

桃热激蛋白101 (Hsp101) 基因和蛋白序列预测与结构分析

CAAS五组

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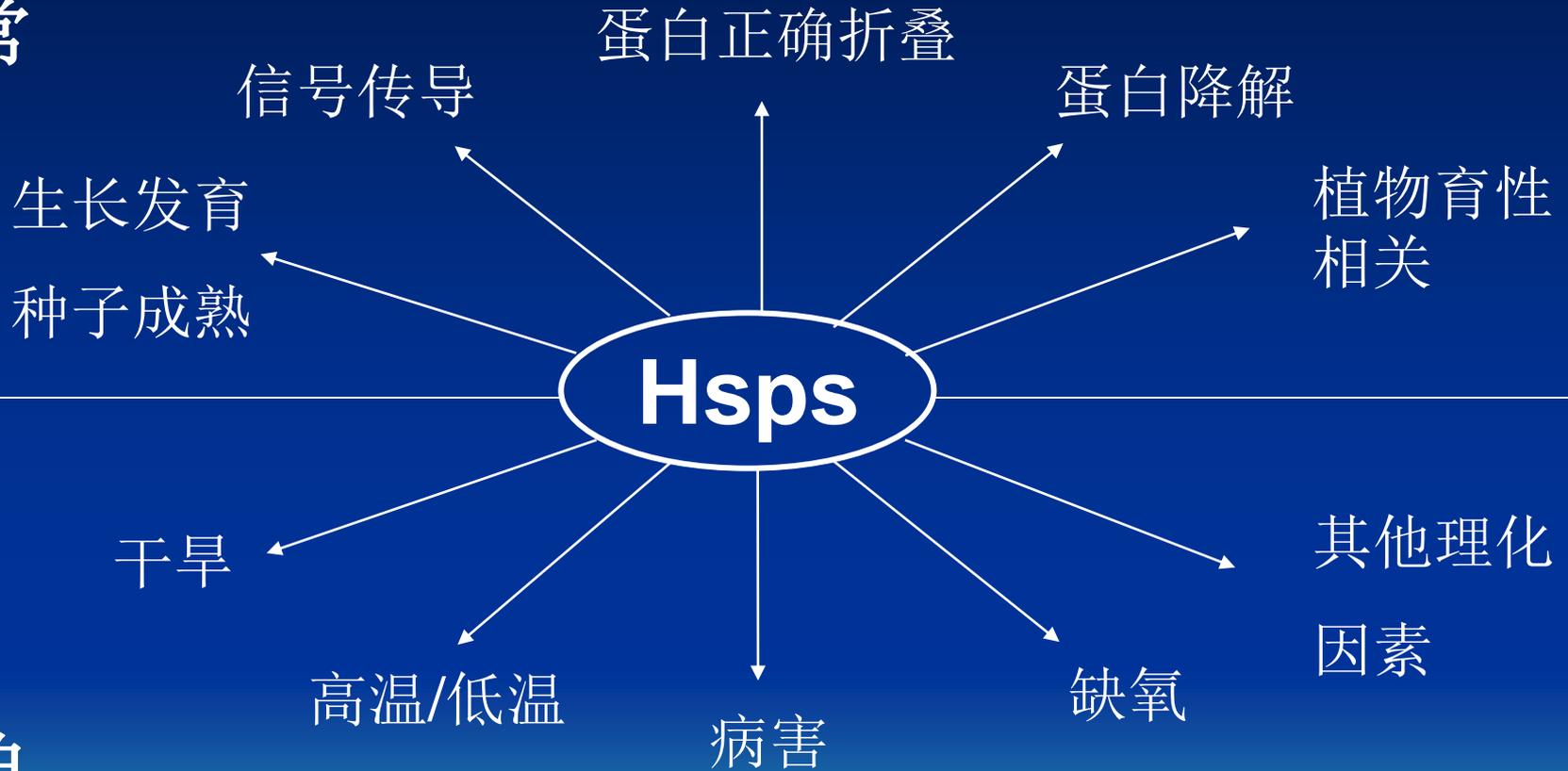


提纲

- 研究背景
- 基因序列与结构预测
- 蛋白序列与结构分析

研究背景

正常



胁迫

稳定蛋白质和膜结构，防止变性蛋白聚合及帮助其再折叠

主要的Hsp家族

Chaperone families

Major functions of chaperone families

Small heat shock proteins
(e.g. Hsp27*)

Prevent the aggregation of other proteins, by collecting protein “garbage”, act as “dustmen” of cells

Hsp60 family

Assistance in protein folding and re-folding

Hsp70 family

Assistance in protein folding and re-folding

Hsp90 family

Stabilize substrate proteins and maintain their active, or inactive state, prevent the aggregation of other proteins, by collecting protein “garbage”, act as “dustmen” of cells

