



# OBP-1蛋白的结构 预测及功能分析

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一、常规性质预测

二、基因结构预测  
及功能分析



# AA序列

☐ F4Y5P0 [UniParc]. FASTA 145 15,689

Last modified June 28, 2011. Version 1.

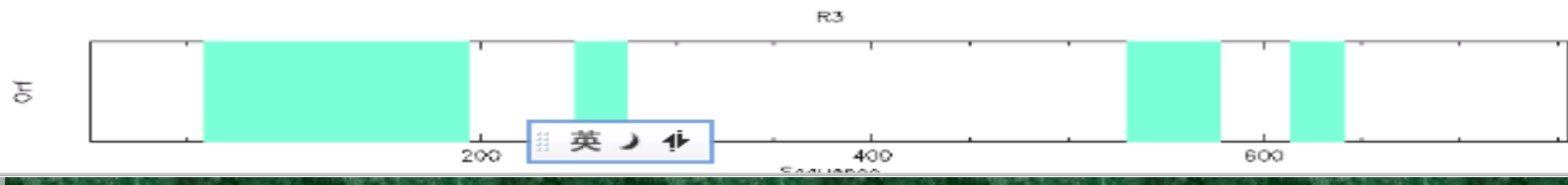
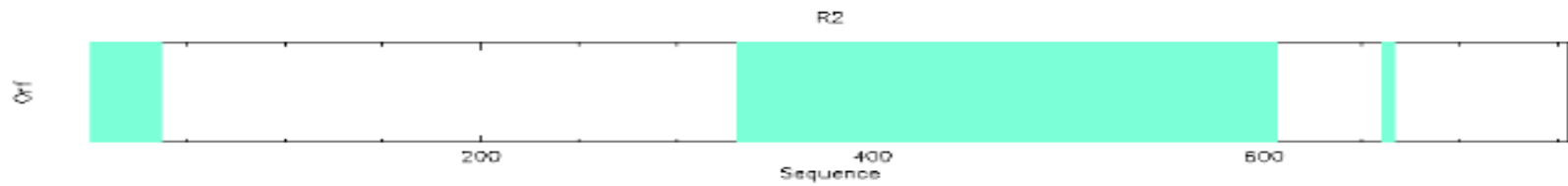
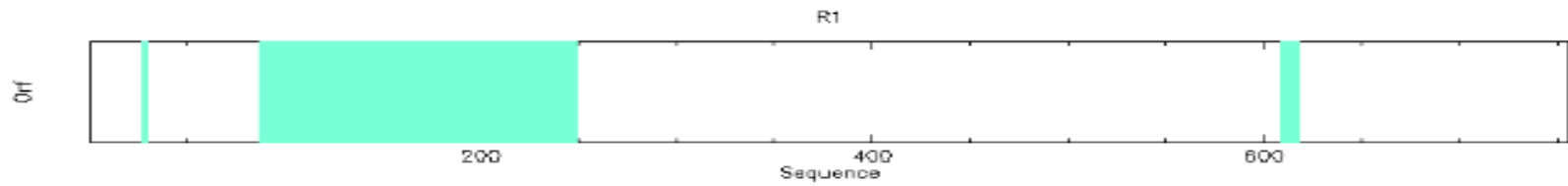
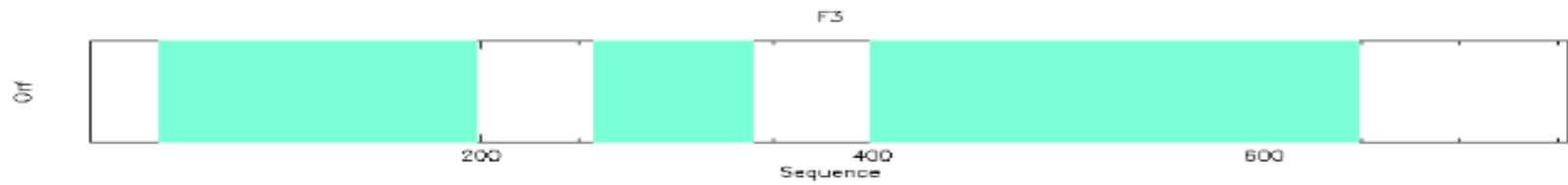
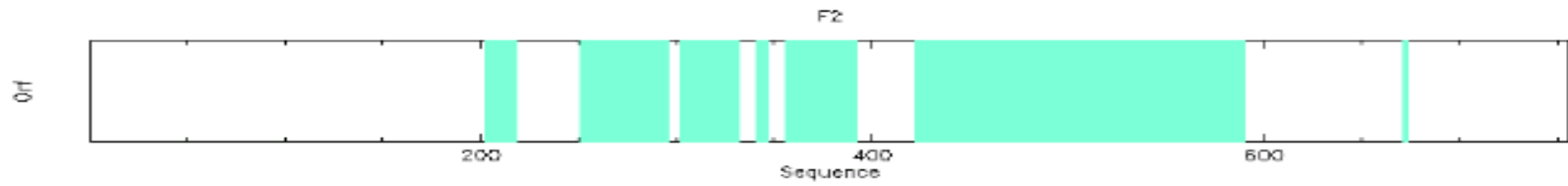
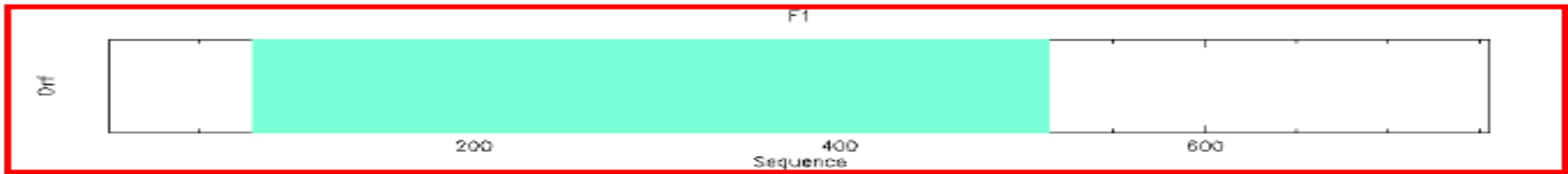
Checksum: C89EA78DF44FA952

```

    10      20      30      40      50      60
MNSLIPVLLV VCAAATRADE QTNAMVAKAF NKCREEFPI S DDEIGGVREK TTIPESHNAK

    70      80      90     100     110     120
CLMACMLREG KMLRDGKYEK ENALIMADVL NKDDPASADK AKQLVETCAG KVGTDAGGDE

    130     140
