

# 走进庆网蛱蝶 ( *Melitaea cinxia* )

——Tpi基因与自然选择



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# *Melitaea cinxia* ( 庆网蛱蝶 )

*Melitaea cinxia* is a sun-loving butterfly, being active only in bright sunshine. Like most fritillaries, it is difficult to follow as it flies with a series of rapid wing beats followed by a short glide. Both sexes are avid nectar feeders, Thrift and Bird's-foot Trefoil being particular favourites. The adults roost, often communally, on flower heads of various grasses.

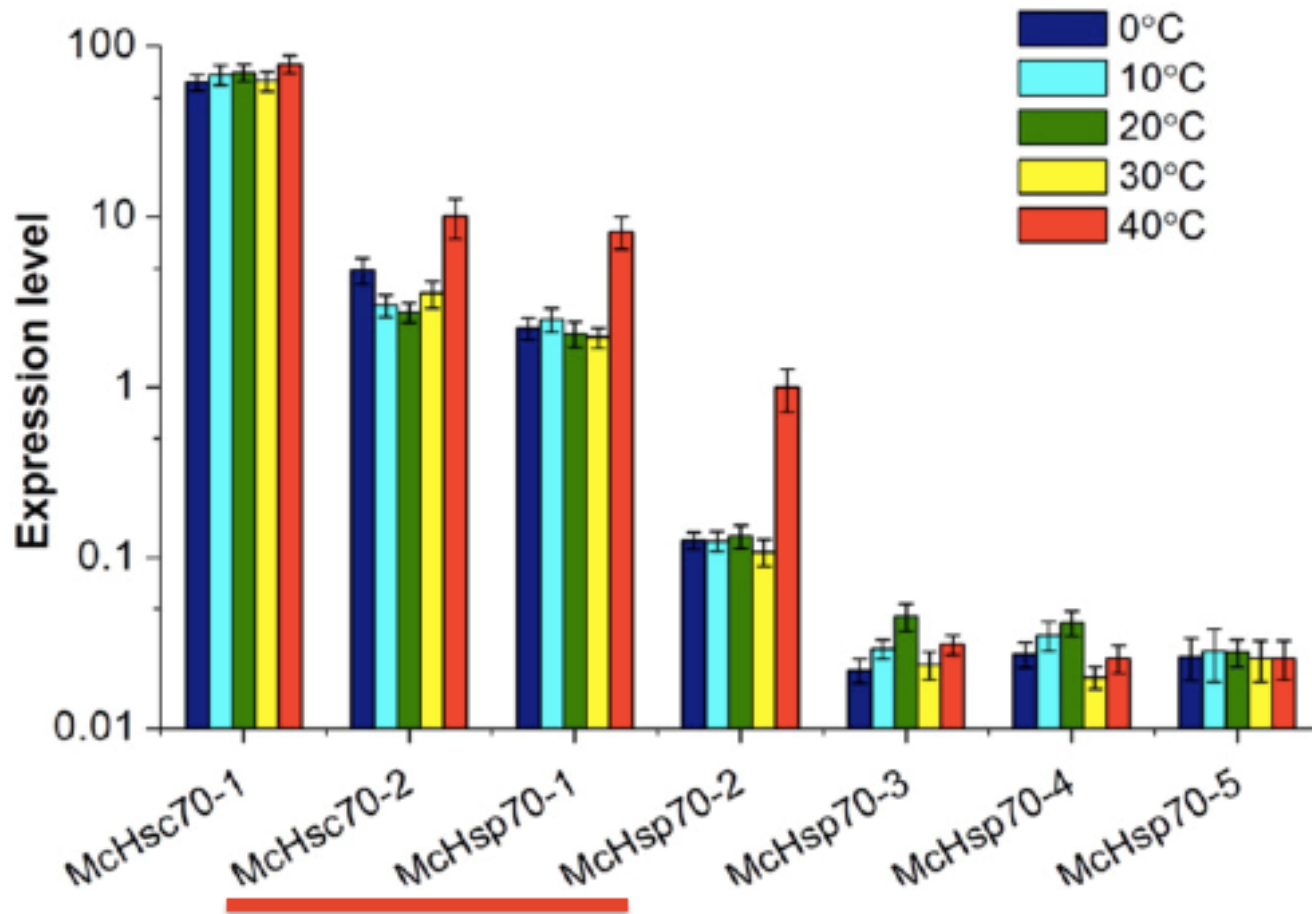


# 出没时间

	Jan				Feb				Mar				Apr				May				Jun				Jul				Aug				Sep				Oct				Nov				Dec							
	1	2	3	4	1	2	3	4	1	2	3	4	1	2	3	4	1	2	3	4	1	2	3	4	1	2	3	4	1	2	3	4	1	2	3	4	1	2	3	4	1	2	3	4	1	2	3	4				
Ovun																					●	●	●	●	●	●																										
Larva	●	●	●	●	●	●	●	●	●	●	●	●	●	●											●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●				
Pupa													●	●	●	●	●	●																																		
Inago																	●	●	●	●	●	●	●	●																												

