



Exploring the Genetic Mechanism of Mitochondrial DNA Inheritance in Angiosperms

Group 4:

Leader : WANG RUI

Members: LI XIN YA

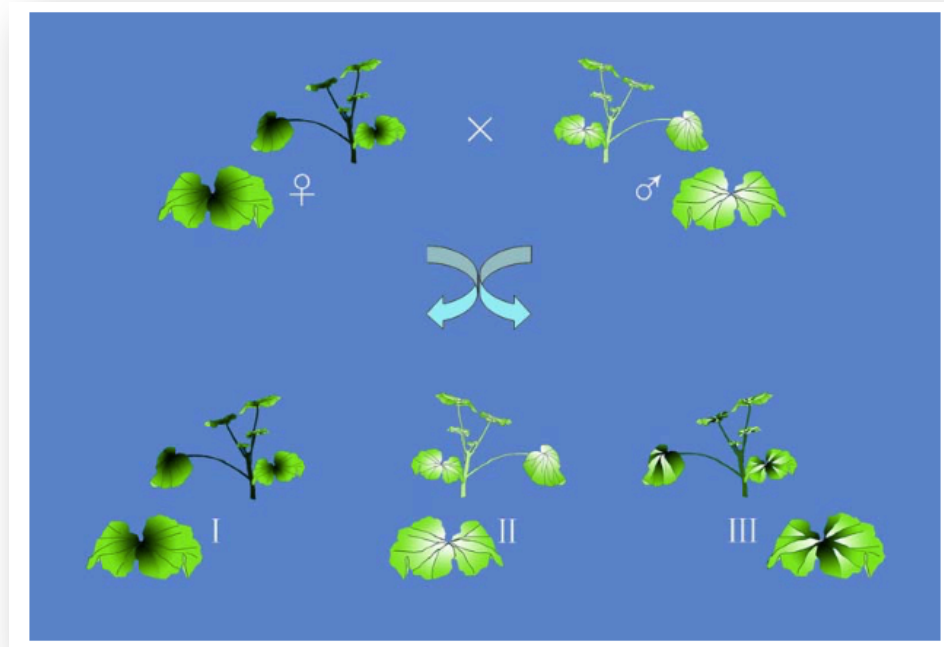
LU QI

Outline

- Background
- Research ideas
- Bioinformatics analysis
- Outlook

Background

- **Non-Mendelian inheritance** : a general term that refers to any pattern of inheritance in which traits do not segregate in accordance with Mendel's laws.



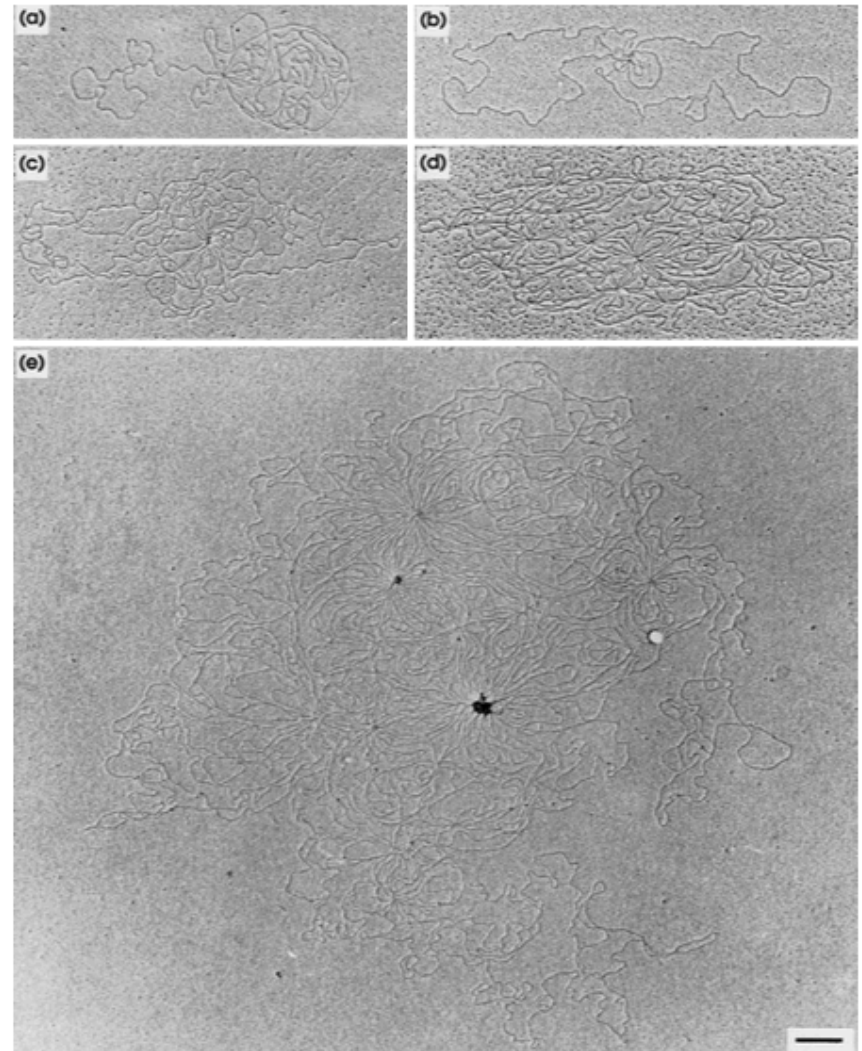
Baur et al., 1909

Background

- Non-Mendelian inheritance of Mitochondrion in plants
 - The degradation of mitochondrial DNA block paternal transmission in the germ cell.(Miyamura et al.,1987)
 - During fertilization process, the cytoplasm of the sperm cell is excluded from the Zygote.Leading to block paternal transmission.(Mogensen,1988)
 - The massive replication of mitochondrial DNA lead to paternal transmission in the sperm cell.(Nagata et al.,1999)

Background

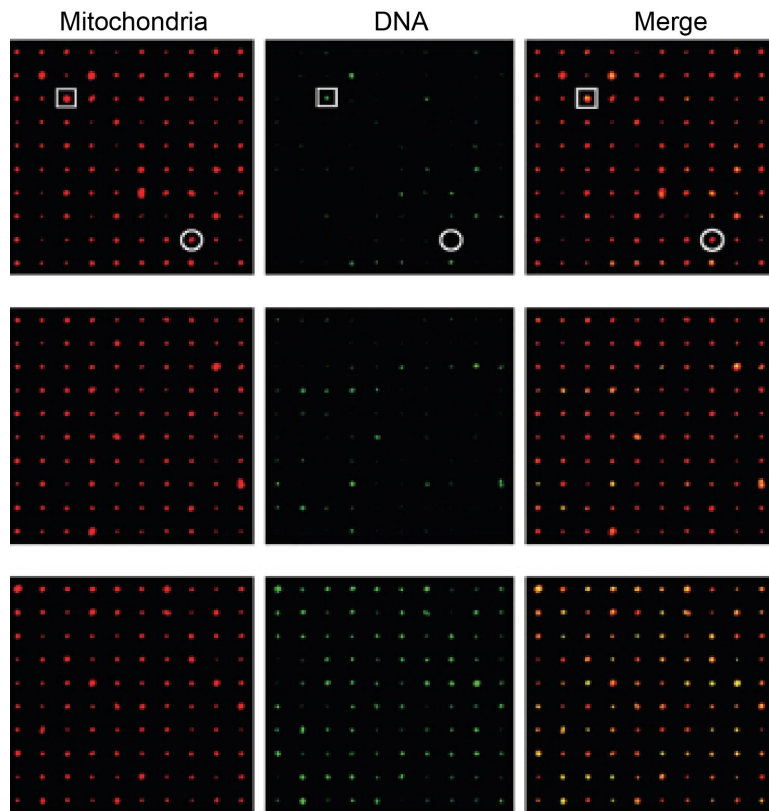
- Electron micrographs of rosette-like structures of mtDNA



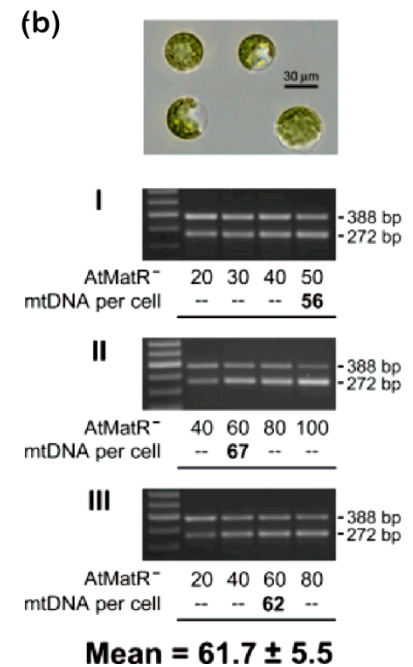
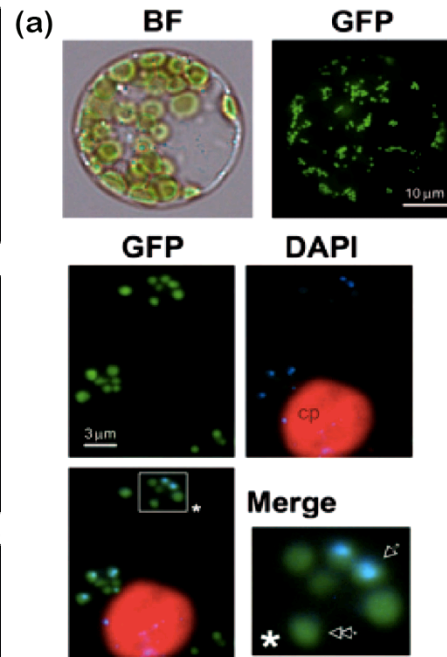
(Steffen Backert et al., 1996)

Background

- The quantity of DNA in plant mitochondria is insufficient.



Takanashi et al., 2006

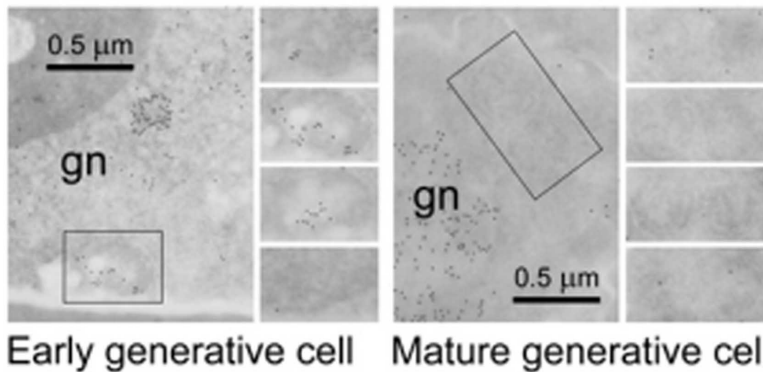
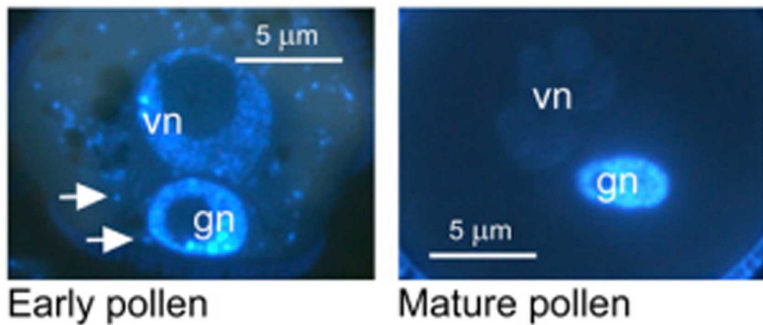


