

# 欧洲云杉 PIFs 的结构与功能分析

Structure and Function Analysis of PIFs in Norway spruce (*Picea abies*)

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# Background

## ***Picea abies***

- Christmas tree
- Easy to transplant
- Widely planted
- Works well for windbreaks
- Grow fast when young
- Important building materials



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- Widely planted
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slow baby period
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Up to 8 years

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Additional lighting at night

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- Q: What are their functions?
- A: We don't know.

# What is PIF?

- PIF: Phytochrome interacting factor
- Function: Transcription activator. Binds to the G-box motif (5'-CACGTG-3') found in many light regulated promoters.
- Domain: HLH (Helix-loop-helix)
- *Arabidopsis thaliana*: PIF1, PIF3, PIF4, PIF5, PIF7

# Outline

4 gene sequences of homology proteins



Physic-chemical characters (Expasy: ProtParam)



Secondary structure prediction (Psipred, PSI-Blast)



Protein Structure & Function prediction (Phyre2, I-TASSER)



Multi-sequence alignment and phylogenetic tree construction (Psi-blast, Mega)

# Physic-chemical Characters

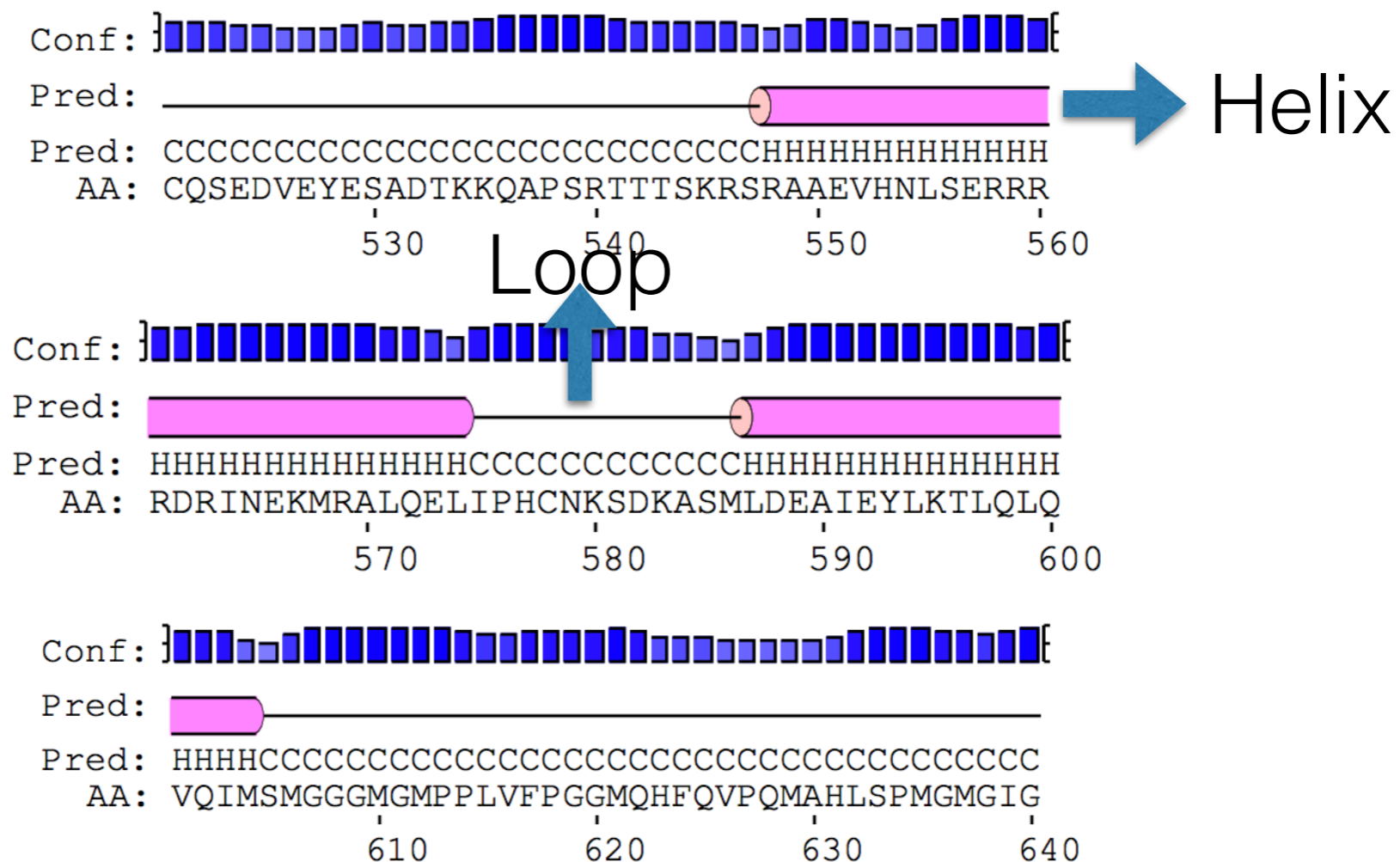
Gene Name	MA_26114g0010	MA_29186g0010	MA_10287127g0010	MA_167128g0010
Number of amino acids	334	662	802	328
Molecular weight	36796.2	72483.6	85160.6	33730
Theoretical pI	7.68	5.87	6.41	8.37
Ext. coefficient	28670	44390	54275	7490
Instability index	67.06	60.25	55.09	47.91
Aliphatic index	69.85	55.77	62.89	51.59
GRAVY	-0.707	-0.791	-0.526	-0.720

