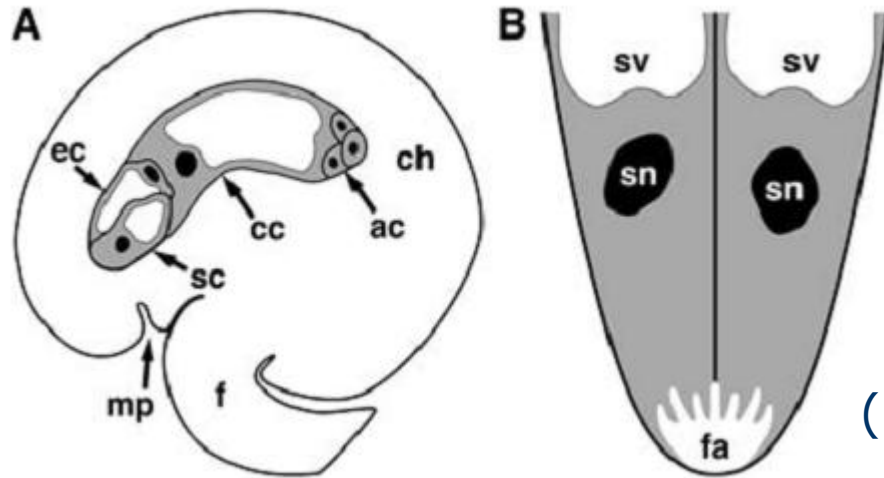




The bioinformatic analysis of Arabidopsis transcription factor MYB98

By G03 (Hao Lihong, Sun Tianshu, Yu He, Wang Chaoyang)
2013.01.11

Why we are interested in MYB98



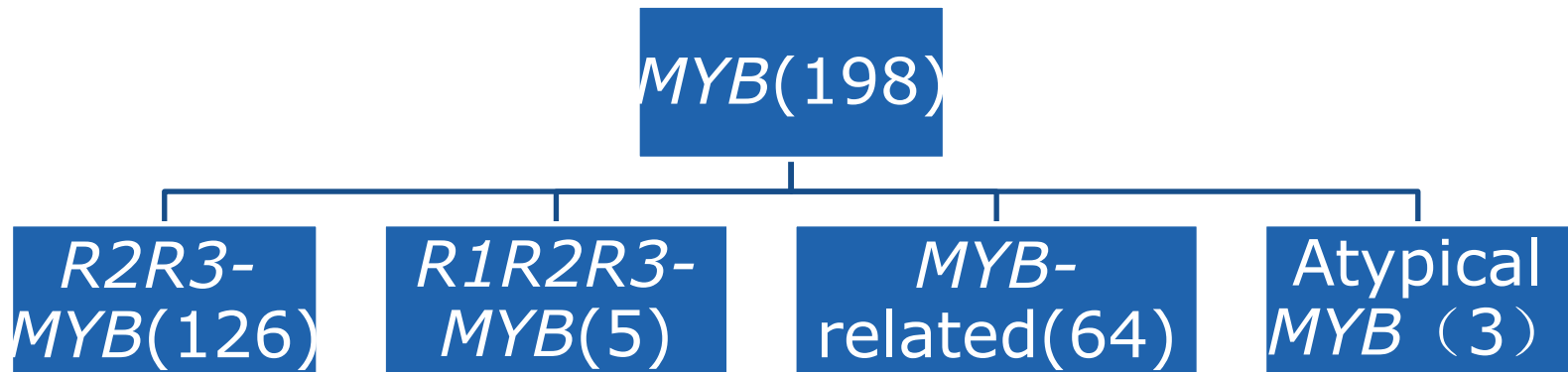
(Ryushiro D. K et al,2005)

- ❖ **Pollen tube guidance is one of the major issues about double fertilization.**
- ❖ **As we know the synergid cells play a central role during this process.**
- ❖ **MYB98 is a synergid cell-specific transcription factor who regulates many key genes involved in this process.**

MYB98 fundamental information

- ❖ **Name:At4g18770.1**
- ❖ **Length of nucleotides:1816bp**
- ❖ **Length of aa:427aa**
- ❖ **Belongs to MYB superfamily ,R2R3-MYB subfamily in *Arabidopsis thaliana***
- ❖ **Encodes a transcription factor**