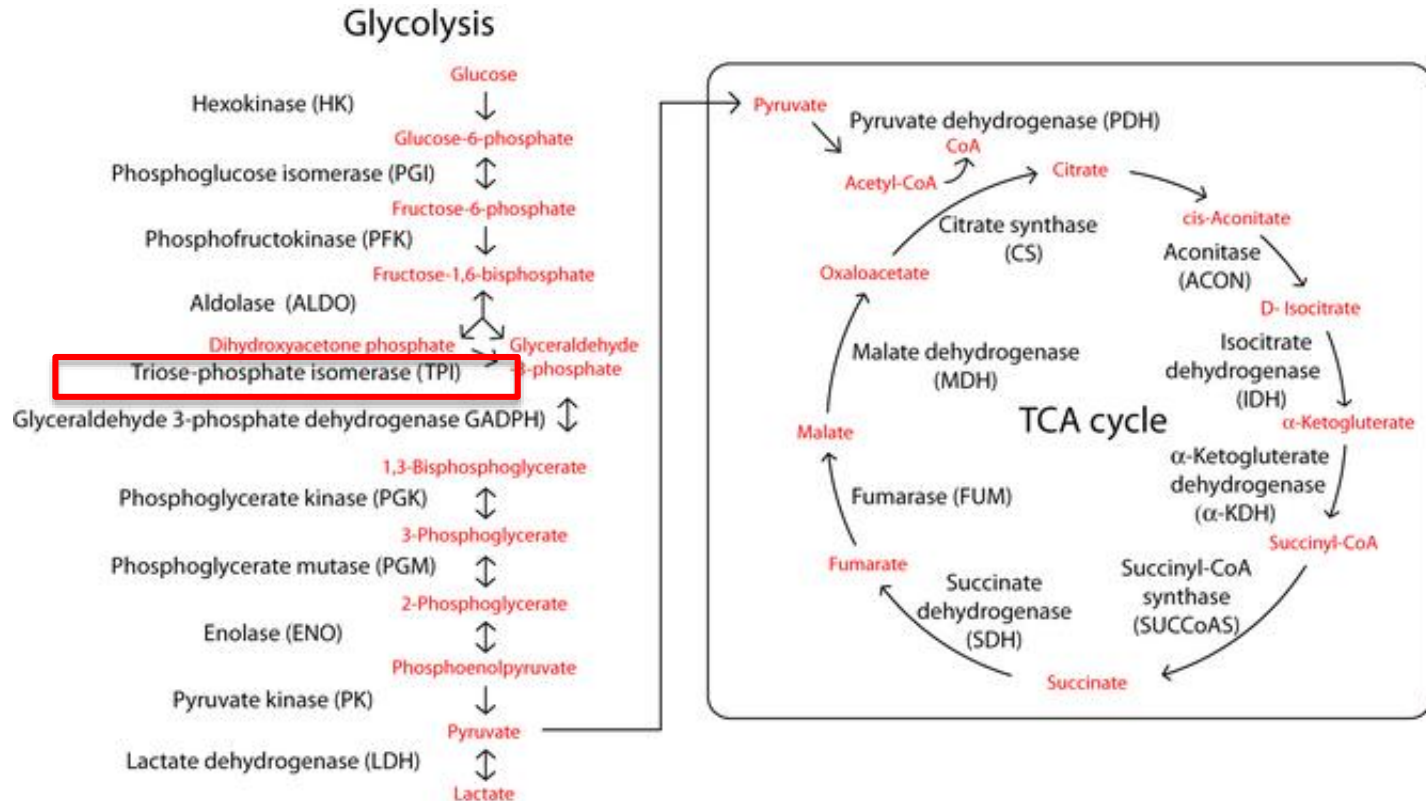
Adults emerge in the second half of May, reaching a peak at the end of the month and at the start of June.

There is typically one generation each year but in good years, when there has been a particularly-early emergence that starts as early as the end of April, there may be a partial second brood that emerges in August.



Expression level of hsp70 genes after exposure to five temperatures for 2 h.

# Nature's inordinate fondness for metabolic enzymes: why metabolic enzyme loci are so frequently targets of selection



# SNP calling

CHROM	POS	REF	ALT
MCINX00436	91854-		
6-PA	isomerase	96716	
scaffold1884	92418	G	A
scaffold1884	92735	T	G
scaffold1884	92755	T	A
scaffold1884	93396	G	A

## GENSCAN Output

View gene model output: [PS](#) | [PDF](#)

GENSCAN 1.0 Date run: 27-Jun-115 Time: 02:05:18

Sequence /tmp/06\_27\_15-02:05:17.fasta : 4863 bp : 29.61% C+G : Isochore 1 ( 0 - 43 C+G%)

Parameter matrix: HumanIso.smat

Predicted genes/exons:

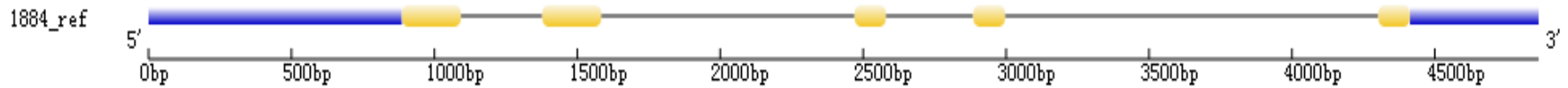
Gn.Ex Type S .Begin ...End .Len Fr Ph I/Ac Do/T CodRg P.... Tscr..

```

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1.06 PlyA - 318 313 6 1.05
1.05 Term - 1093 887 207 1 0 42 38 290 0.993 15.76
1.04 Intr - 1584 1378 207 0 0 61 30 206 0.998 10.45
1.03 Intr - 2580 2471 110 1 2 20 93 154 0.682 8.18
1.02 Intr - 2997 2886 112 0 1 52 75 42 0.648 -1.67
1.01 Init - 4413 4303 111 0 0 71 83 77 0.439 5.76
  
```

# GSDS<sub>2.0</sub>

# Gene Structure Display Server



Legend:

