Structure，function and evolution of plant-specific WOX family

WOX转录因子家族结构、功能及演化分析

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时　　间：2017.01.14

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- 结构分析

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同源异形基因
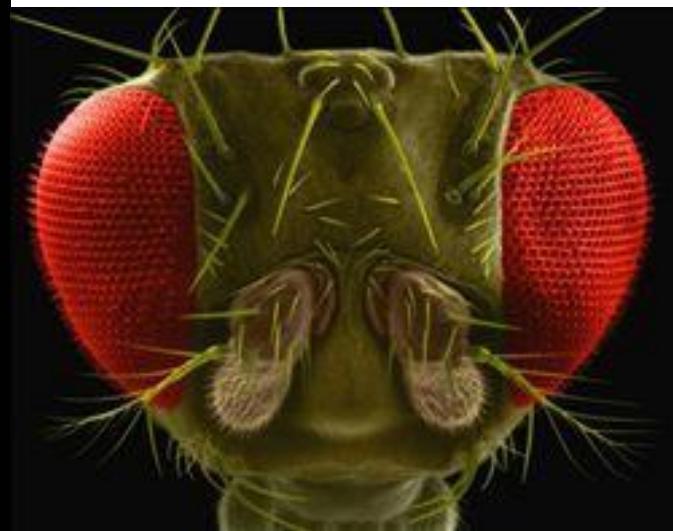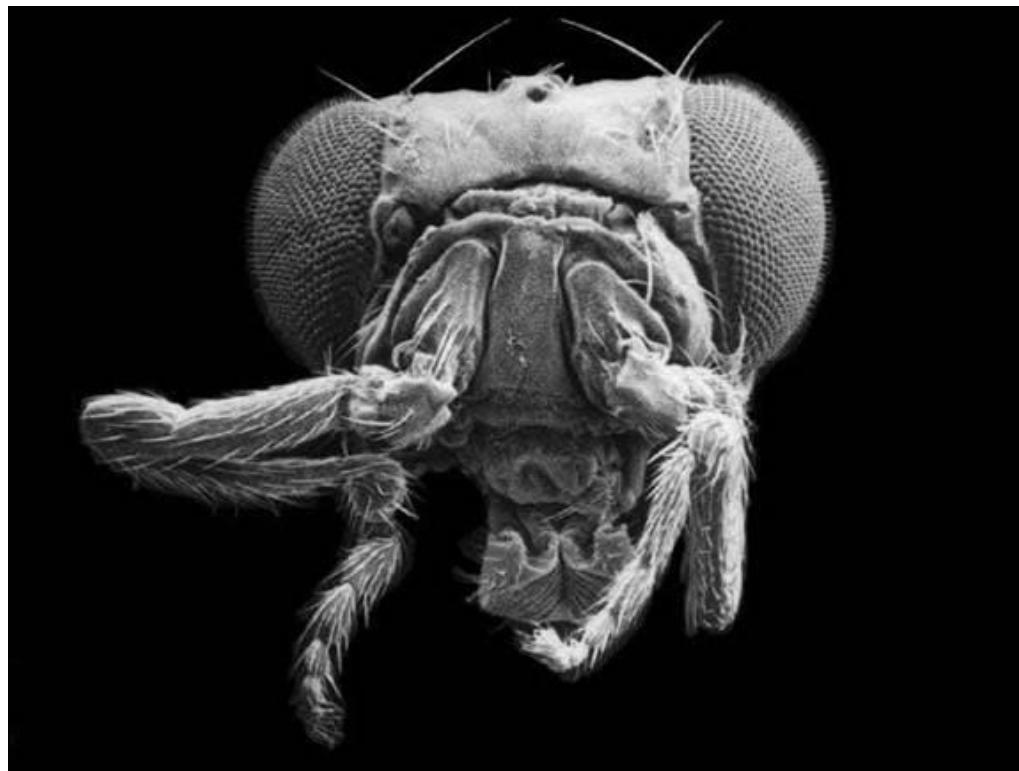
WOX (WUSCHEL related homeobox) gene

Summary of WOX protein expression domains and function

Protein	Alternative name (if any) in species listed	Clade	Expression domain	Function	Species
WUS		WUS clade	SAM, ovule, anther	Stem-cell maintenance, anther and ovule development	*A. thaliana*, snapdragon, petunia
WOX1		WUS clade	Lateral organ primordia	Lateral organ formation	*A. thaliana*, petunia
WOX2		WUS clade	Apical embryo domain	Embryo patterning	*A. thaliana*
WOX3	PRS1 (in maize NS1 and NS2)	WUS clade	SAM, peripheral zone	Promotes cell proliferation, lateral organ formation	*A. thaliana*, maize, petunia, rice
WOX4		WUS clade	Unknown	Unknown	
WOX5		WUS clade	RAM	Stem-cell maintenance	*A. thaliana*, rice
WOX6	PFS2, hos9	WUS clade	Female gametophyte	Prevents differentiation, cold-stress response	*A. thaliana*
WOX7		WUS clade			*A. thaliana*
WOX8		Intermediate clade	Basal embryo domain	Embryo patterning	*A. thaliana*
WOX9	STIMPY	Intermediate clade	Basal embryo domain	Embryo patterning, promote cell proliferation	*A. thaliana*, tomato, petunia
WOX10		Ancient clade	Unknown	Unknown	*A. thaliana*
WOX11		Intermediate clade	SAM and RAM	Crown root development	Rice
WOX12		Intermediate clade	Unknown	Unknown	*A. thaliana*
WOX13		Ancient clade	Root, inflorescence	Floral transition, root development	*A. thaliana*
WOX14		Ancient clade	Root, inflorescence	Floral transition, root development	*A. thaliana*

SAM, shoot apical meristem; RAM, root apical meristem.

