

植物蓝光受体CRY蛋白序列、 结构、功能、进化分析

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List

- Introduction
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Cryptochrome

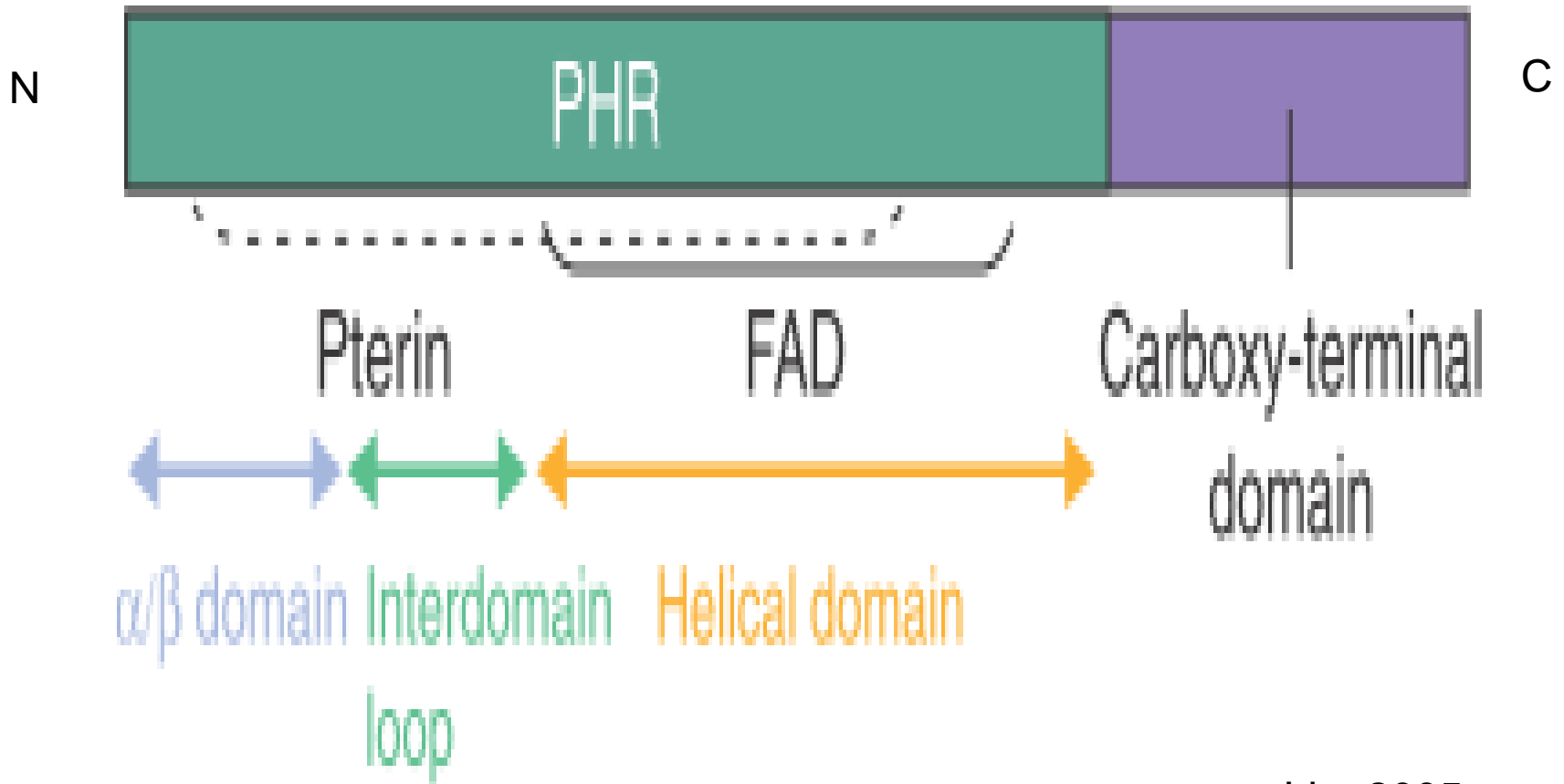
- What is cryptochrome?

photolyase-like, DNA-repair proteins that regulate photomorphogenic development in plants and the circadian clock in plants and animals