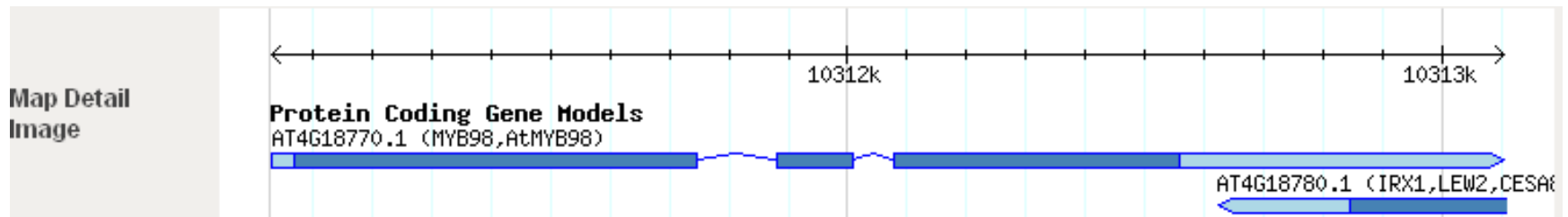
About *A.thaliana* MYB superfamily



- **MYB proteins are a superfamily of transcription factors that play regulatory roles in developmental processes and defense responses in plants.**

(Chen Yanhui et al.2006)

MYB98 gene structure



(From TAIR)

Domain prediction of MYB98 protein



Confidently predicted domains, repeats, motifs and features:

Name	Start	End	E-value
low complexity	42	72	N/A
SANT	216	265	1.61e-17
SANT	268	316	2.76e-16
low complexity	362	379	2.76e-16

SANT : "SWI3, ADA2, N-CoR and TFIIIB" DNA-binding domains

The SANT domain has a strong structural similarity to the DNA-binding domain of Myb-related proteins

Regions

<input type="checkbox"/>	Domain	212 - 267	56	HTH myb-type 1	
<input type="checkbox"/>	Domain	268 - 318	51	HTH myb-type 2	

(From Uniprot)

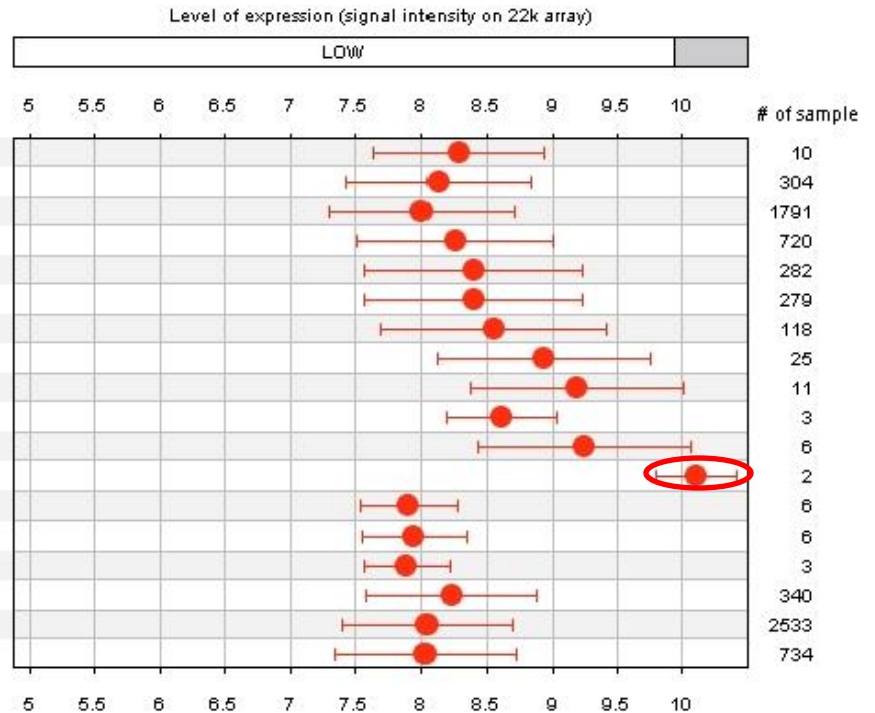
Tissue expression pattern of MYB98 (1)

● AT4G18770

Arabidopsis thaliana (85)

Expand all Collapse all

- callus
- ▶ cell culture / primary cell
- ▶ seedling
- ▼ inflorescence
 - ▼ raceme
 - ▼ flower
 - ▶ stamen
 - ▼ pistil
 - ▼ carpel
 - stigma
 - ▼ ovary
 - ovule
- petal
- sepal
- pedicel
 - ▶ silique
- ▶ shoot
- ▶ roots