Wang et al., 2010

Background

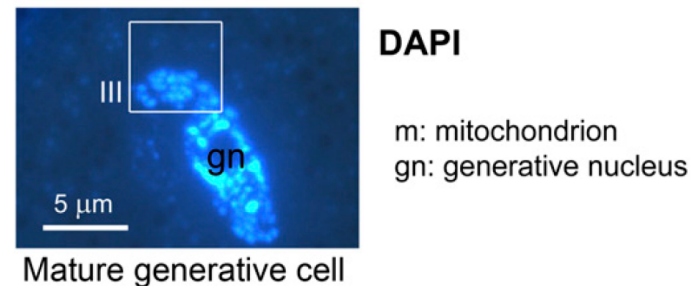
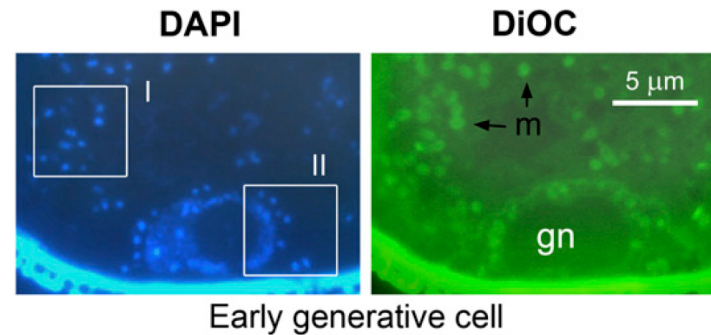
Relationship between mitochondrial DNA and mitochondrial genetic relationship in plant pollen germ cells

Maternal inheritance



Arabidopsis thaliana

Hybrid genetic

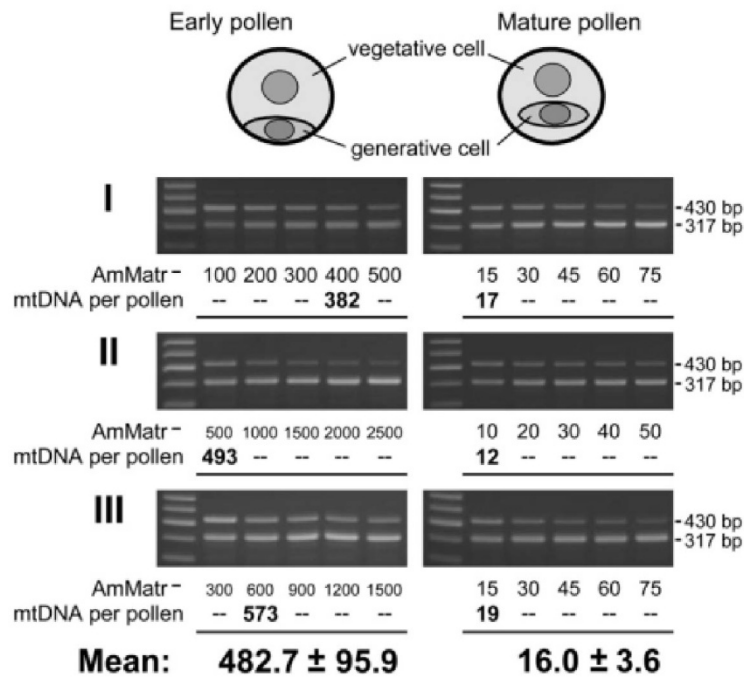


Cucumis sativus

Background

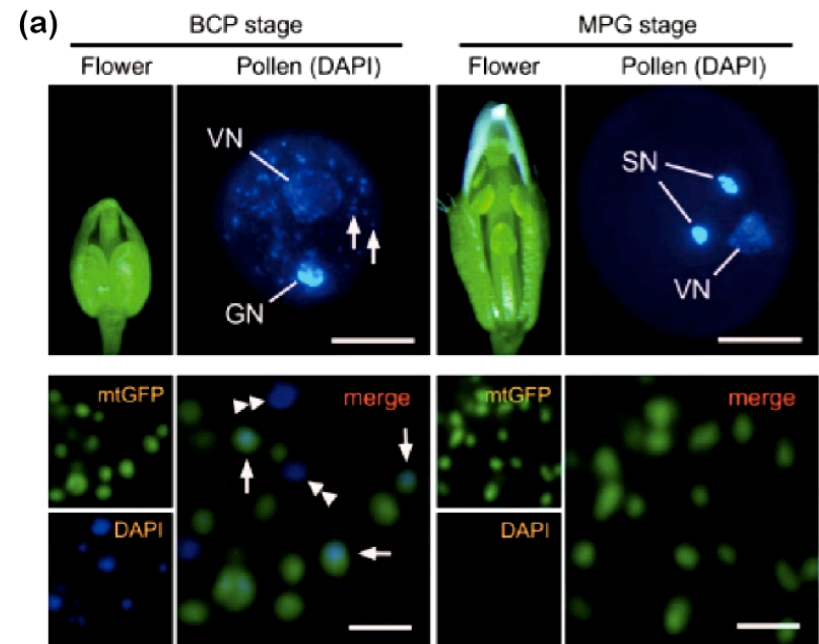
- Most plant pollen vegetative cell mitochondria DNA down to a very low level

Snapdragon



Wang et al., 2010

Arabidopsis thaliana



Cai et al., 2015

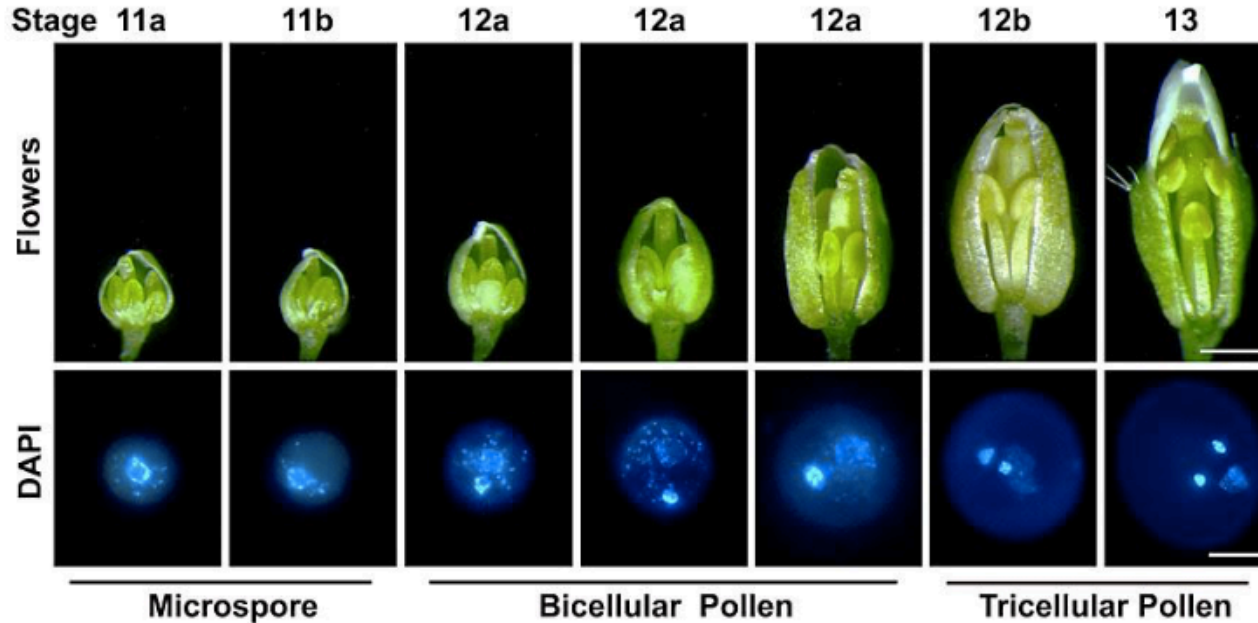
Background

Plant mitochondrial DNA quantity regulation factor

- Whirly2:single stranded DNA binding protein
- mtSSB : single stranded DNA binding protein
- Twinkle : helicase
- POL γ A:polymerase γ A

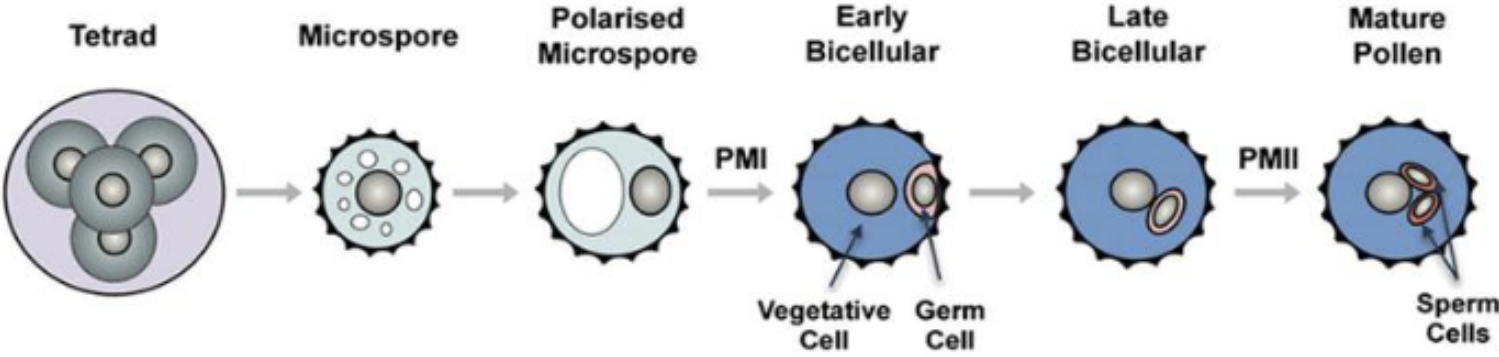
Background

Pollen development process



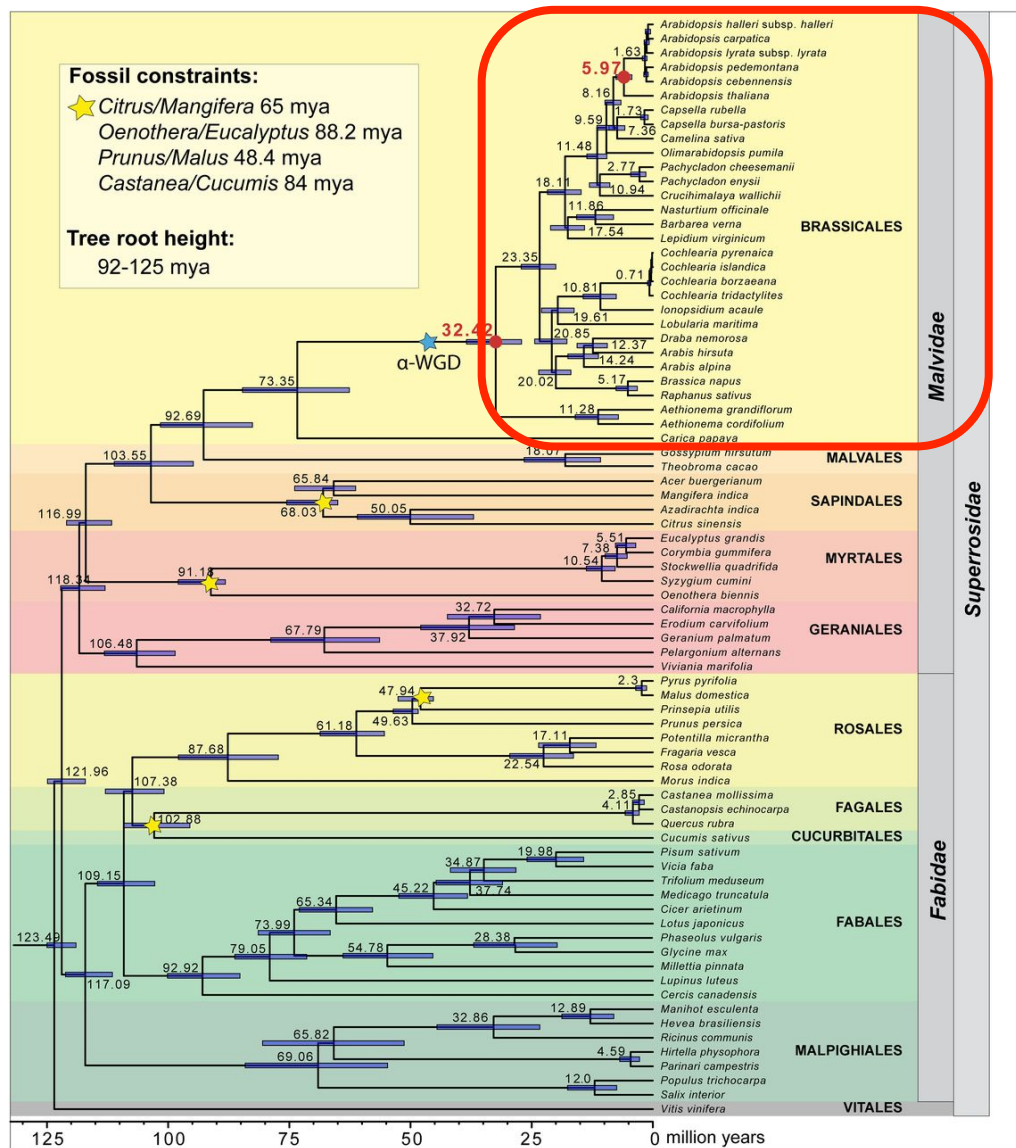
(蔡强博士)