CRY classed into 3 types

- CRY-DASH protein
- Animal CRY
- Plant CRY

General structure of CRY



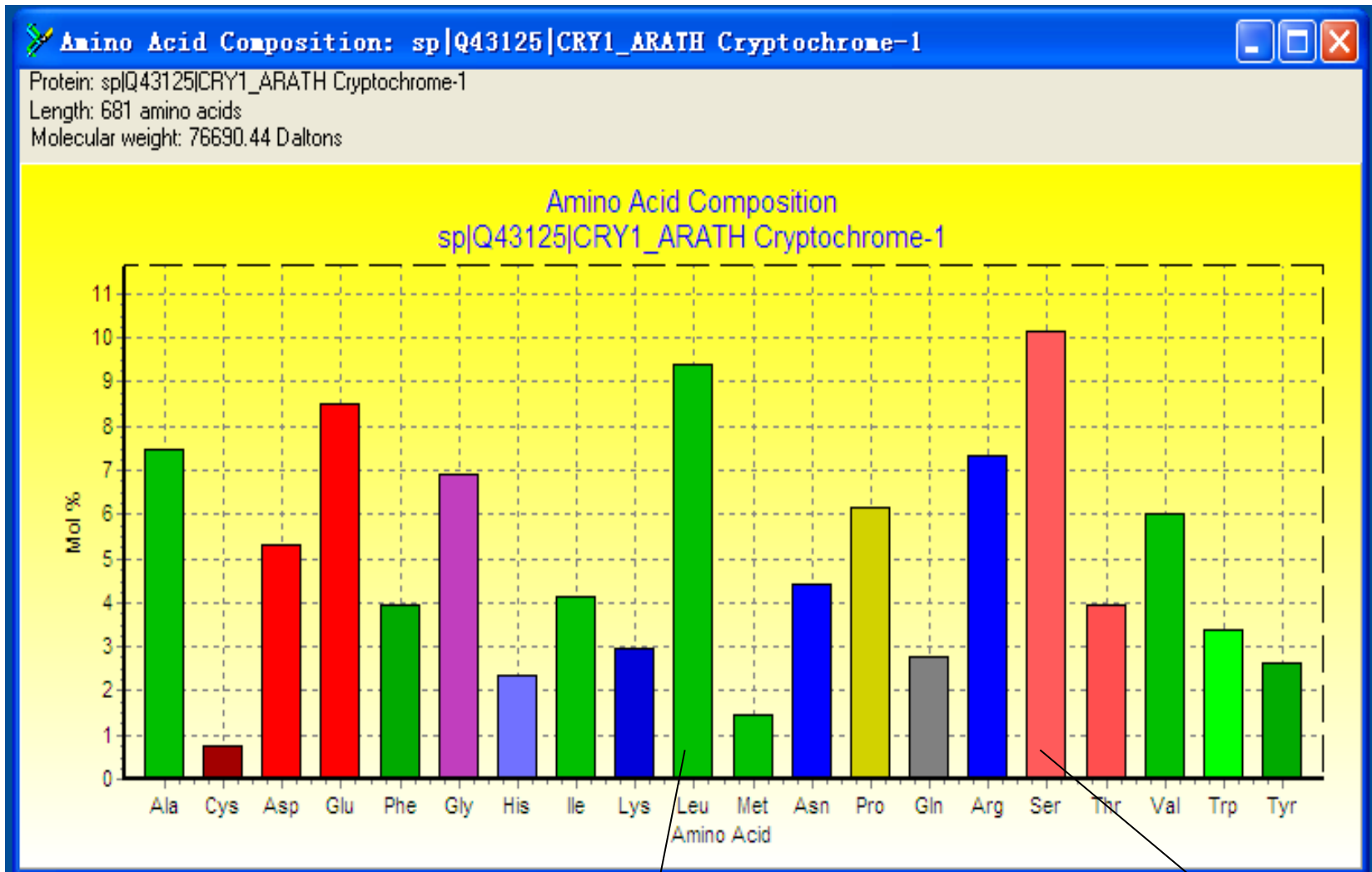
Lin, 2005

Material and method

- Material:

CRY1(ARATH)

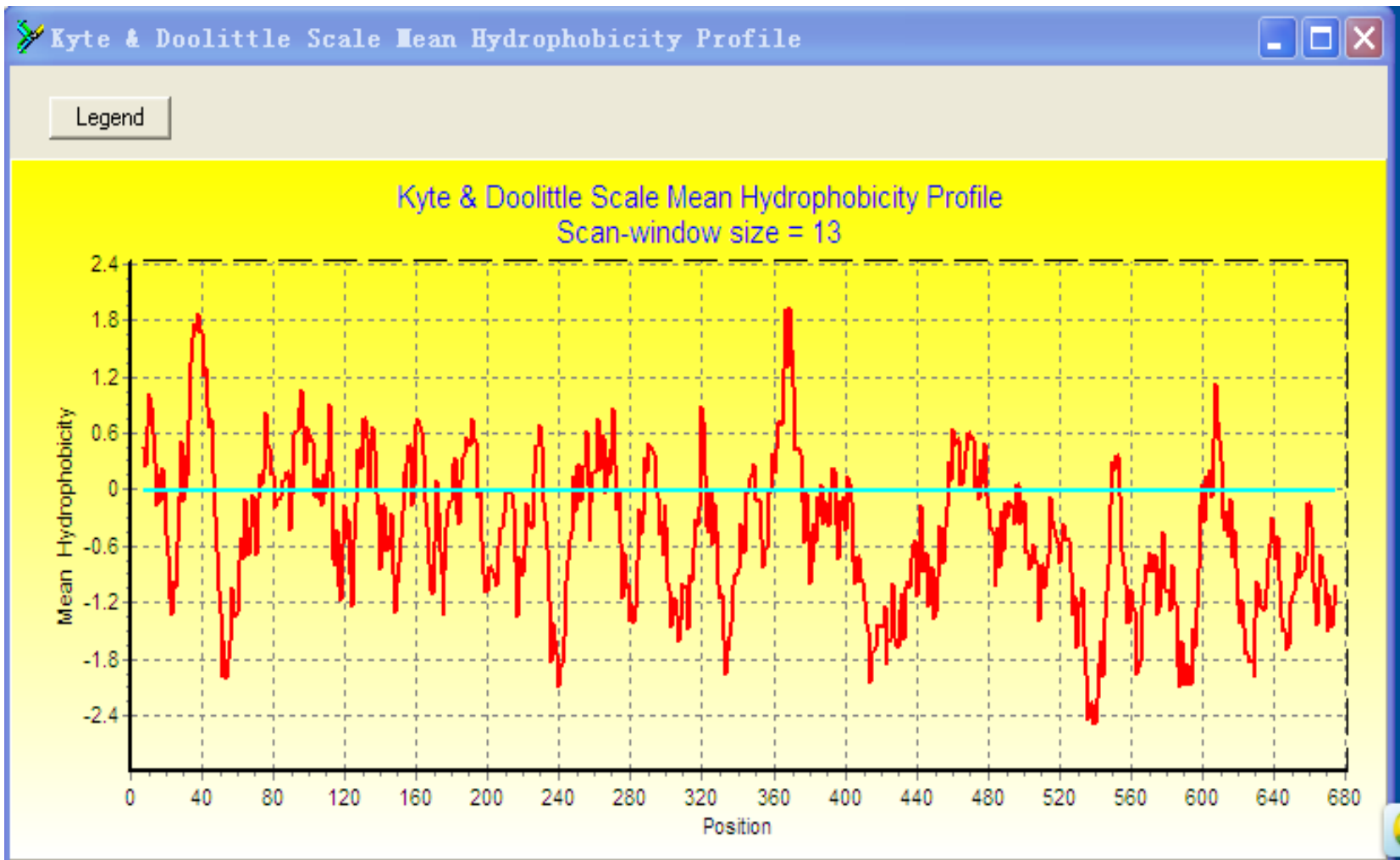
- Method: Bioedit, TMHMM, SMART, Predictprotein;
ClustalX, MEGA 5.0, Weblogo, Swiss-Model



