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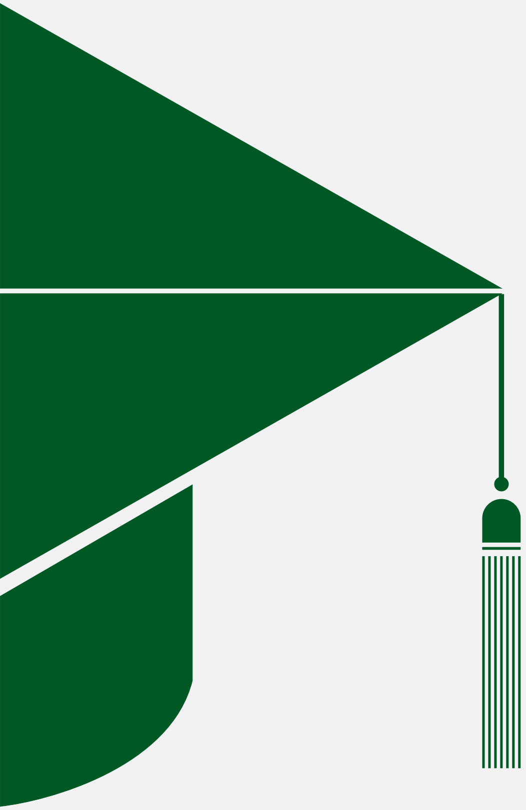


棉蚜P450酶家族基因CYP6CY13的生信分析

汇 报 人： 林妍
时间：2025.04.27

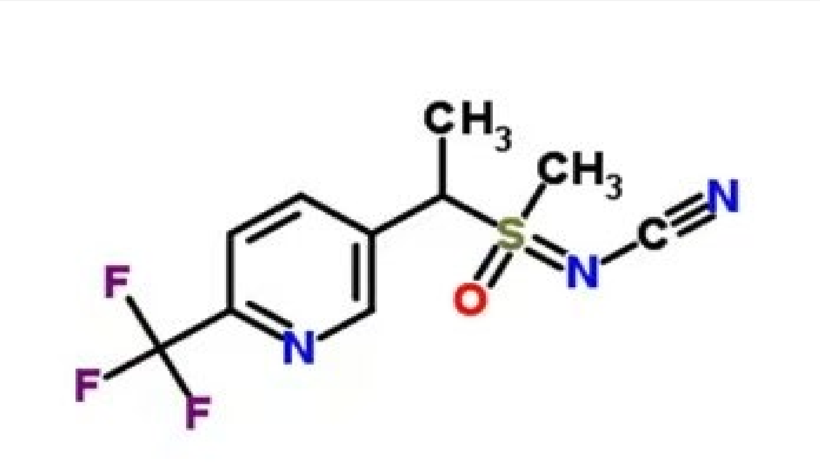
研究背景

来源百度百科（http://baike.baidu.com/l/J9jUJ3ae?bk_share=copy&fr=copy#）

- ➢ 棉蚜是一种严重危害棉花、瓜类、木槿等多种植物的世界性分布的重大农业害虫。
- ➢ 因其具有繁殖速度快、寄主范围广、暴发性强和易于产生抗药性等特点备受人们关注。
- ➢ 当前生产上对于棉蚜的防治主要依赖化学防治。
- ➢ 但由于长期的不合理的使用杀虫剂，国内外大部分棉区的棉蚜对常用杀虫剂产生了严重的抗药性。

来源淘宝（https://e.tb.cn/h.6PswFmh9VkI11SI?tk=9E3FV3GkZOG CZ193 ）

研究背景



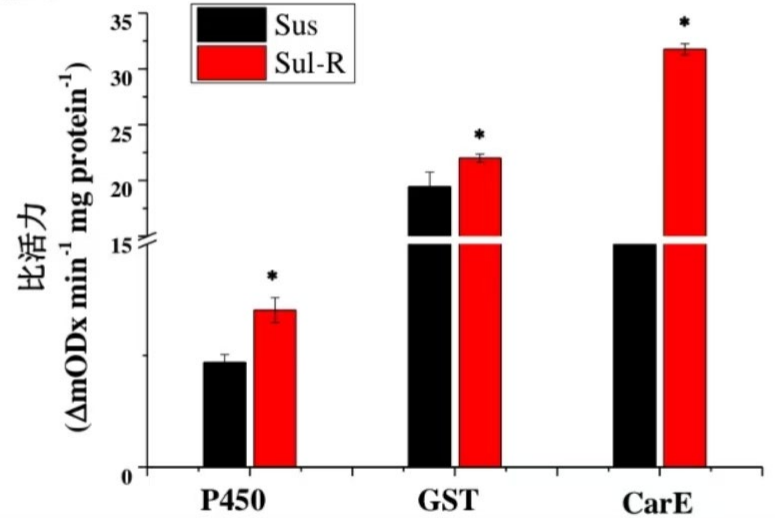
来源百度百科（http://baike.baidu.com/l/XosEJkHj?bk_share=copy&fr=copy#）

- ● 氟啶虫胺腈
- ➢ 化学名称为[甲基[1-(6-三氟甲基-3-吡啶基)乙基]-λ^{6}-亚砜烯基]氰胺，是一种砜亚胺类杀虫剂。
- ➢ 作用于昆虫烟碱型乙酰胆碱受体，会影响昆虫神经系统的正常运行，堵塞其神经通路，最终导致昆虫麻痹，致其死亡

- ➢ 与新烟碱类杀虫剂不同，其拥有 nAChR 独特的结合位点，因此被杀虫剂抗性行动委员会认定为 Group 4C 类杀虫剂。
- ➢ 近年来，不断的有研究报道出我国多个棉区的棉蚜种群都对氟啶虫胺腈产生了不同程度的抗性。
- ➢ 2017 年保定、邯郸两地抗性高达205.39 倍和 197.43 倍的高水平抗性。

研究背景

腈的抗性。



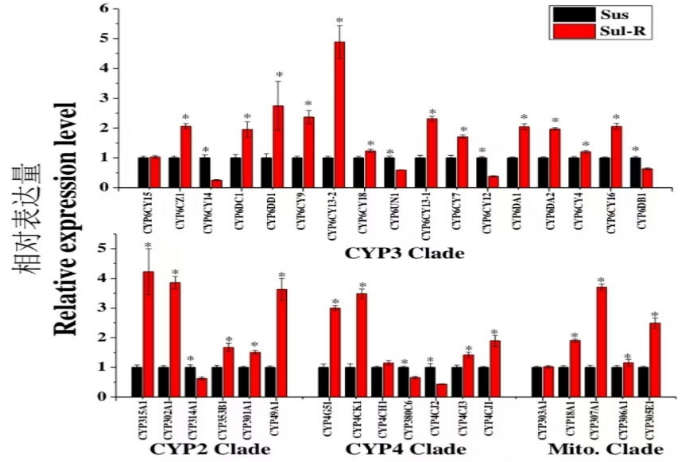


图 3-2 感抗两种群棉蚜 P450 相对表达量

Fig. 3-2 Transcription levels of P450s in the Sus and Sul-R strains determined via real-time PCR.