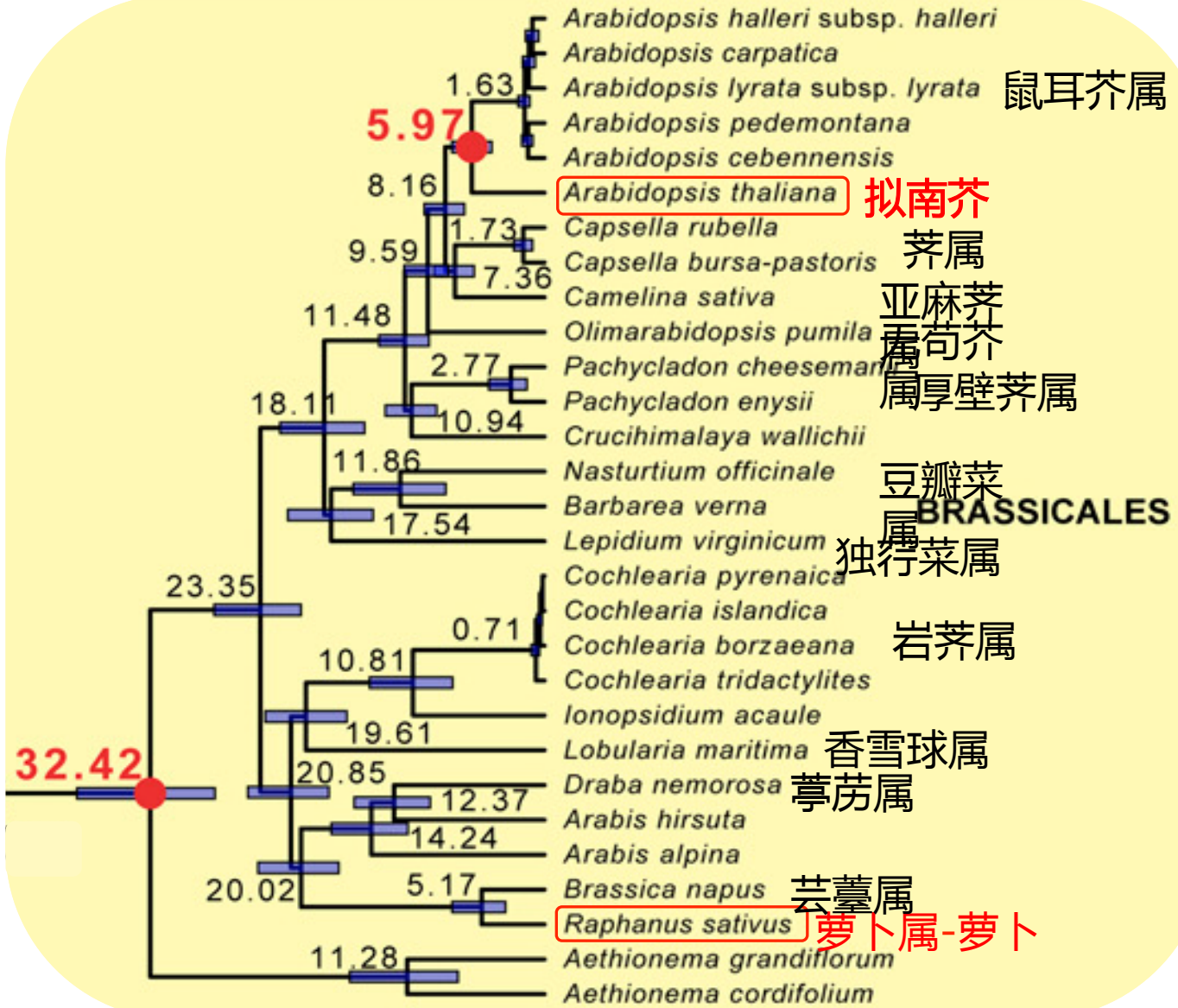
Research ideas



Whirly2 mtSSB Twinkle polymerase

BEAST Analysis of Whole-Chloroplast Genome Sequence Data





Bioinformatics analysis

Whirly2

Subcellular location

Subcellular locationⁱ

- Mitochondrion 🔒 3 Publications ▼

GO - Cellular componentⁱ

- mitochondrion 🔒 Source: TAIR ▼

[Complete GO annotation...](#)

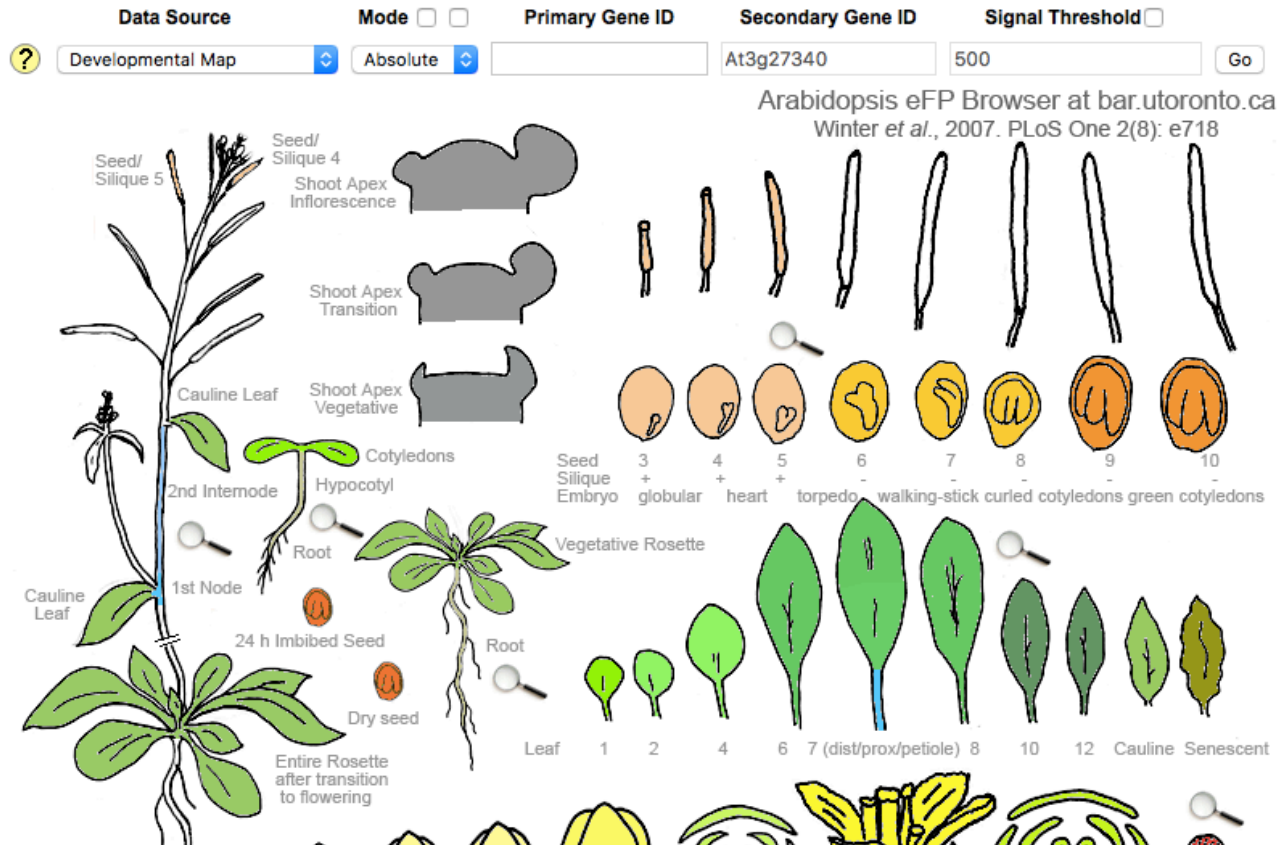
Keywords - Cellular componentⁱ

Mitochondrion



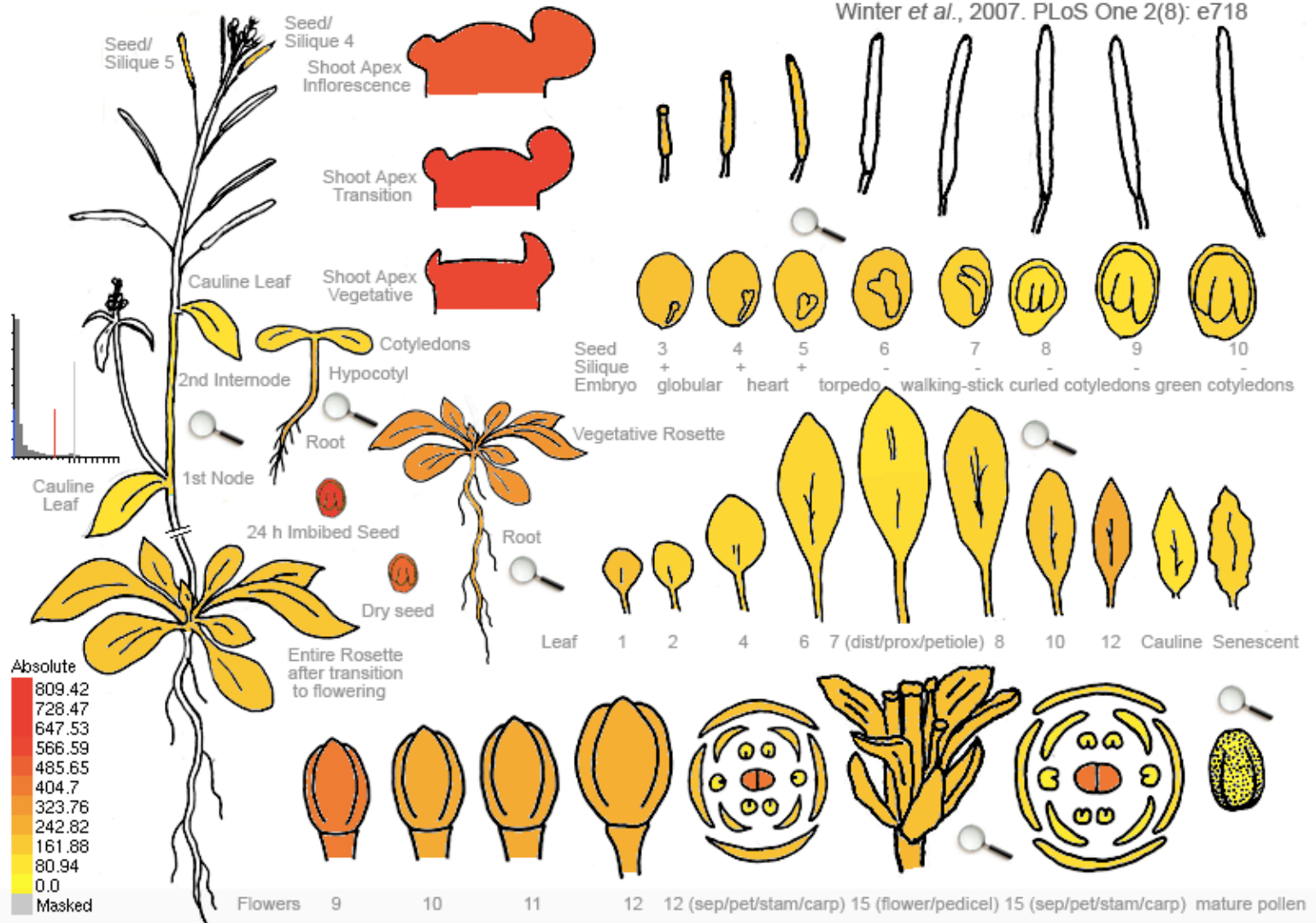
category	relationship type ?	keyword ?
GO Biological Process	involved in	DNA repair, defense response, regulation of transcription, DNA-templated process
GO Cellular Component	located in	chloroplast, mitochondrion
GO Cellular Component	not located in	nucleus
GO Molecular Function	functions in	DNA binding, mRNA binding
Growth and Developmental Stages	expressed during	LP.02 two leaves visible stage, LP.04 four leaves visible stage, LP.06 six leaves visible stage, LP.08 eight leaves visible stage, LP.10 ten leaves visible stage, LP.12 twelve leaves visible stage, flowering stage, mature plant embryo stage, plant embryo differentiation and expansion stage, plant embryo bilateral stage, plant embryo cotyledonary stage, plant embryo globular stage, seed germination stage, leaf senescent stage
Plant structure	expressed in	carpel, cauline leaf, collective leaf structure, cotyledon, flower, flower bud, flower guard cell, hypocotyl, inflorescence meristem, leaf apex, leaf lamina, leaf petiole, plant embryo, pollen, root, seed, sepal, shoot apex, shoot system, vascular leaf

