

# 拟南芥TIR-NBS-LRR类基因AT5G36930的分析

Analysis of gene *AT5G36930*, a member of TIR-NBS-LRR class

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# 目录



研究背景

基因结构及序列分析

蛋白家族演化分析

AT5G36930结构预测

参考文献





马铃薯晚疫病  
爱尔兰大饥荒（1845-1846）

水稻胡麻斑病  
印度孟加拉邦（1943）



葡萄霜霉病  
法国波尔多酿酒危机（1880）

小麦条锈病  
中国大饥荒（1950）



# 研究背景

**植物病害 (plant disease)**：植物受到病原生物的侵染或不良环境因素的干扰，其代谢过程受到影响和破坏，在生理上和组织结构上产生一系列病变，在形态上表现出病态，使植物不能正常生长发育，甚至导致局部或整株死亡，并对农业生产造成损失。

**植物抗病性(resistance)**：植物抵抗病原物破坏和抵抗引起发病的能力。抗病性是植物与其病原生物在长期的协同进化中相互适应、相互选择的结果，是植物普遍存在的、相对的性状，并且是抗病基因（基因型）在外界条件作用下的外在表现（表现型）。



## 研究背景

# gene-for-gene hypothesis

Flor (1956): 亚麻锈病，病菌致病性与亚麻抗病性遗传学系列实验。

对应于病原物方面的每一个决定致病性的基因，寄主方面也存在一个决定抗病性的基因，反之亦然。任何一方的每一个基因只有在另一方相对应的基因的作用下才能被鉴定出来。



# 研究背景

◆ NBS-LRR类基因：植物抗病基因中最重要的一类

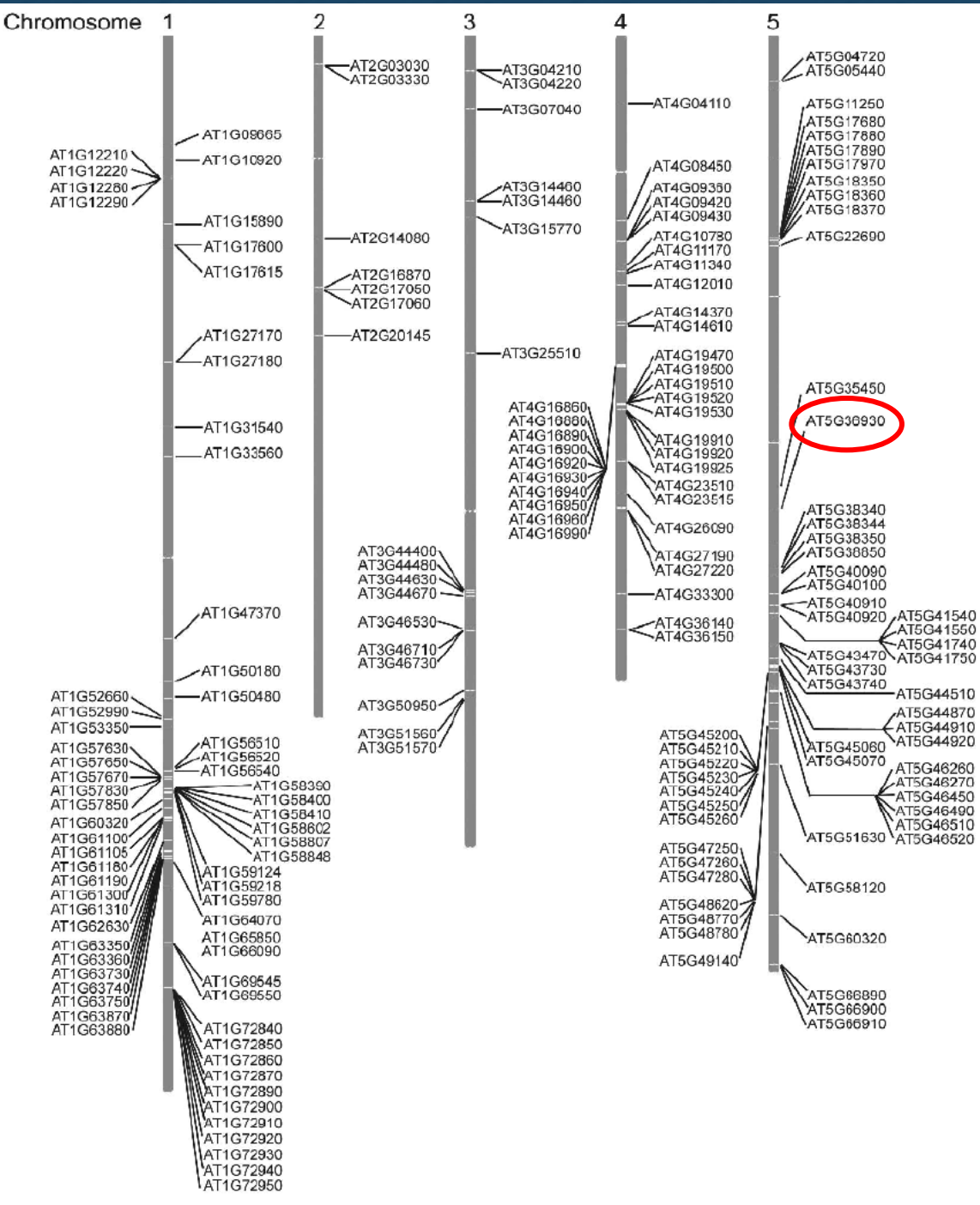
NBS: nucleotide binding site, 存在于真核生物的许多蛋白中, 主要负责ATP的水解以及释放信号。