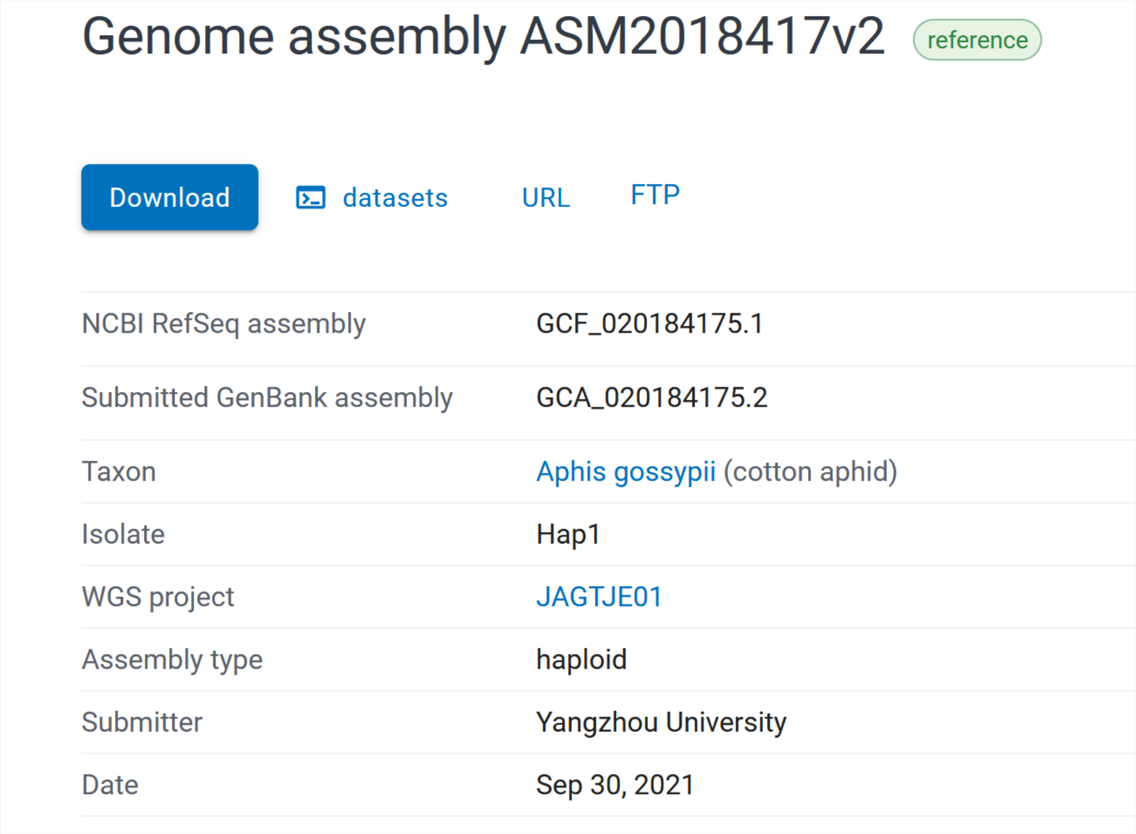
注：图中数值为平均值±标准差。*表示敏感种群与抗性种群差异显著（P<0.05）。

- 相较敏感种群，抗性种群的P450 单加氧化酶、羧酸酯酶和谷胱甘肽 S-转移酶三种解毒酶活力均显著提高。

- 经过对比 P450s基因在感抗种群中的差异表达，发现有 25 条 P450 基因在抗性种群中显著上调表达，其中 CYP6CY13-2 上调倍数最高，为敏感种群的 4.89 倍。

王立. 棉蚜对氟啶虫胺腈的抗性分子机理及药剂胁迫下棉蚜再猖獗机制研究[D]. 北京:中国农业科学院,2022.

基因组信息查询

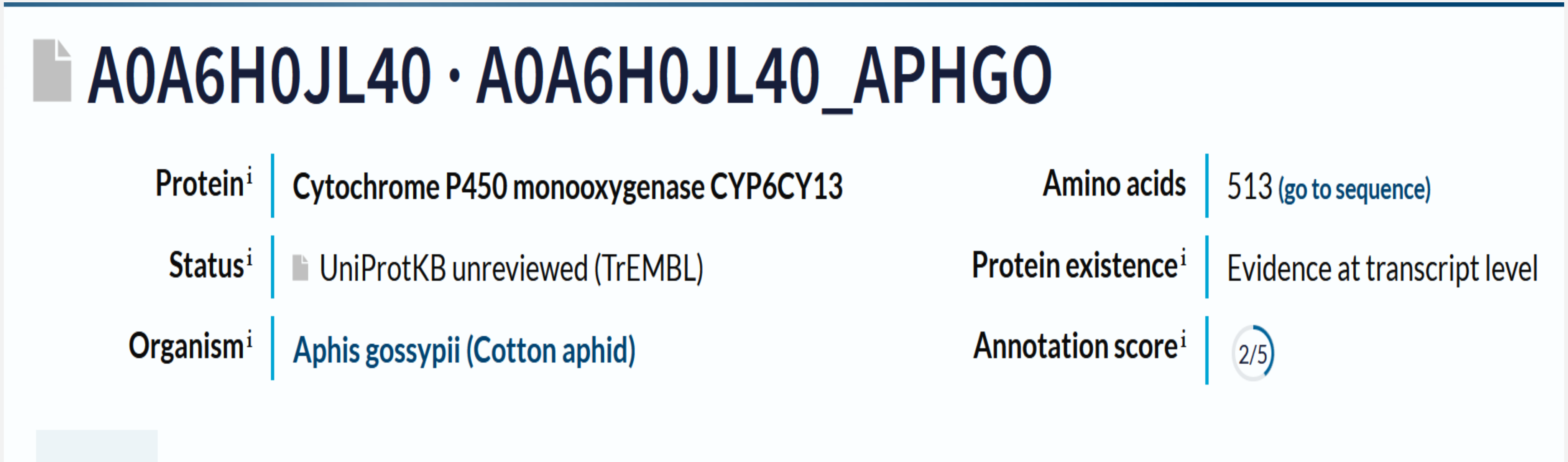


Genome assembly ASM2018417v2 reference

NCBI RefSeq assembly	GCF_020184175.1
Submitted GenBank assembly	GCA_020184175.2
Taxon	Aphis gossypii (cotton aphid)
Isolate	Hap1
WGS project	JAGTJE01
Assembly type	haploid
Submitter	Yangzhou University
Date	Sep 30, 2021