Tissue expression



At1g71260 259942_at ATWHY2

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



Expression analysis

Arabidopsis
Gene Family Profiler

Laboratory of Pollen Biology
Institute of Experimental Botany
Rozvojová 263
165 00 Prague 6 - Lysolaje
Czech Republic

AGI number Gene name BAC locus Family Super family Custom dataset

AGI number:

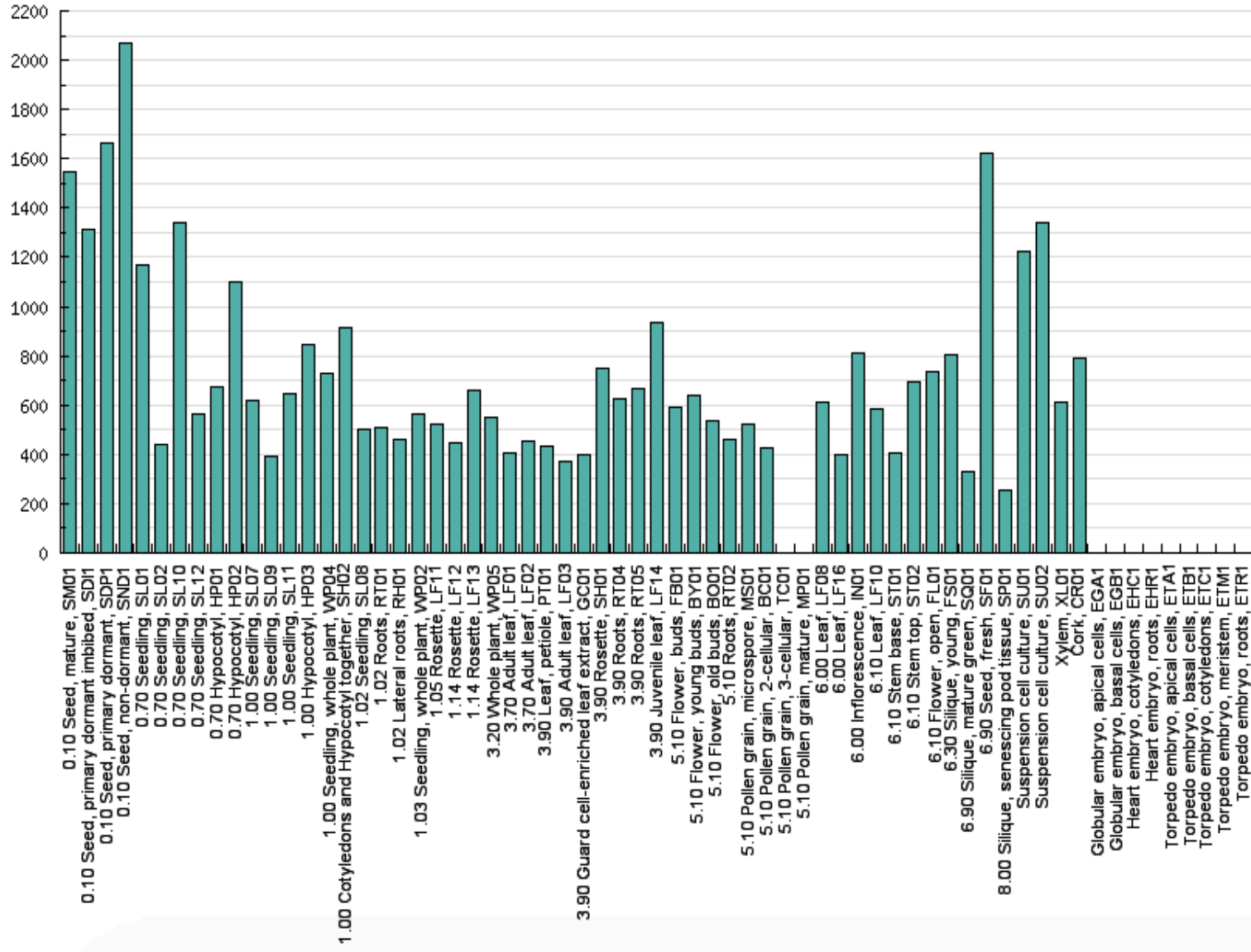
AtGenExpress
 NASCArrays
 MAS5
 MAS4

Search
Methods
Legend
Feedback

Family-oriented gene expression database

Last update: 22 September 2012

© 2005 Nikoleta Duplíšková, Patrik Hovaneč
David Reňák, Barbora Honysová
David Twell, David Honyš



mtSSB

Subcellular location


Representative Gene Model [AT4G11060.1](#)

Gene Model Type protein_coding

Other names: MITOCHONDRially TARGETED SINGLE-STRANDED DNA BINDING PROTEIN, MTSSB

Description mitochondrially targeted single-stranded DNA binding protein (MTSSB); FUNCTIONS IN: single-stranded DNA binding; CONTAINS InterPro DOMAIN/s: Nucleic acid-binding, OB-fold (InterPro:IPR012340), Nucleic acid-binding, OB-fold-like (InterPro:IPR016027), Primosome PriB/single-strand DNA-binding (InterPro:IPR000424); BEST Arabidopsis thaliana protein match is: Nucleic acid-binding, OB-fold-like protein (TAIR:AT3G18580.1)

Map Detail Image

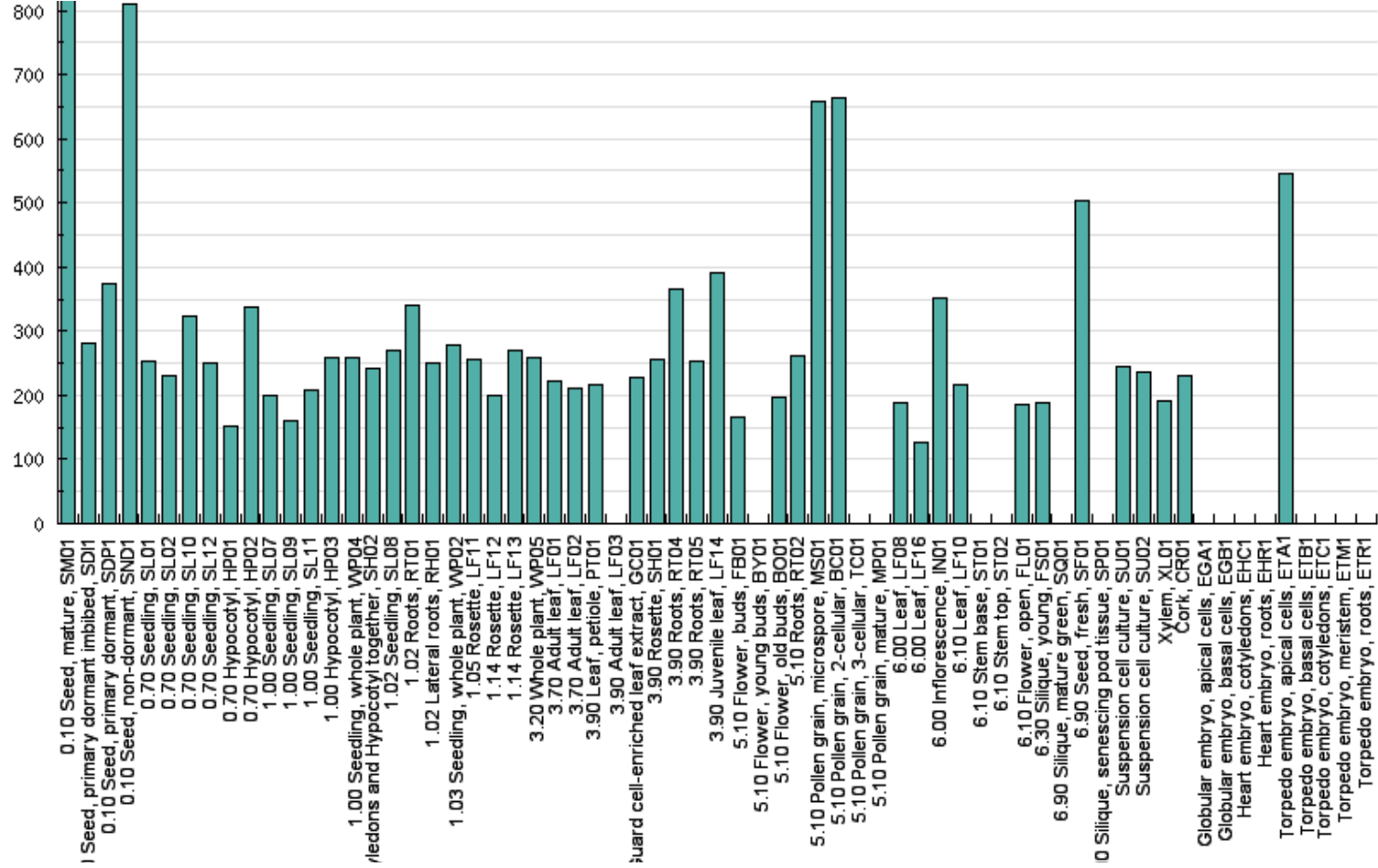


Protein Coding Gene Models
AT4G11060.1 (MTSSB)

Annotations

category	relationship type	keyword
GO Biological Process	involved in	DNA replication
GO Cellular Component	located in	mitochondrion
GO Molecular Function	functions in	single-stranded DNA binding
GO Molecular Function	has	single-stranded DNA binding
Plant structure	expressed in	guard cell

Expression analysis



Twinkle

Subcellular location

Annotations ?

category	relationship type ?	keyword ?
GO Biological Process	involved in	DNA replication, synthesis of RNA primer
GO Cellular Component	located in	chloroplast, mitochondrion
GO Molecular Function	has	5'-3' DNA helicase activity, ATP binding, ATP-dependent DNA helicase activity, DNA primase activity, metal ion binding, single-stranded DNA binding
Plant structure	expressed in	guard cell

[Add My Comment](#)[Hide Comments](#)[Show All Comments](#)

