A

Α	DEG15_pBridge +						-His			pBri	dge +		••	•				-His
	pGAD			뙣	1	1.00	+His		DI	EG15	_pGA	D		۲	1	\$	*	+His
	CML3 pBridge +	25.	!	•	•	N,	-His			pBri	dge +		• •		•			-His
	pGAD			證			+His		C	ML3	_pGA	D				1		+His
	DEG15_pBridge +		۲		A.	•	-His		СМ	L3_1	oBridg	ge +		۲	*	•	٩	-His
	CML3_pGAD		۲	ar.	N		+His		DI	EG15	_pGA	D		۲	\$ <u>.</u>			+His
	DEG15N_pBridge +	•	٠	<u>.</u>	12	19.5	-His		СМ	L3_1	oBridg	ge +		۲	43	••	•	-His
	CML3_pGAD			aș.	:		+His		DE	G151	N_pG	AD		•	-	\$.	:	+His
	DEG15∆N_pBridge		•	•		•	-His		СМ	L3_1	Bridg	ge +	-	•				-His
	+ CML3_pGAD		۲		.4.	•	+His		DEG	G15∆	N_pG	AD				*	*	+His
	DEG15∆1/3N_ pBridge +						-His		CM Di	L3_1 EG15	oBridg 5∆1/3N	ge + N	••	•		•		-His
	CML3_pGAD	pGAD +His pGAD	-	0		*			+His									
	DEG15∆2/3N_ pBridge +						-His		CM D	L3_J EG15	oBridg 5∆2/3N	ge + N_	i.	•	••		•	-His
	CML3_pGAD				20		+His			pG	AD			0	*	a.	1.0	+His
	DEG15		ir	nteraction -	with CML3	1			1	:		•	•	-His				
	DEG15N	+ 					pBridge + pGAD		•	*	4		+His					
	DEG15Δ1/3N								DEG15∆25aa_						-His			
	DEG15A25aa -				-		CML3_pGAD		D			ages.	:		+His			
	DEG15\/75ee -								DEG15∆50aa_		•					-His		
								1	pBridge + CML3_pGAD			۲	3	12		+His		
в	ß-ga	lact	osid	lase	-ass	say			D	EG1	5∆75a	a_						-His
					+/- 1.36	1.07	1.41		pBridge + CML3_pGAD		D				an in		+His	
	12.00				н 9.11	8.23 +/-	7.96 +/- 35 +/- 0.8		Dł	EG15	Δ100a	na_				• •		-His
r units	8.00 -				T -	Πı	$\frac{2}{1}$	1	С	ML3	_pGA	D	۲	10	d:			+His
Mille	6.00 - E	05	.05	33			1		90	.05	90.	90	60	90	07	60 5	à g	
	2.00 0.53 +/- 0	0.31 +/- 0	0.39 +/- 0	.28 +/- 0.(0.42 +/- 0	0.39 +/- 0	0.50 +/- (0.31 +/- 0	0.40 +/- 0	0.39 +/- 0	0.24 +/- 0.	0.24 +/- 0	0/+ +/- 0 1 19 +/- 0 1	
		G15]		ML3]0	ML3	G15	15N 15N	I.,	ML3		NL3	1/3N	NL3	13/3N	игз <mark>1</mark> - -			•
	lge + pG 315 + pG	ge + DE	NL3 + pG	dge + Cl	315 + Cl	L3 + DE	15N + C		AN + C	+ DEG1	/3N + CI	DEG152	%3N + CI	DEG152	5aa + Cl	Uaa + C	Daa + Ch	
	pBric	pBrid	C	pBri	DE	CM	CMLS		DEG1	CML3	DEG15A	CML3 +	DEG15A	CML3 +	EG15Δ2		G15Δ10	
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Figure S1. AtDEG15 interacts with AtCML3 through its N-terminal 25 amino acids. Interaction assay using Y2H was tested by cloning the full-length coding regions of *AtDEG15* and its truncated variants and also *AtCML3* into pBridge and pGAD424, fusing them with the DNA-binding domain or with the DNA-activation domain, respectively, and tested for interaction in both combinations. As negative controls a combination of empty vectors and vectors harbouring one of the constructs were used. (A) Growth on His-free medium (-His) indicates interaction by transcription of the His3-reporter; (+His), positive growth control. Negative controls are shaded in grey. Yeast cultures were diluted from 10^5 cells (left) to 10^1 cells (right) per 50 µl drop applied. (B) Interaction is also demonstrated by transcription of the lacZ reporter (β -gal activity in Miller units). Mean (n=3) +/- SD. Inlay: Schematic representation of AtDEG15 and the various deletion constructs used in A and B: green, AtCML3 binding domain; red, protease domain with plant-specific loop; blue, PTS1.



Figure S2. Binding of AtDEG15 to CaM via its N-terminal domain was confirmed by affinity chromatography on CaM-agarose. (A and B): AtDEG15 was purified from inclusion bodies using 4 M urea and incubated with CaM-agarose in the presence (0.1 mM CaCl_2) or absence of Ca²⁺ (5mM EGTA/EDTA). Bound protein was eluted with either bovine CaM (A) or purified recombinant AtCML3 (B). (C): Affinity chromatography on CaM-agarose using AtDEG15 purified under native conditions. AtDEG15 bound specifically to the matrix in the presence but not in the absence of Ca²⁺, and could be eluted with bovine CaM. (D): DEG15_N comprising only the first 327 amino acids without the protease and C-terminal domains is still able to bind to calmodulin-agarose in a calcium-dependent manner.



Figure S3. Recombinant expression of soluble AtDEG15 yields the full length protein consistently accompanied by various degradation products. AtDEG15 with an N-terminal His-tag and an N-terminal "Xpress epitope" permitting detection of the recombinant fusion protein by appropriate antibodies was expressed in *E.coli* under control of an arabinose-inducible promoter. The protein was purified by HisTrap affinity chromatography under native conditions. Analysis of all fractions by SDS-PAGE and Coomassie staining (A) or Westernblot (B) revealed the full length AtDEG15 protein (76 kDa) as well as varying degradation products probably due to self cleavage.



Figure S4. Recombinant enzymatically active full length AtDEG15 exhibits the characterics of the monomer as a general protease with an intrinsic self-cleavage activity. (A) His-tagged purified AtDEG15 comprising full length protein and C-terminally truncated degradation products was incubated over night at 4°C before affinity chromatography on CaM-agarose under native conditions in the presence (0.1 mM CaCl₂) and absence of Ca²⁺ (5mM EGTA/EDTA). Purified AtDEG15 incubated overnight as well as the different fractions of the affinity chromatography on CaM-agarose were analyzed by SDS-PAGE and Coomassie staining. AtDEG15 full length protein together with its C-terminally truncated versions bound specifically to the matrix in the presence of Ca²⁺ and could be eluted with bovine CaM, but not in the absence of Ca²⁺ (5mM EGTA/EDTA), whereas N-terminally truncated versions could not bind to the CaM-ligand. (B) The AtDEG15_N-terminus lacking the protease domain was stable under these experimental conditions and also bound to the CaM-agarose in a calcium-dependent fashion.



Figure S5. Western Blot analysis of yeast AH109 cells expressing the full-length AtDeg15 and the AtDeg15 Δ 25aa variant with antibodies directed against the binding domain in pBRIDGE [GAL4 (DBD) (RK5C1) Santa Cruz Biotechnology] show immuno-reactive bands of the expected size in both strains and not in the untransformed yeast AH109 used as a negative control.





Figure S6. Crosslinking of a synthetic AtDEG15 peptide with CaM. Crosslinking experiments were performed using a synthetic peptide comprising the first 21 amino acids of AtDEG15 (H2N - MDVSKVVSFSRNFAVLVKVEG - CONH2) and either CaM (A) or egg ovalbumin (B). A cross-linking product between CaM and the peptide can be observed solely in the presence of calcium. No cross-linking product occurs when CaM is replaced by egg albumin.

Ath_DEG15	
Aly_DEG15	
Rco_DEG15	
Maes DEG15	
Potr DEG15	
Proe DEG15	
S1v DEG15	
Cuse DEG15	
Gima DEG15	
Micu DEG15	
Ward DEVILE	
VVI_DEGISA	
VVI_DEGISD	
SODI_DEGIS	
Zema_DEGIS	
Orsa_DEG15	
Seit_DEG15	
Brdi_DEG15	
Phpa_DEG15	MGNLVVVVEEBGGERWATELNSTOLIHVDCERILRDLGVEGGIGLDRQAGGAPRRCTPARTNGGKIAGQCLLSALGVIWNLAGLSGCQFARGHRVDGLGSGFFLICNFEVGVALEGRKGDGEKKVAGILRGKRSGEGNCCGLKSSGIDARDRSSVLFRVIAGDIFRGGCSTQLSLFAAYQRLGIAIALIDTDSYCK
Popa_DEG15	
Didi_DEG15	
Dare_DEG15	
Brf1_DEG15	
HsaTYSND1	
Mmu_DEG15	
Ath DEG1	
Ath DEG2	
Ath DEG3	
Ath DEG4	
Ath DEG5	
3.1 DTG C	
ACD UNIO	
Ach_DEGO Ath_DEG7	
Ath_DEG7 Ath_DEG8	MGDPLERLGS
Ath_DEG7 Ath_DEG8 Ath_DEG8	MGDPLERIGS
Ath_DEG8 Ath_DEG8 Ath_DEG8 Ath_DEG9 Ath_DEG10	MGDPLE RIGS
Ath_DEG6 Ath_DEG7 Ath_DEG8 Ath_DEG9 Ath_DEG10	MGDPLERLGS
Ath_DEG6 Ath_DEG7 Ath_DEG8 Ath_DEG9 Ath_DEG10 Ath_DEG11	MGDPLERIGS
Ath_DEG7 Ath_DEG7 Ath_DEG8 Ath_DEG9 Ath_DEG10 Ath_DEG11 At_DEG12	
Ath_DEG5 Ath_DEG7 Ath_DEG8 Ath_DEG9 Ath_DEG10 Ath_DEG11 At_DEG11 At_DEG13 Ath_DEG13	MGDPLERIGS
Ath_DEG37 Ath_DEG37 Ath_DEG38 Ath_DEG49 Ath_DEG40 Ath_DEG11 At_DEG11 At_DEG13 Ath_DEG14	
Ath_DEG9 Ath_DEG8 Ath_DEG9 Ath_DEG9 Ath_DEG10 Ath_DEG11 At_DEG12 At_DEG13 Ath_DEG14 Ath_DEG16	