Haecker A et al., 2004

WOX (WUSCHEL related homeobox) gene
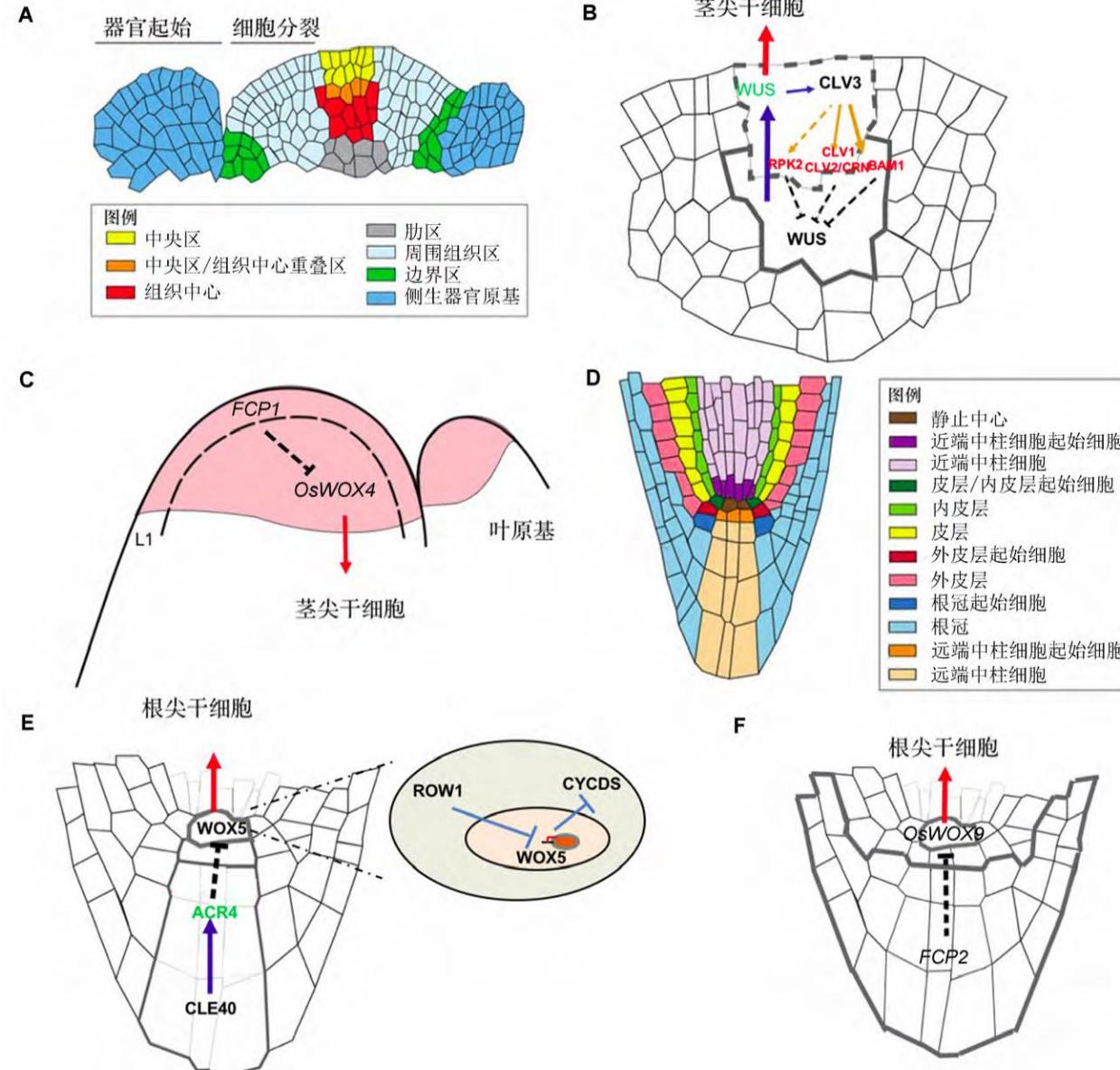
毛果杨（*Populus trichocarpa*）

- 第一个全基因组测序的木本植物

- 林木基因工程研究的模式树种

毛果杨的柔黄花序

香脂杨的叶子和柔黄花序

毛果杨的树皮

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Plant TFDB

Plant Transcription Factor Database

PlantTFDB

v4.0

Previous version: v1.0, v2.0, v3.0

Home BLAST Prediction RegMap ATRM Download Help About Links   Search (e.g., LFY)

Browse by Family

|				
AP2 (4461)	ARF (4578)	ARR-B (2354)	B3 (10609)	BBR-BPC (1256)
BES1 (1549)	C2H2 (17740)	C3H (9693)	CAMTA (1343)	CO-like (2125)
CPP (1612)	DBB (1651)	Dof (5655)	E2F/DP (1781)	EIL (1234)
ERF (21129)	FAR1 (7527)	G2-like (9874)	GATA (5335)	GRAS (9304)
GRF (1876)	GeBP (1564)	HB-PHD (477)	HB-other (2277)	HD-ZIP (8602)
HRT-like (249)	HSF (4574)	LBD (7216)	LFY (253)	LSD (957)
M-type_MADS (7541)	MIKC_MADS (6918)	MYB (22032)	MYB_related (15369)	NAC (19997)
NF-X1 (403)	NF-YA (2461)	NF-YB (3099)	NF-YC (2446)	NZZ/SPL (109)
Nin-like (2766)	RAV (690)	S1Fa-like (359)	SAP (164)	SBP (4168)
SRS (1327)	STAT (214)	TALE (4433)	TCP (4187)	Trihelix (6256)
VOZ (635)	WOX (2358)	WRKY (14549)	Whirly (530)	YABBY (1719)
ZF-HD (2589)	bHLH (28698)	bZIP (15498)		

