

Extra

Functional characterization of a tomato syntaxin involved in powdery mildew resistance

Table S1 Average disease index (DI) scores visually assigned to 11 and four T₂ families obtained after transforming the *Slmlo1* line with the RNAi::*SlPEN1a* and RNAi::*SlPEN1b* constructs. In addition, the average DI scores assigned to the susceptible tomato MoneyMaker and the resistant *Slmlo1* line are listed. NPTII(+) and NPTII(-) indicate T₂ plants carrying the corresponding RNAi construct (+) or not (-).

Family label	Average DI score $\pm$ st dev	Average	Average
		DI score $\pm$ st dev NPTII(+)	DI score $\pm$ st dev NPTII (-)
RNAi:: <i>SlPEN1a</i> _I	1.49 $\pm$ 0.52	1.73 $\pm$ 0.32	0.75 $\pm$ 0.17
RNAi:: <i>SlPEN1a</i> _II	1.11 $\pm$ 0.39	1.22 $\pm$ 0.32	0.5 $\pm$ 0
RNAi:: <i>SlPEN1a</i> _III	0.91 $\pm$ 0.29	1.06 $\pm$ 0.28	0.75 $\pm$ 0
RNAi:: <i>SlPEN1a</i> _IV	0.84 $\pm$ 0.34		
RNAi:: <i>SlPEN1a</i> _V	0.47 $\pm$ 0.11		
RNAi:: <i>SlPEN1a</i> _VI	0.52 $\pm$ 0.16		
RNAi:: <i>SlPEN1a</i> _VII	0.89 $\pm$ 0.26		
RNAi:: <i>SlPEN1a</i> _VIII	0.69 $\pm$ 0.16		
RNAi:: <i>SlPEN1a</i> _IX	0.76 $\pm$ 0.26		
RNAi:: <i>SlPEN1a</i> _X	0.59 $\pm$ 0.12		
RNAi:: <i>SlPEN1a</i> _XI	0.54 $\pm$ 0.09		
RNAi:: <i>SlPEN1b</i> _I	0.95 $\pm$ 0.27	1.06 $\pm$ 0.28	0.78 $\pm$ 0.16
RNAi:: <i>SlPEN1b</i> _II	0.82 $\pm$ 0.31	0.95 $\pm$ 0.35	0.65 $\pm$ 0.22
RNAi:: <i>SlPEN1b</i> _III	0.8 $\pm$ 0.3		
RNAi:: <i>SlPEN1b</i> _IV	0.82 $\pm$ 0.14		
MoneyMaker	3		
<i>Slmlo1</i>	0.62 $\pm$ 0.35		

Table S2 Residues under significant negative selection in SYP1b syntaxins. Residue numbers refer to amino acid position in the AtPEN1 protein. DN-dS values, corresponding p-values and residue position with respect to characteristic syntaxin domains (the three helix domain Ha-Hb- Hc, the Qa-SNARE domain and the membrane-spanning (MS) domain are reported.

Corresponding residue in AtPEN1	dN-dS	p-value	Domain
F5	-3.15883	0.06131	-
S8	-3.1351	0.02213	-
F9	-3.28782	0.09351	-
N43	-3.52804	0.05074	Ha
L44	-2.54257	0.05726	Ha
D50	-3.83057	0.01861	Ha
V51	-3.1351	0.01235	Ha
E52	-3.00033	0.03562	Ha
L58	-2.94697	0.01581	Ha
E73	-2.94552	0.03696	Ha
H79	-3.83057	0.01861	Ha
N80	-3.52804	0.05074	-
A81	-2.35132	0.03704	-
V84	-3.1351	0.01235	-
R88	-3.87355	0.01415	Hb
K90	-3.21478	0.06364	Hb
V95	-2.35132	0.03704	Hb
A98	-3.1351	0.01235	Hb
E110	-4.49517	0.00675	Hb
L112	-2.69996	0.02732	Hb

R114	-2.95551	0.01719	Hb
N116	-3.83057	0.01861	Hb
R120	-2.46381	0.03418	Hb
G124	-2.8307	0.04851	Hb
G126	-2.35132	0.0434	-
P127	-3.1351	0.01235	-
G128	-2.35132	0.03841	-
R133	-2.8257	0.02516	Hc
R135	-2.39318	0.07344	Hc
T136	-2.35132	0.03704	Hc
G141	-2.35132	0.03868	Hc
L142	-2.48174	0.03486	Hc
L146	-1.80166	0.08323	Hc
D148	-3.33705	0.05724	Hc
F153	-3.83057	0.01861	Hc
R157	-2.39325	0.07349	Hc
Y164	-3.83057	0.02885	Hc
V168	-2.35132	0.03704	-
T174	-2.35132	0.03704	-
V175	-2.35132	0.03704	-
T176	-2.35132	0.03704	-
P180	-2.35132	0.03704	-

L188	-2.21353	0.04439	-
T191	-3.1351	0.01235	-
G192	-3.1351	0.01249	-
E193	-2.58975	0.09884	-
E195	-2.93078	0.03733	-
F197	-3.08635	0.06377	-
L198	-2.18715	0.05751	-
A201	-2.35132	0.03704	-
I202	-2.77566	0.03544	-
E204	-2.9842	0.03601	-
G206	-2.35132	0.04295	-
I217	-2.27694	0.05266	-
E219	-2.92783	0.03741	-
R220	-1.6729	0.09756	-
L231	-2.45666	0.06387	Qa SNARE
E233	-4.49517	0.00675	Qa SNARE