	CaM binding							
Ath DEG15		DPKGLKM	RKHAFHOYHSGNA	TLSASGILLPRDIFLSGEV	AAKVLFEAGODMAL	VLTVASVVEPFLI	LGHRTSSSISOD	PVKLIPGA
Aly DEG15	MDVSKVVSFSRNFAVLVKVEGP	DPKGLKM	RKHAFHOYHSGNA	TLS ASGILF PRNILS GGEV	TAKULFEA GOEMAL	VL <mark>T</mark> VASVVEPFLT	LGHRTSSSISOD	<mark>PVKLIPG</mark> A
Rco DEG15		DPKGLKM	RNHAFHLYASGET	TLSASGMILPDTLFHSGLV	KOILGSNGLEGOVLVL	VV <mark>TVAS</mark> VVESFLS	LOORE	
Maes DEG15		DPKGLKM	RKHAFHQYNSGKT	TLS ASGMLL PNTFYEAGLA	KRILGSSCKEGQALAL	VV <mark>TVASIVE</mark> SFLS	PNORDGISOG	RPETIPGA
Potr_DEG15	MCLPEIVDFARNFAVMVRIDGP	DPKGLKM	RKHAFHQYNSGKT	TLS ASGLLLPDTLY DADLA	NRILEGKSQGLGL	VV <mark>TVASVIEPFL</mark> S	SKHRESISQS	RPELIPGA
Prpe DEG15	MCLPEIVDFARNLAVMVRVKGP	<mark>DPKGLKM</mark>	RNHAFHHYHSGTT	TISASGMLLPNTLYDSDVA	QQLFGGDSERSPAL	VV <mark>T</mark> VASIVEPFLS	LOHREGLTOG	RPQLIPGV
Sly DEG15	MCLPEVVDVARNYAVMVRIQGP	DPKGLKM	RKHAFHLYNSGKT	TLSASGMLLPSS-FVNGSV	SEQIOGESKLOSIGGHLI	VLTVASVIEPFVV	OODTSDISKD	KPKLIPGA
Cusa_DEG15	MAKREIVDHARNFAIMVRVQGP	DPKGLKM	QKHAFHQYHSGRT	TLSASGMILPETLYDTRAA	KHLGNYKDQFATL	VL <mark>T</mark> VS <mark>SIFEP</mark> FMF	LOHRDKIHKG	KPELIPGV
Gima DEG15		<mark>DPKGLKM</mark>	RNHAFHQYRSGET	TLSASGVLVPDTLCDSQVA	TRLNGDNCEDRVL	VVTVASVVEPFLS	POORDNIPOVGAAR-	FRTYLIAGV
Migu_DEG15	MCLPEAADFARNFAVMVRVQGP	<mark>DPKGL</mark> KM	RNHAFHHYNSGKT	MLSASGTIFPASNFCN	LESSD-TVL	VL <mark>TAAS</mark> VI <mark>EP</mark> FLI	QQYRENPSKD	KPRLVPGV
Vvi_DEG15a	MCLPEIVDFARNFAVMVRVQGP	<mark>DPKGL</mark> KM	RKHA FHHYHSGKT	TLS ASGMLLPDTLSDISAA	CKHIHSNNDRNSMI	VV <mark>SVASILEP</mark> FLS	LOHRENIS OGS	HPELIHGV
Vvi_DEG15b	MCLPEIVDFARNFAVMVRVQGP	<mark>DPKGL</mark> KM	RKHAFHHYHSGKT	TLSASGMLLPDTLSDISAA	CKHIHSNNDRNSMI	VV <mark>S</mark> VAS IL <mark>EP</mark> FLS	SLQHRENIS QGS	H <mark>PELIHG</mark> V
Sobi_DEG15	METQEIAAAARHFSAMARIVGP	<mark>DPKAVKM</mark>	RRHAFHLHHSGST	TLSASALLLPRGALAEPPP	LL DHICA VHG HVAGDV	AL <mark>TAASLVEP</mark> FLV	AEORNNSGEE	LQPRLVPEV
Zema_DEG15	MEAQEIAAAARHFCAMVRIVGP	<mark>DPKAVKM</mark>	RRHAFHFHHSGST	TLSASALLLPRGALAEPPL	LLDHICSAHGHAAGDV	AL <mark>T</mark> AASLV <mark>EP</mark> FLV	AEQRNNSGEE	<mark>LQPRLVP</mark> ET
Orsa_DEG15	MAPREVAAAARGFSAMARIVGP	<mark>DPKAFKM</mark>	RRHAFHLHQSGST	TLSASALLLPPGSLAEPPP	LLDRICAAHGHAGG-V	AL <mark>T</mark> SASLVEPFLV	EEQRNSPSQE	<mark>L</mark> QPRLVPEA
Seit_DEG15	METQEIAAAARYFAAMARIVGP	DPKAVKM	RRHAFHLHQSGST	TLSASALLLPRGALAEPPP	LLDRICVAHGHAAGDV	AL <mark>T</mark> AASLVEPFLV	AEQRGNPGEE	<mark>F</mark> R <mark>PRLVP</mark> EA
Brdi_DEG15	MEPREIAAAARSFSAMARIVGPVSFSLPTSSPLPLPVTSSREISRNSATLPLCFL	QDPKAVKM	RRHAFHLHQ <mark>SG</mark> ST	TLSASAVIL PPGALAEPPP	P-LLGRVCAAHGHTGG-V	AL <mark>T</mark> SASLVEPFLV	AEQRDSASEE	<mark>LQPRLLP</mark> ET
Phpa_DEG15	ESGRVIVYEVTITMIRRRELTAMAAKAAMDAARLAAVMVRVHGP	<mark>DPKGRKM</mark>	RRHAFFHSESGDT	TILS ASGFLV PCVMNMKKPG	STALGQADLYETTSSEPSVV	VITCAS IVEPFLA	PKSHGISSREVCVVE	PEK-DF <mark>PKLIRG</mark> A
Popa_DEG15	MTITHGSLSACDISKLRQCCVVVRVKGN	DISTASNY	GESSESSALKENKESESQVPTFSHESEGKI	TFSCSGFIINRE	QGI	IL <mark>T</mark> SS <mark>S</mark> IFMPFLS	RRNEQAHYEI	HRDTEIDI
Didi_DEG15	MVNNFSSNGSDFIYNYSNKFNLEEERIPNLRRSCCIVRVSGI	DQSNGTNPI	NFS <mark>YS</mark> SN <mark>G</mark> KI	IFSCSGFILDLE	KGL	II <mark>T</mark> SPTIFLPFII	QQQNDNKRNI	MTESNITK
Dare_DEG15	INTA EEACCVVTVSEQI	LFTPGSENK-		-A <mark>TS</mark> C <mark>SGVFLH</mark> FQ	SGI	VVCS <mark>GIVF</mark> SRFIN	DTLPIKK	DTKILYSE
Brf1_DEG15	MLQEACIVSVSGESSK	SSGNHGEV	T	-GHSCSGVIVDRQ	RGL	VLSHGVAFSPYLF	DEFTSHQVRR	QGWYKPQD
HsaTYSND1	MRRQWG SAMRAA EQAGCMV SASR	AGOPEAG		-PWSCSGVILSRS	<mark>PGI</mark>	VLC <mark>HGGIFVPFL</mark> F	AG-SEVLTAA	<mark>GAVFLPG</mark> D
Mmu_DEG15	MGRQWGPSMRVAEQAGCVVSASR	A <mark>GQP</mark> DAG		-SWSCSGVILSRN	<mark>PG</mark> L	VLC <mark>HGGIFTP</mark> FLF	TG-SAALTQT	<mark>G</mark> TA <mark>FLPG</mark> D
Ath_DEG1							MATTTSC	SLLLSS
Ath_DEG2			MAAS	VANCCFSVLNASVKIQSS	ISS <mark>PWCFVSA</mark> SSLTPRASSN	IKRKSSRSDS <mark>PS</mark> P	ILNPEKNYPGRV	RDE <mark>S</mark> SN
Ath_DEG3			М	ISFLCVR <mark>TVS</mark> RFRSLSRALA	PGFLLLHGNAVPKTAV	FFRQQ <mark>SS</mark> NTRLFS	SYTA <mark>P</mark> S <mark>G</mark> VEENN	SKS <mark>A</mark> LK
Ath_DEG4			M	ILFRFLQTLARFCR	FLLISVL	GFRFSPLLLI	GYVKLQDENKHN	SESALA
Ath_DEG5							MTMALAS	SKAFSS
Ath_DEG6			ML	JFR <mark>SV</mark> HHIVARFSN			S <mark>T</mark> ST <mark>P</mark> I	HRFFYS
Ath_DEG7	QASMATES VMKEDLCLEIDPPLTESVATAEDWRRALGKVVPAVVVLRTTACRAFDTESAGAS YATGFIVLKRRGIILT	RHVVKPGPV	VAEAMFVNREEIPIYPVYRDPVHDFGFFCY	DPSAVQFLTYQEIPLAPEA	AS <mark>VG</mark> LEIR <mark>VVG</mark> NDS <mark>G</mark> EKVSI	LAGTLARL DRDAF	HYKKDGYNDFNTFYI	MQAASGTKGGSSG
Ath_DEG8						MDEDIAKPFVI	PENMMNKEDGLN	<mark>PGG</mark> DS <mark>TG</mark> K
Ath_DEG9			RKNSEK <mark>RG</mark> RKHKRQDASS	AENAGGEVKEASANEASLP	QSPEPVSASEANPSPSRRSR	GRGKKR RLNNES B	AGNORTSSPERS	RSRLHH
Ath_DEG10			M	ILLRSFRTVELLRRISTSSV	SGYRTSPSLL QRCNGFQSYL	PHRVTTTESPFPS	HISRFCSSQSAN	SQNENR
Ath_DEG11			MFFRPCV	HTVGRYSRARVPGLLSSLF	FYRSCNNVLTNSLPTVTTAG	RVSRYGYICRRSS	TSAAERGVFLPF	ALTCRR
At_DEG12				MVSRYSRALLP	TITIS	RIAT	IVL <mark>P</mark> F	ALTRGR
At_DEG13								
Ath_DEG14							MMNFLRR	AVSSSK
Ath_DEG16				MENQVNDISY			VSLIQV	NIVLNK
	200						370	