Distribution of WOX family in different species
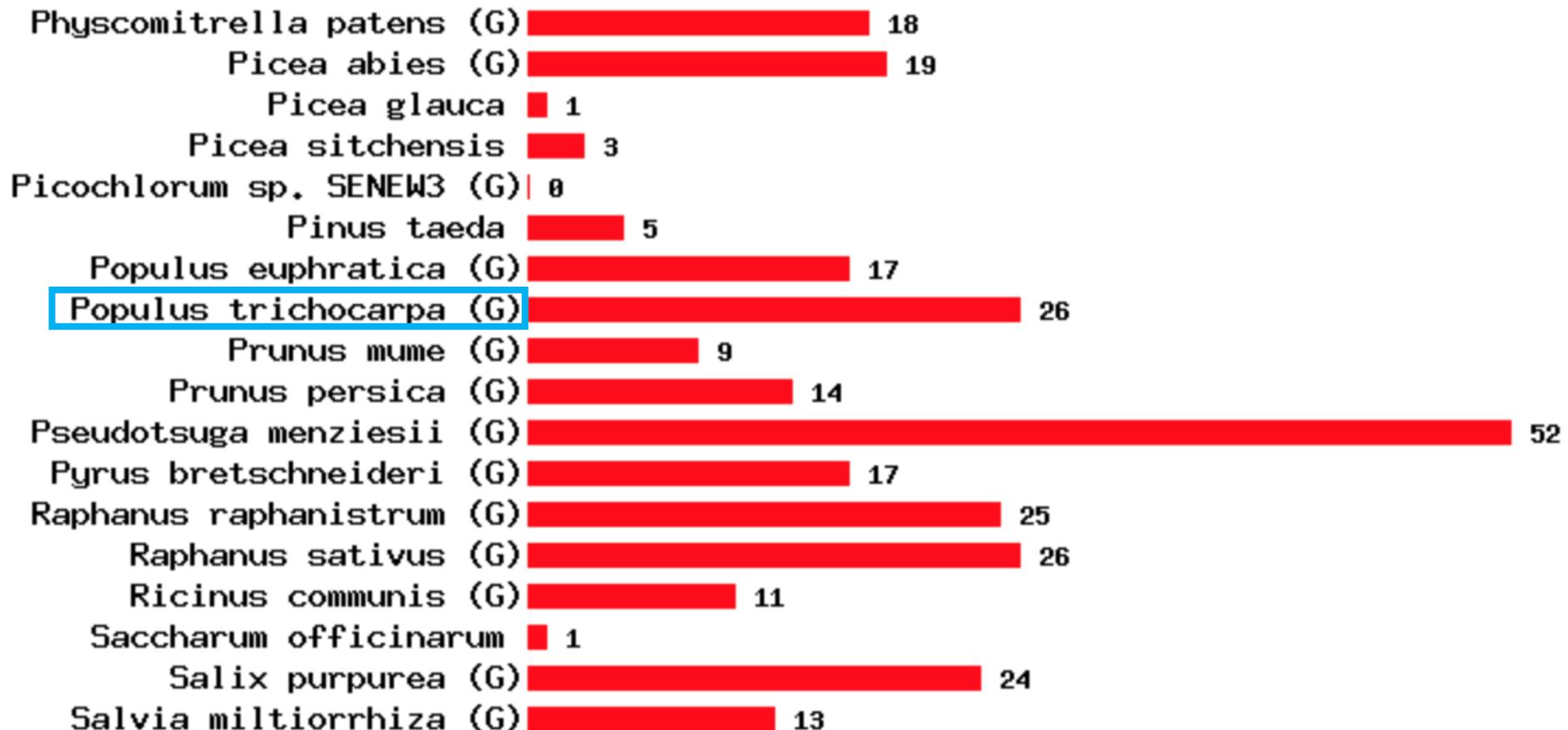
Multiple Sequence Alignment
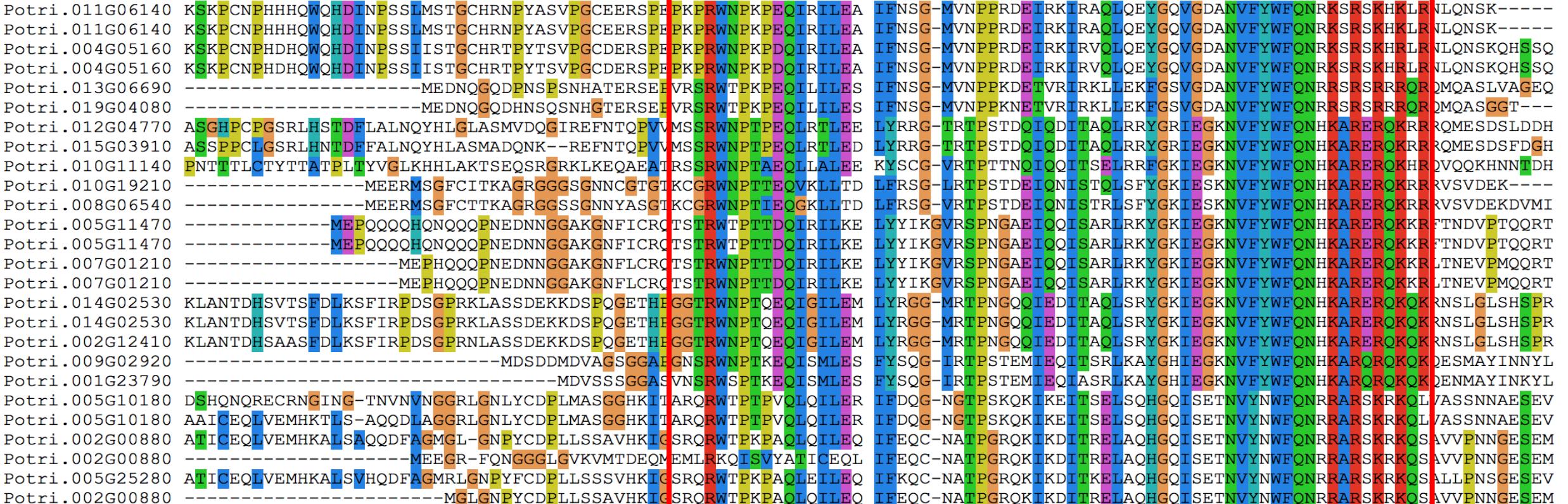
Concerved DNA Binding Domain(~60 aa)