L234	-2.95785	0.01765	Qa SNARE
Q236	-2.94552	0.04219	Qa SNARE
F238	-3.83057	0.01861	Qa SNARE
L244	-2.13677	0.06406	Qa SNARE
V245	-3.1351	0.01235	Qa SNARE
E246	-3.45719	0.06013	Qa SNARE
G249	-2.35132	0.04494	Qa SNARE
Q251	-2.92688	0.04273	Qa SNARE
L252	-2.24543	0.04253	Qa SNARE
I255	-2.22416	0.05519	Qa SNARE
E256	-2.93077	0.03733	Qa SNARE
V259	-2.35132	0.03704	Qa SNARE
R261	-2.64477	0.03867	Qa SNARE
A262	-2.35132	0.03704	Qa SNARE
G269	-2.35132	0.04325	Qa SNARE
L273	-3.09493	0.0138	Qa SNARE

R277	-2.82596	0.0199	Qa SNARE
R284	-2.12025	0.06354	-
C288	-3.49295	0.06064	Membrane-spanning

Table S3 Distribution of *Arabidopsis thaliana*, *Oryza sativa*, *Populus trichocarpa* and *Solanum lycopersicum* syntaxins in subfamilies.

SNARE type	SNARE subfamily	<i>A. thaliana</i>	<i>O. sativa</i>	<i>P. trichocarpa</i>	<i>S.lycopersicum</i>
Qa SNARE	SYP1	9	7	11	10
	SYP2	3	3	3	5
	SYP3	2	1	3	2
	SYP4	3	1	3	2
	SYP8	1	2	2	2
	tot	18	14	22	21

AtPEN1	1	MN-----	DLFSS	SFSRFRSGEPSRRDVAGGGD-GVQMANPAGST
VvPEN1	1	MN-----	DLFSG	SFSRFRSEEPPTS-----VEMTS---ST
HvROR2	1	MN-----	NLFSS	WKRA---GAGGDGDLESGGG-GVEMTAPPGAA
SlPEN1a	1	MN-----	DLFSG	SFSRFRNEEQSPNQESAG-----IQMRQ---QT
SlPEN1b	1	MN-----	DLFSG	SFSRYR--ENDHDQDSHG-----IEMGD---T
AtSYP122	1	MN-----	DLLSG	SFKTSVADGSSPPHS-----H-NIEMSKAKVSG
AtSYP124	1	MN-----	DLFSS	SFKKYTDLKQQAQMD-----DIESGK----
AtSYP123	1	MN-----	DLISS	SFKRYTDLNHQVQLD-----DIESQNVSL--
AtSYP111	1	MN-----	DLMTK	SFMSYVDLKKAAMKDMEAGPDFDLEMAS---T
AtSYP131	1	MN-----	DLLKG	SLEFSRDR---SNRS-----DIESG-HGPGN
AtSYP125	1	MN-----	DLFSN	SFKK-----NQAQLG-----DVEAGQ----
AtSYP132	1	MN-----	DLLKG	S--FELPRGQSSREG-----DVELGEQ---Q
AtSYP112	1	MN-----	DLMTK	SFLSYVELKKQARTDMES--DRDLEKGEDFNFD
Solyc12g005580	1	MN-----	DLFSN	SFKKYQDLKKQTEVD-----DLEGGQDGQ-P
Solyc10g008570	1	MN-----	DLFSP	SLKKYQDLKQQVQMD-----DLELGTGGTGTP
Solyc10g081580	1	MN-----	DLLND	DDNFDA PRHQSNRNG-----DVEMGIQIPMN
Solyc01g056810	1	M-----		
Solyc07g052470	1	MN-----	DLLAD	S-SFIAGKDNASKES-----DIEMGNRFTRS
Solyc06g053760	1	MN-----	DLMTK	SFTSYIDLKKAAMKDVEASPD--LEMGM---T
Solyc02g085090	1	MN-----	DLMTK	SFLSYMELKKQAHL DLET--ERDLEMGO-----
Solyc01g109750	1	M-----	TKSFL	SYVELKKQAMMDVEA--GPD IEMGO-----
Solyc06g062360	1	MSFQD-----		LESGRS---V
Solyc11g066910	1	MSFQD-----		LDSGRS---S
Solyc08g005200	1	MSFQD-----		LESGRP---L
Solyc08g076540	1	MSFQD-----		LEAGRP---L
AtSYP22	1	MSFQD-----		LESGRG---R
AtSYP23	1	MSFQD-----		LEAGRGRSLA
AtSYP21	1	MSFQD-----		LEAGT---R
Solyc06g072760	1	MSFED-----		LES GSSLYVQ
AtSYP41	1	MATRN	RTLLFRKYRNSLR SVRAPLSSSS-----LTGTRSG-GVG PVIEMASTSLLN	
AtSYP43	1	MATRN	RTLLFRKYRNSLR SVRAPMGSSSSSSTLTEHNSLTGAKSG--LGPV IEMASTSLLN	
Solyc01g100170	1	MASRN	RTL VFRKYRDALRSVRIPAGSS-----TSTSSGHGSGPVI ELATTSLLN	
AtSYP42	1	MATRN	RRTVYRKHRDACKSARAPLSLSA-----SDSFGGPV IEMVSGSFSR	
Solyc09g075530	1	MATRN	RIRVFQSYRDTLNENRIPFTTSKDS-----GGPVIEMATT SFLN	
Solyc03g033850	1	M-----		
Solyc04g071730	1	MS-----		
AtSYP81	1	MS-----		
AtSYP31	1	M-GS---	TFRDRTVELH-----SLSQTLKKI	
Solyc07g054140	1	M-ASSG	AWTYRDRTSEFA-----SLSKTLKKI	
AtSYP32	1	MSARH	GQSSYRDRSDEFF-----KIVETLRRS	
Solyc08g067910	1	MPVKV	ASASLRDRTQEFQ-----SIAERLKKS	