CEFAYKMAVC AEEEAKKLGV RPPDF
```



SHOWORF of GQ477022 from 1 to 756

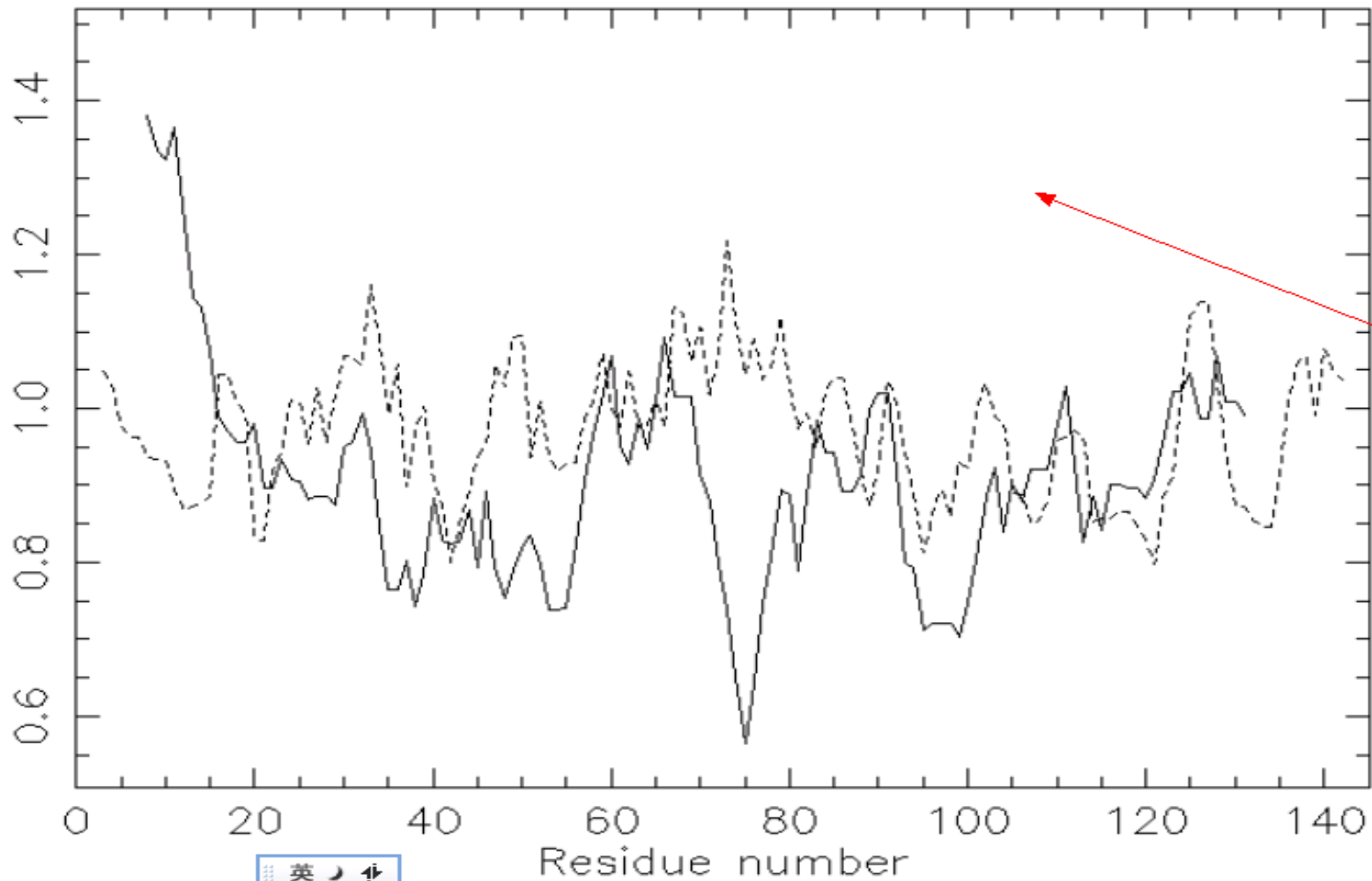
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-----|-----|-----|-----|-----|
1 cggccgggggagacactagcaattttacatcgtccatggttagatcactggtgcgcttcaa 60
F1 1 R P G E T L A I L H R P W * I T G A L Q 6
-----|-----|-----|-----|-----|
61 gaatccacaagcgttatcatgaactcactcattcccgtgtttggtggtttgcgctgct 120
F1 7 E S T S V I M N S L I P V L L V V C A A 26
-----|-----|-----|-----|-----|
121 gcgacgagggcagacgaacaaaccaacgccatggtggccaaagccttcaacaaatgccgg 180
F1 27 A T R A D E Q T N A M V A K A F N K C R 46
-----|-----|-----|-----|-----|
181 gaggaatttcccatcagtgacgatgaaattggcggagtgagggaaaagacgacgattcca 240
F1 47 E E F P I S D D E I G G V R E K T T I P 66
