

Protein Prediction and Structure Analysis of WRKY Transcription Factors Involved in Response to Cold in *Cucumis Sativus*

12组：陈璐 张晓孟 孟姗姗 张吉祥

Background



Protein Sequence Alignment and Phylogeny

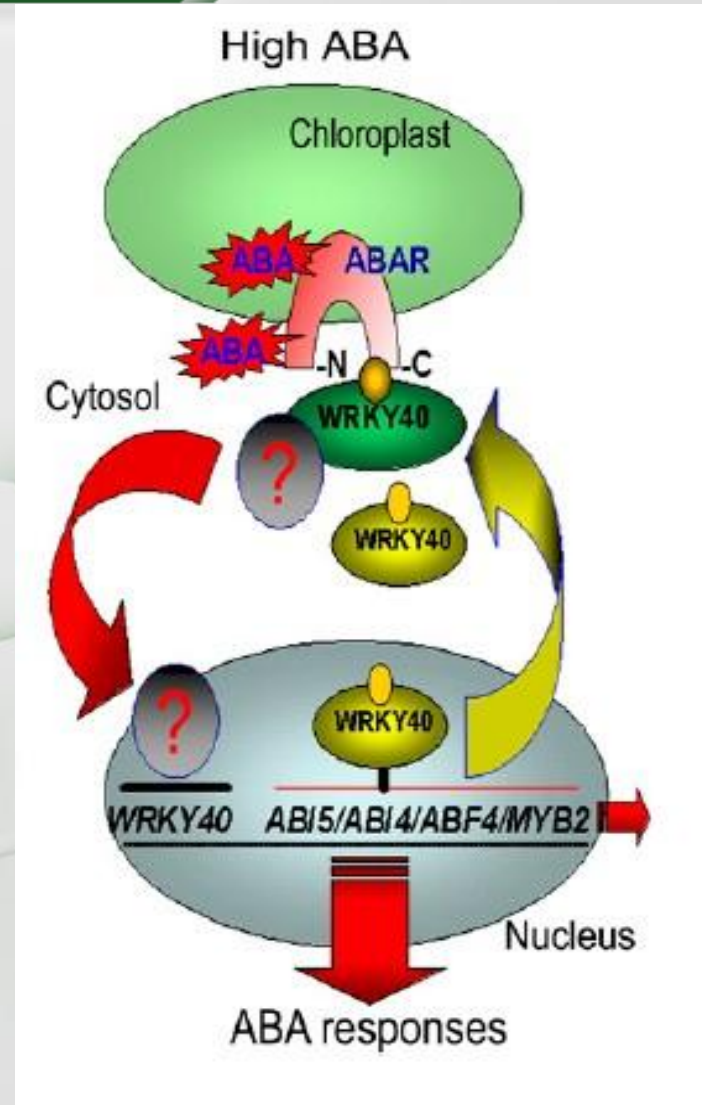
Protein modeling



Future Plan

Transcription factor

- sequence-specific DNA binding
- activate or repress transcription of downstream target genes.



Yi Shang et al. ,2010

WRKY Transcription factor

Group1
AtWRKY20C SEVDILDDGYRWRKYGQKVVRGNPNRSYYKCT--AHGCPVRKHVERAS---HDPKAVITTYEGKHDHDVP
CsWRKY17C SEVDILDDGYRWRKYGQKVVRGNPNRSYYKCT--NVGCPVRKHVERAS---HDPKAVITTYEGKHNHDVP
CsWRKY2C SDIDILDDGYRWRKYGQKVVKGNPNRSYYKCT--NPGCPVRKHVERAS---HDLRAVITTYEGKHNHDVP
CsWRKY15 SEVDILDDGYRWRKYGQKVVKGNPNRSYYKCT--NPGCTVRKHVERAS---HDLKSVITTYEGKHNHDVP
CsWRKY8C TEVDILEDDGYRWRKYGQKVVKGNPNRSYYKCT--SAGCLVRKHVERAS---HDLKCVITTYEGKHNHEVP
CsWRKY37C SEVDLLDDGYRWRKYGQKVVKGNPNRSYYKCT--SAGCNVRKHVERSS---TDSKAVVTTYEGKHNHDVP
CsWRKY39 SNVDKLLDDGYRWRKYGQKVVKGNPNRSYYKCT--YPGCGVRKHIERAS---HDFRAVVTTYEGKHNHDIP
CsWRKY23C SEIDILPDGYRWRKYGQKVVKGNPNRSYYKCT--SLGCPVRKHIERAA---NDMRAVITTYEGKHNHEVP
CsWRKY49C SEVDIVNDGYRWRKYGQKFKGNPNRSYYRCS--SPGCPVKKHVERAS---HDPKIVLTTYEGQHDHVVP
CsWRKY4C GDVGISGDGYRWRKYGQKMYKGNPHPRNYRCT--SAGCPVRKHIESAV---ENPNAVIITYKGVHDHTP
CsWRKY24C TGI EISGKGVWRKYGQKVVKGNLYPRSYRCT--GLKCKARKYVERAS---EDPDSFITTYEGKHNHGIS