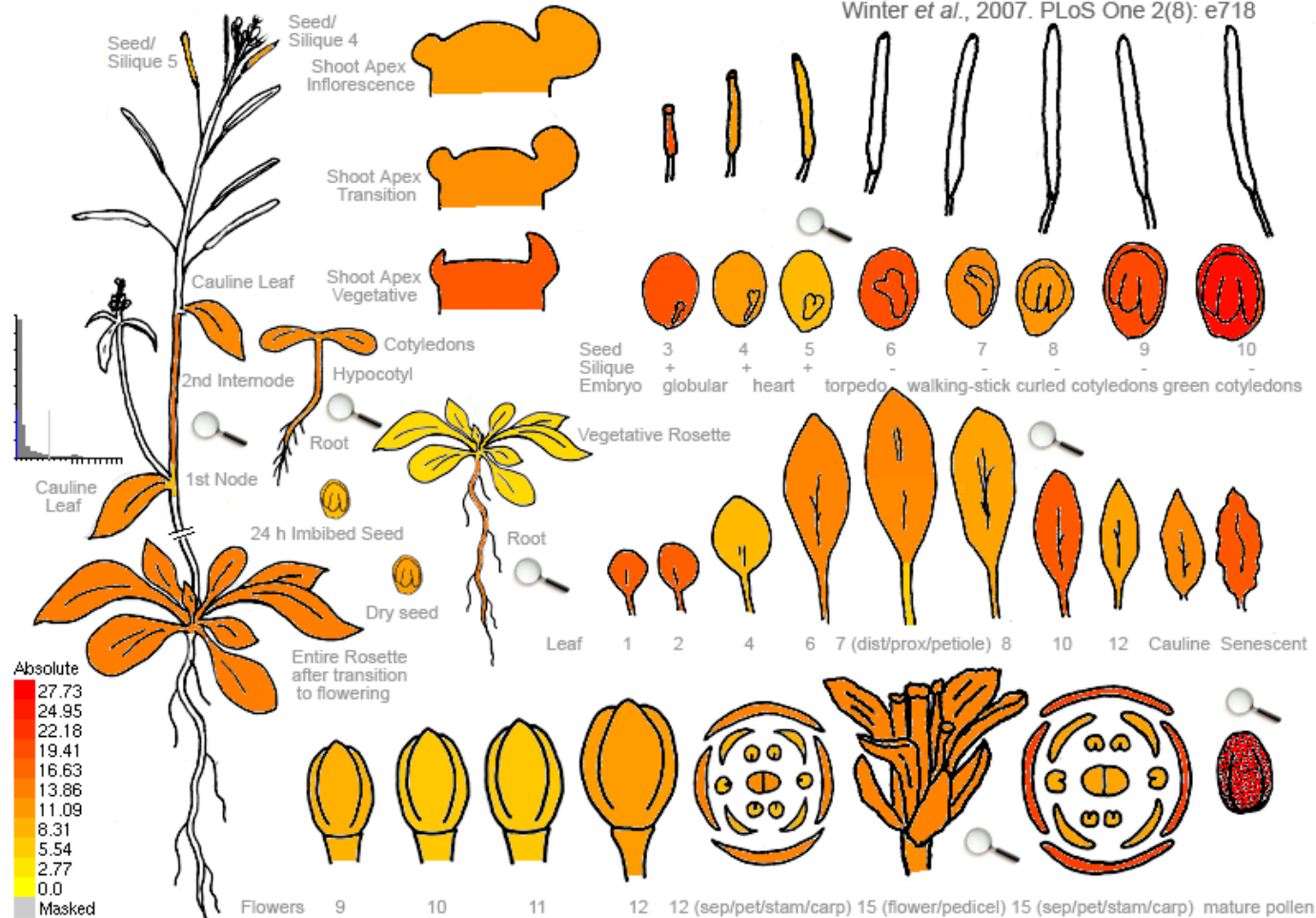
(From Genevestigator)

MYB98 is expressed ubiquitously among almost all the plant tissues, especially in ovule.

Tissue expression pattern of MYB98 (2)

At4g18770 254619_at AtMYB98

Arabidopsis eFP Browser at bar.utoronto.ca
Winter et al., 2007. PLoS One 2(8): e718



eFP Browser by B. Vinegar, drawn by J. Alls 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.