Hsp100 family

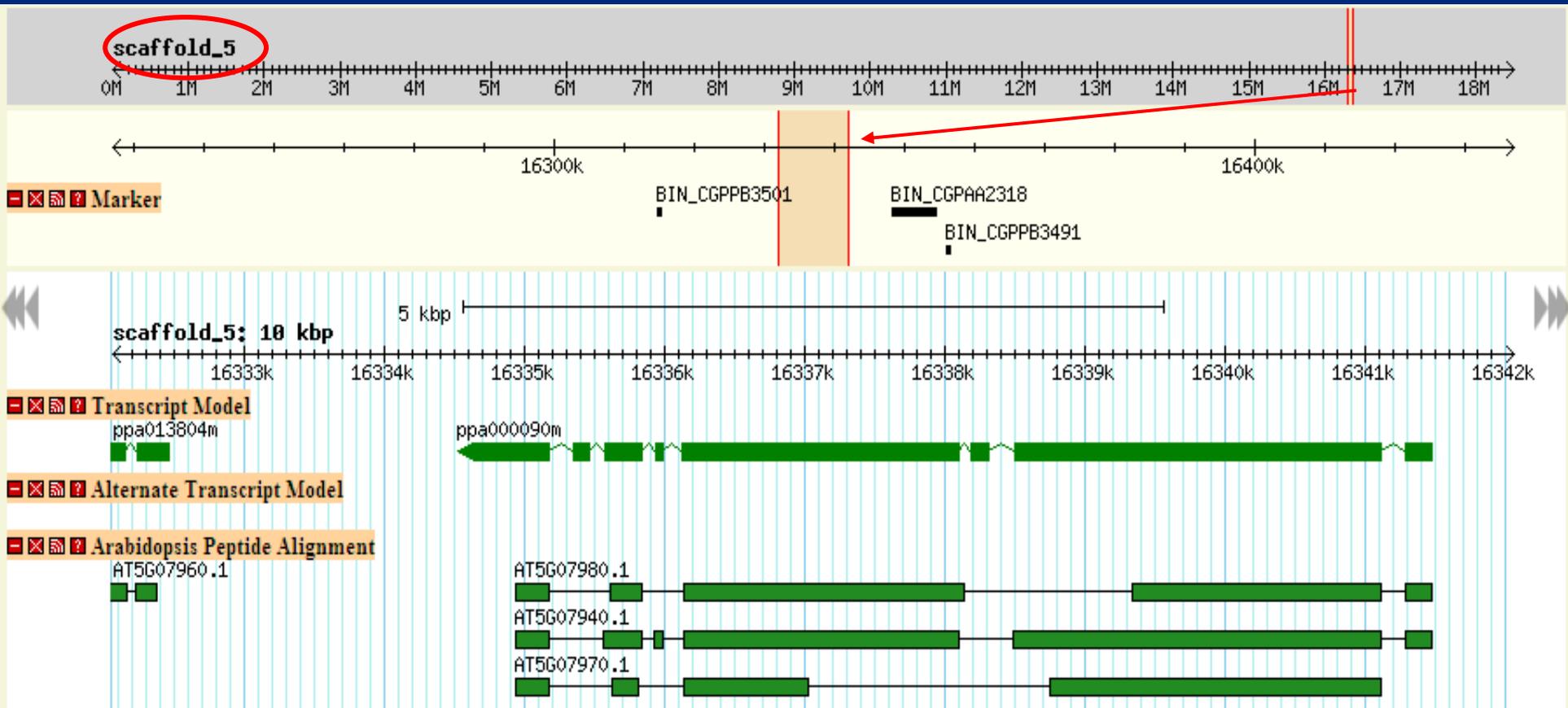
Desegregation of proteins

(P. Csermely & I. Yahara, 2002)