Group3
AtWRKY54 VEAKSSEDRYAWRKYGQKEILNTTFPRSYFRCTHKPTQGCKATKQVQKQD-Q-DSE-MFQITYIGYHTCTAN
CsWRKY34 RTSRTTEDNYGWRKYGQKAIHNTTYPRSYRCTHKFDQGCQATKQVQRMEGD-DSEIMYNITYISDHTCRRP
CsWRKY22 ESCDLVDDGHAWRKYGQKTILNAKYPRNYRCTHKYDQTCQATKQVQRLQ---DNPPKFRTTYGNHTCSNF
CsWRKY20 AIEGSLDDGFAWRKYGQKGILGAKHPRGYRCTHRNLQGCLATKQVQRSD---DDPTIFEITYRGKHS CSQV
CsWRKY50 AVEGPGCDGFSWRKYGQKDILGSKFPRSYFRCSHRFTQGCLATKQVQKSD---NDPTIYEVTYKGRHTCNKA
CsWRKY31 GFEGPHEDGYSWRKYGQKDILGATYPRSYRCTFRNTQNCWAVKQVQRSD---EDPSVFEITYRGKHTCSQG
CsWRKY35 NTELPPDDGFTWRKYGQKEILGSRFPRGYFRCTHQKLYHCPAKKHVQRLD---DDPHTFEVTYRGEHTCHMS

Jian Ling et al. 2011

- contain at least one highly conserved signature domain of about 60 amino acid residues, which includes the conserved WRKYGQK sequence followed by a zinc finger motif.

Eulgem T et al. , 2000

Results: 8

[Genome-wide analysis of WRKY gene family in Cucumis sativus.](#)

1. Ling J, Jiang W, Zhang Y, Yu H, Mao Z, Gu X, Huang S, Xie B.
BMC Genomics. 2011 Sep 28;12:471.

PMID: 21955985 [PubMed - indexed for MEDLINE] **Free PMC Article**

[Related citations](#)

[Capsicum annuum WRKYb transcription factor that binds to the CaPR-10 promoter functions as a positive regulator in innate immunity upon TMV infection.](#)

2. Lim JH, Park CJ, Huh SU, Choi LM, Lee GJ, Kim YJ, Paek KH.
Biochem Biophys Res Commun. 2011 Aug 5;411(3):613-9. Epub 2011 Jul 13.

PMID: 21771584 [PubMed - indexed for MEDLINE]

[Related citations](#)

[Expression and functional analysis of two genes encoding transcription factors, VpWRKY1 and VpWRKY2, isolated from Chinese wild Vitis pseudoreticulata.](#)

3. Li H, Xu Y, Xiao Y, Zhu Z, Xie X, Zhao H, Wang Y.
Planta. 2010 Nov;232(6):1325-37. Epub 2010 Sep 2.

PMID: 20811906 [PubMed - indexed for MEDLINE]

[Related citations](#)

[Male gametophyte-specific WRKY34 transcription factor mediates cold sensitivity of mature pollen in Arabidopsis.](#)

4. Zou C, Jiang W, Yu D.
J Exp Bot. 2010 Sep;61(14):3901-14. Epub 2010 Jul 19.

PMID: 20643804 [PubMed - indexed for MEDLINE] **Free PMC Article**

[Related citations](#)

WRKY Transcription factor- UniProt

Uniprot

Entry	Entry name	Status	Protein names	Gene names	Organism	Length
O22921	WRK25_ARATH	★	Probable WRKY transcription factor 25	WRKY25 At2g30250 T9D9.6	Arabidopsis thaliana (Mouse-ear cress)	393
Q8S8P5	WRK33_ARATH	★	Probable WRKY transcription factor 33	WRKY33 At2g38470 T19C21.4	Arabidopsis thaliana (Mouse-ear cress)	519
O65590	WRK34_ARATH	★	Probable WRKY transcription factor 34	WRKY34 At4g26440 M3E9.130	Arabidopsis thaliana (Mouse-ear cress)	568