数据来源：NCBI

蛋白序列的获取

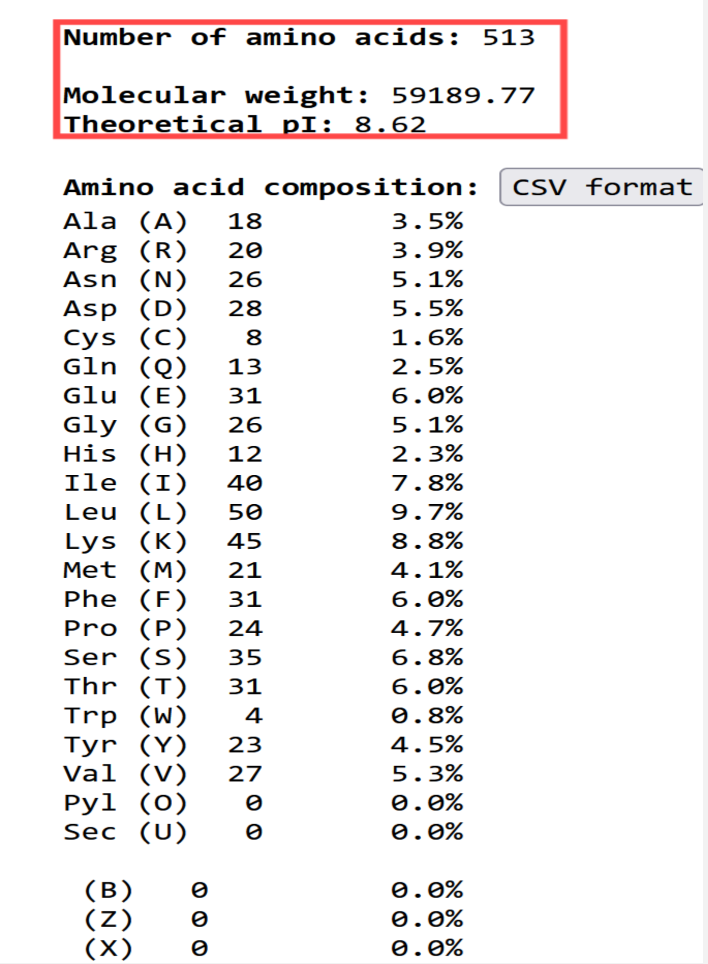


A0A6H0JL40 · A0A6H0JL40_APHGO

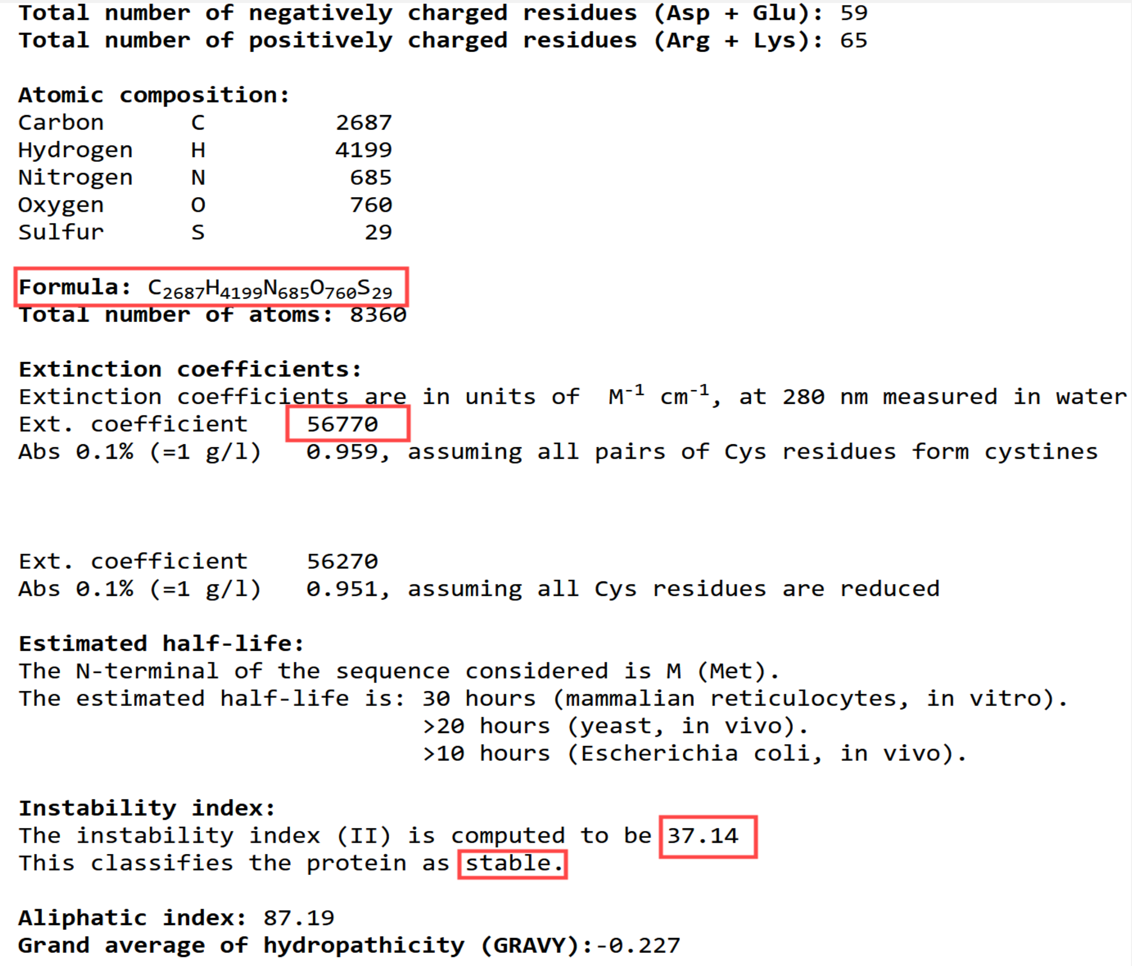
Protein	Cytochrome P450 monooxygenase CYP6CY13	**Amino acids**	513 (go to sequence)
Status	UniProtKB unreviewed (TrEMBL)	**Protein existence**	Evidence at transcript level
Organism	Aphis gossypii (Cotton aphid)	**Annotation score**	2/5

数据来源：UniProt

蛋白理化性质分析



```
Number of amino acids: 513

Molecular weight: 59189.77
Theoretical pI: 8.62

Amino acid composition:  CSV format
Ala (A)  18        3.5%
Arg (R)  20        3.9%
Asn (N)  26        5.1%
Asp (D)  28        5.5%
Cys (C)   8        1.6%
Gln (Q)  13        2.5%
Glu (E)  31        6.0%
Gly (G)  26        5.1%
His (H)  12        2.3%
Ile (I)  40        7.8%
Leu (L)  50        9.7%
Lys (K)  45        8.8%
Met (M)  21        4.1%
Phe (F)  31        6.0%
Pro (P)  24        4.7%
Ser (S)  35        6.8%
Thr (T)  31        6.0%
Trp (W)   4        0.8%
Tyr (Y)  23        4.5%
Val (V)  27        5.3%
Pyl (O)   0        0.0%
Sec (U)   0        0.0%

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

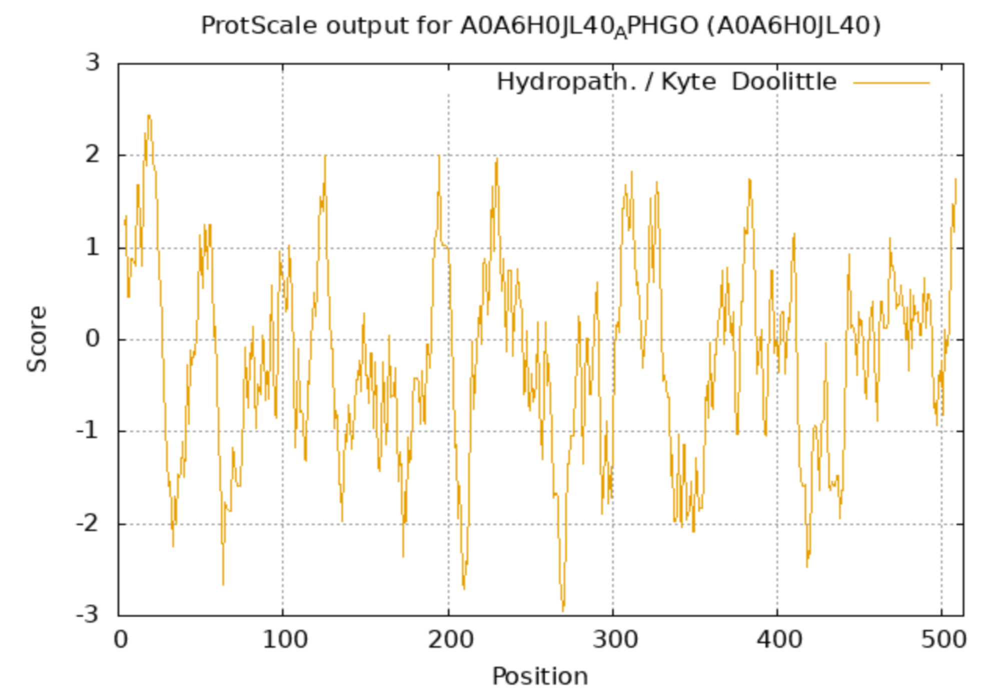


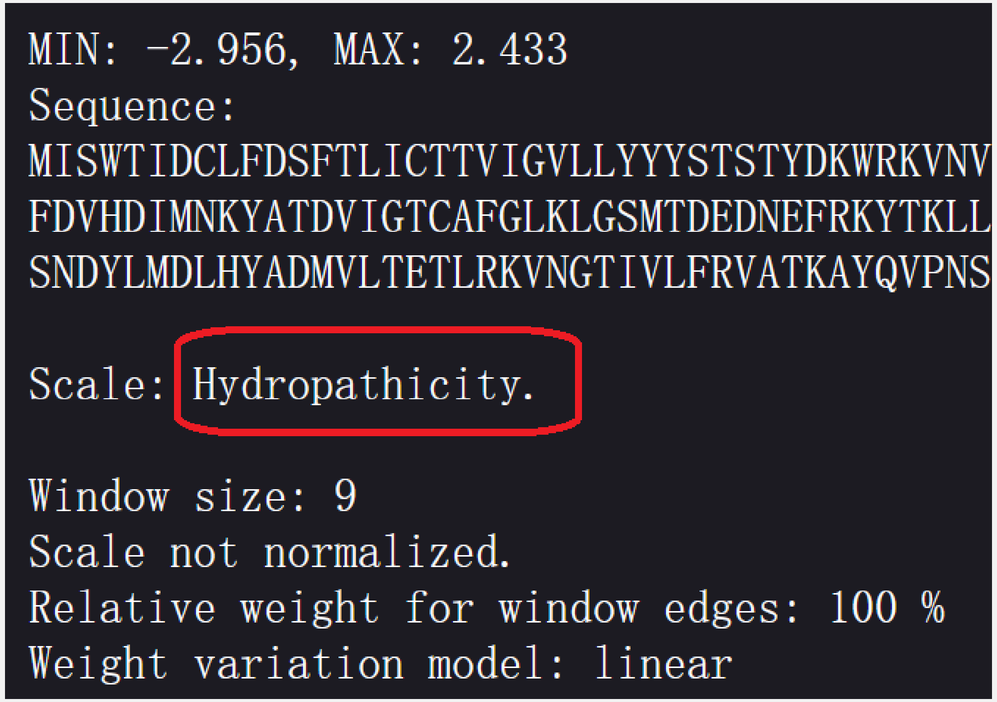
```
Total number of negatively charged residues (Asp + Glu): 59
Total number of positively charged residues (Arg + Lys): 65