LRR: Leucine-rich repeat, 富含亮氨酸重复, 蛋白质互作的平台和蛋白质活化作用的调控构件。

(1) TIR-NBS-LRR 类型基因: N端包含一个TIR (Toll and interleukin-1 receptor) 结构。

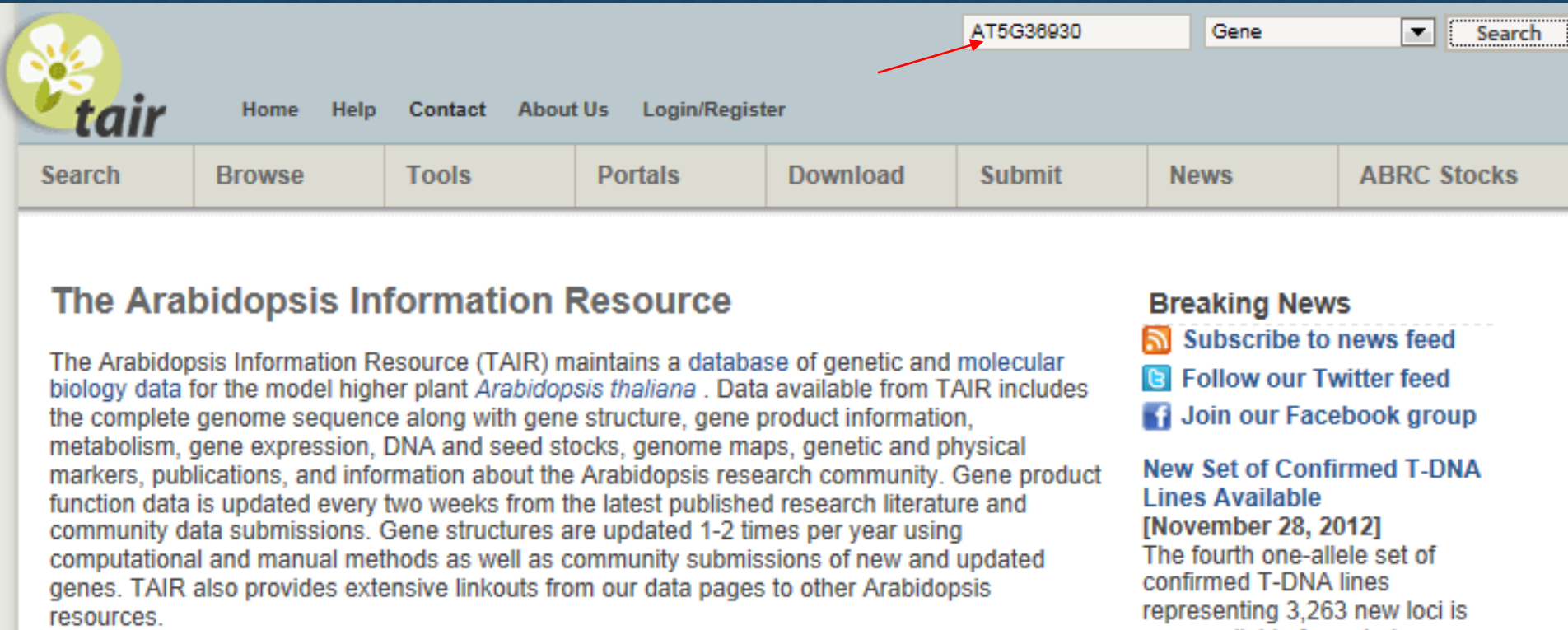
(2) CC-NBS-LRR 类型基因






拟南芥全基因组中共有204个NBS-LRR类基因，大多位于1号和5号染色体上，其中71.6%的NBS-LRR类基因分布在基因簇内。

# 基因结构及序列分析






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## The Arabidopsis Information Resource

The Arabidopsis Information Resource (TAIR) maintains a [database](#) of genetic and molecular biology data for the model higher plant *Arabidopsis thaliana*. Data available from TAIR includes the complete genome sequence along with gene structure, gene product information, metabolism, gene expression, DNA and seed stocks, genome maps, genetic and physical markers, publications, and information about the Arabidopsis research community. Gene product function data is updated every two weeks from the latest published research literature and community data submissions. Gene structures are updated 1-2 times per year using computational and manual methods as well as community submissions of new and updated genes. TAIR also provides extensive linkouts from our data pages to other Arabidopsis resources.

### Breaking News

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-  [Join our Facebook group](#)

### New Set of Confirmed T-DNA Lines Available

**[November 28, 2012]**  
The fourth one-allele set of confirmed T-DNA lines representing 3,263 new loci is

TAIR: 可以为研究者提供完整的基因组序列、基因结构、基因产物、代谢过程、基因表达、DNA和种子库、遗传和物理标记、发表文献以及拟南芥研究的相关信息。具有信息全面、更新速度快、数据量大、权威性高和影响范围广等优点。





## Locus: AT5G36930

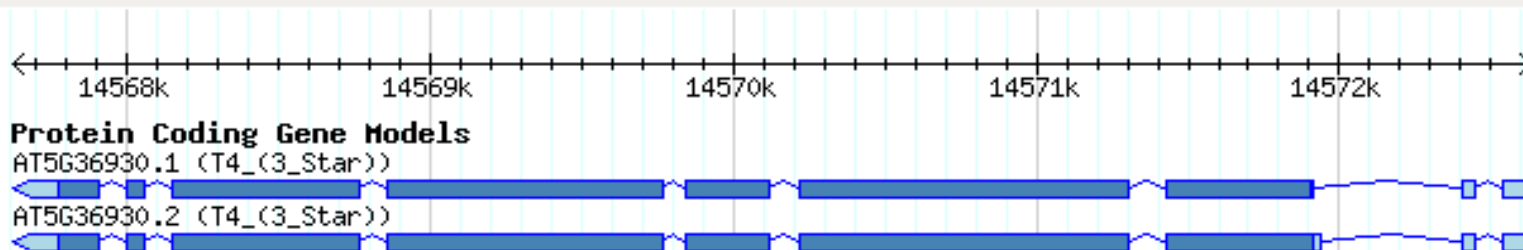
Date last modified	2008-04-22
TAIR Accession	Locus:2167457
Representative Gene Model	<a href="#">AT5G36930.2</a>
Gene Model Type	protein_coding

### Other names:

**Description**  Disease resistance protein (TIR-NBS-LRR class) family; FUNCTIONS IN: transmembrane receptor activity, ATP binding; INVOLVED IN: signal transduction, defense response, apoptosis, innate immune response; LOCATED IN: intrinsic to membrane; EXPRESSED IN: 19 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: NB-ARC (InterPro:IPR002182), Toll-Interleukin receptor (InterPro:IPR000157), Disease resistance protein (InterPro:IPR000767); BEST Arabidopsis thaliana protein match is: disease resistance protein (TIR-NBS-LRR class), putative (TAIR:AT5G17680.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLINK).