WRKY Transcription factor- UniProt

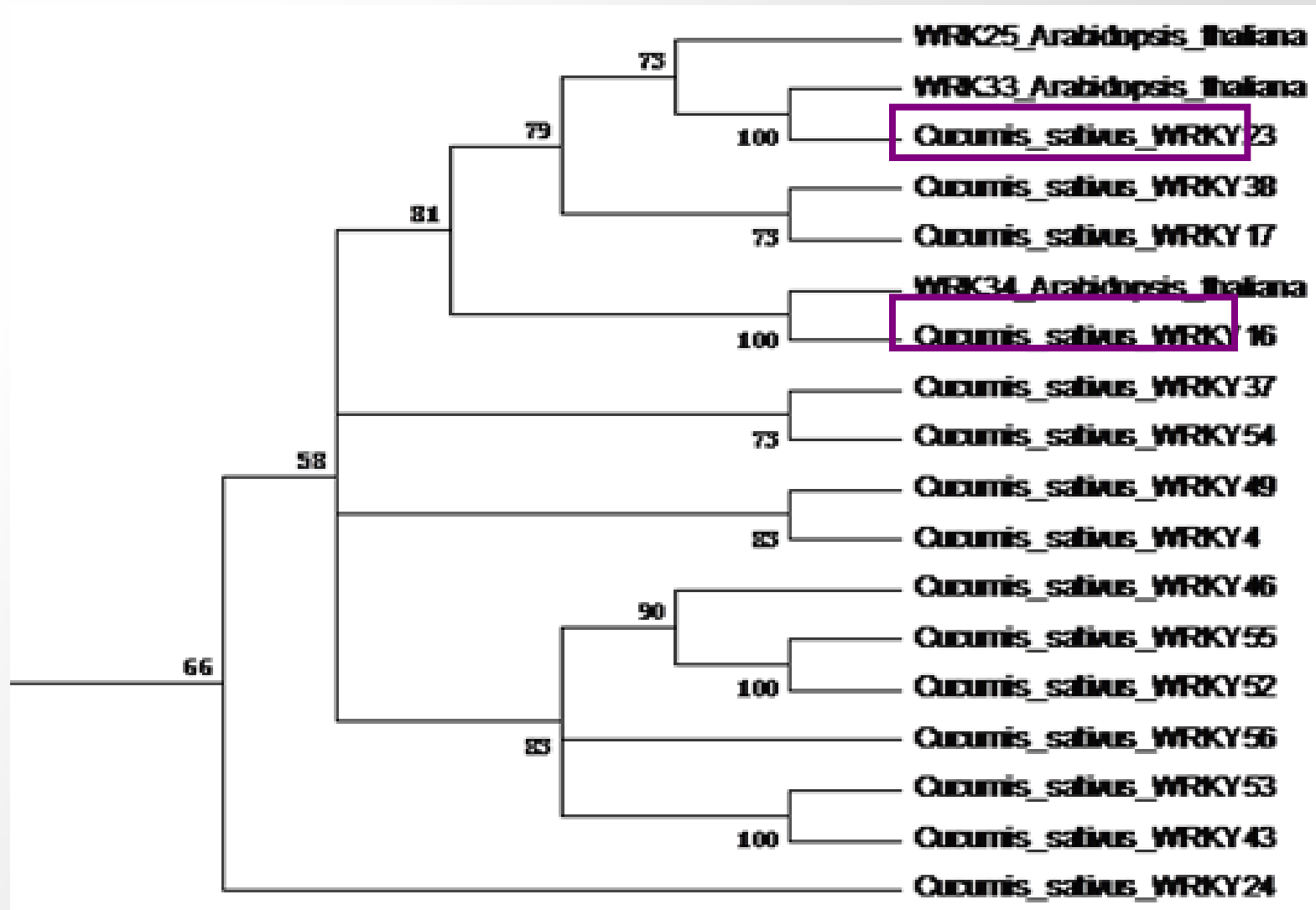
Uniprot

› Restrict term "wrky" to [gene name \(33\)](#), [protein name \(34\)](#)

› Expand search to "[Cucumis sativus \(Cucumber\) \[3659\]](#)" to include lower taxonomic ranks

Entry	Entry name	Status	Protein names	Gene names	Organism	Length
E7CEW1	E7CEW1_CUCSA	★	WRKY protein	WRKY9 WRKY10	Cucumis sativus (Cucumber)	348
E7CEV9	E7CEV9_CUCSA	★	WRKY protein	WRKY5	Cucumis sativus (Cucumber)	282
E7CEX6	E7CEX6_CUCSA	★	WRKY protein	WRKY33	Cucumis sativus (Cucumber)	383
E7CEY5	E7CEY5_CUCSA	★	WRKY protein	WRKY51	Cucumis sativus (Cucumber)	352
E7CEX3	E7CEX3_CUCSA	★	WRKY protein	WRKY25	Cucumis sativus (Cucumber)	350
E7CEW4	E7CEW4_CUCSA	★	WRKY protein	WRKY14	Cucumis sativus (Cucumber)	293
E7CEW7	E7CEW7_CUCSA	★	WRKY protein	WRKY18	Cucumis sativus (Cucumber)	336
E7CEY3	E7CEY3_CUCSA	★	WRKY protein	WRKY49	Cucumis sativus (Cucumber)	433
E7CEX0	E7CEX0_CUCSA	★	WRKY protein	WRKY22	Cucumis sativus (Cucumber)	280