Atomic composition:
Carbon      C        2687
Hydrogen    H        4199
Nitrogen    N         685
Oxygen      O         760
Sulfur      S          29

Formula: C2687H4199N685O760S29
Total number of atoms: 8360

Extinction coefficients:
Extinction coefficients are in units of  M-1 cm-1, at 280 nm measured in water
Ext. coefficient    56770
Abs 0.1% (=1 g/l)   0.959, assuming all pairs of Cys residues form cystines



Ext. coefficient    56270
Abs 0.1% (=1 g/l)   0.951, assuming all Cys residues are reduced

Estimated half-life:
The N-terminal of the sequence considered is M (Met).
The estimated half-life is: 30 hours (mammalian reticulocytes, in vitro).
                            >20 hours (yeast, in vivo).
                            >10 hours (Escherichia coli, in vivo).

Instability index:
The instability index (II) is computed to be 37.14
This classifies the protein as stable.

Aliphatic index: 87.19
Grand average of hydropathicity (GRAVY):-0.227
```

数据来源：ExPASy-ProtParam

蛋白理化性质分析

亲疏水性分析



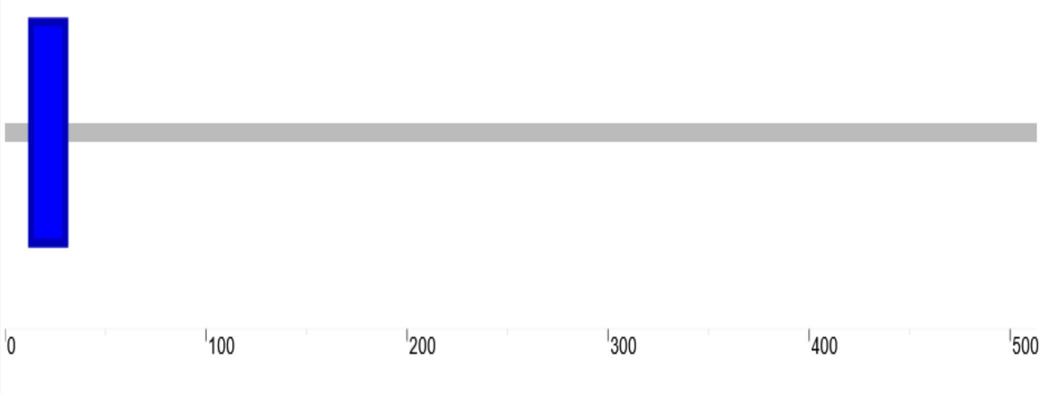


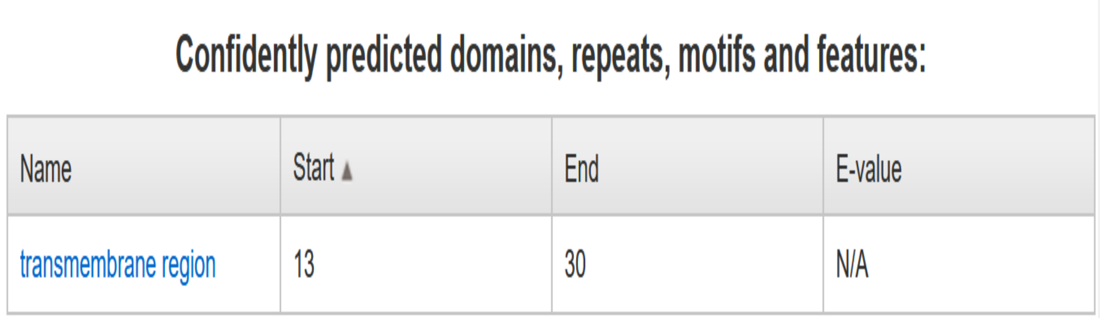
```
MIN: -2.956, MAX: 2.433
Sequence:
MISWTIDCLFDSFTLICTTVIGVLLYYYSTSTYDKWRKVNV
FDVHDIMNKYATDVIGTCAFGLKLGSMTDEDNEFRKYTKLL
SNDYLMDLHYADMVLTETLRKVNGTIVLFRVATKAYQVPNS

Scale: Hydropathicity.

