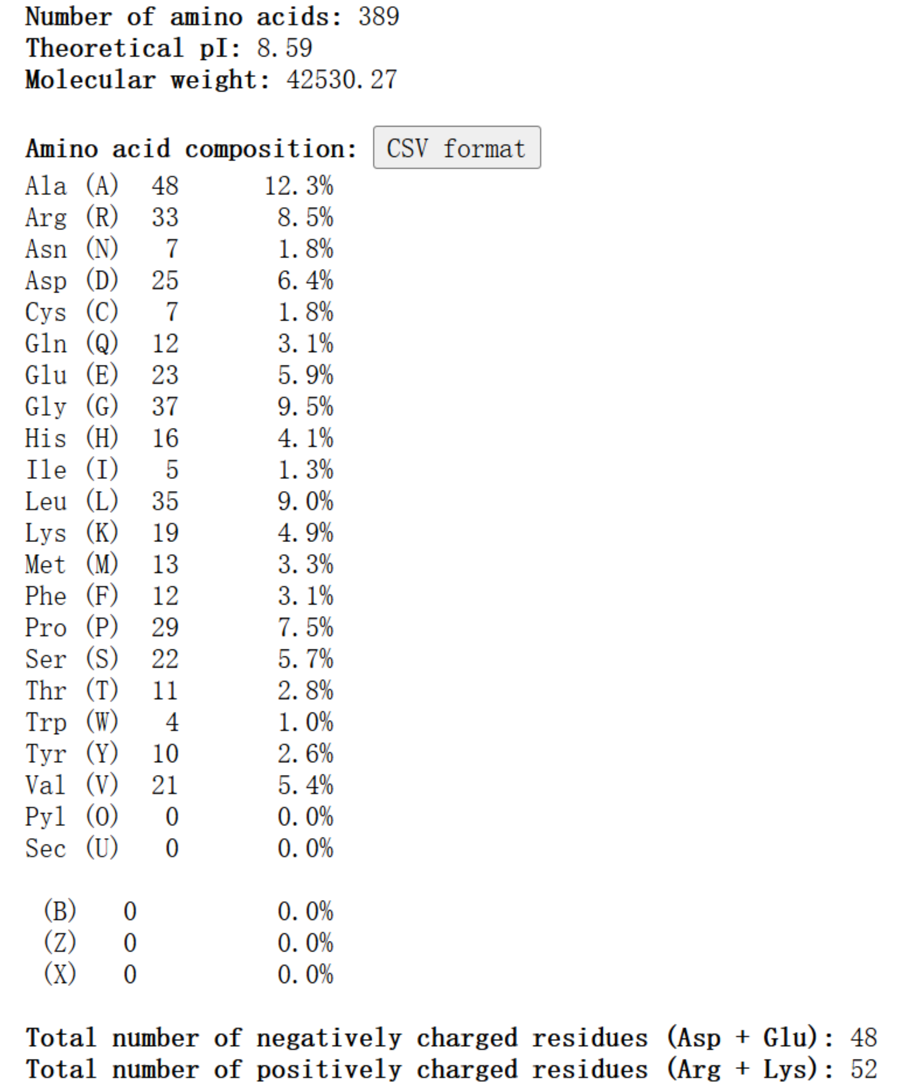
```
Instability index:
The instability index (II) is computed to be 64.28
This classifies the protein as unstable.

Aliphatic index: 92.00
Grand average of hydropathicity (GRAVY):0.253
```



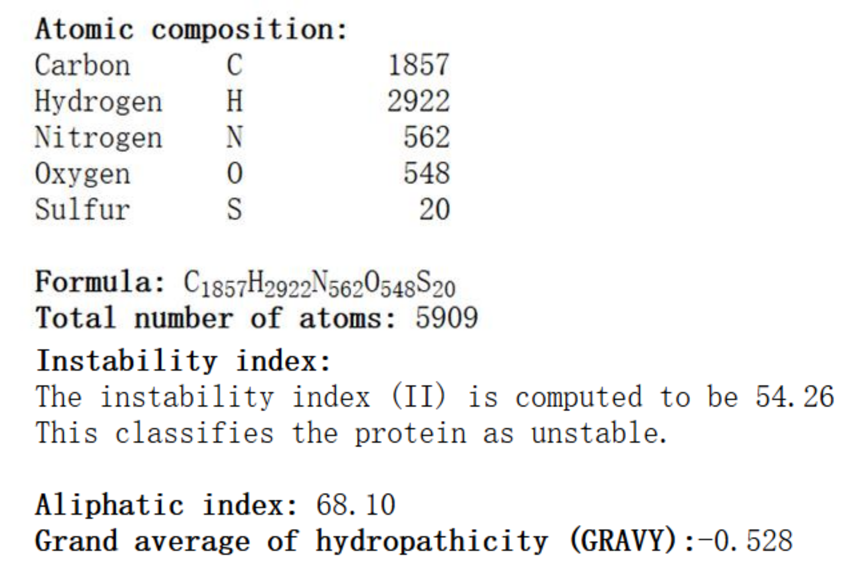
应用 ExPASy 系统中的 ProtParam 软件（https://web.expasy.org/protparam/）分析基本理化性质；

应用在线软件 ProtScale（https://web.expasy.org/protscale/）分 析 亲疏水性

APO2理化性质的预测分析



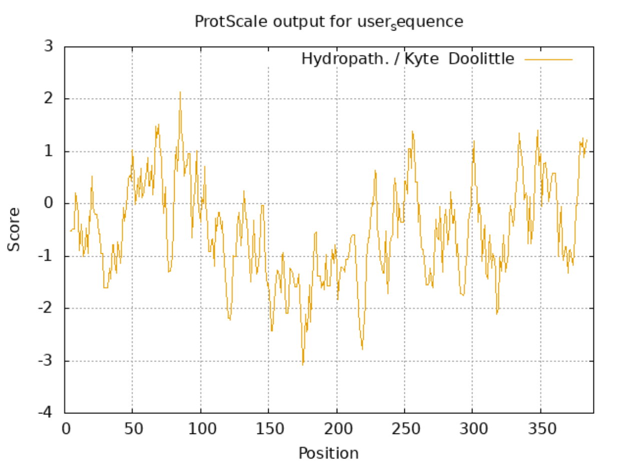
```
Number of amino acids: 389
Theoretical pI: 8.59
Molecular weight: 42530.27

Amino acid composition: [CSV format]
Ala (A)  48        12.3%
Arg (R)  33         8.5%
Asn (N)   7         1.8%
Asp (D)  25         6.4%
Cys (C)   7         1.8%
Gln (Q)  12         3.1%
Glu (E)  23         5.9%
Gly (G)  37         9.5%
His (H)  16         4.1%
Ile (I)   5         1.3%
Leu (L)  35         9.0%
Lys (K)  19         4.9%
Met (M)  13         3.3%
Phe (F)  12         3.1%
Pro (P)  29         7.5%
Ser (S)  22         5.7%
Thr (T)  11         2.8%
Trp (W)   4         1.0%
Tyr (Y)  10         2.6%
Val (V)  21         5.4%
Pyl (O)   0         0.0%
Sec (U)   0         0.0%

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

Total number of negatively charged residues (Asp + Glu): 48
Total number of positively charged residues (Arg + Lys): 52
```



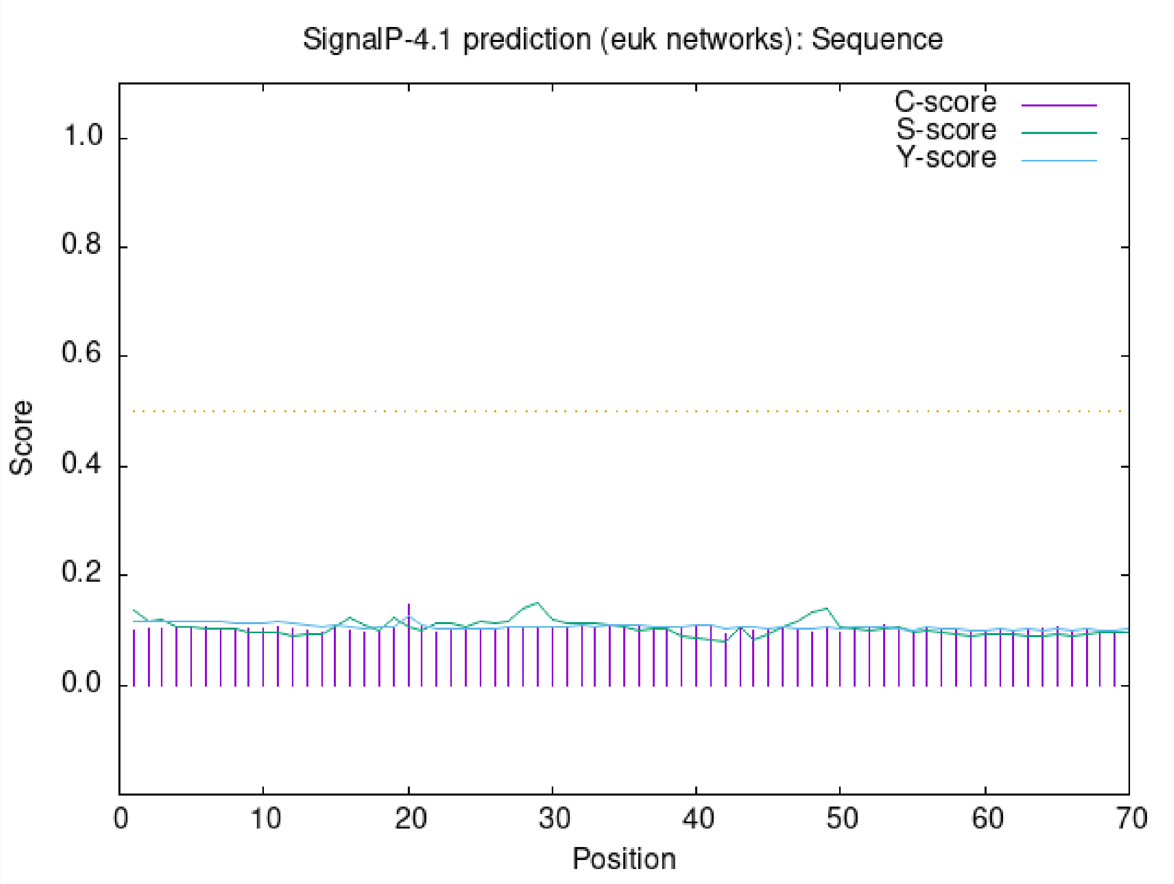
```
Atomic composition:
Carbon      C          1857
Hydrogen    H          2922
Nitrogen    N           562
Oxygen      O           548
Sulfur      S            20
```