AtPEN1	40	G---GVNLDKFFEDVESVKEELKE-----LDRLNETLSSCHEQS
VvPEN1	28	A---GVNLDKFFEDVESIKEELRE-----MESLQQKLHDAHEQS
HvROR2	37	A---GASLDRFFEDVESIKDDLRE-----LERIQRSLHDGNESEG
SlPEN1a	33	G---GVNLDKFFEDVETIKDELKE-----LEKIHTQLHNSHEQS
SlPEN1b	30	G---GVNLDKFFEDVEAIKDELDKN-----LEKIYAQLQSSNEKS
AtSYP122	35	GSCHGGNNLDTFFLDVEVVEDLKE-----LDRLCHNLRSSNEQS
AtSYP124	29	---E-TMNLDKFFEDVENVKDNMKG-----VETLYKSLQDSNEEC
AtSYP123	32	---D-SGNLDEFFGYVESVKEDMKA-----VDEIHKRLQDANEES
AtSYP111	37	KADKMDENLSSFLEEA EYVKAEMGL-----ISETLARIEQYHEES
AtSYP131	30	SG---DLGLSGFFKKVQEIEKQYEK-----LDKHLNKLQGAHEET
AtSYP125	24	---E-TMNLDKFFEDVENVKDDMKG-----VEALYKKLQDSNEEC
AtSYP132	29	GG---DQGLDEFFKKVQVIDKQYDK-----LDKLLKKLQASHEES
AtSYP112	39	FSPADEENL SGFFQEIEETIKTLIEE-----ITHLLLDLQNLNEET
Solyc12g005580	33	G-TE-SIDLAKFFEDVENVKEDMKD-----VEKFHKKLQESNEES
Solyc10g008570	34	SHNE-SIDLAKFFEDVENVKEDMKE-----VEKLHKRLQDSNEES
Solyc10g081580	34	SG---ELGLDDFFKKVQYIEKQYGR-----LNELLQKLQDAHEES
Solyc01g056810	2	-----LALSLIDAHEES
Solyc07g052470	33	QS---DSGLDSFNKQIQEIEKQYDR-----LSGLLKTLKDANEET
Solyc06g053760	35	Q---MDQNLTAFLAEA EKVKLEMNS-----IKEILRRLQDTNEES
Solyc02g085090	34	LSRTDEDNLSNFFRETEAVKGD IQE-----ITNLLMDLQNLNEET
Solyc01g109750	30	LDPTDERNLSKFFEEVAVIKSD MEE-----INNLLVLNLQDLNRKT
Solyc06g062360	13	GPRRGFM-----NG-KQ-----DTTQAVA
Solyc11g066910	13	GPRRSNV-----NG-KQ-----DATQALA
Solyc08g005200	13	GSRRFQT-----NG-KQ-----DPTQAVA
Solyc08g076540	13	GPRRGYM-----NG-KQ-----DPTQAVA
AtSYP22	13	STRKFN-----GG-RQ-----DSTQAVA
AtSYP23	16	SSRNING-----GGSRQ-----DTTQDVA
AtSYP21	12	SPAPNRF-----TGGRQ-----QRPS-SRGDPSQEVA
Solyc06g072760	16	GGSRWE-----RQTTQ-----AITNPSASDNRSIV
AtSYP41	51	PNRS-YAPISTEDP-GTS-SKGAIT-----VGLPPAWVDVSEEIS
AtSYP43	59	PNRS-YAPVSTEDP-GNS-SRGTIT-----VGLPPDWVDVSEEIS
Solyc01g100170	50	PNRS-YAPLSTEDP-GTS-SNGPVT-----VGLPPAWVDLSDEIT
AtSYP42	47	SNHSSYAPLNSYDP-GPS-SSDAFT-----IGMPPAWVDDSEEIT
Solyc09g075530	45	SNRS-YAPLSTEDDLGPSTSRDAFT-----LGLPPAWVDVSEEVA
Solyc03g033850	2	-----HKPRQRLGFTRA AI
Solyc04g071730	3	-----KVRDRTEDFKDV AHRSA LSLGYDESKTAALLASFIMHKPRQKSGFTRAAL
AtSYP81	3	-----RFRDRTEDFKDSVRNSAVSIGYNESKVASTMASFIIHKPKERSPF TKA AF
AtSYP31	23	-GAIPSVHQ-----DEDDPASSKRS-----SPGSEFNKKASRIGLGIKETSQKITRLAK--
Solyc07g054140	27	AGTTGSDHE-----PQQNSASSTTKVLQIPDRSEFNKKASRIGLTIHQTFQKIDRLAK--
AtSYP32	28	IAPAPAAANNVPYGNRNDGARRED----LINKSEFNKRASHIGLAINQTSQKLSKLAKRI
Solyc08g067910	28	FS---SVQNGSISTSTSSGSRSEEQRTTIAMQSEFNRRASKIGFGIHQTSQKLAKLAK--