Window size: 9
Scale not normalized.
Relative weight for window edges: 100 %
Weight variation model: linear
```

数据来源：ExPASy-ProtScale

蛋白理化性质分析

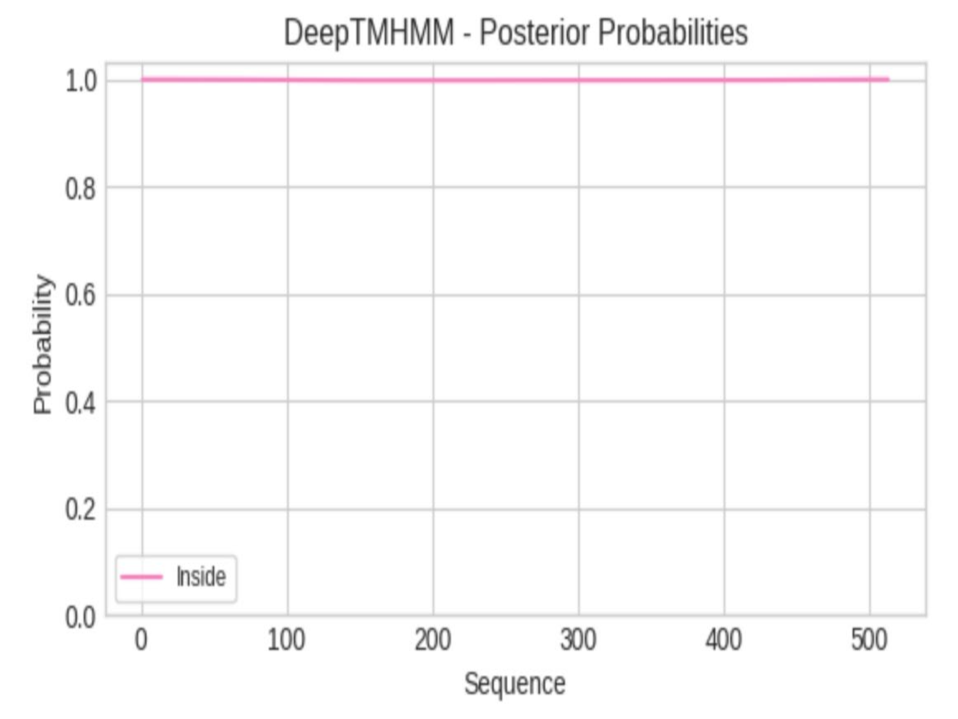
跨膜结构域预测





Confidently predicted domains, repeats, motifs and features:

Name	Start ▲	End	E-value
transmembrane region	13	30	N/A

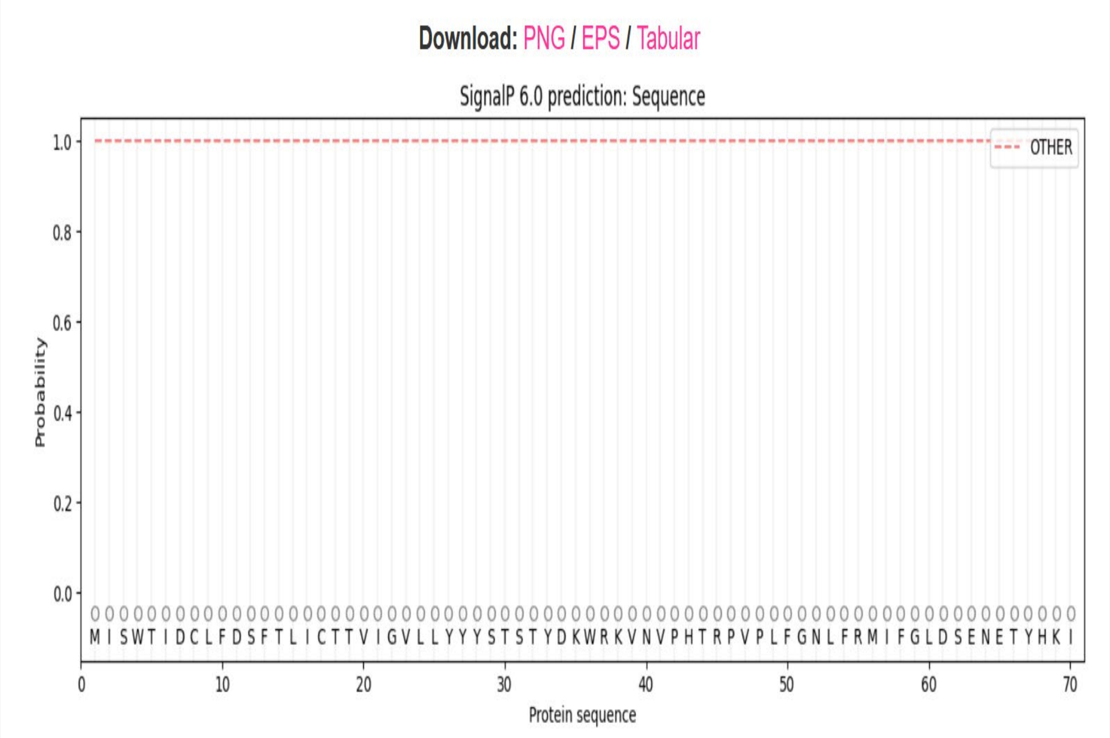


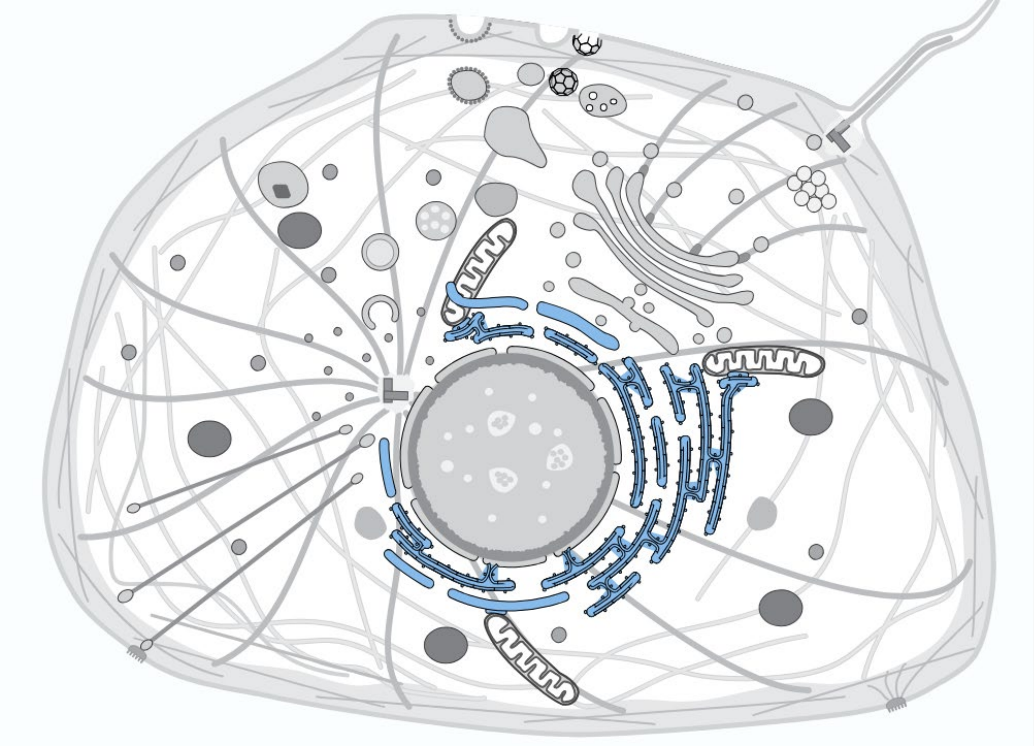
数据来源：SMART

数据来源：TMHMM

蛋白理化性质分析

信号肽和亚细胞定位



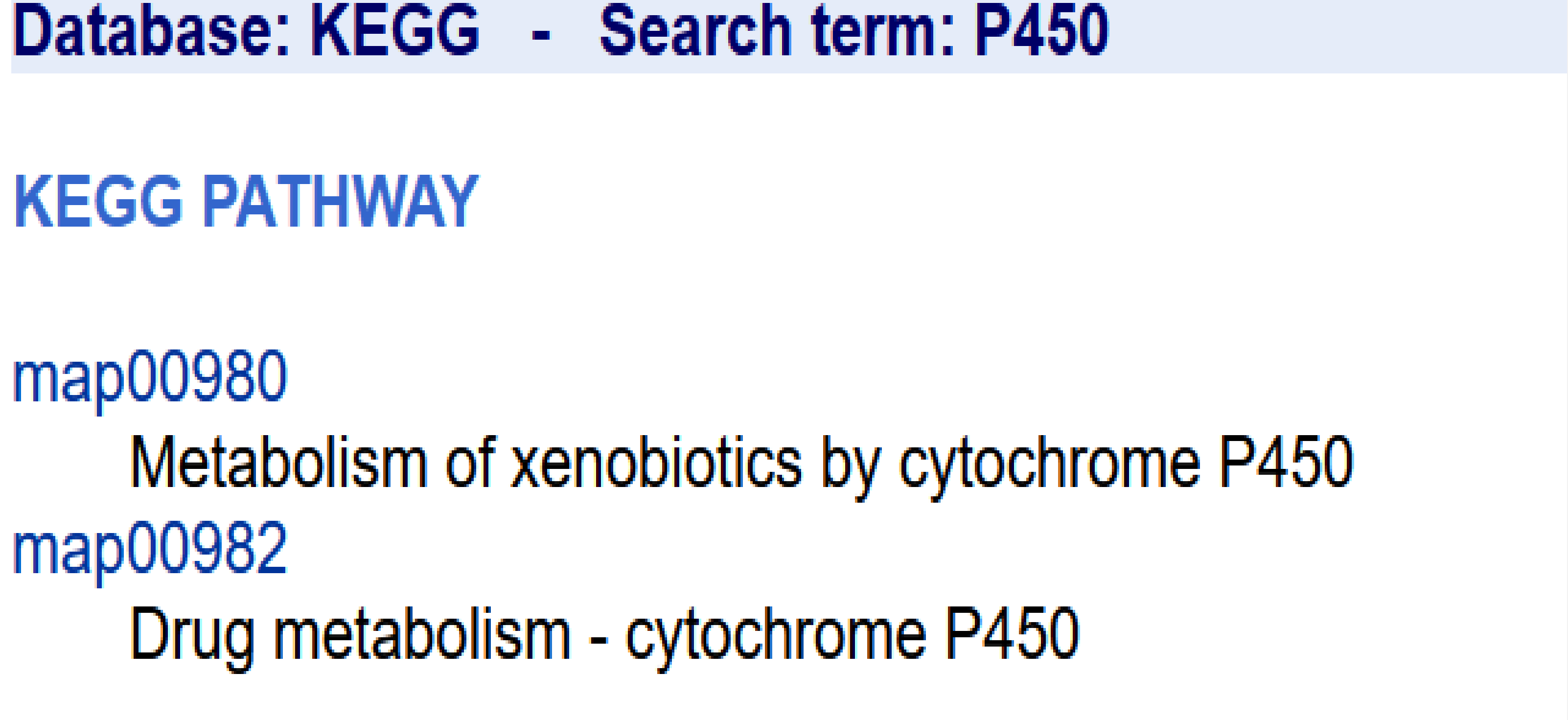


数据来源：SignalP-6.0

数据来源：UniProt

蛋白理化性质分析

代谢通路



Database: KEGG - Search term: P450

KEGG PATHWAY

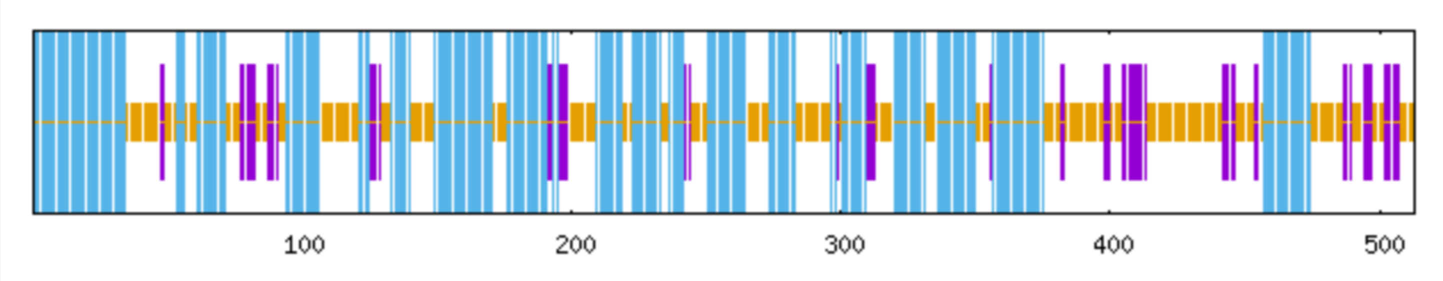
map00980
Metabolism of xenobiotics by cytochrome P450
map00982
Drug metabolism - cytochrome P450

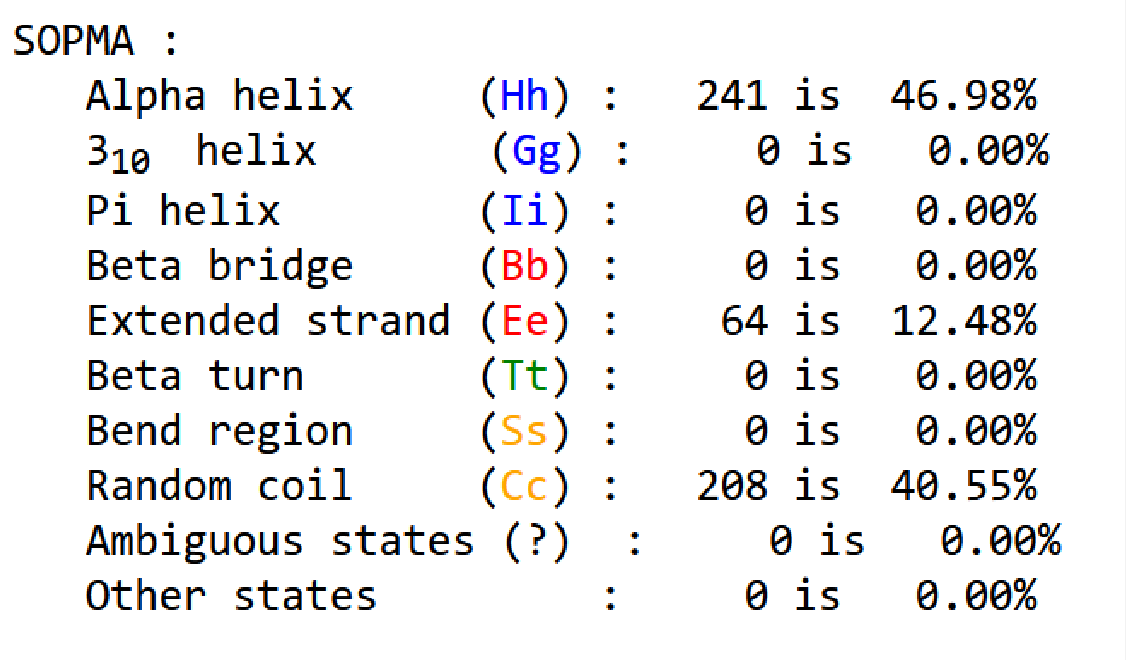
异种生物代谢、药物代谢

数据来源：KEGG

蛋白结构预测

二级结构



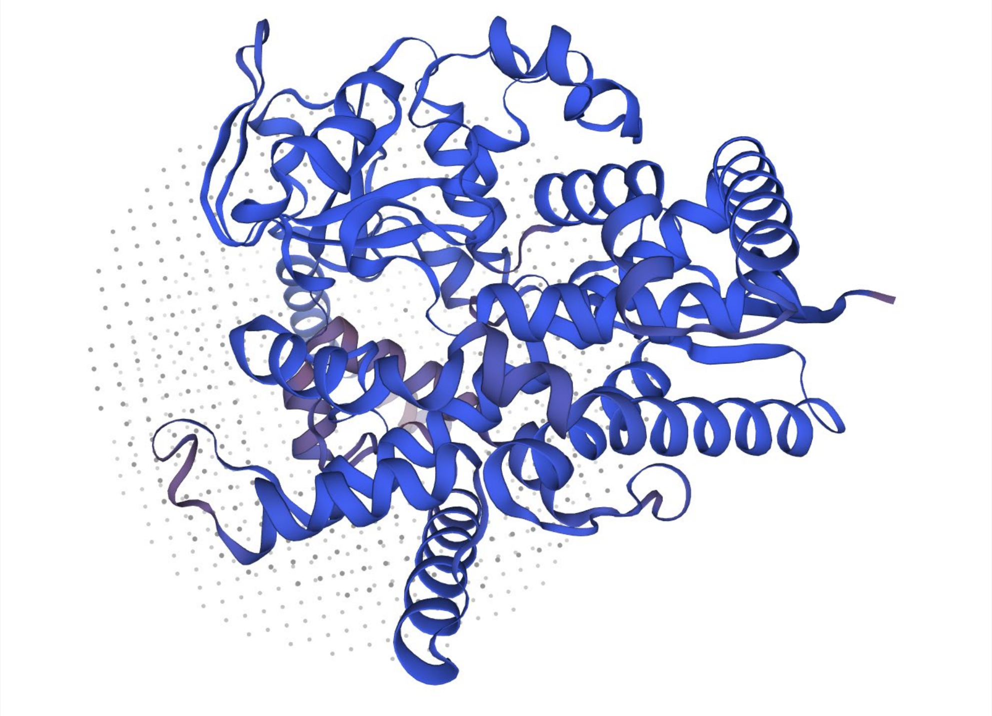