**Other Gene Models**  [AT5G36930.1](#)

### Map Detail Image



**Annotations**

category	relationship type	keyword
GO Biological Process	involved in	defense response, signal transduction

Annotations ?	category	relationship type ?	keyword ?
	GO Biological Process	involved in	defense response, signal transduction
	GO Cellular Component	located in	cytoplasm, intracellular
	GO Molecular Function	has	ADP binding
	Growth and Developmental Stages	expressed during	4 anthesis stage, 4 leaf senescence stage, C globular stage, D bilateral stage, E expanded cotyledon stage, F mature embryo stage, LP.02 two leaves visible stage, LP.04 four leaves visible stage, LP.06 six leaves visible stage, LP.08 eight leaves visible stage, LP.10 ten leaves visible stage, LP.12 twelve leaves visible stage, petal differentiation and expansion stage
	Plant structure	expressed in	cauline leaf, collective leaf structure, cotyledon, flower, hypocotyl, inflorescence meristem, leaf apex, leaf lamina base, pedicel, petal, petiole, plant embryo, seed, sepal, shoot apex, shoot system, stamen, stem, vascular leaf

**生物学功能**

Annotation Detail

RNA Data			
One-channel Arrays	array element name ?	avg. signal intensity (std. error)	avg. signal percentile (std. error)
	249639_AT	57.527 (1.353)	39.324 (0.497)

Associated Transcripts ?	type	number associated	<b>芯片数据</b>
	EST	( 14 )	

Chromosome	5
------------	---

Nucleotide Sequence ?	full length CDS	full length genomic	full length cDNA
-----------------------	-----------------	---------------------	------------------

Protein Data ?	name	length(aa)	molecular weight	isoelectric point	domains( # of domains)
	AT5G36930.2	1191	136030.0	6.3881	Disease resistance protein:IPR000767(4) Toll-Interleukin receptor:IPR000157(4) NB-ARC:IPR002182(1)

**序列信息**

greater than half the expression value.

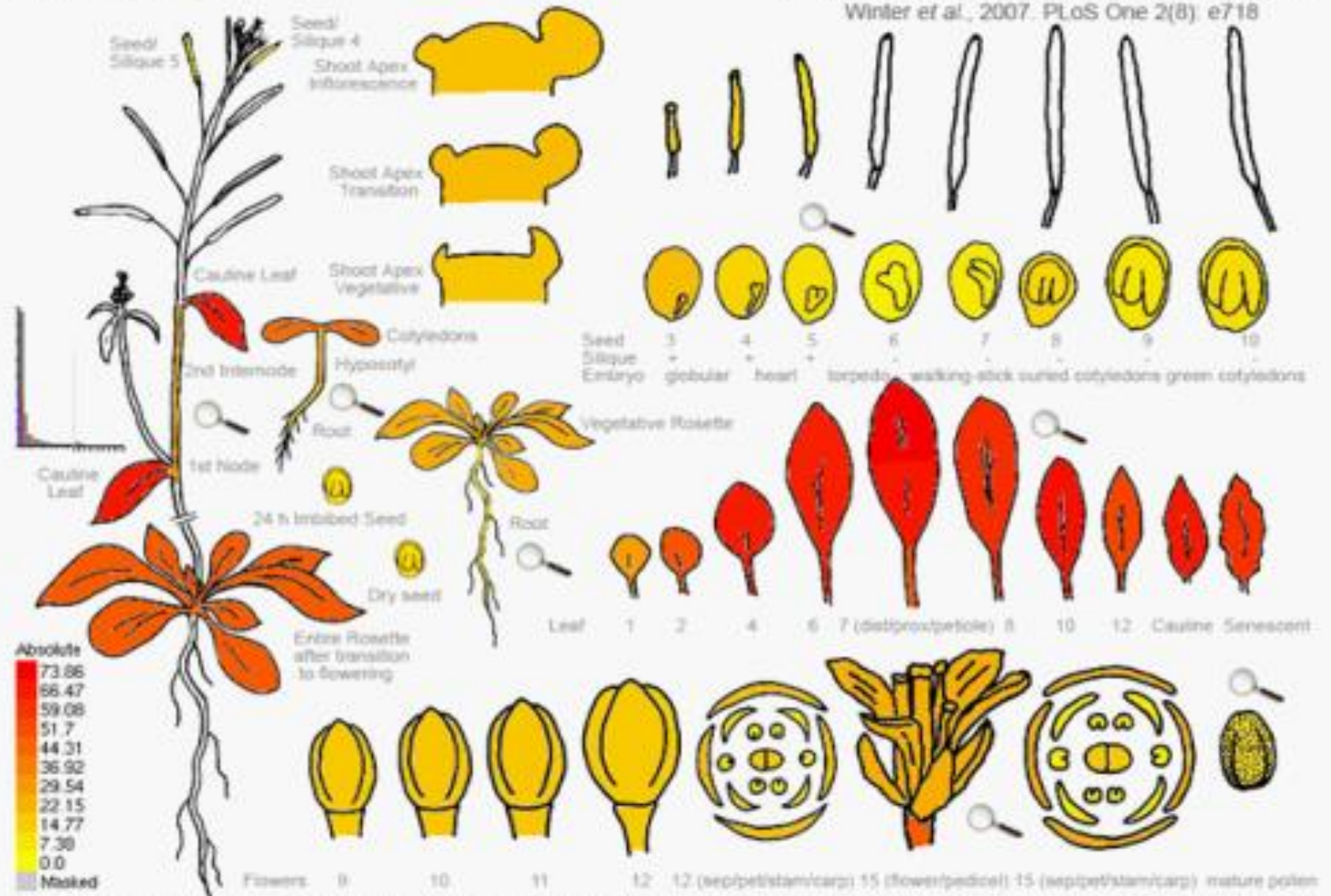
# e-FP browser



At5g36830 249638\_at

Arabidopsis eFP Browser at bar.utoronto.ca

Winter et al., 2007. PLoS One 2(8): e718



eFP Browser by B. Virejat, drawn by J. Alle and N. Provart. Data from Gene Expression Map of Arabidopsis Development. Schmid et al., 2005, Nat. Gen. 37:501, and the Nambara lab for the imbibed and dry seed stages. Data are normalized by the GCOS method, TGT value of 100. Most tissues were sampled in triplicate.