WEBLOGO DNA Binding Domain Logo
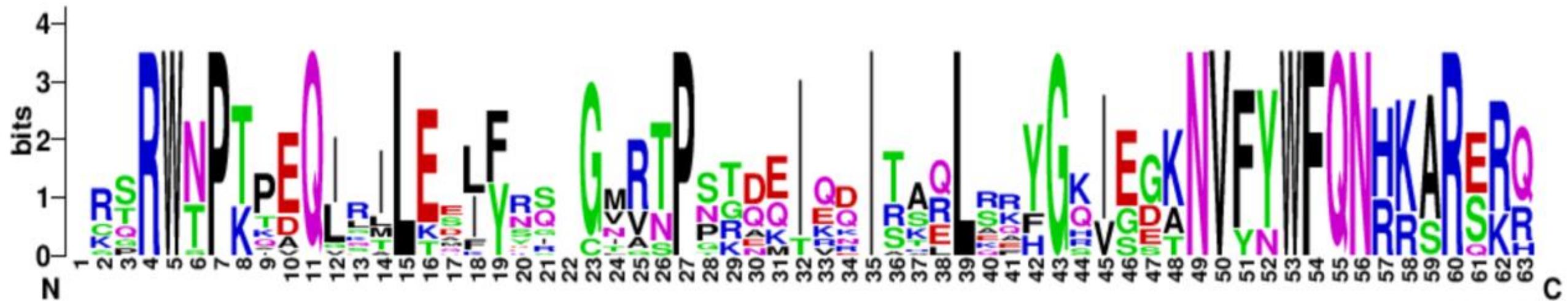
非极性疏水氨基酸（P、F、W、V）：位于螺旋疏水内部；

