## 棕色棉查尔酮合成酶的生物信息 学分析

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## 主要内容

一:研究背景

二: 基因分析

三: 蛋白质分析

### 一: 研究背景:

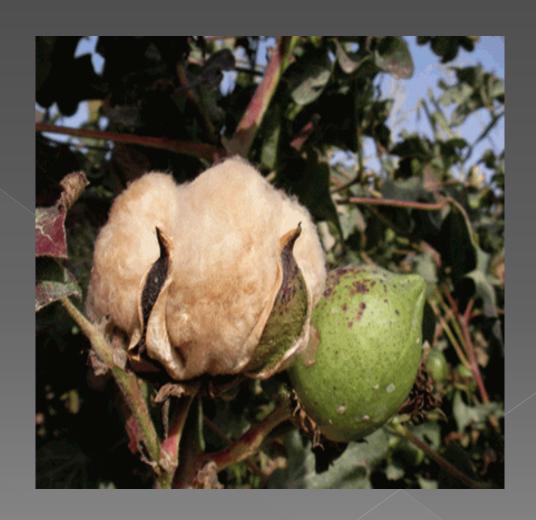
1:棉花

棉花是锦葵科,棉 属植物的种籽纤维, 是世界上主要的农 作物之一, 也是我 国重要的经济作物, 目前,我国棉花产 量位于世界前列。



#### 2: 彩棉

- 彩棉用现代生物工程技术培育出来的一种在棉花吐絮时纤维就具有天然色彩的新型纺织原料。
- 彩色棉制品有利于人体 健康,舒适:亲和皮肤, 不起静电,不起球.透汗 性好。
- 彩色棉制品在纺织过程 中减少印染工序;迎合了 减少了对环境污染。



#### 3:查尔酮合成酶

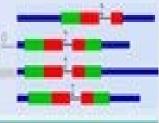
查尔酮合成酶(chalcone synthase,CHS)是生物类黄酮合成的关键酶,它催化丙二酰辅酶A的3个乙酸基和对羟苯丙烯酰辅酶A的1个乙酸基缩合,产生柚配基查尔酮和生松素查尔酮。

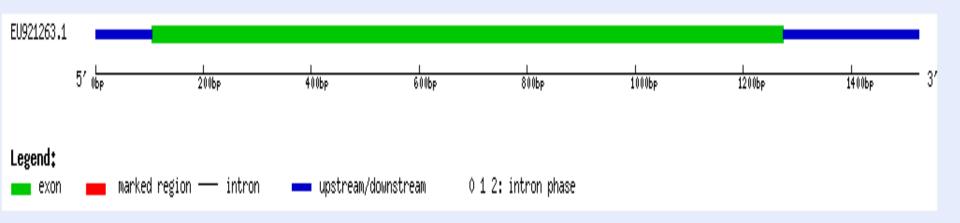
研究表明,通过荧光定量PCR检测显示:该基因在彩棉纤维细胞中优先表达,且在棕色棉纤维中的表达量远高于其近等基因系白色棉,由此推断,该基因可能在彩棉色素形成中发挥重要作用。

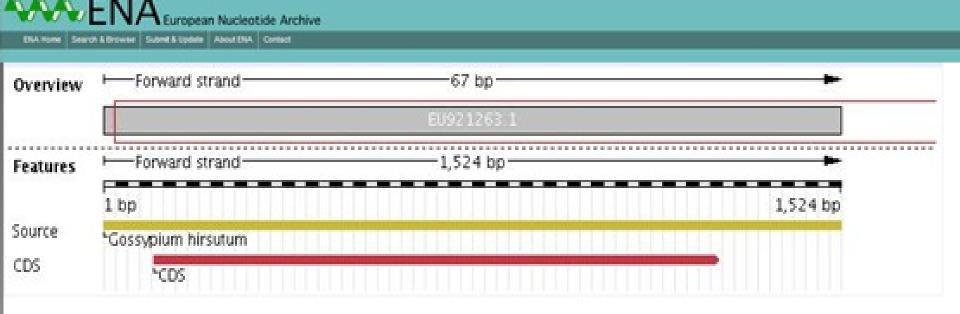
对该基因进行进一步分析,有利于改善彩棉 颜色单调,着色不均匀的的缺点,育成更好的 彩色棉品种。