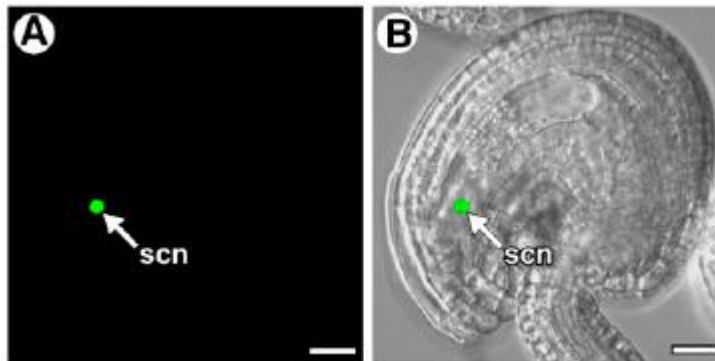
Subcellular location prediction



MYB98 [details](#) nucl: 14.0

```
----- Final Results -----  
nucleus --- Certainty= 0.760(Affirmative) < succ>  
microbody (peroxisome) --- Certainty= 0.191(Affirmative) < succ>  
mitochondrial matrix space --- Certainty= 0.100(Affirmative) < succ>  
endoplasmic reticulum (membrane) --- Certainty= 0.000(Not Clear) < succ>  
  
----- The End -----
```

(From PSORT)



(Jayson A.Punwani et al.2007)

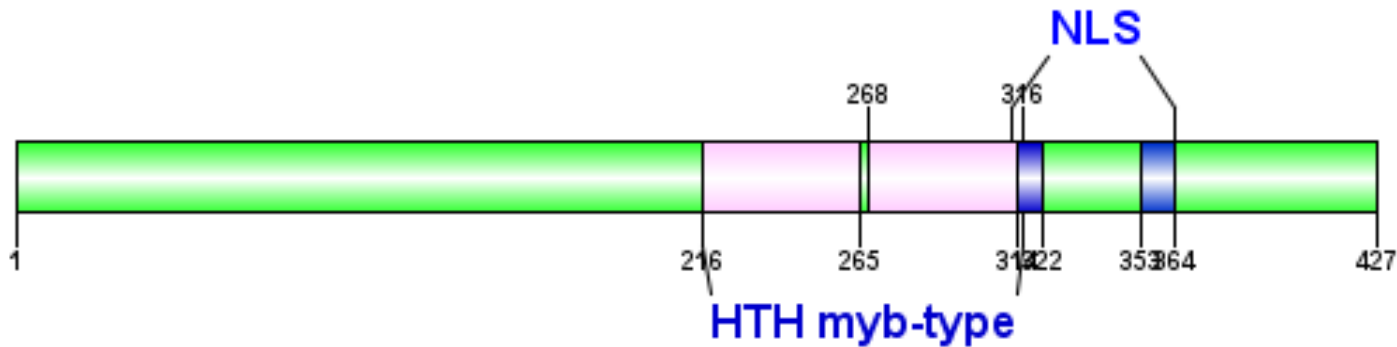


(By NLS tradamus)