# 序列分析

## BLAST:

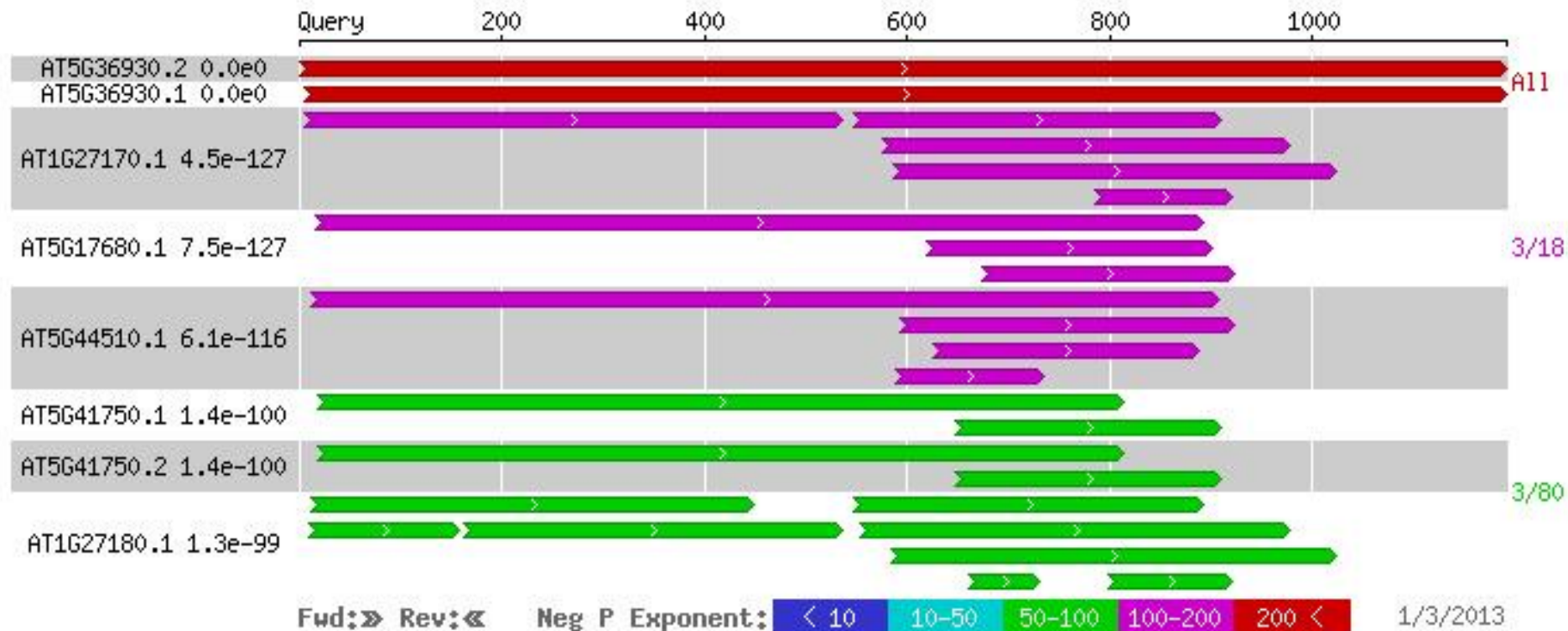
TAIR BLAST Results:

### Summary of BLAST Results Help

The graph shows the highest hits per range.

Data have been omitted in the Summary Graphic: 8/100 hits displayed.

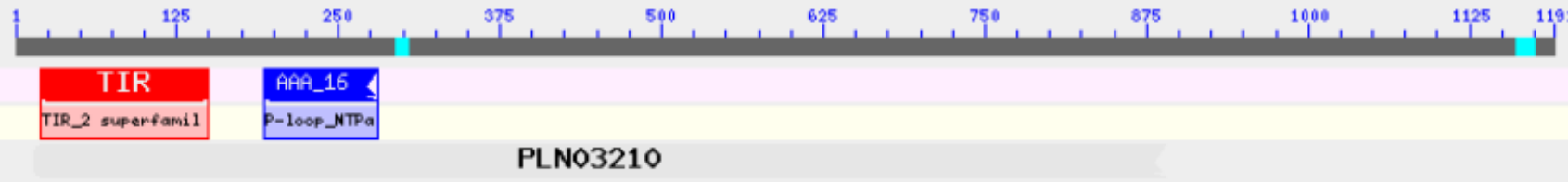
| Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:14567771



# BLAST:

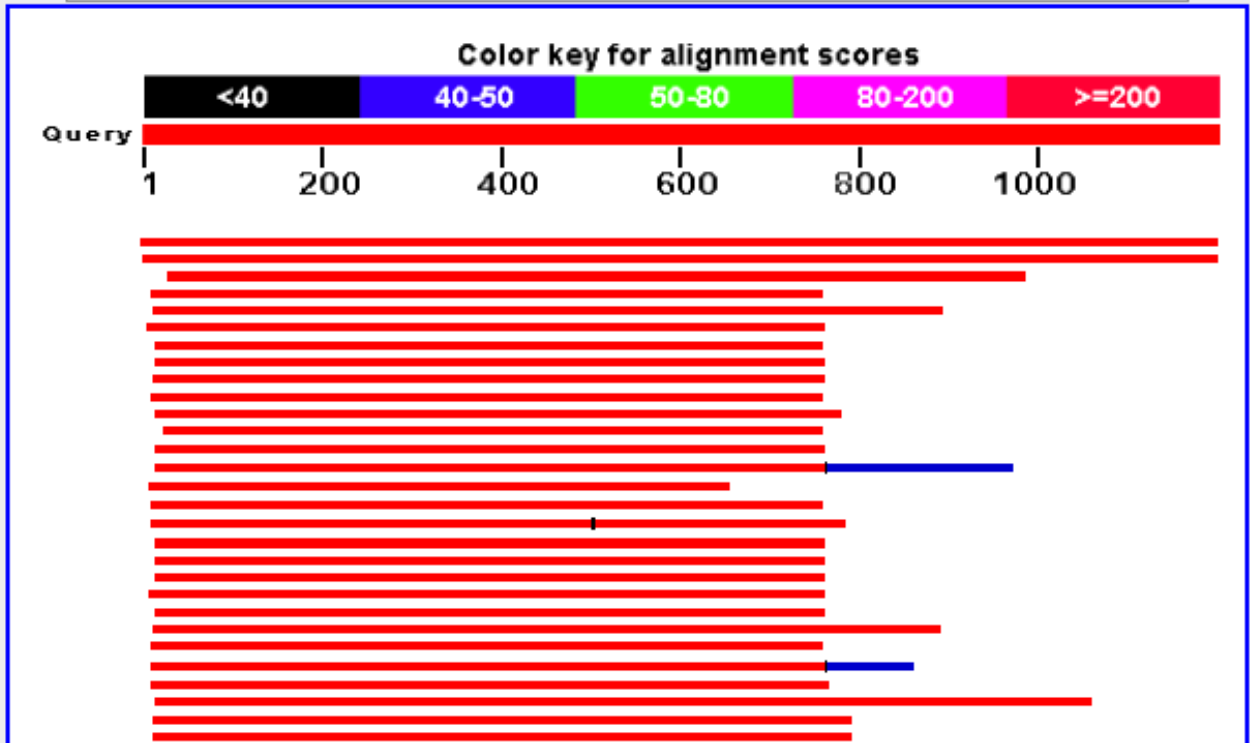
NCBI BLAST Results:

Putative conserved domains have been detected, click on the image below for detailed results.

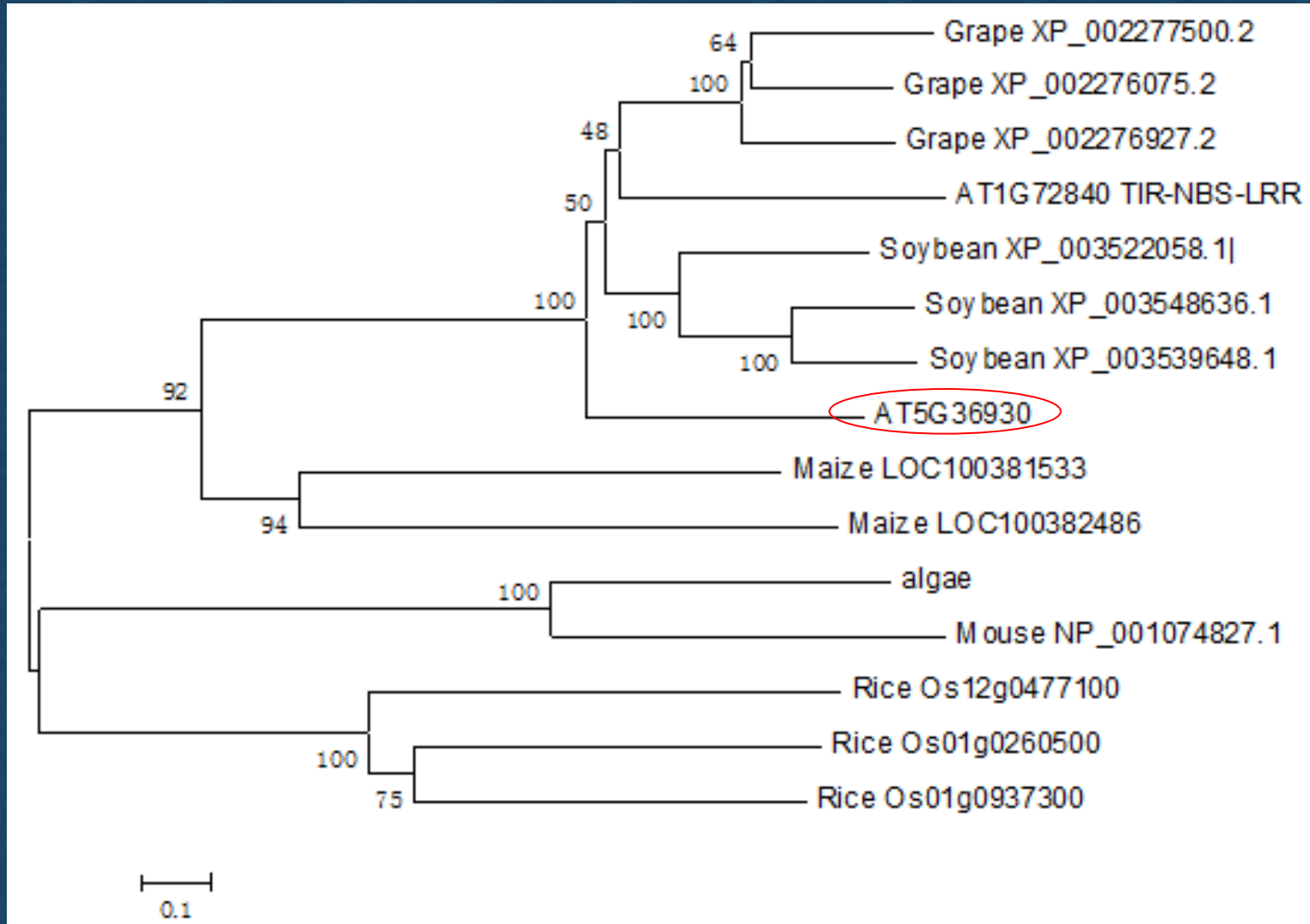


Distribution of 158 Blast Hits on the Query Sequence

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

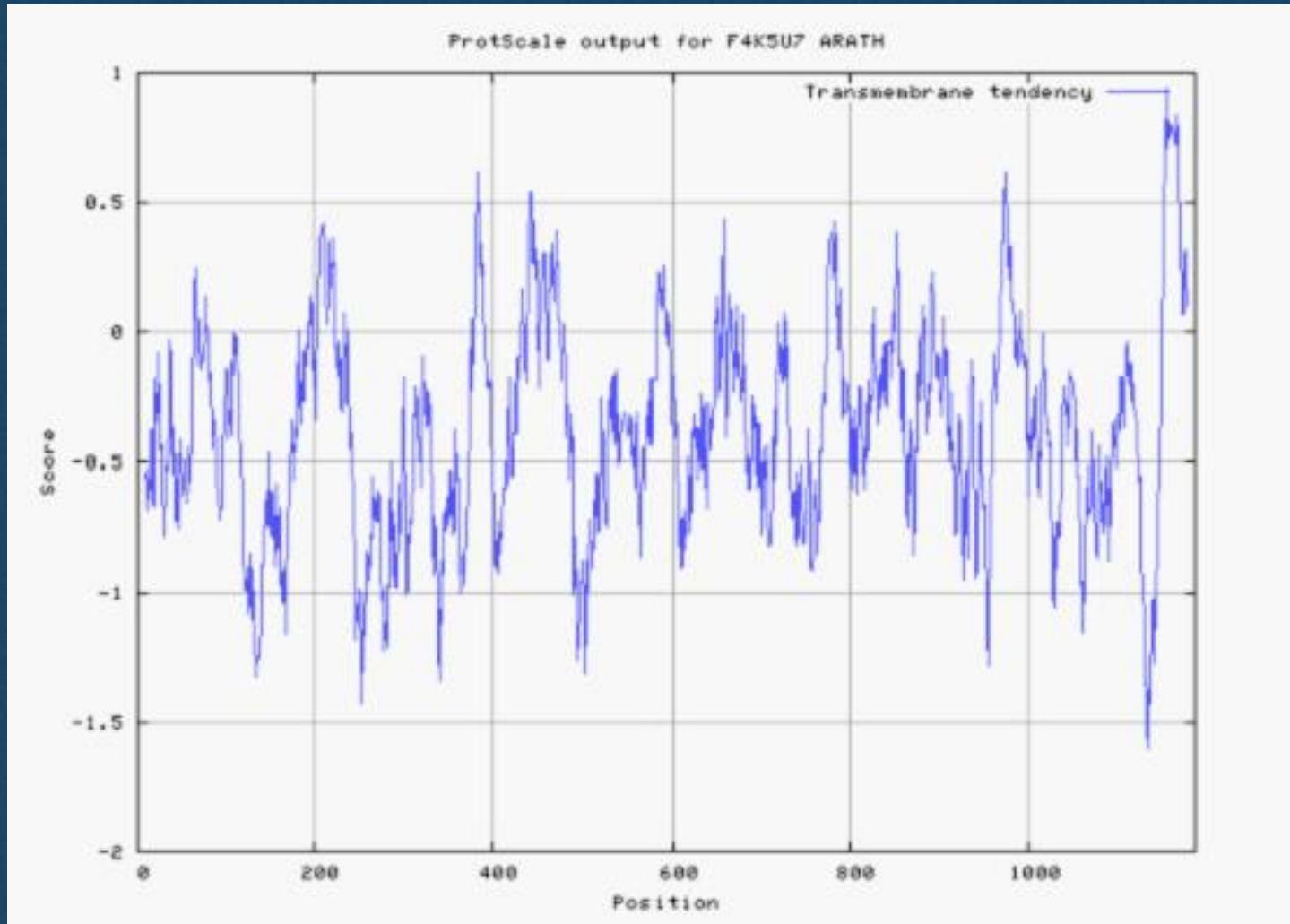