CDS upstream/ downstream Intron

## Intron

Color Shape  Line width  px Intron rescale  Display intron phase

## CDS

Color Shape  Filled  Height  px

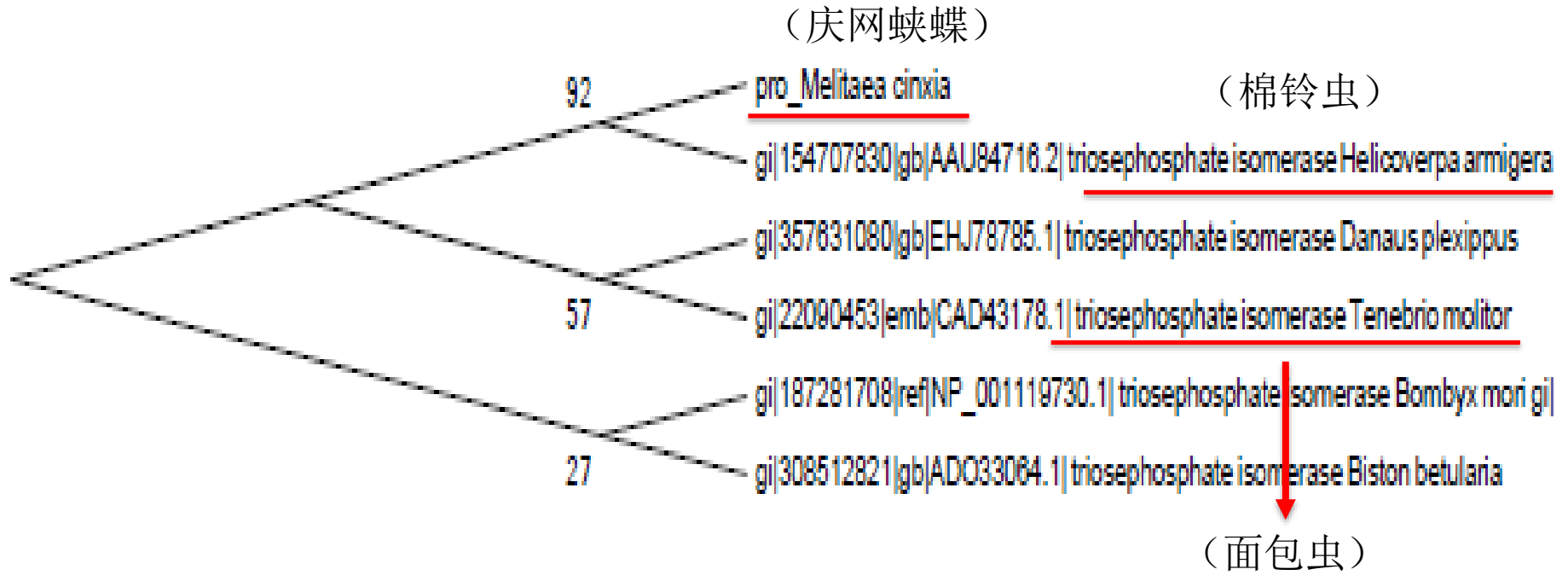
## UTR

Color Shape  Filled  Height  px

# Secondary Structure Prediction and Comparison



# Phylogeny Tree



# Amino acid comparison

Range 1: 1 to 248 [Graphics](#)

▼ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps
461 bits(1187)	3e-170	Compositional matrix adjust.	224/248(90%)	236/248(95%)	0/248(0%)
Query 1	MGRKFFVGGNWKMNQDKKQVTEIVETLKKGPLDPNVEVVGVPPIYLAYVQSIVPGTISV				60
Sbjct 1	MGRKF+VGGNWKMNQDK Q+ EIV LKKGPLDPN EVVIGVPPIYLAYV+SIVP TI V				60
Query 61	AAQNCWKVAKGAFTGEISPAMIKDIGANWVILGHSERRTIFGEKDELVAEKVAHALENGL				120
Sbjct 61	AAQNCWKV KGAFTGEISPAMIKD+GANWVILGHSERR IFGEKDELVAEKVAHALE+GL				120
Query 121	KVIACIGETLEEREAGKTEEVVFRQTKALLPAIGNNWANVVLAYEPVWAI GTGKTASPQQ				180
Sbjct 121	KVIACIGETLEEREAGKTEEVVFRQTKALLPAIGNNWANVVLAYEPVWAI GTGKTA+PQQ				180
Query 181	AQDVHASLRNWLSANASPDVAASVRIQYGGSVTGANAKELASCPDIDGFLVGGASLKPEF				240
Sbjct 181	AQ+VHASLRNWLS+NASPDVA +VRIQYGGSVT ANAKELA+ PDIDGFLVGGASLKPEF				240
Query 241	VDIVNATQ	248			
Sbjct 241	VEIVNATK	248			

Amino acids differences<sup>↓</sup>

K18N	T26N	S60G	A203Q <sup>↓</sup>
T21N	V36A	A70D	G215A <sup>↓</sup>
E25N	G56D	S60G <sup>↓</sup>	

# Secondary Structure

- Secondary structure prediction

**Jpred 4**  
Incorporating Jnet

A Protein Secondary Structure Prediction Server

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**Phyre<sup>2</sup>**

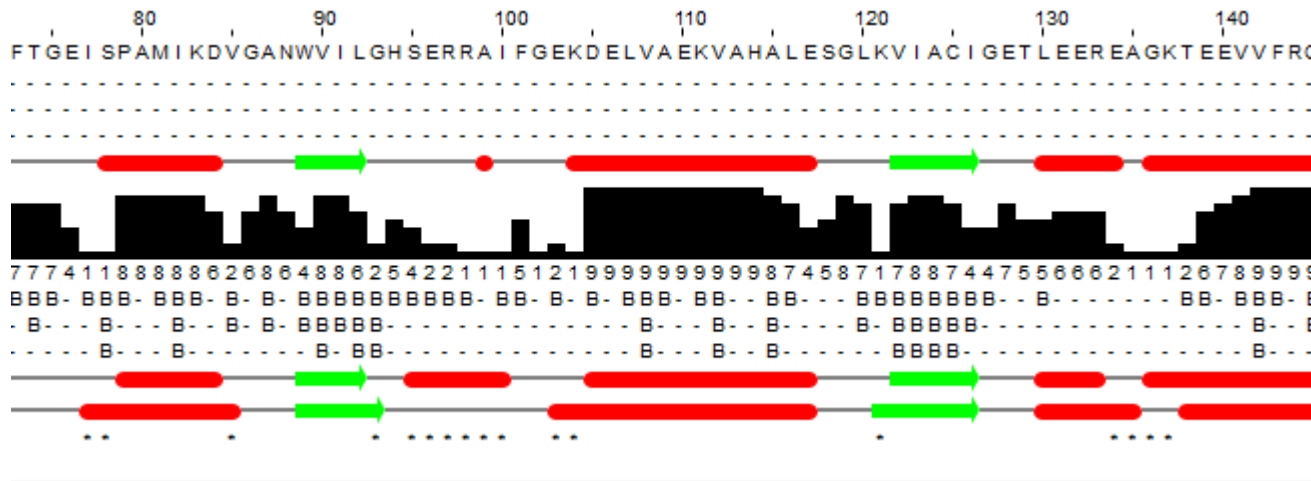
Protein Homology/analogy Recognition Engine V 2.0

