Functional analysis and protein structure prediction of gene 6-SFT in Triticum aestivum

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Content

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Background

2. Fructan
one of the ways for plant to resist stress
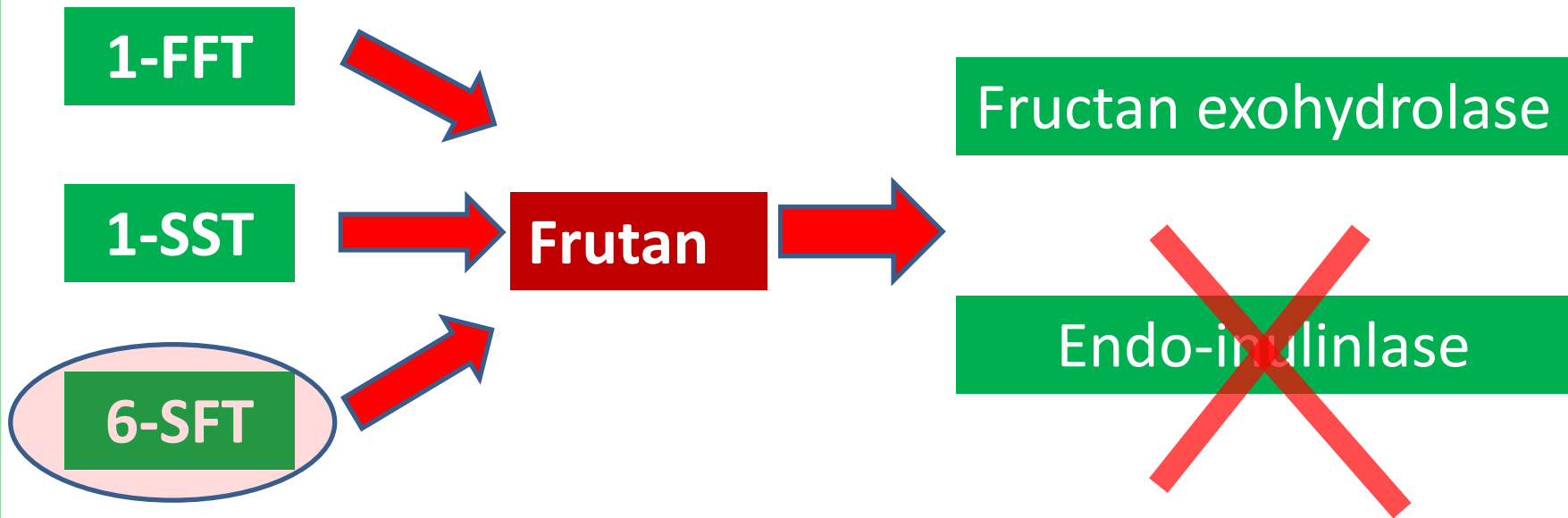
fructan → Tolerance Cold and Drought

fructan → Tolerance Salt Waterloge and Poor

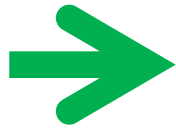fructan → Tolerance Metal poisoning in soil

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3.Enzymes related to Fructan metabolic

1-FFT

1-SST → Frutan → Fructan exohydrolase

6-SFT

Endo-inulinlase
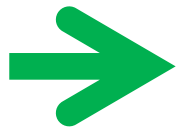
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4.Study progress