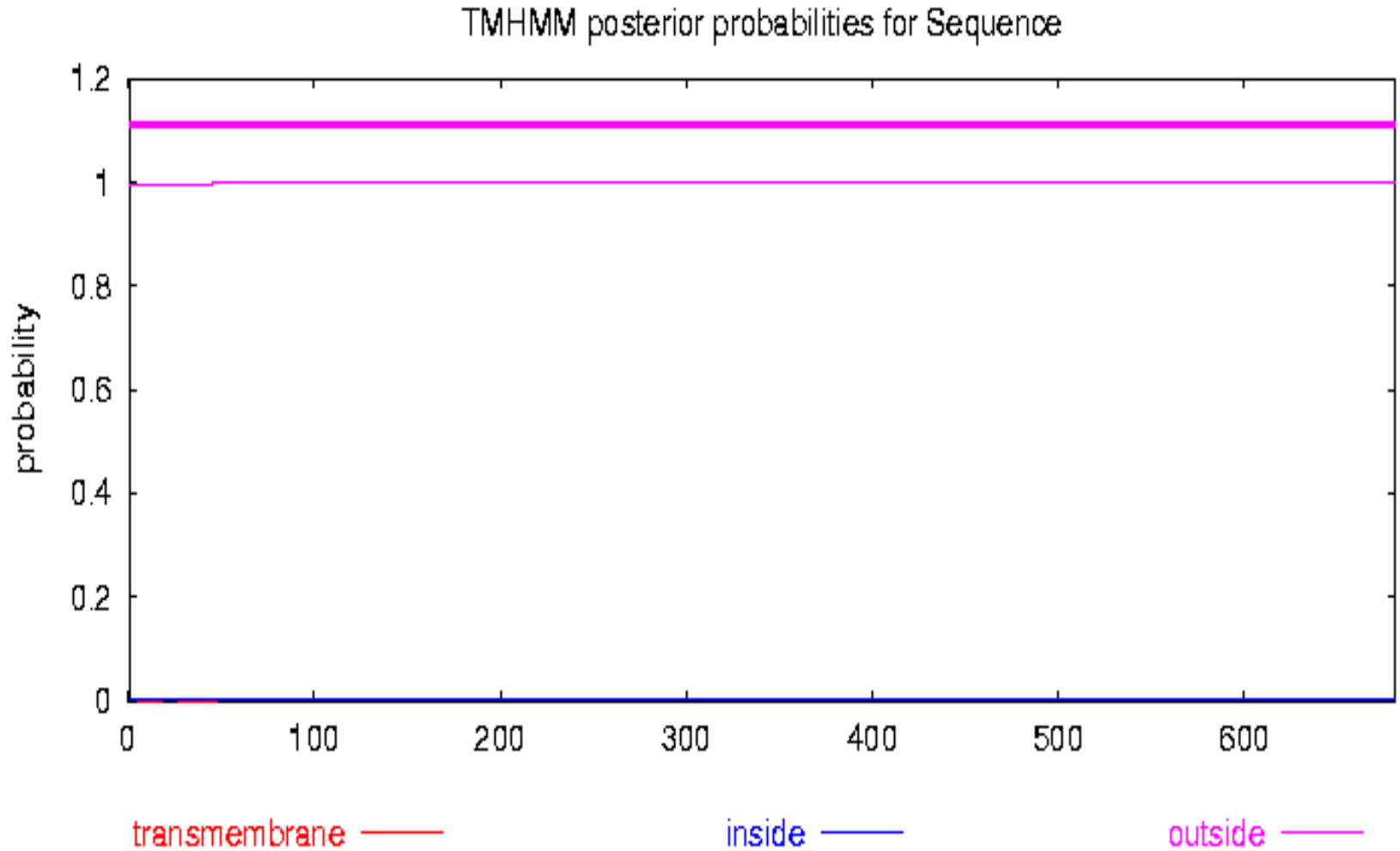
二聚化

磷酸化

- Bioedit分析CRY1蛋白的氨基酸组成



- Bioedit分析CRY1蛋白的疏水性分析



- TMHMM分析CRY1蛋白的跨膜域



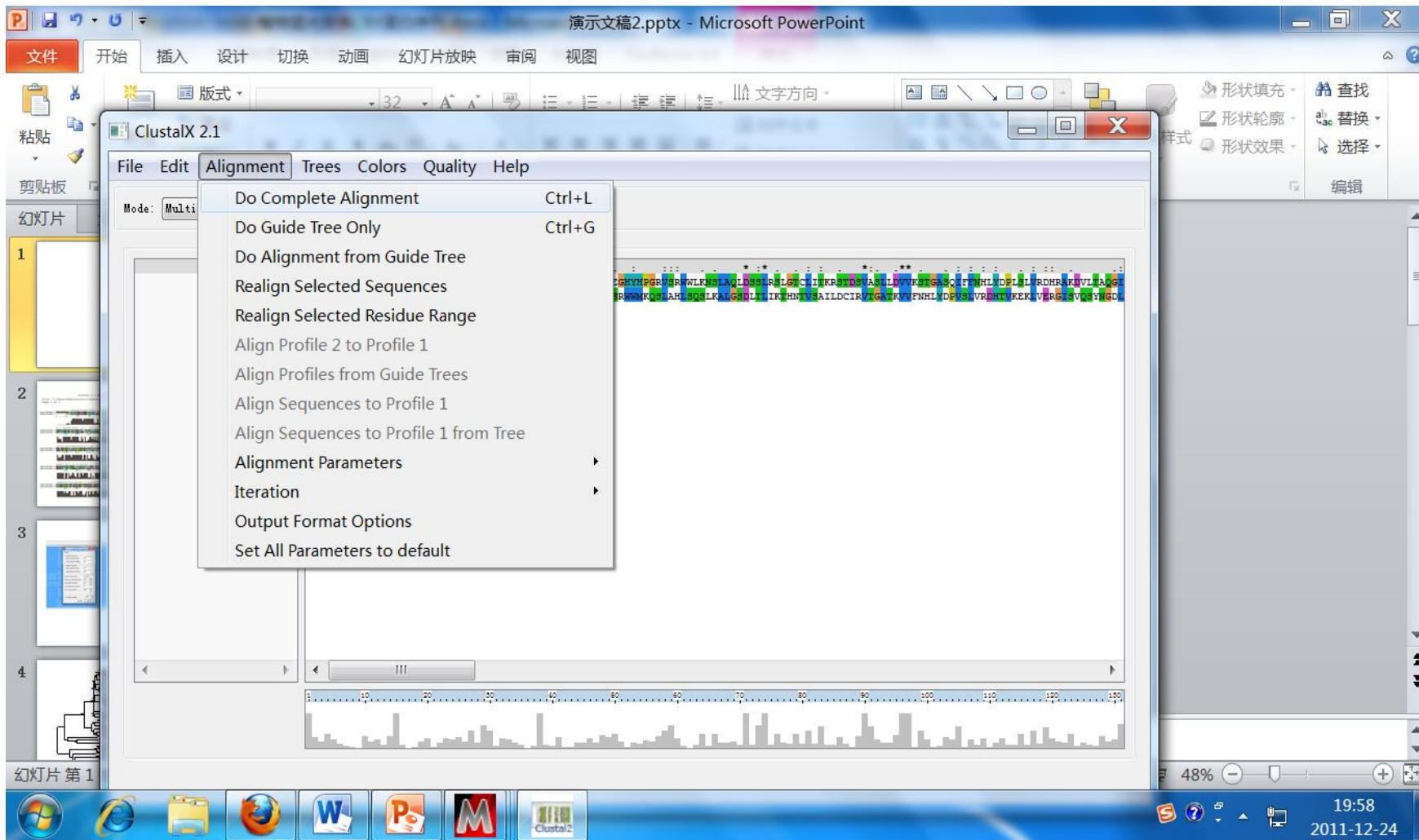
| Name | Begin | End | E-value |
|---------------------|-------|-----|----------|
| Pfam:DNA_photolyase | 14 | 181 | 2.70e-43 |
| Pfam:FAD_binding_7 | 215 | 492 | 1.20e-88 |
| Pfam:Cryptochrome_C | 519 | 629 | 9.90e-29 |

- SMART预测CRY1蛋白的结构域

Predicted secondary structure composition

| sec str type | H | E | L |
|--------------|-------|------|-------|
| % in protein | 32.16 | 5.87 | 61.97 |