UCL Department Of Computer Science

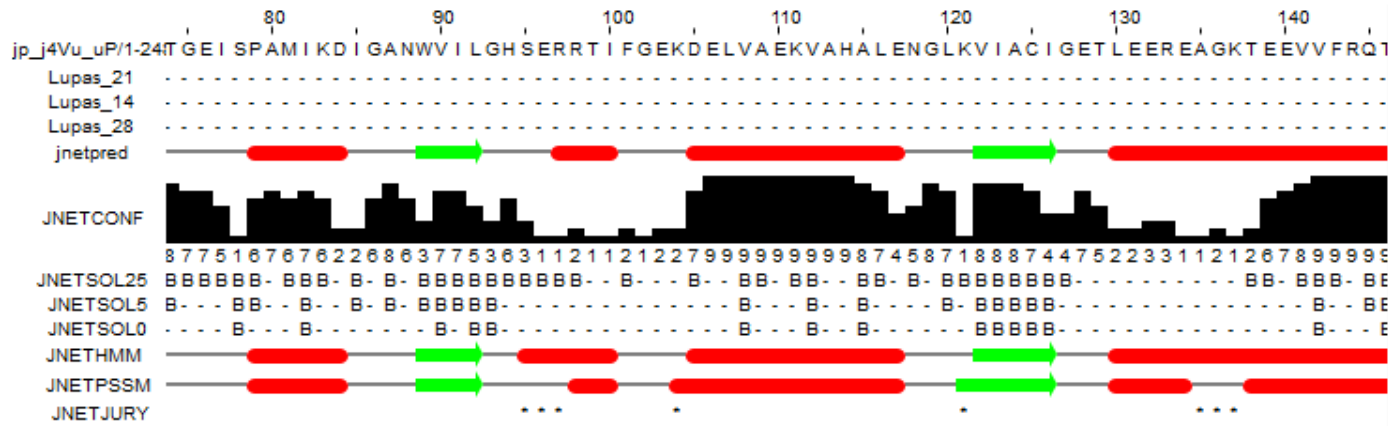
Bioinformatics Group



- Prediction from Jpred
- *Melitaea cinxia*

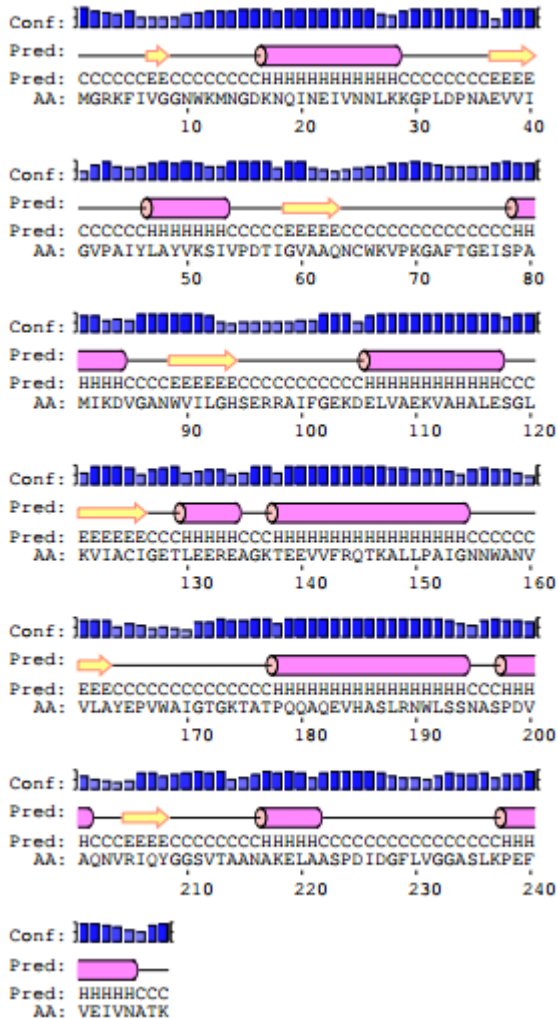


- *Helicoverpa Armigera*

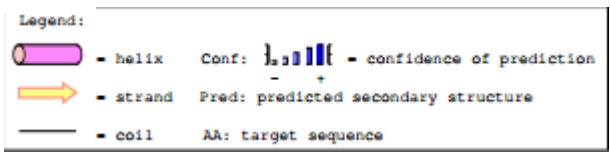
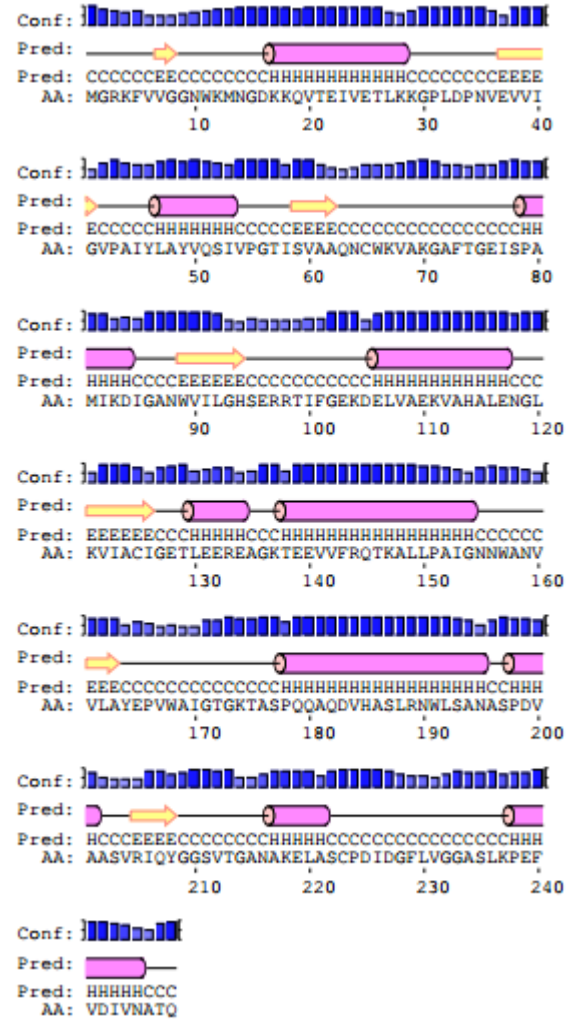