# Secondary structure predictions

UCL Department Of Computer Science

Bioinformatics Group

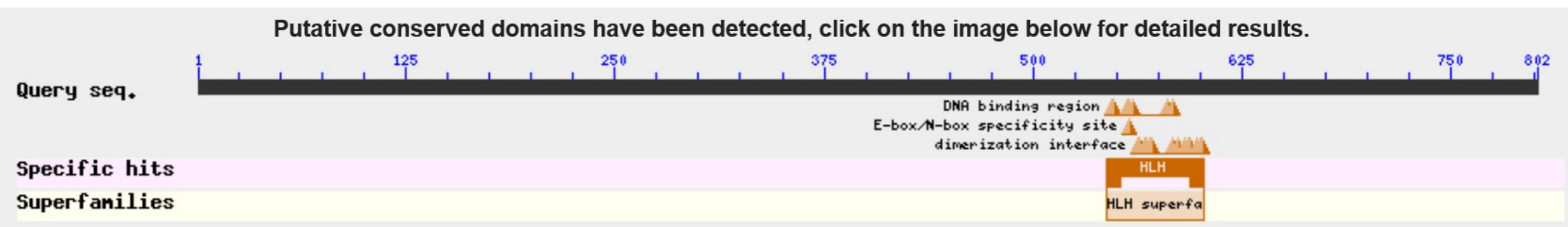
## The PSIPRED Protein Sequence Analysis Workbench