Hsp101基因序列与结构预测

EST序列~150bp → BLAST → 桃基因组序列
<http://www.rosaceae.org/>



基因组序列6.7kb

拟南芥和葡萄的Hsp101基因大小在**6.3-6.5kb**

推测该DNA片段包含一个基因



FGENESH基因预测

FGENESH 2.6 Prediction of potential genes in Dicot_arab genomic DNA

Seq name: scaffold_5:16357000..16363699

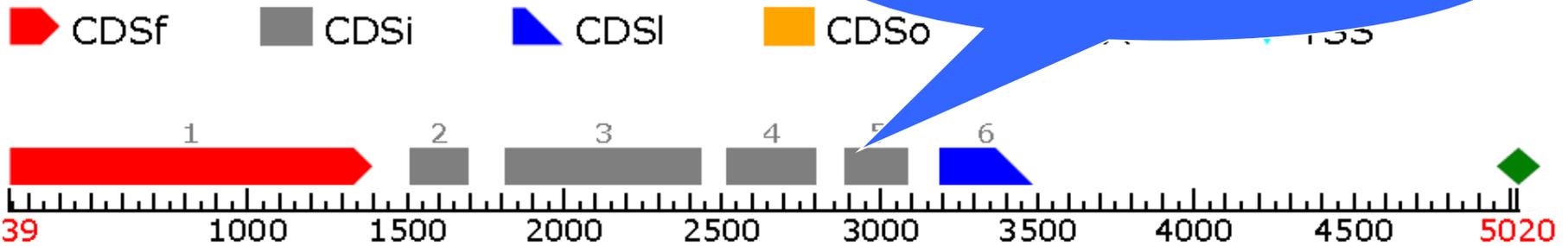
Length of sequence: 6700

Number of predicted genes 1: in +chain 1, in -chain 0.

Number of predicted exons 6: in +chain 6, in -chain 0.

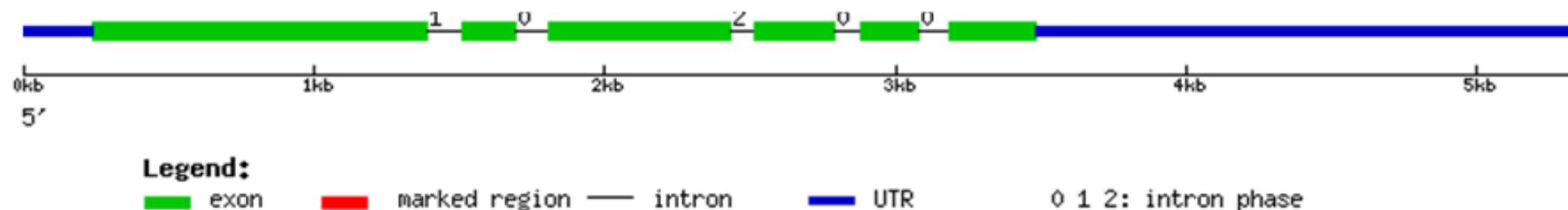
Positions of predicted genes and exons: Variants: 10

一个基因，6个外显子



1	+	1	CDSf	239	-	1388	177.57	239	-	1387	1149
1	+	2	CDSi	1510	-	1691	33.32	1512	-	1691	180
1	+	3	CDSi	1809	-	2431	94.53	1809	-	2429	621
1	+	4	CDSi	2513	-	2792	35.98	2514	-	2792	279
1	+	5	CDSi	2884	-	3081	26.47	2884	-	3081	198
1	+	6	CDSl	3185	-	3481	48.93	3185	-	3481	297
1	+		PolA	5020			1.06				

用DSDS显示基因结构 (<http://gsds.cbi.pku.edu.cn>)