Formula: $C_{1857}H_{2922}N_{562}O_{548}S_{20}$

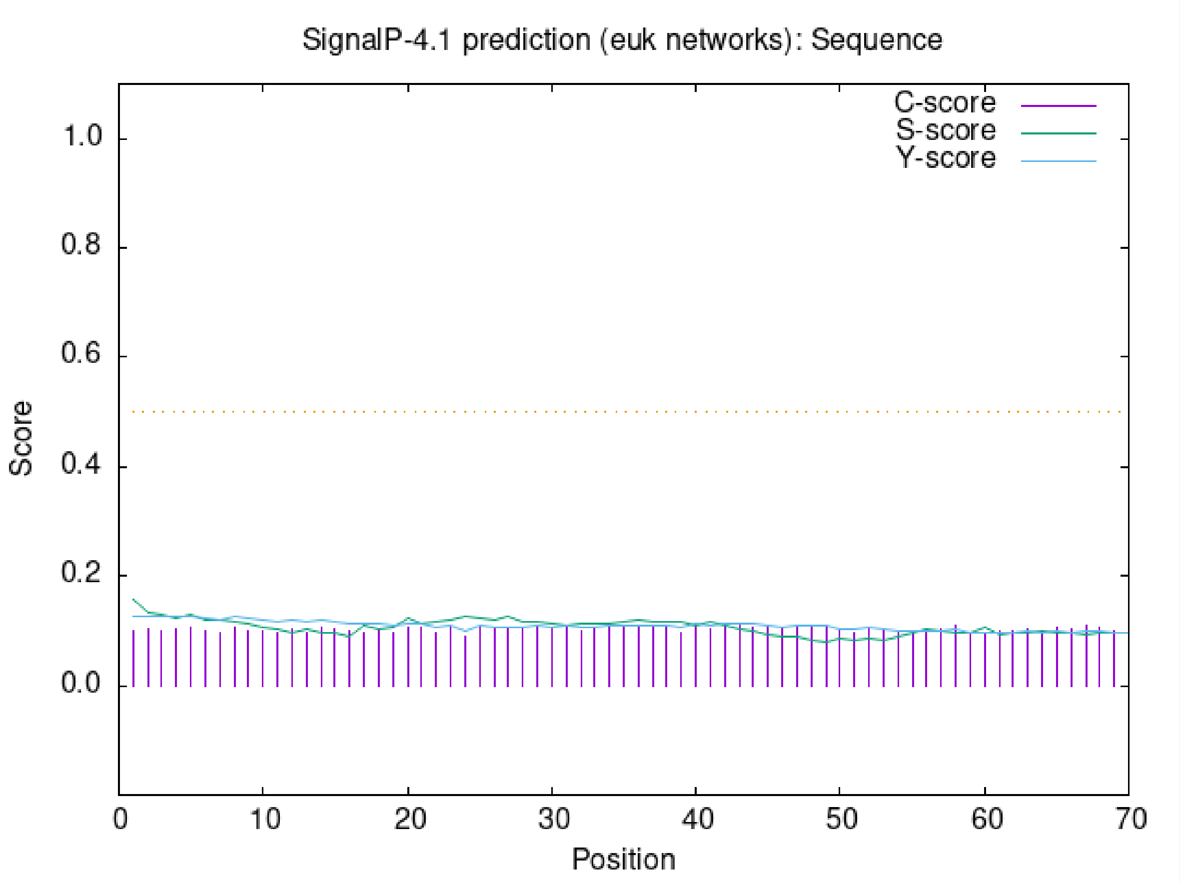
```
Total number of atoms: 5909
Instability index:
The instability index (II) is computed to be 54.26
This classifies the protein as unstable.

Aliphatic index: 68.10
Grand average of hydropathicity (GRAVY):-0.528
```



APO1与APO2的信号肽预测分析



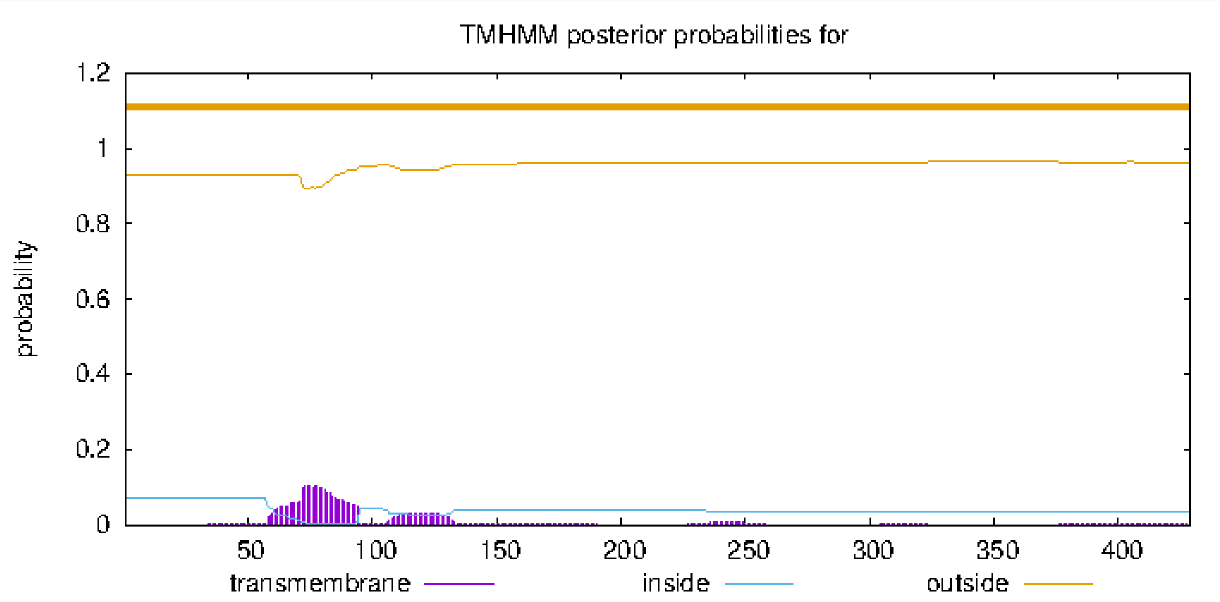
APO1



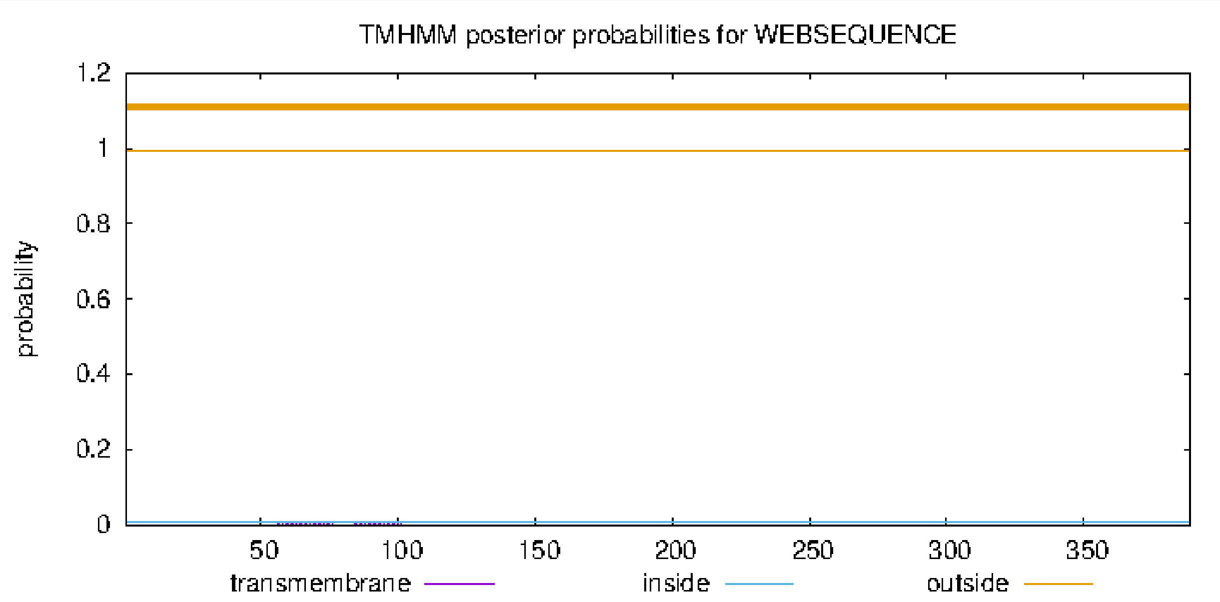
APO2

应用https://services.healthtech.dtu.dk/services/SignalP-4.1/预测信号肽结构

APO1与APO2跨膜结构的预测分析



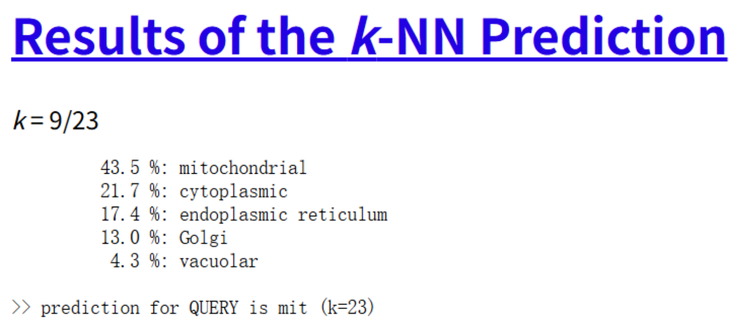
APO1



APO2

应用https://services.healthtech.dtu.dk/services/TMHMM-2.0/预测跨膜结构

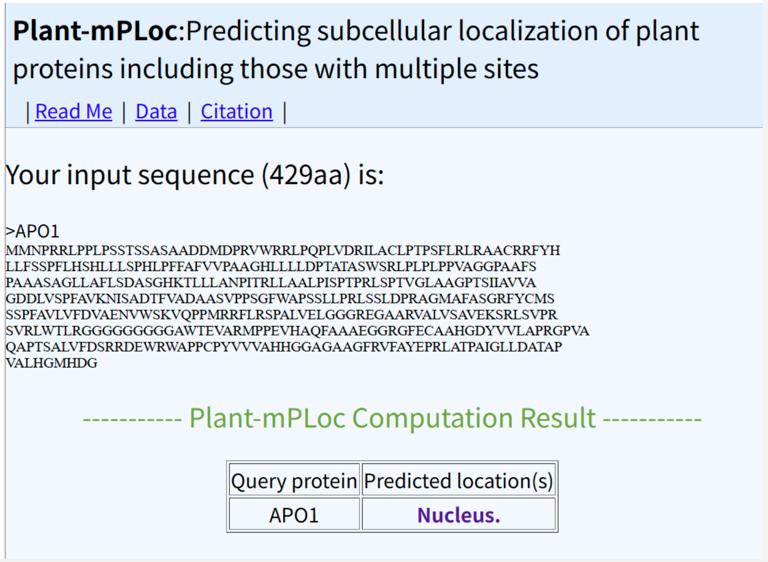
APO1亚细胞定位的预测分析



Results of the *k*-NN Prediction

k = 9/23

```
     43.5 %: mitochondrial
     21.7 %: cytoplasmic
     17.4 %: endoplasmic reticulum
     13.0 %: Golgi
      4.3 %: vacuolar

>> prediction for QUERY is mit (k=23)
```