Publication ?	author/title	source	associated loci	date
	Towle-Weicksel, J B, Cao, Y, Crisl... Chimeric proteins constructed from bacteriophage T7 gp4 and a putative primase-helicase from <i>Arabidopsis thaliana</i>	MOLECULAR BIOLOGY REPORTS	AT1G30680	2014
	Diray-Arce, J, Liu, B, Cupp, J D, ... The <i>Arabidopsis</i> At1g30680 gene encodes a homologue to the phage T7 gp4 protein that has both DNA primase and DNA helicase activities	BMC PLANT BIOLOGY	AT1G30680	2013
	Dal Bosco, C, Lezhneva, L, Biehl, ... Inactivation of the chloroplast ATP synthase gamma subunit results in high non-photochemical fluorescence quenching and altered nuclear gene expression in <i>Arabidopsis thaliana</i> .	JOURNAL OF BIOLOGICAL CHEMISTRY	AT1G01080 AT1G01090 AT1G01250 AT1G01290 AT1G01500 AT1G01520 AT1G01550 AT1G01690 AT1G01730 AT1G01860 AT1G01950 AT1G02020 AT1G02060 AT1G02070 AT1G02150 AT1G02170 AT1G02260 AT1G02560 AT1G02680 AT1G02730 more...	2003

Diray-Arce et al. *BMC Plant Biology* 2013, **13**:36
<http://www.biomedcentral.com/1471-2229/13/36>



RESEARCH ARTICLE

Open Access

The *Arabidopsis* At1g30680 gene encodes a homologue to the phage T7 gp4 protein that has both DNA primase and DNA helicase activities

Joann Diray-Arce[†], Bin Liu[†], John D Cupp, Travis Hunt and Brent L Nielsen^{*}

DNA POLYMERASE GAMMA

Subcellular location

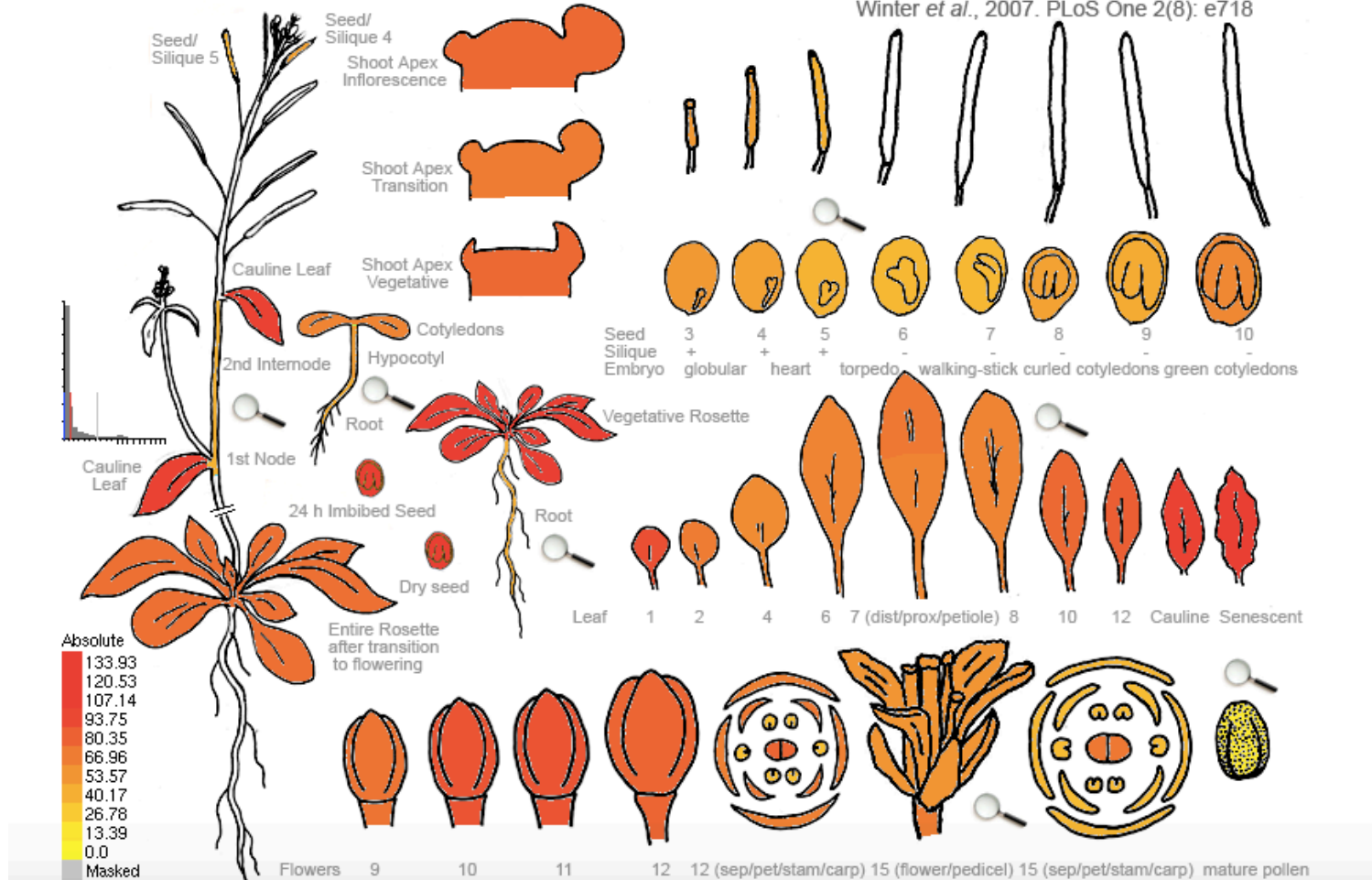
Annotations ?	category	relationship type ?	keyword ?
	GO Biological Process	involved in	DNA repair, DNA replication, mitochondrial DNA replication, plastid DNA replication
	GO Cellular Component	located in	chloroplast, mitochondrion, nucleus, plastid
	GO Molecular Function	functions in	DNA binding
	GO Molecular Function	has	3'-5' exonuclease activity, 5'-3' exonuclease activity, DNA binding, DNA-directed DNA polymerase activity
	Growth and Developmental Stages	expressed during	LP.02 two leaves visible stage, LP.04 four leaves visible stage, LP.06 six leaves visible stage, LP.08 eight leaves visible stage, LP.10 ten leaves visible stage, LP.12 twelve leaves visible stage, flowering stage, mature plant embryo stage, petal differentiation and expansion stage, plant embryo bilateral stage, plant embryo cotyledonary stage, plant embryo globular stage, vascular leaf senescent stage
	Plant structure	expressed in	carpel, cauline leaf, collective leaf structure, cotyledon, flower, flower pedicel, guard cell, hypocotyl, inflorescence meristem, leaf apex, leaf lamina base, petal, petiole, plant embryo, root, seed, sepal, shoot apex, shoot system, stamen, stem, vascular leaf