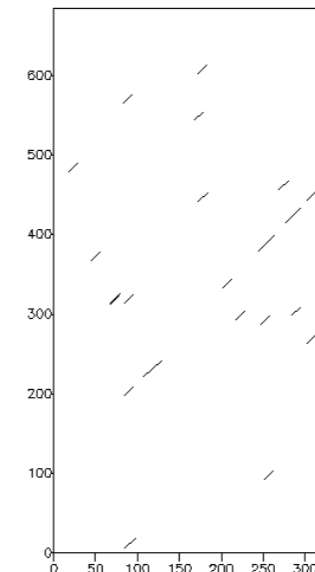
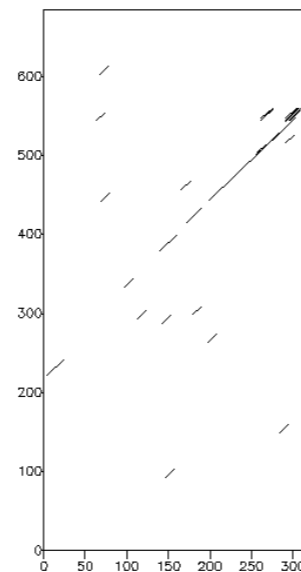
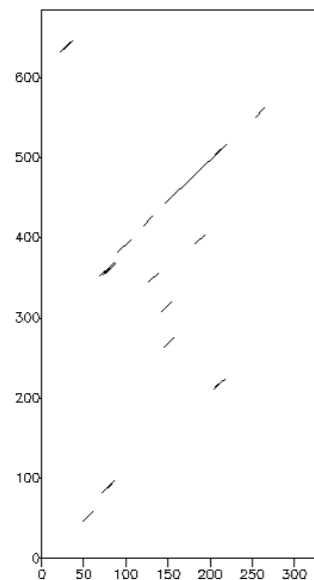
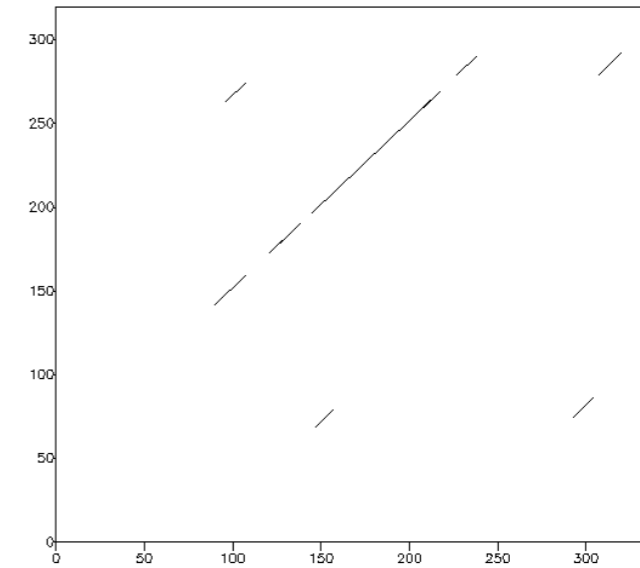
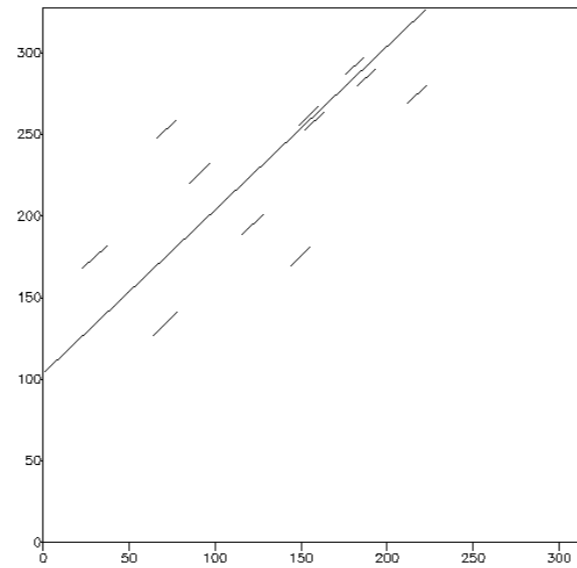
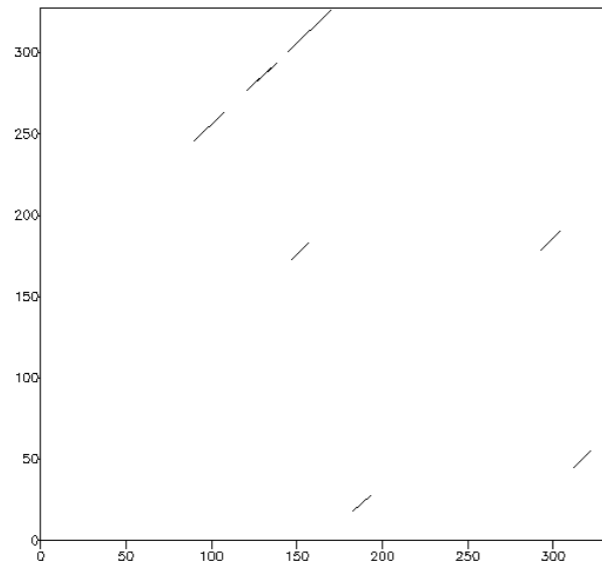