Ath_DEG15	MIEIMVEGQLKSEKEAPFWVPAQLLSL	VDVPVSSAALQSLIEASSGSKDS-GWDIGWSLVSAANGSQPSINIEHYS	KPLMQLDEPHNANFMAKSATR
Aly_DEG15	RIEIMVEGQLKSGEEAPFWVPAQLLSL	VDVPVSSAALQSLIEASSGSKDS-GWDVGWSLVSAANGSQPSTKIEHYS	KPLMQLDEPLNANFMAKSATR
Rco_DEG15	SMYQERWGMERVAEGSLDKGTSYWHTARLIRL	VDVAESSLALQSLVES <mark>S</mark> LGSLDH-GWEIGWSLASHDNGHRNSMDVIQTQVS	KAQVGESGNPTLVSKTSTR
Maes_DEG15	QIDVMLEEKLCLERDAEGSLDKGASSWFTAELIRL	VDIPLSSLAVQSLIES <mark>S</mark> SGTLDH-GWEVGWSLASYDSGPRNFMGVTQTQIED	G NI E FIEGQRHLGMGESGNTSLMSKKTTR
Potr_DEG15	QIDVMAEGKSDLRNGADGGLDKGTSHWLRAQVIRL	<mark>VDVPL</mark> SSLALQSLVEA <mark>S</mark> SGSMNH-GWEVGWSLASPENGSQSFMDVVQTQTEH	G NA <mark>SI</mark> AESQRRARE-ESSN <mark>P</mark> SINGKSTTR
Prpe_DEG15	QIDIMVEDEMRFHKDSE-DLDKGPPCWFAAQLLML	IDVPASAVALQSVIEASLSSPDH-GWEVGWSLASHGNAPQTQRNAP	FFVNLDCDSTSSVMDNQVDSAVGQLGNSSLTGKSTTR
Sly_DEG15	QIDILREGEIKLQNDLK-ESSKEGLNWLPAELLRV	<mark>VDIPV</mark> SSAAVQSLIE <mark>GS</mark> SSSIEH- <mark>GWE</mark> VGWSLAAYGNAHQSFINTKRRQVEQ	MEFPSQTPTVEAQSSLPSVIGTSTTR
Cusa_DEG15	QIDIMVEG ISRDSDVSK-TPHWHAAHLLAL	YDIPTSATALQSVMDASIDSLHQ-RWEVGWSLASYTNGSPSFRDSLRGQIEN	EKRT <mark>EVG</mark> SQKFLDLEGSSKNNDLTIR
G1ma_DEG15	QIDVMTEETNEKSNRGTPCWLLAQLLSL	VDIPASSNCLQSLIEASLGLPEH-EWESTRQSGPMRCSCFKCKGSFCEGSGGMLFIKLLFMG	LYLMIHAFGKVVSRKTLIVIMKDWLREDLAVQVLCTNHLLEWQFLVF
Migu_DEG15	QIDILMEDKSMM-DGNMEALPWLSAELLKM	VNIPQSSAAVQSLIEASCGSLEN-SWEVGWSLASHSRGPQNVLEGSR	
Vvi_DEG15a	QIDVMVEENNSE-EIDKKAPHWLPVQLLAL	LASYTGDSHTLVDAIQTQLTGIFVKLKAEADCLD	FLDGFRFSSGLKISLVYVEHQLEVDCNAKSSIEG-QRHFMVGDSSHPSLMGKSTAR
Vvi_DEG15b	QIDVMVEENNSE-EIDKKAPHWLPVQLLAL	LASYTGDSHTLVDAIQTQ	
Sobi_DEG15	RLDVLVEQGSAQDGKSGPPRWLPARLLAM	IADANQKQVENDTRADSALSLLRHEE-FIRRPTWDVGWSLADANQKQVENDTRCSLKS	NRNNASIESVDPLMLSKSATR
Zema_DEG15	RLDVFVEYELGNAQDGKSGPPRWLPARLLAM	VDVPTAAVSALSLLRHDDSFIRRPTWDVGWSLADANQKQVSLFIESKSSLES	NRNNSSLESVDSLMLAKSATR
Orsa_DEG15	HLDVLVEHEE SRNIGGG KTGAPRWLSARLLAILYFS	QQDSTVGLLVVDVQASADSVLSLLQHEGSLIRSSSWDVCWSLADVNQKQVDNDARYSLEC	NRKNAYAESTE <mark>PPMLA</mark> KSATR
Seit_DEG15	RLDVLVEHET LGNTRDGKSGPPQWLSARLLAM	LANVNEKQVENDIRSSPAS	NRNHASVESMDPLMLAKSATR
Brdi_DEG15	CLDVLVEHEELGNIIDGDSGAPQWLSAQLLAM		NRKNAYAESIEPSMLAKSATR
Phpa_DEG15	EVDILVEVP-DLSEKGSGYSGEHSVCWLPGQLLAV	VDVPAAGAALQDLLDVHGGSVKG-VWEVGWALAPVEDNAQQLH SLLTSEILTETQLQEDVAS	QHDLKGDKRPVAHAVAGVSRLGMAAAAATKIAVLSVGSHG
Popa_DEG15	MCNNNRQIKEEDIKSSNSGGSGGS	GSGQSIYNKSSDERIYDPLKDWIQCRFHQLIEVDQSIMDIVDLLKSYFVIGSSKS	LSLVLLKASSPLTVDP
Didi_DEG15	NTKNSIEKILSLINIDIILESDII	NIRNNVNEDYSDDKIYDPVNSWRSCKFIDYLSCSQKTINTLNQLKNHFILSNQSSG	FESSFGLIVLEINDKS <mark>SLI</mark> INRQQ
Dare_DEG15	SFKKKTKVFVDYTHFCANPTD	RRKTSRREAHLVMLINCLEFQDAFHKIFKGPENWDFYSGGLDT	RFLTWFALLKVP
Brf1_DEG15	TDRFNIEVIVRPRSEKGQPEASDRFLQPIQQPIPAATT -	AGGKLASELDSPPEKKCSAELLLLWRCIDFDDAVRKLMPKYDNWHFDEPPNNPADSRRDPSHQIEA	VQSCVKTDWMAEVSLSWFALLKLK
HsaTYSND1	SCRDDLRLHVQWAPTAAGPGGGAERGRPGLCTPQCASL-	EPGPPAPSRGRPLOPRLPAELLILLSCPAFWAHFARLFGDEAAEQWRFSSAARDD	EVSEDEEADQLRALGWFALLGVR
Mmu_DEG15	SC SDDLRLHVQWGPTAASPAGRADQELPGLCTPQCASLG	/LEPGAPSRARARPLOPPRPAOLLLLLSCPAFRSHFARLFGADAVDOWHFVSSAPDD	AVSEEEEEDQLRALGWFALLRVQ
Ath_DEG1	TLFLHSPPSSHLSFFNLSSSRSS	<mark>PISLYP</mark> IRSKR <mark>YF</mark> RILSKLSLNDNNRDDDDDTLHF TPF SAVK <mark>P</mark> FFLLC <mark>T</mark>	SVALSFSLFAAS <mark>P</mark> AVESASAFVVS <mark>T</mark> PKKLSVALSFSLFAASPAVESASAFVVSTP
Ath_DEG2	PPQKMAFKAFGSPKKEKKESLSDFSRDQQTDPAKI	HDASFLNAVVKVYCTHTAPDYSLPWQKQRQFTSTGSAFMIGDCKLLTNAHCVE	HDTQVKVKRRGDDRKYVAKVLVRGVDCDI
Ath_DEG3	NKLPPGKEVSSKDAKEKITTS	AIDLALNSVVKVFTVSSKPRLFQPWQITMQSESTGSGFVISGKKILTNAHVVA	NQTSVKVRKHGSTTKYKAKVQAVGHECDL
Ath_DEG4	SGTDAKQPEAAENVTSS	SIDFAVNSVVKVFTVYSMPSVLQPWRNWPQQESGGSGFVISGKKILTNAHVVA	DHIFLQVRKHGSPTKYKAQVRAIGHECDL
Ath_DEG5	IFNTLSPINQSKFVLACSGSN	HVDVIDRR-RRINIFGSSLALTSSLLGSNQQRLPMES	KEEEL
Ath_DEG6	PSLLRRRSSFNASLISRCCSSVS	DVDVARDAVVKIFSFSREPNVVQPWQT-TEKEYSSSGFAISGRRILTNAHVVG	DHLYLQVRKHGSPTKYKAEVKAFRYGCDLDHLYLQVRKHGSPTKYKAEVKAFRYGCDL
Ath_DEG7	SPVIDWQGRAVALNAGSKSSSASAFFLPLQRVVRALSFL	<mark>igksidsrtdkpkavhiprgtlomtflhkg</mark> fdeirrlglrseteqvvrhas <mark>ptg</mark> etgmlvvdsvvpsgpadkhl <mark>epgd</mark> vl	VRVNGTVLTGFLNLENLLDDGVGQILELEIERGGQPLSVSVSVQDLHSITPDHFLEVSGAVIHPLSYQQARN
Ath_DEG8	AMTSKPKEKKIPHYLRASTGSCHD	LC KYGKRQIPVEKPWRSETKKIFKKSLDDNLNETLKPGSEKMKKKVREVEKNEGT	DDSFEVIKREVVKYQASGVSSG
Ath_DEG9	SDTKNGDC SNGMIVSTTTES IPAAP SWETVV	KVVPSMDAVVKVFCVHTEPNFSLPWQRKRQYSSGSSGFIIGGRRVLTNAHSVE	HHTQVKLKKRGSDTKYLATVLAIGTECDI
Ath_DEG10	HTTLSSPVSSRRVNNRKISRRRKAGKELSISPAAD	AVDLALDSVVKIFTVETSPSYFLPWQNKSQRESMGSGFVISGRKIITNAHVVA	DHSFVLVRKHGSSIKHRAEVQAVGHECDLDHSFVLVRKHGSSIKHRAEVQAVGHECDL
Ath_DEG11	NIHSIHEDEKKLERWKKIEESHP	LDELVLDSVVKVFSNSTEYSKSKPWKTLDQKSSRGTGFAIAGRKILTNAHVVMAM	NDHTFVDVKRHGSQIKYKAKVQKISHECDL
At_DEG12	KIHTMSKDEEWWKKIRKSPP	VDELMLESVVEVFTDETKYSKVKPWQTLNQESYGGSGFAIAGKKLLTNAHVVEGM	NDHIFVHVKRHGSQVKYKAKVQKIAHECDL
At_DEG13			NHILVLVIKRGSPKKYKAEVKAIGRECDL
Ath_DEG14	RSELIRIISVATATSGILYASTN		EAPINDEKGVSVEASDSSS
Ath_DEG16	NIILWLGSATPRALR	DIDLAQDSVVKIFSFEREPNVVQPWQT-TEKEYSSSGFAISGRRILTNAHVVG	DHSYLQVRKHGSPTKYKAEVKAFG
		440	