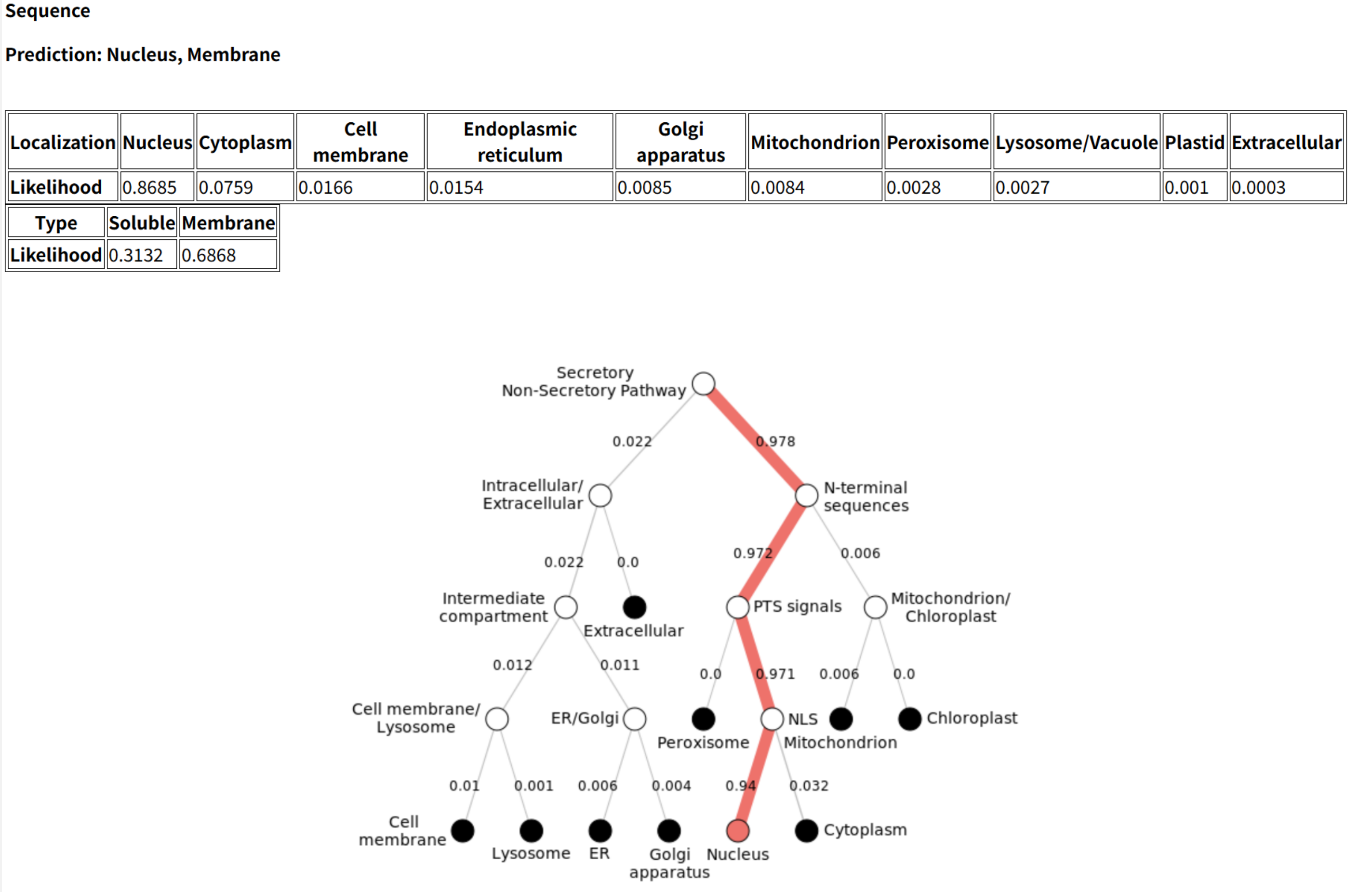
Plant-mPLoc:Predicting subcellular localization of plant proteins including those with multiple sites

Your input sequence (429aa) is:

```
>APO1
MMNPRRLPPLPSSTSSASAADDMDPRVWRRLPQPLVDRILACLPTPSFLRLRAACRRFYH
LLFSSPFLHSHLLLSPHLPFFAFVVPAAGHLLLLDPTATASWSRLPLPLPPVAGGPAAFS
PAAASAGLLAFLSDASGHKTLLLANPITRLLAALPISPTPRLSPTVGLAAGPTSIIAVVA
GDDLVSPFAVKNISADTFVADAASVPPSGFWAPSSLLPRLSSLDPRAGMAFASGRFYCMS
SSPFAVLVFDVAENVWSKVQPPMRRFLRSPALVELGGGREGAARVALVSAVEKSRLSVPR
SVRLWTLRGGGGGGGGGAWTEVARMPPEVHAQFAAAEGGRGFECAAHGDYVVLAPRGPVA
QAPTSALVFDSRRDEWRWAPPCPYVVVAHHGGAGAAGFRVFAYEPRLATPAIGLLDATAP
VALHGMHDG
```

----------- Plant-mPLoc Computation Result -----------

Query protein	Predicted location(s)
APO1	**Nucleus.**



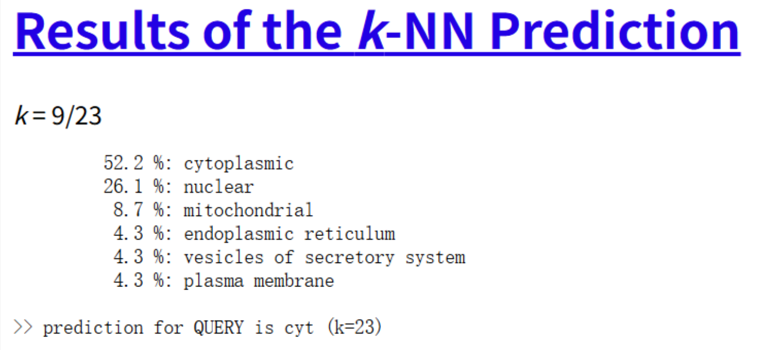
Sequence

Prediction: Nucleus, Membrane

Localization	Nucleus	Cytoplasm	Cell membrane	Endoplasmic reticulum	Golgi apparatus	Mitochondrion	Peroxisome	Lysosome/Vacuole	Plastid	Extracellular
Likelihood	0.8685	0.0759	0.0166	0.0154	0.0085	0.0084	0.0028	0.0027	0.001	0.0003

Type	Soluble	Membrane
Likelihood	0.3132	0.6868

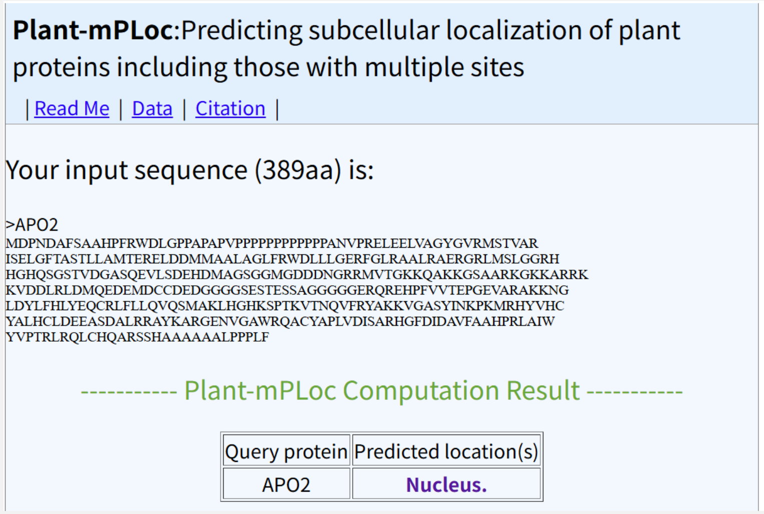
APO2亚细胞定位的预测分析



Results of the *k*-NN Prediction

k = 9/23

```
52.2 %: cytoplasmic
26.1 %: nuclear
 8.7 %: mitochondrial
 4.3 %: endoplasmic reticulum
 4.3 %: vesicles of secretory system
 4.3 %: plasma membrane

>> prediction for QUERY is cyt (k=23)
```



Plant-mPLoc:Predicting subcellular localization of plant proteins including those with multiple sites