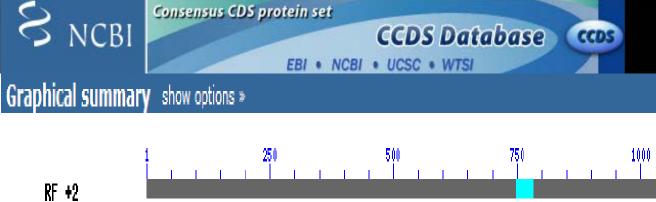


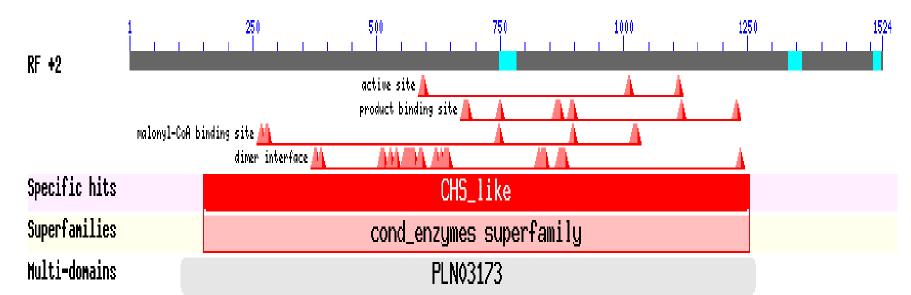
## GSDS Gene Structure Display Server





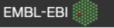






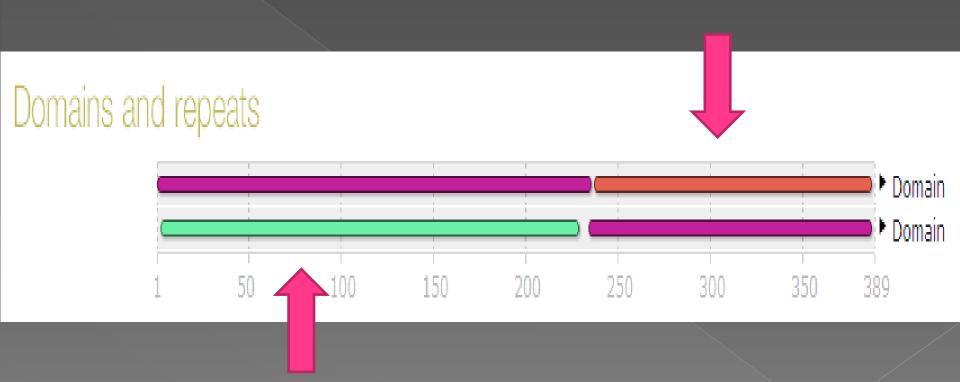


List of domain hits			0
Description	Pssmld	Multi-dom	E-value
HCHS_like[cd00831], Chalcone and stilbene synthases; plant-specific polyketide synthases (PKS) and related	238427	yes	2.46e-155
+1PLN03173[PLN03173], chalcone synthase; Provisional	178717	yes	0e+00



#### InterProScan

Chalcone/stilbene synthase, C-terminal



Chalcone/stilbene synthase, N-terminal

#### 等电点和分子量分析



#### Compute pl/Mw

#### Theoretical pl/Mw (average) for the user-entered sequence:

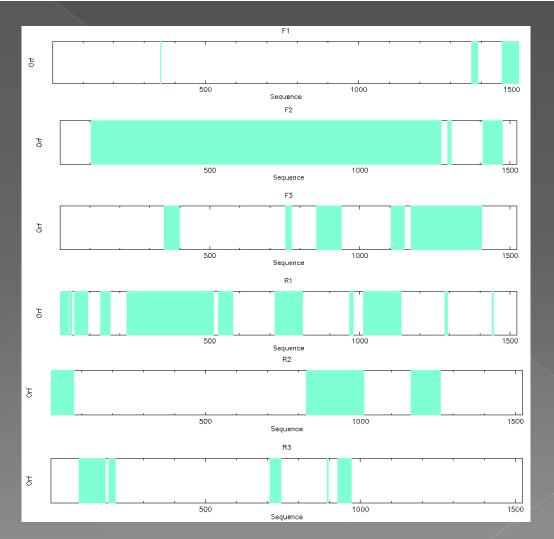
10	2 <u>0</u>	3 <u>0</u>	4 <u>0</u>	5 <u>0</u>	6 <u>0</u>
MVTVEEVRKA	QRAQGPATVL	AIGTSTPPNC	VDQSTYPDYY	FRITNSEHKT	ELKEKFKRMC
7 <u>0</u>	8 <u>0</u>	9 <u>0</u>	10 <u>0</u>	11 <u>0</u>	12 <u>0</u>
EKSMIKKRYM	YLTEEILKEN	PNVCEYMAPS	LDARQDMVVV	EVPKLGKEAA	TKAIKEWGQP
13 <u>0</u>	14 <u>0</u>	15 <u>0</u>	16 <u>0</u>	17 <u>0</u>	18 <u>0</u>
KSKITHLVFC	TTSGVDMPGA	DYQLTKLLGL	RPSVKRLMMY	QQGCFAGGTV	LRVAKDLAEN
19 <u>0</u>	20 <u>0</u>	21 <u>0</u>	22 <u>0</u>	23 <u>0</u>	24 <u>0</u>
NKGARVLVVC	SEITAVTFRG	PSDTHLDSLV	GQALFGDGAA	AVIIGADPMP	EIEKPMFEIV
25 <u>0</u>	26 <u>0</u>	27 <u>0</u>	28 <u>0</u>	29 <u>0</u>	30 <u>0</u>
SVAQTILPDS	DGAIDGHLRE	VGLTFHLLKD	VPGLISKNIE	KSLVEAFQPL	GISDWNSLFW
31 <u>0</u>	32 <u>0</u>	33 <u>0</u>	34 <u>0</u>	35 <u>0</u>	36 <u>0</u>
IAHPGGPAIL	DQVEAKLALK	PEKLRATRHV	LSEYGNMSSA	${\tt CVLFILDEMR}$	KKSREDGLQT
37 <u>0</u>	38 <u>0</u>				
TGEGLEWGVL	FGFGPGLTVE	TVVLHSVAA			
Theoretical	pl/Mw: 6.12 /	42668.39			

#### 4: 基因中可能的读码框





plotorf(v6.0.1) - Plot potential open reading frames in a nucleotide sequence



#### 分析CHS全长mRNA序列读码框特征



>2\_ORF2 Translation of in frame 2, ORF 2, threshold 100, 407aa STPPTPHHHMLFVIIRKRMVTVEEVRKAQRAQGPATVLAIGTSTPPNCVDQSTYPDYYFR ITNSEHKTELKEKFKRMCEKSMIKKRYMYLTEEILKENPNVCEYMAPSLDARQDMVVVEV PKLGKEAATKAIKEWGQPKSKITHLVFCTTSGVDMPGADYQLTKLLGLRPSVKRLMMYQQ GCFAGGTVLRVAKDLAENNKGARVLVVCSETTAVTFRGPSDTHLDSLVGQALFGDGAAAV IIGADPMPEIEKPMFEIVSVAQTILPDSDGAIDGHLREVGLTFHLLKDVPGLISKNIEKS LVEAFQPLGISDWNSLFWIAHPGGPAILDQVEAKLALKPEKLRATRHVLSEYGNMSSACV LFILDEMRKKSREDGLQTTGEGLEWGVLFGFGFGLTVETVVLHSVAA

