	Name	Accession number	Species
	PATC139978	-	Phalaenopsis aphrodite
	PATC127710	-	Phalaenopsis aphrodite
	PATC150554	-	Phalaenopsis aphrodite
	PbTPS5	MW645242	Phalaenopsis bellina
	PbTPS7	MW645243	Phalaenopsis bellina
	PbTPS9	MW645244	Phalaenopsis bellina
	PbTPS10	MW645245	Phalaenopsis bellina
TDC L	FhLin	AFP23421.1	Freesia hybrid cultivar
113-0	VvPNRLin	ADR74209.1	Vitis vinifera
	MdOCS-RG1	AGB14628.1	Malus domestica
	SITPS38	AEP82768.1	Solanum lycopersicum
	VvaTerP	NP_001268216.1	Vitis vinifera
	PmIspS	AAQ84170.1	Pueraria montana var. lobata
	PtIspS	AAQ16588.1	Populus tremuloides
	MdRGAFS1	AAX19772.1	Malus domestica
	PcAFS1	AAT70237.1	Pyrus communis L.
	PbTPS3	MW645240	Phalaenopsis bellina
	PbTPS4	MW645241	Phalaenopsis bellina
	OsDTC2/KS8	XP_015617513.1	Oryza sativa
	OsDTC1/KS7	BAC56714.1	Oryza sativa
TDC = /f	SITPS24/KS	AEP82778.1	Solanum lycopersicum
1PS-e/1	MdRGEKS	AFG18184.1	Malus domestica
	LnTPS3	AKQ19359.1	Laurus nobilis
	AdAFS1	ACO40485.1	Actinidia deliciosa
	VvPNENerGl	ADR74220.1	Vitis vinifera
	PdTPS	XP_017696375.1	Phoenix dactylifera

**Supplementary Table S1** Information of *TPS* genes used for phylogenetic analysis in Fig. 1.

**Supplementary Table S2** Information of *TPS* genes used for phylogenetic analysis in Supplementary Fig. S1.

Subfamily	Name	Accession No.	Species	Function/Product	
TPS_b	FhLin	AFP23421.1	Freesia hybrid cultivar	linalool	
	VvPNRLin	ADR74209.1	Vitis vinifera	(3R)-linalool	
	MdOCS-RG1	AGB14628.1	Malus domestica	$(E)$ - $\beta$ -ocimene	
	SITPS38	AEP82768.1	Solanum lycopersicum	α-bergamotene	
	VvaTerP	NP_001268216.1	Vitis vinifera	(-)-alpha-terpineol	
115-0	PmIspS	AAQ84170.1	Pueraria montana var. lobata	isoprene	
	PtIspS	AAQ16588.1	Populus tremuloides	isoprene	
	MdRGAFS1	AAX19772.1	Malus domostica	(E,E)-a-farnesene	
	PcAFS1	AAT70237.1	Pyrus communis L.	(E,E)-a-farnesene	
	AmMyr	AAO41727.1	Antirrhinum majus	myrcene	
	AtTPS14	NP_176361.2	Arabidopsis thaliana	(3S)-linalool	
TPS-g	GmNES	AEE92791.1	Glycine max	nerol	
	ZmTPS2	NP_001105854.1	Zea mays	linalool, (E)- nerolidol, and (E,E)- geranyllinalool	
TPS-a	Cstps1	AAQ04608.1	Citrus sinensis	valencene	
	MdGDS-RG1	AGB14625.1	Malus domestica	germacrene-D	
	SITPS12	AEP82783.1	Solanum lycopersicum	$\beta$ -caryophyllene and $\alpha$ -humulene	
	NtEAS	AFJ04408.1	Nicotiana tabacum	5-epi-aristolochene	
	EhTPS	XP_010910563.1	Elaeis guineensis	_	
	OsCyc2	BAD42452.1	Oryza sativa	ent-copalyl diphosphate	
TPS-c	SITPS41	AEP82765.1	Solanum lycopersicum	Unknown	
	SrCPS	AAB87091.1	Stevia rebaudiana	ent-copalyl diphosphate	
	OsDTC2/KS8	XP_015617513.1	Oryza sativa	stemar-13-ene	
	OsDTC1/KS7	BAC56714.1	Oryza sativa	ent-cassa-12,15-diene	
	SITPS24/KS	AEP82778.1	Solanum lycopersicum	ent-kaurene	
	MdRGEKS	AFG18184.1	Malus domestica	ent-kaurene	
TPS-e/f	LnTPS3	AKQ19359.1	Laurus nobilis	geranyllinalool	
	AdAFS1	ACO40485.1	Actinidia deliciosa	(E,E)-a-farnesene	
	VvPNENerGl	ADR74220.1	Vitis vinifera	( <i>E</i> )-Nerolidol and ( <i>E</i> , <i>E</i> )-Geranyl linalool syn	
	PdTPS	XP_017696375.1	Phoenix dactylifera	_	