Predictprotein预测CRY1蛋白的二级结构成分

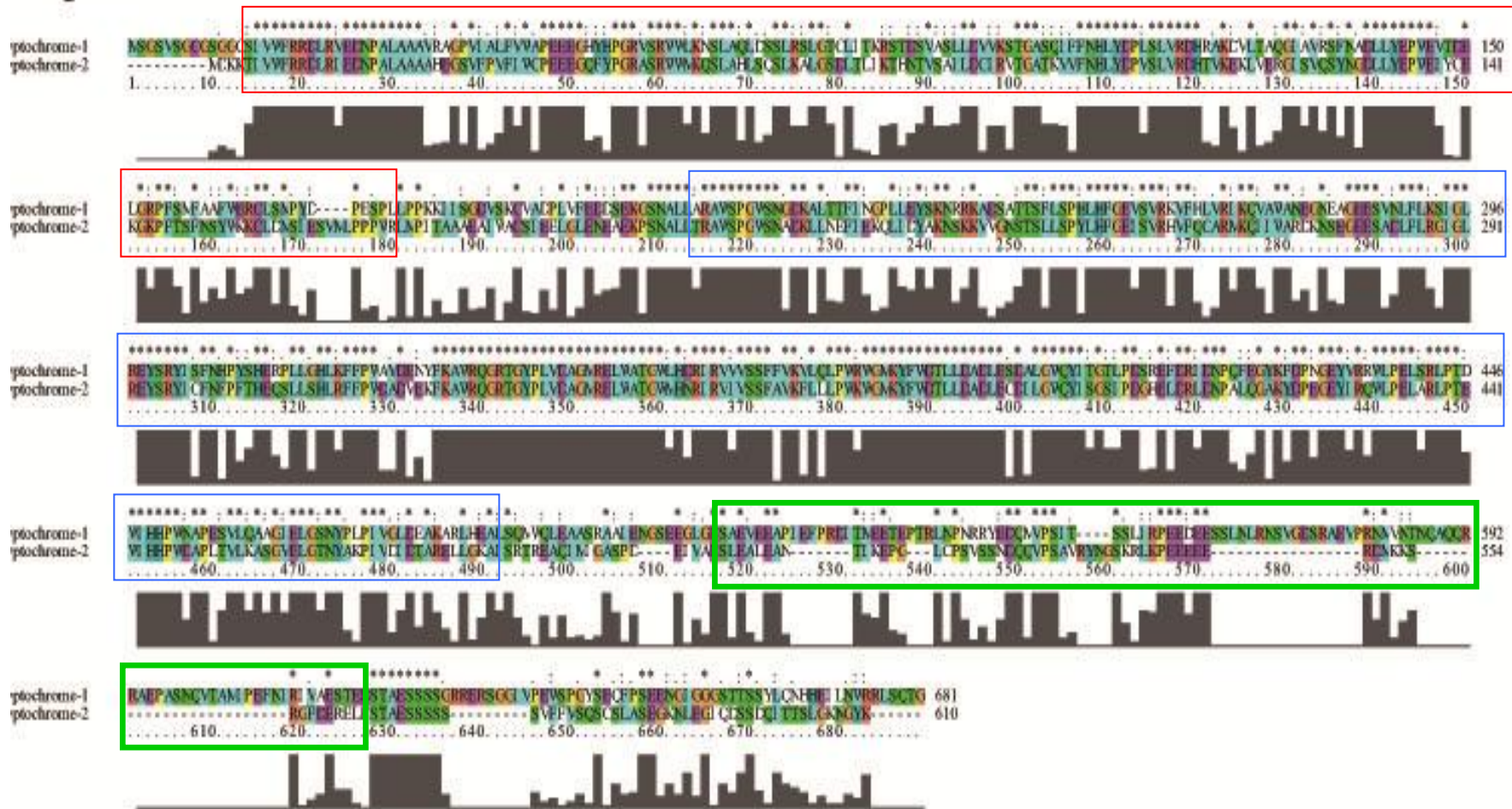


ClustalX软件进行序列比对

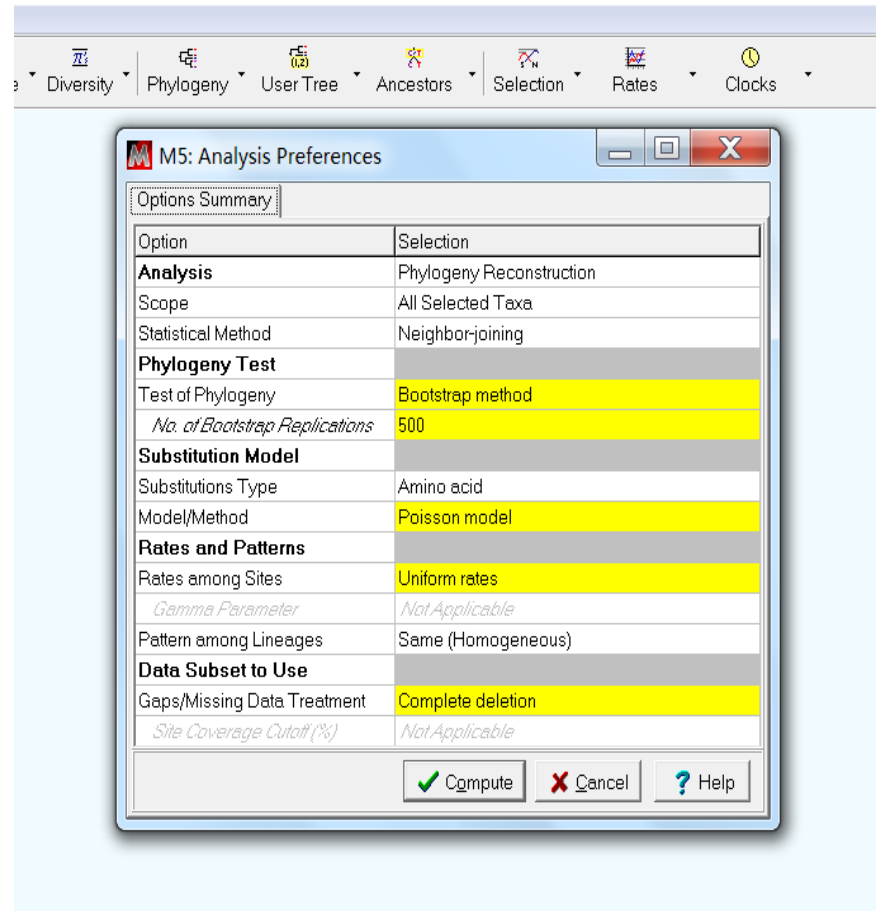
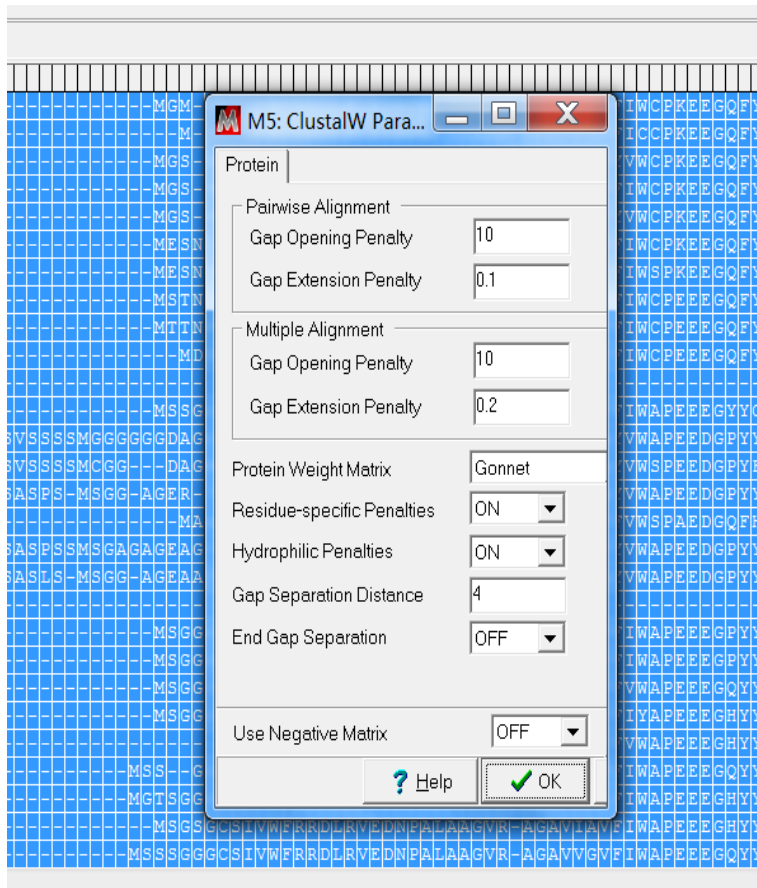
CLUSTAL 2.1 MULTIPLE SEQUENCE ALIGNMENT