#### 用SixPack分析得到的氨基酸序列与 GeneBank中提供的氨基酸序列进行比对

#### Pairwise Alignment Result

LENGTH	SCORE	IDENTITY	SIMILARITY	GAPS
407	2008.0	389/407 (95.6%)	389/407 (95.6%)	18/407 ( 4.4%)

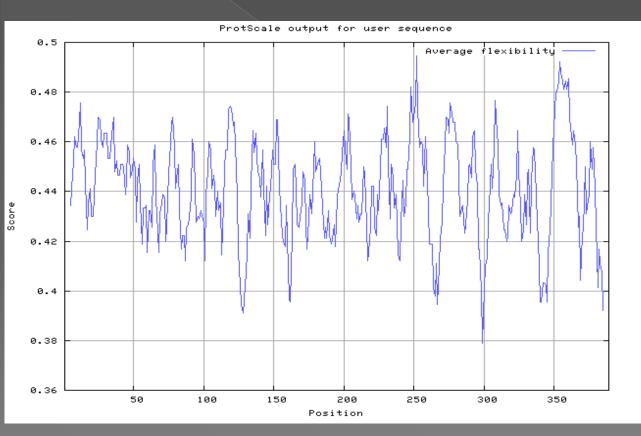
Species/Abbrv		Ŧ	÷	¥	÷	# #	<del>1</del>	#	T T T		# #	<b>†</b> †	ļ		L L	÷		Ŧ Ŧ	¥	Ť Ť	<b>.</b>	<u>.</u>	T T T		Ŧ	<u>.</u>	Ť Ť	##	#	Ť Ť	¥	#	# #	‡	Ť Ť	‡	T T T		T T
1. Q9M5B2 PETHY		MV	ΤV	Œ	Y R B	A	RA	EG:	A	VM	AΙ	GT	AT.	Tl	(C)	ΒQ	ST	Y P	DΥ	YF	RI	I N S	S <mark>B</mark> H	KT	I L	KE	K <mark>e</mark> k	RM	CE	K S M	IK	KR	Y <mark>M</mark> H	LΙ	EE	ΙL	E N P	SM(	CEY
2. CHSY VITVI		ΜV	SVZ	YΕ	IRK	A	RA	EG	A	۷L	ΑI	GT	N T	A	ICV	ΥQ	A D	Y P	DΥ	YF	RI	TNS	S E H	ΜT	I L	KE	KFK	RM	CE	K S M	ΙN	KR	Y <mark>M</mark> H	LΙ	EE.	ILK	ENP	NV(	C <mark>A</mark> Y
3. E9JWE4 PYRPY		ΜV	ΤV	Œ	V R B	A	RA	EG	A	۷L	AΙ	GT:	3 T	P	(CV	DQ	AΤ	Y P	DΥ	YF	RI	T N S	S E H	K T	ΙL	KE	K F	R M	CD	K S M	ΙK	T R	Y M Y	LΙ	EE.	ΙL	EN P	TV(	CEY
4. CHS5 PEA		ΜV	s <mark>v</mark> s	S E	IRK	A	RA	EG	A	ΙL	AΙ	GT	A N	A	(CV	EQ	ST	Y P	ΙF	YF	RI	T N S	S E H	KT	ΙL	KQ	K F (	R M	CD.	K S M	ΙN	RR	Y <mark>M</mark> Y	LΤ	EE.	IL	EN P	S V (	CEY
5. CHS5 SOYBN		ΜV	s V	Œ	IRÇ	AO	RA	EG	A	VM	AΙ	GI	A T	P	(CV	ם סַם	ST	Y P	DΥ	YF	RI	T N S	H	M T	ΕL	KE	K F K	RM	CD	K S M	ΙK	KR	Y <mark>M</mark> Y	LN	E E	ΙL	ENP	S V (	CAY
6. CHS8 MEDSA		MV	s <mark>v</mark> s	E	IRI	A	RA	E G	A	ΙL	AΙ	GT	A N	A	IC.	EQ	ST	y p	ΒF	YF	KI	I N S	S E H	KT	Į,	KE	Ε	RM	CD	KSM	IK	RR	Y M Y	LI	EE	ILK	EN P	S V (	CEY
7. CHS5 TRISU		ΜV	SVZ	I E	IRC	ΑO	RA	EG	Α	ΙL	AΙ	GT	A N	A	KV	EO	AΤ	y p	ΡF	YF	KI	I N S	S B H	K V	I	KE	F	RM	CD	K S M	ΙK	SR	YMY	LT	EE	IL	EN P	S V (	CEY
8. CHSS SORBI Species/Abbrv	MAAA * * * *	. ▼ V * *	. V	*	V R R	A 0	RA + +	I C	A	VL * *	AI  ∗ •	<b>C</b> T	A	<u>A</u>	ICV	# #	A I	Y D	P Y	Y F	N I	K + + +	H	M ₩	<u>I</u>	# # #	K F K	R M + +	C I	S 0	I R  ÷	K R	YMH	L + +	# #	Y L A	E N D	N M (	CAY
1. Q9M5B2 PETHY	MAPS	L	A R	Б	VV	۷	V P	L	K	AΑ	QK.	ΑI	E 7	G	PΚ	SK	ΙT	H L	V F	T	18	V	М	gc	DY.	ĮL:	KI	LG	LR	sv	ΚR	LM	MYQ	QG	CF	A G G	IVL	RL	AK D
2. CHSY VITVI	MAPS	LD	A R	D	1VV	V	V P I	L	K	AΑ	A K	ΑI	EV	Ġ,	PΚ	SK	IT	H L	VF(	T	[ S <mark>(</mark>	V	M	<mark>G</mark> A	DY.	ĮL:	KI	LG	LK	sV	ΚR	LM	MY Q	QG	CF	A G G	IVL	RLA	AK D
3. E9JWE4 PYRPY	MAPS	LD	A R	1	1 V V	۷	V P I	L	KE	AΑ	ΙK	ΑI	ΕV	Ġ,	PΚ	SK	IT.	H L	VF(	T	I 8 <mark>9</mark>	V	M	<mark>G</mark> A	DY.	ĮL:	ΚI	LG:	LR	SV	ΚR	LM	MY Q	QG	CF	A G G	TVL	RL	AK D