-----|-----|-----|-----|-----|
241 gagtctcataatgcaaaaatgtctcatggcctgcatgttgcgagaaggcaaaaatgttgaga 300
F1 67 E S H N A K C L M A C M L R E G K M L R 86
-----|-----|-----|-----|-----|
301 gatgaaaatacgaaaaaggaaaacgctcttataatggctgatgtgctgaacaaggatgat 360
F1 87 D G K Y E K E N A L I M A D V L N K D D 106
-----|-----|-----|-----|-----|
361 cctgcctctgctgataaagcaaaaacagctttagaaacatgtgcaggcaaaagtgggaca 420
F1 107 P A S A D K A K Q L V E T C A G K V G T 126
-----|-----|-----|-----|-----|
421 gatgcaggtggggacgaatgocgagtttgcttacaaaatggctgtgtgocgctgocggaagaa 480
F1 127 D A G G D E C E F A Y K M A V C A A E E 146
-----|-----|-----|-----|-----|
481 gcaagaagccttggagtgctcctccagacttcaagtaccaaaaatttcaattgtattga 540
F1 147 A K K L G V R P P D F * V P K F Q L Y * 7
-----|-----|-----|-----|-----|
541 tacaccaccatcgacttgcacaccaaatttcaggcattcctcgtctcttgatcccacca 600
F1 1 Y T T I D F A H Q I S G I P R L L I P P 20
-----|-----|-----|-----|-----|
601 aagtcatcacattaccatctcgtaaatttaagacctttcatttcttataattaagacttt 660
F1 21 K S S H Y H I V N L R P F I S Y N * D F 2
-----|-----|-----|-----|-----|
661 aatacatattatgtaaactctggtggttaattgctgggttcacgaaaaaataaaaactcctac 720
F1 3 N T Y Y V N L V V I A G F T K K * N S Y 3
-----|-----|-----|-----|-----|
721 aattacaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 756
F1 4 N Y K K K K K K K K K K K K 15

```

# 跨膜螺旋分析

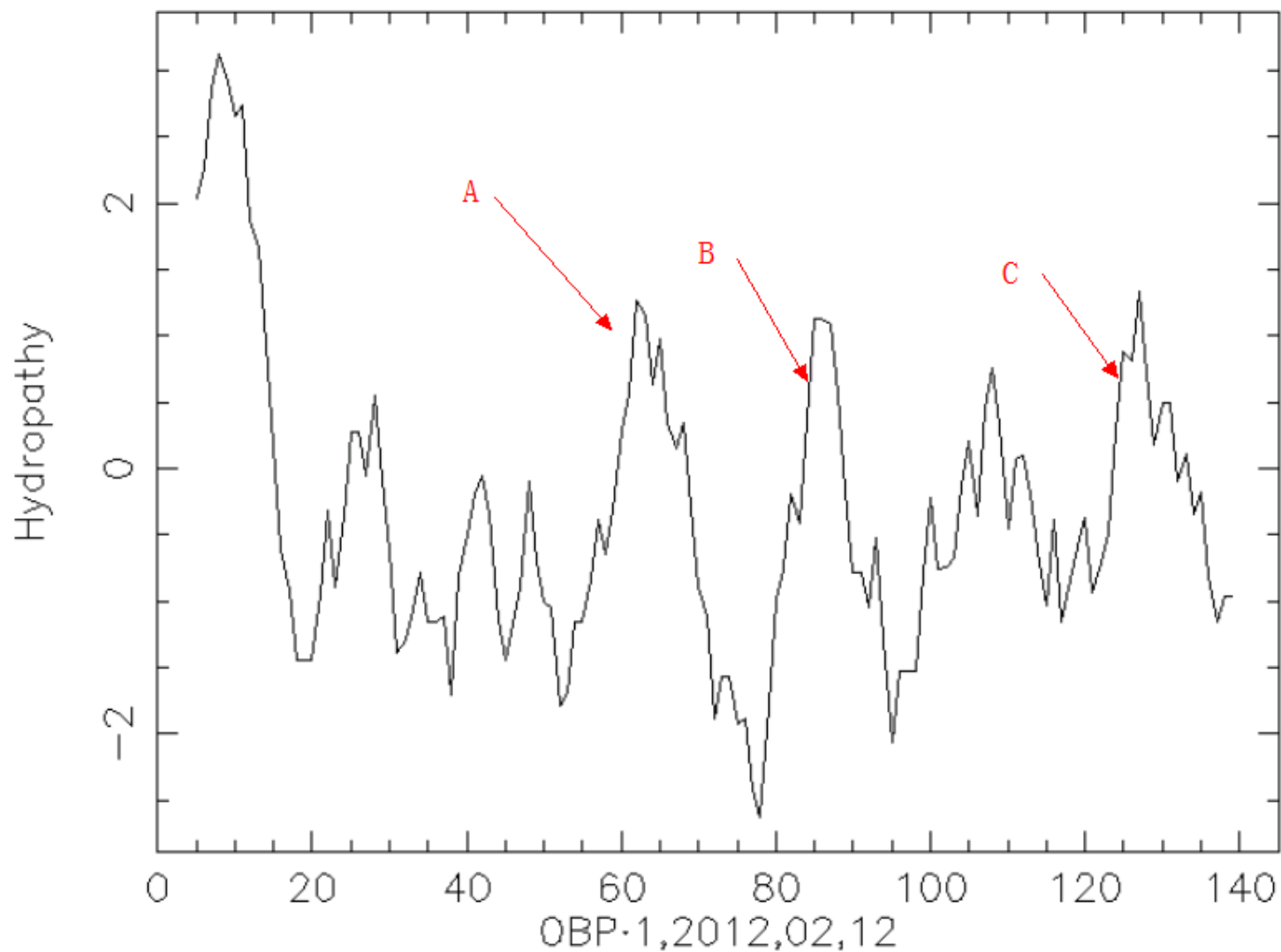
Tmap



没有跨膜螺旋

# 亲脂性分析

Kyte-Doolittle Plot