Tissue expression

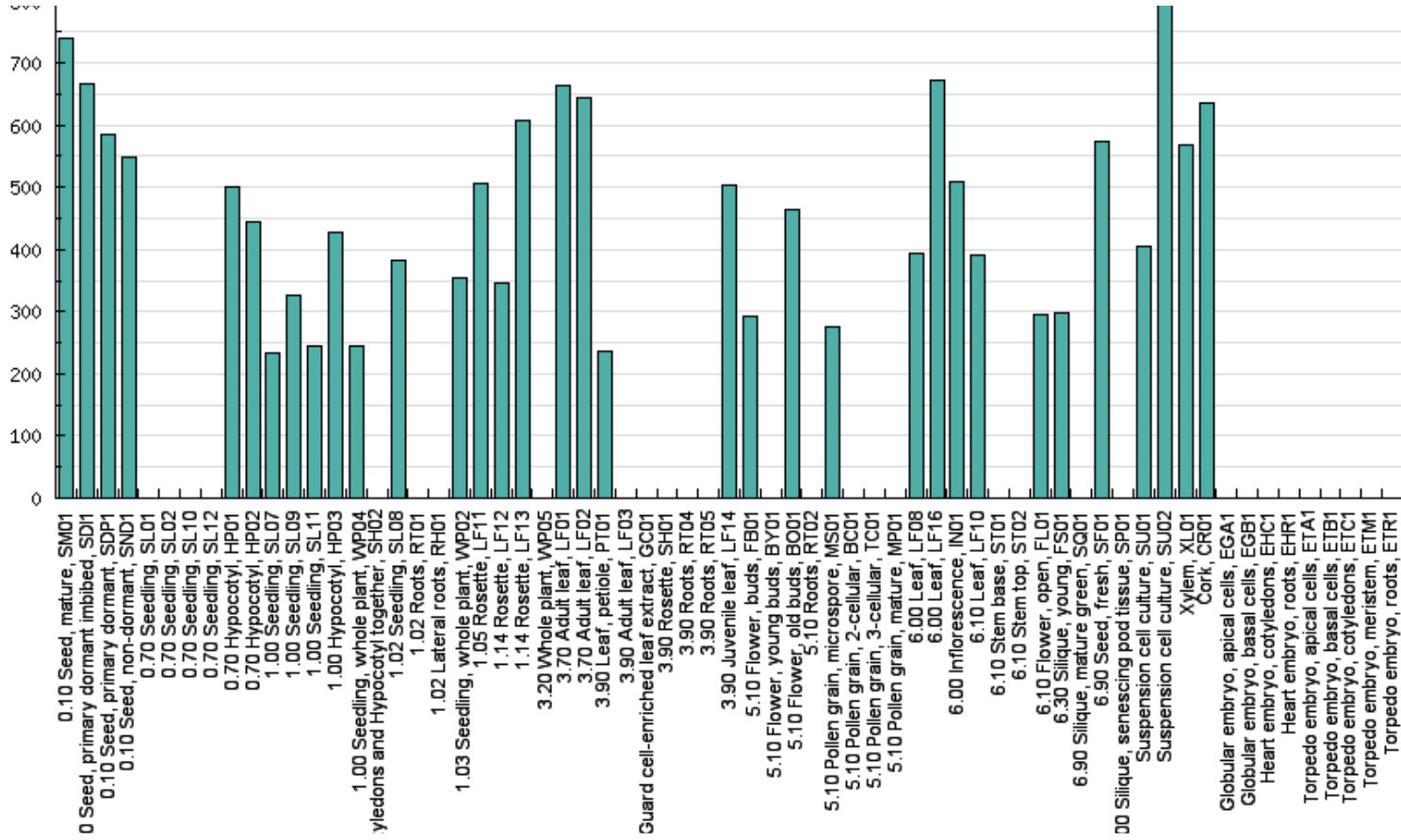
At1g50840 256204_at POLGAMMA2

Arabidopsis eFP Browser at bar.utoronto.ca

Winter et al., 2007. PLoS One 2(8): e718



Expression analysis



Sequence Alignment

Alignment –Atwhy2

```
Q8VYF7 WHY2_ARATH      1  MMKQARS-----LLSRSLCDQ-SKSLFEASTLRGFASWSNSSTPGRGFPGKDAAPSGR      53
D9J034 WHY2_SOLTU      1  MLKVSRLHLPNRQLLHKKLPGEQVKGSIWQHAINTFAGFST----VRQNVVADAGKREGR      56
      *: *  ** : *  : * :  : : ** : *  *  ** *  **

Q8VYF7 WHY2_ARATH      54  LFAPYSIFKGGKAALSVEPVLPSFTEIDSGNLRIDRRGSLMMTEMPAIGERKYDWEKKQKF      113
D9J034 WHY2_SOLTU      57  VFAPYSVFKGKAALSAPRLPTFNRLDSGGVKNRRGVIMLTFWPSVGERKYDWEKRQLF      116
      :*****:*****:* ** * : : * * : : : * * : * * * : * * : * * : * *

Q8VYF7 WHY2_ARATH      114  ALSPTTEVGSLSISMGSKDSSEFFHDPSMKSSNAGQVRKSLSVKPHADGSGYFISLSVNNSI      173
D9J034 WHY2_SOLTU      117  ALSATEVGSLSISMGTRDSSEFFHDPSMLSSNAGQVRKSLSIKPNADGSGYFISLSVNNN      176
      *** ***** : : ***** ***** : * : ***** *

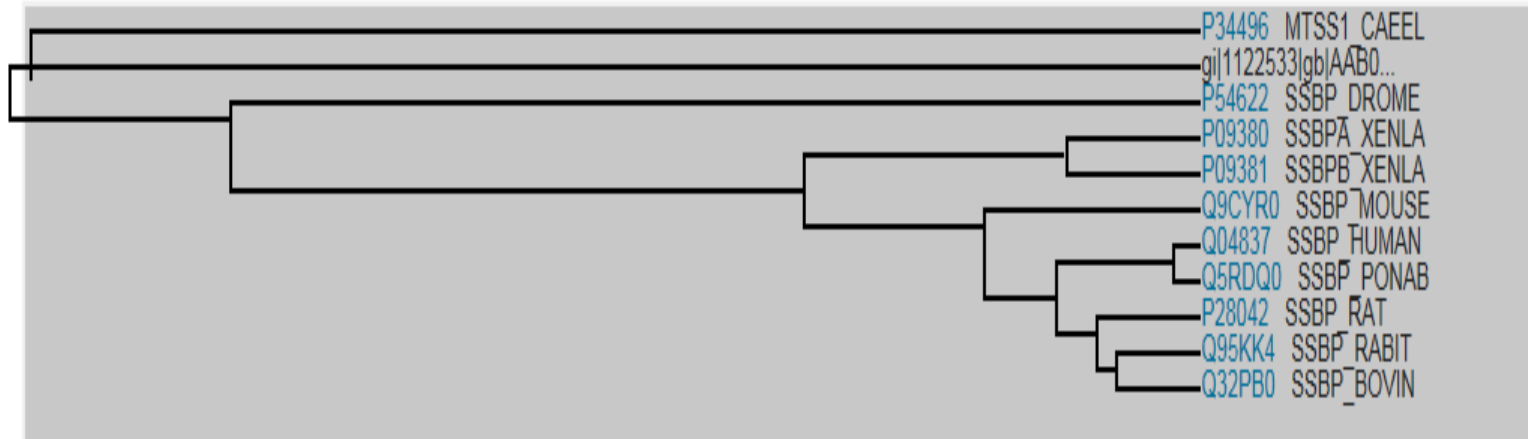
Q8VYF7 WHY2_ARATH      174  LKTNDYEVVPVTKAEFAVMKTAFSFALPHIMGNRLTGHVNTALPSRNVSHLKTEPQLE      233
D9J034 WHY2_SOLTU      177  LKTNDREIVPVTTAEFAVMRTAFSFAALPHIMGWRFTNRPSEISQSP---SKVVPQLME      233
      ***** * * * * * : * * * * * : * * : : . . * . . : *

Q8VYF7 WHY2_ARATH      234  LEWDK      238
D9J034 WHY2_SOLTU      234  AEWDR      238
      ***:
```

Alignment -mtSSB

P54622	SSBP DROME	1	-----MQHTRRMLNPLLTGLR	16
P09380	SSBP ^A XENLA	1	-----MFHRPALQVFR	11
Q04837	SSBP HUMAN	1	-----MFRRPVLQVLR	11
P09381	SSBP ^B XENLA	1	-----MFHRPVLQVFR	11
Q9CYR0	SSBP MOUSE	1	-----MFRRPVLQVFR	11
P28042	SSBP ⁻ RAT	1	-----MFRRPVLQVFR	11
Q5RDQ0	SSBP ⁻ PONAB	1	-----MFRRPVLQVLR	11
Q95KK4	SSBP ⁻ RABIT	1	-----MFRRPALQVLR	11
Q32PB0	SSBP ⁻ BOVIN	1	-----MFRRPVVQVLR	11
P34496	MTSS1 CAEEL	1	-----MLRSLSTISKSTVRCMSLT SKMAAEQPSKQEVDDLFA-----	37
gi 1122533 gb AAB0509..		1	MNSLAIRVSKVLRSSS-ISPLAISAEGRGSKSWFSTGPIDEGVEEDFEENVTERPELQPHG	59
P54622	SSBP DROME	17	NLPARGATTTTAAAPAKVEKTVNTVTLLGRVGADEQLRGSQ-EHPVVTESVAHTNYKY-	74
P09380	SSBP ^A XENLA	12	QFARC---QSTDS--VILERSINKVQLLGRVGDQFVMRQAEQKNPVTIFSLATNELWRSG	66
Q04837	SSBP HUMAN	12	QFVRH---ESETTSLVRLERSLNRVHLLGRVGDQFVLRQVEGKNPVTIFSLATNEMWRSG	68
P09381	SSBP ^B XENLA	12	QFARC---QSTDLSAILERSMKNVQLLGRVGDQFVMRQADGKNPVTIFSLATNELWRSG	68
Q9CYR0	SSBP MOUSE	12	QFVRH---ESEVASSLVRLERSLNRVQLLGRVGDQFVMRQVEGKNPVTIFSLATNEMWRSG	68
P28042	SSBP ⁻ RAT	12	QFVRQ---ESEVASSLVRLERSLNRVQLLGRVGDQFVMRQVEGKNPVTIFSLATNEMWRSG	68
Q5RDQ0	SSBP ⁻ PONAB	12	QFVRH---ESETASSLVRLERSLNRVHLLGRVGDQFVLRQVEGKNPVTIFSLATNEMWRSG	68
Q95KK4	SSBP ⁻ RABIT	12	QFVRH---ESEIASSLVRLERSLNRVQLLGRVGDQFVMRQVEGKNPVTIFSLATNEMWRSG	68
Q32PB0	SSBP ⁻ BOVIN	12	QFVRH---ESEVASSLVRLERSLNRVQLLGRVGDQFVMRQVEGKNPDTIFSLATNEMWRSG	68
P34496	MTSS1 CAEEL	38	EKPKH-----HNPEQRRHAYSVNKVELVGGVALDPLYKTGRNGKPYLIENIINSYFKQQ	92
gi 1122533 gb AAB0509..		60	VDPRK-----GWGFRGVHRAIICGKVGQAELOKILRNGRTVITIVGIGGMFDQR	109
			:: . : * * . * : . * : * :	
P54622	SSBP DROME	75	-----ENGDWQRITDWRVWVFKPNLRDVTVLEYLKKQRTMVOGKITIYGEI-TDQQNQ	127
P09380	SSBP ^A XENLA	67	ESETFHTAGDVNQKITWHRISVFRPGLRDVAYQYVKKGARLLVEGKIDYGEY-TDKNNVR	125
Q04837	SSBP HUMAN	69	DSEVYQ-LGDVSOQKITWHRISVFRPGLRDVAYQYVKKGSRIYLEGKIDYGEY-MDKNNVR	126
P09381	SSBP ^B XENLA	69	ENEVFPQAGDVNQKITWHRISVFRPGLRDVAYQYVKKGARLLVEGKIDYGEY-TDKNNVR	127
Q9CYR0	SSBP MOUSE	69	DSEVYQ-MGDVSOQKITWHRISVFRPGLRDVAYQYVKKGARIFVEGKVDYGEY-MDKNNVR	126
P28042	SSBP ⁻ RAT	69	DNEAYQ-MGDVSOQKITWHRISVFRPGLRDVAYQYVKKGARIFVEGKVDYGEY-MDKNNVR	126
Q5RDQ0	SSBP ⁻ PONAB	69	DSEVYQ-LGDISQKITWHRISVFRPGLRDVAYQYVKKGSRIYLEGKIDYGEY-MDKNNVR	126
Q95KK4	SSBP ⁻ RABIT	69	DNETYQ-MGDVSOQKITWHRISVFRPGLRDVAYQYVKKGSRIYVEGKVDYGEY-MDKNNVR	126
Q32PB0	SSBP ⁻ BOVIN	69	ENETYQ-MGDVSOQKITWHRISVFRPGLRDVAYQYVKKGSRIYVEGKVDYGEY-TDKNNVR	126
P34496	MTSS1 CAEEL	93	D-----GTTLDQTERHAVSVFQKQA-EILSKTIKKGSRMLMVGRLHYSGGQKDEQGNR	144
gi 1122533 gb AAB0509..		110	LV----GATNQPKPAQWHRIAVHNEVLGSYAVQKLAKNSSVYVEGDIETRVY-NDSSISE	164
			. : * : * . . : : * . : : * : * . . .	
P54622	SSBP DROME	128	KTSTSI-IA---DDVLF---FRDANN-----	146
P09380	SSBP ^A XENLA	126	RQATTI-IA---DNIIF---LSDLRDKL-----	146
Q04837	SSBP HUMAN	127	RQATTI-IA---DNIIF---LSDQKEKE-----	148
P09381	SSBP ^B XENLA	128	RQATTI-IA---DNIIF---LTDLRDKP-----	148
Q9CYR0	SSBP MOUSE	127	RQATTI-IA---GKKLV---VHSVS-GCSL---EGLA	152
P28042	SSBP ⁻ RAT	127	RQATTI-IA---DNIIF---LSDQAREKPL---NG--	151
Q5RDQ0	SSBP ⁻ PONAB	127	RQATTI-IA---DNIIF---LSDQKEKE-----	148
Q95KK4	SSBP ⁻ RABIT	127	RQATTI-IA---DNIIVF---LSDQKEKA-----	148
Q32PB0	SSBP ⁻ BOVIN	127	RQATTI-IA---DNIIF---LSDQKEKP-----	148
P34496	MTSS1 CAEEL	145	TQRNTYIAQTVOPLAR-----AARENPDQH-----	170
gi 1122533 gb AAB0509..		165	VKSIPE-ICVRRDGKIRMIKYGESISIKISFDELKEGLI	201