细菌 ➡️ 大肠杆菌　欧文式菌　链球菌

真菌 ➡️ 曲霉菌
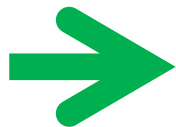
植物 ➡️ 大麦　洋蓟　富贵草

Structure and function of 6-SFT

1.Get the protein and gene sequence

UniProt › UniProtKB → protein

↓

NCBI — National Center for Biotechnology Information → { GENE, CDS, promoter }

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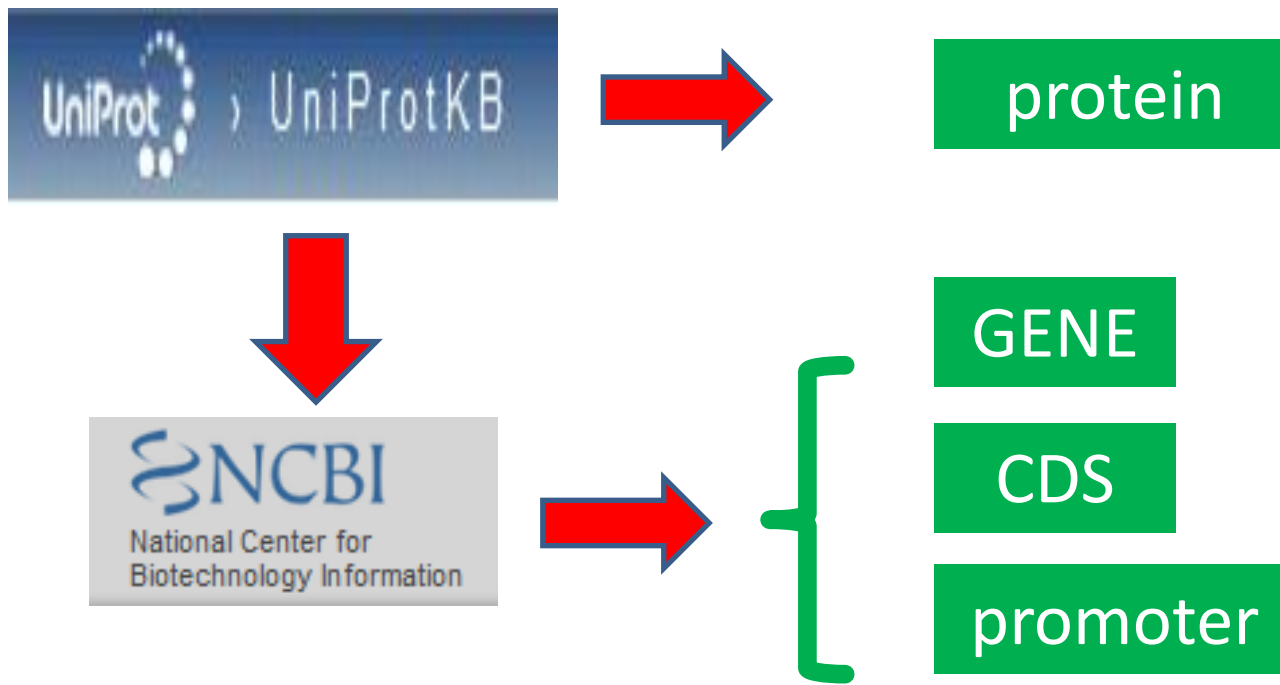
2.The structure of 6-SFT

DOTTUP

Displays a wordmatch dotplot of two sequences
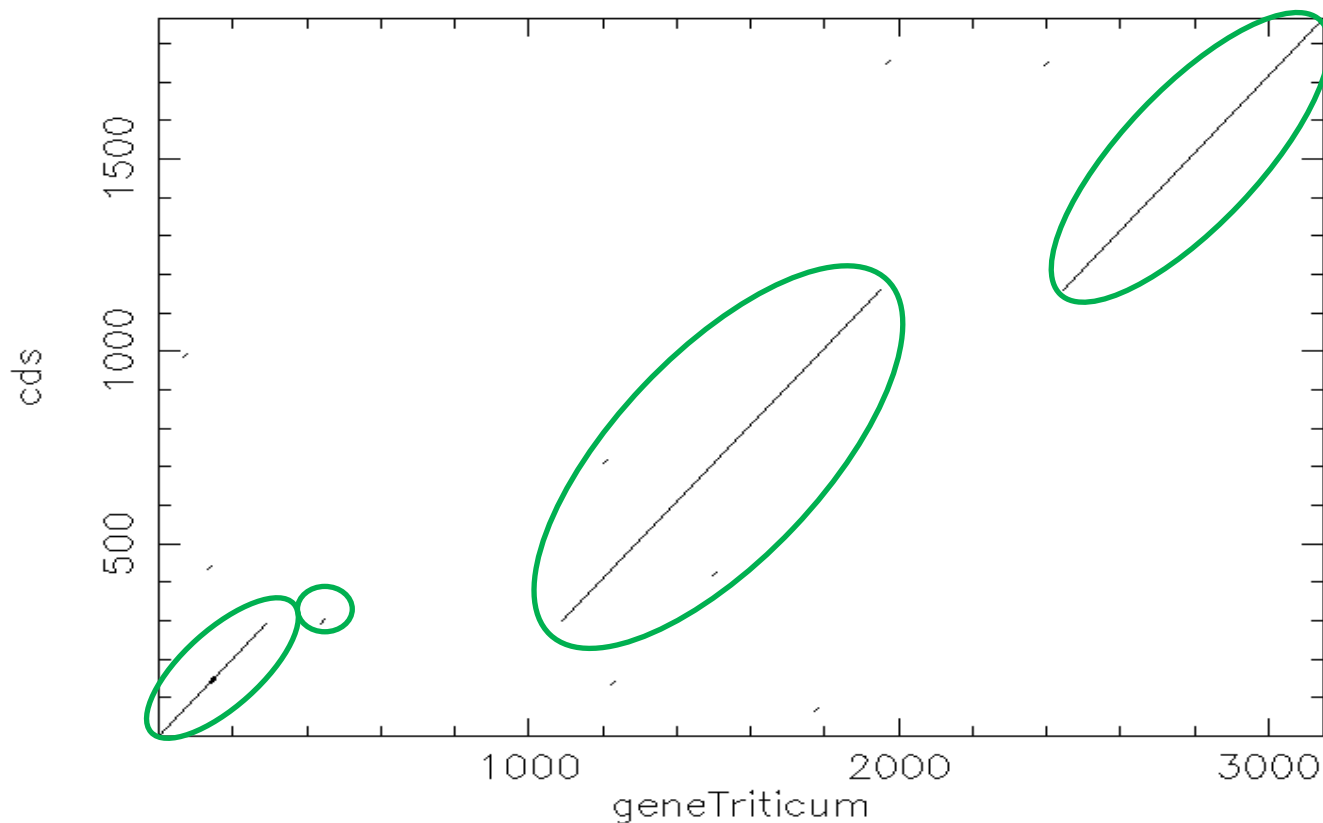
3.Prediction of promoter