#### **Supplementary Figure legends**

**Supplementary Figure S1.** (A) Phylogenetic analysis of the subfamilies of putative *TPS* genes with *TPS* genes identified from other species (detailed information in Supplemental Table 2). *TPS* genes from *P. bellina* are in bold black and from *P. aphrodite* in bold grey. Bootstrap values were calculated as a percentage of 1000 replicates, with values > 50 shown. The scale bar represents 0.2 substitutions per site. (B) Comparative gene expression analysis using heatmap analysis of *TPS* genes in transcriptomic data for blooming day (Dd), 3 days post-anthesis (D+3), D+5 and D+13 in *P. bellina* and microarray data for bud and flower in *P. aphrodite*. Hierarchical clustering was performed by the centroid linkage method with uncentered correlation. The heatmap and dendrogram of the clustered data were visualized by using Java TreeView (2.11) (Freudenberg et al., 2009). The color scale ranged from red (highest expression) to white to green (lowest expression).

**Supplementary Figure S2.** Plant morphology for (A) *P. bellina* and (B) *P.* I-Hsin Venus. *P. bellina* has strong floral scent but has one flower in the spike at one time, while *P.* I-Hsin Venus has less scent but is floriferous.

**Supplementary Figure S3.** An alternative-splicing model was proposed to account for the appearance of pre-stop MTPS transcripts, PbTPS5-2 and PbTPS10-1. Gene structure analysis of *PbTPS5* and *PbTPS10* showed that both genes contain one normal transcript and one pre-stop transcript, which might result from intron retention because of alternative splicing. TSS, transcription start site.