# Secondary structure predictions

## PSI-Blast

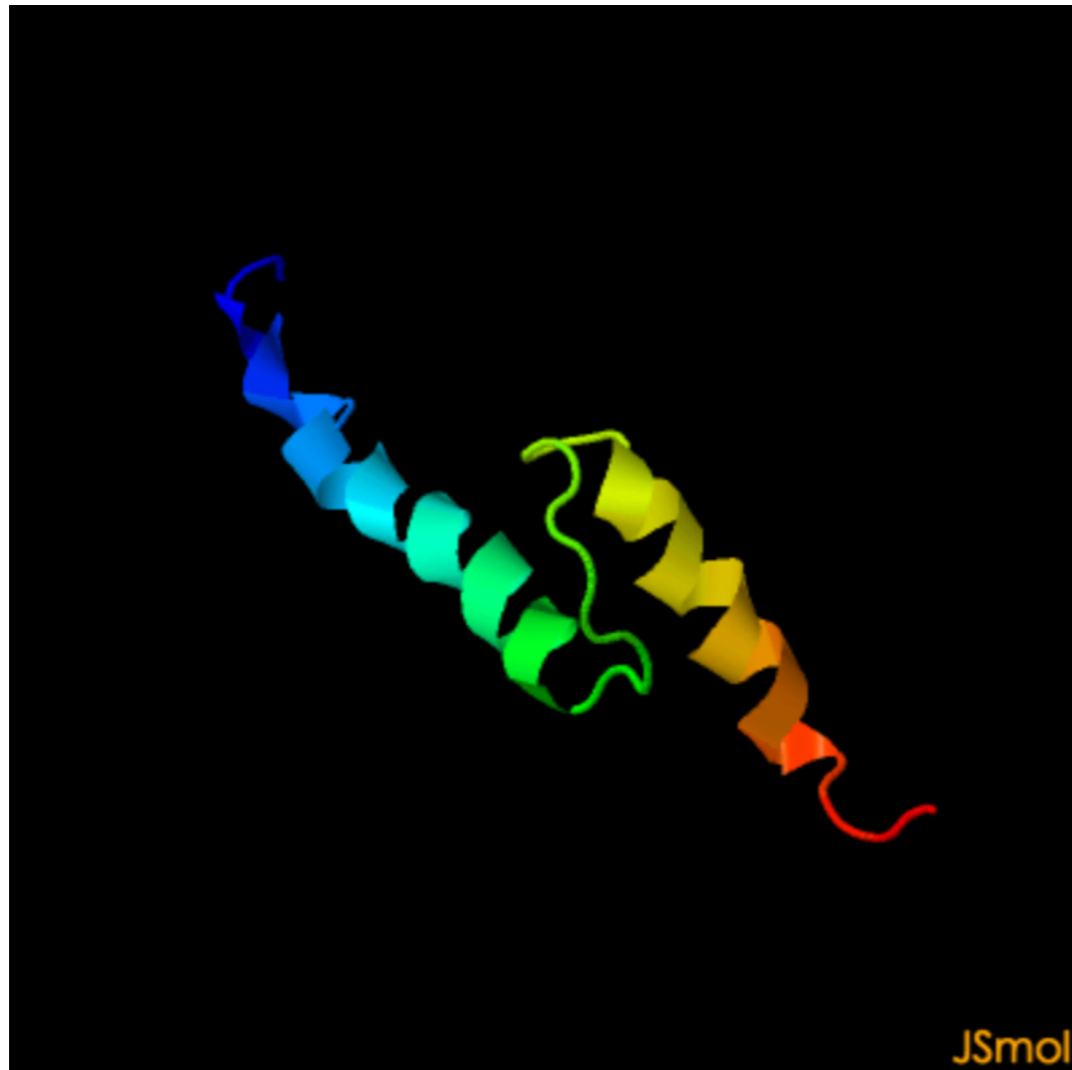


# Sequence Alignment (DotMatch)



HLH Domain

# Structure prediction (Phyre2)



## Top template information

**Fold:**HLH-like

**Superfamily:**HLH, helix-loop-helix DNA-binding domain