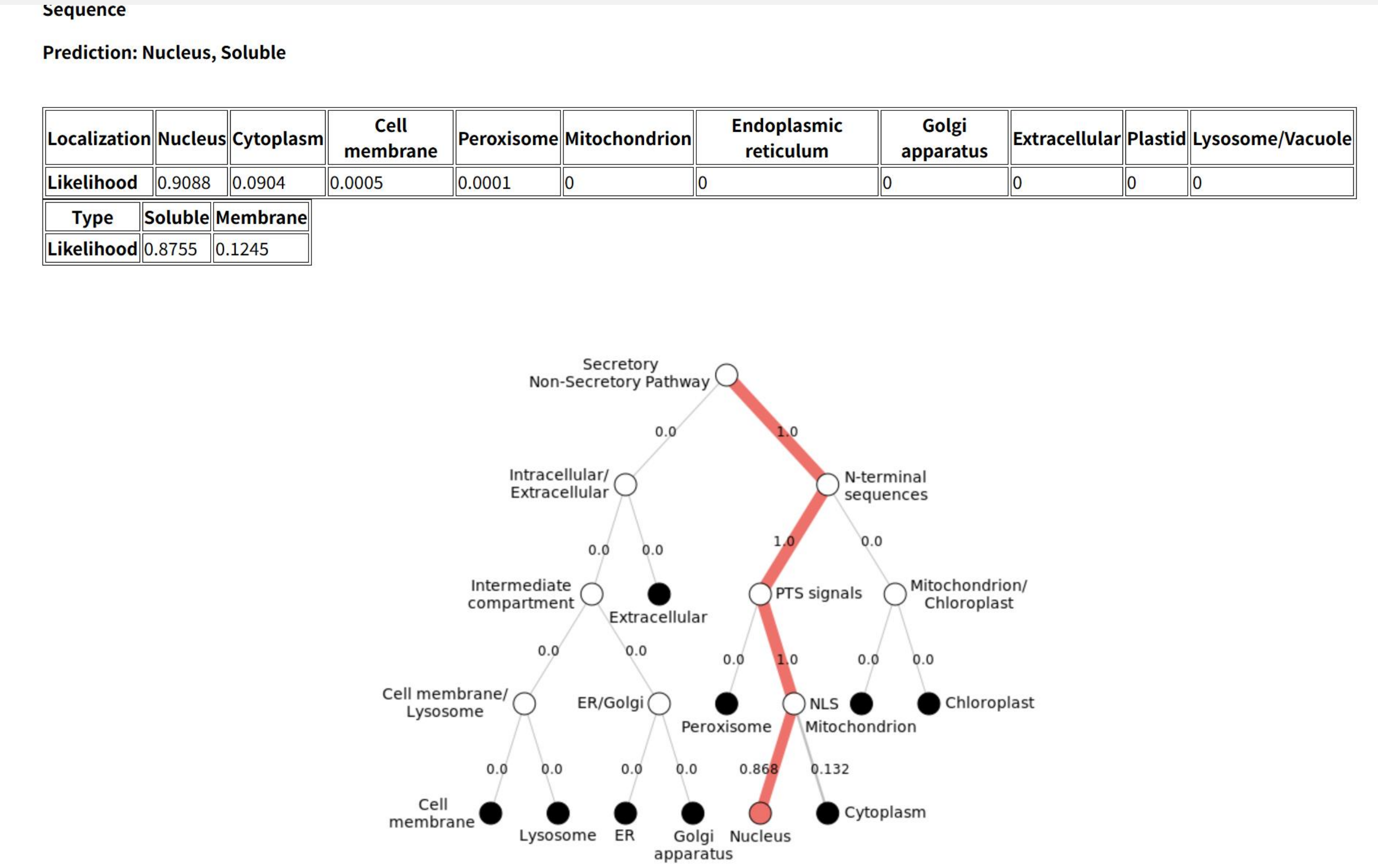
| Read Me | Data | Citation |

Your input sequence (389aa) is:

```
>APO2
MDPNDAFSAAHPFRWDLGPPAPAPVPPPPPPPPPPPPANVPRELEELVAGYGVRMSTVAR
ISELGFTASTLLAMTERELDDMMAALAGLFRWDLLLGERFGLRAALRAERGRLMSLGGRH
HGHQSGSTVDGASQEVLSDEHDMAGSGGMGDDDNGRRMVTGKKQAKKGSAARKGKKARRK
KVDDLRLDMQEDEMDCCDEDGGGGSESTESSAGGGGGERQREHPFVVTEPGEVARAKKNG
LDYLFHLYEQCRLFLLQVQSMAKLHGHKSPTKVTNQVFRYAKKVGASYINKPKMRHYVHC
YALHCLDEEASDALRRAYKARGENVGAWRQACYAPLVDISARHGFDIDAVFAAHPRLAIW
YVPTRLRQLCHQARSSHAAAAAALPPPLF
```

----------- Plant-mPLoc Computation Result -----------

Query protein	Predicted location(s)
APO2	**Nucleus.**



Sequence

Prediction: Nucleus, Soluble

Localization	Nucleus	Cytoplasm	Cell membrane	Peroxisome	Mitochondrion	Endoplasmic reticulum	Golgi apparatus	Extracellular	Plastid	Lysosome/Vacuole
Likelihood	0.9088	0.0904	0.0005	0.0001	0	0	0	0	0	0

Type	Soluble	Membrane
Likelihood	0.8755	0.1245

明德格物 博学笃行

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Part 3

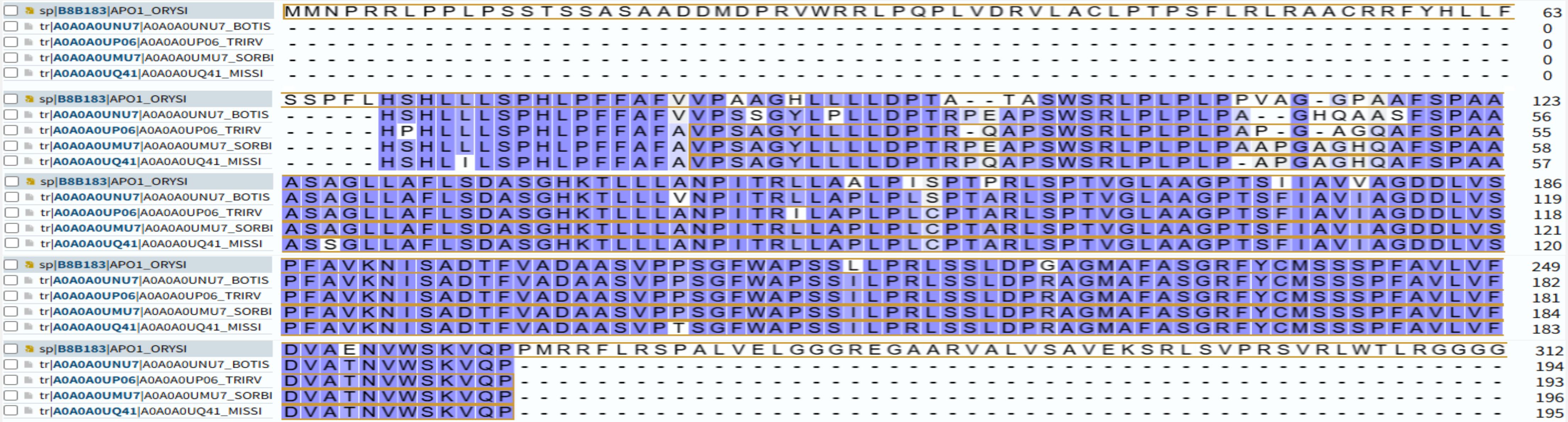
序列保守性与系统发育分析

序列比对

APO1序列比对

Tool: UniProt

Species	Scientific name	Accession	AA Length
Rice	*Oryza sativa*	B8B183	429
Sorghum	*Sorghum bicolor*	A0A0A0UMU7	196
Yellow bluestem	*Bothriochloa ischaemum*	A0A0A0UNU7	194
Ravanna grass	*Tripidium ravennae*	A0A0A0UP06	193
Chinese silver grass	*Miscanthus sinensis*	A0A0A0UQ41	196