Supplementary Figure S4. Phylogenetic analysis of *Clarkia* linalool synthase (in blue dots) and *PbTPS3*, *PbTPS4* and other plants terpene synthases. Sequence analysis was performed with MEGA5 to create a tree using the nearest neighbor-joining method. The numbers at each node represent the bootstrap values. The accession numbers of sequences used are as follows: Perilla frutescens limonene synthase (AAG31438.1), Gossypium arboretum cadinene synthase (CAA65289.1), Cucurbita maxima entkaurene synthase (AAB39482.1), Clarkia breweri S-linalool synthase (AAC49395.1), Gossypium hirsutum cadinene synthase (AAC12784.1), Citrus limon gama-terpinene synthase (AAM53943.1), Citrus limon limonene synthase 2 (AAM53946.1), Pisum sativum copalyl diphosphate synthase (AAB58822.1), Mentha aquatic linalool synthase (AAL99381.1), Abies grandis pinene synthase (AAB71085.1), Abies grandis limonene synthase (AAB70907.1), Mtntha piperita farnesene synthase (AAB95209.1), Solanum lycopersicum germacrene C synthase (AAC39432.1), Salvia officinalis cineole synthase (AAC26016.1), Salvia officinalis bornyl diphosphate synthae (AAC26017.1), Salvia officinalis sabinene synthase (AAC26018.1), Cinnamomum tenuipile geraniol synthase (CAD29734.2), Mentha spicata limonene synthase (AAC37366.1), Clarkia concinna linalool synthase (AAD19839.1), Clarkia breweri linalool synthase 2 (AAD19840.1), Nicotiana tatbcum aristolochene synthase (AAA19216.1), Arabidopsis thaliana copalyl diphosphate synthase (AAA53632.1), Zea mays copalyl diphosphate synthase (AAA73960.1), Gossypium arboretum cadinene synthase (AAD51718.1), Artemisia annua linalool synthase (AAF13356.1), Abies grandis phellandrene synthase (AAF61453.1), Abies grandis terpinolene synthase (AAF61454.1), Abies grandis limonene/pinene synthase (AAF61455.1), Arabidopsis thaliana geranyllinalool synthase (Q93YV0.1), Actinidia deliciosa ocimene/farnesene synthase (ACO40485.1), Orvza sativa Japonica Group linalool synthase (ACF05530.1), Solanum lycopersicum terpene synthase (AEP82769.1), Solanum lycopersicum linalool/nerolidol synthase (AEP82767.1), Antirrhinum majus ocimene synthase (AAO42614.1), Antirrhinum majus myrcene synthase (AAO41727.1), Arabidopsis thaliana terpene synthase 14 (NP 001185286.1), Medicago truncatula chloroplast terpene synthase 3 (AAV36466.1), Glycine max nerol synthase (AEE92791.1), Medicago truncatula terpenoid synthase (ABE80305.1), and Medicago truncatula terpenoid synthase (ABE91630.1).

**Supplementary Figure S5.** (A) GC-MS of *N. tabaccum* transiently overexpressing *PbTPS5* and *PbTPS10* with or without *PbGDPS*. (B) Quantification of tetrahydromyrcenol detected in various experiments. (C) The peaks labeled in (A) are as follows: 1: Tetrahydromyrcenol; 2: Nonanol; 3: Decanal; 4: Ethyl-hexanol; 5: Dodecene; 6: Decene.

**Supplementary Figure S6.** VOCs detected in flowers of (A) *P. aphrodite* and (B) *P.* Sogo Yukidian 'V3' overexpressing various genes, and internal non-volatile terpenoids in flowers of (C) *P. aphrodite*, and (D) *P.* Sogo Yukidian 'V3' overexpressing various genes. Different numbers show the different independent line.

**Supplementary Figure S7.** Functional characterization of purified recombinant proteins of *PbTPS3* and *PbTPS4* with FDP and GGDP added as the substrates. (A) PbTPS3+FDP, (B) PbTPS3+GGDP, (C) PbTPS4+FDP, and (D) PbTPS4+GGDP, and No monoterpene products were detected in any reactions.

**Supplementary Figure S8.** Multiple alignment of amino acid sequences of the *TPS-e/f* subfamily of *P. equestris*, *P. bellina* and other plants. *PbTPS3* and *PbTPS4* from *P. bellina*, *LIS* from *C. concinna*, *LIS2* from *C. concinna*, *S-LIS* from *C. breweri*, *AFS1* from *A. deliciosa*, and *GES* from *A. thaliana*. The red boxes indicate the three conserved motifs of DDXXD and NSE/DTE, respectively. The red line is the conifer diterpene internal sequence (CDIS). *PbTPS3* and *PbTPS4* share 62.4% identity.

**Supplementary Figure S9.** (A) Expression of *PbTPS3* vegetative organs with high expression in leaf but very low expression in root and stalk. (B) VOCs emitted from leaf were mostly ( $\beta$ )-cis-oicmene. (C) Structure of ( $\beta$ )-cis-oicmene.

**Supplementary Figure S10.** The binding domains of plant defense transcription factor on the promoter sequences of *PbTPS3* and *PbTPS4*. (A) The gene promoter was indicated as 2,000 bp upstream from the translation start site. (B) WBOXATNPR1 is marked with a blue box, and WRKY71OS is marked with a green box.