WRKY Transcription Factor Phylogeny



Domains within the query sequence of 720 residues

1 100 200

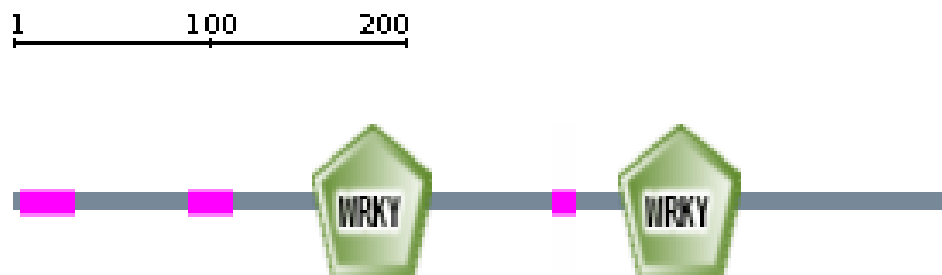


Name	Begin	End	E-value	Reason
EH	46	118	1.71e+03	threshold
Btz	281	437	1.34e+05	threshold
A4_EXTRA	285	432	5.32e+02	threshold
Pfam:FAR1	301	361	8.80e+01	overlap
Pfam:WRKY	303	361	8.00e-30	overlap
internal repeat 1	304	375	3.97e-18	overlap
Pfam:Ogr_Delta	311	348	8.90e+00	overlap
CTD	384	536	1.59e+05	threshold
Glyco_25	389	490	2.15e+03	threshold
SPT2	422	490	8.30e+04	threshold
Pfam:FAR1	506	579	1.00e+00	overlap
Pfam:WRKY	518	577	3.70e-30	overlap
GYR	519	536	2.35e+03	threshold
internal repeat 1	519	591	3.97e-18	overlap
Pfam:Ogr_Delta	530	555	1.10e+01	overlap
ZnF_C2H2	542	560	3.60e+02	threshold

Confidently predicted domains, repeats, motifs and features:

Name	Begin	End	E-value
low complexity	157	169	-
low complexity	263	276	-
WRKY	303	361	1.00e-34
WRKY	518	577	6.83e-37

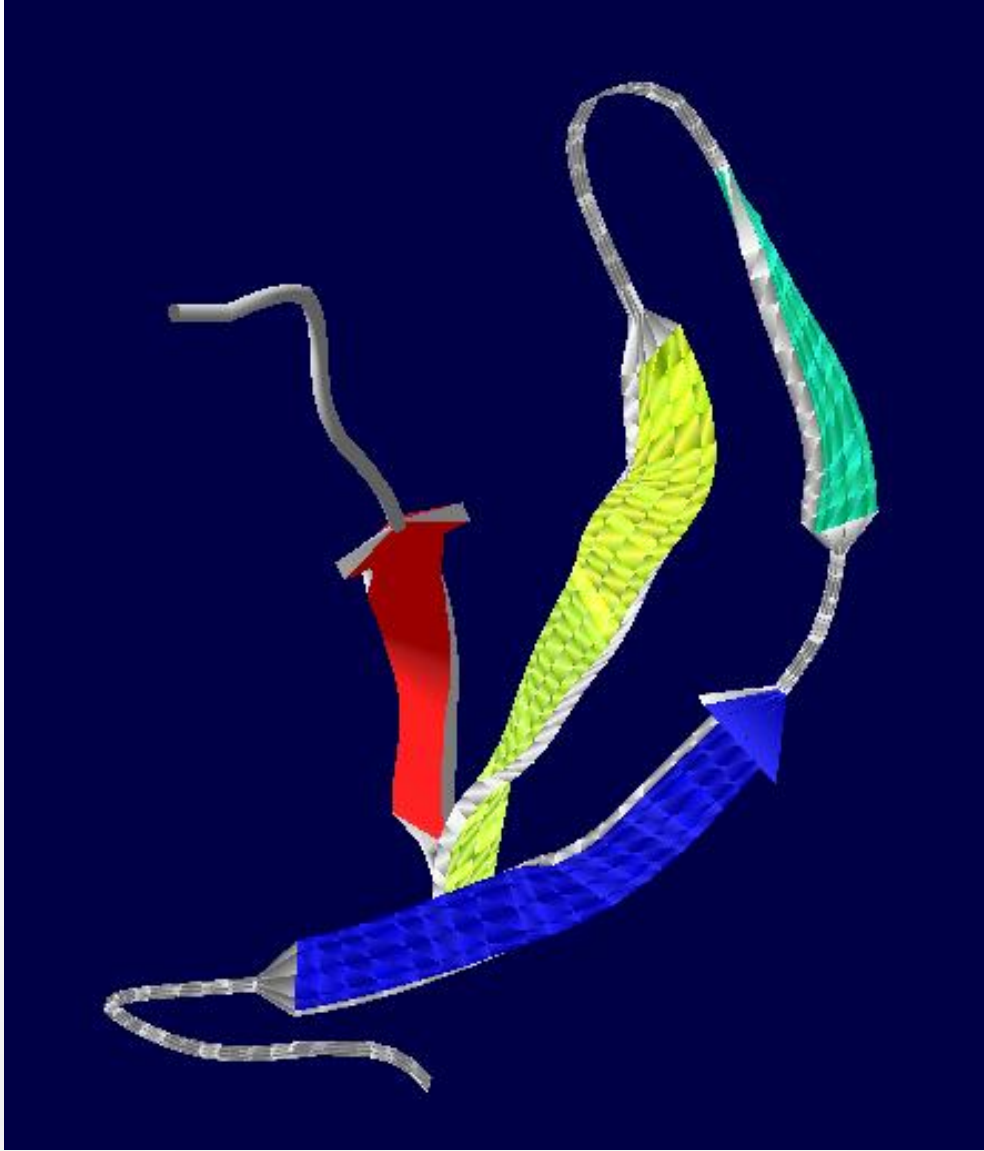
Domains within the query sequence of 452 residues