```
SOPMA :
   Alpha helix      (Hh) :   241 is  46.98%
   3_10  helix      (Gg) :     0 is   0.00%
   Pi helix         (Ii) :     0 is   0.00%
   Beta bridge      (Bb) :     0 is   0.00%
   Extended strand  (Ee) :    64 is  12.48%
   Beta turn        (Tt) :     0 is   0.00%
   Bend region      (Ss) :     0 is   0.00%
   Random coil      (Cc) :   208 is  40.55%
   Ambiguous states (?)  :     0 is   0.00%
   Other states          :     0 is   0.00%
```

数据来源：SOPMA

蛋白结构预测

三级结构



数据来源:SWISS-MODEL

Oligo-State
Monomer

GMQE
0.91

We predict the structure to have a transmembrane segment.

☑ Show / Hide

Template

A0A2S2P6M2.1.A Putative Cytochrome p450

AlphaFold DB model of A0A2S2P6M2_SCHGA (gene: Cyp6a13_4, organism: Schizaphis graminum (Green bug aphid))

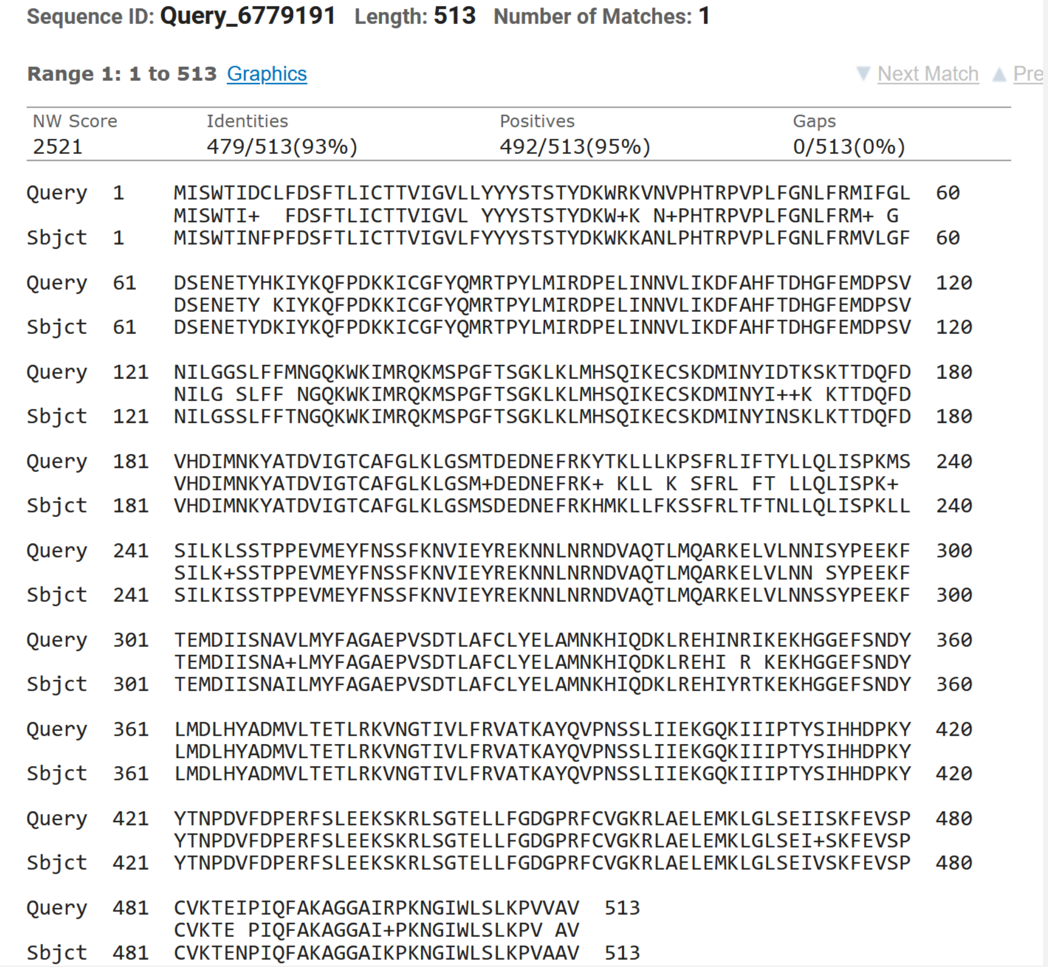
Seq Identity
85.13%

Coverage

Model-Template Alignment