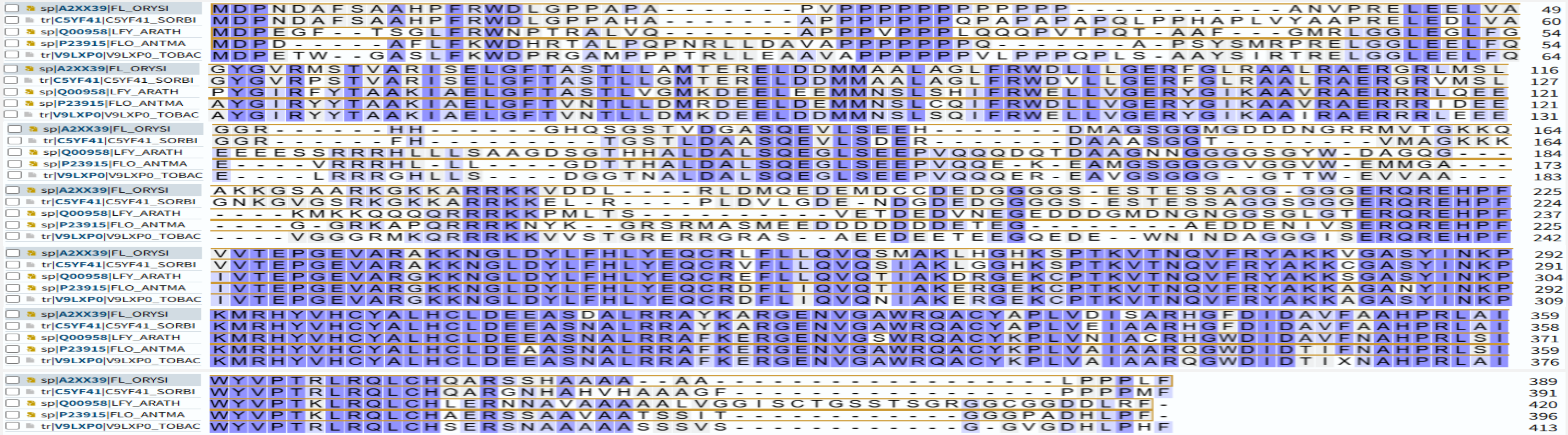
```
☐ sp|B8B183|APO1_ORYSI                MMNPRRLPPLPSSTSSASAADDMDPRVWRRLPQPLVDRVLACLPTPSFLRLRAACRRFYHLLF   63
☐ tr|A0A0A0UNU7|A0A0A0UNU7_BOTIS      ---------------------------------------------------------------    0
☐ tr|A0A0A0UP06|A0A0A0UP06_TRIRV      ---------------------------------------------------------------    0
☐ tr|A0A0A0UMU7|A0A0A0UMU7_SORBI      ---------------------------------------------------------------    0
☐ tr|A0A0A0UQ41|A0A0A0UQ41_MISSI      ---------------------------------------------------------------    0

☐ sp|B8B183|APO1_ORYSI                SSPFLHSHLLLSPHLPFFAFVVPAAGHLLLLDPTA--TASWSRLPLPLPPVAG-GPAAFSPAA  123
☐ tr|A0A0A0UNU7|A0A0A0UNU7_BOTIS      ------HSHLLLSPHLPFFAFVVPSSGYLPLLDPTRPEAPSWSRLPLPLPA--GHQAASFSPAA   56
☐ tr|A0A0A0UP06|A0A0A0UP06_TRIRV      ------HPHLLLSPHLPFFAFAVPSAGYLLLLDPTR-QAPSWSRLPLPLPAP-G-AGQAFSPAA   55
☐ tr|A0A0A0UMU7|A0A0A0UMU7_SORBI      ------HSHLLLSPHLPFFAFAVPSAGYLLLLDPTRPEAPSWSRLPLPLPAAPGAGHQAFSPAA   58
☐ tr|A0A0A0UQ41|A0A0A0UQ41_MISSI      ------HSHLILSPHLPFFAFAVPSAGYLLLLDPTRPQAPSWSRLPLPLP-APGAGHQAFSPAA   57

☐ sp|B8B183|APO1_ORYSI                ASAGLLAFLSDASGHKTLLLANPITRLLAALPISPTPRLSPTVGLAAGPTSIIAVVAGDDLVS  186
☐ tr|A0A0A0UNU7|A0A0A0UNU7_BOTIS      ASAGLLAFLSDASGHKTLLLVNPITRLLAPLPLSPTARLSPTVGLAAGPTSFIAVIAGDDLVS  119
☐ tr|A0A0A0UP06|A0A0A0UP06_TRIRV      ASAGLLAFLSDASGHKTLLLANPITRILAPLPLCPTARLSPTVGLAAGPTSFIAVIAGDDLVS  118
☐ tr|A0A0A0UMU7|A0A0A0UMU7_SORBI      ASAGLLAFLSDASGHKTLLLANPITRLLAPLPLCPTARLSPTVGLAAGPTSFIAVIAGDDLVS  121
☐ tr|A0A0A0UQ41|A0A0A0UQ41_MISSI      ASSGLLAFLSDASGHKTLLLANPITRLLAPLPLCPTARLSPTVGLAAGPTSFIAVIAGDDLVS  120

☐ sp|B8B183|APO1_ORYSI                PFAVKNISADTFVADAASVPPSGFWAPSSLLPRLSSLDPGAGMAFASGRFYCMSSSPFAVLVF  249
☐ tr|A0A0A0UNU7|A0A0A0UNU7_BOTIS      PFAVKNISADTFVADAASVPPSGFWAPSSILPRLSSLDPRAGMAFASGRFYCMSSSPFAVLVF  182
☐ tr|A0A0A0UP06|A0A0A0UP06_TRIRV      PFAVKNISADTFVADAASVPPSGFWAPSSILPRLSSLDPRAGMAFASGRFYCMSSSPFAVLVF  181
☐ tr|A0A0A0UMU7|A0A0A0UMU7_SORBI      PFAVKNISADTFVADAASVPPSGFWAPSSILPRLSSLDPRAGMAFASGRFYCMSSSPFAVLVF  184
☐ tr|A0A0A0UQ41|A0A0A0UQ41_MISSI      PFAVKNISADTFVADAASVPTSGFWAPSSILPRLSSLDPRAGMAFASGRFYCMSSSPFAVLVF  183

☐ sp|B8B183|APO1_ORYSI                DVAENVWSKVQPPMRRFLRSPALVELGGGREGAARVALVSAVEKSRLSVPRSVRLWTLRGGGG  312
☐ tr|A0A0A0UNU7|A0A0A0UNU7_BOTIS      DVATNVWSKVQP---------------------------------------------------  194
☐ tr|A0A0A0UP06|A0A0A0UP06_TRIRV      DVATNVWSKVQP---------------------------------------------------  193
☐ tr|A0A0A0UMU7|A0A0A0UMU7_SORBI      DVATNVWSKVQP---------------------------------------------------  196
☐ tr|A0A0A0UQ41|A0A0A0UQ41_MISSI      DVATNVWSKVQP---------------------------------------------------  195
```

序列比对

APO2序列比对

Tool: UniProt

Species	Scientific name	Accession	AA Length
Rice	*Oryza sativa*	A2XX39	389
Sorghum	*Sorghum bicolor*	C5YF41	391
Tobacco	*Nicotiana tabacum*	V9LXP0	413
Snapdragon	*Antirrhinum majus*	P23915	396
Mouse-ear cress	*Arabidopsis thaliana*	Q00958	420



```
☐ sp|A2XX39|FL_ORYSI        MDPNDAFSAAHPFRWDLGPPAPA-------PVPPPPPPPPPPPP-----------ANVPRELEELVA   49
☐ tr|C5YF41|C5YF41_SORBI    MDPNDAFSAAHPFRWDLGPPAHA-------APPPPPPPQPAPAPAPQLPPHAPLVYAAPRELEDLVA   60
☐ sp|Q00958|LFY_ARATH       MDPEGF--TSGLFRWNPTRALVQ-------APPPVPPPLQQQPVTPQT-AAF---GMRLGGLEGLFG   54
☐ sp|P23915|FLO_ANTMA       MDPD-----AFLFKWDHRTALPQPNRLLDAVAPPPPPPPQ-------A-PSYSMRPRELGGLEELFQ   54
☐ tr|V9LXP0|V9LXP0_TOBAC    MDPETW--GASLFKWDPRGAMPPPTRLLEAAVAPPPPPPVLPPPQPLS-AAYSIRTRELGGLEELFQ   64

☐ sp|A2XX39|FL_ORYSI        GYGVRMSTVARISELGFTASTLLAMTERELDDMMAALAGLFRWDLLLGERFGLRAALRAERGRLMSL  116
☐ tr|C5YF41|C5YF41_SORBI    GYGVRPSTVARISELGFTASTLLGMTERELDDMMAALAGLFRWDVLLGERFGLRAALRAERGRVMSL  127
☐ sp|Q00958|LFY_ARATH       PYGIRFYTAAKIAELGFTASTLVGMKDEELEEMMNSLSHIFRWELLVGERYGIKAAVRAERRRLQEE  121
☐ sp|P23915|FLO_ANTMA       AYGIRYYTAAKIAELGFTVNTLLDMRDEELDEMMNSLCQIFRWDLLVGERYGIKAAVRAERRRIDEE  121
☐ tr|V9LXP0|V9LXP0_TOBAC    AYGIRYYTAAKIAELGFTVNTLLDMKDEELDDMMNSLSQIFRWELLVGERYGIKAAIRAERRRLEEE  131

☐ sp|A2XX39|FL_ORYSI        GGR------HH------GHQSGSTVDGASQEVLSEEH-------DMAGSGGMGDDDNGRRMVTGKKQ  164
☐ tr|C5YF41|C5YF41_SORBI    GGR------FH---------TGSTLDAASQEVLSDER-------DAAASGGT--------VMAGKKK  164
☐ sp|Q00958|LFY_ARATH       EEEESSRRRHLLLSAAGDSGTHHALDALSQEGLSEEPVQQQDQTDAAGNNGGGGSGYW-DAGQG---  184
☐ sp|P23915|FLO_ANTMA       E----VRRRHL-LL----GDTTHALDALSQEGLSEEPVQQE-K-EAMGSGGGGVGGVW-EMMGA---  173
☐ tr|V9LXP0|V9LXP0_TOBAC    E----LRRRGHLLS----DGGTNALDALSQEGLSEEPVQQQER-EAVGSGGG--GTTW-EVVAA---  183

☐ sp|A2XX39|FL_ORYSI        AKKGSAARKGKKARRKKVDDL----RLDMQEDEMDCCDEDGGGGS-ESTESSAGG-GGGERQREHPF  225
☐ tr|C5YF41|C5YF41_SORBI    GNKGVGSRKGKKARRKKEL-R----PLDVLGDE-NDGDEDGGGGS-ESTESSAGGSGGGERQREHPF  224
☐ sp|Q00958|LFY_ARATH       ----KMKKQQQQRRRKKPMLTS----------VETDEDVNEGEDDDGMDNGNGGSGLGTERQREHPF  237
☐ sp|P23915|FLO_ANTMA       ----G-GRKAPQRRRKNYK--GRSRMASMEEDDDDDDDETEG--------AEDDENIVSERQREHPF  225
☐ tr|V9LXP0|V9LXP0_TOBAC    ----VGGGRMKQRRRKKVVSTGRERRGRAS--AEEDEETEEGQEDE--WNINDAGGGISERQREHPF  242

☐ sp|A2XX39|FL_ORYSI        VVTEPGEVARAKKNGLDYLFHLYEQCRLFLLQVQSMAKLHGHKSPTKVTNQVFRYAKKVGASYINKP  292
☐ tr|C5YF41|C5YF41_SORBI    VVTEPGEVARAKKNGLDYLFHLYEQCRVFLLQVQSIAKLGGHKSPTKVTNQVFRYAKKCGASYINKP  291
☐ sp|Q00958|LFY_ARATH       IVTEPGEVARGKKNGLDYLFHLYEQCREFLLQVQTIAKDRGEKCPTKVTNQVFRYAKKSGASYINKP  304
☐ sp|P23915|FLO_ANTMA       IVTEPGEVARGKKNGLDYLFHLYEQCRDFLIQVQTIAKERGEKCPTKVTNQVFRYAKKAGANYINKP  292
☐ tr|V9LXP0|V9LXP0_TOBAC    IVTEPGEVARGKKNGLDYLFHLYEQCRDFLIQVQNIAKERGEKCPTKVTNQVFRYAKKAGASYINKP  309

☐ sp|A2XX39|FL_ORYSI        KMRHYVHCYALHCLDEEASDALRRAYKARGENVGAWRQACYAPLVDISARHGFDIDAVFAAHPRLAI  359
☐ tr|C5YF41|C5YF41_SORBI    KMRHYVHCYALHCLDEEASNALRRAYKARGENVGAWRQACYAPLVEIAARHGFDIDAVFAAHPRLAI  358
☐ sp|Q00958|LFY_ARATH       KMRHYVHCYALHCLDEEASNALRRAFKERGENVGSWRQACYKPLVNIACRHGWDIDAVFNAHPRLSI  371
☐ sp|P23915|FLO_ANTMA       KMRHYVHCYALHCLDEAASNALRRAFKERGENVGAWRQACYKPLVAIAARQGWDIDTIFNAHPRLSI  359
☐ tr|V9LXP0|V9LXP0_TOBAC    KMRHYVHCYALHCLDEEASNALRRAFKERGENVGAWRQACYKPLVAIAARQGWDIDTIXNAHPRLAI  376

☐ sp|A2XX39|FL_ORYSI        WYVPTRLRQLCHQARSSHAAAA--AA------------------LPPPLF                   389
☐ tr|C5YF41|C5YF41_SORBI    WYVPTRLRQLCHQARGNHAHVHAAAGF-----------------PPPPMF                   391
☐ sp|Q00958|LFY_ARATH       WYVPTKLRQLCHLERNNAVAAAAALVGGISCTGSSTSGRGGCGGDDLRF-                   420
☐ sp|P23915|FLO_ANTMA       WYVPTKLRQLCHAERSSAAVAATSSIT------------GGGPADHLPF-                   396
☐ tr|V9LXP0|V9LXP0_TOBAC    WYVPTRLRQLCHSERSNAAAAASSSVS------------G-GVGDHLPHF                   413
```