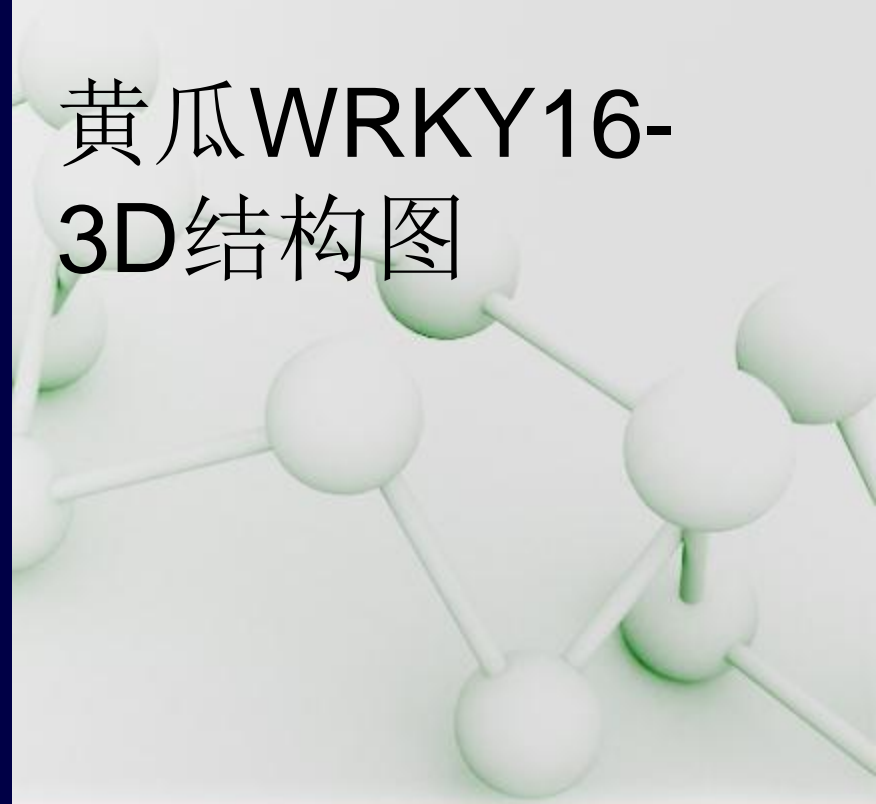
Confidently predicted domains, repeats, motifs and features:

Name	Begin	End	E-value
low complexity	4	31	-
low complexity	86	108	-
WRKY	145	203	5.30e-34
low complexity	263	274	-
WRKY	294	353	1.68e-36

Name	Begin	End	E-value	Reason
Pfam:FAR1	77	203	3.40e+02	overlap
PhnA_Zn_Ribbon	100	147	1.00e+05	threshold
CG-1	107	199	2.28e+04	threshold
Pfam:CG-1	112	164	2.70e-03	overlap
Pfam:DNA_pol3_tau_4	117	166	3.20e+00	overlap
Pfam:WRKY	145	203	8.00e-31	overlap
internal repeat 1	147	217	7.74e-24	overlap
SEP	203	278	2.19e+03	threshold
Pfam:DNA_pol3_tau_4	203	270	1.70e+01	overlap
Pfam:DNA_pol3_tau_4	276	314	5.40e+02	overlap
Pfam:FAR1	286	355	4.00e-01	overlap
Pfam:WRKY	294	353	7.10e-31	overlap
Pfam:CG-1	294	309	7.00e+02	overlap
internal repeat 1	296	365	7.74e-24	overlap
CBF	308	366	3.32e+03	threshold