AtPEN1	76	KT L HN A KAVKD--LRSKMD-----GDVGV--AL K KAKMIKV K LEAL-----DR
VvPEN1	64	KT L HNANSVKE--LRSRMD-----SHVSL--AL K KAKLIKRL E AL-----DR
HvROR2	73	KSLHDASAVRA--LRSRMD-----ADVAA--AI K KAKVVKLRL E SL-----DR
SlPEN1a	69	KT L HNAKNVKD--LRKKMD-----NDVSL--AL K KAKFIKVRL E AL-----DR
SlPEN1b	66	KT L HNAKAVKD--LRSKMD-----DDVSL--AL K KAKFIKVRL E AL-----DR
AtSYP122	75	KT L HNANAVKE--LKKKMD-----ADVTA--AL K TARRLKGNL E AL-----DR
AtSYP124	65	KTVHNAKKVKE--LRAKMD-----GDVAQ--VLKRVKMIKQKLEAL-----EK
AtSYP123	68	KTVHDSKAVKK--LRARM-----SSVTE--VLKRVKMIKTKLVAL-----EK
AtSYP111	77	KG V HKAESVKS--LRNKIS-----NEIVS--GLRKA S IKSKLEEM-----DK
AtSYP131	67	KAVTKAPAMKS--IKQRME-----RDVDE--VGRISRFIK G KIEEL-----DR
AtSYP125	60	KTVHNAKKVKE--LRAKMD-----GDVAM--VLKRVKIIKQKLEAL-----EK
AtSYP132	66	KSVTKAPAMKA--IKKTME-----KDVDE--VGS I ARFIK G KLEEL-----DR
AtSYP112	79	KSTHSTKIIRG--LRDRME-----SNIVT--ISRKANTVKT L IETL-----EK
Solyc12g005580	71	KL V HNAKTVKE--IRSRMD-----SDVSQ--VLKRVKMIK G KLEAL-----ER
Solyc10g008570	73	KTVHSAKKVKD--IRARM-----SDVTL--VLKRVKIIK G KLEGL-----ER
Solyc10g081580	71	KAVTKASAMKA--IKQRME-----KDVDE--VGKIARV I KSKIEEL-----DK
Solyc01g056810	14	KAVTKATAMKA--IKQRME-----KDVDE--VSKVARFIK S KIEGL-----DK
Solyc07g052470	70	KSVTKASAMKA--IRKRME-----KDIDE--VGKIARNV K AKIEAT-----NK
Solyc06g053760	72	KSLHKPEALKS--MRDRIN-----SDIVA--VLKKARAI R SQLEEM-----DR
Solyc02g085090	74	KTTHGPKVIRG--IRDRMD-----SDMVS--VLRKAKIV K AKLEAL-----DK
Solyc01g109750	70	KSAPSAKILQG--HRDQIN-----SDIIT--VLRKAKMIK T RLELL-----DK
Solyc06g062360	31	SGIFQINTAVS--TFQR-----LVNTLGTPKDTPE--LRDKLHKTRLHIGQL-----VK
Solyc11g066910	31	SGIFQINTAVS--TFQR-----LVNTLGTPKDTPE--LRDKLHKTRLHIGQL-----VK
Solyc08g005200	31	SGIFQINTAVS--TFQR-----LVNTLGTPKDTPE--LRDKLHKTRVHIGQL-----VK
Solyc08g076540	31	SGIFQINTAVS--TFQR-----LVNTLGTPKDTPE--LREKLHKTRVHIGQL-----VK
AtSYP22	30	SGIFQINTGVS--TFQR-----LVNTLGTPKDTPE--LREKLHKTRLHIGQL-----VK
AtSYP23	35	SGIFQINTSVS--TFHR-----LVNTLGTPKDTPE--LREKLHKTRLYIGQL-----VK
AtSYP21	38	AGIFRISTAVN--SFFR-----LVNSIGTPKDTLE--LRDKLQKTRLQISEL-----VK
Solyc06g072760	43	VGVFQINTALT--NFQR-----LVNTLGTPKDTLQ--LRHKLHSTRQQIAEL-----IK
AtSYP41	88	VNIQRARTKMA--ELGKAHAKALMP S FG---DGKE--DQHNIESLTQEITFL-----LK
AtSYP43	96	VYIQRARTKMA--ELGKAHAKALMP S FG---DGKE--DQHQIETLTQEVTFL-----LK
Solyc01g100170	87	ANVHRVRTKMS--ELAKAHAKALMP S FG---DGKE--DQRRIEALTHEITDL-----LK
AtSYP42	85	FNIQKVRDKMN--ELAKAHKALMP T FG---DNKG--IHREVEMLTHEITDL-----LR
Solyc09g075530	84	ASIHQAQVKLA--DLKKCHAKALTP S FG---DGRE--DQNVIEVLTMEITDI-----LR
Solyc03g033850	16	KTLESIGTLEQFLMKHKKDYVDLHRTTEQERDSIEHEVTIFVKSCKEQIDVLRNSINEED
Solyc04g071730	53	KTLESIGTLEQFLMKHKKDYVDLHRTTEQERDSIEHEVTIFVKSCKEQIDVLRNSINEED
AtSYP81	53	KTLD S IKEL E LFMLK H RKDYVDLHRTTEQE K DSIEQEVA A FIKACKEQIDILINSIRNEE
AtSYP31	71	-----LAKQS-----TIFNDRTVEIQELTVLIRNDITGLNMA L SDLQ
Solyc07g054140	80	-----LAKRS-----SIFDDPSKEIQELTTSIKNDITS L NVGVS D LQ
AtSYP32	84	RMVLR S R T DLFSVAKRT-----SVFDDPTQEIQELTVVIKQEISALNSALVDLQ
Solyc08g067910	83	-----LAKRT-----SVFDDPTTEIQELTAVIKQDITALNSAVVDLQ