碱性氨基酸（L、R）：与特定位点的DNA结合；

其他不带电荷氨基酸（E、N、Q、G）：可能在二级结构的稳定

中起到一定作用。

Analysis of α-helix

ExPASy： ProtScale

alpha-helix/Delage&Roux

— alpha-helix

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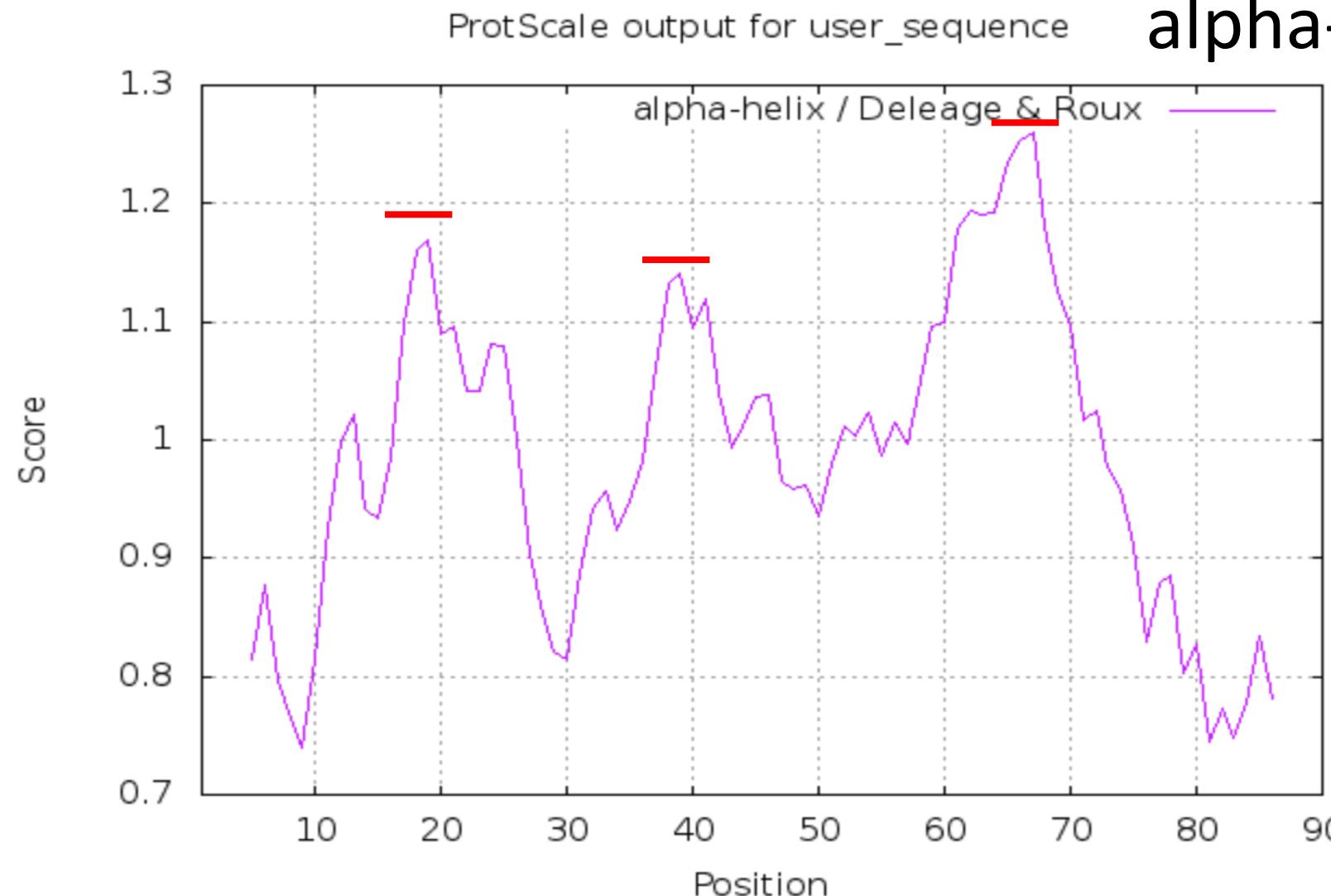
拟南芥的WOX转录因子进化树
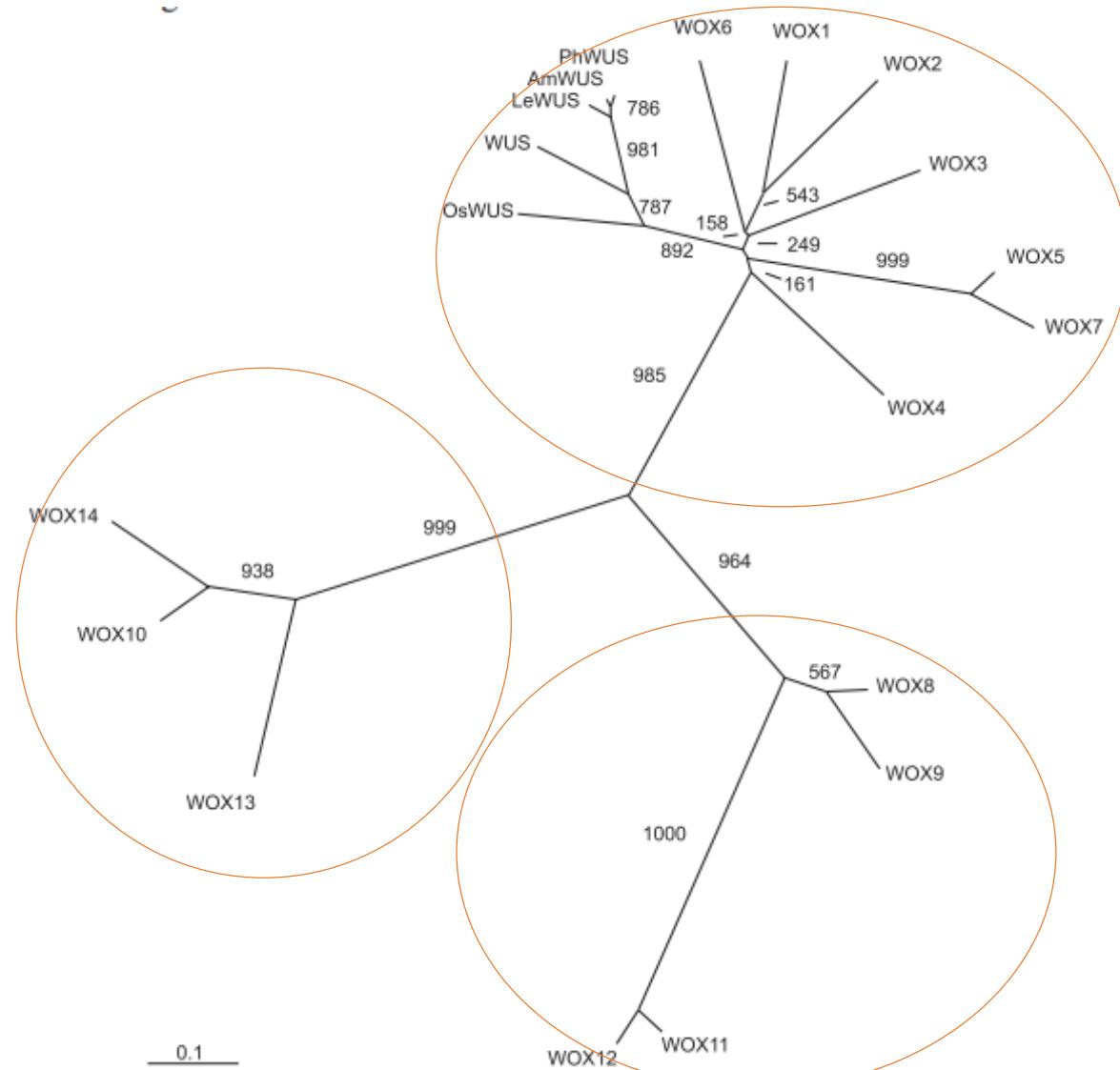
Haecker A et al., 2004