MYB98 protein structure

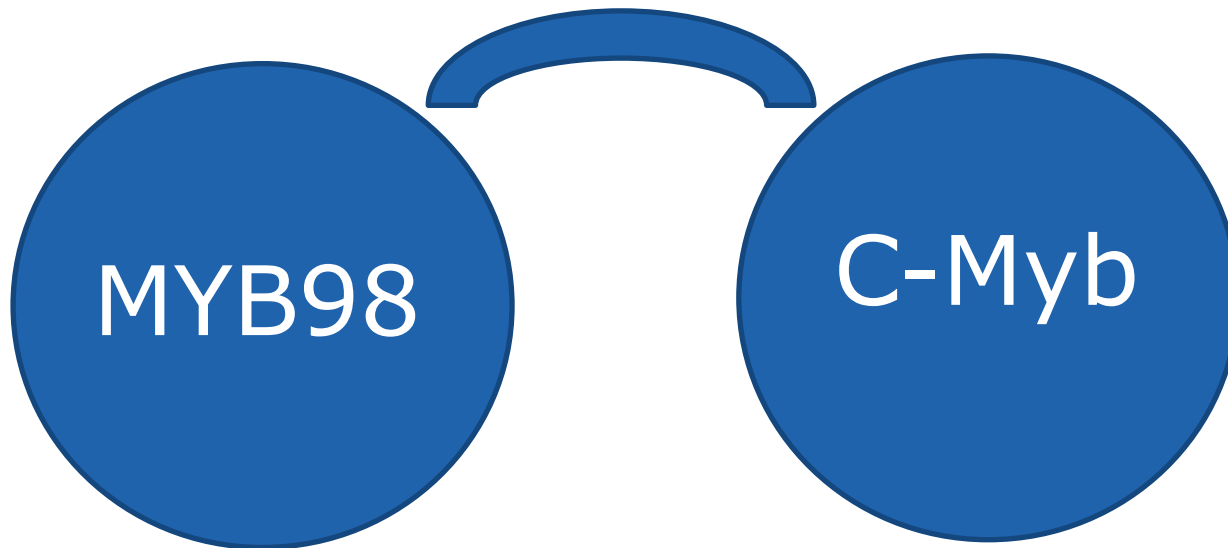


(Ryushiro D. Kasahara et al, 2005)



(By myself with DOG software)

Any linker



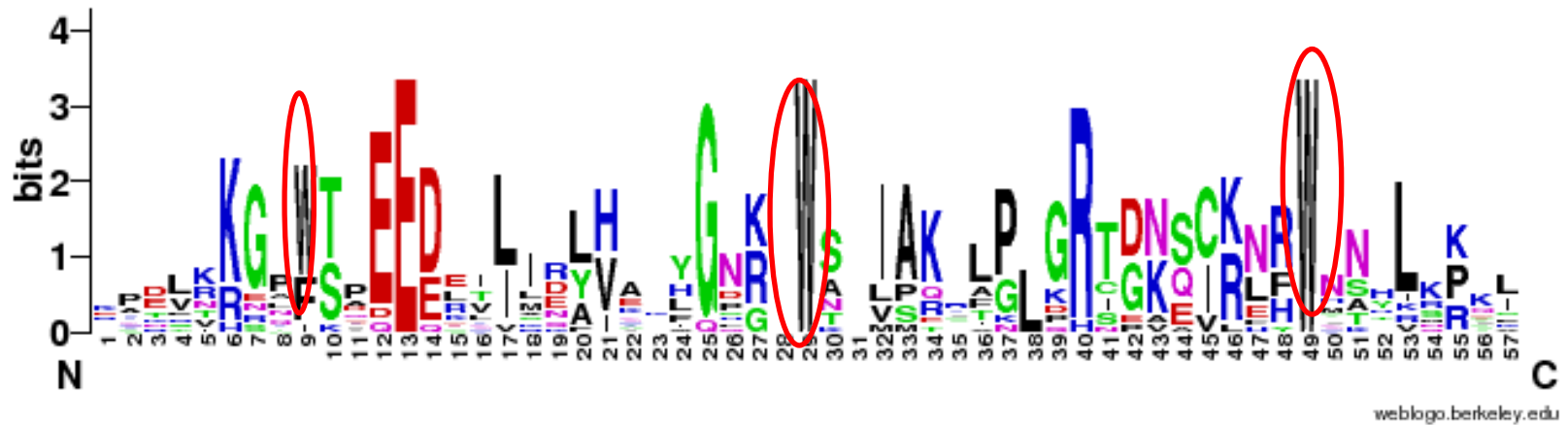
MYB98 VS. c-Myb

	★		★		★		
1	NPELIKGPWTKEEDQRVIELVQKYGPKRWSVIAKHLKGRIGKQCRERWHNHLNPEVKKTS	60	P06876	MYB_MOUSE			
1	KSTLVKGQWTAEDRVL IQLVEKYGLRKWSHIAQVLPGRIGKQCRERWHNHLRPDIKKE	60	Q9S7L2	MYB98_ARATH			
	: ** ** ***: **:***:*** **: ** : * *****.***: ** :						
61	WTEEDRIIYQAHKRLGNRWAEIAKLLPGRTDNAIKNHWNSTMRRKV	107	P06876	MYB_MOUSE			
61	WSEEDRVLIEFHKEIGNKWAEIAKRLPGRTE NSIKNHWNATKRRQF	107	Q9S7L2	MYB98_ARATH			
	*:*****: : **.:***:***** *****:*****:* **:.:						

★ ★ ★ (By Uniprot)

- The Myb domain is a DNA binding motif found in 1999 in the vertebrate protooncogene *c-Myb*;
- The Myb domain in *c-Myb* consists of three imperfect tandem Myb repeats referred to as R1,R2 and R3;
- The Myb repeats form a heix-turen-helix structure;
- Most plant MYB proteins contain only the R2 and R3 Myb repeats.