# • Prediction from Psipred

## • *Melitaea cinxia*



## • *Helicoverpa Armigera*

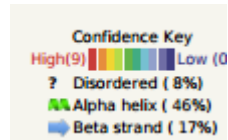
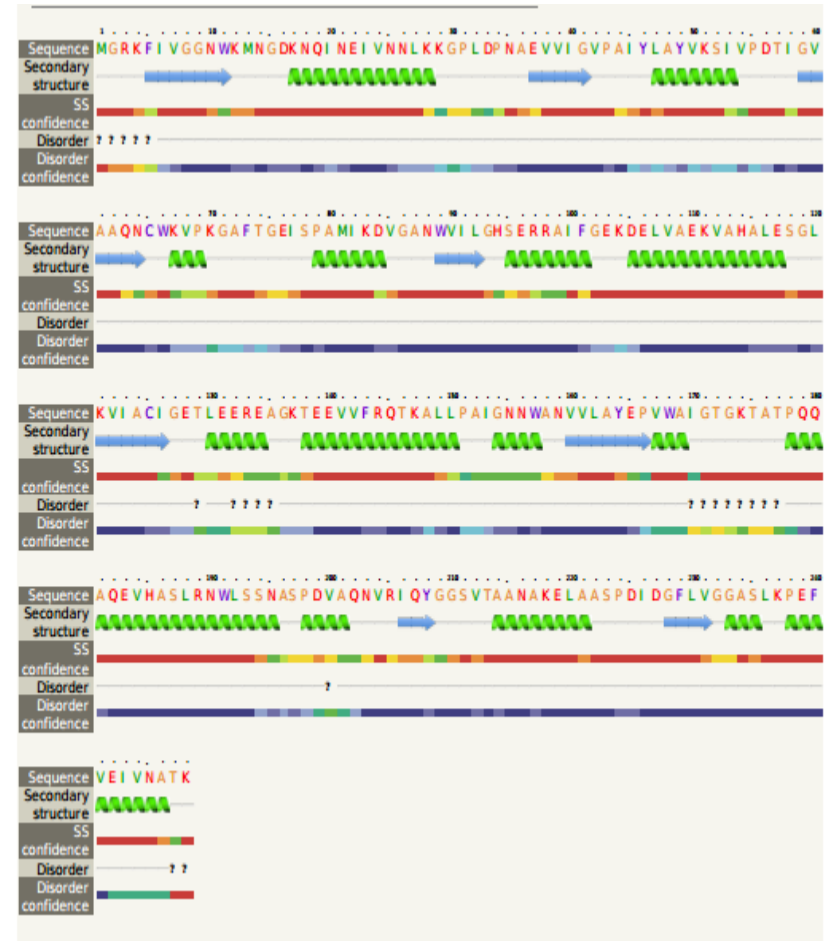