结果分析

INTERPRETATION OF RESULT

1

APO1

水稻、高粱、白羊草、蒲苇和芒草5种禾本科植物中的APO1蛋白序列是高度保守的。

2

APO2

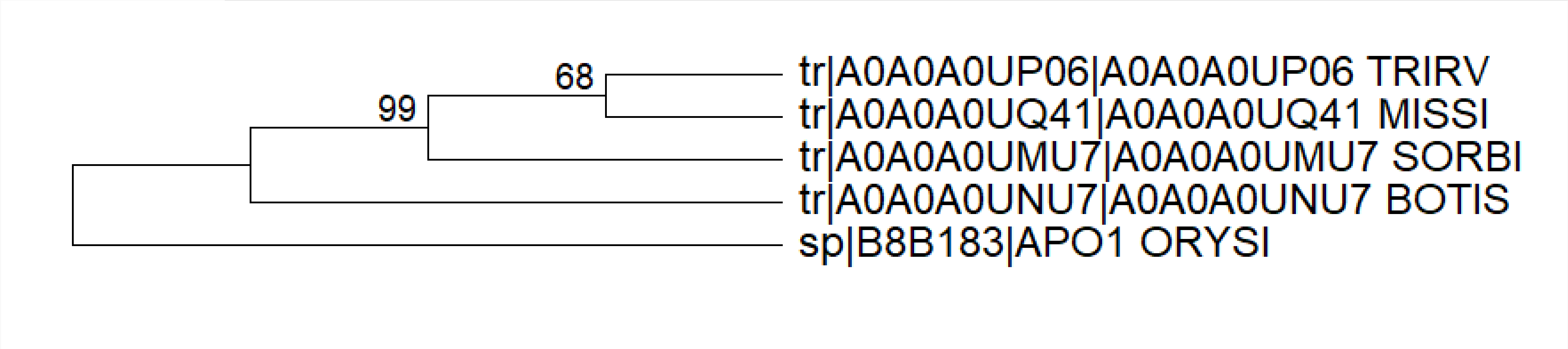
在植物界不同物种中，APO2同源的概率是很大的，它们编码的氨基酸序列中有大量的保守结构域。

系统发育分析

APO1系统发育分析

Tool: UniProt

Species	Scientific name	Accession	AA Length
Rice	*Oryza sativa*	B8B183	429
Sorghum	*Sorghum bicolor*	A0A0A0UMU7	196
Yellow bluestem	*Bothriochloa ischaemum*	A0A0A0UNU7	194
Ravanna grass	*Tripidium ravennae*	A0A0A0UP06	193
Chinese silver grass	*Miscanthus sinensis*	A0A0A0UQ41	196



系统发育分析

APO2系统发育分析

Tool: UniProt

Species	Scientific name	Accession	AA Length
Rice	*Oryza sativa*	A2XX39	389
Sorghum	*Sorghum bicolor*	C5YF41	391
Tobacco	*Nicotiana tabacum*	V9LXP0	413
Snapdragon	*Antirrhinum majus*	P23915	396
Mouse-ear cress	*Arabidopsis thaliana*	Q00958	420

结果分析

INTERPRETATION OF RESULT

1 APO1

荻草与中国芒草同属一个分支（支持率 68%），二者遗传关系最接近；
上述 2 条序列，与高粱、黄须芒草共同聚为一支（支持率 99%），说明这 4 条序列的亲缘关系较近；

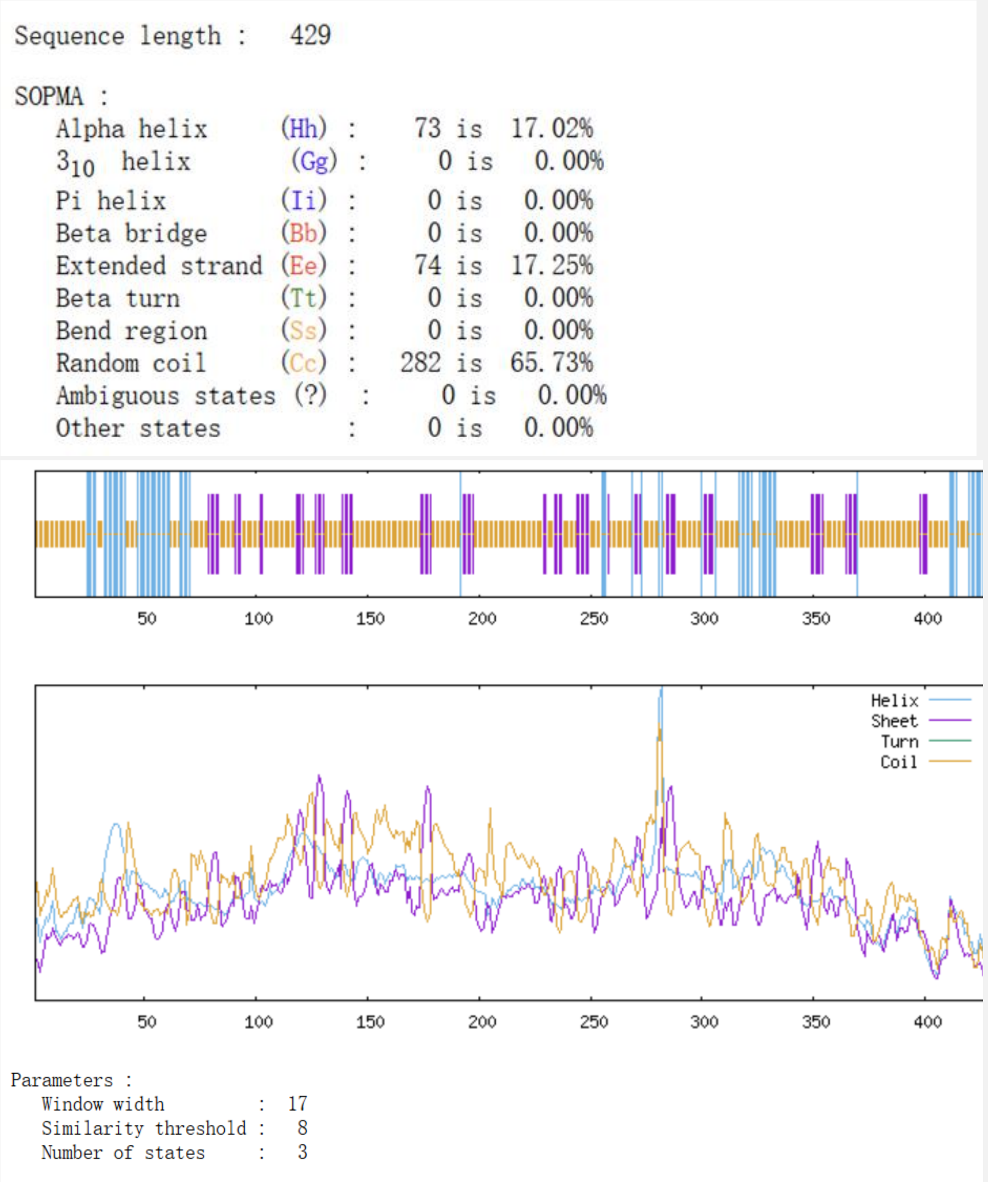
2 APO2

烟草与金鱼草聚为一支（支持率 100%）；
水稻与高粱聚为一支（支持率 100%）；
拟南芥 处于上述两个子分支的上游分支中，与这 4 种蛋白的亲缘关系介于两者之间。

Part 4

潜在互作区域结构预测

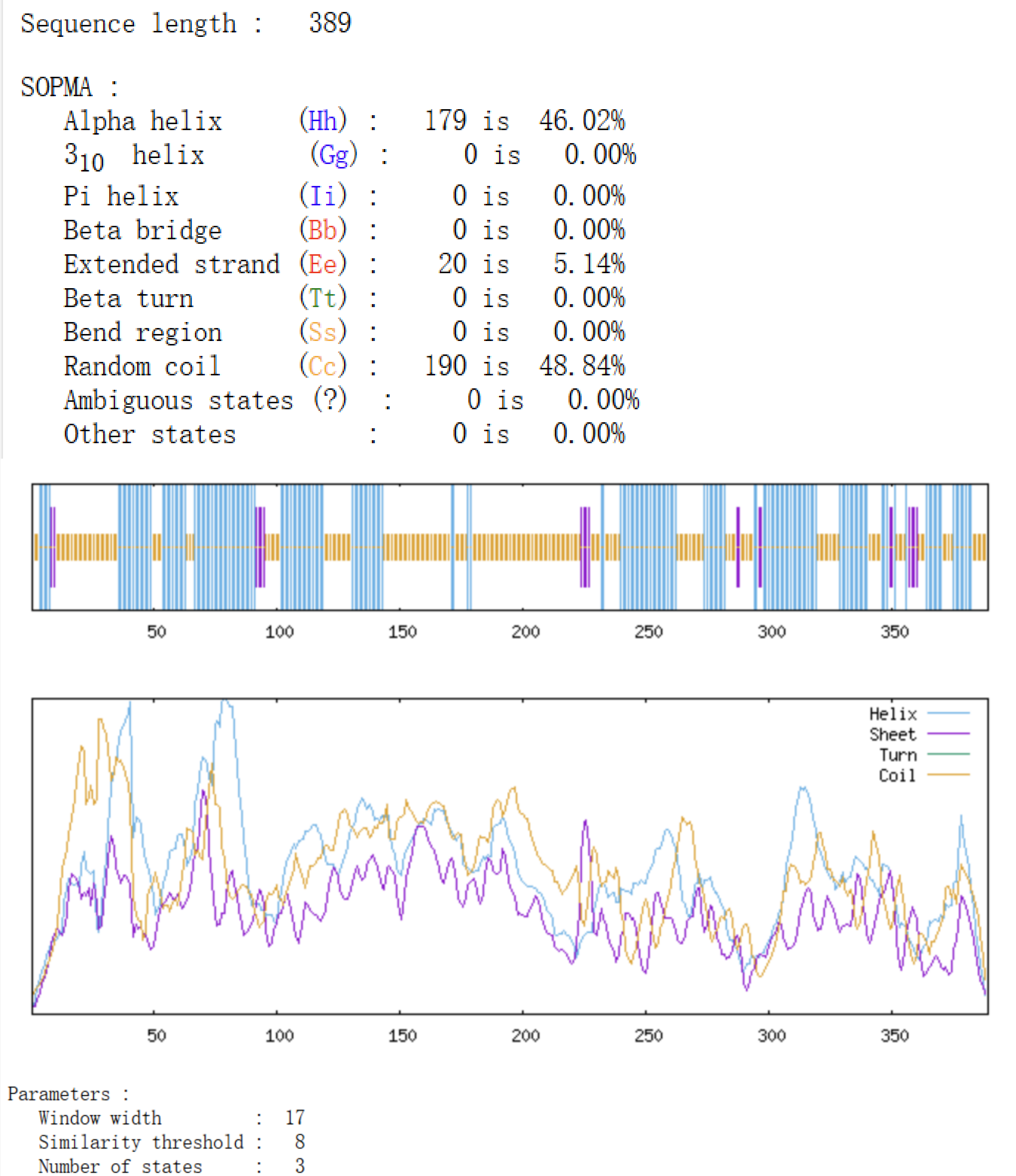
APO1与APO2二级结构分析



```
Sequence length :    429

SOPMA :
   Alpha helix      (Hh) :    73 is  17.02%
   3_10  helix       (Gg) :     0 is   0.00%
   Pi helix         (Ii) :     0 is   0.00%
   Beta bridge      (Bb) :     0 is   0.00%
   Extended strand  (Ee) :    74 is  17.25%
   Beta turn        (Tt) :     0 is   0.00%
   Bend region      (Ss) :     0 is   0.00%
   Random coil      (Cc) :   282 is  65.73%
   Ambiguous states (?)   :     0 is   0.00%
   Other states          :     0 is   0.00%
```

```
Parameters :
   Window width          :  17
   Similarity threshold :   8
   Number of states      :   3
```