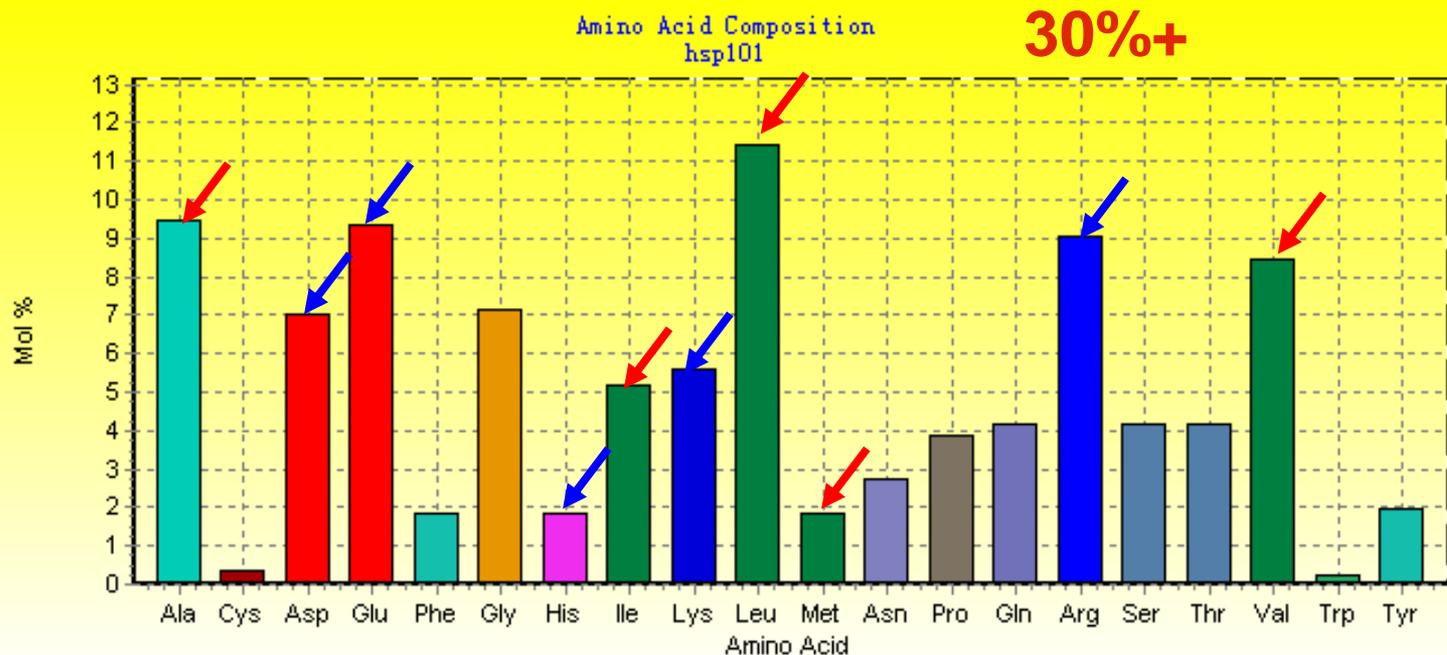


得到了**2730bp**的**mRNA**序列

蛋白序列与结构分析

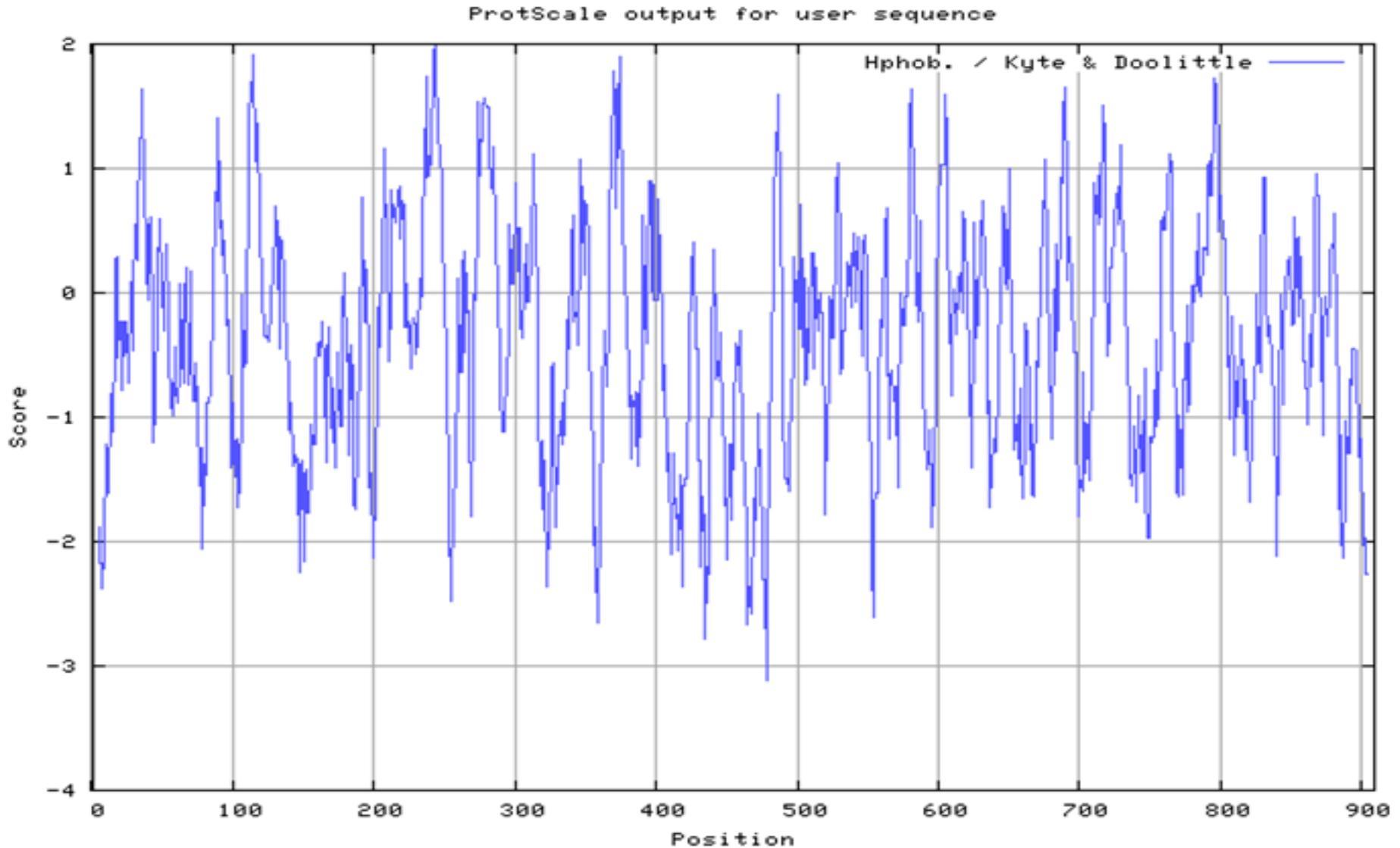
编码蛋白Hsp101长909个氨基酸残基

氨基酸	数目	百分比%
L	104	11.44
I	47	5.17
V	77	8.47
M	17	1.87
D	64	7.04
E	85	9.35
R	82	9.02
K	51	5.61
A	86	9.46
C	3	0.33
F	17	1.87
G	65	7.15
H	17	1.87
N	25	2.75
P	35	3.85
Q	38	4.18
S	38	4.18
T	38	4.18
W	2	0.22
Y	18	1.98