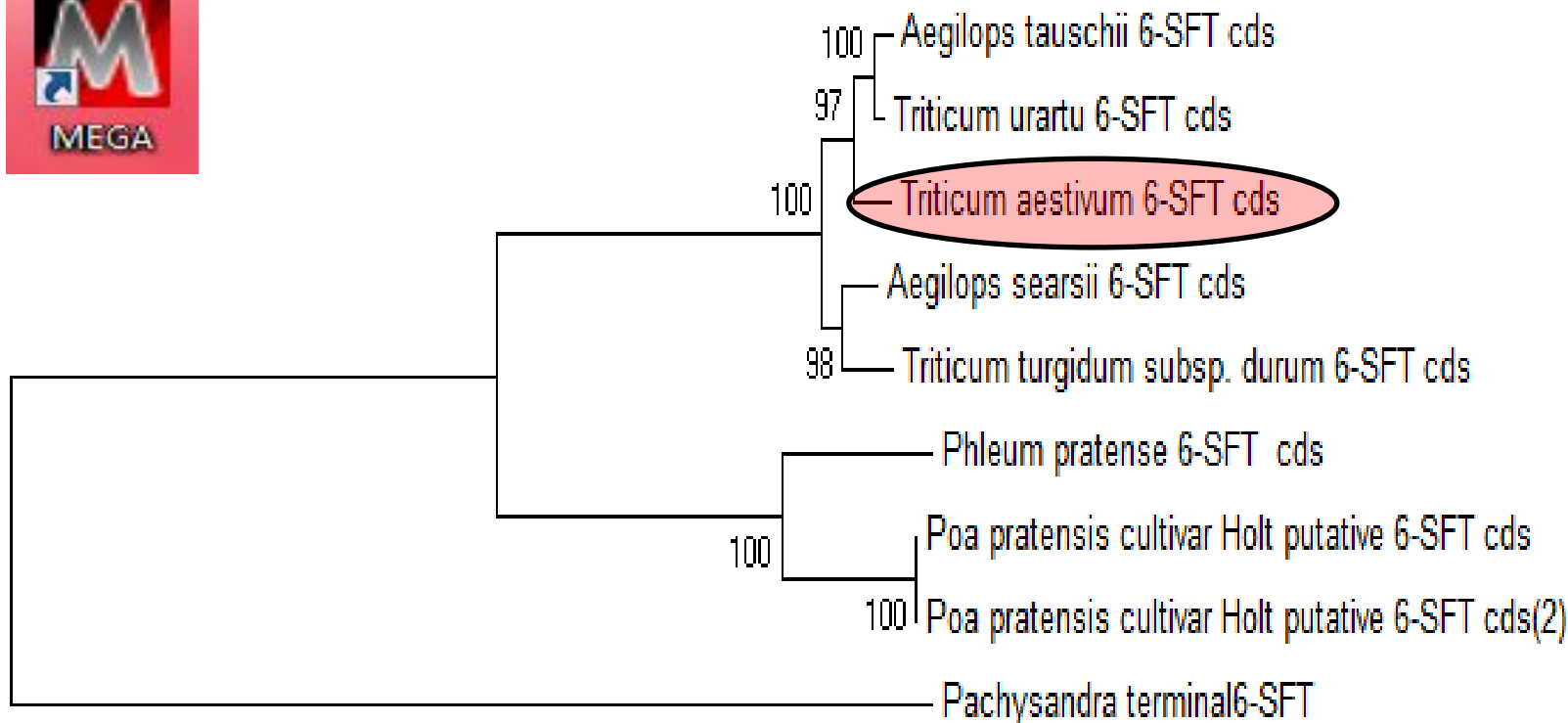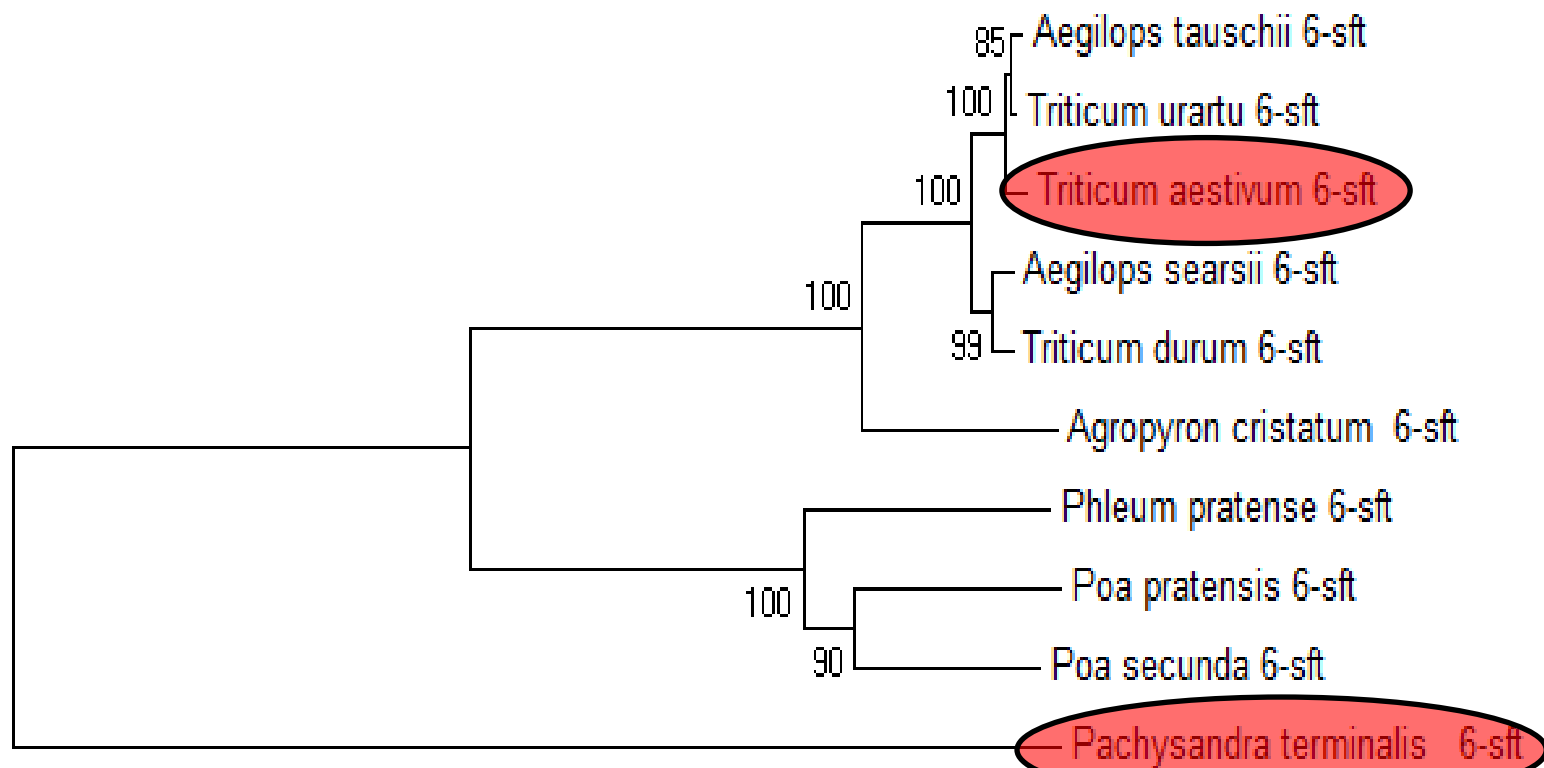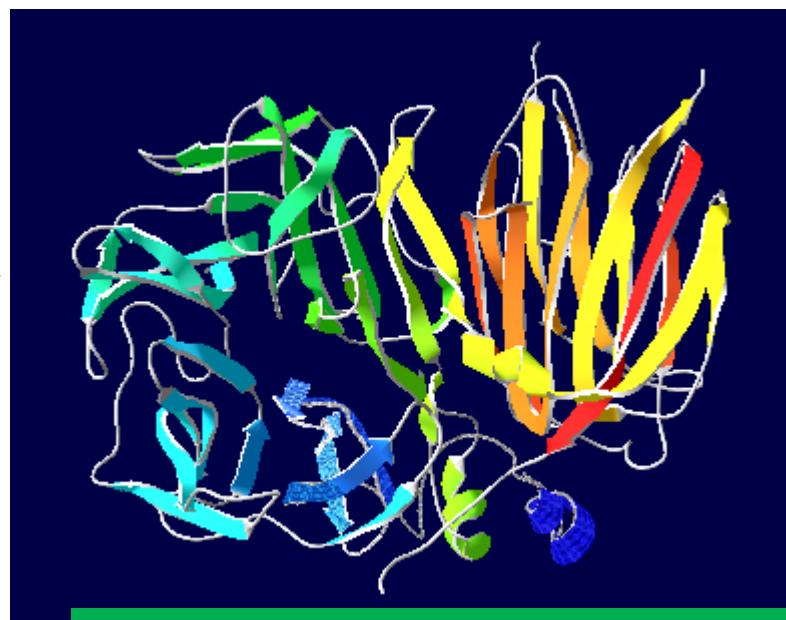| element	function
TATA-box	core promoter element around -30 of transcription start
CAAT-box	common cis-acting element in promoter and enhancer regions
MYB	cis-acting regulatory element involved in drought-inducibility
LTR	cis-acting element involved in low-temperature responsiveness
GARE	gibberellin-responsive element
ABRE	cis-acting element involved in the abscisic acid responsiveness
Circadian	cis-acting regulatory element involved in circadian control