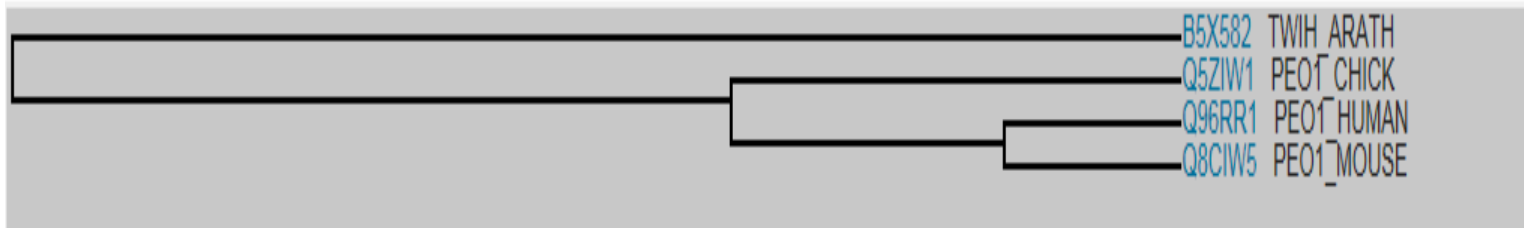
Tree-mtSSB



Alignment-Twinkle

Q96RR1	PEO1_HUMAN	1	-----MWVLLRSGYP-LRLLPLRGEWM	22
Q8CIW5	PEO1_MOUSE	1	-----MWLLLRRAYP-LRLLPLRGEWV	22
B5X582	TIWIH_ARATH	1	MRFLRLRQIHFRLKLSCSMSVLMGSKQFLFCLLPSPFASYPSSPSYSSSRQVSSV----	55
Q5ZIW1	PEO1_CHICK	1	-----MAAVPLRRCRASGRFLPLRGGAR	24
			* : :	
Q96RR1	PEO1_HUMAN	23	GRGLRNLAPGP-PR--RRYRK-----ETIQALDMP-----VLPVTATELRQ	62
Q8CIW5	PEO1_MOUSE	23	GRGLRSLAPGP-PR--RRYRK-----EALPALEMP-----VSPVITTELRQ	62
B5X582	TIWIH_ARATH	56	SRFRFVLA SRPVS KNSPYVQRTNGLSSYNSIPRVVTPVDTEVEADKRVVLSRLVTLRR	114
Q5ZIW1	PEO1_CHICK	25	SRGASVWAAGPGRVAQ--RRYRK-----DVLPEPGGA-----APAVSVTELRQ	65
			* * : * : * : *	
Q96RR1	PEO1_HUMAN	63	YLRGHGIPFDGHSGLRALSPFAESSQLKQG--IGVITTSFLFDKTIHGHLFCMTSLAEGS	121
Q8CIW5	PEO1_MOUSE	63	YLRRAHGIPFDGHSGLRALSPFPVSSDIKNEKKDAPTSFCLFDKTIHGHLFCMTSLAEGS	122
B5X582	TIWIH_ARATH	115	KLAEGQVDAA--NCPGQHS--GLICPTCEGGNSGKSLFLFAPD-----GSSAT	161
Q5ZIW1	PEO1_CHICK	66	YLRAGGIPFDGYSGLHAPSLFGPELP-----PAAGPPTLFDKTIHGHLFCMTSLAEGG	120
			* : * : * : * : * : *	
Q96RR1	PEO1_HUMAN	122	WEDFOASVEGSGDGAREG----F--LLSKAPEFEDSEVRRWNRAIPWEIPDQEEVQ	174
Q8CIW5	PEO1_MOUSE	123	WEDLOASVEGSGDGAKEG----V--LLREGPEAEVREVLRWNRAPWEIPDPEEAQ	175
B5X582	TIWIH_ARATH	162	WNCFRGKCGLRGGVPRADGGLASAD-----PI---EKVERKIVTEGTELEPLCDEI---	208
Q5ZIW1	PEO1_CHICK	121	WODLQAVELRHRGVPAPGPDEGEREEEEAEARRAREDARRWERALPGEILLDEETR	180
			* : * : * : * : * : *	
Q96RR1	PEO1_HUMAN	175	LADTMEGLTKVIDDTLRFVRYLSPAR--SLVFPWFSPGGSGRLGKLLLEAKCOGDGVS	232
Q8CIW5	PEO1_MOUSE	176	LARVMEGLTKVIDDTLRFVRYLSAR--SLVFPWFSPGGSGRLGKLLLEAKCOENGWV	233
B5X582	TIWIH_ARATH	209	--QDYFAARALSRKTLERNRMQKIGDEIVTAFTYVQRGELVSC-----KYR-----S	255
Q5ZIW1	PEO1_CHICK	181	ATKAAGIAPLADGTLKRFVRYLRAAK--ALVFPWFAPRDAALRGLKLLVAEQRGDAVS	238
			* : * : * : * : * : *	
Q96RR1	PEO1_HUMAN	233	YEETIPRPSAYHNLFGLPLISRRDAEVVLTRELSLALNOSTGLPTLTLRGTICLPP	292
Q8CIW5	PEO1_MOUSE	234	YVETIPRPGYHNLFGPLISRRDIEVVVLTRELSLALSOSTGLPTLSLRGTIVCLPP	293
B5X582	TIWIH_ARATH	256	LTKMFFQERKIRRIYGLDDLEK--TSEVLIIVEGIEIKLAMEEAGFLNCVSVEDSAPKVS	314
Q5ZIW1	PEO1_CHICK	239	YTEETIPRFDAYRNLFGPLIGRRDAEVVLTRELSLALALHQATGVPCLALRGTATILPP	298
			* : * : * : * : * : *	
Q96RR1	PEO1_HUMAN	293	A-L-----LPYLEQFRRIVFWLGDRLRSWEAAKLFARKLNPKRCFLVRP	335
Q8CIW5	PEO1_MOUSE	294	A-L-----LPYLEQFRRIVFWLGDRLRSWEAAKLFARKLNPKRCFLVRP	336
B5X582	TIWIH_ARATH	315	SKEIPSEDKDKYKFLWNCNDYLKKAASRIVIAIDGEGPQAMAEETARRLCKERCWRVWK	374
Q5ZIW1	PEO1_CHICK	299	A-L-----LPYLEQFRRIVFWLGDRLRSWEAAKLFARKLNPKRCFLVRP	341
			* : * : * : * : * : *	
Q96RR1	PEO1_HUMAN	336	GDOQ-PRPLEALN-----GGFN-LSRIILRTALEAWHKSIVSFRQLREEVL---GELS NVE	385
Q8CIW5	PEO1_MOUSE	337	GNQQ-PRPLEALN-----QGLS-LPRIILRTALEAWHKSIVSFRQLREEVL---GELS NVE	386
B5X582	TIWIH_ARATH	375	PKKSEDEHFKDANVLMKSGPHLLEKALDAAEYPIPLGLFSFKDFDFEIDAYYDRTHGHE	434
Q5ZIW1	PEO1_CHICK	342	GDLQ-PRPLEALN-----RGLN-LTKIIRAALEAGHKATVVSFRQLREEVF---GELANSE	391
			* : * : * : * : * : *	
Q96RR1	PEO1_HUMAN	386	QAAGLRMSRFPDLNRLKGRHRKGELTVFTGPTSGSKITTFISEYALDLCQGVNLTGWSFE	445
Q8CIW5	PEO1_MOUSE	387	QAAGVRRMSRFPDLNRLKGRHRKGELTVFTGPTSGSKITTFISEYALDLCQGVNLTGWSFE	446
B5X582	TIWIH_ARATH	435	YGVSTGKKNLDNLYS----VVEGELTVFTGPIPSGRSEWIDAML---CNLNHSVGVKFAI	487
Q5ZIW1	PEO1_CHICK	392	QVAGVKMARFPDLNRLKGRHRKGELTVFTGPTSGSKITTFISEYALDLCQGVNLTGWSFE	451
			* : * : * : * : * : *	
Q96RR1	PEO1_HUMAN	446	I----SNVRLARVMITC-----FAEGRLL-----EDQLDKYDHWADR--FEDLPLYFMT	487
Q8CIW5	PEO1_MOUSE	447	I----SNVRLARVMITC-----FAVTRLL-----EEDLDKYEEWADR--FEDLPLYFMT	488
B5X582	TIWIH_ARATH	488	CSMENKVRDHARKLEKHKIKKFFDADYGRSVQORMSVEEKDEGKKVINDTETYPYI---RCE	544
Q5ZIW1	PEO1_CHICK	452	I----NNIRLAKIMITC-----FATRRL-----EDQLELYDEWADR--FEDLPLYFMT	493
			* : * : * : * : * : *	
Q96RR1	PEO1_HUMAN	488	FHGQQSRTVIDTMOHAVYVYDICHVVIDNLOFMGHEQLSDRIAQAQDYIIGVFRKEAT	547
Q8CIW5	PEO1_MOUSE	489	FHGQQSRSVIDTMOHAVYVYDVCHVIDNLOFMGHEQLSSDRIAQAQDYIVGAFRKEAT	548
B5X582	TIWIH_ARATH	545	MDSLPSLDWVLERAKAAVLRVYGRGLVVIDPYNELDHQRTPRQTEYVVSQMLTKIKRESQ	604
Q5ZIW1	PEO1_CHICK	494	FHGQQNKTVLDTMOHAVYVYDITHVVIDNLOFMGHEQLSADRLLAAQDFIVGAFRKEAT	553
			* : * : * : * : * : *	