黄瓜WRKY16-
3D结构图



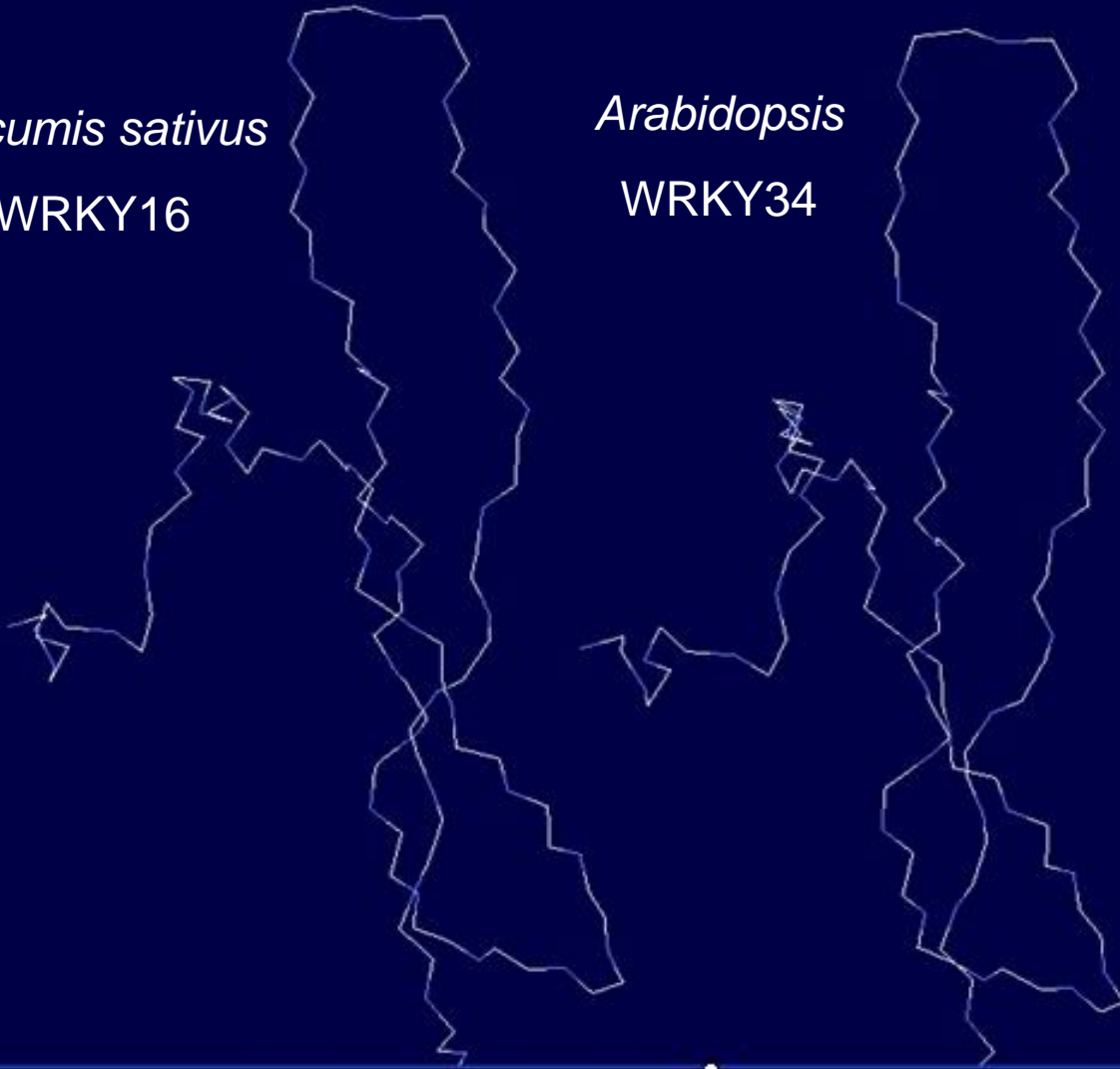
WRKY Transcription factor-SPDBV

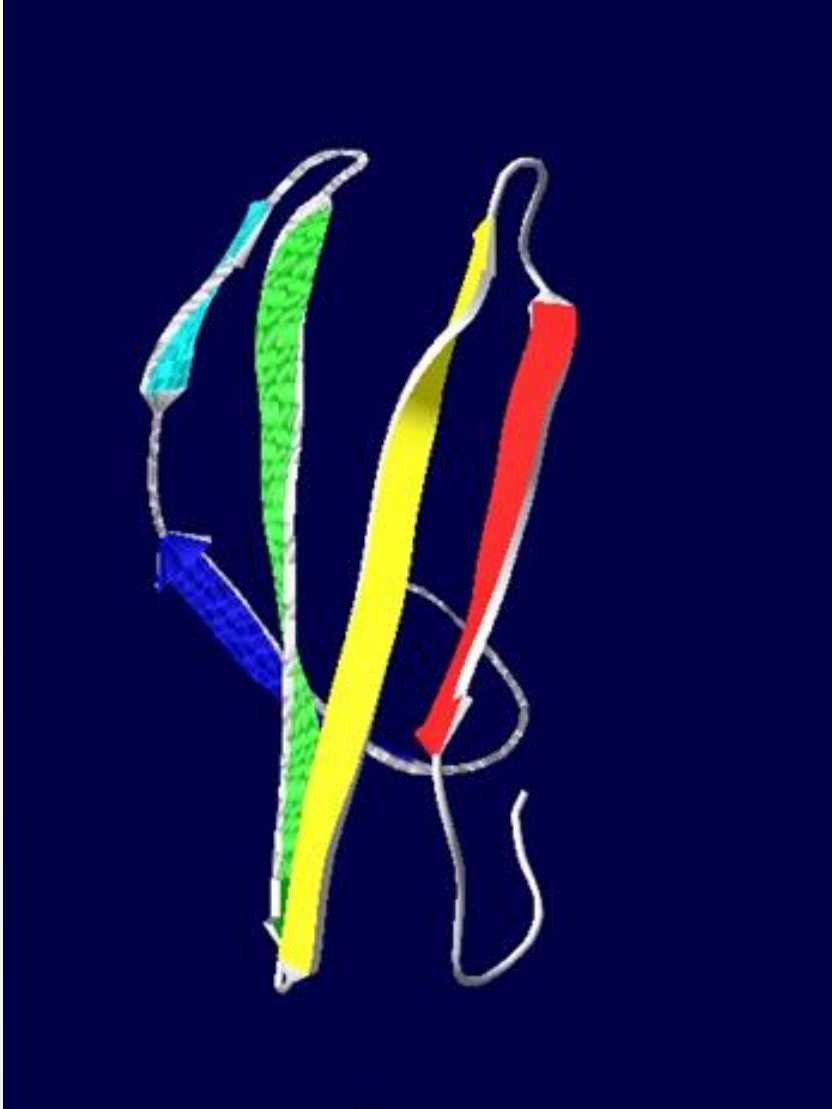
Cucumis sativus

WRKY16

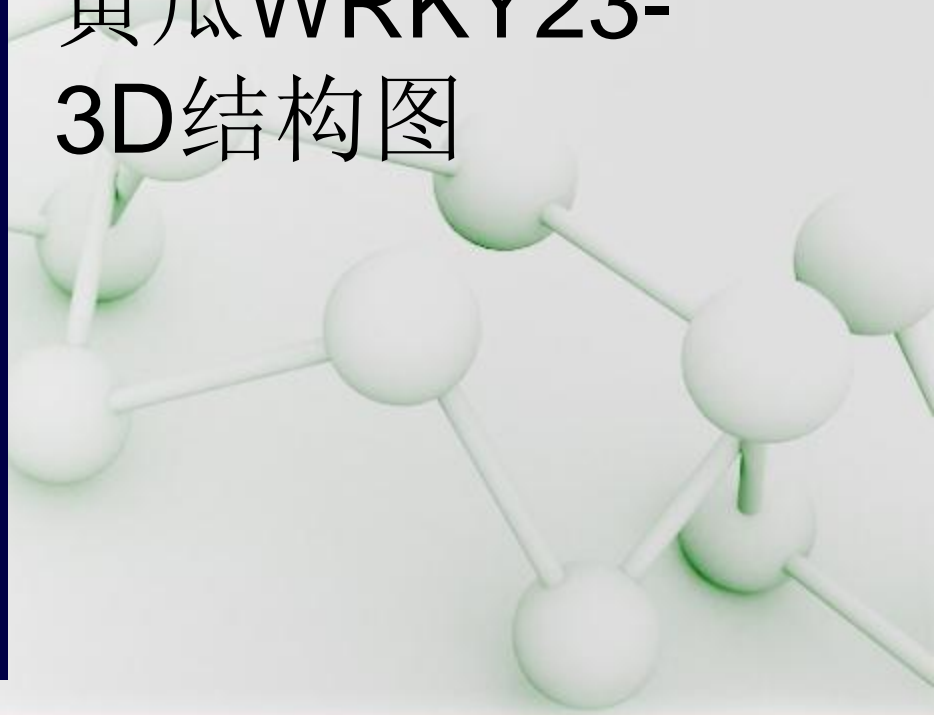
Arabidopsis

WRKY34





黄瓜WRKY23-
3D结构图



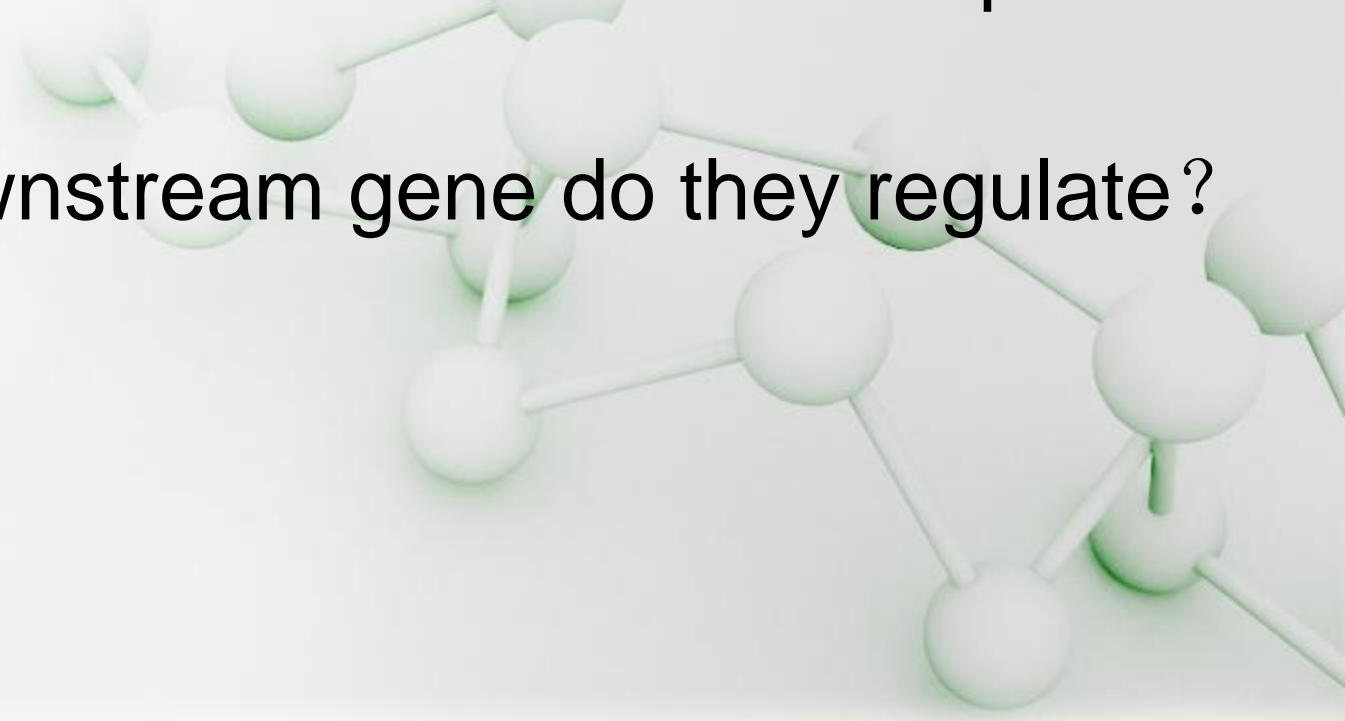
WRKY Transcription factor-SPDBV

Cucumis sativus
WRKY23



Arabidopsis
WRKY33



- 1、 Do the WRKY 16 and WRKY 23 have NLS(Nuclear Localization Signal)?
 - 2、 Do the WRKY 16 and WRKY 23 response to cold?
 - 3、 Which downstream gene do they regulate?
-
- 