Ath_DEG15	MAILGV-PLSLLGQPSMNF	ASSSSKGETLVALGSPFGILSPVNFF	NSVSTGSIANSYPSGS	-LKKSLMIADVRCLPGMEGAPVFA	KNGHLIGILIRPLROK	SGVEIGLVVP	WGAITTACSHLLLEEPSVE	GKASQWGSEVLSVKSD
Aly_DEG15	MALLGV-PLSLLGQPNMKF	ASSSSKGETLVALGSPFGILSPVNFF	NSVSTGSIANCYPSGS	LKKSLMIADVRCLPGMEGAPVFDI	KN <mark>GHLIGILIRPL</mark> RQ K M	R <mark>SGVEIQLVVP</mark>	WGAITTACSHLLLEEPSEA	GKASKWGSEALNVKSD
Rco_DEG15	IALLGV-SLNLKDLPIITI	SPSIIRGDSLLTVGSPFGVLSPVHFF	NSLEMGSVANCYPARS	-SNVSLVMADIRCLPGMEGAPAFG	EC GDFIGILT RPL RQKS	TGAEIQLVIP	WEATATACGDLLLKEP QNA	EEGIAINKENLNAVENAYS
Maes_DEG15	IAILGV-FLSLKVLPNIEI	PPSSRRGVSLLAVGSPFGVLSPVHFF	NSLSVGSIANCYPARS	-SNVSLLMADIRCLPGMEGGPVFGI	ONAHFIGILIRPLROKS	SSGAEIQLVIP	WEALATACSDLLLKEP QNA	EKGTHINKENLNAVGNACS
Potr_DEG15	VAILGV-FLHLKDLPNFEI	SASSERGEFLLAVGSPFGVLSPVHFF	NSLSVGSIANCYPPRS	-SDISLLMADIRCLPGMEGSPVFCH	ENSNFIGILIRPLRQKS	S <mark>SGAEIQLVIP</mark>	WEATALACSDLLLKEP QNA	EKGIHINKENLNAVGNAYS
Prpe_DEG15	IAILGVSLIS-KDVPNITI	SSSTKK <mark>GD</mark> FLVAVGSPFGVLSPVHFF	NSIS <mark>MG</mark> SIS <mark>NCYPP</mark> NS	-TYSSLLMADIRCLPGGEGGPVLNI	EHAQLIGILIRPLROK	F <mark>SGAEIQLVI</mark> S	WEALATACSDLLQKEPRYA	EKGIYY DKRNLNAVGKTFLADS
Sly_DEG15	IALLRVPSNPYEDPPPLKV	SPWSRRGDLLLAMGSPFGILSPSHFS	NSISVGTIANSYPPNS	-LNKALLIADIRCLPGMEGSPVLG	EHAELIGVLSRPLRQKA	ATAAEIQMVIP	WEATTSACASYLQEERQTG	RKIHFNNGNLISVKK-ESSSN
Cusa_DEG15	KDMPNISI	SPSRQRGSFLLAVGSPFGVLSPVHFL	NSLSVGSISNCYPPSS	-LSKSLIMADMRCLPGMEGCPVFDH	EKAR <mark>LIGVLI</mark> R <mark>PL</mark> VHYI	TGAEIQLLIP	WGAIATACSGLLLG-TCNV	GERIDNDNRCIGAVGNMAVNKE
G1ma_DEG15	YLSGYFLFLFILFSLLGFLLQTVIDLLDSKV	SAMNKRGDFLLAVGSPFGVLSPMHFF	NSISVGCIANCYPPHS	-SDGSLLMADIRCLPGMEGSPVFSH	EHACLIGVLIRPFRQKA	AY <mark>GAEIQLVIP</mark>	WDAIVTASSGLLHKRP QNT	QKGLCNQEGNLYAAGSVPFSDT
Migu_DEG15	YGPISDKN	IC PASNSFQIFLEFSEYFGGVSWQHLS		TKCLPGMEGSPVFSI	EHARFIGLLTRPLRQK	SGTEVQMVIP	WEAVASACSDLLQDDLHS	KKIDYNNGNLNTVGN-MLS
Vvi_DEG15a	IALLGVSSINSKDLPNIAI	SPSNKRGDLLLAMGSPFGVLSPVHFF	NSISVGSIANCYTPSP	-SRRSLLMADIRCLPGMEGGPVFNI	EHAQ <mark>LIGILT</mark> RPLRQK	IGGAEIQLVIP	WEALATACCDLLQKEVQNE	GEMKHYNRGNLNAVGKKYLFSG
Vvi_DEG15b	IALLGVSSINSKDLPNIAI	SPSNKRGDLLLAMGSPFGVLSPVHFF	NSIS <mark>VGSIANCYTP</mark> SP	-SRRSLLMADIRCLPGMEGGPVFNI	EHAQLIGILTRPLRQK	I <mark>GGAEIQLVIP</mark>	WEALATACCDLLQKEVQNE	GEMKHYNRGNLN
Sobi_DEG15	IAILGISTFNSNDARCINV	SVMQQRGDPLLIVGSPFGLMSPFHFF	NSISVGAVANCLPPCT	-VRSSLLMADIHCLPGMEGAPVFDH	RNSCLVGLLMNPLRQK	SSNIEVQLVIT	WDAICMEWNSKKLDEIGRA	PRELPNGKNTDSKSMELRHGYN
Zema_DEG15	IAILGISTSNLNDARRINV	SVMQQRGDPLLIVGSPFGLMSPFHFF	NSVS <mark>VGAVANCLPP</mark> CT	-ARSSLLMADMHCLPGMEGAPVFD	QNSCLVGLLMNPLTQKC	SSNIEVQLVIT	WDAICTEWNSKKLEEIERP	PRKLPNDKNTDSKSMELRHVYN
Orsa_DEG15	IAILGVSNLNSSNTRCINV	SLMQQRGDSLLIMGSPFGILSPVHFF	NSISVGVVANCLPPGT	-ARSSILLMADVHCLPGMEGAPVFDH	KNSCLVGMLMKPLRQRC	SSTEVQLVIT	WDAICNAWNSDKLERIGHP	PSELVDDKSSDCKYKESCVADK
Seit_DEG15	IAILGISTVNSNNERQIDV	SVMQHRGDPLLIAGSPFGLLSPFHFF	NSISVGAVANFLPPCA	-VRCSLLMADIQCLPGMEGAPVFDH	RNSCLVGLLMNPLRQK	SSSVEVQLVIT	WDAICTGWNNMKLVEIERE	PSKLPNDKNEESKMMELKHPDN
Brdi_DEG15	IAILGVSSLTSSNEIHINV	SPAPORGESLLVVGSPFGILSPFHFF	NSISVGAVANCLPPGA	-VRSSLLMADIHCLPGMEGAPVFDI	KNSCLVGMLMKPLRQRC	SSIQVQLVIT	WDGICTAWSSNKLEGIEQA	SNDLLDDKNADSKMVESCAMDN
Phpa_DEG15	DSSALNTCLKKRHQLSKVSNGLSKMPTGHVI	AEQKRRGDSLIAVGSPFGALSPLHFQ	NSVSVGIVSNLWPPTR	-GPPSILIMADVRCLPGMEGGPVFDH	ERGNLVGMLTRPLRQRO	GAAEVQLLT QDVTHFVAN	MHMQLVMTTDVLLPVLQRVGIN	VGVLCNTKSPDVQLQPSASAMLVENSSFET
Popa_DEG15	AIDQVRFAQ	STHIKTGERISIVASPFGFISPTIFL	NSVSSGIICNKIAARPY	-SHPSLFLTDARCLPGSEGAAVFNS	SR <mark>GEVIAIVTPPI</mark> RA <mark>K</mark> I	DEKT <mark>PFNLAS</mark> LLP	-THTFLEYLLKTDLVAK	
Didi_DEG15	IEHQQHQHRINSSVIIGN	ISVDVRS <mark>GNSVYVVGSPFGFISP</mark> TMFL	NSISNGIVCN		KDGLLIGFIAPPIRSK	NDKL <mark>PFTLSPVLP</mark>	-IHSFLPRIESQLSIYP	
Dare_DEG15	TSPNCPCKETIPWMKS	-GSLKKGCHVIACGSPFGGLCPDLFM	NTISKGIVSNLAGD	ENALILTDARCLPGTEGGGVFIS	SKG-GTSYLVGLIASPLCWKS	SE-EWIGLTLVCS	VHLILKNMLQTEGSIKETL	
Brf1_DEG15	ESEKGAESSAVVG	VEQAQIGSPVMAVGTPFGVLCPSVFM	NSLAKGIVCNTAGK	GGALILTDARCLPGTEGGPLLT	DR <mark>DG</mark> KWMLLGLVAAPLCWK	AN-EWIGLSLVCS	FHAVLDSLAHLVP	
HsaTYSND1	LGQEEVEEERGPAMAVSF	LGAVPKGAPLLVCGSPFGAFCPDIFL	NTLSCGVLSNVAG	PLILLTDARCLPGTEGGGVFT	AR PAGALVALVVAPL CWK	AG-EWVGFTLLCA	AAPLFRAARDALHRLPHST	
Mmu_DEG15	RG-AAAEERRGPVVTVAF	LGAVVKGAPLLACGSPFGAFCPDIFL	NTLSRGVLSNAAG	PILLTDARCLPGTEGGGVFA	AR PAGALVALVAAPL CWK	AR-EWVGLTLLCA	AAPLLQVARWALARLHPGS	
Ath_DEG1	QTDELATVRLFQENTP-SV	VYITNLAVRQDAFTLDVLEVPQ	GEGEG FVWDKQGHIVT	NYHVIRGASDLRVIL	ADQTTFDAKVVG-		FDQDKDVAVLR	
Ath_DEG2	ALLSVESEDFWKGAEPLRI	GHLPRLQDSVTVVGYPLGGDTISVTK	GVVSRIEVTSYAHGSS	DLLGIQIDAAINPGNSGGPAFNI	DQGECIGVAFQVYRSEI	ETENIGYVIPTTV	VSHFLTDYERNGKYTGYPC	
Ath_DEG3	AILEIDNDKFWEGMNPLEI	GDIPSMQDTVYVVGYPKGGDTISVSK	GVVSRVGPIKYSHSGT	ELLAIQIDAAINNGNSGGPVIM	NKVAGVAFESLCY-	-SDSIGYIIPTPV	IRHFLNAIEESGEDVSFGS	
Ath_DEG4	AILEIDNEEFWEDMIPLEI	GEIPSLDESVAVFGYPTGGDSVSITK	GYVSRVEYTRYAHGGT	TLLAIQTDAAINPGNSGGPAIIC	NKMAGVAFQKDPS	-ADNIGYIIPTPV	IKHFLTAVEENGQYGGFCT	
Ath_DEG5	EEEEERNVNLFQKTSP-SV	VYIEAIELPKTSSGDILTDEENGKIE	GTGSGFVWDKLGHIVT	NYHVIAKLATDQFGLQRCKVSLV	DAKGTRFSKEGKIVG-		LDPDNDLAVLK	
Ath_DEG6	AILGIDSEEFWEDINPLEI	GGIPFIGETVYALGYPRGGDTISVTK	SIVTRVEPOKYSHSSI	KMYVYTSGGSTNKFYSG	QINKKIYDGR			
Ath_DEG7	FRFPCGLAYVADPGYMLFRAGVPRHA	IIKKVANEDISSLGDLVSVLSKLSRG	AR <mark>VP</mark> LEYMSH T DRHRKK <mark>SV</mark> LV	TIDHHEWYAPPQLYTRNDSSGLWDA	AKPAIEPASVSPSIGNNGFP	ISQDISLCHHDTEPMHEVN	VRGVTDIAAIMETSSGDGSQND	FGSEAKKORVDEDSSDGIAANGSLYGSEFKSDDA
Ath_DEG8	MRKPEVLIISSCDETPVKQ	IKKKTTLSSKLKPSPDLGSRSSENVD.	ALK <mark>P</mark> KVLKKS <mark>Y</mark> SALT <mark>T</mark> SKPKV	NHEKVVAS PVLKPKMGKRNDGKDEI	OGKVKKGTVSSRVASKI	KAPVTPRASLSPR	LSVRLAGSSSLRKSQSLKA	
Ath_DEG9	ALLTVTDDEFWEGVSPVEF	GDLPALQDAVTVVGYPIGGDTISVTS	GVVSRMEILSYVHGST	ELLGLQIDAAINSGNSGGPAFNI	DKGKCVGIAFQSLKHEI	DAENIGYVIPTPV	IVHFIQDYEKHDKYTGFPV	
Ath_DEG10	AILVVDSEVFWEGMNALEL	GDIPFLQEAVAVVGYPQGGDNISVTK	GVVSRVEPTQYVHGAT	QLMAIQIDAAINPGNSGGPAIM	NKVAGVAFQNLSG	-AENIGYIIPTPV	IKHFINGVEECGKYIGFCS	
Ath_DEG11	AILEIDSDEFWKGMNPLEI	GDIPPLOEVVSVVGGENICITK	GLVLRVETRIYDYSDS	DLLSIQIDATINDENSGGPVIM	NKVVGVVYEIG	FVIPTPI	IKHFITSVQESRQYSCFGS	
At_DEG12	AILEIDSDEFWKGMNPLEF	GDIPPLNEIVYVVGYPKAGETICVTK	GVVTGVKTGNYLRSST	KLLTIHIDATTYGGNSGGPVIT	DKVLGVLFQILGD-	-KKSTGVVIPTPI	IRHFITGAEESSHNAVFGS	
At_DEG13	AILVIESKEFWEDMNPLEI	GDMPFLQESVNVIGYPTGGENISVT K	GVVSRIESMDYAHGAI	NLPAIQTDAAMNPGNSGGPVCIC	NKVVGVAFQTLGH	-SNNIGCLIPAPV	VKHFITGVEKTGQYVGFCS	
Ath_DEG14	KPSNGYLGRDTIA	NAAARIGPAVVNLSVPQGFHGISMGK	SIGSGTIIDADGTILT	CAHVVVDFQNIRHSSKGRVDV	TLQDGRTFEGVVVN-		ADLQSDIALVK	
Ath_DEG16	IFGARR	YTFIGETIYALGYPRDGDIISVTK	GIVTRVEPOKYAHSSI	EILTIQTDACINGGKSGGPVVM	NKVAGVVFENDSP	- <mark>S</mark> DK		
			50	0		720730	740	760