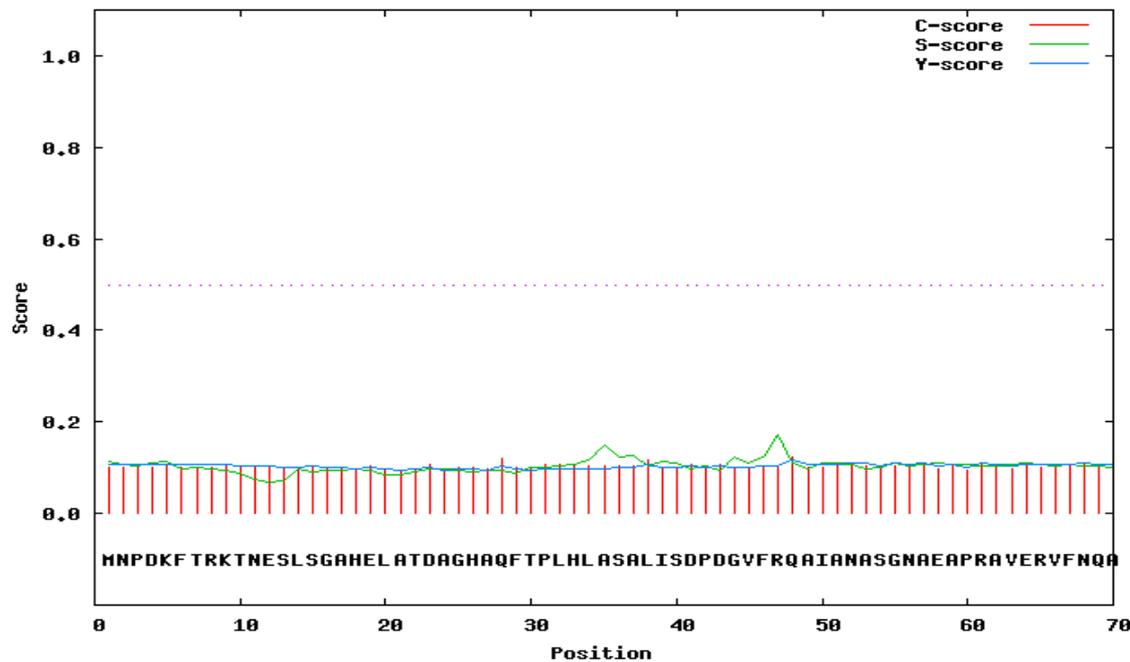


Bioedit计算氨基酸组成

ProtScale疏水性分析



SignalP-4.0 prediction (euk networks): hsp101



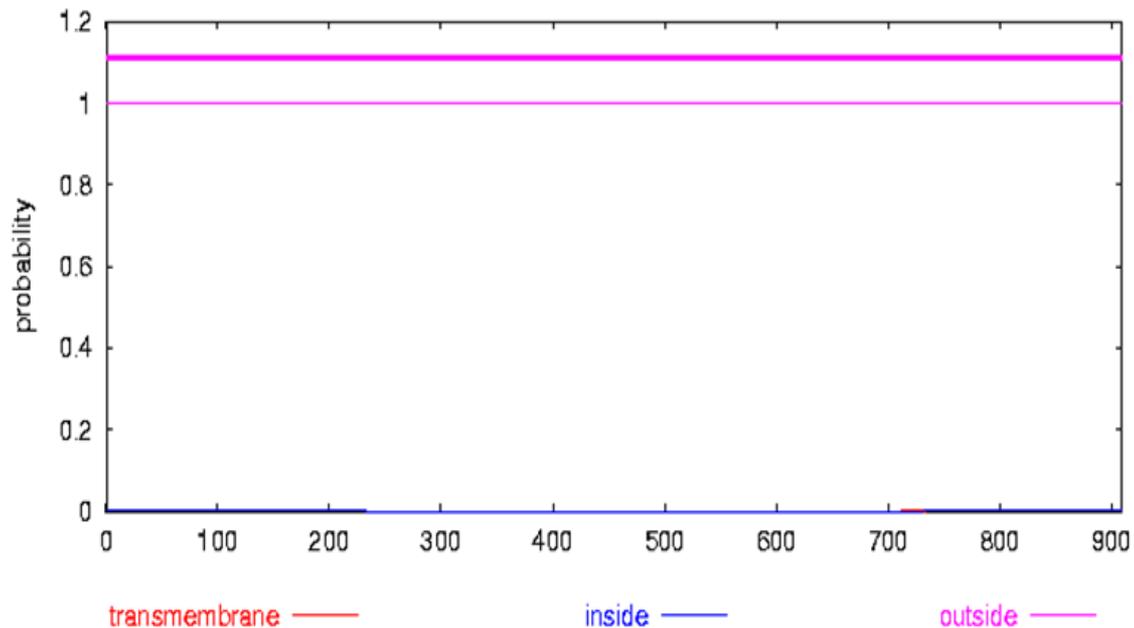
SignalP 4.0 Server

信号肽预测

TMHMM

跨膜预测

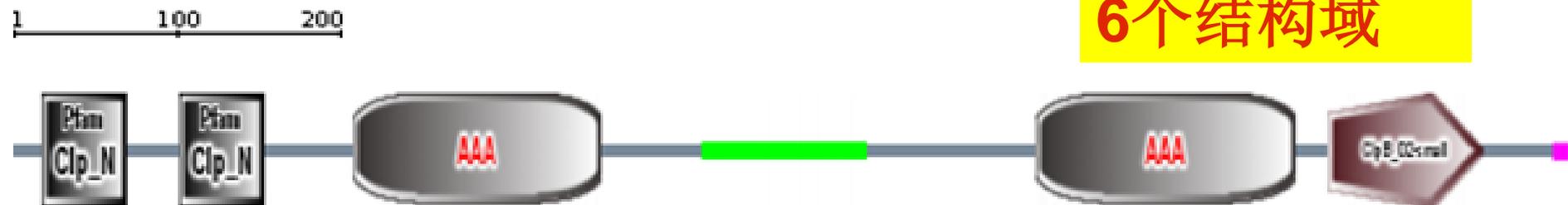
TMHMM posterior probabilities for hsp101



SMART结构域预测