```
      Model_01 MISWTIDCLFDSFTLICTTVIGVLLYYYST  30
A0A2S2P6M2.1.A MISWTINCLTDSFTVICTTVIGVLLYYYST  61

      Model_01 STYDKWRKVNVPHTRPVPLFGNLFRMIFGL  60
A0A2S2P6M2.1.A STHGKWRKANVPHTRPVPLFGNLFRTTLGL  91

      Model_01 DSENETYHKIYKQFPDKKICGFYQMRTPYL  90
A0A2S2P6M2.1.A ESEKETFDKIYKQFPDKKICGLYQMRTPYL 121

      Model_01 MIRDPELINNVLIKDFAHFTDHGFEMDPSV 120
A0A2S2P6M2.1.A MIRDPELINNVLIKDFAHFTDHGFKLDPSV 151

      Model_01 NILGGSLFFMNGQKWKIMRQKMSPGFTSGK 150
A0A2S2P6M2.1.A NFLASSLFFTNGQKWKIMRQKMSPGFTSGK 181

      Model_01 LKLMHSQIKECSKDMINYIDTKSKTTDQFD 180
A0A2S2P6M2.1.A LKLMHSQIKKCSKDMIDYIDAKSKTTDQFD 211
```

双序列比对



Sequence ID: Query_6779191 **Length: 513** **Number of Matches: 1**

Range 1: 1 to 513 Graphics

```
NW Score      Identities            Positives              Gaps
2521          479/513(93%)          492/513(95%)           0/513(0%)

Query  1    MISWTIDCLFDSFTLICTTVIGVLLYYYSTSTYDKWRKVNVPHTRPVPLFGNLFRMIFGL  60
            MISWTI+  FDSFTLICTTVIGVL YYYSTSTYDKW+K N+PHTRPVPLFGNLFRM+ G
Sbjct  1    MISWTINFPFDSFTLICTTVIGVLFYYYSTSTYDKWKKANLPHTRPVPLFGNLFRMVLGF  60

Query  61   DSENETYHKIYKQFPDKKICGFYQMRTPYLMIRDPELINNVLIKDFAHFTDHGFEMDPSV  120
            DSENETY KIYKQFPDKKICGFYQMRTPYLMIRDPELINNVLIKDFAHFTDHGFEMDPSV
Sbjct  61   DSENETYDKIYKQFPDKKICGFYQMRTPYLMIRDPELINNVLIKDFAHFTDHGFEMDPSV  120

Query  121  NILGGSLFFMNGQKWKIMRQKMSPGFTSGKLKLMHSQIKECSKDMINYIDTKSKTTDQFD  180
            NILG SLFF NGQKWKIMRQKMSPGFTSGKLKLMHSQIKECSKDMINYI++K KTTDQFD
Sbjct  121  NILGSSLFFTNGQKWKIMRQKMSPGFTSGKLKLMHSQIKECSKDMINYINSKLKTTDQFD  180

Query  181  VHDIMNKYATDVIGTCAFGLKLGSMTDEDNEFRKYTKLLLKPSFRLIFTYLLQLISPKMS  240
            VHDIMNKYATDVIGTCAFGLKLGSM+DEDNEFRK+ KLL K SFRL FT LLQLISPK+
Sbjct  181  VHDIMNKYATDVIGTCAFGLKLGSMSDEDNEFRKHMKLLFKSSFRLTFTNLLQLISPKLL  240