	protease domain *	plant specific loop within protease domain	protease domain *
Ath DEG15	ASIPACVAIEKAMESVCLITVNDGVWASGIILNEHGLILITNAHLLE	WRYGKGGVYGEGFKPYV-LGAEEFSSTGSKFWEOKSOT-LPRKAPRNHYSSYGENIREYKHNFLOTGHRD	IRVRLCHLDSWIWCPANVVYICKEOLDIALLOLEYVPG
Alv DEG15	TSIPACVAIEKAMESVCLITVNDGVWASGIILNEHGLILTNAHLLE	WRYGKGGVYGEGNDAGLKPYV-LGADEFSSTGGKVWECKSOT-LPRKAPANLYSAVGENI REYKHNFLOTGHRD	IRVRLCHLDSWTWCTANVVYICKEOLDIALLOLEYVPG
Rco DEG15	HESDGPFSYKYEHFNSHCSSTLPVEKVMASYCLITIDEGIWASGVLLNDOGLVLTNAHLLE	WRFGKTTINGGRNRTKSGALF-LPPEGSVIPGHSNVDSYRGSOMPLNKAKIMDSSVFDOTKGDOLSLSYSGHRN	IRVRLDHFNPWIWCDAKVIYVSKGPLDVALLOLEYVPD
Maes DEG15	HESDGPLCFEYEPLKTYCPSSLPVEKVKASYCLITIDEGVWASGVLLNDRGLIL/TNAHLLE	WRFGKTTASGGRNGTNSEAVF-LLPEESSFHGYSHVDNHKKSLR-FOPEAVKRMNSLVLDHSKGYOLNLSYKGHRN	IRVRLDHVNPWIWCDAKVVYVCKGPLDVALLOLEYVPD
Potr DEG15	SSSDGPFPLKHEHHISYCSSPPPVEKAMASICLITIDELVWASGVLLNDOGLILTNAHLLE	PWRFGKTTVNGGEDGTKLODPF-IPPEEFPRYSEVDGHEKTOR-IPPKTLNIMNSSVADESKGYKLSLSYKGPMN	IRVRLDHADPWIWCDAKVVHVCKGPLDVALLOLEHVPD
Prpe DEG15	HDSNGPITHIOEHLYSNCSSPSHIEKAIGSVCLITMDDGVWASGVFLNKOGLILTNAHLLE	WRFGKRTASDGKHGSNSEALSDGPVSPRHSELYGKOKGEG-FLPRIENNADLFVGDEYGGHKLSSSYRGHEN	RVRLDHTDPWTWCDAKVVYICKGPLDVSLLOLKHIAD
Sly DEG15	SIODGPINYTOEHLLTGSVPPSLIEKANTSICLITVDDGAWASGVLLNKOGLLLTNAHLLE	WREGKTSVNG YNT KSDVVF - TTSNOSEHPGDDKFT I HHRNKY - LLOKELKTPOFL VNNEOGSFRVNLANTSSRT	RVRLDFMDPWVWTNAEVVHVSRGPLDVALLOLOLVPD
Cusa DEG15	OKLEGGFSSIOESSGCSRPFPFKIEKAVASVCLVTMGEGIWASGVLLNSOGLILTNAHLIE	WRFGKTNVGGEKSIENAKLLO-SHTEHSPCSMNNSVFGGOEIGN-IEPNASKNGNILLHNOLEDNKLSFPNYGRRN	LHVRLSHAEPWIWCDAKLLYICKGSWDVALLOLEOIPE
Gima DEG15	DKLDVCSRNKHEHLYFGSSSPLPIEKAMTSVCLVTIGDGVWASGVLLNSOGLILTNAHLLE	WRFGKEHVNGGGYGTNSEKIS-SMLEGTAYVVN-RVESNOVSOTSPLKMPILYPFAANEOGGYKSSPTYDNHRN	IRVRLDHIKSWVWCDAKVVYVCKGPWDVALLOLESVPD
Migu_DEG15	KORILPOPVSPIEDAMNSICLITSDDGSWASGVLLNKQGLVLTNAHLLE	WRFGKTAAN AGYQLMCGHTNHRN	IRVRLDFMDPWMWSDAKIVYISKGPMDIALLQLEIVPH
Vvi_DEG15a	HDSDGPFNSMHQQPDCCSPPLSLIEKAMASICLVTIDDGVWASGVVLNSQGLILTNAHLLE	WRFGKTVARGGRCGAEPEIPF-IPSEESVYCRDEGTYSHQKSQD-LLPKTLKIAGSSVMDGHGGYKSSSTYRGHRN	IRIRLDHTDPRIWCDARVVYVSKGPLDIALLQLEFVPG
Vvi_DEG15b	AQPDCCSPPLSLIEKAMASICLVTIDDGVWASGVVLNSQGLILTNAHLLE	PWRFGKTSQDFSTYRGHRN	IRIRLDHTDPRIWCDARVVYVSKGPLDIALLQLEFVPG
Sobi_DEG15	YGRFVSSMVNKINQHCISPPLLREAISAVVLVTVSDTSWASGIVLNKRGLVLTNAHLLE	WRFGRTSPSDLQASFTGEHLNAGENK-SQPE-GKFSNEDAVNHNVSLFNLGFKREKR	ISVRLDHAERQIWCNASVVFISKGPLDVALLQIDKVPI
Zema_DEG15	YVRVFSSTDNKTNQHCISPRSLREAISAVVLVTVGDTSWASGIVLNKRGLVLTNAHLLE	PWRFGRTSPSDLQASFAGEHLNAGENK- <mark>SLQP</mark> QQGKISNEDAVKHKVSSFNLGFKRGK	ISVRLDHEERQIWCNASVVFISKGPLDVALLQIEKVPV
Orsa_DEG15	HRRFVPNSANNLNQYDVS-PSLTEAISSVVLVTVSETSWASGIILNKNGLIMTNAHLLE	PWRFGRTSPLGLQN	ISVRL <mark>DHG</mark> ERKTWCNASVVFISK <mark>GPLD</mark> VALL <mark>O</mark> ME <mark>KTP</mark> I
Seit_DEG15	YGRFVSSTVNKINQYCISSPSIREAISAVVLVTVGDSSWASGIVLNKGGLVLTNAHLLE	PWRFGRTSPLGAQ	ISVRLDHAERQVWCSASVVFISKGPLDVALLQMEEVPI
Brdi_DEG15	YRRSVSISANHHNQYRIP-ASLKEAISEVVLVKVGDTSWASGIVLNKNGLILTNAHLLE	PWRFGRTSPLGLQNEITSLTGEHVREVENK-LLQSQECKMSNQDAVKHEAPLFNLGFKREKR	ISVRL <mark>DHG</mark> KRQ T WCSASVVFISK <mark>GPLD</mark> VALLQL <mark>E</mark> MVAI
Phpa_DEG15	QPCRPGSIESHSTYQAMQYVPSAVERAVTSVVLITIGDGAWASGVILNKTGLILTNAHLLE	PWRFGKPRMVPSPVNGSIPKDEGFPLSCDESQEDLALNQLQEEEISKGVSTSRTSSWPTDVSQKNYGR	IRVRLDHRQPRSWHAARPVYVSQGPLDIALLQLESPPP
Popa_DEG15	PLISNSVLSLSPLQTSLSLLDRQKHNIVLVKFKDTWGSGVLISSNGYILTNAHILA	PSISALHKASNDSNNAVGYPAHMFKDYRVEIRVDYAALIG	KETIGGHMWYNGRIEYISHTHLDIALLKIVCDDS
Didi_DEG15	KYRLSNSLSVSCFDPIQQSVNDCQNSIVLVQFKNSWGSGVLISESGYILTNAHLII	PSIPLITNQTKQTKS <mark>SPQP</mark> FPIELYKDKKVDLR <mark>I</mark> SSNEIINNNGS	SSLHQSENSSFIWCKGTIEYISHTHLDIALIKIDQHDLSILLNDQKKHEP
Dare_DEG15	-TGVSSQLVNGSLQAPL-TANRGSGLELYPGVVLVETGWLWGSGVLLNQNLVLTCRHVVD	EKSELTVKVNS <mark>GG</mark> R	FHTVRGKVLYSSVVSSPYDIAIVELQEAFHTVRGKVLYSSVVSSPYDIAIVELQEAFHTVRGKVLYSSVVSSPYDIAIVELQEA
Brf1_DEG15	WPLIPAAAVIHSIQEPPHPALSQVEKSIVMIEAGEIWGSGVVVHVDESKVYLLICRHVIG	-SSS KVKVVMCHAQ	KVRVTGNVVYATPSESVYDLAVVEFPNP
HsaTYSND1	-AALAALLPP-EVGVPWGLPLRDSGPLWAAAAVIVECGTVWGSGVAVAPRLVVTCRHVSP	REAARVLVRSTT <mark>P</mark> K	SVAIWGRVVFATQETCPYDIAVVSLEED
Mmu_DEG15	-ASLSVLLPPPDVSTPRGLPLRDLGPPWAAAAVLVECGTVWGSGVVVAPRLVVTCRHVAP	REAA RVLV <mark>H</mark> SAT <mark>P</mark> K	NVAIWGQVVFATQETSPYDIAVVSLEEE
Ath_DEG1	IDAPKNKLRPIPVGVSADLLVGQKVFAIGNPFGLDHTLTTGVISG		LRREISSAATGRPIQDVIQTDAAINPGNSGGPLLDS
Ath_DEG2	IGVLLQKLENPALRECLKVPTN-EGVLVRRVEPTSDASKVLKEGD		VIVSFDDLHVGCEGTVPFRSSERIAFRYLISOKFAG
Ath_DEG3	INLTYQKMDNDQLRKDFKMSDKMTGILINKINPLSDVHKVLKKDD		IILAIDGVPIGNDSSVHFRKKERITFKHLVSMKKPC
Ath_DEG4	LDISYQLMENSQLRNHFKMGPEMTGILINEINPLSDAYKRLRKDD		IILAIDDVLIGNDAKVTFRNKERINFNHFVSMKKLD
Ath_DEG5	IETEGRELNPVVLGTSNDLRVGQSCFAIGNPYGYENTLTIGVVSG		LGREIPSPN-GKSISEAIQTDADINSGNSGGPLLDS
Ath_DEG6			
Ath_DEG7	METETTVLRDFEGATALSANASLAERAIEPALVMFEVHVPPSCSLDGVHSQHFFGTGIIIYHSS	INGLAVVDKNTVAISASDVMLSFAAF <mark>P</mark> VEI <mark>PG</mark> EVVFLHPVHNYALIAYNPSAMDPASASVIRAAELLPEPALQRGDS	VYLVGLSRNLQATSRKSIVTNPCAALNIGSADSPRYRATNMEVIELDTDFGSSFSG
Ath_DEG8	ASSSSRQNQKPRPVNRTDEFNKQLDDYPVEEKTLHVVEMETTNN		VVSENDQNQQGFVEPFLPPLPPTQSTPKDDECTVS
Ath_DEG9	IGIEWQKMENPDLRKSMGMESHQKGVRIRRIEPTAPESQVLKPSD		IILSFDGVNIANDGTVPFRHGERIGFSYLISQKYTG
Ath_DEG10	MGVSCOPMENGELRSGFOMSSEMTGVLVSKINPLSDAHKILKKDD		VLLAFDGVPIANDGTVPFRNRERITFDHLVSMKKPD
Ath_DEG11	LDLSYQSLENVQIRNHFKMSHEMTGILINKINSSSGAYKILRKDD		IILAIDGVPIGNDEKVPFQNKRRIDFSYLVSMKKPG
At_DEG12	LVLSCQSMKNAQIRNHFKMSPETTGILINKINSSSGAHKILRKDD		IILAIDGVPVLSEMRRISFNHFISMKKPD
At_DEG13	LNLSYQHMD-AQTRSHFKMNSEMTGILIYNINQHSDALNILKKYD		VILSIDGVAIENDGTVIIPNRERTRLDDLVSLKQLG
Ath_DEG14	IKSKTPLPTAKLGFSSKLRPGDWVIAVGCPLSLQNTVTAGIVSC		VDRKESDLGLGGKHREYLQTDCSINAGNSGGPLVN
Ath_DEG16			
	90	860	0