(A)



**(B)** 







0.2







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4.5									
(1)	1 ,10	20	30	40	50	60	70	80	90
PeMTPS6 (1)	MB	HSHAIEKMRME	LFSSSANL	FALLPVSAYE	TSLVVMVPD	PNDQ	MFPGYLDWVI	RSO-NTLG	FWLDDHPQ
PbTPS3 (1)	<mark>ME</mark>	QSQA <mark>VERMK</mark> KD	LFSPSANL	FTLLPI <mark>SAYE</mark>	TAWVAMIPH	PDDP	LF SEYLDWVA	AR <mark>NQ</mark> -NIM <mark>G</mark>	FWFEDHVH
PbTPS4 (1)	MLME	LSQVVERLRRE	LFSSS <mark>A</mark> GL	FTLLPV <mark>SAYE</mark>	<mark>T</mark> AW <mark>V</mark> AM <mark>V</mark> PD	PNDP <mark>TR</mark> P	MFPQCLD <mark>WV</mark> I	RS <mark>Q</mark> -DAL <mark>G</mark>	FWFD <mark>D</mark> HMH
LIS_Clarkia_concinna (1)	MQPITKSSSTSS	LEFLVDKVKRE	SL <mark>SSS</mark> SDTQ	NL <mark>FLS</mark> A <mark>S</mark> P <mark>YD</mark>	TAWLA <mark>L</mark> IPH	PHHHH-HHGP <mark>P</mark>	M <mark>F</mark> EK <mark>CL</mark> Q <mark>W</mark> II	LHNQ-TPQ <mark>G</mark>	FWTAAAG-
LIS2_Clarkia_breweri (1)	MLS	IQSH <mark>VDEIKR</mark> -	G <mark>S</mark> LW	NLR <mark>LS</mark> P <mark>SAYD</mark>	<mark>T</mark> AWLA <mark>L</mark> IPD	PDDP <mark>TR</mark> P	M <mark>F</mark> AK <mark>CM</mark> H <mark>WL</mark>	<mark>V</mark> Q <mark>NQ</mark> -SME <mark>G</mark>	FWAADD
S-LIS_Clarkia_breweri (1)	MQLITNFSSSSS	LQFLVDKVKRE	SL <mark>SSS</mark> SNTQ	NL <mark>FLS</mark> T <mark>S</mark> P <mark>YD</mark>	<mark>T</mark> AWLA <mark>L</mark> IPH	PHHHH-HHGRE	M <mark>F</mark> EK <mark>CLQ</mark> WII	LHNQ-TPQ <mark>G</mark>	FWAAAG
APS1_Actinidia_deliciosa (1)	MEPLLFS	IQTLVHQVKQE	<mark>IFSS</mark> TFD <mark>L</mark>	YSFVSP <mark>S</mark> AYD	TAWLAMIPH	PKQN <mark>S</mark> CE	K <mark>F</mark> KG <mark>CLD</mark> WII	LD <mark>NQ</mark> -KEA <mark>G</mark>	<mark>YW</mark> G
GES_Arabidopsis_thaliana (1)	MKSSYGSSSN <mark>D</mark>	LHAF <mark>V</mark> NE <mark>IK</mark> GE	IQLSNINLDP	YSEVSPSAYD	TAWL SMIEE	DINVDDNELKE	MFQGCLDWIN	C <mark>NQ</mark> NARE <mark>G</mark>	FWMNSTSY
5				and a second second					—— Section 2
(91)	91 ,100	,110	,120	,130	,140	,150	,160	170	180