Domains within the query sequence of 909 residues

6个结构域



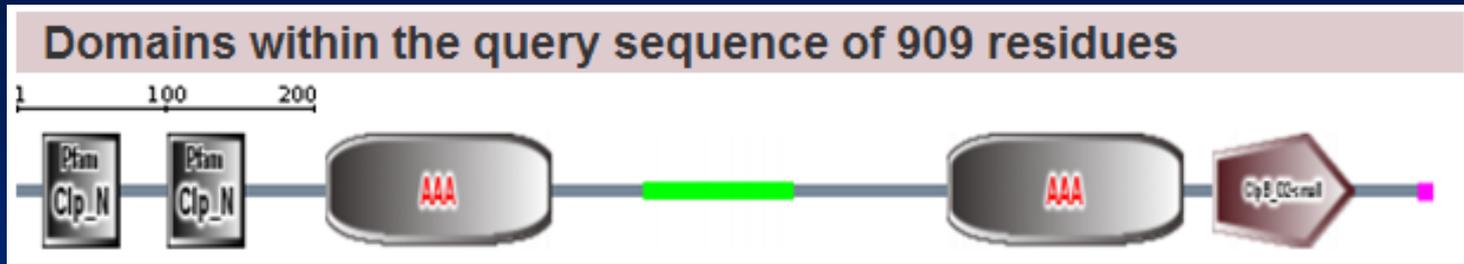
Name	Begin	End	E-value
Pfam:Clp_N	17	67	7.70e-10
Pfam:Clp_N	97	147	1.40e-07
AAA	199	344	2.81e-11
coiled coil	403	500	-
AAA	597	749	4.64e-12
ClpB_D2-small	767	858	3.15e-26
low complexity	899	909	-