File: H:/a1.ps
Page 1 of 1

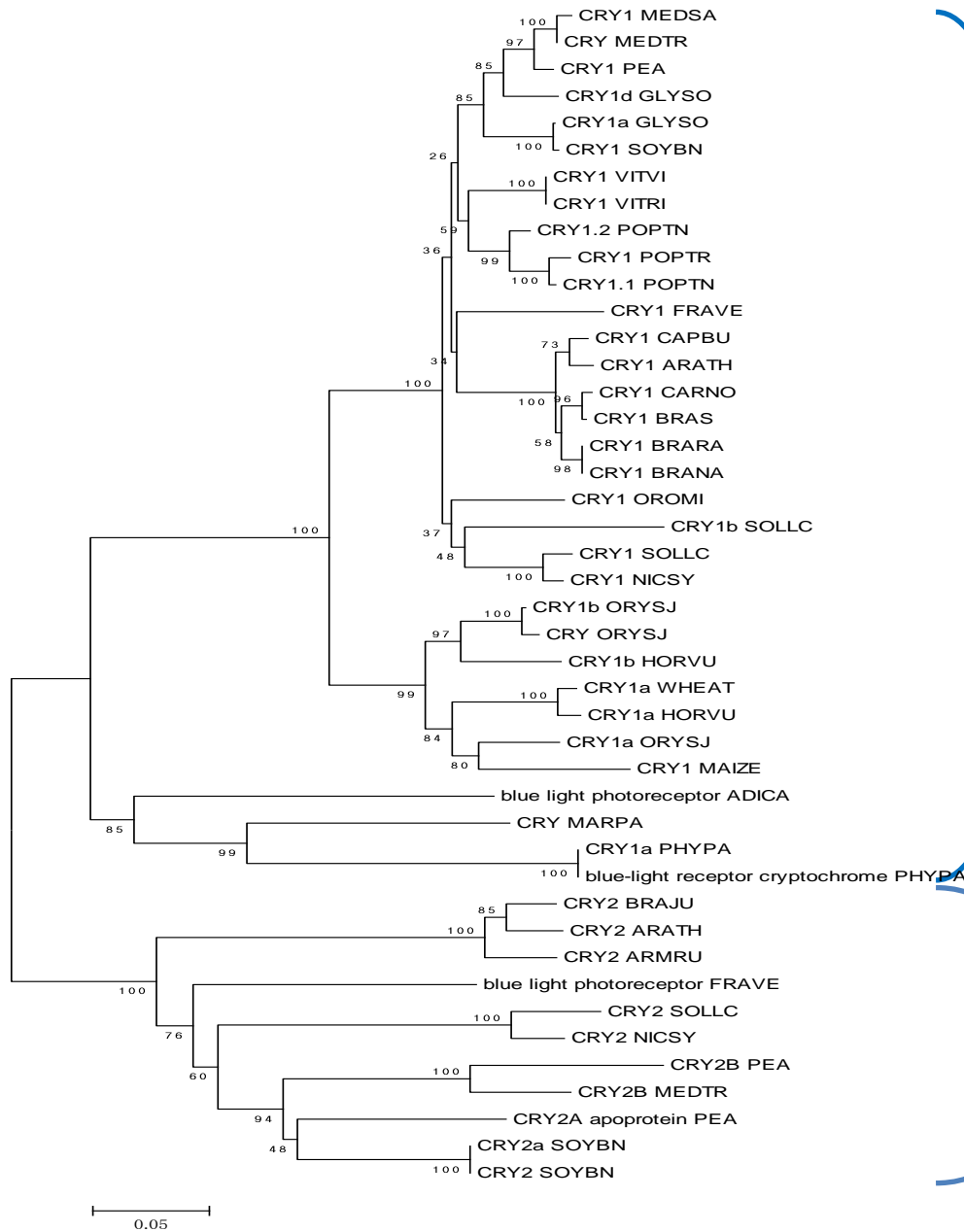
Date: Sat Dec 24 20:40:45 2011



拟南芥 CRY1、CRY2旁系序列比对结果



MEGA软件进行进化树构建分析



CRY1

CRY2

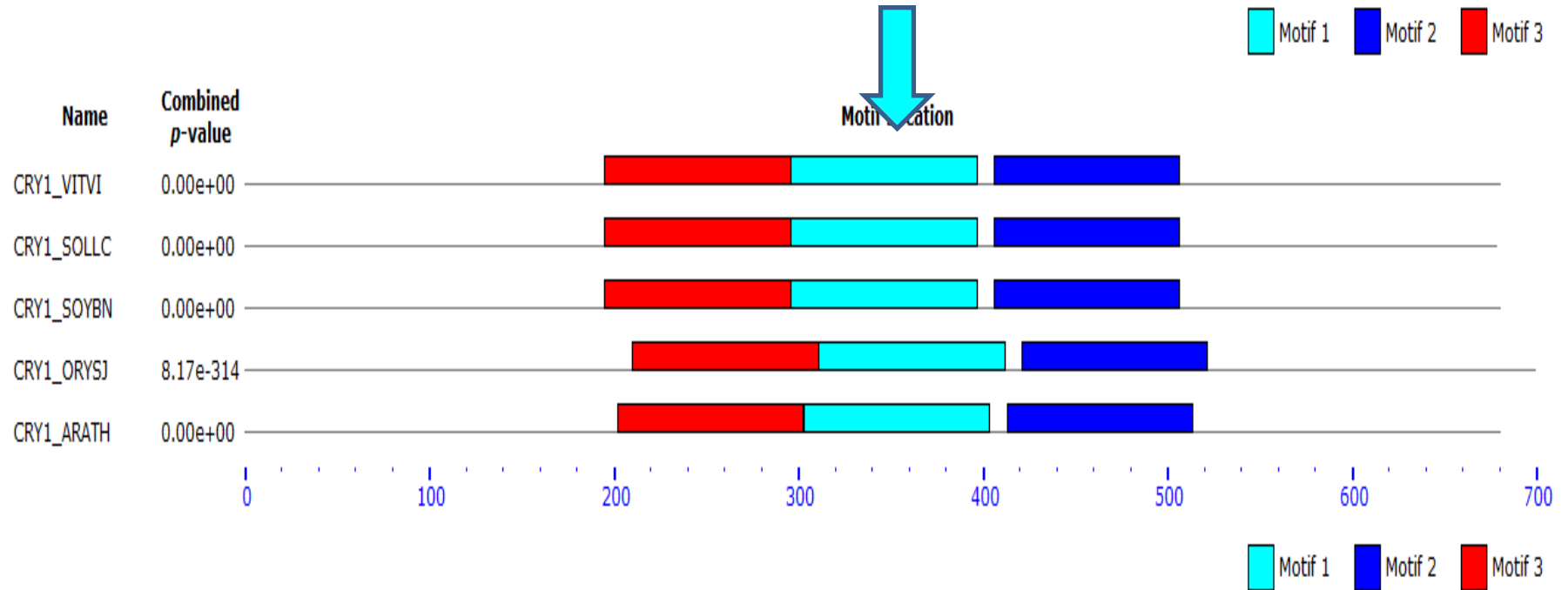
直系CRY蛋白进化树结果

Non-overlapping sites with a p -value better than 0.0001.