PeMTPS6 (73)	DHRRELKS	NES-QWTAADV	VGTLACLIAL	KT <mark>WEI</mark> DGFSH	K <mark>INKGL</mark> EF <mark>L</mark>	RD <mark>NMEKVL</mark> WKI	RKS <mark>K</mark> QDGDEA	AGLLRR <mark>W</mark> IL	M <mark>VELA</mark> EAK
PbTPS3 (73)	EQCGKDLDHHETI	NYKRQWNSADL	MATLTCLIAL	KT <mark>WEI</mark> TGF SR	K <mark>INKGL</mark> KF <mark>L</mark>	GD <mark>NMEEF</mark> KMF	-ES <mark>K</mark> DESDKU	VGLQR-WSL	M <mark>VELA</mark> EAK
PbTPS4 (75)	EQCGLDLDHQELN	NYMHQRSVDL	MATLACLIAL	KIWEIDAFTH	K <mark>INKGL</mark> KFL	RD <mark>NMEKELRK</mark> M	IRKR <mark>K</mark> EDGDEA	ARLLYMCFL	MLELAKAK
LIS_Clarkia_concinna (88)	DNIS	DTDDDVTLDCL	LSTLACLVAL	KRWQLAPD	MIHKGLEF <mark>V</mark>	HRNTERLVMKC	2KPSDVPP	RWFTIMFPA	ML <mark>ELA</mark> GAS
LIS2_Clarkia_breweri (67)	D	IDTEPVALDCL	PATLACLIAL	KRWGAAPN	NINKGLGFF	ERNVEELLLR	GKLSDVPP	RWFTVTFLA	MLELAIAS
S-LIS_Clarkia_breweri (87)	DNIS	DTDDDVTLDCL	LSTLACLVAL	KRWQLAPD	MIHKGLEFV	NRNTERLVMK (	2KPSDVPP	RWFTIMFPA	MLELAGAS
APS1_Actinidia_deliciosa (73)	EC	DHDGLPTIDSL	PATLACMVAL	RTWGVSEK	HINKGLAFI	HANSTTLLKEF	YD-H <mark>LPP</mark>	RWFVI <mark>V</mark> FPA	MVEVAQAA
GES_Arabidopsis_thaliana (89)	TTVADGR	DEDGEKDMCIL	TSTLACVVAL	QKWNIGCF	HIHKGTRYI	ERNTEMIIGKY	IN-EEGSY <mark>P</mark>	RWFAIKFTG	TLELAQKL
	101 100	200	210	220	220	240	250	200	Section 3
(181)	181 ,190	200	210	220	230	240	250	260	270
PeMTP96 (157)	GLKVFP-AAQHIK	DGPFNKF <mark>K</mark> LNG	TKINCRLEDE	TIERIVMREI	AFE	Ns	GSELYRSE	PSTTACAFM	TG <mark>GN</mark> QAYK
PbTPS3 (161)	GLKVFP-TFQRIK	NGISNEFELNR	TKIKCSEEDE	TIERIVKREI	AFE	Ns	GSELFRSE	PSATACAFM	ISGNQTYK
PbTPS4 (165)	GLIVFPAVAQQIK	NELFNEFEVNA	TKIKRTEEDG	MVERIVMREI	AFE	N8	GSELFR <mark>S</mark> E	PSATACAFM	ISGDQTYK
LIS_Clarkia_concinna (164)	GLRVDFSENLNRI	LVELTQNRDDI	LTREEVGERK	QYSPLLLFLE.	ALPAQSYDS	DVLKQIIDKKI	SSDGSLFQSE	PSATARAYM	ITGNTRCL
LIS2 Clarkia breweri (141)	GLKVAFPDNLIK	LDELFENRNT	LLREELSDKT	OYAPLLMFLE	ALPPSYVKL	DDLNOYLERNI	GNDGSLYOSE	PSATARAYM.	ATGNTKCL Continu
(071)	271 200	200	200	210	220	220	240	250	
(271)	2/1 200	290	200	210	92U	200	240	200	360
PeMTP36 (229)	TYLQNLFVDC-QH	GVPPTYMMDKD	<b>AIKTGTA</b> DHT	ERLGCAEHFT	EDIKNVIDI	QYKEWIVEELC	APNKNNVA	AFQLYKDSL.	AFRL LRMK