AtPEN1	115	ANAANRSLP-GCGPGSSSDRTRTSVLNGLRKKLRDMSMDSFNRLRELISSE--YRETVQRR
VvPEN1	103	SNAANRSLP-GCGPGSSSDRTRTSVVGNGLRKKLRDSMDAFTSIRNQISSE--YRETVQRR
HvROR2	112	ANAANRSVA-GCGPGSSDTRTRTSVVAGLRKKLRDAMESFSSLRSRITSE--YRETVARR
SlPEN1a	108	SNAANRSVP-GCGPGSSSDRTRTSVVGNGLRKKLQESMNQFNELRQRMASE--YRETVQRR
SlPEN1b	105	SNASNRSLP-GCGPGSSSDRTRTSVVGNGLRKKLQESMNQFNELRQKMASE--YRETVQRR
AtSYP122	114	ANEVNRSLP-ESGPGSSSDRTRTSVVGNGLRKKLKDEMEKFSRVRETITNE--YKETVGRM
AtSYP124	104	ANANSRNVS-GCGPGSSDTRTRTSVVSGLGKKLKDLMDSFQGLRARMNAE--YKETVERR
AtSYP123	107	SNAQRKVA-GCGPGSSADTRTRTSVVSGLGKKLKDMDDFQQLRRTKMATE--YKETVERR
AtSYP111	116	ANKEIKRLS-G----TPVYRSRTAVTNGLRKKLKEVMMEFQGLRQKMMSE--YKETVERR
AtSYP131	106	ENLENRTKP-GCGKGTGVDRTRTATTIAVKKKFKDKISEFQTLRQNIQQE--YREVVERR
AtSYP125	99	ANANSRNVP-GCGPGSSDTRTRTSVVSGLGKKLKDLMDSFQGLRARMNNE--YKETVERR
AtSYP132	105	ENLANRQKP-GCAKSGVDRSRTATTLSLKKKLDKMAEFQVLRENIQQE--YRDVVDNR
AtSYP112	118	RNVANR---TSFKEGSCVDRTRTSITNGVRKKLRDTMSEFHRLRERIFAD--YREDLKRK
Solyc12g005580	110	SNAHRKIS-GCGPGSSADTRTRTSVVSGLGKKLKVLMDDFQGLRTRMNDE--YKETVARR
Solyc10g008570	112	SNVANRKNL-GCGPGSSADTRTRTSVVSGLGKKLKVLMDDFQALRAKMNSE--YKDTVARR
Solyc10g081580	110	ENLANRNKP-GCGKGSVDRSRTATTVSLKKKFKDKMAEFQTLRENIHHE--YREVVERR
Solyc01g056810	53	ENLSNRSKP-GCGKGSVDRSRTATTVSLKKKLDKMSFQTLRENIHNE--YREVVERR
Solyc07g052470	109	ENLANLQKP-GCGKGTSDRSRTNMTNSLTKKFRDVMTEFQTLRQRIDNE--YREVVERR
Solyc06g053760	111	SNAINRRLS-GCKEGLVDTRTSVAVTNGLRKKLKELMDFQGLRQRMTE--YKETVGRR
Solyc02g085090	113	SNVGNRKL SVAYAQSSVDRTRVSMNSGLRVKLRDIMNDFQALREKILSD--YKDCLERR
Solyc01g109750	109	SNLDNRGVS-----GSPVDRTRISVTNGLRKLRDMNDFQCLRENIVAE--HKEGLRKQ
Solyc06g062360	76	DTSKLKQASETDHRVEVSASKKITDAKLAKDFQAVLKEFQKAQRLAAER--ETAYTPFI
Solyc11g066910	76	DTSKLKQASETDHRIEVSASKKITDAKLAKDFQAVLKEFQKAQRLAAER--ETSYPFV
Solyc08g005200	76	DTSKLKQASETDHHDVSASKKITDAKLAKDFQAVLKEFQKAQRLAAER--ETAYTPFI
Solyc08g076540	76	DTSKLKQASETDHRVEVSASKKITDAKLAKDFQAVLKEFQKAQRLAAER--ETAYTPFV
AtSYP22	75	DTSKLKEASETDHQSGVNPSKKIADAKLAKDFQAVLKEFQKAQQTAAER--ETTYTPFV
AtSYP23	80	DTSKLKEASETDHQRGVNQKKKIVDAKLAKDFQAVLKEFQKAQRLAAER--ETVYAPLV
AtSYP21	83	NTSAKLKEASEADLHGSASQIKKIADAKLAKDFQSVLKEFQKAQRLAAER--EITYTPVV
Solyc06g072760	88	ETSANLKQAIGSNRHSQSSVTKKIANAKLAKDFQSVLKKFQRAQLAAQR--EAAFTPSI
AtSYP41	135	KSEKQLQRLSASGPSSEDSNVRKNV-QRSLATDLQLLSMELRKKQSTYLKR-----
AtSYP43	143	KSEKQLQRLSAGPSEDSNVRKNV-QRSLATDLQNLSMELRKKQSTYLKR-----
Solyc01g100170	134	RSEKQLQRLSAGLSEDSNVRKNV-QRSLATDLQSLSMELRKKQSTYLKR-----
AtSYP42	132	KSEKRLQMLSTRGPSEESNLRKNV-QRSLATDLQNLSMELRKKQSTYLKR-----
Solyc09g075530	131	KSQKKLQKLSASGSCEDSNVRKNV-QRSLATDLQNLSSVELRRMQSPLYLKQ-----
Solyc03g033850	76	ANSKGWLGLKGDNLNADTIAHKHGVVLIISEKLHSHVTSQFDQLRAIRFQDAINRVTPRRN
Solyc04g071730	113	ANSKGWLGLKGDNLNADTIAHKHGVVLIISEKLHSHVSSQFDQLRAIRFQDAINRVTPRRK
AtSYP81	113	ANSKGWLGLPADNFNADSIHKHGVVLIISEKLHSHVTAQFDQLRATRFQDIINRAMPRRK
AtSYP31	108	TLQNMELADGNYSQ--DQVGHYTAVCDDLKTRLMGATKQLQDVLTTSENMMKAHENRKQL
Solyc07g054140	117	ALQDMDVADGTHSK--DTIVHCTAICDDLKTRLMAATKSFQEALTIRTKNMKAHEDRKQI
AtSYP32	133	LFRSSQNDEGNNSRDRDKSTHSATVVDDLKYRLMDTTKEFKDVLTMRTENMKVHESRRQL
Solyc08g067910	120	LHSNARNESGNS----DTTSHSTTVDDLKNRLMTATKEFKDVLTMRTENMKVHENRRQM