4. CHS5 PEA	MAPS	LD	A R	1	1V V	V	V P	L	KE	AΑ	V K	ΑI	ΞV	g	PΚ	SK	IT	HL:	IF(	T	T 8 <mark>9</mark>	V	М	G A	DY.	L	KI	LG	LR	ΥV	ΚR	YM	MY Q	QG	CF	AGG	IVL	RL	AK D
5. CHS5 SOYBN	MA <mark>P</mark> S	LD	A R	D	1V V	M	V P	L	KE	AΑ	ΙK	ΑI	EV	Ġ	PΚ	SK	IT	HL:	IF(	T	[ S <mark>9</mark>	V	М	<mark>G</mark> A	DY.	L	KI	LG	LR	SV	ΚR	YM	MY Q	QG	CF	A G G	ΤVL	RL	AK D
6. CHS8 MEDSA	MAPS	LD	A R	D	1 V V	V	V P	L	KE	AΑ	V K	ΑI	EV	g	PΚ	SK	IT	HL:	IV(	T	[ S	V	M	G A	DY.	QL	KI	LG	LR	ΥV	ΚR	Y M I	MY Q	QG	CF	A G G	TVL	RL	AK D
7. CHS5 TRISU	MAPS	LD	A R	D	1V V	VE	V P	L	KE	AΑ	V K	ΑI	EV	G	PΚ	SK	IT	HL:	IF(	T	I S C	V	M	G A	DY.	L	ΚI	LG	LR	ΥV	ΚR	YM	MY Q	QG	CF	A G G	TVL	RL	AK D
8. CHS5 SORBI Species/Abbrv	MAPS	L *	ARO	<b>1</b>	V V	V =	V P	LO	K A	AA ++	H K	AI,		G *	₽ K	5 K	II:	H L	VF(	*	5 (	V *	M ₽ + +	GA	D Y	L	K M	LG	LR:	s V	N R ÷	LMI	MYO	o <mark>G</mark>	CFA	A G G	TVL	RVI	A K D
1. Q9M5B2 PETHY	LAEN	NK	g A R	V	VV	CS	Ī	ΑV	7 T E	RG	P N	DI	L	SI	VG	ΟA	LF	G D	GA (	A		I G	100	IP	gν	R	LF	I.	V S Z	AAO	ΤL	L	SH	GA	I	HL	R E V	GL	FH
2. CHSY VITVI	LAEN	ΝA	GSR	VI	VV	CS	I	ΑV	/ <b>T</b> F	RG	<b>9</b> S	DTI	L	SI	VG	O A	LF	G D	GAZ	/A/	7 I I	I G A		DT	ΚI	L	LF	L	V S I	ΑAO	ΤI	LP	DSE	GΑ	I	HL	R E V	GL	FH
	LAEN	NK	G A R	V	VV	CS	I	A١	TE	RG	<b>9</b> S	DTI	L	SI	VG	QΑ	LF	G D	GA	, A	7 I I	I G	D P	V P	ΕV	K	LF	L	V S Z	ΑAQ	ΙI	L	DSD	G A	ID	HL	R E V	G L	FH
4. CHS5 PEA	LAEN	NK	G A R	V	VV	CS	V	A١	TE	RG	<b>9</b> S	DT	L	SI	VG	QA	LF	G D	G A A	AAI	, I	7 G S	DP	ΙP	ΙΙ	K	ΙF	M	۷v	Ι <mark>Α</mark> Ω	TI.	A	DSE	GΑ	ID	HL	R E A	G L	FH
5. CHS5 SOYBN	L A E N	NK	G A R	V	VV	CS	I	A١	ľ	RG	P T	DT	L	SI	VG	QΑ	LF	GD	G A A	/A/	ĮΙ	7 G	D P	LP	- <mark>∨</mark>	K	LF	ĞΓ	V v	ΑQ	ΙI	LP	DSE	<mark>G</mark> A	ID	HL	R E V	G L	FH
3. E9JWE4 PYRPY 4. CHS5 PEA 5. CHS5 SOYBN 6. CHS8 MEDSA	LAEN	NK	G A R	V	VV	CS	V	A١	TE	RG	<b>9</b> S	DT	L	SI	VG	QA	LF	G D	GA	AΑΙ	ΙI	7 G S	D P	VP	I	K	ΙF	E M	V v	Ι <mark>Α</mark> Ω	ΙI.	A P	DSE	GG	ID	HL	REA	GL	FH
7. CHS5 TRISU	LAEN	NK	G A R	V	VV	CS	V	ΑV	/ T E	RG	<b>9</b> S	DT	L	5 I	VG	QA	LF	GD(	GAZ	ΙΑΙ	ΙIΙ	7 G	I D P	VP	ΙĮ	BK E	ΙF	E M	٧n:	Ι <mark>Α</mark> Ω	II.	ΑP	085	GΑ	I	HL	R E A	G L	FH
8. CHS5 SORBI	LAEN	N R	<mark>g</mark> a r	V	VV	CS	I	A١	/TE	RG	<b>9</b> S	E S I	L	S	IV G	QA	LF	G D	GAZ	I A I	/IV	I <mark>G</mark> I	o D	DΕ	R V	R	LF	ĞΓ	V S Z	A S Q	ΙI	L	DSE	<mark>G</mark> A	ID	HL	R E V	G L	FH