**Family:**HLH, helix-loop-helix DNA-binding domain

## Confidence and coverage

Confidence:

**99.1%**

Coverage:

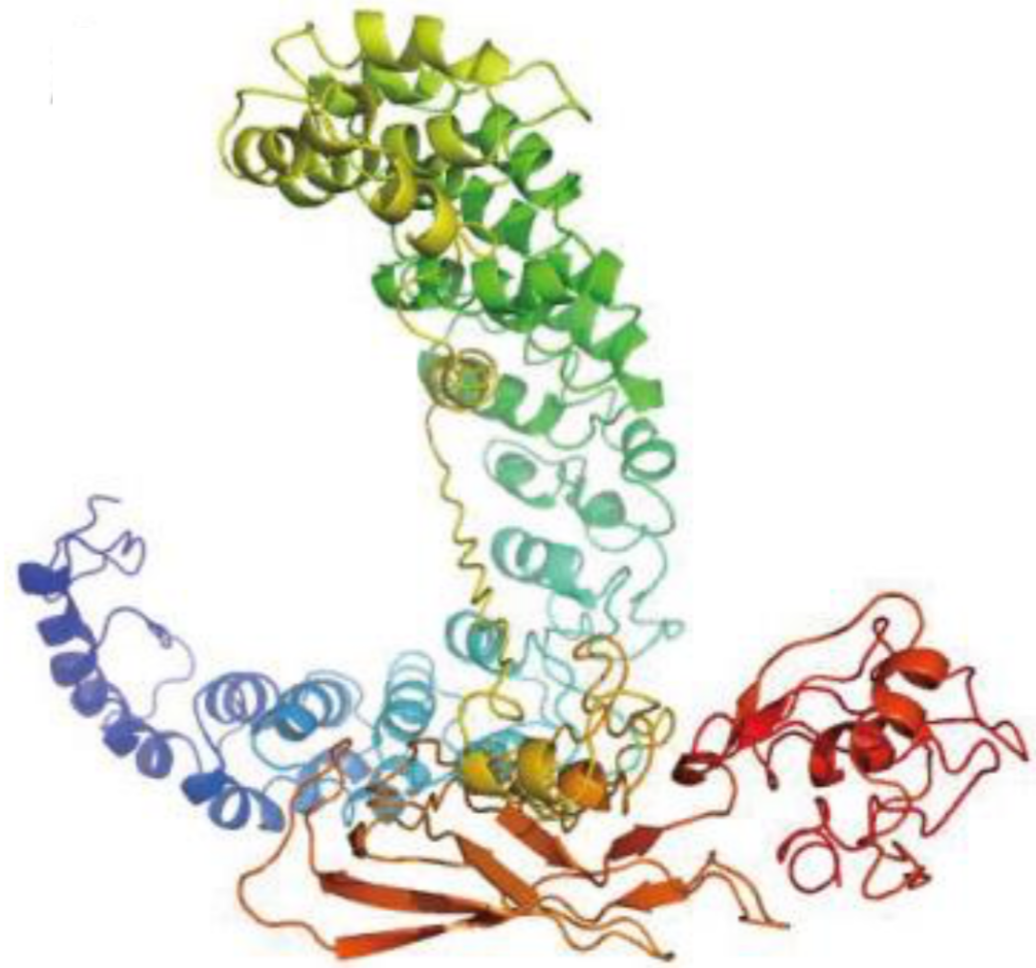
**7%**

53 residues ( 7% of your sequence) have been modelled with 99.1% confidence by the single highest scoring template.