4.Function of the gene

pomoter

CDS

ATG

	circadian		MYB		GARE
	CAAT		LTR		TATA-box

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cds

gene

1-FFT

1-SST

6-SFT

6. Phylogenetic Tree

Aegilops tauschii 6-sft
85
100
Triticum urartu 6-sft
100
Triticum aestivum 6-sft
Aegilops searsii 6-sft
100
99
Triticum durum 6-sft
Agropyron cristatum 6-sft
Phleum pratense 6-sft
Poa pratensis 6-sft
100
90
Poa secunda 6-sft
Pachysandra terminalis   6-sft

0.02

protein

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Protein structure

1.Chose the model

Pachysandra terminal

2.Protein sequence alignment

```
#=======================================
#
# Aligned_sequences: 2
# 1: 6-sft
# 2: E3PQS3_9MAGN
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 686
# Identity:      311/686
# Similarity:    425/686    (62.0%)
# Gaps:           97/686
#
#
#
#=======================================
```

NEEDLE

Needleman-Wunsch global alignment of two sequences

Pachysandra terminalis

VS

Triticum aestivum

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3.Resault and compare

SWISS-MODEL
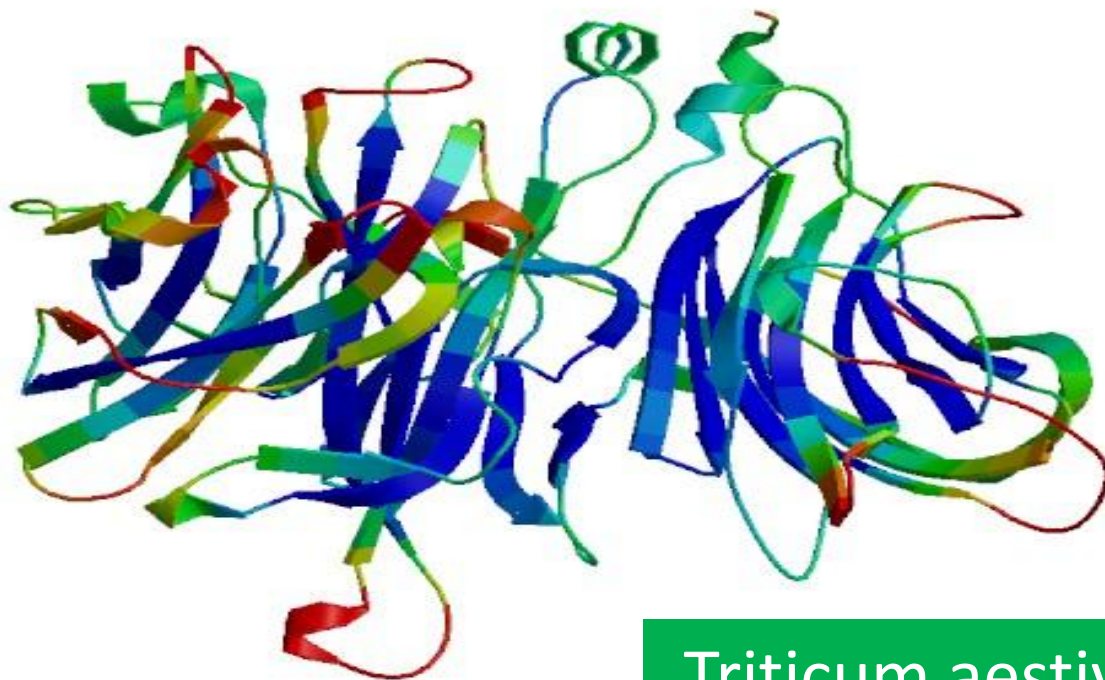
Triticum aestivum

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Magic fit

model

Ta

no

yes
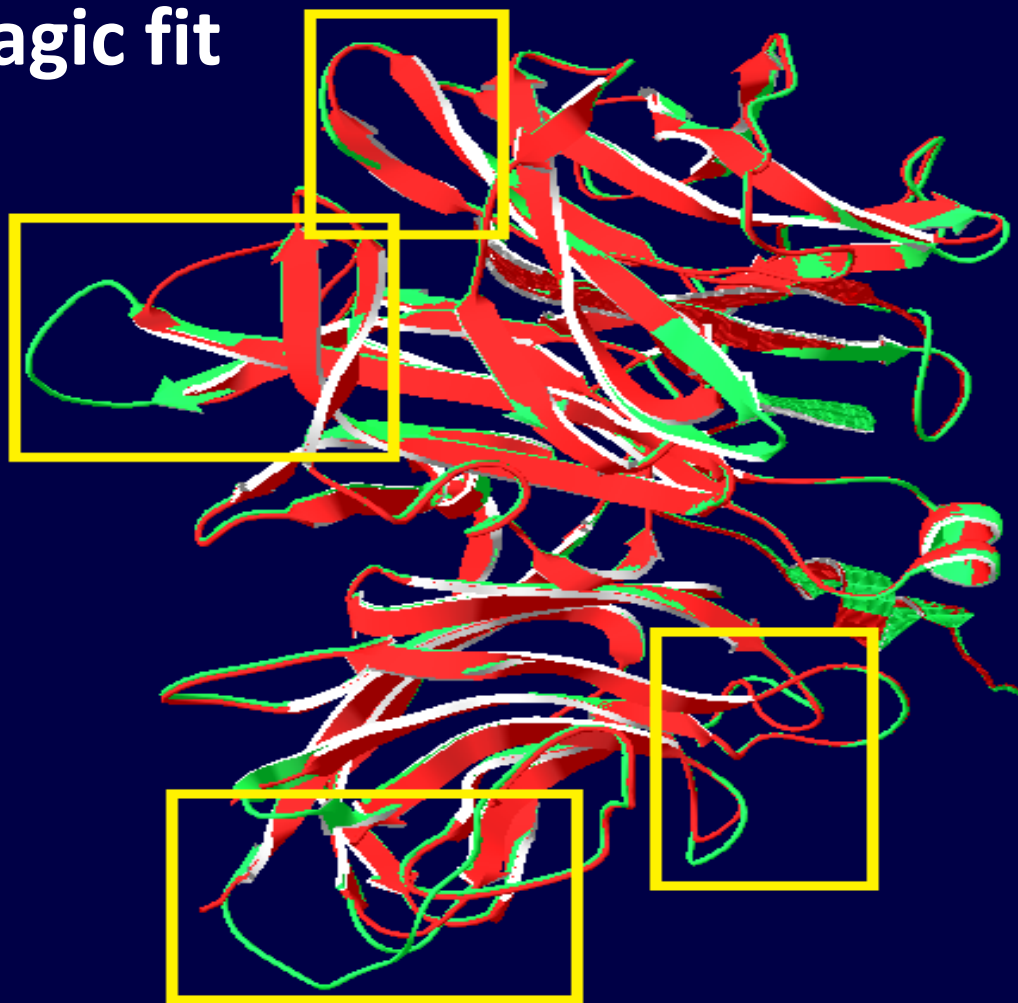
CHINESE ACADEMY OF AGRICULTURAL SCIENCES
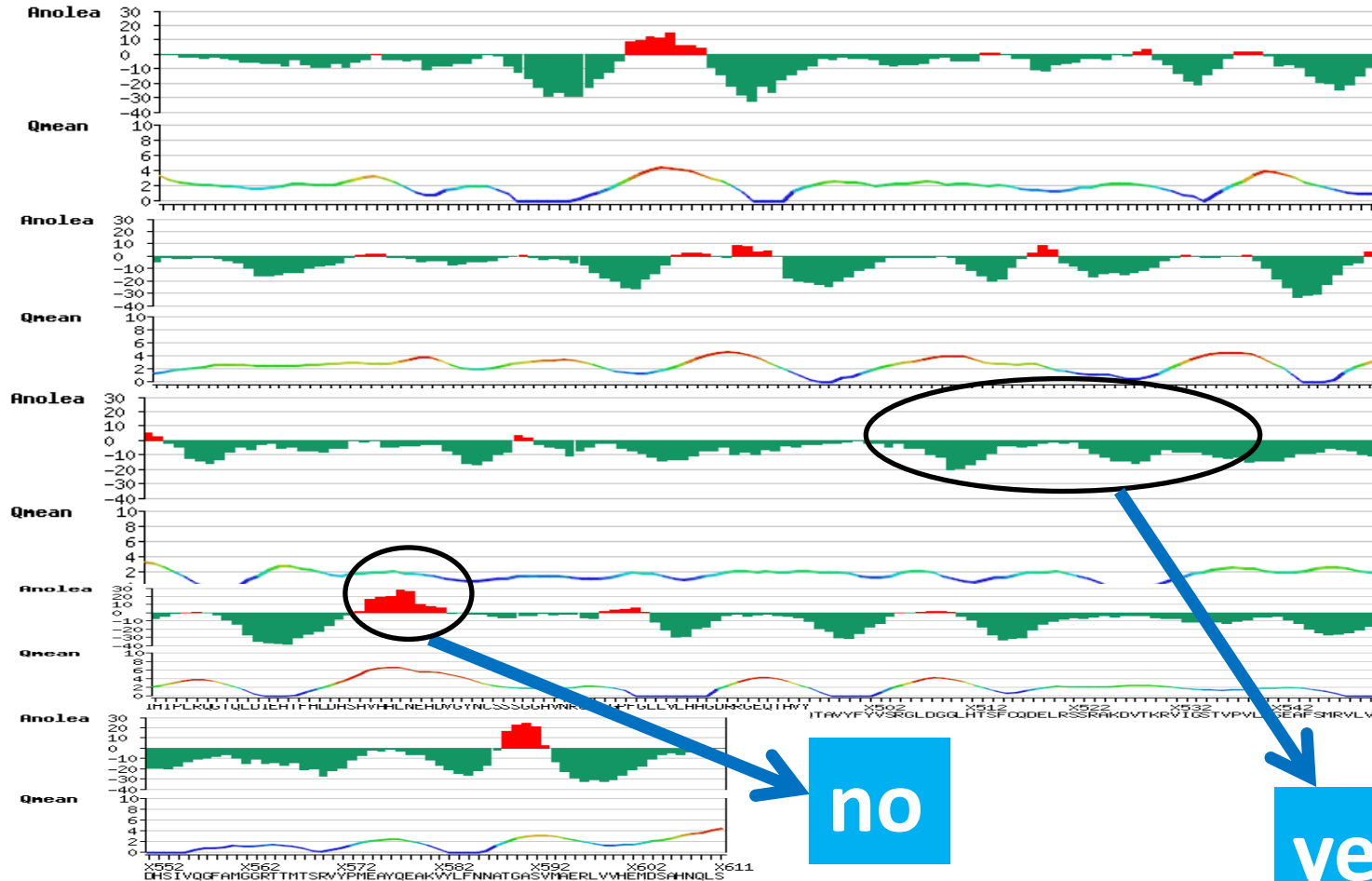
5. Analysis of TranMen