与蛋白酶或其他基底结合的结构域

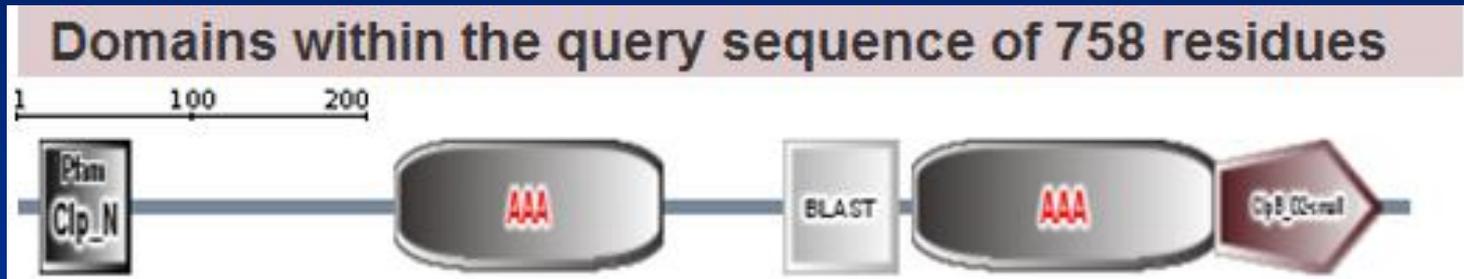
ATP酶结构域，ATP结合与水解

多聚化相关

Hsp101



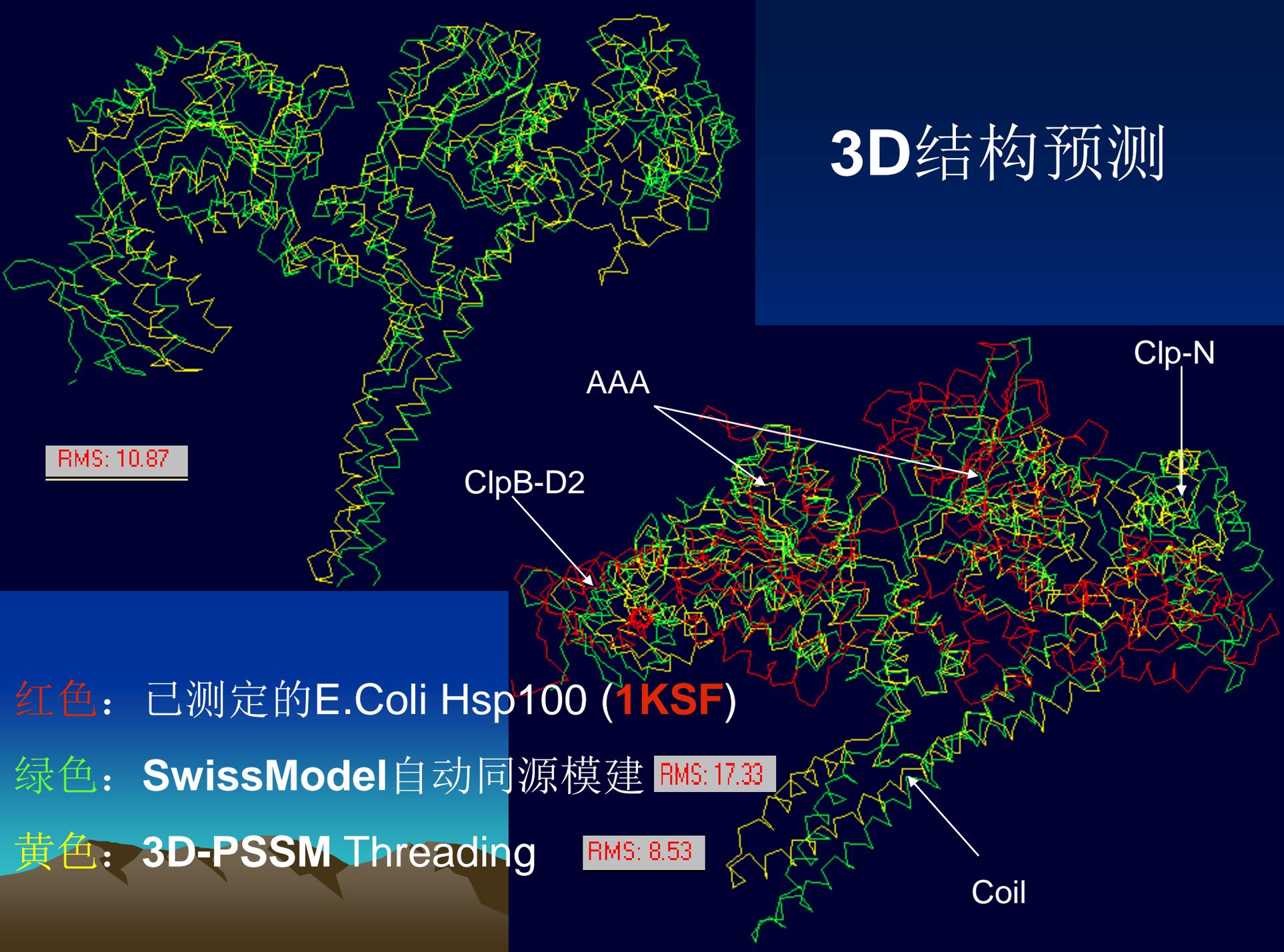
Hsp100



与E. Coli的Hsp100结构极类似（M. Agrawal et al. 2003），其晶体结构以测定，PDB ID为**1KSF**

问题：结构基本相同，为什么同源模建失败？

3D结构预测



红色: 已测定的E.Coli Hsp100 (**1KSF**)