#### 序列比对

● 序列比对发现,棉花查尔酮CHS基因与葡萄、 矮牵牛、梨、黄蜀葵等同源性较高。均达到 90%以上。

#### 蛋白质柔性分析





#### scale values:

Ala: 0.360

Arg: 0.530

Asn: 0.460

Asp: 0.510

Cys: 0.350

Gln: 0.490

Glu: 0.500

Gly: 0.540

His: 0.320

Ile: 0.460

Leu: 0.370

Lys: 0.470

Met: 0.300

Phe: 0.310

Pro: 0.510

Ser: 0.510

Thr: 0.440

Trp: 0.310

Tyr: 0.420

Val: 0.390

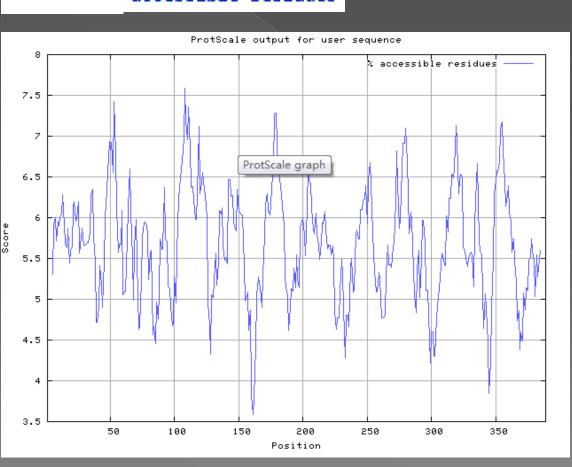
蛋白质柔性越高,蛋白质稳定性越好。

#### 蛋白质溶剂可及性分析



ProtScale

accessible residues



scale values:

Ala:6.600

Arg:4.500

Asn:6.700

Asp:7.700

Cys:0.900

Gln:5.200

Glu:5.700

Gly:6.700

His:2.500

lle: 2.800

Leu:4.800

Lys:10.300

Met:1.000

Phe:2.400

Pro:4.800

Ser:9.400

Thr:7.000

Trp:1.400

Tyr:5.100

Val:4.500

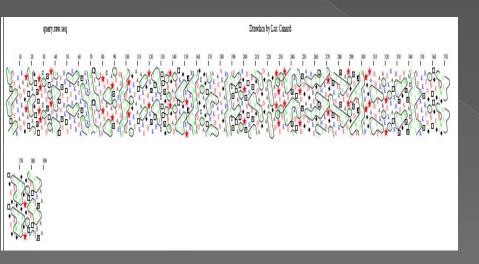
溶剂可及性越高,越有利于与DNA结合

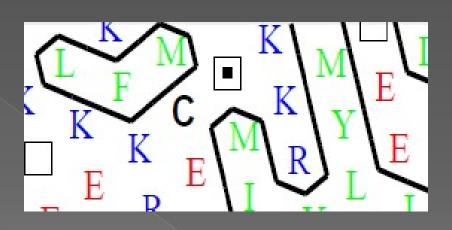
#### 蛋白质中疏水氨基酸基团分析:



**HCA 1.0.2** 

**Hydrophobic Cluster Analysis.** 





绿色:非极性氨基酸,也是疏水氨基酸。

蓝色:极性氨基酸,带正电的亲水氨基酸。

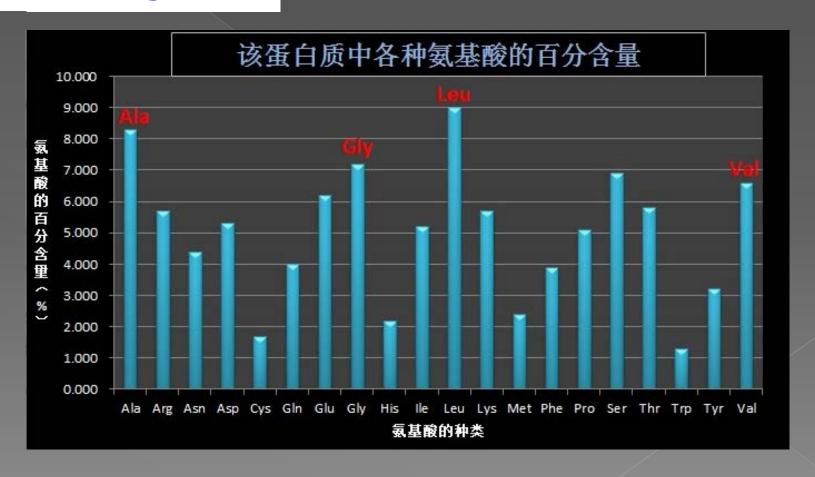
红色:极性氨基酸,带负电的亲水氨基酸。

#### 蛋白质氨基酸组成分析



ProtScale

A.A. composition



### 二级结构分析



Service

 $\label{eq:garnier} \textbf{garnier(v6.0.1)} \text{ -} \text{Predicts protein secondary structure using GOR method}$ 