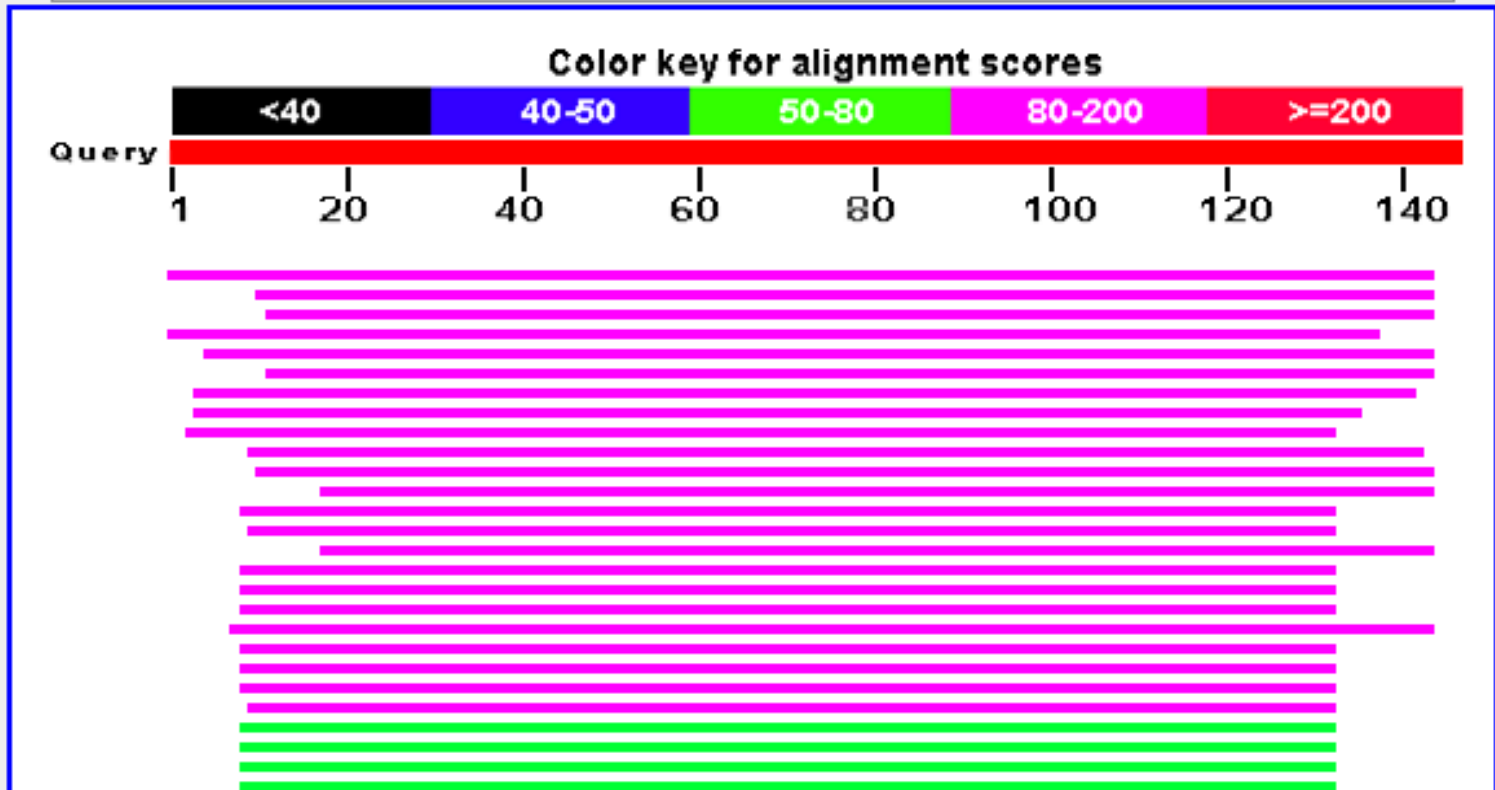


# BLAST对苜蓿盲蝽气味结合蛋白进行同源性搜索

[\[nomy reports\]](#) [\[Distance tree of results\]](#) [\[Multiple alignment\]](#)

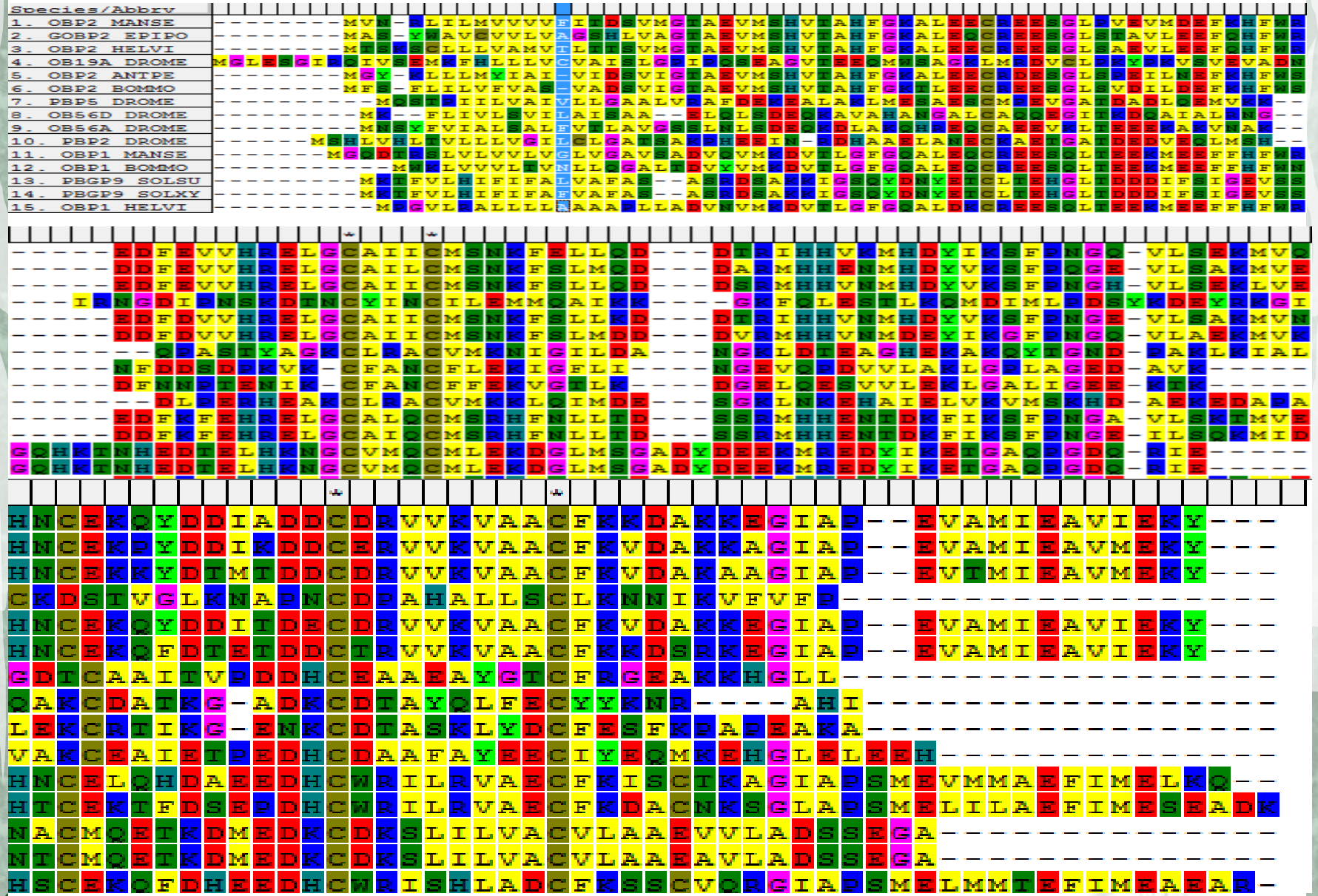
## Distribution of 48 Blast Hits on the Query Sequence

Mouse-over to show defline and scores, click to show alignments

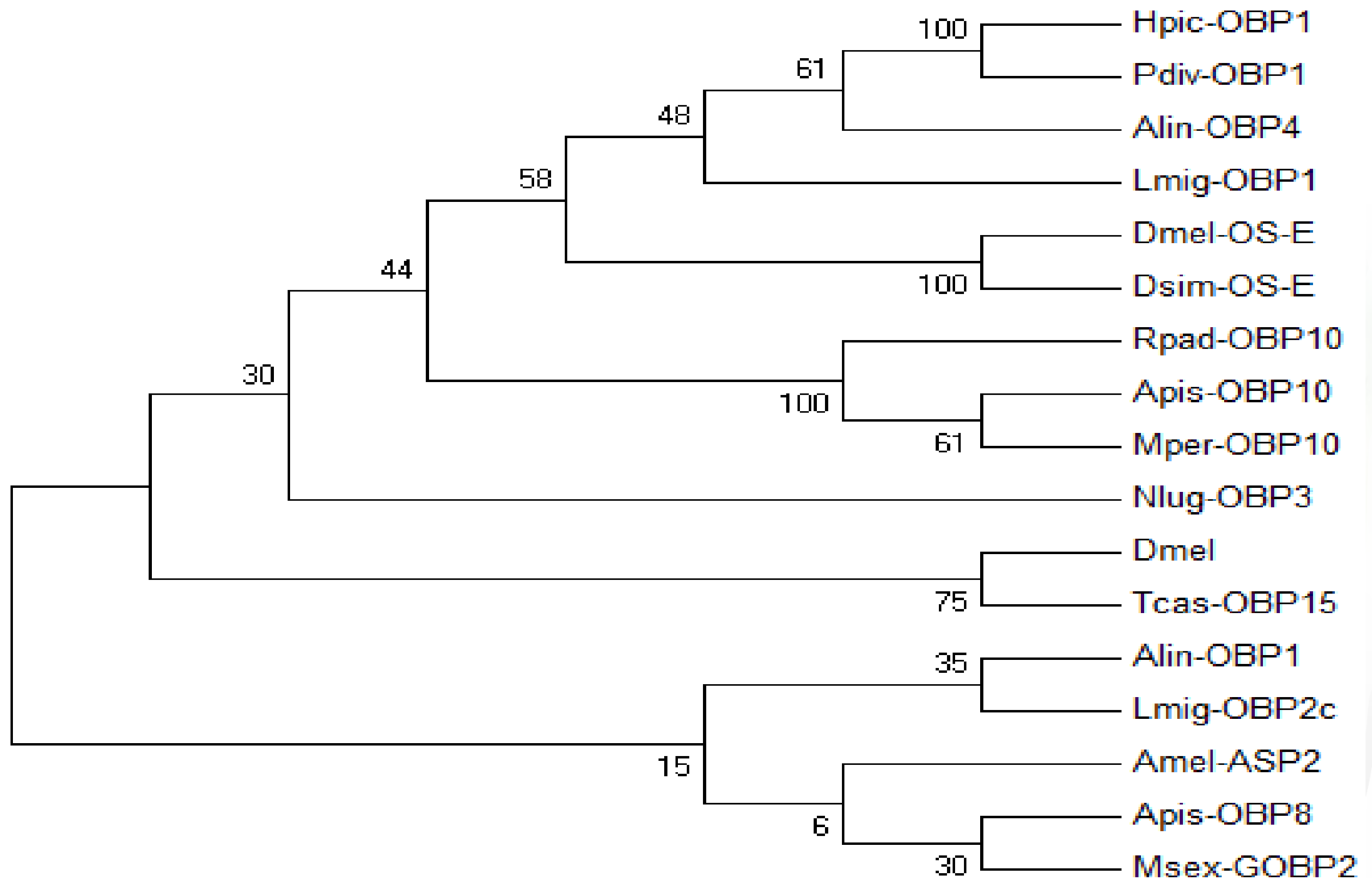




# 苜蓿盲蝽气味结合蛋白Alin-OBP1与其它已知昆虫OBP的多重联配



# 苜蓿盲蝽气味结合蛋白Alin-OBP1与其他已知昆虫 气味结合蛋白的系统发育树



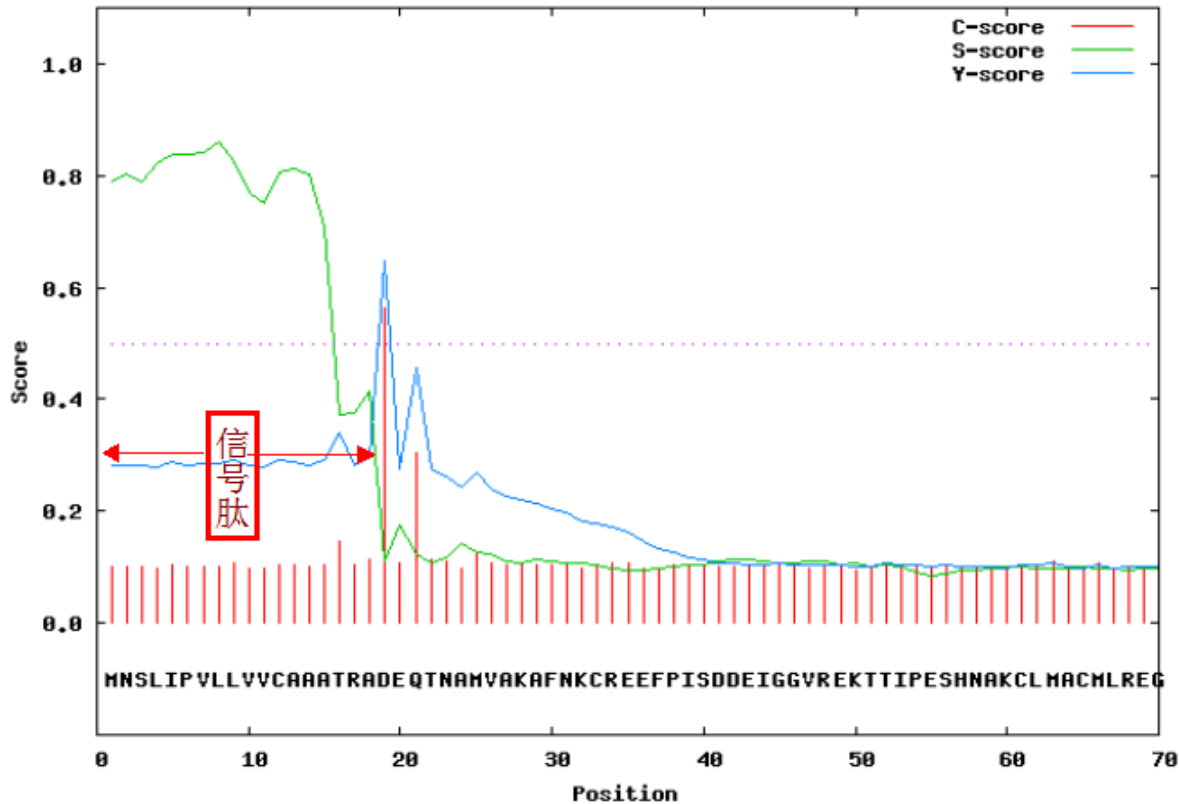


# 信号肽预测

# SignalP-4.0 euk predictions

>GQ477022\_1\_79 - 513\_Adelphocoris lineolatus odorant-binding protein 1 mRNA, complete cds.

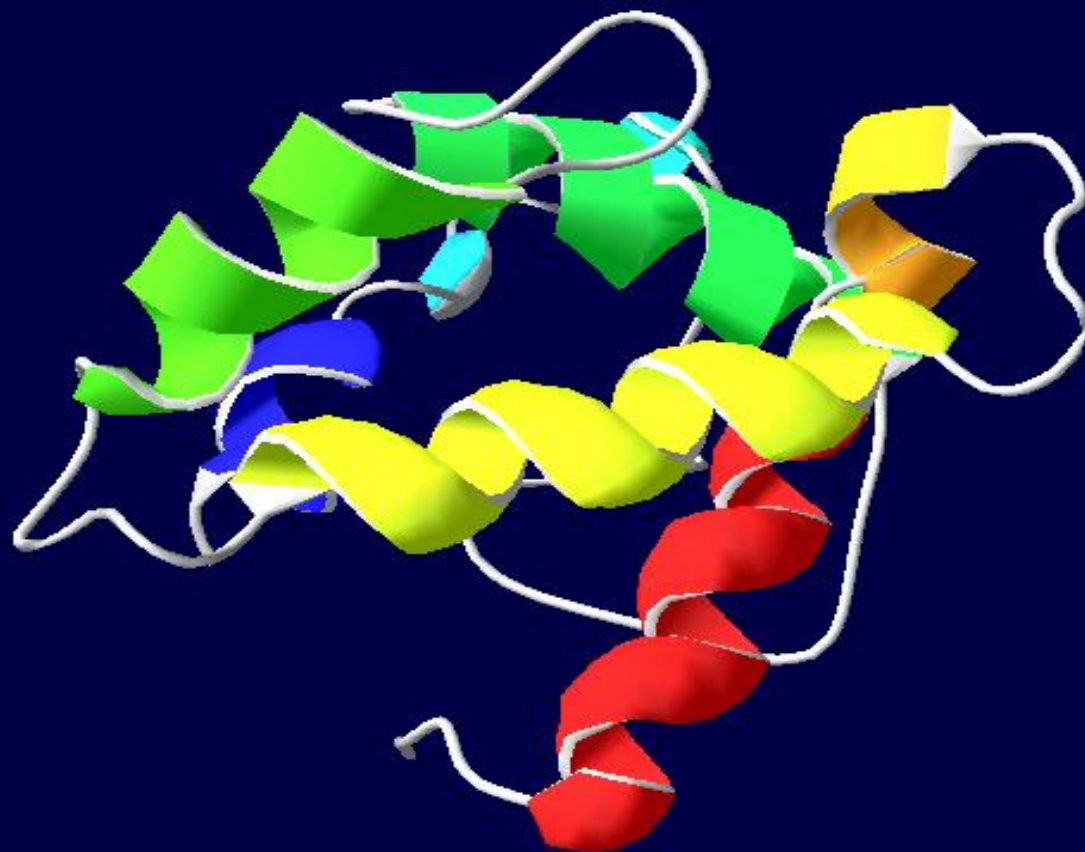
SignalP-4.0 prediction (euk networks): GQ477022\_1