# Structure Prediction (I-TASSER)



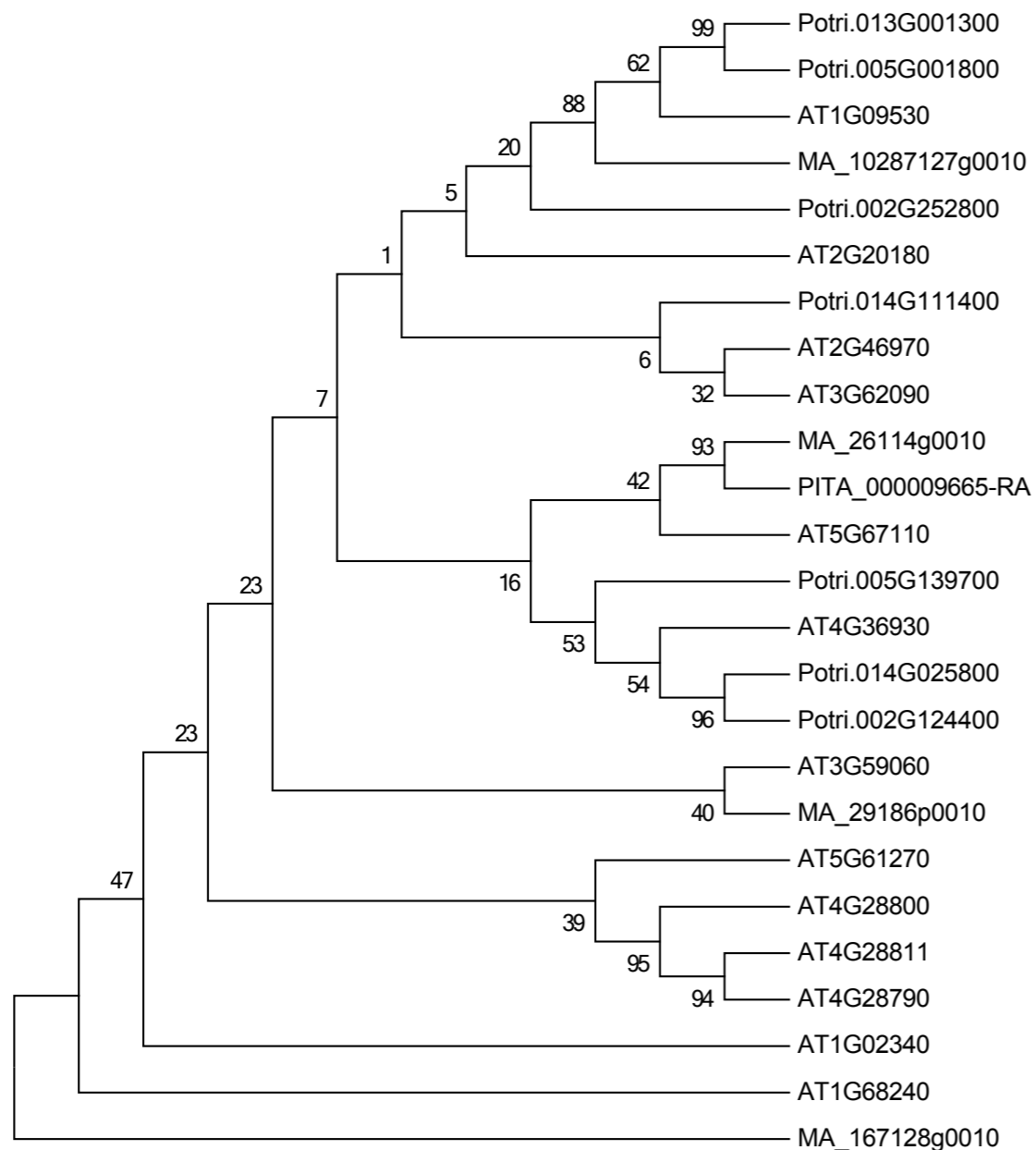
Iterative Threading  
ASSEMBly Refinement