protease domain *

Ath_DEG15	EPAMLETTANVERGEFGPRCGLSPSICSGVVAVVHAKRELNTOSISGEVAEPAMLETTAVHPGGSGGAVINSS-GHMIGLVTSNARH-GAGTVIPHLANBIPCAVLAPIFKEAEL-MONTILIOTLOPSELSSIWALMPSLSPRTEQSL
Aly_DEG15	EPAMLETTAAVHPGGEGGAVLNES-GHMIGLVTENARH-GAGTLIPHLNPSIPCAULAPIFKEAEL-OPSEELEIVALMPSLEPKTEQSL
Rco_DEG15	HIPAMLETTAAVHPGGBGGAVINES-GRMIGL/VENAEH-GGGEVIPHLNPEIPCALLAPIPEFARG-TKUISLLQNLDRPNQQLSEVWALMPSLEHKPSPPL
Maes_DEG1	HIPAMLETTAVHPGGSGGAVINSE-GHMIGLITSNARH-GGGTVIPHLNPSIPCALLAPIPEPARD-LQDISLLVNLD-LPNQHLSSVWALMPSLSPKPSPHL
Potr_DEG1	HIPAMLETTAAVHPGGSGGAVVNSE-GHMIGLVTSKAKH-GGGTVIPHLNPSIPCAVLAPIFDFAKL-MRDISLLQNLDRPMEHLSSVAALMPPLSFKPSPPL
Prpe_DEG1	HISPIAKDESSESVGEKAVVVGHGLEGERCGESEESCSGVVAKVVGAKEPLSYOPNOPGHTQGHEPVMLETTAAVHPGGGGGAVINSD-GHMIGLVTENAEH-GGGTVIPHLNEEIPCAALLPIFKEAKG-MODISLLOVLDOPNKYISSVWALMPPVEPKPPPL
Sly_DEG15	ELCPITVDFMRPSPGSKAYILGHGLFGPRCDFLPBACVGAIAKVVEAKRPLLDQSCLGGNPAMLETTAAVHPGGSGGAVVNSE-GHMIALVTSNARH-GGGTVIPHLNFSIPCAALKPIFKFAED-WQDLLPLEYLDKPMEQLSEVWALTPPLSSKQSPSL
Cusa_DEG1	YPANLETTAXYPGGSGAVVNSE-GHMIGLYTSNARH-GRGVIPHLNFSIPCAALEPIHRFSKD-MEDLSVVKVLDEPNEQLSSYHKGDSLEYPANLETTAXYPGGSGGAVVNSE-GHMIGLYTSNARH-GRGVIPHLNFSIPCAALEPIHRFSKD-MEDLSVVKVLDEPNEQLSSIWALMSQRSPKPSYPANLETTAXYPGGSGGAVVNSE-GHMIGLYTSNARH-GRGVIPHLNFSIPCAALEPIHRFSKD-MEDLSVVKVLDEPNEQLSSIWALMSQRSPKPSYP
G1ma_DEG1	EHFPANLETTAAIHPGASGGAIINGD-GHMIGLFGPKHGFFPSVCSGVVAKVVEAKTPQSYLSVQPEHLHMHEHFPANLETTAAIHPGASGGAIINGD-GHMIGLVTSNARH-SGGAIIPQLNFSIPSAALAPIVNFSKA-MEDLSLLRILDEPMEYLSEVWALMRPSYPNPHPM
Migu_DEG1	· QlCPIVVDIDCPSPGSKAYVIGHGLFGP RCDFR PSACLGVIAKVIEAT RS PH NSSEQ PAMLETTAAVHPGSSGGAVVNS N-GHMIGLV TSNAKH-GGG TVIPHLNF S IPCAALEPILKFSKD-MQDITILEELEKPNEHLSEVWALMPPLYPKPDPVPDI
Vvi_DEG15	NDICPIIMDFACPSAGSKAYVIGHGLFGPRCDFFPSVCVGEVAKVVKSKMPLSCQSSLQENILEDFPAMLETTAAVHAGGSGGAVVNSE-GHMIGLITSNARH-GGGTVIPHLNFSIPCAALQAVYKFSKD-MQGMSLLLDLDKPNEHLSEVWALMPPL&PKPGPSLPML
Vvi_DEG15	»DICPIIMDFACPSAGSKAYVIGHGLFGPRCDFFPSVCVGEVAKVVKSKMPLSCQSSLQENILEDFPAMLETTAAVHAGGSGGAVVNSE-GHMIGLITSNARH-GGGTVIPHLNFSIPCAALQAVYKFSKD-MQGMSLLLDLDKPNEHLSEVWALMPPLSPKPGPSLPML
Sobi_DEG1	: ElNTIRPEFVCPTAGESVYVVGHGLFGPRSGLSSELE SGVVSKVVQIPSNQLSHLASALE TDH BLIPVMLQTTAAVHPGASGGVLVNEH-GLMVGIITSNAKH-GGGSTIPHLNFEIPCKLLVALFKYSAIGKLVILEQLDKPNEVLSEVWALAPESSPFV
Zema_DEG1	BINTIRPEFVCPTAGEPVTVVGHGLFGPRSGLHSELYSGVVSKVVQIPANQLSHLARA-EADBINVGLGTTAAVHPGAEGGVLVNTH-GLMVGIITSNAKH-GGGSTIPHLNFEIPCKLLVAVFEYSANGNLVVLEQLDKPNEVLSEVWALAPESSPFV
Orsa_DEG1	BLCAIRPEFVCPTAGESVYVVGHGLLGPRSGLSSELESGVVSKIVKIPSTQHSQLSSEVEVN
Seit_DEG1	ELNTIRPEFVCPTAGESVTVVGHGLFGPRSGLCSELESGVVSKVVQIPSTQLSHPSGTVEAHMDMPVMLQTTAXVHPGAEGGMLVNEH-GLMVGIVTSNAKH-GGGSTIPHLNFEIPCKELEIIFKYSENEEPAILEQLDKPMKVLSEVWALAPESSQFI
Brdi_DEG1	ElCAIRPEFICPTAGESVYVVGHGLLGPRSGLCSELESGVVSKIVKIPSAOHSHLSSSLEAETPMT PVMLQTTAAVHPGAEGGVLINEH-GRMVGLITSNAKH-GGGTTIPRLMFEIPCNELEMVFKYSANEDETILEQLDKPMELLSEVWALAQTPASLPFL
Phpa_DEG1	ASKAAMLQTTAAVHPGGSGGAVVSGE-GHNIGLVTSNARH-SGGTVIPFLNFSVP¥AALVPVFEFASSADSDWSRLEELDKPNDQLAAVWALVPPTPPRPSPPPFF
Popa_DEG1	
Didi_DEG1	·IKFQHVICNPILNPKYGESVFVLGYPLIPPTQNPPISVTKGIISNIVYVDNC
Dare DEG1	
Brf1 DEG1	
HsaTYSND1	LDDVPIPVPAEHFHEGEAVSVVGFGVFGOSCGPEVTSGILSAVVOVNGT
Mmu_DEG15	LIGVPTPVPAGHFHEGEPVSVVGFGVFGQACGPSVTSGILSAVVRVDGSPVMLQTTCAVHGGSSGGDLIGIVASNTRDINTGATYPHLNFSIPITVLQPALKQYSQ-TGDLGGLRELDHTTEPVRVVWRLQRPL
Ath_DEG1	
Ath DEG2	DIAEIGIIRAGEHKKVQVVLRPRVHLVPYHIDGGQPEYITVAGLVFTPLSEPLIEEECEDTIGLKLLTKARYEVARFRGEQIVILEQVLANEVNIGYEDMNNQQVLKFNGIPIRNIHHLAHLIDMCKDKVLVFEFED-NYVAVLEREASNSASLCILKDYGIPSEREADLEPYVDPIDD
Ath DEG3	ETALLKVLREGKEYEFNESLKSVPPLVPKRQYDKEASYYIFGGLVFLPLTKPYIDSSCVSESALGKMPKKAGEQVVIIEQILTEGILTGYSIFEDFQVKKVNGVQVHNLKHLVKLVEECCTETVRMDLEK-DKVITLDYKSAKKVTSKILKSLKIPSAVSEDLQPKQQNKRSK
Ath DEG4	ETVLLOVLRDGKEHEFHIMVKPVPPLVPGHOVDKLPSYVIFAGFVFVPLTOPVIDSTLICNCAIKYMPEKAGEOLVIIE
Ath_DEG5	YGHTIGVNWATFTRKGSGMESGVNFAIPIDTVVRWPYLIVYGTAYR-DRF-DRF-DRF-DRF-DRF-DRF-DRF-DRF-DRF-DR
Ath DEG6	
Ath_DEG7	ALTDEOGRIRAIWGSFSTOVKYSSTSSEDHQFVRGIPVWAISQVLEKIITGGNGPALLINGVKRPMPLVRILEVELVPGTDKRDGNGTTRVI
Ath DEG8	ETE EVENTEGSNEAESEEEEIGLSNGEKKPRAARKEGDSADEAARKLRFRRGTIVDP DTVGEKARKLKFRRGRGLGEDKAQDAQVRRSFKKREDIREEVNEDGEKVVLRHODVQEKDAQGLFNNVIEETASKLVEARKSKVKALVGAFETVISLQESEKARKLKFRRGRGLGEDKAQDAQVRRSFKKREDIREEVNEDGEKVVLRHODVQEKDAQGLFNNVIEETASKLVEARKSKVKALVGAFETVISLQES
Ath DEG9	DSALVKVLRNKEILEFNIKLATHKRLIPAHISCKPPSYFIVACFVFTYSVPYLRSEYCKEYEFDAPVKLLEKHLHAMACSVDEQLVVVSQVLVSDINICYEEIVNTQVVAFNCKPLKELEGACVVCCDEYMKFNLCY-DQIVVLDTKTAKEATLDILTTHCIPSAMSDDLKTEERN
Ath DEG10	ETALVKVLREGKEHEFSITLRPLOPLVPVHOFDQLPSYYIFAGFVFVPLTOPYLHEYGEDWYNTSP-RTICHRALKDLPKKAGQQLVIVSQVLMDDINTGYERLAELQVNKVNGVEVNNLRHLCQLIENCNTEKLRIDLDESRVIVLNYGSAKIATSLILKRHRIASAISSDLLIEQNLETEL
Ath DEG11	ORLADDINEGYOELYGAOVEKVNGVEVKNLKHLCELIECETEDLRLEFKN-HKVLVLNYESAKKATLOILEREKIKSVISKDICLPMLLDDPF
At DEG12	
At DEG13	
Ath DEG14	
Ath DEG16	
Sector Constants of Constants o	