<b>5573</b>	нининининин	IQGFHIOLH	IGISTEFAC	DQSIIIDIII	ннн
	ппппппппппппппппппппппппппппппппппппппп			eeeee eee	
sheet	т.		E E TT TTT		EE
turns coil	•		ccc	• • •	cccc
COTT	- 60	. 79		. 90	_ 188
	ELKEKFKRMCEKS				
boliv	HHHHHHHHHHHH				
sheet				EEEE	EEEE
turns		_	тт		EEEE
coil					
COLL	. 110	. 120		. 140	. 150
	EVPKLGKEAATKA				
holiv	нининининини		3. 1 1 111 2 1 6 1		HH
sheet			EEEEEE		EEEEE
turns		т.		TTTT T	T
coil		ccc.		ccc	·c
COLL	. 169		. 180		- 200
	RPSVKRLMMYQQG				
helix	нн		нинининн		
sheet	EEEEEEE			EEEEEEE	FFFFFF
turns				т	т
	т	TTTTT		Т	T CC
turns coil	T CC	C	. 239	-	-
	T T CC . 219	TTTTT C - 220		. 240	. CC - 250
	T CC	TTTTT C - 220	VIIGADPMPE	. 240	. CC . 250 Vaqtilpds
coil	T T CC . 219	TTTTT C . 220 ILFGDGAAA HHHH	VIIGADPMPE HF	. 240 EIEKPMFEIUS	. CC . 250 Vaqtilpds
coil helix	T T CC . 210 PSDTHLDSLUGQA EEEEEEEE	TTTTT C . 220 ILFGDGAAA HHHH	VIIGADPMPE HF	. 240 EIEKPMFEIUS	CC 250 Vaqtilpds Hh
coil helix sheet	T T CC 210 PSDTHLDSLUGQA EEEEEEEE	C 220 LFGDGAAA HHHH	VIIGADPMPE HF	. 240 :IEKPMFEIUS ННИННИННИН	CC 250 VAQTILPDS HH EEEE
coil helix sheet turns	T T CC - 210 PSDTHLDSLUGQA EEEEEEEE T CCCC	C 220 LFGDGAAA HHHH	VIIGADPMPE HH EEEE	. 240 :IEKPMFEIUS НИННИННИНН	CC 250 VAQTILPDS HH EEEE T C C
coil helix sheet turns	T T CC - 210 PSDTHLDSLUGQA EEEEEEEE T CCCC	C 270	VIIGADPMPE HH EEEE CCCC . 280	. 240 :IEKPMFEIUS ИННИНИНИННИ . 290	CC 250 UAQTILPDS HH EEEE T C C . 300
coil helix sheet turns	T T CC . 210 PSDTHLDSLUGQA EEEEEEEE T CCCC . 260 DGAIDGHLREUGL	C 270	VIIGADPMPE HH EEEE CCCC . 280	. 240 EIEKPMFEIUS IНННННННННН . 290 ISLUEAFQPLG	CC 250 UAQTILPDS HH EEEE T C C . 300
coil helix sheet turns coil	T T CC . 210 PSDTHLDSLUGQA EEEEEEEE T CCCC . 260 DGAIDGHLREUGL	C 270	VIIGADPMPE HE EEEE CCCC . 280 PGLISKNIEK	. 240 EIEKPMFEIUS IНННННННННН . 290 ISLUEAFQPLG	CC 250 UAQTILPDS HH EEEE T C C . 300
coil helix sheet turns coil helix	T TCC 210 PSDTHLDSLUGQA EEEEEEEE T CCCC 260 DGAIDGHLREUGL HH HHHHH	TTTTT C 220 LFGDGAAA EEE CC . 270 .TFHLLKDU	VIIGADPMPE HE EEEE CCCC . 280 PGLISKNIEK	. 240 EIEKPMFEIUS IНННННННННН . 290 ESLUEAFQPLG IНННННН	CC . 250 VAQTILPDS HH EEEE T C C . 300 ISDWNSLFW
coil helix sheet turns coil helix sheet	T TCC 210 PSDTHLDSLUGQA EEEEEEEE T CCCC 260 DGAIDGHLREUGL HH HHHHH	C 278 . TFHLLKDV	VIIGADPMPE HE EEEE CCCC . 280 PGLISKNIEK	. 240 ЕІЕКРМБЕІ US ІННИННИНННН . 290 (SLUEAFQPLG ІННИННН Е	CC . 250 VAQTILPDS HH EEEE T C C . 300 ISDWNSLFW
coil helix sheet turns coil helix sheet turns	T T T CC CC . 310	C 270  TFHLLKDU	VIIGADPMPE HH EEEE CCCC . 280 PGLISKNIEK HHHHHHHHHH	. 240 :IEKPMFEIVS  НННННННННН . 290  SLVEAFQPLG  ННННН E TT C . 340	CC CCC . 350
coil helix sheet turns coil helix sheet turns	T T T CC CC	C 270  TFHLLKDU	VIIGADPMPE HH EEEE CCCC . 280 PGLISKNIEK HHHHHHHHHH	. 240 :IEKPMFEIVS  НННННННННН . 290  SLVEAFQPLG  ННННН E TT C . 340	CC CCC . 350
coil helix sheet turns coil helix sheet turns	T T T T CC . 210 PSDTHLDSLUGQA EEEEEEEE T CCCC . 260 DGAIDGHLREUGL HH HHHHH E T CC . CC . 310 IAHPGGPAILDQU	TTTTT C 220 LFGDGAAA EEE CC 270 TFHLLKDUIHHHH E TT C 320	UIIGADPMPE HH EEEE CCCC 280 PGLISKNIEK HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	. 240 EIEKPMFEIUS HHHHHHHHHHH  . 290 SSLUEAFQPLG HHHHHHH  E TT C 340 .SEYGNMSSAC	CC CCC . 350
helix sheet turns coil helix sheet turns coil	T TCC . 218 PSDTHLDSLUGQA EEEEEEEE T CCCC . 269 DGAIDGHLREUGL HH HHHHH E T CC CC . 318 IAHPGGPAILDQU	TTTTT C 220 LFGDGAAA EEE CC 270 TFHLLKDUIHHHH E TT C 320	UIIGADPMPE HH EEEE CCCC . 280 PGLISKNIEK HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	. 240 EIEKPMFEIUS HHHHHHHHHHH  . 290 SSLUEAFQPLG HHHHHHH  E TT C 340 .SEYGNMSSAC	CC . 250 VAQTILPDS HH EEEE T C C C . 300 ISDWNSLFW ETT T CC CCC . 350 ULFILDEMR
helix sheet turns coil helix sheet turns coil	T TCC . 218 PSDTHLDSLUGQA EEEEEEEE T CCCC . 269 DGAIDGHLREUGL HH HHHHH E T CC CC . 318 IAHPGGPAILDQU	TTTTT C 220 LFGDGAAA EEE CC 270 TFHLLKDUIHHHH E TT C 320	UIIGADPMPE HH EEEE CCCC 280 PGLISKNIEK HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	. 240 EIEKPMFEIUS HHHHHHHHHHH  . 290 SSLUEAFQPLG HHHHHHH  E TT C 340 .SEYGNMSSAC	CC . 250 VAQTILPDS HH EEEE T CC . 300 ISDWNSLFW E TT CC . 350 ULFILDEMR HHHHHHHH