# Multi-sequence alignment (MEGA)

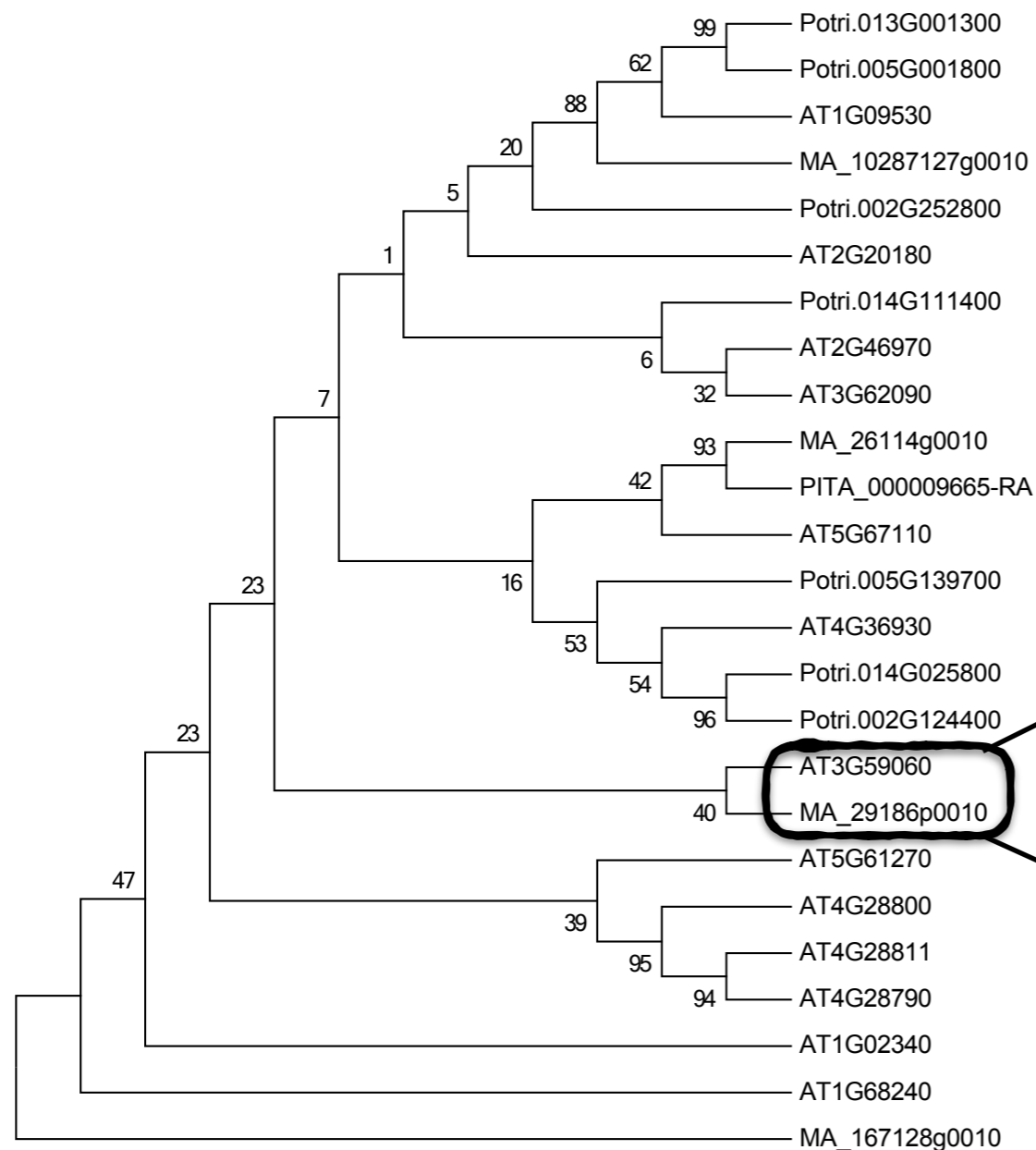
Species/Abbrv	Group Name	
1. AT4G36930		G G S S G T R V V A V V G A G F I D E - V D C E E E
2. AT4G28800		A A H D L G R K G K A V A V E A A G T S S G V C K A E E E
3. AT1G09530		G P S E S S L L X R K H S I I D - I D C H S E E
4. AT5G67110		V G Y G V F E G D K - - - - - V A F E H K
5. AT3G59060		S G T S V I D R K K E V M D A D E F - - - - - V V S S D
6. AT2G20180		K G K A V A M A A I E I T G S S V V K N S I E E E E
7. AT4G28811		A V E G L G R R G K E V A E I A G T V Y G V K A E E E E
8. AT4G28790		A V E G L G R R G K A V A I E I A G T V Y G V K A E E E E
9. AT2G46970		T S R D L C C L K R K Y G D I F F F S Y L L A S S D
10. AT3G62090		F E D S E G M Y L S L I D D - - - - - - - - - -
11. AT1G68240		F I F G V K K L D E K K - - - - - - - - - -
12. AT5G61270		A F F E S G R L K A R G D R D F R G S E R R D E E
13. AT1G02340		K H E E P K K R R I V L - - - - - - - - - -
14. MA_26114g0010		G G R V I K S K K V L M G I K D - - - - - I E C S S Q
15. MA_10287127g0010		R A G R E A L S K R G R D L E D - - - - - S E C S S E
16. MA_167128g0010		S F S R P A A A M A L S I G S A - - - - - S G L S S I
17. MA_29186p0010		S G R E P C L R C K R F G E E D - - - - - S G C S S E
18. PITA_000009665-RA		K S S E V I K S S K V L M G I K D - - - - - I E C S S Q
19. Potri.014G111400		K I K G K P D R G K S I D L A I S S I C - - - - - S R G A S N
20. Potri.013G001300		R P S D D P L E L K R R R D I E E - - - - - S E G P S E