AtPEN1	172	YFTVTGENPDERTL-----	DR
VvPEN1	160	YFTVTGENPDEKTV-----	DL
HvROR2	169	YFTVTGSQPDEATL-----	DT
SlPEN1a	165	YFTVTGENPDEGTL-----	DT
SlPEN1b	162	YYTVTGENPDEAVL-----	DT
AtSYP122	171	CFTVTGEYPDEATL-----	ER
AtSYP124	161	YFTITGEQADEQTI-----	EN
AtSYP123	164	YFTVTGQKADEETV-----	EK
AtSYP111	169	YFTVTGEHANDEMI-----	EK
AtSYP131	163	VFTVTGQRADEEAI-----	DR
AtSYP125	156	YFTITGEKADEQTI-----	DN
AtSYP132	162	VYTVTGERADEDTI-----	DE
AtSYP112	173	YFLATGEEPSNEDM-----	EK
Solyc12g005580	167	YFTVTGEKADDGLI-----	EN
Solyc10g008570	169	YFTVTGENADDELI-----	DN
Solyc10g081580	167	VFTVTGNRADEETI-----	DR
Solyc01g056810	110	VYTVTGNRADEETI-----	DR
Solyc07g052470	166	VITVTGTRPDEETI-----	NN
Solyc06g053760	168	YFTVTGEHPDEEVI-----	DK
Solyc02g085090	171	YYNETGKEPNEEVI-----	EK
Solyc01g109750	162	YSNANGKEPSEEAI-----	EK
Solyc06g062360	134	PQAVLPSSYTDGEV-----	DV
Solyc11g066910	134	PQAVLPSSYTNSEI-----	DV
Solyc08g005200	134	PQAVLPSSYTASEV-----	DV
Solyc08g076540	134	PQAVLPSSYTASEI-----	DV
AtSYP22	133	PQSALPSSYTAGEV-----	D-
AtSYP23	138	HKPSLPSSYTSSEI-----	DV
AtSYP21	141	TKE-IPTSYNAPEL-----	DT
Solyc06g072760	146	SQEI--NSSRSIEI-----	QI
AtSYP41	184	---LRQQKE--DGM-----	DL
AtSYP43	192	---LRLQKE--DGA-----	DL
Solyc01g100170	183	---LQQQKEGPDGV-----	DL
AtSYP42	181	---LQQQKEGQDEV-----	DL
Solyc09g075530	180	---LRLQSEGH DGL-----	DL
Solyc03g033850	136	RKSTTKSNAAEASA-----	SI
Solyc04g071730	173	RKN TTKSNAAETSV-----	SS
AtSYP81	173	PKRVIKE---ATPI-----	NT
AtSYP31	166	FSTKNAVD--SP-----PQNNAKSVPEPPPWSSSSNPFGNLQQPLLPLNTGAPPGS	
Solyc07g054140	175	FSTNLSRE--NP-----LK---QPTAEPPPWSTCQS-----LTAID--AQGSN	
AtSYP32	193	FSSNASKESTNPFVRQRPLAAKAAASESV-PLPWANGSS-----SSSS	
Solyc08g067910	176	FSSSTSKEASNPFMRQRPLASRNTASTSASPPPWAN-DS-----PSSS	