H: α-螺旋

S: *B*一折叠

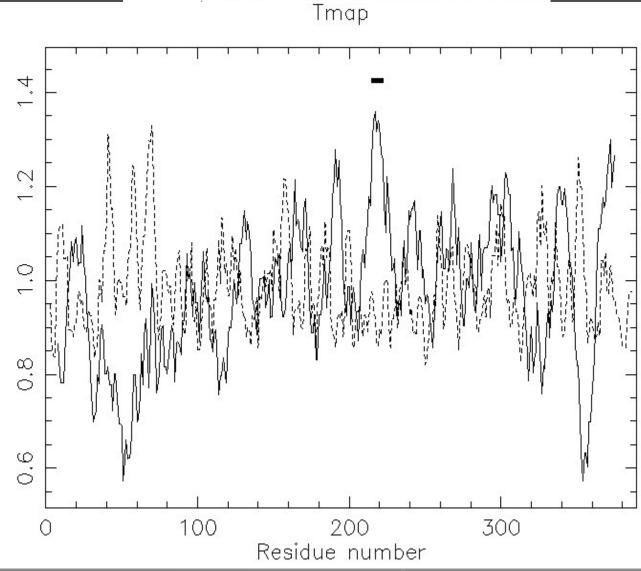
T: 第一转用

C: 卷曲

#### 跨膜螺旋预测

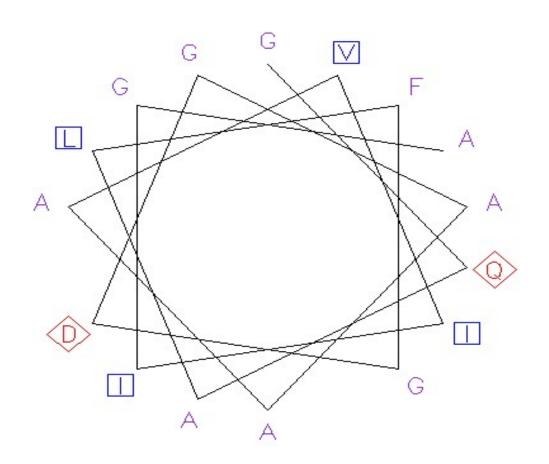
Service tmap(v6.0.1) - Predict and plot transmembrane segments in protein sequences

Start 211 End 226 TransMem Sequence GQALFGDGAAAVIIGA

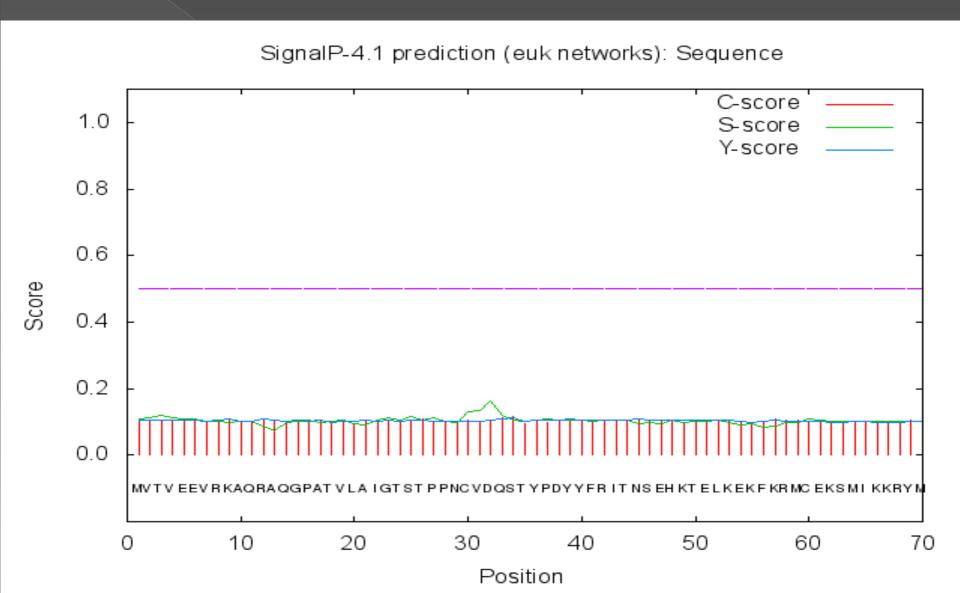


#### 螺旋轮构建

Helical wheel of raw::635887



#### 信号肽预测-无信号肽切割位点



#### 亚细胞定位



#### TargetP 1.1 Server - prediction results

Technical University of Denmark

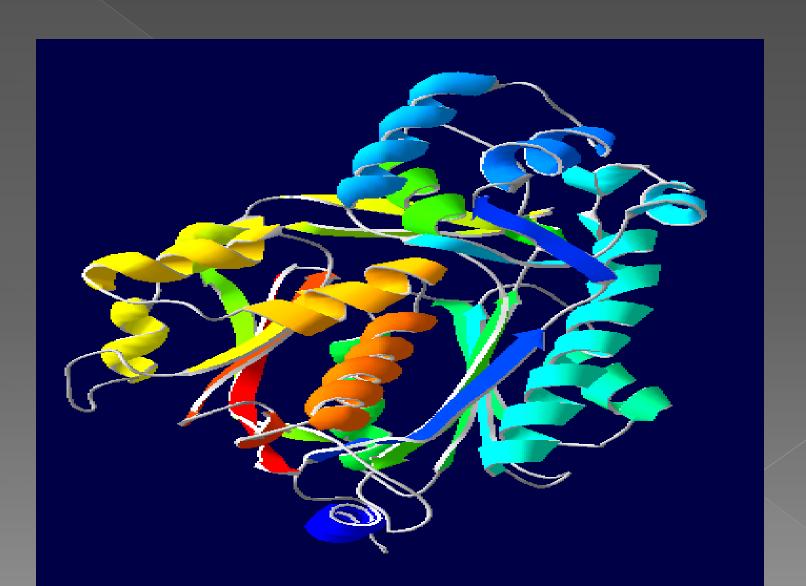
Cleavage site predictions included.