21. Potri.005G001800		R A S D D P L E L K R R R D I E E - - - - - S E G P S E
22. Potri.014G025800		- - - - - V S K R G G V V E D D L G D - - - - - F S C D S E
23. Potri.005G139700		S G V R I R L I M S E P D H E - - - - - C D C E S E
24. Potri.002G124400		V S S G I S K R R G A V E D D L G D - - - - - F S C D S E
25. Potri.002G252800		E L P A L M S P V E D R R K G R E E E - - - - - A E C S F I A I S I I M A E G V P O S V A I R K T A S A D S S K P L G R R D A A M P L K D A E F F A D A K K R I R G S M S K R S R A A E V H L S E R R R D R I E K M E A L E L I P R C N

# Phylogenetic tree construction (MEGA)



- Neighbor-Joining method
- Bootstrap: 1000
- Amino acid sequence (ORFFinding → aa sequence)

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*Arabidopsis thaliana*

*Picea abies*

# GO (Gene Ontology) Analysis

GO ID	Description
GO:0007623	circadian rhythm
GO:0003677	DNA binding
GO:0009693	ethylene biosynthesis
GO:0005634	nucleus
GO:0009585	red, far-red light phototransduction
GO:0006355	regulation of transcription, DNA-dependent
GO:0003700	transcription factor activity
GO:0030528	transcription regulator activity



# Conclusion

- **Physic-chemical characters prediction:** Guide experiment
- **Secondary structure prediction:** Conserved domain identification
- **Structure prediction:** Function prediction
- **Multi-sequence alignment and phylogenetic tree construction:** Understand PIFs' function