- Prediction from Phyre2

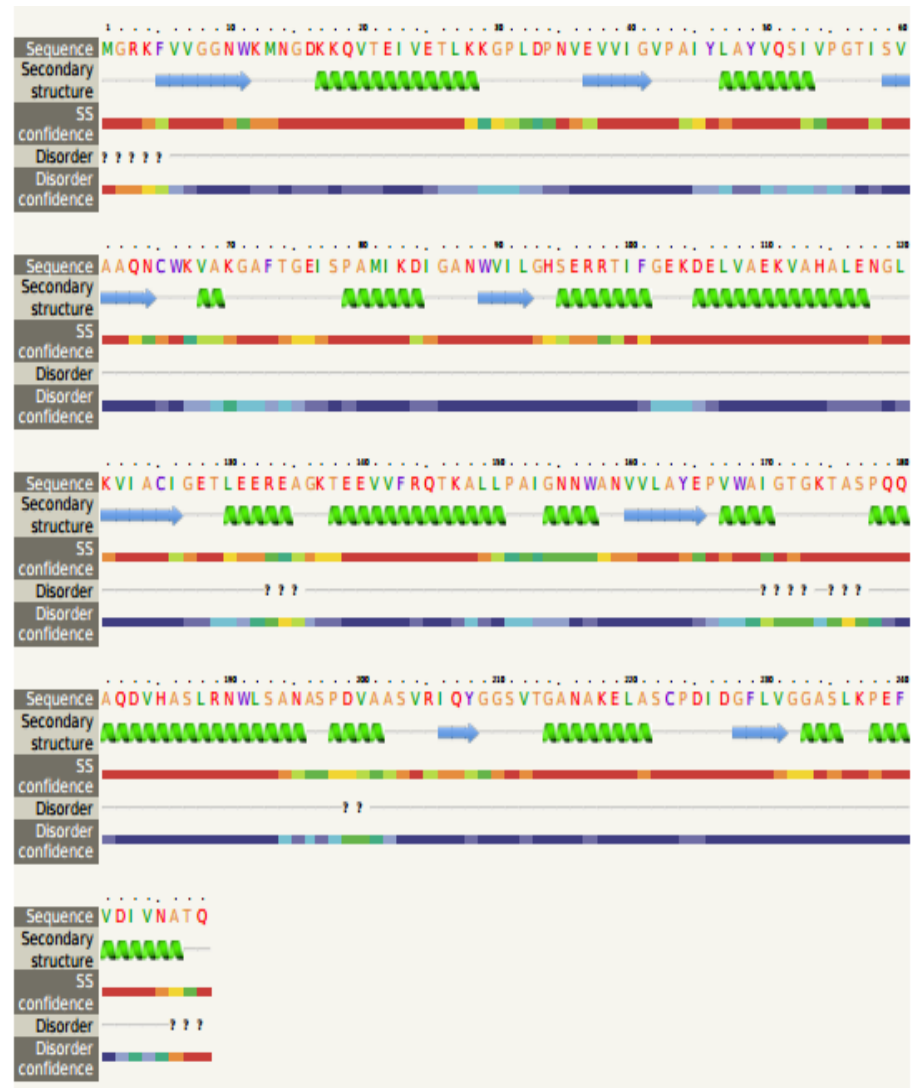
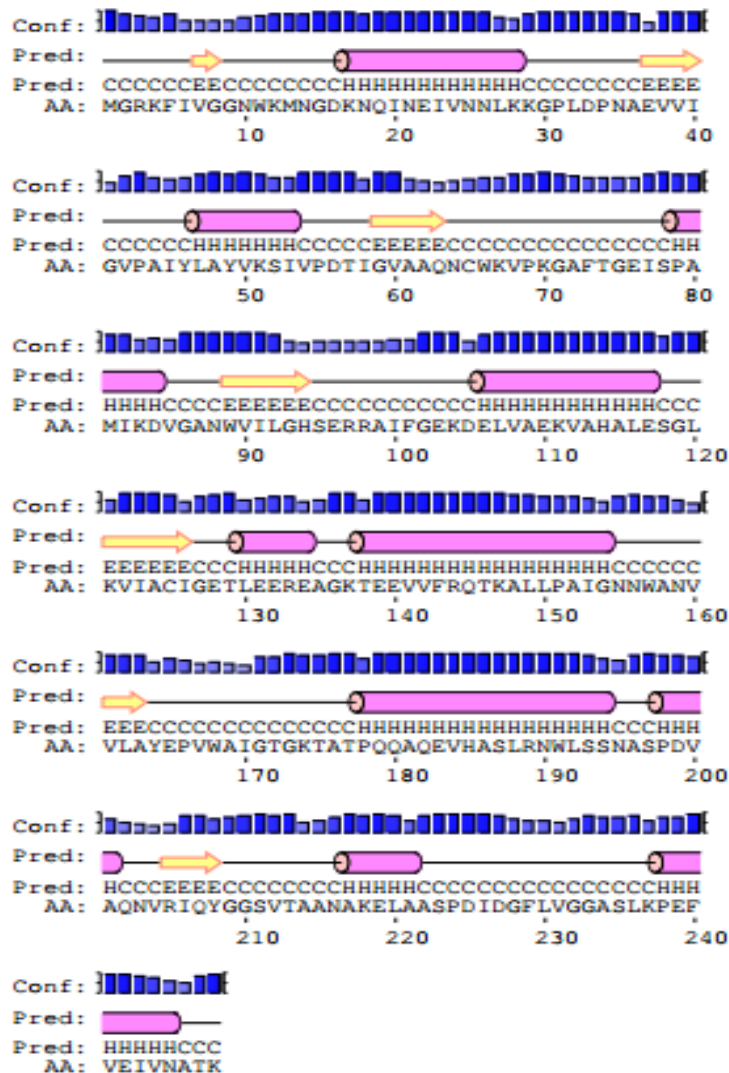
- *Melitaea cinxia*



- *Helicoverpa Armigera*



# • Prediction differences of Psipred and Phyre2





# BIOZENTRUM

Universität Basel  
The Center for Molecular Life Sciences

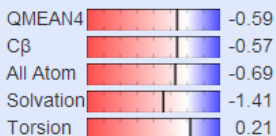
# SWISS-MODEL



Model 01

### Oligo-State

MONOMER



### Ligands

None



### GMQE

0.94

### QMEAN4

-0.59



### Template

Seq Identity

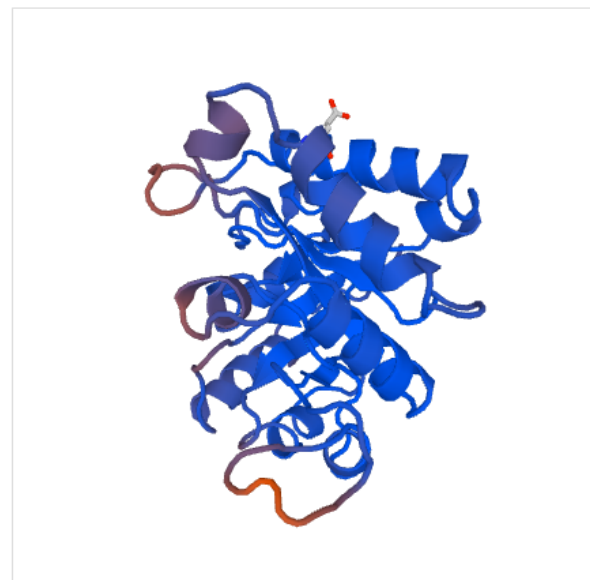
Coverage

Description

template_upload.1.A	77.96%		Polypeptide
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### Model-Template Alignment

Model_01	MG	<b>RK</b> FIVGGNWKMGDKNQINEIVNNLKKGPLDPNAEVVIGVPAIYLAYVKSIVPDTIGVAAQNC	65
template_upload.1.A	--	RKFVVGGNWKMGDKRQINEIIGFLKSGPLNQDTEVVVGVPAIYLELVRTCVPASIGVAAQNC	64
Model_01		<b>WKVPKGAFTGE</b> ISPAMIKDVGANWVILGHSERRAIFGEKDELVAEKVAHALESGLKVIACIGETL	130
template_upload.1.A		YKVPKGAFTGEISPAMIKDVGADWVILGHSERRQIFGESDELIAEKVCHALESGLKVIACIGETL	129
Model_01		<b>EERE</b> AGKTEEVVFRQTKALLPAIGNNWANVVLAYEPVWAIGTGKTATPQQAQEVHASLRNWLSSN	195
template_upload.1.A		EEREAGKTEEVVFRQTKAIAAKV-NDWSNVVIAIYEPVWAIIGTGKTATPQQAQDVHKALRQWICEN	193
Model_01		<b>ASPDVAQNVRIQY</b> GGSVTAANAKELAAASPDIDGFLVGGASLKPEFVEIVNATK	248
template_upload.1.A		IDAKVGNIRIQYGGSVTAANCKELASQPDIDGFLVGGASLKPEFVDIINARQ	246