Tmap
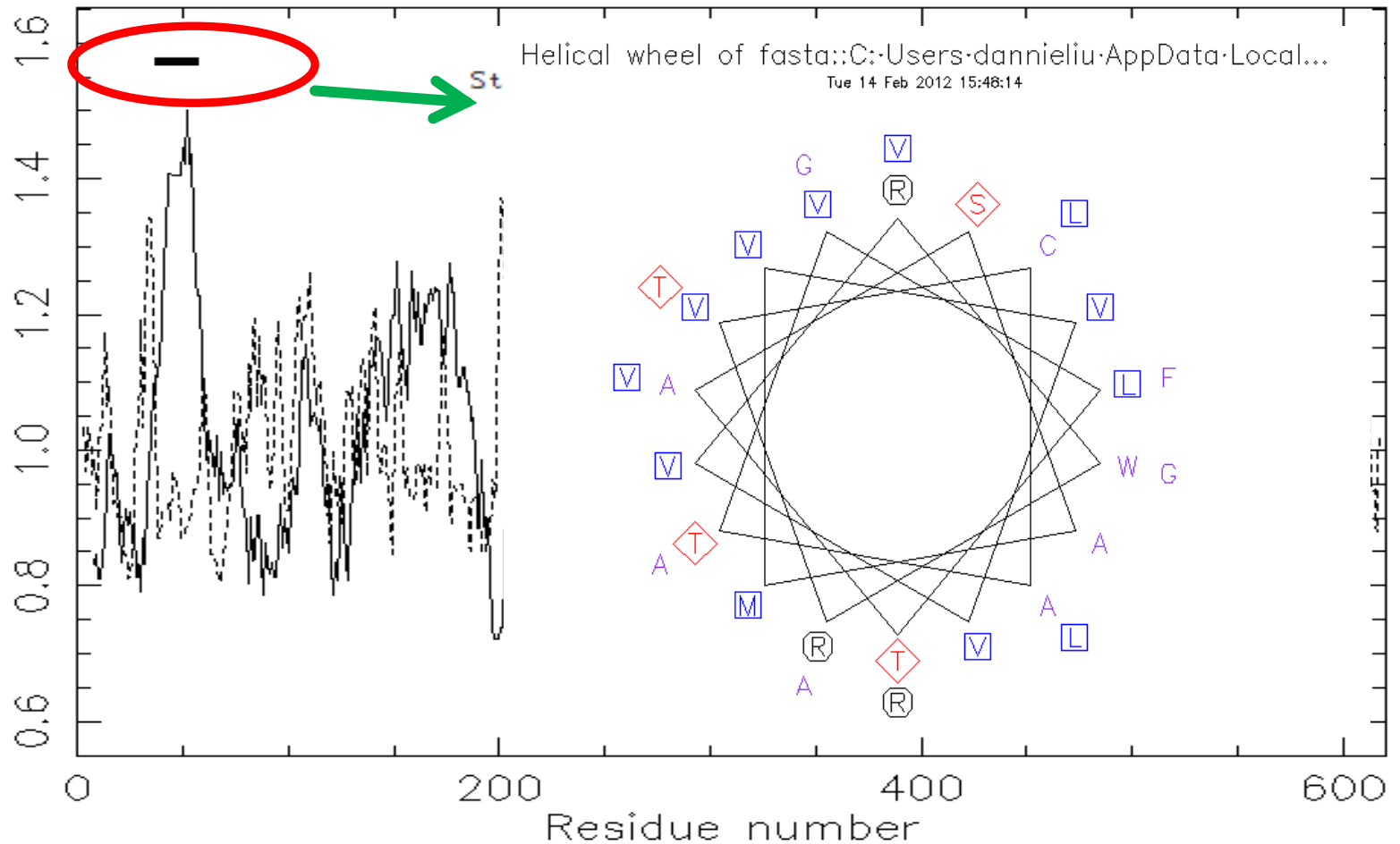
6. How does the enzyme works

membrane

outside

Inside
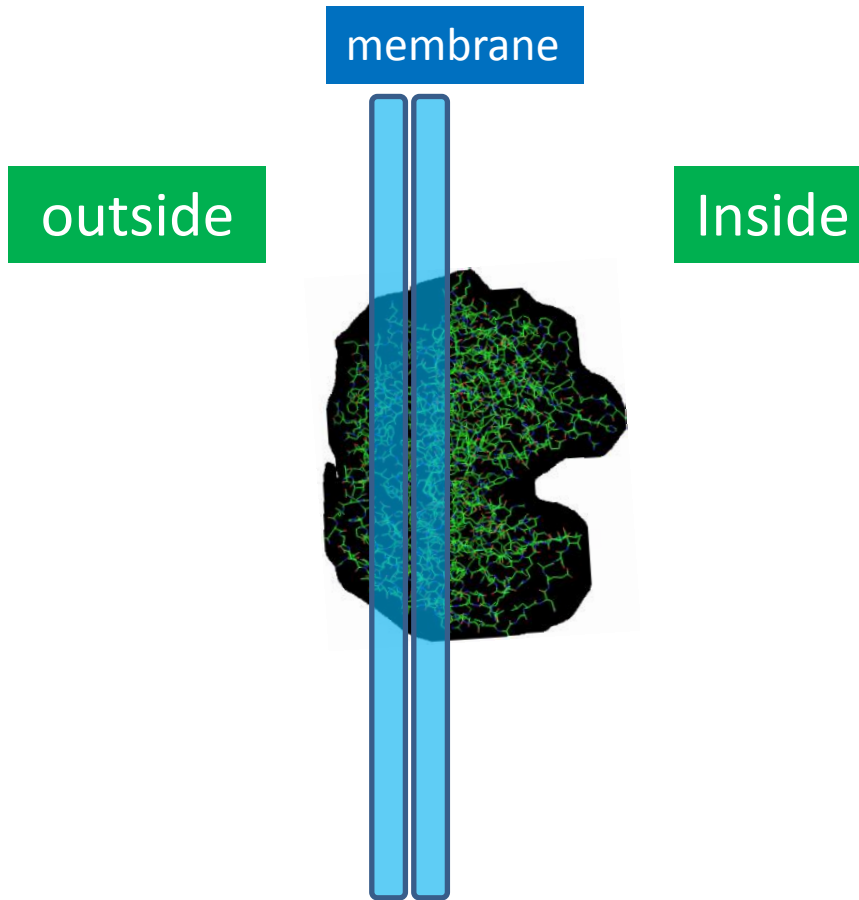
Summary

Through the analysis of the 6-SFT we can predict the function the gene

According to alignment we get the information about 6-SFT in other species

The prediction of the protein's structure can help us to know how it works

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Thanks all students

Thanks
for your
attention!

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