PbTPS3 (233)	TYLQNLLVDC-QC	GVPPTYFVDKD	<b>VIKLWVV</b> DHI	ERLGCAEHFS	EDIRHVMDH	QYREWIAEELC	APIKNNVA	FKLYKDSL.	AFRLLRMK
PbTPS4 (238)	IYLENLIVDC-OH	GVPPIFFVDKD	<b>NKIWV</b> DLL	ERLGCAKHFR	EDIRHVMDR	QYRKWIAEELC	DIPKKEDI	AFQIYKDSL.	AFRILRMH
LIS_Clarkia_concinna (254)	SYLHSLTNSCSNG	GVPSFYPVDDD	THDTAWANGT	TRSGLTEHLI	PEIDHLLLK	VQ <mark>KNYKYK</mark> KAS	PKSLYGI	AAELYKDSL.	AFWLLRVN
LIS2_Clarkia_breweri (231)	SYLKSLTNTYLDG	GVPSLYCMDEE	T O O T AW AN O T	VRPGLTEYFV	PETEGITFO	VEQNYKCKRSE	PPRNALHNV	VAELYKDSL.	AFWLLRIN
S-LIS_Clarkia_breweri (253)	SYLHSLINSCONG	GVPSFYPVDDD	THDTAWANGT	TREGLIEHLI	PEIDHLLK	VQKNYKYKKAS	PKSLYSI	AAELYRDSL.	AFWL LRVN
APS1 Actinidia deliciosa (233)	AYLESLVOKR-PG	GVPTMYPMDGE	LVSLCLVNOI	ORLGLAEHFT	EELEENLKL	TYENYKNOESP	E-MKDSYLVE	PTKIYKDSL.	AFRITERMH
CEC Anabidanaia thaliana (200)	NUT OUT HOUSE DU		T THE OWNER T		T T T T T T T T		n where		
GES_Arabidopsis_thaliana (260)	AYLONLVOKC-PN	GVPOKYPL VED	LIKLSMVNLI	EST <mark>GLG</mark> EFFG	I <mark>EIE</mark> HVL <mark>E</mark> Q	VY SRYEEKDFE	R-MPMSYLAI	D-Q <mark>L<mark>H</mark>K<mark>DSL</mark></mark>	AFRMLRMH
GES_Arabidopsis_thaliana (260)	A <mark>YLQNLVQ</mark> KC-PN	GVPOKYPINED	L <mark>IKL</mark> SMVNLI	est <mark>glg</mark> effg	I <mark>EIE</mark> HVL <mark>E</mark> Q	VYSRYEE <mark>KD</mark> FE	R-MPMS <mark>Y</mark> LAI	D-Q <mark>L<mark>H</mark>KDSL.</mark>	AFRMLRMH —— Section 5
GES_Arabidopsis_thaliana (260)	A <mark>YLQNLVO</mark> KC-PN	GVPOKYPLED	LIKLS <mark>MVN</mark> LI	EST <mark>GLGEFF</mark> G	IE <mark>IEHVLE</mark> Q	VYSRYEEKDFE	R-MPMS <mark>Y</mark> LAI	D-Q <mark>L<mark>H</mark>K<mark>DSL</mark>.</mark>	AF <mark>RMLRM</mark> H —— Section 5
GES_Arabidopsis_thaliana (260)	A <mark>ylqnlvqkc-p</mark> n	GVPOKYPLAED		EST <mark>GLGEFF</mark> G	IE <mark>IE</mark> HVL <mark>E</mark> Q	VYSRYEEKDFE	R-MPMS <mark>Y</mark> LAI	D-Q <mark>LH</mark> KDSL.	AFRMLRMH — Section 5
GES_Arabidopsis_thaliana (260)	A <mark>ylqnlvqkc-p</mark> n	GVPQKYPL <mark>N</mark> ED	DDXXD	estglgeffg motif	IE <mark>IBHVL</mark> EQ	VYSRYEEK <mark>D</mark> FE	R-MPMS <mark>y</mark> lai	D-Q <mark>LH</mark> KDSL.	AFRMLRMH — Section 5 — Section 7