# Measure	Position	Value	Cutoff	signal peptide?
max. C	19	0.563		
max. Y	19	0.647		
max. S	8	0.860		
mean S	1-18	0.734		
D	1-18	0.694	0.450	YES

Name=GQ477022\_1 SP='YES' Cleavage site between pos. 18 and 19: TRA-DE D=0.694 D-cutoff=0.450 Networks=SignalP-noTM

# 基于Swiss-modle的蛋白结构预测



# SWISS-MODEL

Workunit: P000002 Title:OBP

1

145

## Model Summary:

### Model information:

Modelled residue range: 21 to 143  
Based on template: 2wcjA (1.40 A)  
Sequence Identity [%]: 21.26  
Evaluate: 2.6E-20

### Quaternary structure information:

Template (2wcj): MONOMER  
Model built: SINGLE CHAIN

### Quality information:

QMEAN Z-Score: -2.522

### Ligand information:

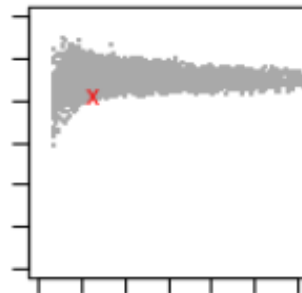
Ligands in the template: M21: 1, MG: 1.  
Ligands in the model: none.

## Global Model Quality Estimation:

### QMEAN4 global scores:

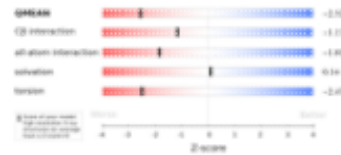
QMEANscore4: Estimated absolute model quality:

0.559



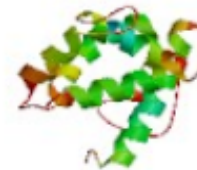
Z-Score: -2.522