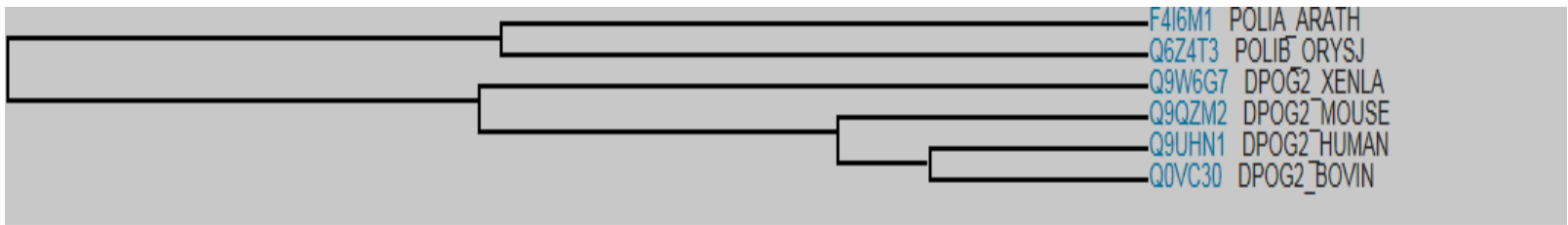
Tree-Twinkle



Alignment-DNA polymerase gamma2

Q9UHN1	DPOG2_HUMAN	94	GCHPGFGLGVELRKNLAAEWWSIVVVFREQVFPVDA	LHHK-----P-----G	136
Q9QZM2	DPOG2_MOUSE	68	GCHARFGLGVELRKNLASQWWSIVVVFREQVFAVDSLHOE	-----P-----G	110
F4I6M1	POLIA_ARATH	173	-----KERTTTRSTTATL-NKELIGIT--QSEPVVSLPRKGLDVGDNMVDNPKGEGTOR	-----P-----G	223
Q0VC30	DPOG2_BOVIN	94	GCHPGLGELGIELRKNLAAEWWSIVVVFREQVFPVDA	LHRE-----P-----G	136
Q9W6G7	DPOG2_XENLA	79	GCH-NLGEELGVELRKNLVAQWWSIVVVFREQVLGIDLHHL	-----S-----T	120
Q6Z4T3	POLIB_ORYSJ	167	VANNDIKELNLLDGSKEEIPWHDSIVVE--SSLPKVSKSETTLVVDKAI	-----S-----T	213
Q9UHN1	DPOG2_HUMAN	137	PLLPGDSAFRLVSAETLREILQDKELSKEQLVAFLENVLKTS	SGKIREN-----	185
Q9QZM2	DPOG2_MOUSE	111	SSQPRDSAFRLVSPESIREILQDREPSKEQLVAFLENLLKTS	SGKIRATL-----	159
F4I6M1	POLIA_ARATH	224	PLISDKSGTANGNKNTV-AISKVERSTE----PSNVRENLGKTYDKVLIVDNVQAAKD	-----P-----G	277
Q0VC30	DPOG2_BOVIN	137	PSLPVDNGFRLVSAETLREILQDKELSKEQLVAFLENLLNTS	SGKIREN-----	185
Q9W6G7	DPOG2_XENLA	121	PSSAPEKPLLAICTOHL-----KELPRDQLVKWLED	PAGKLEFLRHE-----	163
Q6Z4T3	POLIB_ORYSJ	214	---PNKKEHKRITRVTLNIIPDKASLSTE----SKNARKLLATTYDKVLVVDNVESARS	-----P-----G	265
Q9UHN1	DPOG2_HUMAN	186	----LHGALHEYVNCLE-----LVNKRLEYGLAQIGVCFHPVFDIK	----QIRNG----	227
Q9QZM2	DPOG2_MOUSE	160	----LHGALHEYVNCLE-----LVNKRLEFGLAQIGVCFHPVSNLN	----QTPSS----	201
F4I6M1	POLIA_ARATH	278	TVAKLVNQFRNHVHSCDTEVSGIEVKEETEVVDHGEL-ICFSIYCGP--EADFGNGKSCI	-----P-----G	333
Q0VC30	DPOG2_BOVIN	186	----LHGALHEYVSYLD-----LVNKRLEFGLAQIGVCFHPVSDIK	----QTPDG----	227
Q9W6G7	DPOG2_XENLA	164	---LYGALLEYVPSME-----LVNKRMEFGLAEIGKCEHSIPEER	----NKGTI----	205
Q6Z4T3	POLIB_ORYSJ	266	VVKLITTKYKGFVHACDTEVANIDVKEETEVVGHGEV-ICFSIYSGNSDGEADFGNGKTCI	-----P-----G	324
Q9UHN1	DPOG2_HUMAN	228	--VKSIGEKTEASIV---WETPRTSNQNLDFWLRHRLQWWRK	FAMSPSNESSSDCQDEE	282
Q9QZM2	DPOG2_MOUSE	202	--VTRVGEKTEASIV---WETPRTSSQNLDFWLRHRLLWWRK	FAMSPSNESSSADCQDEL	256
F4I6M1	POLIA_ARATH	334	WVDVLCENGREVLAEFKPYEEDSFRKRVHNYNSDSHII--RNHGIEISGTHA-----	-----P-----G	384
Q0VC30	DPOG2_BOVIN	228	--VKSIGEKTEASIV---WETSARTASQNLDFWLRHRLQWWRK	FAMSPSNESSSGDCQDEA	282
Q9W6G7	DPOG2_XENLA	206	--LPRIGERTVASIV---WSSPKSSGQDQYWRQRQLQWWRK	FAQSPGSGSCNDIQDQG	260
Q6Z4T3	POLIB_ORYSJ	325	WVDVLD--GGRDVVMEFAPFEEDPSIKKVVHNYNSDSHVI--ENCIGIKVAGTHA-----	-----P-----G	374
Q9UHN1	DPOG2_HUMAN	283	GRKGNKLYYFPWGKELIETLWNLGDHELLHMYPGNVSKLHGRDGRKNV	VPCVLSVNGDL	342
Q9QZM2	DPOG2_MOUSE	257	GRKGSKLYYFPWGKEPIETLWNLGDQELLHTYPGNVSTIQGRDGRKNV	VPCVLSVSGDV	316
F4I6M1	POLIA_ARATH	385	-----P-----G	-----P-----G	384
Q0VC30	DPOG2_BOVIN	283	GRKGNRLYYFPWGKEPIETLWNLGDHELLHMYPGSVAQVHGRDGRKNV	VPSVLSINGDL	342
Q9W6G7	DPOG2_XENLA	261	GRKSSLIQYEFPPWGRETIIETLCNMDDSAFQMHGPGCTTKLQARDGRKS	VVPHVWVSGDL	320
Q6Z4T3	POLIB_ORYSJ	375	-----P-----G	-----P-----G	374
Q9UHN1	DPOG2_HUMAN	343	IRGMLAYLYDSFOLTENSFTR-----KKNLHRKVLKLFHPC	LAPIKVALD	386
Q9QZM2	DPOG2_MOUSE	317	DLGTLAYLYDSFOLAENSFAR-----KKSQRKVKLKFHPC	LAPIKVALD	360
F4I6M1	POLIA_ARATH	385	DTMHMLRRLWDSARRIKGGYSLEALTSDPKVLGGTQTKEEAEFLGKISMKTIIFGRKRLKKD	-----P-----G	444
Q0VC30	DPOG2_BOVIN	343	IRGMLAYLYDSFOLTENSFTR-----KKNLHRKVLKLFHPC	LAPIKAALD	386
Q9W6G7	DPOG2_XENLA	321	IRGMLAYLYDSFOLAENSFAR-----KKSQRKVKLKFHPC	LAPIKVALD	364
Q6Z4T3	POLIB_ORYSJ	375	DTMHMLRRLWDSARRIKGGYSLEGLTNDHRIMNAVL--KDIHKTGKISMKTIIFGRKRVKKN	-----P-----G	432
Q9UHN1	DPOG2_HUMAN	387	VGRGPTVELRQVCGQLFNELLENGISVWPGVLEITMOSSELEQLY	-----P-----G	429
Q9QZM2	DPOG2_MOUSE	361	VGKGPTEVLRQVCGLLNELLENGISVWPGVSETVHSSLEQLH	-----P-----G	403
F4I6M1	POLIA_ARATH	445	GSEKIVVI-----PPVEELQREDREARISVSALDAISTLKLYESMTKKLQMLDWHLDGK	-----P-----G	499
Q0VC30	DPOG2_BOVIN	387	VGRGPTVELRQVCGQLFNELLENGISVWPGVLEITVQSSLEQLY	-----P-----G	429
Q9W6G7	DPOG2_XENLA	365	MGKGPTEGLRLVCGQLSSELRQGGYVWPGVQETLHGSLEQLY	-----P-----G	407
Q6Z4T3	POLIB_ORYSJ	433	GSEKTIISI-----EPVKLQREDRELNICSSSLDSMTLKLYESLKNKLEAKEIFDGC	-----P-----G	487
Q9UHN1	DPOG2_HUMAN	430	-----SKYDEMSILEFTVIVTETLLENGLIH-----LRSRDTIMKEMMHISKLRDELI	-----P-----G	476
Q9QZM2	DPOG2_MOUSE	404	-----SKYDEMSVLESVIVTETLLENGLIQ-----LRSRDTIMKEMMHISKLRDELV	-----P-----G	450
F4I6M1	POLIA_ARATH	500	PVLGRTMLDFEHEFRWPPGELIVVQMEAGILVDREYLAEIEKVAKAEQQVAGSRFRNWS	-----P-----G	559
Q0VC30	DPOG2_BOVIN	430	-----SKYDEMSILEFTVIVTETLLENGLIQ-----LRSRDTIMKEMMHISKLRDELV	-----P-----G	476
Q9W6G7	DPOG2_XENLA	408	-----TKYDKMGLVLEFTVIVSESTLENGLLQ-----VRSRDTILKETHVSKVRDELV	-----P-----G	454
Q6Z4T3	POLIB_ORYSJ	488	PR--GTMYDFEYWRPFGALLVQMETEGMFDVDRAYLSEIEKTAVVERKLAADKFRKWS	-----P-----G	545

Tree-DNA polymerase gamma2



Structure analysis

- Whirly2: single stranded DNA binding protein
- mtSSB : single stranded DNA binding protein
- Twinkle : helicase
- POL γ A: polymerase γ A

Untitled Project Created: today at 16:36

Summary Templates Models

Model Results

Order by: GMAQE

Oligo-State: Homo-tetramer
Ligands: None (matching prediction)

Global Quality: GMAQE 0.41, QMEAN -7.90

Local Quality:

Completion:

Quality Metric	Value
QMEAN	-7.90
CP	-4.78
All Atom	-2.90
Solvation	-1.06
Torsion	-6.02

Template: 1qvc.1.D
Seq Identity: Coverage: Description: DNA primase/helicase

Model-Template Alignment

```

Model_01_MNLSLAIRVSKVRSRISIS 80
Model_01_BMNSLAIRVSKVRSRISIS 80
Model_01_CMNSLAIRVSKVRSRISIS 80
Model_01_DMNSLAIRVSKVRSRISIS 80
1qvc.1.D 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
Model_01_A QAPLQKILNQRVTFIF 80
Model_01_B QAPLQKILNQRVTFIF 80
Model_01_C QAPLQKILNQRVTFIF 80
Model_01_D QAPLQKILNQRVTFIF 80
1qvc.1.D 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
Model_01_A ISSVKSIFKCVRRDGR 80
Model_01_B ISSVKSIFKCVRRDGR 80
Model_01_C ISSVKSIFKCVRRDGR 80
Model_01_D ISSVKSIFKCVRRDGR 80
1qvc.1.D 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

```

Summary Templates Models

Model Results

Order by: GMAQE

Oligo-State: Monomer
Ligands: None (matching prediction)

Global Quality: GMAQE 0.40, QMEAN -6.58

Local Quality:

Completion:

Quality Metric	Value
QMEAN	-6.58
CP	-4.92
All Atom	-2.78
Solvation	-1.85
Torsion	-5.52

Template: 1q57.1.G
Seq Identity: Coverage: Description: DNA primase/helicase

Model-Template Alignment

```

Model_01_MNRLDLPQIFRFLSCSMVLMGSKQFLPCLLRFPSAFYSPSSRQVSVSRFPVLSRPFVRSRPFYQRTGQ 80
1q57.1.G 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
Model_01_LSXNSIPFPPVPTVEADKRVVLSLVLRLKRLAEGVDAREKCPDGGHSLICPTCEGNSGKSLSLPIADGSSA 160

```

Untitled Project Created: today at 16:36

Summary Templates Models

Model Results

Order by: GMAQE

Oligo-State: Monomer
Ligands: None (matching prediction)

Global Quality: GMAQE 0.36, QMEAN -6.15

Local Quality:

Completion:

Quality Metric	Value
QMEAN	-6.15
CP	-4.06
All Atom	-2.96
Solvation	-1.95
Torsion	-5.15

Template: 1q57.1.F
Seq Identity: Coverage: Description: DNA primase/helicase

Model-Template Alignment

```

Model_01_CSMVLMGSKQFLPCLLRFPSAFYSPSSRQVSVSRFPVLSRPFVRSRPFYQRTGSLSSNSIPVPTVDT 80
1q57.1.F 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
Model_01_EVADRKRVVLSRLVLRKLAEGVDAREKCPDGGHSLICPTCEGNSGKSLSLPIADGSSATMCFRKGKGGVR 160
1q57.1.F 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
Model_01_A DGGSLASADPIEKVRKITEGIELEPLCDRIQDFAARASIKYLRNNAVQKRLGDDIVIAETMGRHLSVSKYR 240
1q57.1.F 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
Model_01_LTKMFPQRHYRRLYGLDDIKYSEVIVGSDIKLMSRDPINCVSVDGAPAKVSSKRLPSHDKDKTKYFLN 320
1q57.1.F 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
Model_01_CNDYLKASRIVVATDGGDQDQAMRERARLQKRCRWVVMKSSDDEHPKDNVLMKSGPHLKRALIDARYPIL 400
1q57.1.F 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
Model_01_LPSFDFPDIDAYDRTGRHGYGVSDMKNIDNLYS VVDEGLVTVGIDNSGKSNIDAMCLNNSVGMFALC 480
1q57.1.F 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
Model_01_EHNDKRNKLLKIKKRPFDADYGRVQMDVRRGRKRNNDYFIFKRNHSLSLVYKSNANVAVK 560
1q57.1.F 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
Model_01_LYIIVDLYVDELDGQVTRDTYEVSMQKTIKFDQNSCHVQVFAEKQQLQWHDGAFNLYDSGASPIK 640
1q57.1.F 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
Model_01_CDNGIVHRNDSNAQDILVQVQKRVKRVAGQIGDDVLYDRTGYSYSSVPCMPERRSPKRY 720
1q57.1.F 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

```

Summary Templates Models

Model Results

Order by: GMAQE

Oligo-State: Monomer
Ligands: None (matching prediction)

Global Quality: GMAQE 0.03, QMEAN -4.43

Local Quality:

Completion:

Quality Metric	Value
QMEAN	-4.43
CP	-3.00
All Atom	-1.80
Solvation	-0.61
Torsion	-0.02

Template: 4kcp.1.A
Seq Identity: Coverage: Description: Single-stranded DNA-binding protein WHY2, mitochondrial

Model-Template Alignment

```

Model_01_AHMKQARSLSSICDQKRSFEASTLRFQFAHNSNSTPGRQFPQDAARFSSGLFAYFIPGKALVSEVLPSP 80
4kcp.1.A 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
Model_01_CMKQARSLSSICDQKRSFEASTLRFQFAHNSNSTPGRQFPQDAARFSSGLFAYFIPGKALVSEVLPSP 160
4kcp.1.A 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
Model_01_DMKQARSLSSICDQKRSFEASTLRFQFAHNSNSTPGRQFPQDAARFSSGLFAYFIPGKALVSEVLPSP 240
4kcp.1.A 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
Model_01_AHMLIDRSLMLTFPFAKGRKDWKQKTFALSTEVQSLIMQKSDSFPDFKMSKSNADQKSLVSHAD 320
4kcp.1.A 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
Model_01_CHMLIDRSLMLTFPFAKGRKDWKQKTFALSTEVQSLIMQKSDSFPDFKMSKSNADQKSLVSHAD 400
4kcp.1.A 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
Model_01_AHYFSLVSNSSLKTDFVYVVKAFPMKATAFALFIMGNMLLHVTALPSRYSVSLTEPQLEWDK 480
4kcp.1.A 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
Model_01_CHYFSLVSNSSLKTDFVYVVKAFPMKATAFALFIMGNMLLHVTALPSRYSVSLTEPQLEWDK 560
4kcp.1.A 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
Model_01_HYFSLVSNSSLKTDFVYVVKAFPMKATAFALFIMGNMLLHVTALPSRYSVSLTEPQLEWDK 640
4kcp.1.A 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

```

At1g50840

AT1G71260

Outlook

- Paternal inheritance

Protection of mitochondrial DNA in sperm cells

- RNA-seq

To explore the key protein in the paternal inheritance

Acknowledgement

- Professor Luo jingchu
- Professor Sodmergn
- Group 04 memebbers
- All the classmates

Thank fou your listening!