AtPEN1	188	LIS---	TGES---	ERFLQKAIQE-Q-GRGRVLDTINEI	I-----	-QERHDAVKDIEKN
VvPEN1	176	LIS---	TGES---	ETFLQKAIQE-Q-GRGRVLDTISEI	I-----	-RERHESVKELERN
HvROR2	185	LAE---	TGEG---	ERLLQRAIAEQQGRGEVLGVVAEI	I-----	-QERHGAVADLERS
SlPEN1a	181	LIS---	TGQS---	ETFLQKAIQE-Q-GRGQVMDTVMEI	I-----	-QERHEAVKELEARN
SlPEN1b	178	LIS---	TGQS---	ETFLQKAIQE-Q-GRGQVMDTIMEI	I-----	-QERHEAVKEIERN
AtSYP122	187	LIS---	TGES---	ETFLQKAIQE-Q-GRGRILDTINEI	I-----	-QERHDAVKDIEKS
AtSYP124	177	LIS---	SGES---	ENFLQKAIQE-Q-GRGQILDITSEI	I-----	-QERHDAVKEIEKN
AtSYP123	180	LIS---	SGES---	ERFLQKAIQE-Q-GRGQVMDTLSEI	I-----	-QERHDTVKEIERS
AtSYP111	185	II T---	--DNAGGEF	LTRAIQEH-KGKGVLLETVVEI	I-----	-QDRYDAAKEIEKS
AtSYP131	179	LIE---	TGDS---	EQIFQKAIREQ-GRGQIMDTLAEI	I-----	-QERHDAVRDLEKK
AtSYP125	172	LIA---	SGES---	ENFLQKAIQE-Q-GRGQILDITSEI	I-----	-QERHDAVKEIEKN
AtSYP132	178	LIE---	TGNS---	EQIFQKAIREQ-GRGQVMDTLAEI	I-----	-QERHDAVRDLEKK
AtSYP112	189	MIS---	GSGS---	CSDLVKTFEVKPEM	-----	-DLKTKERHEAVNDIKRS
Solyc12g005580	183	LIS---	SGES---	ESFLQKAIQE-Q-GRGQIMDTISEI	I-----	-QERHDAVKEIEKN
Solyc10g008570	185	LIS---	SGES---	ESFLQKAIQE-Q-GRGQIMDTISEI	I-----	-QERHDAVKEIEKN
Solyc10g081580	183	LIE---	TGDS---	EQIFQKAQQQ-GRGQIMGTLAEI	I-----	-QERHDAVRELERK
Solyc01g056810	126	LIE---	TGDS---	EQIFQKAIREQ-GRGQIMDTLAEI	I-----	-QERHDAVRELERK
Solyc07g052470	182	LIE---	TGNS---	EQIFQNAIQGM-GRGQVLSTVEEI	I-----	-QERHDAVKEIERK
Solyc06g053760	184	LIS---	SGNGQGGEF	LSRAIQEH-GRGKVLETVVEI	I-----	-QDRHDAAKEIEKS
Solyc02g085090	187	MVS---	GE-----	SGKVQIFAAKTEM	-----	-NLDDKDRHEAVMDIKKS
Solyc01g109750	178	NMQ---	ERVI-----	EKG VVE-	-----	-NQDRHEAVKEIQKS
Solyc06g062360	150	SSD---	KGQE-----	QRALLVESRRQEVLLLLDNEISF	---NEAIIIEEREQGIQEVQQQ	
Solyc11g066910	150	SSD---	KSQE-----	QRALLVESRRQEVVLLDNEISF	---NEAIIIEERDQGIQEVQQQ	
Solyc08g005200	150	ASD---	KSQE-----	QRALLVESRRQDVLYLDNEIAF	---NEAIIIEERDLGIQEVQQQ	
Solyc08g076540	150	SSG---	KSPE-----	QRALLVESRRQEVLLLDNEIAF	---NEAIIIEEREQGIQEIQQQ	
AtSYP22	148	-----	KVPE-----	QRAQLQESKRQELVLLDNEIAF	---NEAVIEEREQGIQEIHQQ	
AtSYP23	154	NGD---	KHPE-----	QRALLVESKRQELVLLDNEIAF	---NEAVIEEREQGIQEIQQQ	
AtSYP21	156	ESL---	RISQ-----	QQALLLQSRREQVVFLDNEITF	---NEAIIIEEREQGIREIEDQ	
Solyc06g072760	160	SSS---	ISPE-----	SSSILLESKRQDVVQLEHEIVF	---NK AIIIEEREQGMIEIQQQ	
AtSYP41	195	EMN---	LSRN-----	RYR-PEEDDFGDML-NEHQMSKIKKSEEVSVEREKEIQOVVES		
AtSYP43	203	EMN---	LNGS-----	RYK-AEDDDFD DMVFSEHQMSKIKKSEEISI EREKEIQOVVES		
Solyc01g100170	196	EMN---	LNGS-----	HSR-RDDDDLDDLGFNEHQMAKLK KSEAFTVERERE IQOVVES		
AtSYP42	194	EFN---	VNGK-----	MSRLDEEDELGGMGFDEHQTIKLKEGQHVS AERERE IQQVLGS		
Solyc09g075530	193	EMN---	EKKS-----	SFL---DDD FNDVGFT ELQMATGQKDEQFTA ERERE IRQVLKS		
Solyc03g033850	152	SLDPDMKR DSEVRDNDVSQAAPMRVQE-Q-LLDDETALQVELNSLL----	DSVQETETN			
Solyc04g071730	189	NLDPNMKR DSEGLGDPDTQAAPIRVQE-Q-LLDDETALQVELNSLL----	DSVQETETK			
AtSYP81	186	TLG----	NSESIEPDEIQAQPRRLQQQQLLDDKETALQVELSNLL----	DGARQTETK		
AtSYP31	216	QL--RRRSAIENAP----	SQMEMSLLQQTVPKQENYS	-----	-QSRAVALHSVESR	
Solyc07g054140	211	QL--RRRLASDNPP----	SNELEMSMLQDQVP RQESYS	-----	-QS RATALQNVEST	
AtSYP32	235	QLVPWKPGEGESSPLLQSQSQQQQQQ QMVPLQDTYM	-----	-QGRAEALHTVEST		
Solyc08g067910	218	QLFPRKQGDGDTQPLLOD----	QQQQQQQQQIVPLQDSYM	-----	-QSRAEALQNVEST	