使用MEGA6，多序列比对拟南芥和毛果杨的WOX家族蛋白，构建系统进化树，采用邻接法，选择Poisson Model，Bootstrap 检验次数设为100次
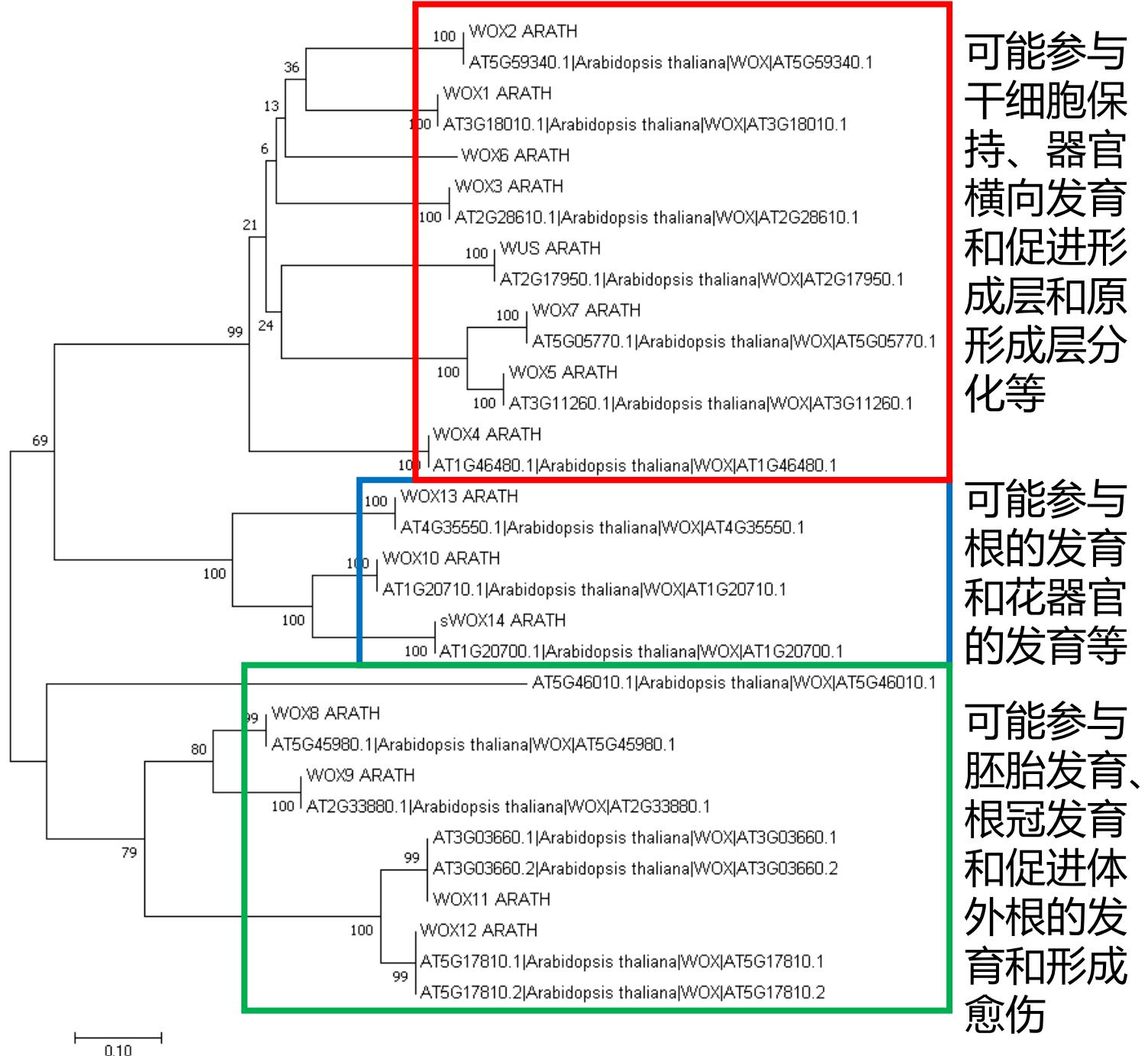
可能参与干细胞保持、器官横向发育和促进形成层和原形成层分化等

可能参与根的发育和花器官的发育等

可能参与胚胎发育、根冠发育和促进体外根的发育和形成愈伤

目录

WOX蛋白的结构分析 -以At-WUS和Pt-WOX为例

- Sturcture: ~60 amino acids composing 3 helices, and 2 helix and 3 helix form a Helix-Turn-Helix (HTH) motif .

- Function: DNA binding. (have preference of 5'-TAAT-3')
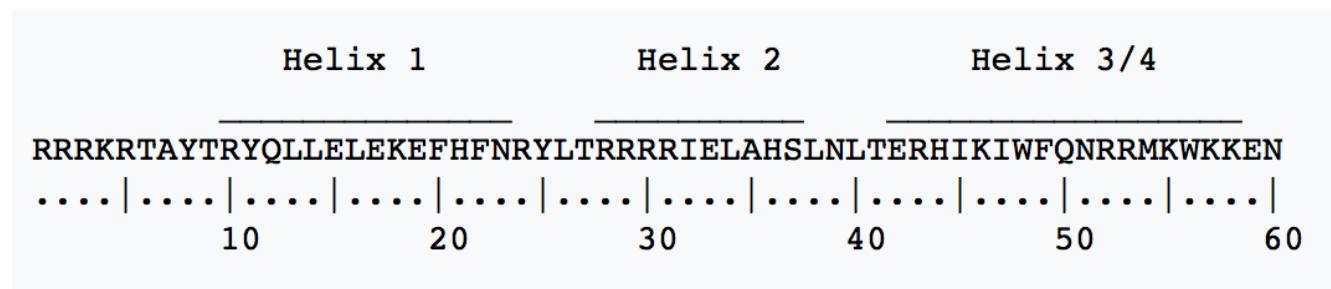
Consensus homeodomain from Wikipedia

At-WUS in UniProt

Q9SB92 (WUS_ARATH)