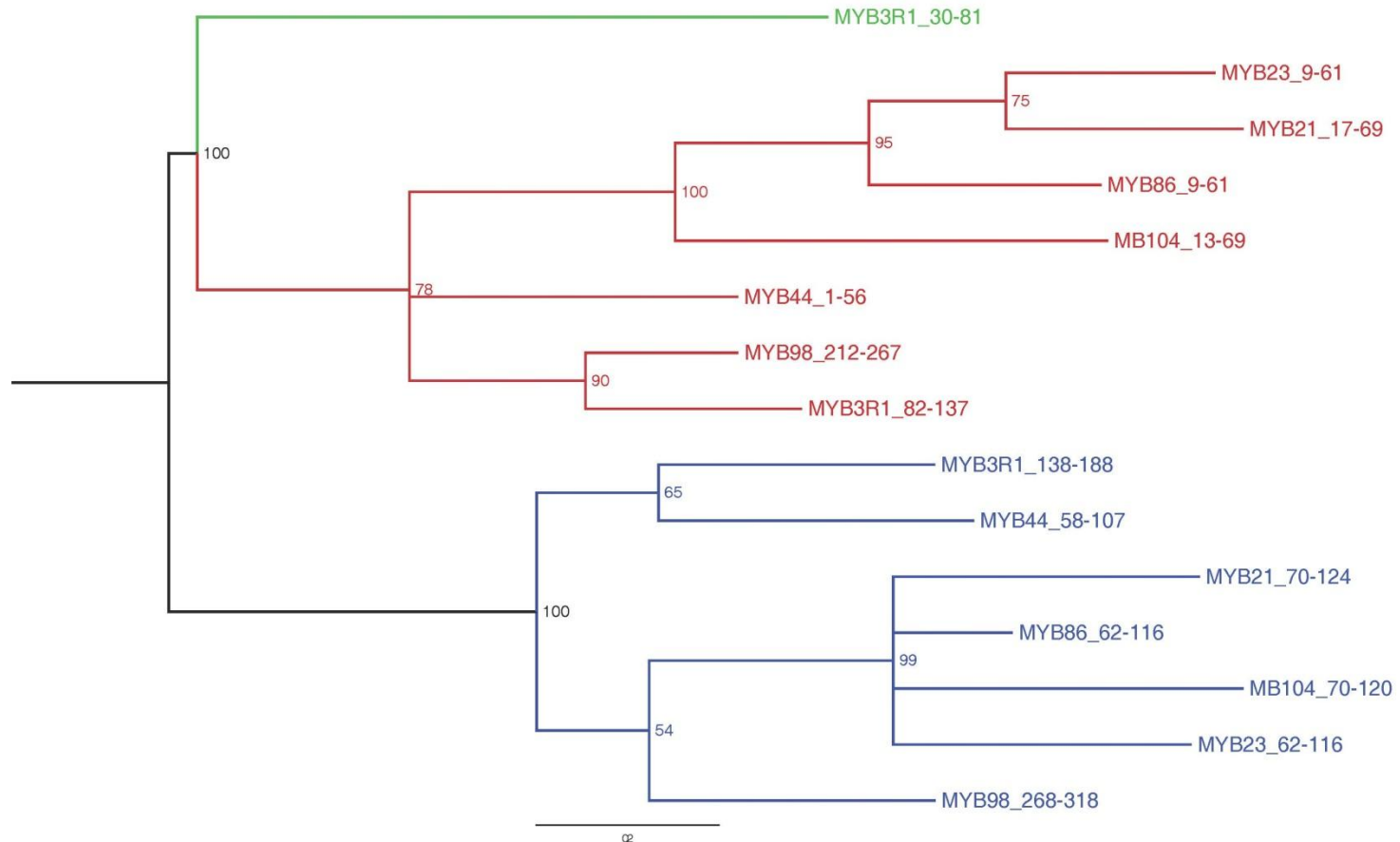
About the myc-repeat domain(1)