	PTS	
Ath_DEG15	PNLPKLLKQDMFVKPTQDMFVKPT	709
Aly_DEG15	PNLPKLLKKLSRDVIPSKLKLSRDVIPSKL	713
Rco_DEG15	SNLPESLLDEVLRSSTRLGKVGSFSNEIBPSKL	729
Maes_DEG15	LNLPFSLV	756
Potr_DEG15	PSLPESILEKLFRGTPQLGKAKSISSVIIPSKL	752
Prpe_DEG15	PHMPESLRQDAFTKPTQLGKAGRLSNDAVPSKL	755
Sly_DEG15	LHLPILPREAMLKNATOLGKVERLPNKLVOSKLGDSNDDAKGSKFAKFIADC	753
Cusa_DEG15	PGLPQLLGREVLRKPTLHNEGERLLPSDIVRSKL	747
G1ma_DEG15	HDPPQSVTAGKEGVISKEVIASKL	794
Migu_DEG15	QKFPIERINKGTTKGSRFAKFIADRNELLNKTDERGMARSSFINDLIIPSKLFINDLIIPSKL	614
Vvi_DEG15a	PNLPOSIL	798
Vvi_DEG15b	PNLPQSLLNEVFKKPTQLGKVEMLANEIIPSKLEDNK-EGKGSRFAKFIAER	682
Sobi_DEG15	sss <mark>p</mark> e kgk e ekvlefs <mark>kfl</mark> sd <mark>k</mark> <mark>goal</mark> kstadlkelf <mark>r</mark> yk t psktyk t pskt	717
Zema_DEG15	RSS <mark>P</mark> QQALKSNVDLKELF <mark>R</mark> YK <mark>TPSKI</mark> YKTPSKI	722
Orsa_DEG15	sts <mark>p</mark> Qegl ksikd i eA FLR DRIPSKIDRIPSKIDRIPSKI	736
Seit_DEG15	DNPPQATLKSSTDLKELFKRMMPSKMRMMPSKM	722
Brdi_DEG15	SSS <mark>P</mark> QEGLKSRTDIEAFLKSRTDIEAFLKSRTDIEAFLKSRTDIEAFLK	760
Phpa_DEG15	RRHPRVPVSQE	1068
Popa_DEG15	LQPLQKQPPQTTGNGCNTENINSLMAKLRKYAEFLEKITNTPQTEAANCNTENINSLMAKL	662
Didi_DEG15	TISTSTSPIAGDNNNKLOSKLDNNNKLOSKL	679
Dare_DEG15	I08KL	521
Brf1_DEG15	KPILQSKI	569
HsaTYSND1		566
Mmu_DEG15	SEVPRSKL	568
Ath_DEG1		381
Ath_DEG2	TQALDQGIGDEPVSNLEIGFDGIVWA	607
Ath_DEG3	V <mark>P</mark> PKSKER	559
Ath_DEG4		436
Ath_DEG5		323
Ath_DEG6		215
Ath_DEG7	nwcgcvvqdphpavralgflpeeghgvyvtrwchgspahryglyalqwivevngkktpdlnafadatkelehgqfvrirtvhlngkprvltlkgdlhywptwelrfdpetalwrrnilkalq	1097
Ath_DEG8		507
Ath_DEG9		592
Ath_DEG10	ASCSAV	586
Ath_DEG11	kdnkinlipw <mark>svip</mark> lmfdfs	555
At_DEG12		491
At_DEG13	SSTRLY	410
Ath_DEG14		429
Ath_DEG16		198
	119012001210122012301240125012601270128012901300	

Figure S7. Sequence alignement of peroxisomal processing proteases from plants, animals and cellular slime molds and of DEG proteases in Arabidopsis used for construction of the phylogenetic tree (Fig. 7). The **CaM-binding domain** at the N-terminus of DEG15 from dicots and monocots (also boxed in red within the sequences), the protease domain in the plant, animal and cellular slime mold DEG15 with their catalytic triade His, Asp and Ser (*), the plant specific loop within the protease domain and the **PTS1** at the C-terminus are indicated above the sequences. Amino acids conserved among the sequences are coloured according to the *Clustal X Colour Scheme*: orange, G; yellow, P; green, T, S, N, Q; blue, W, L, V, I, M, A, F; cyan: H, Y; magenta: E, D; red: K, R. For accession numbers see supplemental Tab. S2A. Sequence alignments were obtained by ClustalX 2.0 [Thompson JD, Gibson TJ, Plewniak F, Jeanmougin F, Higgins DG (1997) The CLUSTAL_X windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. Nucleic Acids Res 25:4876-4882] and phylogenetic tree construction was performed by maximum likelihood using tree-puzzle-5.2 [Strimmer K, von Haeseler A (1996) Quartet puzzling: A quartet maximum-likelihood method for reconstructing tree topologies. Mol Biol Evol 13:964-969].

Figure S8: Amino acids of the entire beta-casein sequence (224 aa) including the presequence (amino acid residues 1-15) and the mature beta-casein (amino acid residues 16-224) with the AtDEG15 cleavage sites indicated by arrows.

MKVLILACLVALALA-RELEELNVPGEIVESLSSSEESITRINKKIEKFQSEEQQQTEDELQDKIHPFAQTQSLVYPFPGPIPNSLPQNIP PLTQTPVVVPPFLQPEVMGVSKVKEAMAPKHKEMPFPKYPVEPFTESQSLTLT;DVENLHLPLPLLQS;W;M;HQ PHQPLPPTVM;FPPQ;S;VLSLSQSKVLPVPQKAVPYPQRDMPIQAFLL;YQEPV;LGPVR;GPFPIIV

Beta-casein peptides obtained by cleavage with recombinant AtDEG15

aa-position beta-casein	pept	tide sequence
144-157	TD	OVENLHLPLPLLQS W
159-171	WM	IHQPHQPLPPTVM∥Ë
159-176	WM	IHQPHQPLPPTVMFPPQS∥V
160-171	М∥Н	IQPHQPLPPTVM F
160-175	МH	IQPHQPLPPTVMFPPQ S
160-176	МH	IQPHQPLPPTVMFPPQS V
208-217	LY	ZQEPVLGPVR G
213-224 C-term	V	_GPVRGPFPIÏV

Figure S9. *Dictyostelium discoideum* DEG15. XP_641938: The protein sequence as it is published in the database contains long repeat regions of N, Q and S that don't match the other cellular slime mold *Polysphondylium pallidum* DEG15 and would cause long gaps in the alignment of DEG proteins (Fig. S4). DiDi_DEG15: Protein sequence without the long repeat regions of N, Q and S as it was used for the alignment of DEG proteins.