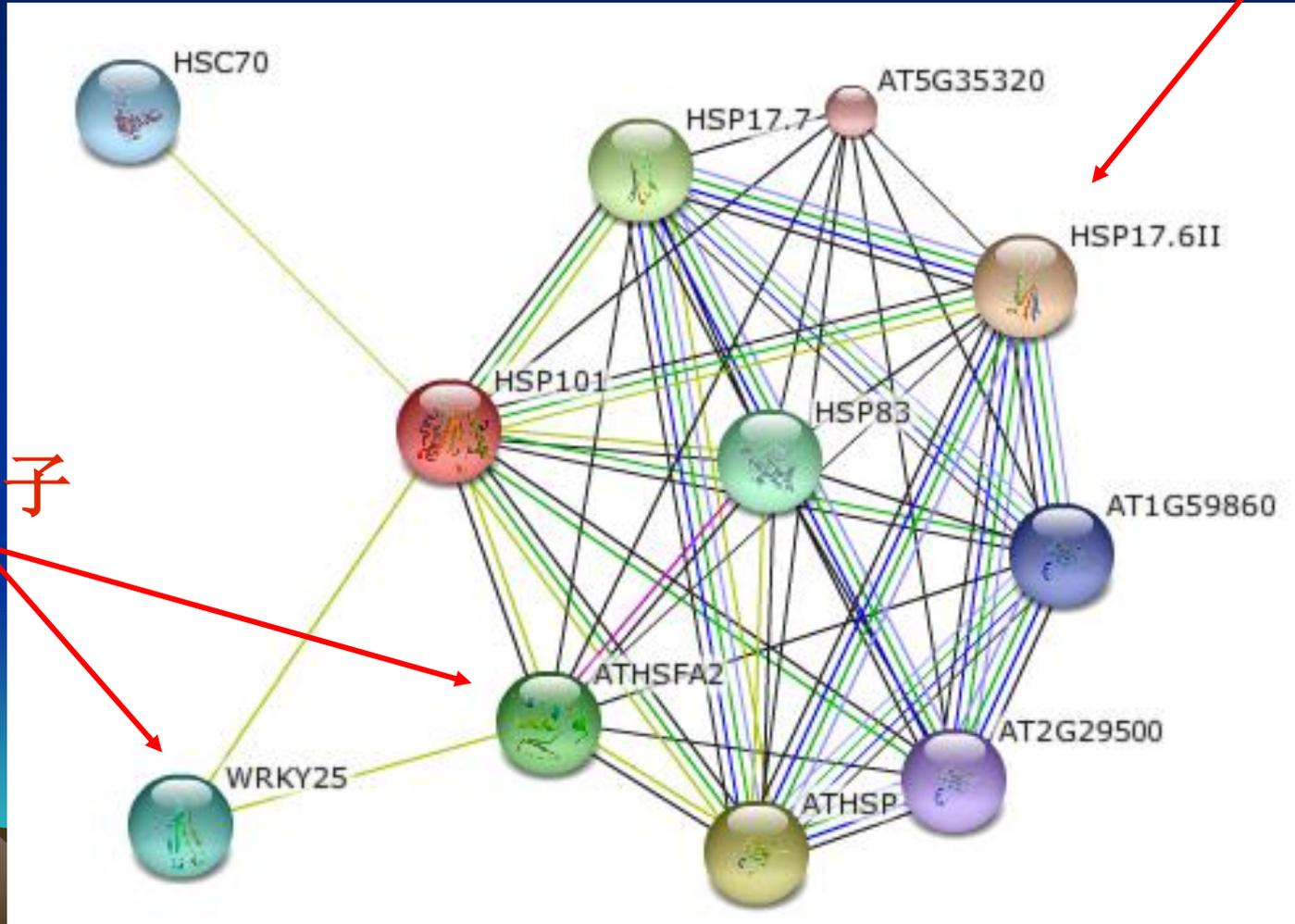
绿色: **SwissModel**自动同源模建 RMS: 17.33

黄色: **3D-PSSM Threading** RMS: 8.53

String蛋白相互作用

A. Thaliana

小热激蛋白家族



转录因子

参考文献

- 王吉龙, 癌胚抗原CEA 三维空间结构同源模建
- Vierling E. The roles of heat shock proteins in plants
- Cermely P. and Yahara I. Heat shock proteins
- M. Agarwal et al. molecular characterization of rice Hsp101
- 陈建南, 曲军. 温度, 热激蛋白与高粱与性变化
- Guanfeng W. and Xuening W. Molecular analysis of common wheat genes encoding three types of cytosolic heat shock protein 90 (Hsp90): functional involvement of cytosolic Hsp90s in the control of wheat seedling growth and disease resistance

致谢

- 感谢尊敬的罗老师
- 感谢CAAS



谢谢！

请大家批评指正！