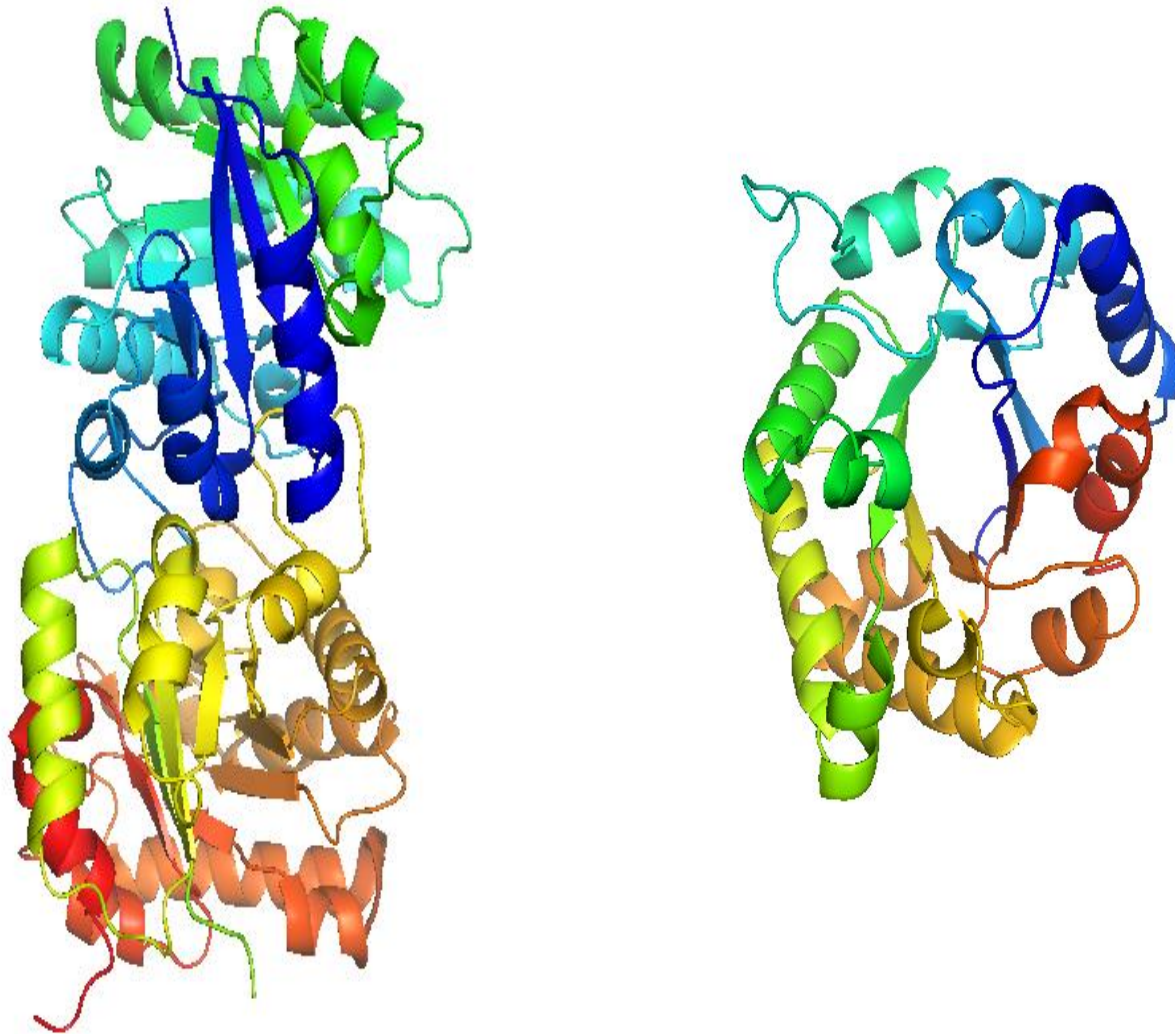


View

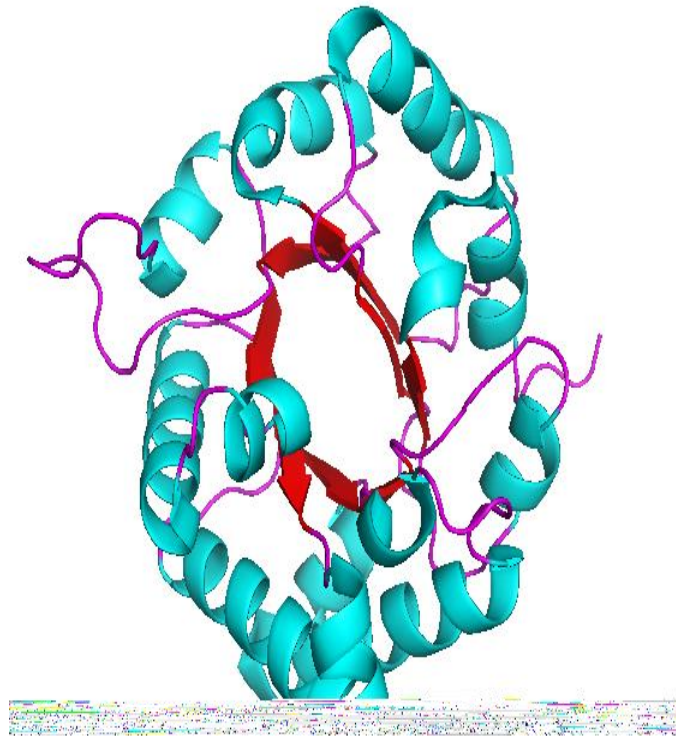




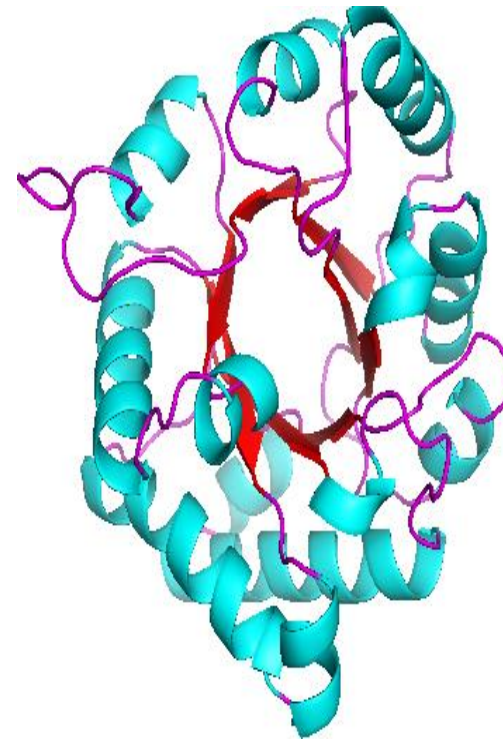
# Structure of Tpi of Tenebrio molitor



# Tpi subunit comparison

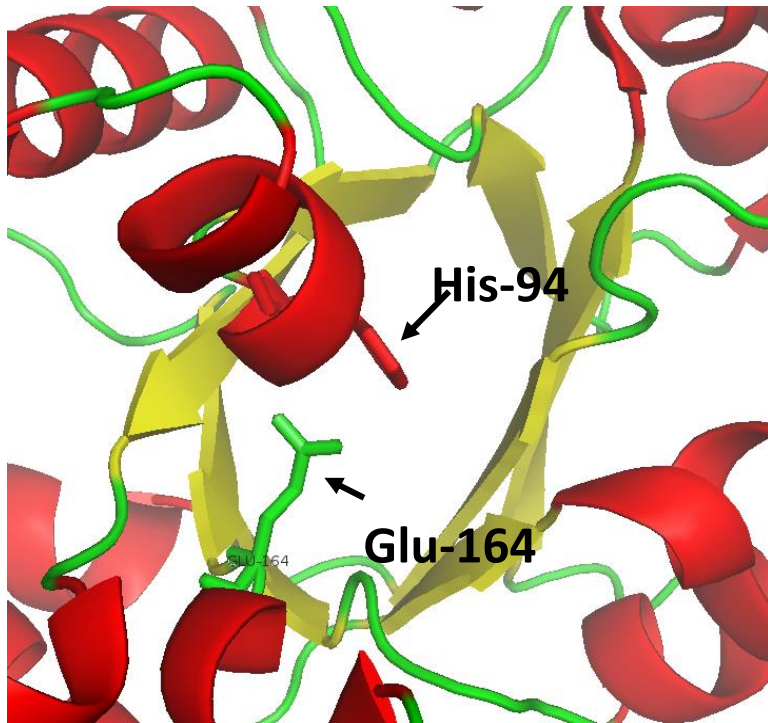