Using PLANT networks.

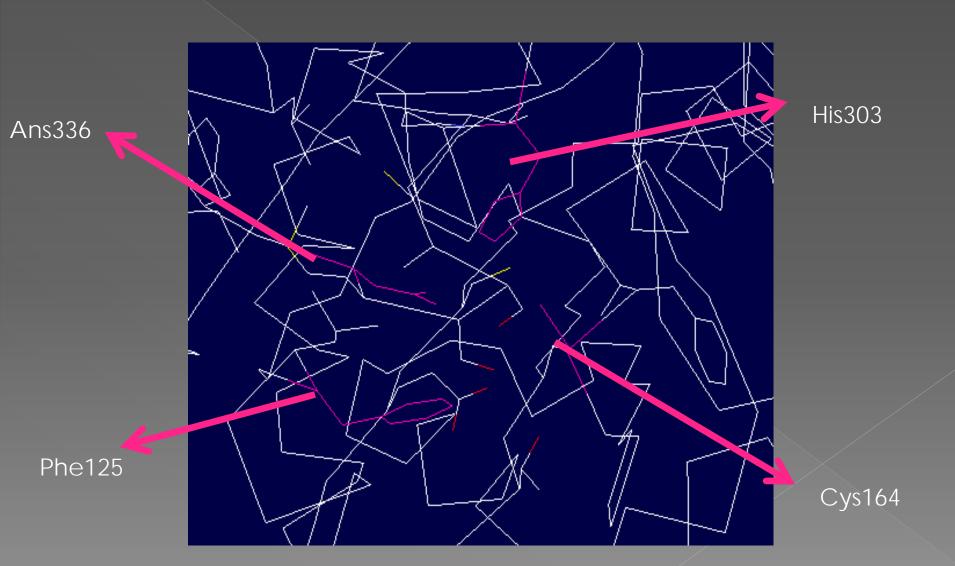
Name	Len	cTP	mTP	SP	other	Loc	RC	TPlen
Sequence	389	0.029	0.486	0.063	0.671	_	5	-
cutoff		0.000	0.000	0.000	0.000			

cTP: 叶绿体mTP: 线粒体

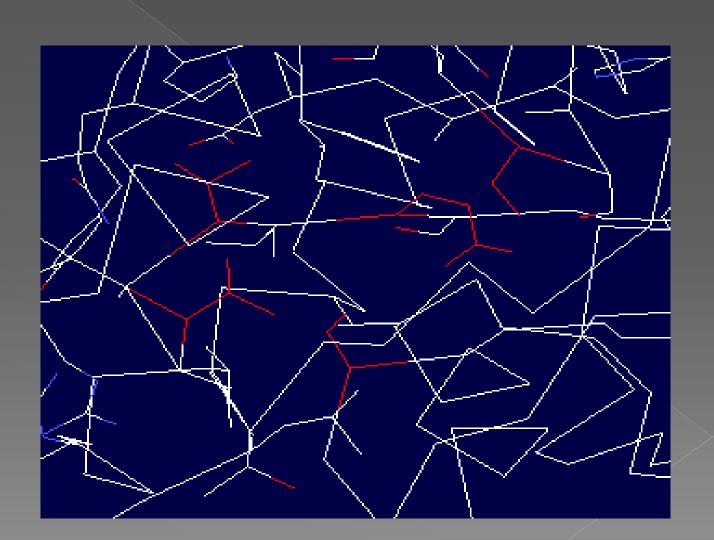
## 同源建模



### 四个酶活性位点



## 5个组成底物结合口袋位点

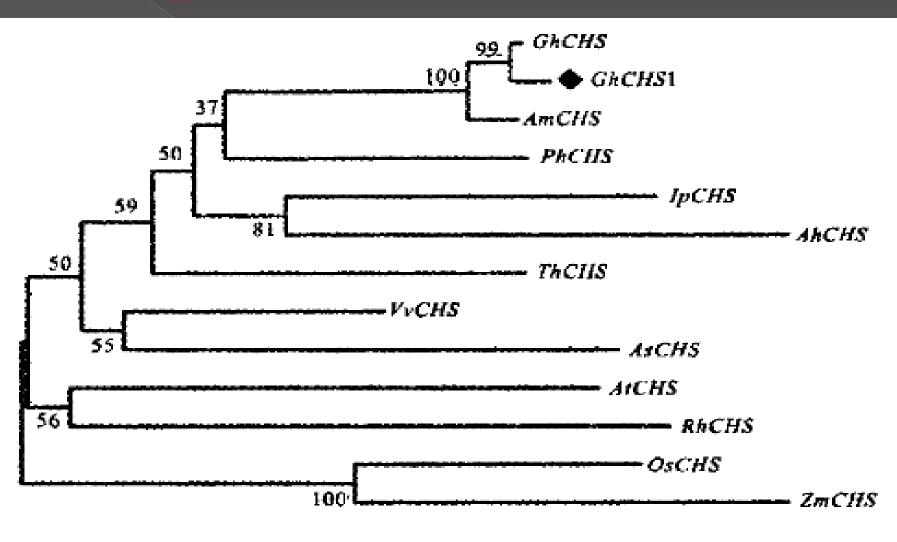


# 7个组成环化反应口袋的结合位点



### 构建进化树

0.02



CHS在进化上与陆地棉、黄蜀葵等最为接近, 与水稻、玉米进化关系最远,可能与棉花和黄 蜀葵属于棉葵科而且是双子叶植物,而玉米、 水稻是单子叶植物有关

# Thank you!