# 序列比对和系统发育分析



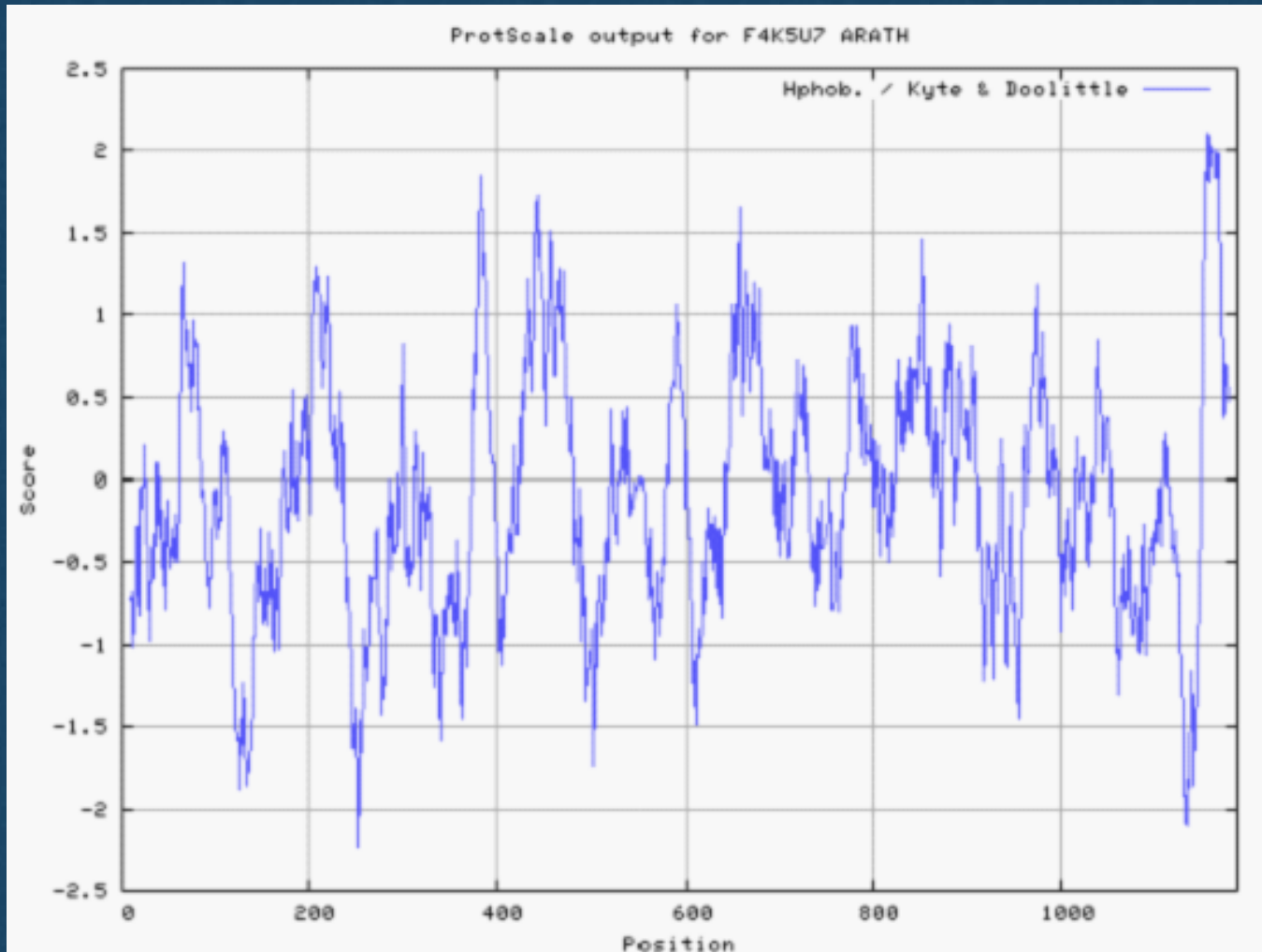
# 蛋白结构预测

Proscale: Transmembrane tendency



# Proscale: 亲疏水性分析

(Hphob. / Kyte & Doolittle window size=19)

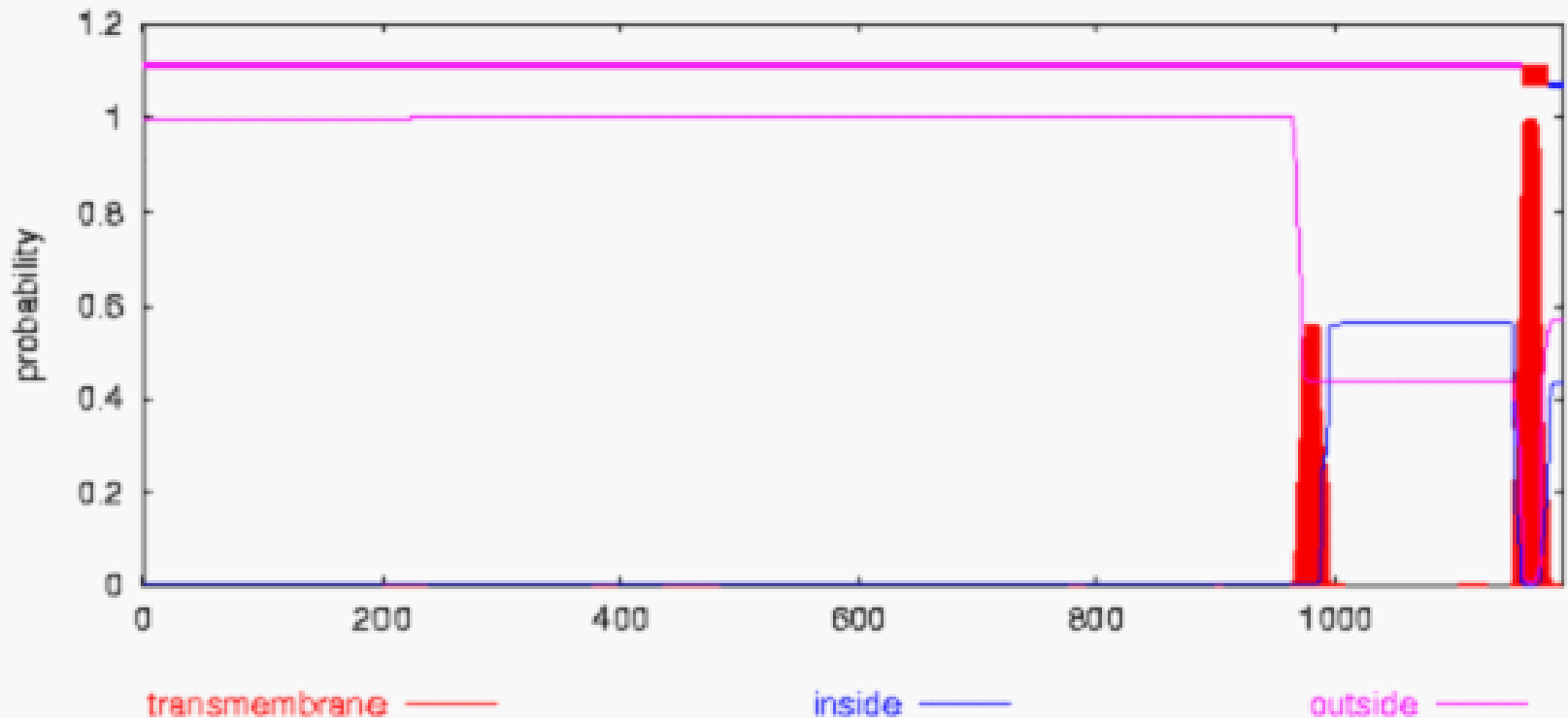




# TMHMM result

```
# AT5G36930.2 Length: 1191
# AT5G36930.2 Number of predicted TMHs: 1
# AT5G36930.2 Exp number of AAs in TMHs: 34.59076
# AT5G36930.2 Exp number, first 60 AAs: 0
# AT5G36930.2 Total prob of N-in: 0.00443
AT5G36930.2    TMHMM2.0    outside    1 1156
AT5G36930.2    TMHMM2.0    TMhelix   1157 1179
AT5G36930.2    TMHMM2.0    inside    1180 1191
```