APO1

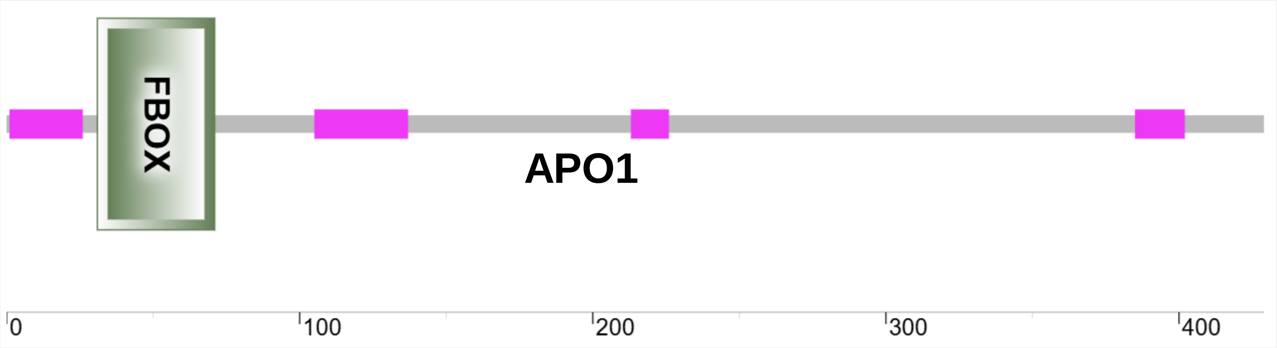


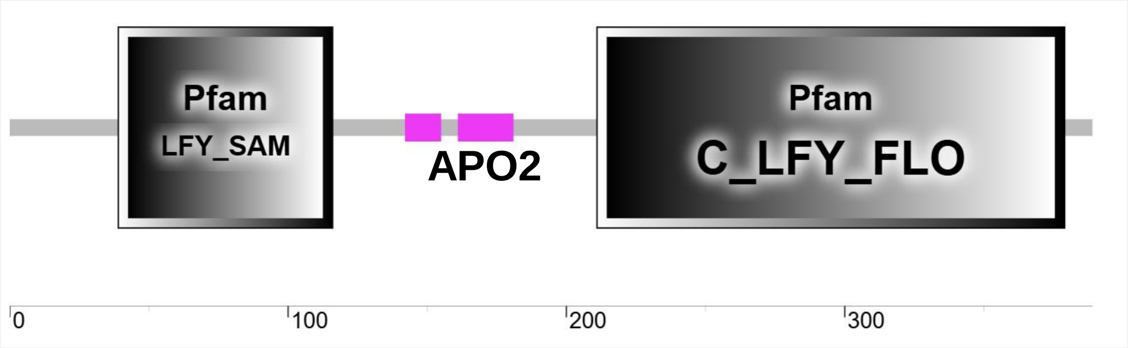
```
Sequence length :    389

SOPMA :
   Alpha helix      (Hh) :   179 is  46.02%
   3_10  helix       (Gg) :     0 is   0.00%
   Pi helix         (Ii) :     0 is   0.00%
   Beta bridge      (Bb) :     0 is   0.00%
   Extended strand  (Ee) :    20 is   5.14%
   Beta turn        (Tt) :     0 is   0.00%
   Bend region      (Ss) :     0 is   0.00%
   Random coil      (Cc) :   190 is  48.84%
   Ambiguous states (?)   :     0 is   0.00%
   Other states          :     0 is   0.00%
```

```
Parameters :
   Window width          :  17
   Similarity threshold :   8
   Number of states      :   3
```