GES_Arabidopsis_thaliana (260)	AXLONLVOKC-PN	GVPOKMPINED	DDXXD	estglgeffg motif 580	IEIEHVLEQ 590	VYSRYEERDFE 600	R-MPMSYLAI 610	D-Q <mark>LHRDSL</mark>	AFRMLRMH — Section 5 — Section 7 630
GES_Arabidopsis_thaliana (260) (54 PeMTPS6 (49)	A <mark>XLONLVOKC-PN</mark> 1) 541 550 5) <b>AVASSICPPINI</b>		DDXXD	estglgeffg motif 580 Kapldelft	IEIEHVLEQ 590	600	R-MPMSYLAI β10 PNALDNLVHD	D-QLHKDSL 620	AFRMLRMH — Section 5 — Section 7 630 GYDVRKII
GES_Arabidopsis_thaliana (260) (54 PeMTP56 (49 PhTP53 (49	A <mark>YLONLVOKC-PN</mark> 1) 541 550 5) AVA 881 CPBINI 9) ATA 881 CPBINI	560 550 D SRKEAAKCAT	DDXXD	ESTGLGEFFG motif 580 KAPLDELFI KASLDELFI	IBIEHVLEQ 590 LTDALQRMDC LTDALQRMDC	OV SRVEEKDFE 600 SEFLTGHSKVI SEFLTGHSKVI	F-MPMSYLAI 610 FNALDNLVHD	620 620 <b>ISQKSFKRY</b>	AFRMLRMH — Section 5 — Section 7 630 GYDVKKIL GYVKKIL
GES_Arabidopsis_thaliana (260) (54 PeMTP36 (49 PbTP53 (49 PbTP54 (49	ATLONIVORG-PN 1) 541 550 5) ATA SICPPIN 9) ALASSICPPIN 0 AMA STCIPIN	560 560 D SRKEAA KCAT D SRKEAA KCAT D SRKEAA VKEAU	DDXXD 570 FIAV DDFFD LITI DDFFD	BSTGLGEFFG motif 580 KAPLDELFI KASLDELFI EASLHDLSI	590 590 LTDALQRWD LTDALQRWD LTDALQRWD	600 600 607 LIG GHSKVI 67 CLIGSHSRVI 67 CLIGSHNRVI	β10 β10 PNALD NL VHD PNALD NL VHD PTBLD NL VHD	620 F20 F20 F20 F20 F F F F F F F F F F F	AFRMLRMH Section 5 
GES_Arabidopsis_thaliana (260) (54 PeMTP56 (49 PbTPS3 (49 PbTPS3 (49 PbTP54 (48 LIS_Clarkia concinna (52	AVLONIVORO-PN 1) 541 550 5) AVASSICPINI 9) AIASSICPINI 0) AMASSTCIPINI 0) AFASSTCIPINI 0) AFASSTCIPINI	560 D SRKEAA KCAT D SRKEAA KCAT D SRKEAA KCAT D SRKEAA KCAT D SRKEAA KCAT	DDXXD 570 FIAW DDFFD LITI DDFFD VITV DDFFD	BSTGLGEFFG motif 580 KAPLDELFI KASLDELFI EASLHDISI EGSMDDIEK	590 590 LTDAL QRMD LTDAL QRMD LTDAL QRMD LTDAY RRMD	600 56 F L TG HSK VI 56 F L TG HSK VI 57 C L TG HSK VI 57 C L TG HSK VI 58 C J G SH NK VI	β10 β10 FNALDNLVHD FTBLDHLVHD FTBLDHLVFD FEALDDLVNB	620 620 13 QK SF KRY 13 QK SF KRY 13 LK IF KQH VRLKCF QQN	A F RMLRMH Section 5 Section 7 630 GYDVKKIL GYDVKKIL GHDLKKHL GQDLKNNL
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