BLAST	Align	Format	Add to basket	History		Feedback

**Protein** | Protein WUSCHEL

Gene | WUS

Organism | *Arabidopsis thaliana (Mouse-ear cress)*

Status | Reviewed - Annotation score: ⊙⊙⊙⊙⊙ - Experimental evidence at protein level[i]

- Length: 292
- DNA binding domain: 34-99
- Compositional bias：123-156，His rich
- No experimental structures found with sequence identity >90%

Structure of Pdx1

--P70118 (PDX1_MESAU)

Helix 2

Helix 3

5'-TAAT-3

Robert B. Rose, *Biochemistry,* 2006
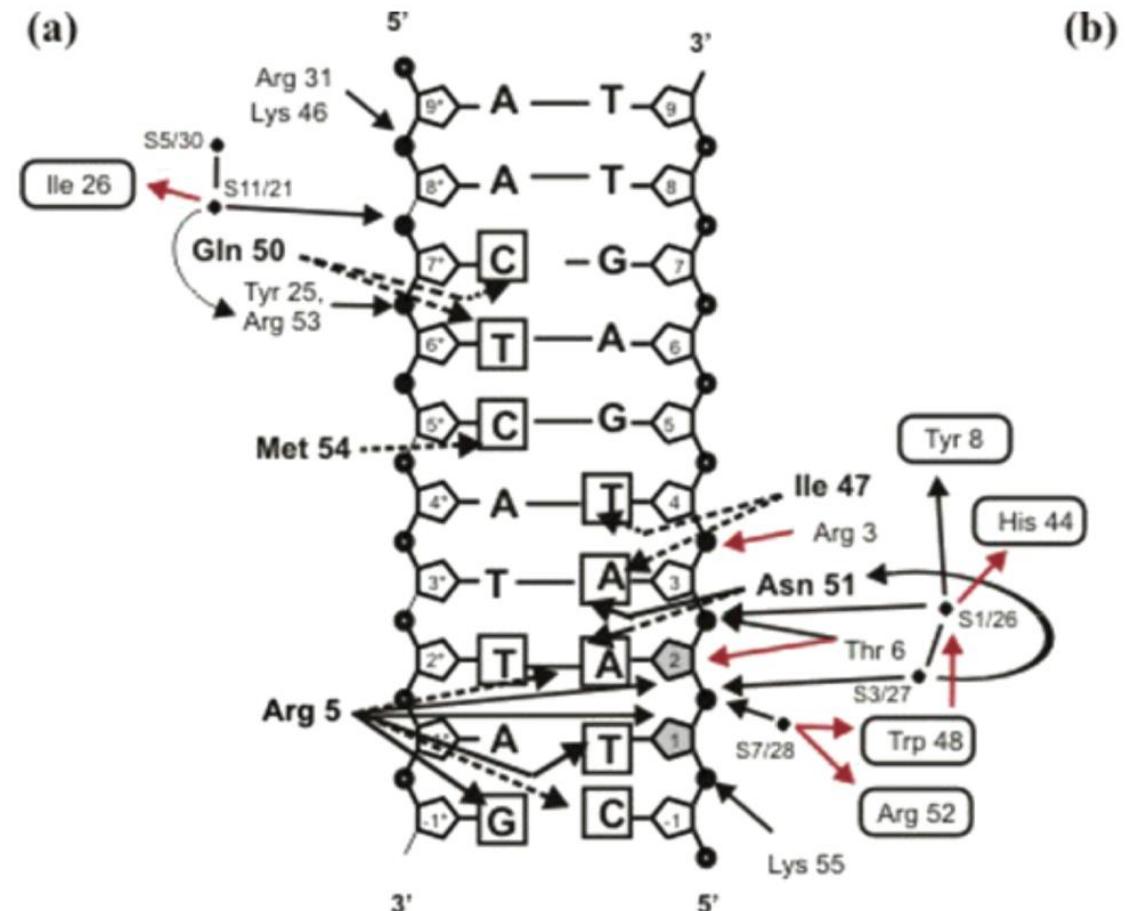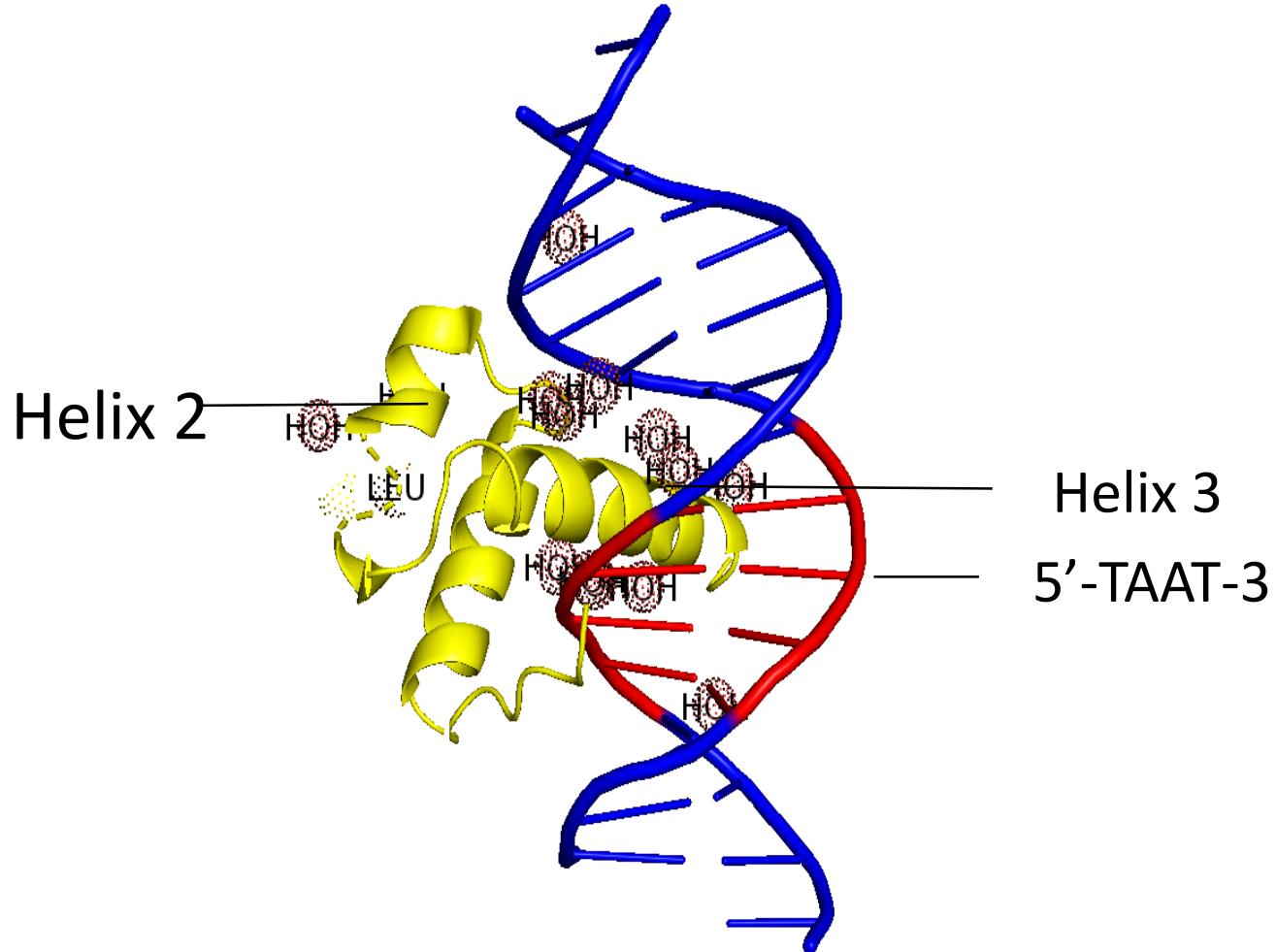
3D Structure (Predictied by Phyre2)