- Pro. Jiang, Pro. Luo
- Ying Zhang
- Lu Chen, Jixiang Zhang, Shanshan Meng



References

- Eulgem T, Rushton PJ, Robatzek S, Somssich IE: The WRKY superfamily of plant transcription factors. *Trends Plant Sci* 2000, 5:199-206.
- Jian Ling, Weijie Jiang*, Ying Zhang et al. Genome-wide analysis of WRKY gene family in *Cucumis sativus*. *BMC Genomics* 2011, 12:471.
- Yi Shang, Lu Yan, Zhi-Qiang Liu, et al. The Mg-Chelatase H Subunit of *Arabidopsis* Antagonizes a Group of WRKY Transcription Repressors to Relieve ABA-Responsive Genes of Inhibition. *Plant Cell* 2010, Vol. 22: 1909–1935.
- Changsong Zou, Wenbo Jiang and Diqiu Yu. Male gametophyte-specific WRKY34 transcription factor mediates cold sensitivity of mature pollen in *Arabidopsis*. *Journal of Experimental Botany* 2010, Vol. 61, No. 14: 3901–3914.

Thanks

thank you

A 3D molecular model of a network structure, possibly representing a protein or a material, with white spheres and connecting rods. The model is positioned in the lower right quadrant of the slide, partially overlapping the 'thank you' text.