weblogo.berkeley.edu

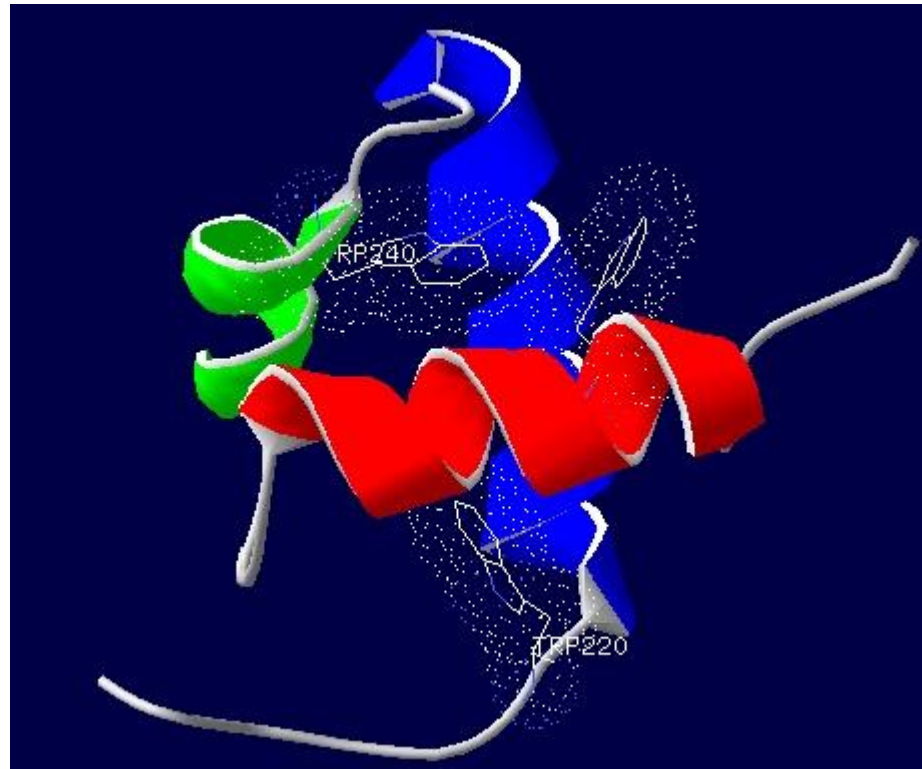
From the result ,we also can see that three trp residues are conserved.

About the myc-repeat domain(2)



While R1 forms a clade with R2, R2 and R3 separate with each other clearly.

Swiss model—homology modeling



- The figure shows the structure of a single HTH Myb-type repeat, three conserved TRP residues form its hydrophobic core.
- The third helix is found to be a recognition helix.

(Ogata, K et al.1992,1994)

Phosphorylation site prediction



Species: Arabidopsis thaliana
Protein: AT4G18770.1
Description: MYB98, AtMYB98; myb domain protein 98
MapMan: 27.3.25 RNA.regulation of transcription.MYB domain transcription factor family
Substrate for Kinase: AT3G59790.1 - ATPMPK10, MPK10; MAP kinase 10

Sequence

```
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50
1...50 M E N F V D E N G F A S L N Q N I F T R D Q E H M K E E D F P F E V V D Q S K P T S F L Q D F H H L
51...100 D H D H Q F D H H H H H G S S S S H P L L S V Q T T S S C I N N A P F E H C S Y Q E N M V D F Y E T
01...15 K P N L M N H H H F Q A V E N S Y F T R N H H H H Q E I N L V D E H D D P M D L E Q N N M M M R M
51...20 I P F D Y P P T E T F K P M N F V M P D E I S C V S A D N D C Y R A T S F N K T K P F L T R K L S S
01...25 S S S S S W K E T K K S T L V K G Q W T A E E D R V L I Q L V E K Y G L R K W S H I A Q V L P G R
51...30 I G K Q C R E R W H N H L R P D I K K E T W S E E E D R V L I E F H K E I G N K W A E I A K R L P G
01...35 R T E N S I K N H W N A T K R R Q F S K R K C R S K Y P R P S L L Q D Y I K S L N M G A L M A S S V
51...40 P A R G R R R E S N N K K K D V V V A V E E K K K E E E V Y G Q D R I V P E C V F T D D F G F N E K
```

(From PhosPhAt)

There are many predicted serine/threonine and tyrosine sites in the MYB98 sequence.

Future work

- ❖ **Try to figure out genes regulated by MYB98;**
- ❖ **Through dominant negative and dominant active approaches to find out the function of myb 98;**
- ❖ **protein-protein interaction;**