Turn
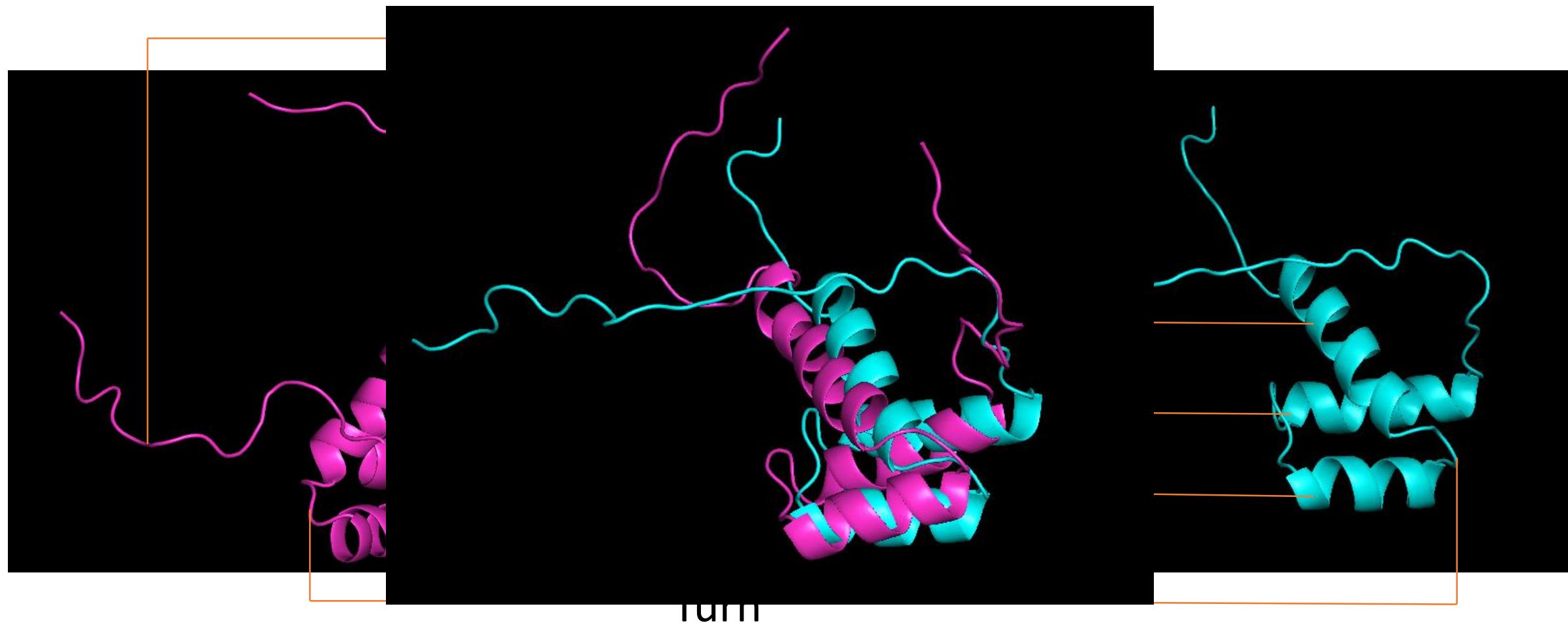
Pt-WOX (69-153/172)   At-WUS (18-103/292)

参考文献

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致 谢

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