>XP 641938

>DiDi DEG15

MVNNFSSNGSDFIYNYSNKFNLEEERIPNLRRSCCIVRVSGIDQSNGTNPNLQSTRSRSFSYSSNGKIIFSCSGF ILDLEKGLIITSPTIFLPFILQQQNDNKRNIMTESNITKNTKNSIEKILSLINIDIILESDIINIRNNVNEDYSD DKIYDPVNSWRSCKFIDYLSCSQKTINTLNQLKNHFILSNQSSGFESSFGLIVLEINDKSSLIINRQQIEHQQHQ HRINSSVIIGNSVDVRSGNSVYVVGSPFGFISPTMFLNSISNGIVCNCIQLFLIDARSLPGNEGSGVFNKDGLLI GFIAPPIRSKNDKLPFTLSPVLPIHSFLPRIESQLSIYPKYRLSNSLSVSCFDPIQQSVNDCQNSIVLVQFKNSW GSGVLISESGYILTNAHLIIPSIPLITNQTKQTKSSPQPFPIELYKDKKVDLRISSNSIINNNQSSSLHQSSNSS FIWCKGTIEYISHTHLDIALIKIDQHDLSILLNDQKKHEPIKFQHVICNPILNPKYGESVFVLGYPLIPPTQNPP ISVTKGIISNIVYVDNCAVSYQTTASVHSGNSGGGLFDLKGNFLGIVTCNAKQKNGLIITELNFSIPATSLIHFF HYANGTDEMGLNLMRSTSTDKFLKALWKLQITPPPLSNTNKNINNTNTISTSTSPIAGKKYSEFLTKMNDNNKI QSKL

Table S1. List of primers used in this study

Primer name	5'-3' sequence
Y2HDEG15fw	ACGTACGAATTCATGGATGTGTCTAAAG
Y2HDEG15rev	TGCATCGTCGACAGGGATCACATC
Y2HDEG15∆1/3N fw	TCGATCGAATTCAGTAGTAGTATCTCTC
Y2HDEG15Δ2/3N fw	TCGATCGAATTCGTCCCCTTAAGTTTAC
Y2HDEG15∆N fw	TCGATCGAATTCGCACAAGTGGCTATTG
Y2HDEG15N rev	AGCTAGGTCGACAACACCATCATTG
Y2HDEG15∆C rev	AGCTAGGTCGACTCAGGTGCCAAGACTGC
Y2HDEG15A25AS fw	GCATCGAATTCATGTTGAAGATGAGGAAGCATGC
Y2HDEG15Δ50AS fw	GCATCGAATTCATGCCAAGAGATATTTTTTTGAG
Y2HDEG15∆75AS fw	GCATCGAATTCATGTTGACCGTTGCATCTGTTG
Y2HDEG15∆100AS fw	GCATCGAATTCATGGTGAAGCTTATTCCGGGTGC
Y2HCAM fw	ACGTACGAATTCATGGATCAAGCGGAGC
Y2HCAM rev	TGCATGGTCGACTCCTAAGGCGGC
Y3HCAM fw	AAGGTGGCGGCCGCATGGATCAAGCGGAGCTTGC
Y3HCAM rev	CCCGAAGATCTTTACAAGTTTGATCCTAAGGCG
pETDEG15fw	CGATCGATCGAATTCTGGATGTGTCTAAAGTTGTCAGC
pETDEG15rev	CCTTAGCTCGAGTCATAACTTGCTAGGGATCACATCACG
pETDEG15Δ1/3N fw	CGATCGATCGAATTCAGTAGTAGTATCTCTCAGGATCCGG
pETDEG15Δ2/3N fw	CGATCGATCGAATTCGTCCCCTTAAGTTTACTGGGTCAACC
pETDEG15ΔN fw	CGATCGATCGAATTCTGGGCTTCTGGTATTATTCTTAACG
pETDEG15∆loop fw	CACCTCAGGAGCTCCTCAAGCAGGTGAGCATTTG
pETDEG15∆loop rev	CGATCGATCGAGCTCGGGCATAGAGACATACGTGTGCG
pETDEG15∆C rev	CTCAGCTCGAGTCATAACTTGCTACATGGGATGCTGAAGTTGAGATGCGG
pETCML3 fw	ATCGATCGAATTCATGGATCAAGCGGAGCTTGC
pETCML3 rev	CCTTAGGTCGACCAAGTTTGATCCTAAGG
pCAMBIA fw	CGATCGATCAGATCTATGGGCAGCAGCCATCATCATC
pCAMBIA ∆C rev	CCTCAGCACGTGCTCGAGTCATAACTTGCTAGGGATC
pCAMBIA rev	CCTCAGCACGTGCTCGAGTCATAACTTGCTACATGG
pCAMBIA CML3-bd fw	ACTGACCATGGACATGGATGTGTCTAAAG
pCAMBIA CML3-bd rev	TCAGTAGATCTAACTTTGGATCAGGGCC

fw, forward; rev, reverse.

Denotation	Organism	Accession-Nr.	Localization	Domain-structure
Ath_DEG15	Arabidopsis thaliana	NP_174153	SKL (peroxisome)	no PDZ-domain
Aly_DEG15	Arabidopsis lyrata	XP_002893523	SKL (peroxisome)	no PDZ-domain
Rco_DEG15	Ricinus communis	XP_002509448	SKL (peroxisome)	no PDZ-domain
Potr_DEG15	Populus trichocarpa	XP_002305124/POPTR_4s04650	SKL (peroxisome)	no PDZ-domain
Cusa_DEG15	Cucumis sativus	Cucsa046320	SKL (peroxisome)	no PDZ-domain
Glma_DEG15	Glycine max	Glyma13g31080	SKL (peroxisome)	no PDZ-domain
Migu_DEG15	Mimulus guttatus	mgf007197	SKL (peroxisome)	no PDZ-domain
Prpe_DEG15	Prunus persica	ppa001854	SKL (peroxisome)	no PDZ-domain
Maes_DEG15	Manihot esculenta	4.1_003779m + 4.1_018442m.g	SKL (peroxisome)	no PDZ-domain
Vvia_DEG15	Vitis vinifera	XP_002273997	SKL (peroxisome)	no PDZ-domain
Vvib_DEG15	Vitis vinifera	CBI30593	SKL (peroxisome)	no PDZ-domain
Sobi_DEG15	Sorghum bicolor	XP_002441322	SKI (peroxisome)	no PDZ-domain
Zema_DEG15	Zea mays	GRMZM2G162699	SKI (peroxisome)	no PDZ-domain
Orsa_DEG15	Oryza sativa	EEE64231	SKI (peroxisome)	no PDZ-domain
Seit_DEG15	Setaria italica	SiPROV003192	SKM (peroxisome)	no PDZ-domain
Brdi_DEG15	Brachypodium distachyon	Bradi2g21020	SKI (peroxisome)	no PDZ-domain
Phpa_DEG15	Physcomitrella patens	XP_001775762	SRL (peroxisome)	no PDZ-domain
Popa_DEG15	Polysphondylium pallidum	EFA82668	AKL (peroxisome)	no PDZ-domain
Didi_DEG15	Dictyostelium discoideum	XP_641938	SKL (peroxisome)	no PDZ-domain
Darer_NP_001	Danio rerio	XP_690168	SKL (peroxisome)	no PDZ-domain
Brfl_DEG15	Branchyostome floridae	XP_002609926	SKI (peroxisome)	no PDZ-domain
HsaTYSND1	Homo sapiens	NM_173555	SKL (peroxisome)	no PDZ-domain
Mumu_NP082188	Mus musculus	XP_125636 XP_002509448	SKL (peroxisome)	no PDZ-domain
Ath_DEG1	Arabidopsis thaliana	XM_002667490	chloroplasts	1 PDZ-domain
Ath_DEG2	Arabidopsis thaliana	AF245171	chloroplasts	1 PDZ-domain, elongated C-terminus
Ath_DEG3	Arabidopsis thaliana	NM_105236	mitochondria	1 PDZ-domain, elongated C-terminus
Ath_DEG4	Arabidopsis thaliana	NM_105237	mitochondria	1 PDZ-domain, elongated C-terminus
Ath_DEG5	Arabidopsis thaliana	NM_117947	chloroplasts	truncated, no PDZ-domain
Ath_DEG6	Arabidopsis thaliana	NM_103994	chloroplasts	no PDZ-domain
Ath_DEG7	Arabidopsis thaliana	NM_111209	nucleus (?)	2 protease-domains (1 inactiv), 4 PDZ-domains
Ath_DEG8	Arabidopsis thaliana	NM_123346	chloroplasts	1 PDZ-domain
Ath_DEG9	Arabidopsis thaliana	NM_123384	chloroplasts	1 PDZ-domain, elongated C-terminus
Ath_DEG10	Arabidopsis thaliana	NM_123053	mitochondria	1 PDZ-domain, elongated C-terminus
Ath_DEG11	Arabidopsis thaliana	NM_112526	mitochondria	1 PDZ-domain, elongated C-terminus
Ath_DEG12	Arabidopsis thaliana	NM_112527	mitochondria	1 PDZ-domain, elongated C-terminus
Ath_DEG13	Arabidopsis thaliana	NM_123420	unknown	1 PDZ-domain, elongated C-terminus
Ath_DEG14	Arabidopsis thaliana	NM_122648	mitochondria	1 PDZ-domain
Ath_DEG16	Arabidopsis thaliana	NM_148132	chloroplasts	1 PDZ-domain, elongated C-terminus

Table S2A: DEG proteases from plants, animals and cellular slime molds for alignement (Fig. S7) and phylogenetic tree (Fig. 7)

Denotation	Organism	Accession-Nr.	encoded protein	catalytic aa	PTS1
Metr_DEG15	Medicago trunculata	Medtr2g017690	608 aa	His-Asp-Ser	truncated
Metr_DEG15	Medicago trunculata	Medtr2g017700	194 aa	truncated	truncated
Aqco_DEG15	Aquilegia coerulea	AcoGoldSmith_v1.004744m.g	461 aa	His-Asp-Ser	SKL
Capa_DEG15	Carica papaya	evm.TU.supercontig_373.8	502 aa	His-Asp-Ser	SKL
Potr_DEG15	Populus trichocarpa	POPTR_0011s05510	729 aa	His-Asp-Ser	SKL
	Volvox carteri f. nagariensis	XP002956349	1088 aa	Asp-Ser	SRL
	Micromonas sp. RCC299	XP002505560	708 aa	Asp-Ser	SKL

Table S2B: DEG15 proteases from plants (truncated sequences) and peroxisomal proteases from green algae