### Score components:

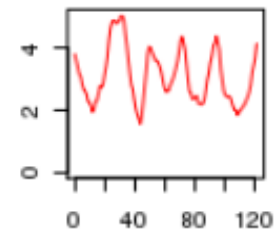


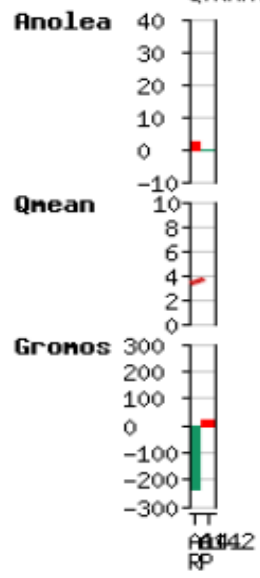
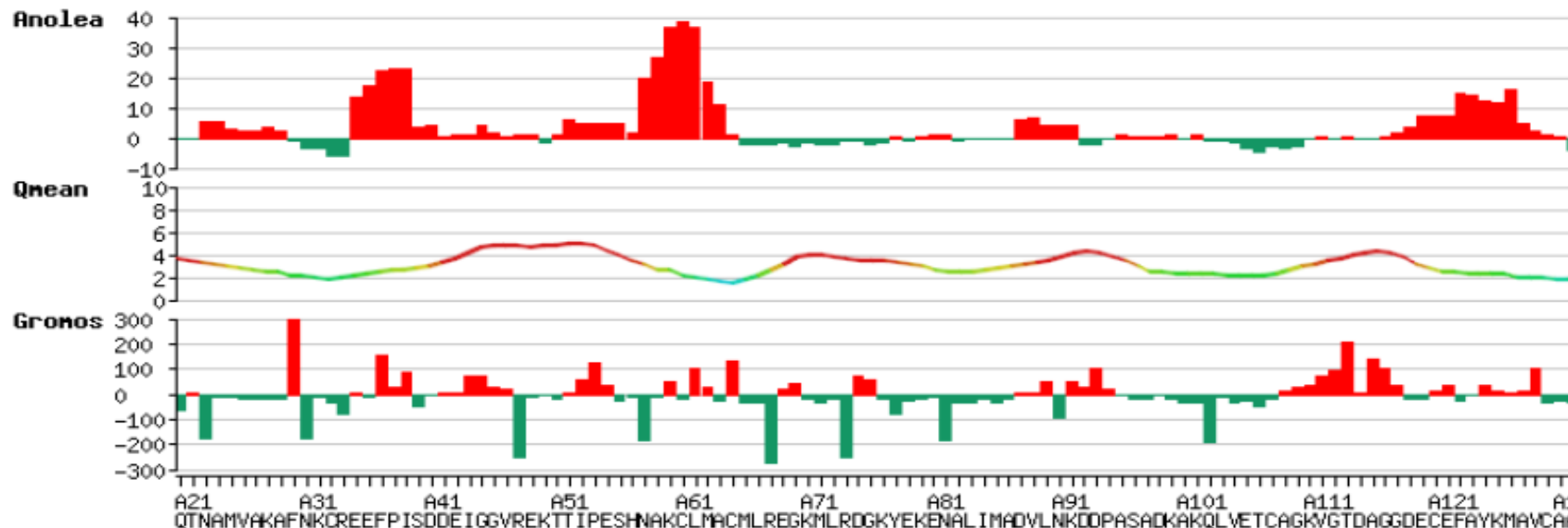
### Local scores:

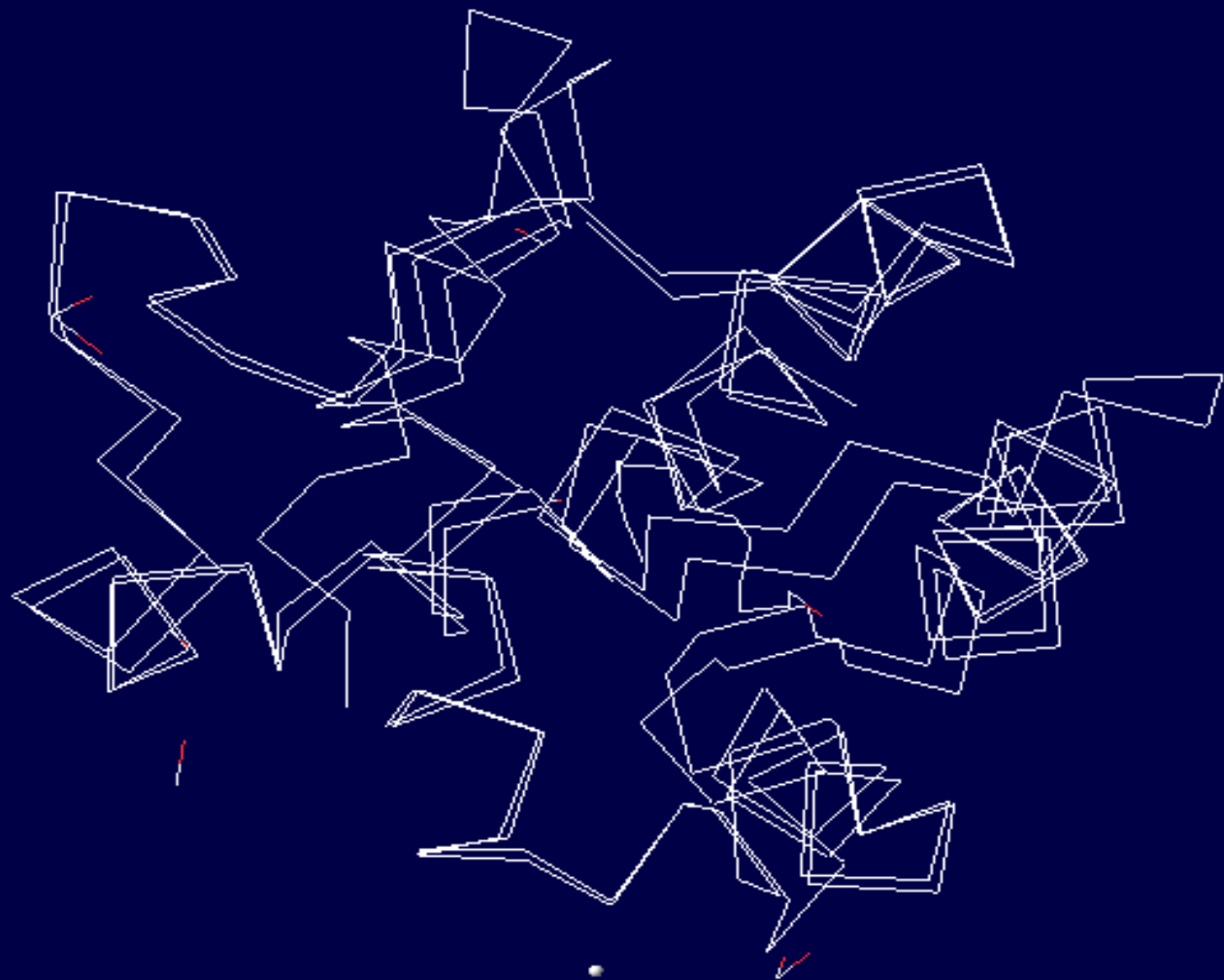
Coloring by residue error:



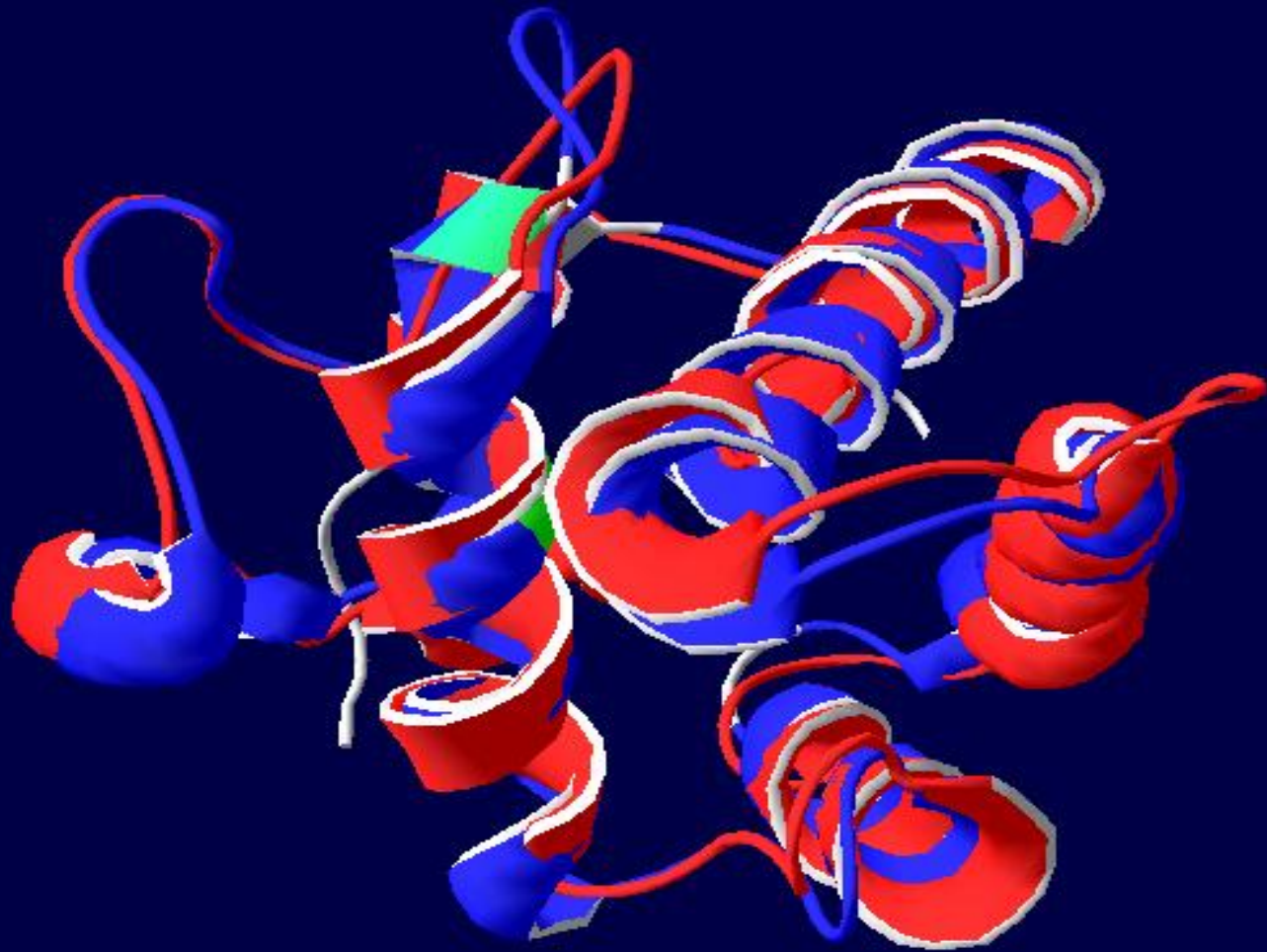
Residue error plot:

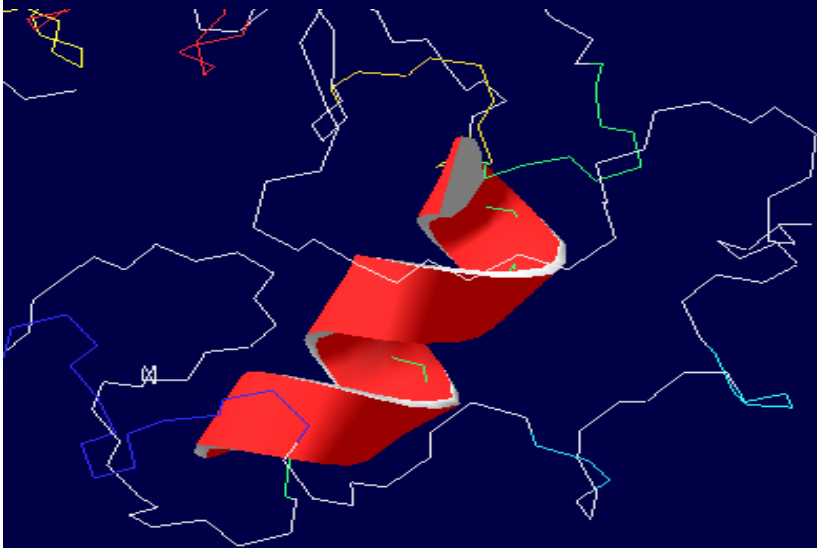
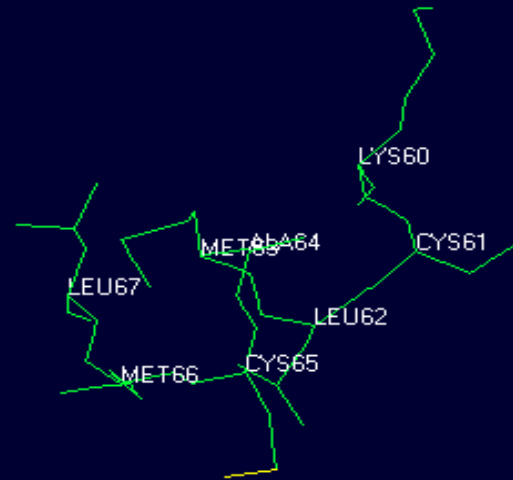
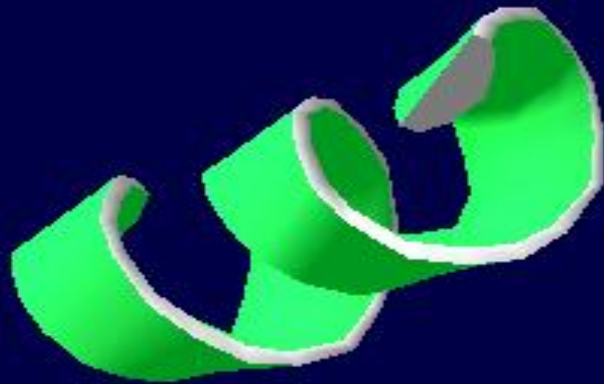


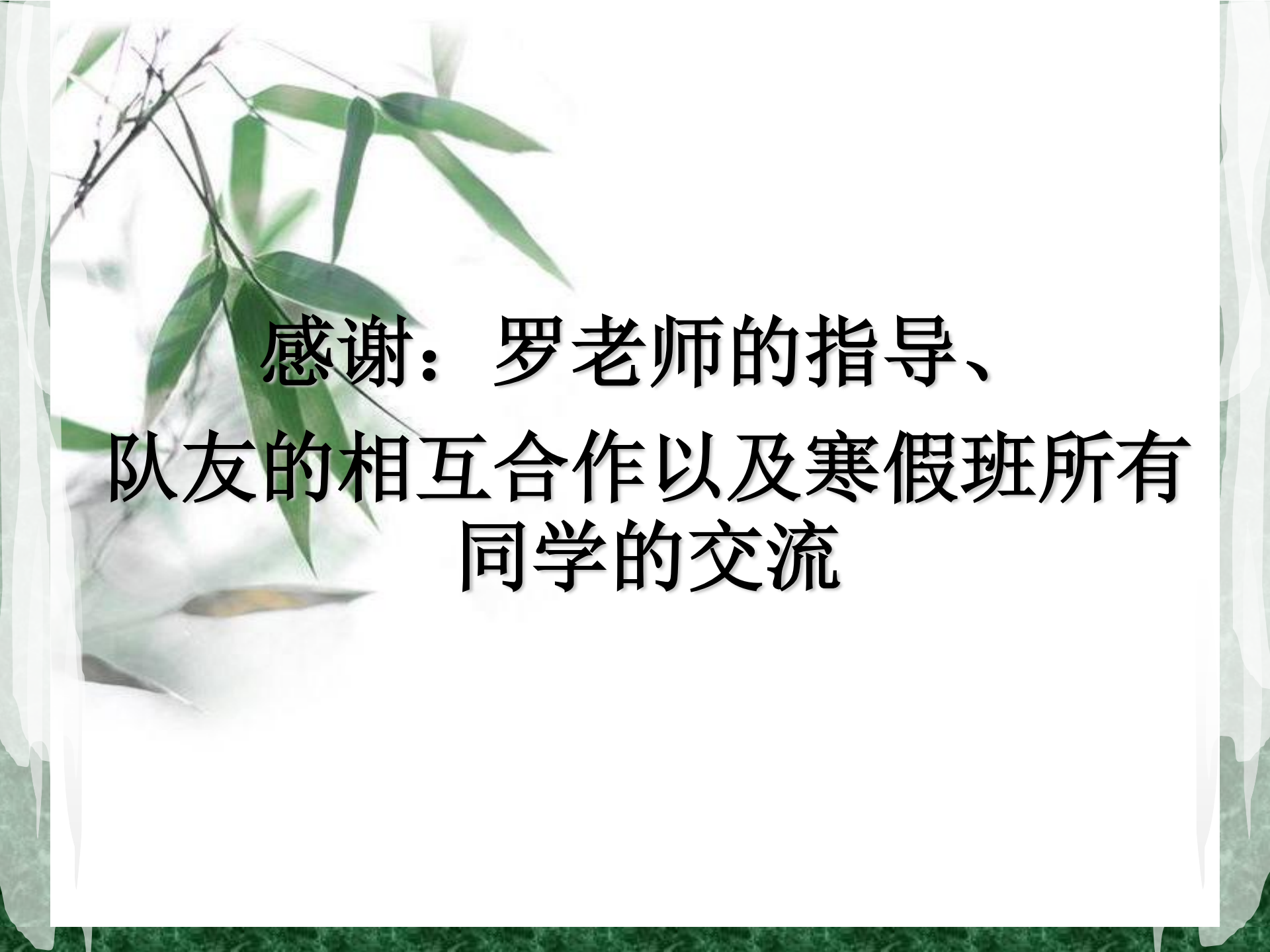












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