Query  241  SILKLSSTPPEVMEYFNSSFKNVIEYREKNNLNRNDVAQTLMQARKELVLNNISYPEEKF  300
            SILK+SSTPPEVMEYFNSSFKNVIEYREKNNLNRNDVAQTLMQARKELVLNN SYPEEKF
Sbjct  241  SILKISSTPPEVMEYFNSSFKNVIEYREKNNLNRNDVAQTLMQARKELVLNNSSYPEEKF  300

Query  301  TEMDIISNAVLMYFAGAEPVSDTLAFCLYELAMNKHIQDKLREHINRIKEKHGGEFSNDY  360
            TEMDIISNA+LMYFAGAEPVSDTLAFCLYELAMNKHIQDKLREHI R KEKHGGEFSNDY
Sbjct  301  TEMDIISNAILMYFAGAEPVSDTLAFCLYELAMNKHIQDKLREHIYRTKEKHGGEFSNDY  360

Query  361  LMDLHYADMVLTETLRKVNGTIVLFRVATKAYQVPNSSLIIEKGQKIIIPTYSIHHDPKY  420
            LMDLHYADMVLTETLRKVNGTIVLFRVATKAYQVPNSSLIIEKGQKIIIPTYSIHHDPKY
Sbjct  361  LMDLHYADMVLTETLRKVNGTIVLFRVATKAYQVPNSSLIIEKGQKIIIPTYSIHHDPKY  420

Query  421  YTNPDVFDPERFSLEEKSKRLSGTELLFGDGPRFCVGKRLAELEMKLGLSEIISKFEVSP  480
            YTNPDVFDPERFSLEEKSKRLSGTELLFGDGPRFCVGKRLAELEMKLGLSEI+SKFEVSP
Sbjct  421  YTNPDVFDPERFSLEEKSKRLSGTELLFGDGPRFCVGKRLAELEMKLGLSEIVSKFEVSP  480

Query  481  CVKTEIPIQFAKAGGAIRPKNGIWLSLKPVVAV  513
            CVKTE PIQFAKAGGAI+PKNGIWLSLKPV AV
Sbjct  481  CVKTENPIQFAKAGGAIKPKNGIWLSLKPVAAV  513
```

数据来源:NCBI

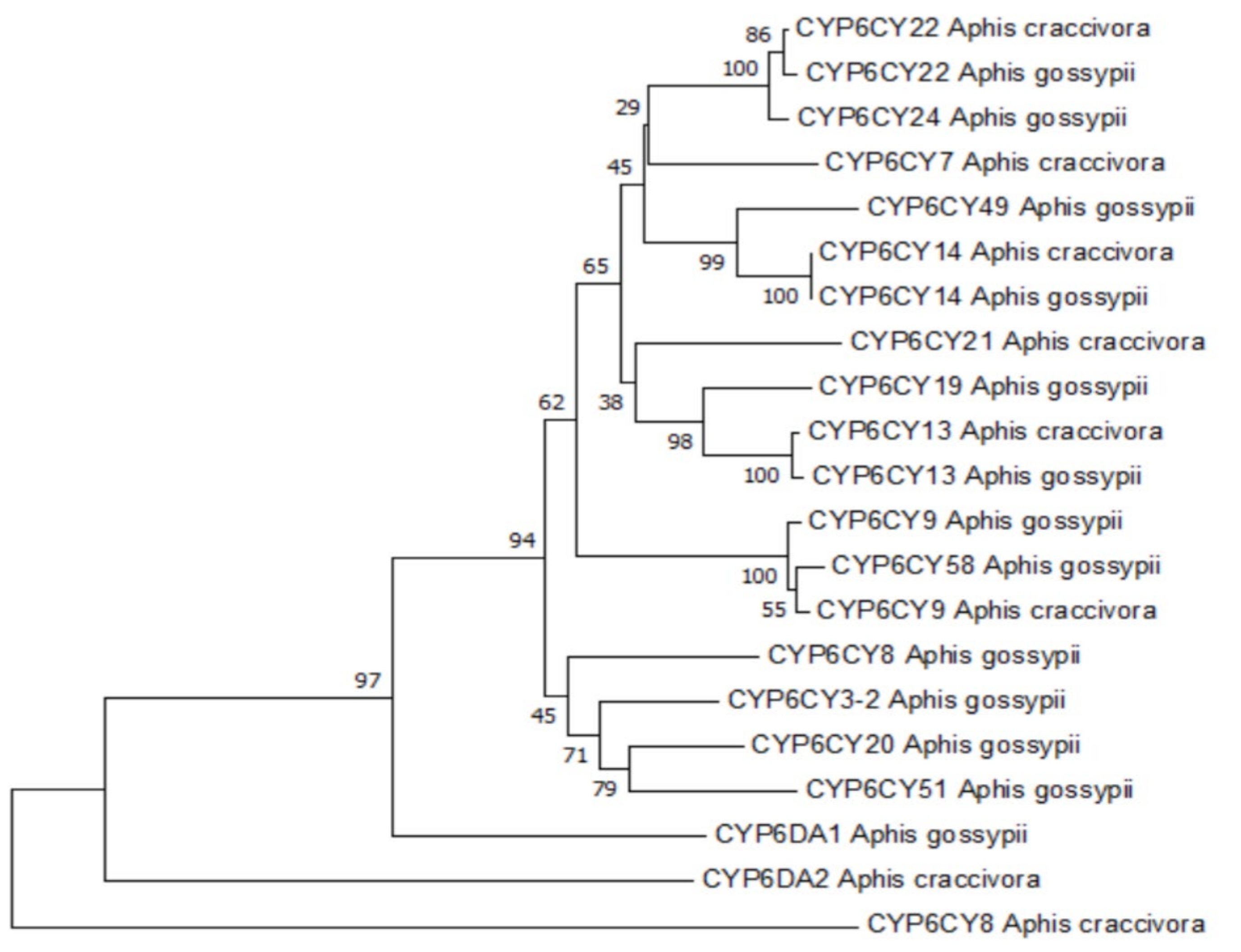
多序列比对

模式生物果蝇P450家族部分基因

数据来源:Uniprot

系统发育分析

棉蚜P450家族基因
、花生蚜P450家族基因



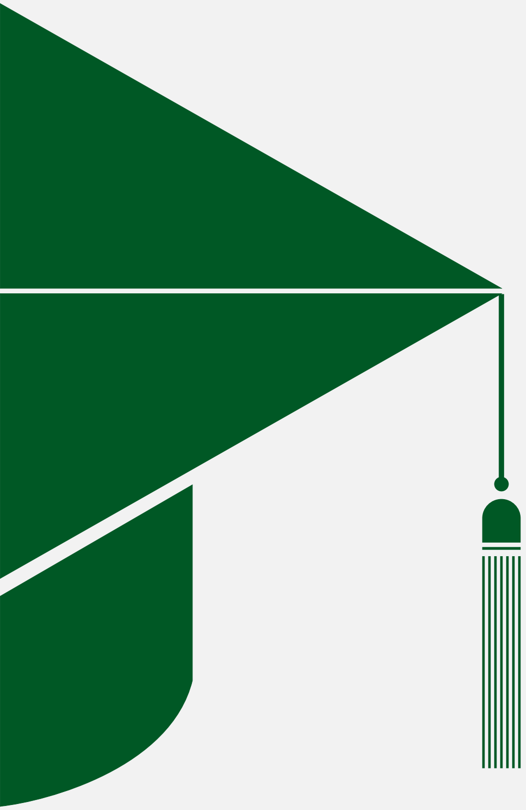
数据来源:MEGA7

总结

- 了解CYP6CY13蛋白的基本信息，包括理化性质、二级结构、三级结构等；
- 了解也知道了棉蚜与花生蚜两个相关物种的基因很相似，可以参考对黑豆蚜的研究来为棉蚜的研究提供大致思路；
- 接下来的计划是深入研究该蛋白，在基因水平、蛋白质水平、代谢水平、转录水平方面对该蛋白如何参与棉蚜对氟啶虫胺腈的抗性产生过程进行深入研究。

中国农业科学院

CHINESE ACADEMY OF AGRICULTURAL SCIENCES



请老师同学批评指正