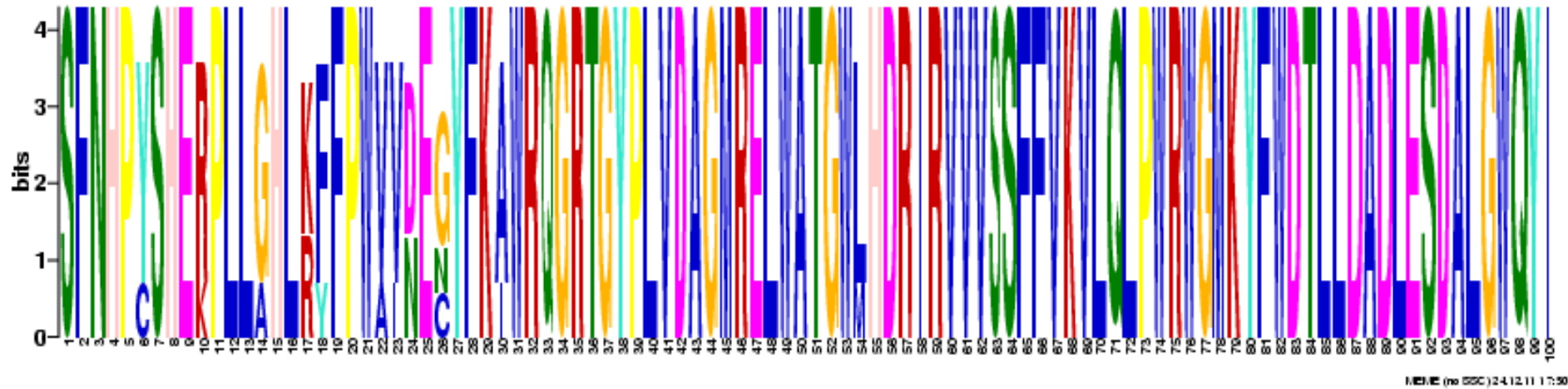
The height of the motif "block" is proportional to $-\log(p\text{-value})$, truncated at the height for a motif with a p -value of 1×10^{-4} .

Click on any row to highlight sequence in all motifs. The motif blocks have tool tips with more information.