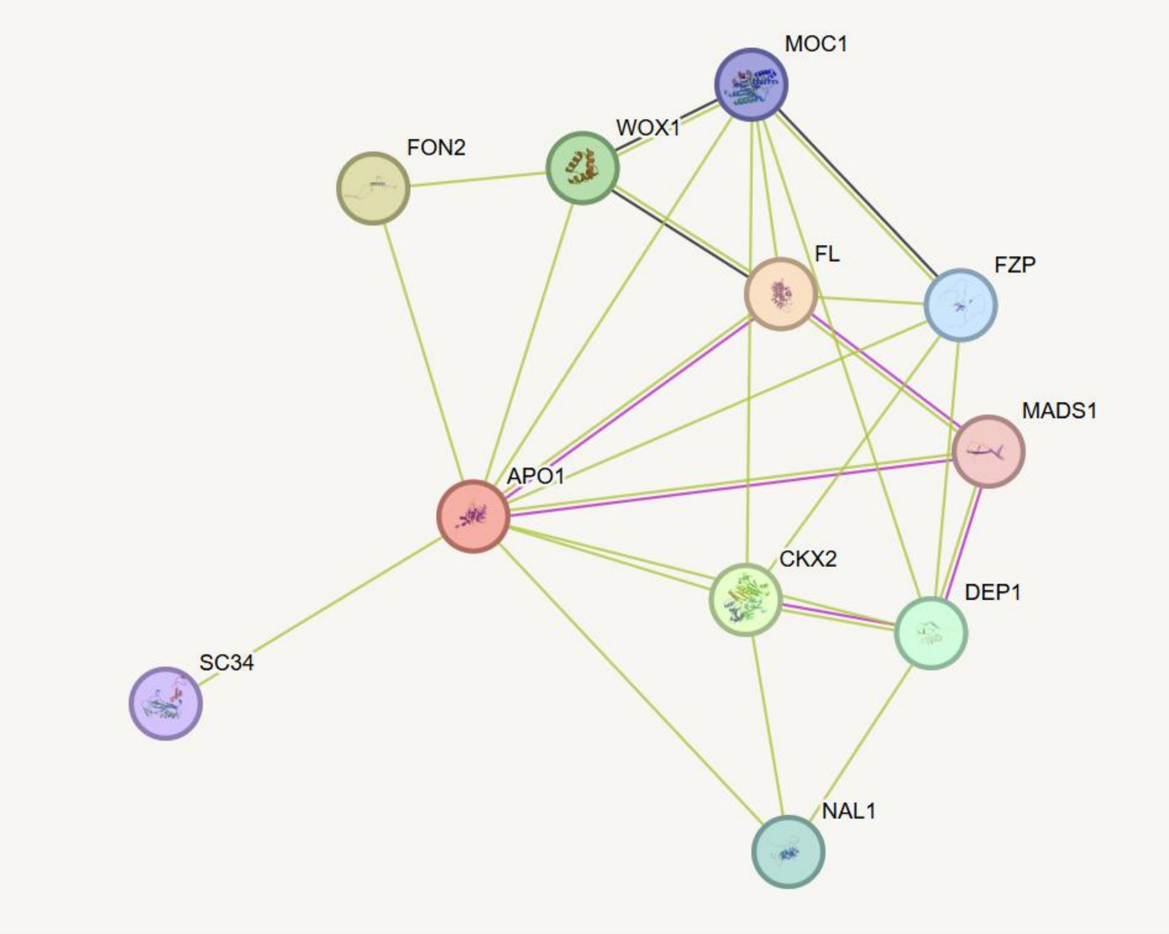
APO2

APO1与APO2蛋白互作的预测





APO1与APO2蛋白互作的预测



APO1与APO2的蛋白质三维结构预测

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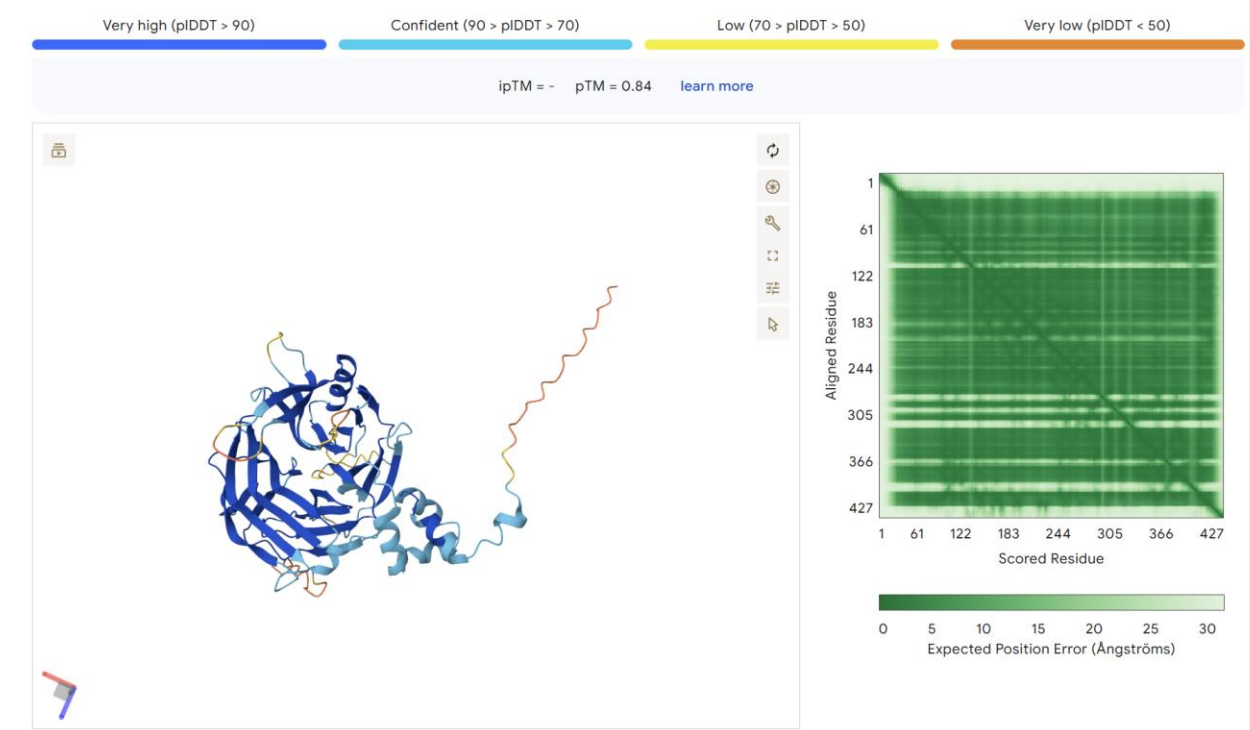
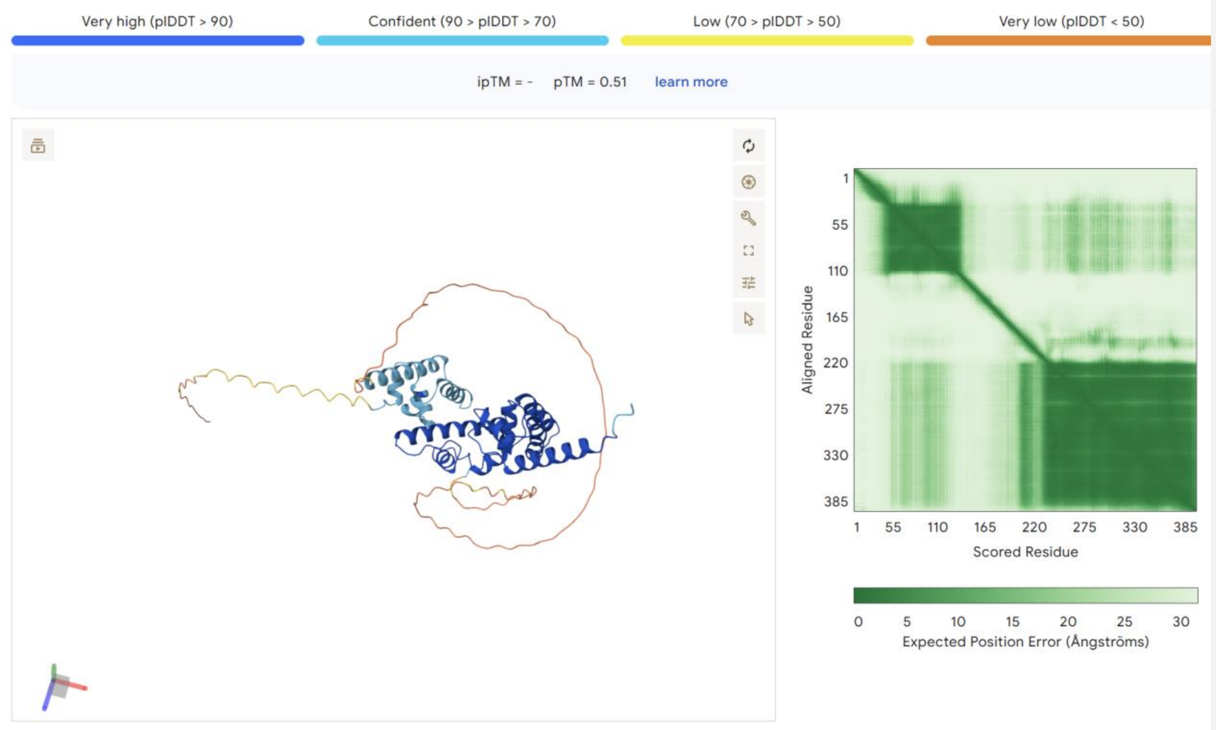


ipTM = - pTM = 0.84

APO1

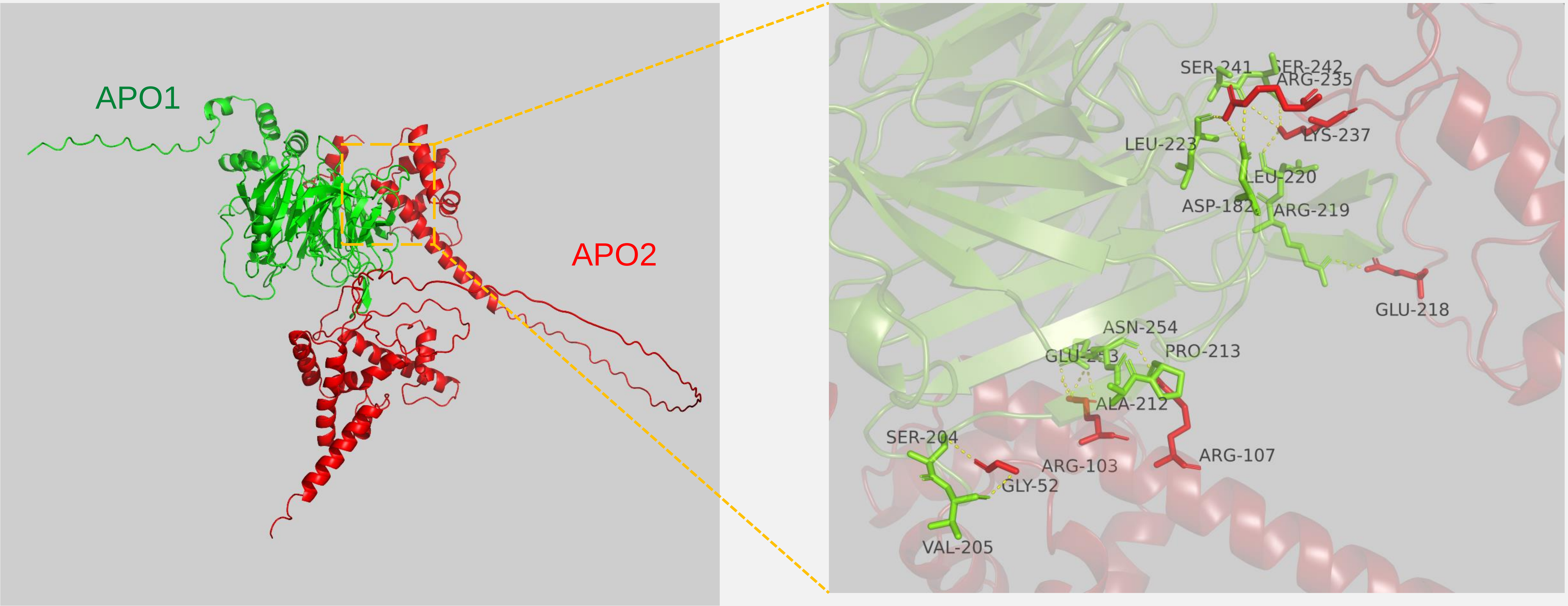


ipTM = - pTM = 0.51

APO2

https://alphafoldserver.com/

Pymol可视化互作位点



PYMOL

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CAAS

Part 5

讨论与总结

讨论

(1) 从生信角度看 APO1–APO2 互作的合理性

- APO1 与 APO2 在表达部位与亚细胞定位上具有重叠
- 均为非跨膜、非分泌蛋白，为直接或复合体互作提供空间基础

(2) 进化保守性支持互作功能的重要性

- 系统发育分析显示 APO1 / APO2 在禾本科中高度保守
- 保守区域与预测互作区域存在重叠，提示该互作机制可能在进化中受到选择

(3) 结构层面对互作位点的支持

- AlphaFold 预测结构显示候选互作区域位于蛋白表面
- 二级结构与疏水性分析表明该区域具备形成稳定蛋白–蛋白界面的可能性

(4) 本研究的局限性

- 生信预测不能替代实验验证
- 尚无法区分直接互作或通过复合物间接互作

APO1与APO2蛋白互作的预测

通过生物信息学分析，我们预测了 APO1–APO2 潜在的互作区域，并发现这些区域在进化上具有较高保守性，因此推测其在穗发育调控中具有功能意义。下一步工作将重点放在互作关系的实验验证以及关键互作位点的功能解析，从而将生信预测结果转化为可验证的生物学结论。

小组成员照片

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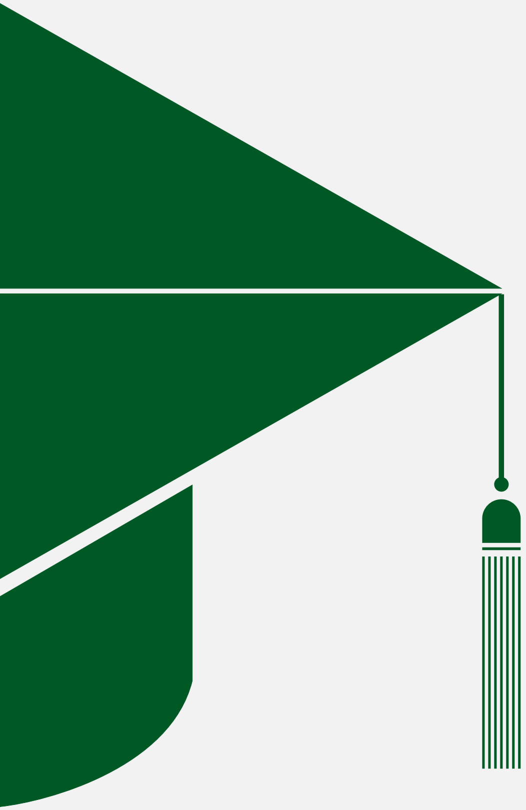

中国农业科学院

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演示完毕 感谢聆听！

汇报人：吴春雪　　**小组成员：吴春雪、樊泰延、肖晋瑜、秦超琦**