TMHMM posterior probabilities for AT5G36930.2



# Pfam预测结构域

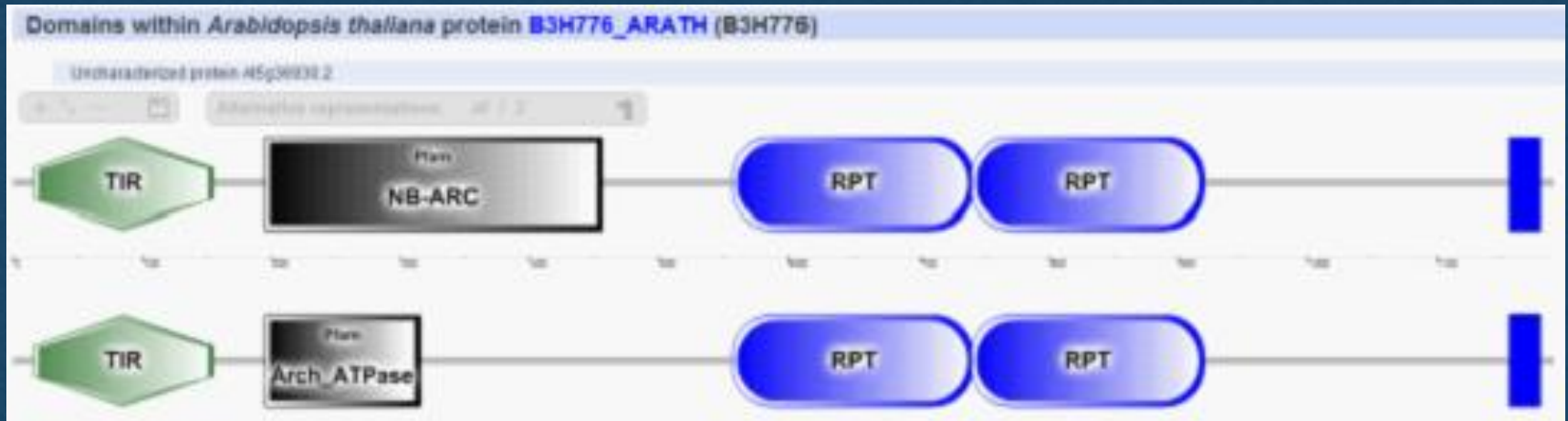
## Pfam domains

This image shows the arrangement of the Pfam domains that we found on this sequence. Clicking on the domain names below gives the domain boundaries for each of the domains.



Source	Domain	Start	End
Pfam A	<a href="#">TIR</a>	19	151
Pfam A	<a href="#">NB-ARC</a>	195	456
low_complexity	n/a	294	304
transmembrane	n/a	377	396
	n/a	911	1190
transmembrane	n/a	1152	1172
low_complexity	n/a	1161	1175

# Smart预测蛋白结构域



## Confidently predicted domains, repeats, motifs and features:

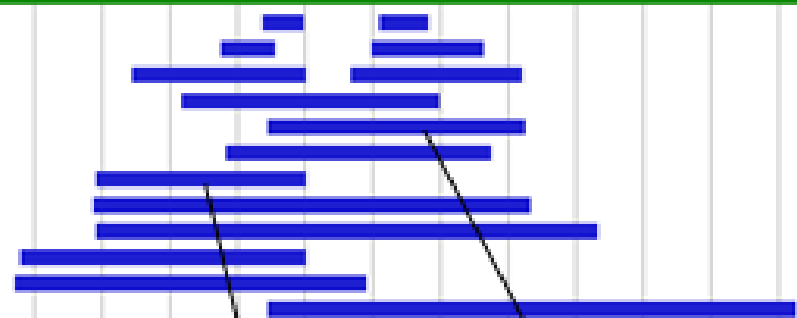
Name	Start ▲	End	E-value
<a href="#">TIR</a>	16	155	9.55e-43
<a href="#">Pfam:Arch_ATPase</a>	195	315	0.0092
<a href="#">Pfam:NB-ARC</a>	195	456	2.1e-39
<a href="#">internal repeat 1</a>	557	741	1.83e-8
<a href="#">internal repeat 1</a>	740	920	1.83e-8
<a href="#">transmembrane region</a>	1157	1179	1.83e-8

# 同源模建

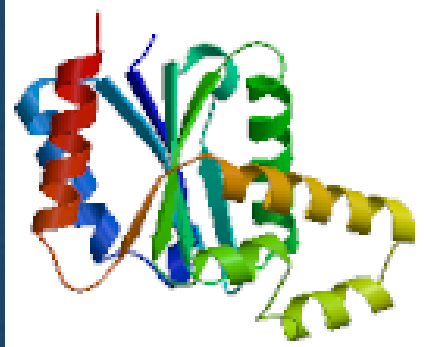
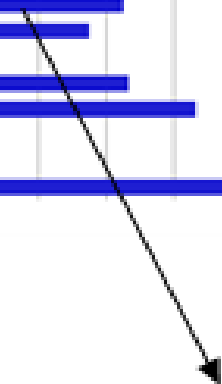
Workunit: P000003 AT5G36930.2 - Overview

1

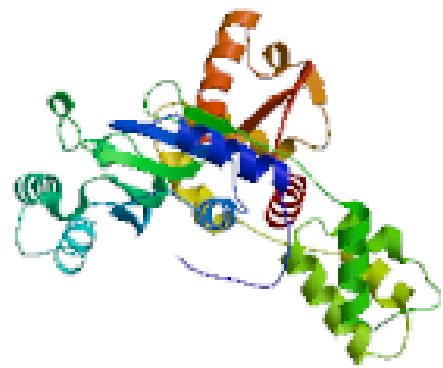
1191



click on model here



TIR domain



ATPase



# References

- Peter Brodersen, Morten Petersen, Henrik Bjorn Nielsen et. al. (2006). Arabidopsis MAP kinase 4 regulates salicylic acid- and jasmonic acid/ethylene-dependent responses via EDS1 and PAD4. *The Plant Journal* 47, 532–546.
- Xiaoping Tan, Blake C Meyers, Alexander Kozik *et al.* (2007). Global expression analysis of nucleotide binding site-leucine rich repeat-encoding and related genes in Arabidopsis. *BMC Plant Biology* 7: 56.
- Li Chunlai, Zhang Huaiyu. (2004). Research Advance of Resistance Gene Analogs in Plant. *Molecular Plant Breeding* 2(6): 853-860.
- Wang Yan, Li Zhaoyang, Tang Xinlong et. al. (2006). Bioinformatic Analysis of the NBS-LRR Gene Family in *Arabidopsis thaliana*. *Chinese Agricultural Science Bulletin* 25(15): 40-45.
- Li Feng, Zhang Ying, Fan Xiucui, Zhang Guohai, Liu Chonghuai. (2011). Research Advance of Resistance Gene NBS-LRR Type in Plant. *Fenzi Zhiwu Yuzhong* 9, 1784-1790.



致

感谢罗老师一个学期以来的认真授  
课和耐心的指导！

谢

感谢助教的负责和帮助！

感谢小组所有成员！



Thank you!

1/22/2013