FAD





Weblogo FAD domain 保守序列分析



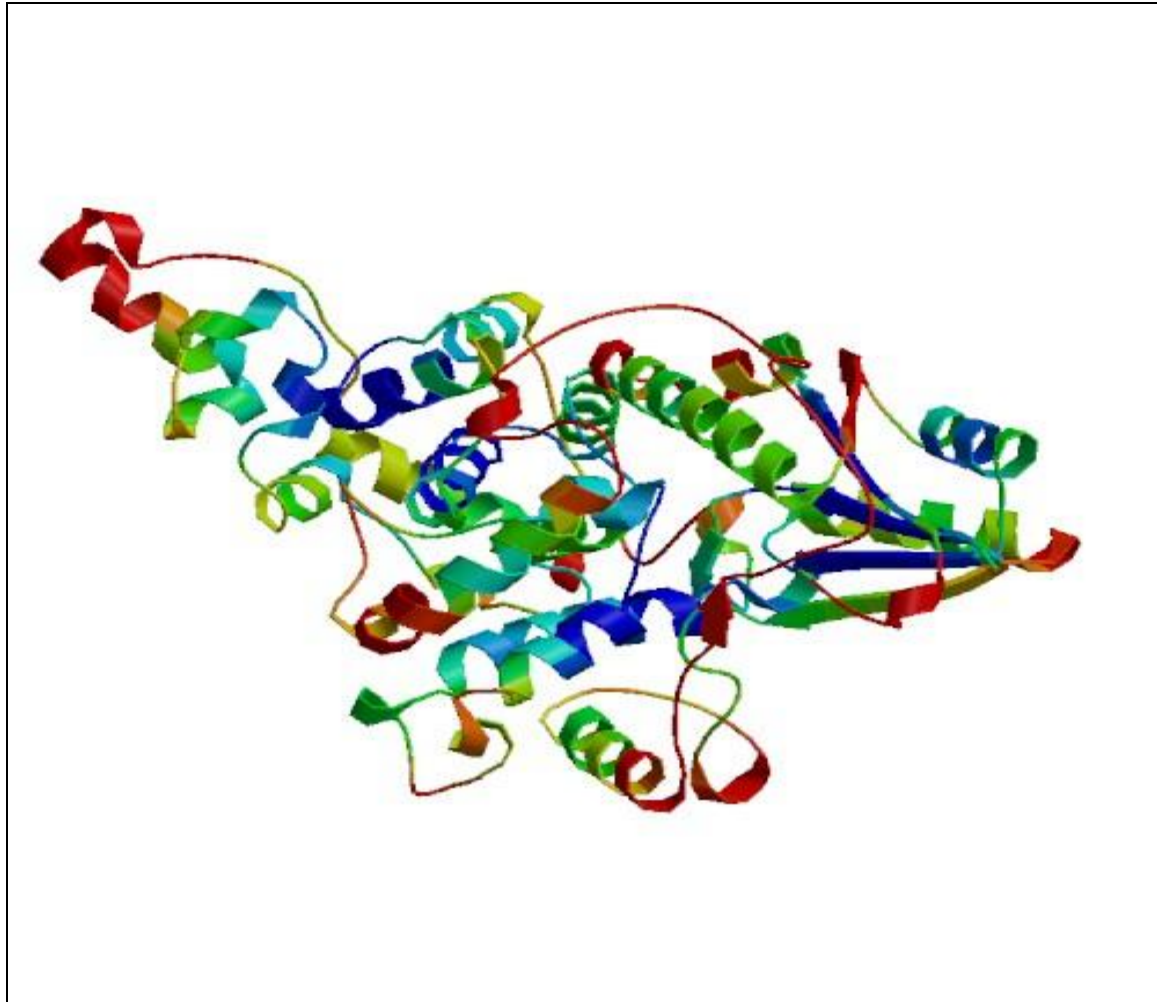
FAD 序列保守性分析 拟南芥，
水稻，葡萄，茄子，大豆

Search for Template

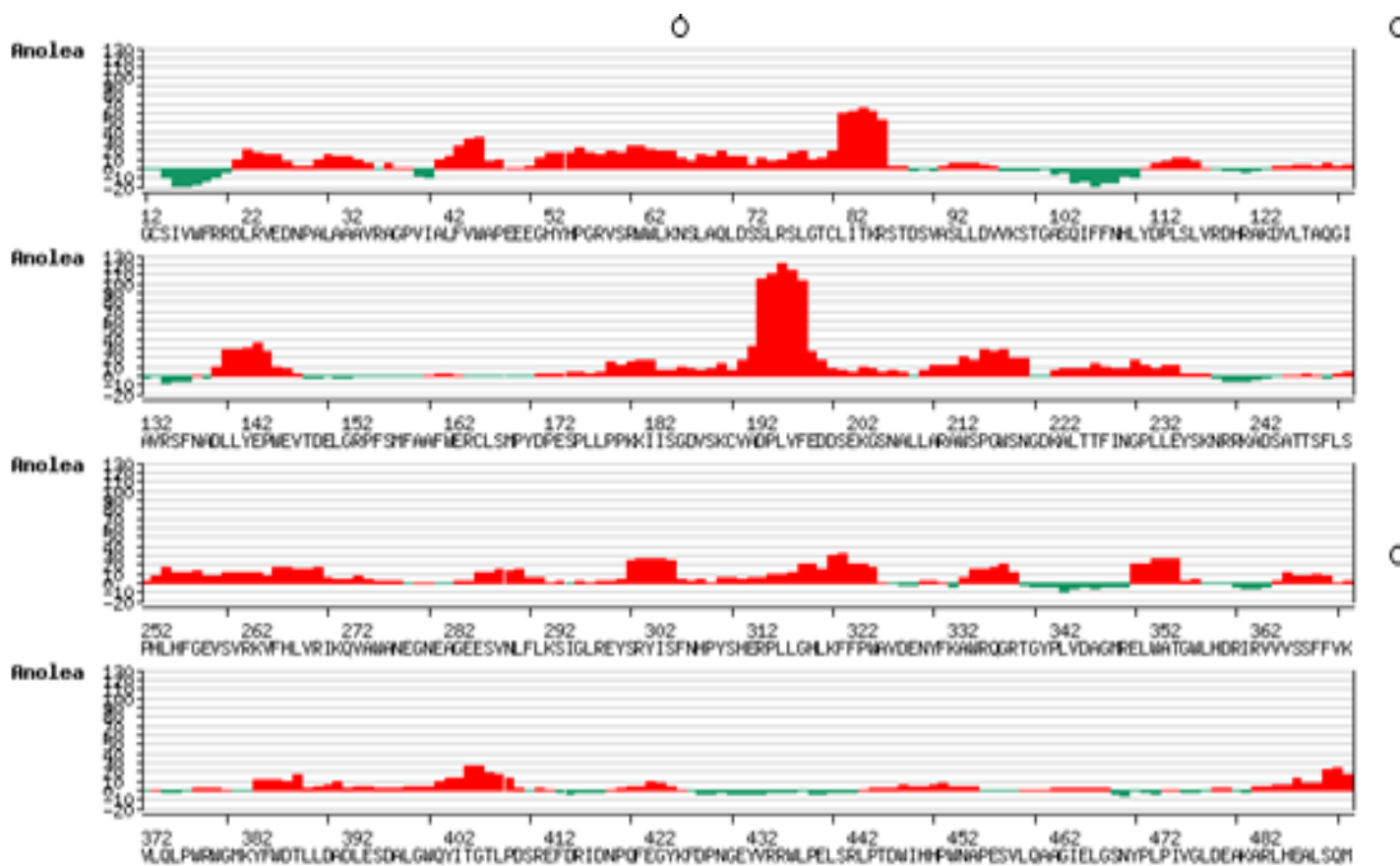
Sequences producing significant alignments:

| <u>Accession</u> | <u>Description</u> | <u>Max score</u> | <u>Total score</u> | <u>Query coverage</u> | <u>E value</u> | <u>Max ident</u> | <u>Links</u> |
|------------------------|---|----------------------|--------------------|-----------------------|----------------|------------------|---|
| 1U3C_A | Chain A, Crystal Structure Of The Phr Domain Of Cryptochrome 1 Fr | 1052 | 1052 | 74% | 0.0 | 100% |  |
| 1DNP_A | Chain A, Structure Of Deoxyribodipyrimidine Photolyase >pdb 1DNP | 205 | 205 | 68% | 9e-59 | 31% |  |
| 1OWL_A | Chain A, Structure Of Apophotolyase From Anacystis Nidulans >pdb | 190 | 190 | 63% | 3e-53 | 30% |  |
| 1TEZ_A | Chain A, Complex Between Dna And The Dna Photolyase From Anacy | 190 | 190 | 63% | 4e-53 | 30% |  |

Swiss-Model Workspace: Alignment mode 方式



利用Anolea评估程序来检测模型的健康度， Anolea计算每个氨基酸（横坐标）和周围环境相互作用的能量（纵坐标）正值以红色表示，负值以绿色表示能量越高越不稳定。



Thank you