*Tenebrio molitor*

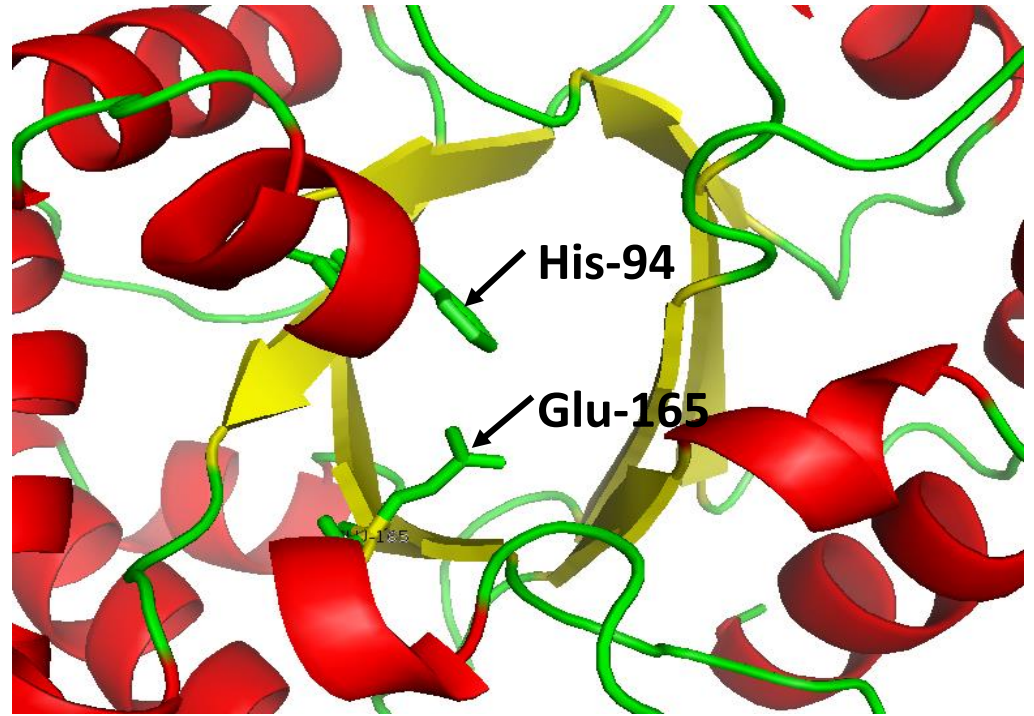


*Melitaea cinxia*

# Active site comparison



*Tenebrio molitor*



*Melitaea cinxia*

# 感想

- 收获颇丰，得到了很多生物信息的相关知识
- 学会如何对一个未知蛋白（序列）进行分析。
- 感谢罗老师一学期的付出！感谢G06成员！

Thank you !