AtPEN1	231	I	R	E	T	H	Q	V	F	L	D	M	A	V	L	V	E	H	Q	G	A	Q	I	D	D	I	E	S	H	V	G	R	A	S	S	F	I	R	G	G	T	D	Q	I	Q	T	A	R	V	Y	Q	K	N	T	R	-----						
VvPEN1	219	I	K	E	T	H	Q	V	F	L	D	M	A	V	L	V	Q	A	Q	G	E	Q	I	D	D	I	E	S	Q	V	A	R	A	N	S	F	V	T	G	G	T	Q	Q	I	Q	T	A	R	K	H	Q	I	S	S	R	-----						
HvROR2	229	I	L	E	I	Q	Q	V	F	N	D	M	A	V	L	V	A	A	Q	G	E	Q	I	D	D	I	E	G	H	V	G	R	A	R	S	F	V	D	R	G	R	E	Q	L	Q	V	A	R	K	H	Q	K	S	S	R	-----						
SlPEN1a	224	I	K	E	T	H	Q	V	F	M	D	M	A	V	L	V	E	S	Q	G	A	Q	I	D	D	I	E	S	Q	V	N	R	A	N	S	F	V	R	G	G	A	Q	Q	L	E	V	A	R	K	H	Q	K	S	S	R	-----						
SlPEN1b	221	I	K	E	T	H	Q	V	F	L	D	M	A	V	L	V	E	S	Q	G	E	Q	I	D	D	I	E	S	Q	V	N	R	A	N	S	F	V	R	G	G	A	Q	Q	L	Q	V	A	R	K	H	Q	K	N	T	R	-----						
AtSYP122	230	I	N	E	T	H	Q	V	F	L	D	M	A	V	L	V	E	H	O	G	A	Q	I	D	D	I	E	G	N	V	K	R	A	N	S	L	V	R	S	G	A	D	R	I	V	K	A	R	F	Y	O	K	N	T	R	-----						
AtSYP124	220	I	I	E	T	H	Q	V	F	L	D	M	A	A	L	V	E	S	Q	G	Q	I	D	D	I	E	S	H	V	S	K	A	S	S	F	V	R	R	G	T	D	Q	L	Q	D	A	R	E	Y	Q	K	S	S	R	-----							
AtSYP123	223	I	L	E	T	H	Q	V	F	L	D	M	A	A	L	V	E	A	Q	G	N	I	D	D	I	E	S	N	V	S	K	A	S	S	F	V	M	R	G	T	D	Q	L	H	G	A	K	V	L	Q	R	N	N	R	-----							
AtSYP111	229	I	L	E	T	H	Q	V	F	L	D	M	A	V	L	V	E	S	Q	G	E	Q	I	D	D	I	E	H	H	V	I	N	A	S	H	Y	V	A	D	G	A	N	E	L	K	T	A	K	S	H	Q	R	N	S	R	-----						
AtSYP131	222	I	L	D	I	Q	Q	V	F	L	D	M	A	V	L	V	D	A	Q	G	E	M	I	D	N	I	E	N	M	V	S	S	A	V	D	H	V	Q	S	G	N	N	Q	L	T	K	A	V	K	S	Q	K	S	S	R	-----						
AtSYP125	215	I	L	E	T	H	Q	V	F	L	D	M	A	A	L	V	E	A	Q	G	Q	I	D	D	I	E	S	H	V	A	K	A	S	S	F	V	R	R	G	T	D	Q	L	Q	D	A	R	E	Y	Q	K	S	S	R	-----							
AtSYP132	221	I	L	D	I	Q	Q	I	F	L	D	M	A	V	L	V	D	A	Q	G	E	M	I	D	N	I	E	S	Q	V	S	S	A	V	D	H	V	Q	S	G	N	T	A	L	Q	R	A	K	S	L	Q	K	N	S	R	-----						
AtSYP112	227	I	N	R	I	H	Q	V	F	L	D	M	A	V	L	V	E	T	Q	G	D	R	I	D	D	I	E	A	N	V	A	N	A	G	S	F	V	S	G	T	N	S	L	Y	A	N	Q	M	K	K	K	T	K	-----								
Solyc12g005580	226	I	I	E	T	H	Q	I	F	L	D	M	A	A	L	V	E	A	Q	G	Q	I	D	D	I	E	S	H	V	A	H	A	S	S	F	V	R	R	G	T	E	Q	L	Q	E	A	R	E	I	Q	K	S	S	R	-----							
Solyc10g008570	228	I	I	E	T	H	Q	I	F	L	D	M	A	A	L	V	E	A	Q	G	Q	I	D	D	I	E	S	H	V	A	H	A	S	S	F	V	R	R	G	T	E	Q	L	T	E	A	R	E	L	Q	K	S	S	R	-----							
Solyc10g081580	226	I	L	E	I	Q	Q	I	F	L	D	I	A	V	L	V	D	A	Q	G	D	M	I	D	N	I	E	S	Q	V	S	T	A	V	D	H	V	Q	S	G	T	T	A	L	Q	K	A	K	L	Q	K	N	S	R	-----							
Solyc01g056810	169	I	L	E	I	Q	Q	I	F	L	D	M	A	V	L	V	D	A	Q	G	D	M	I	D	N	I	E	S	Q	V	S	A	A	V	D	H	V	Q	S	G	N	T	A	L	Q	K	A	K	S	L	Q	R	N	S	R	-----						
Solyc07g052470	225	I	L	D	I	H	Q	I	Y	L	D	M	A	V	L	V	E	A	Q	G	D	L	I	D	N	I	E	T	Q	V	R	Y	A	V	D	H	V	N	M	G	T	D	A	L	Q	T	A	K	S	L	Q	K	K	S	R	-----						
Solyc06g053760	230	I	L	E	T	H	Q	I	F	L	D	M	A	V	L	V	E	A	Q	G	E	K	M	D	D	I	E	H	H	V	N	A	A	Q	Y	V	N	D	G	A	K	N	I	K	T	A	K	K	Y	Q	K	S	S	R	-----							
Solyc02g085090	222	I	D	K	I	H	Q	V	F	L	D	M	A	V	L	V	E	T	Q	G	E	Q	I	D	D	I	E	H	N	M	A	I	A	G	S	F	I	S	G	T	N	S	L	F	Y	A	K	Q	Q	K	K	G	R	-----								
Solyc01g109750	205	I	V	E	I	H	Q	V	F	L	D	M	A	V	L	V	E	T	Q	G	D	Q	M	N	I	E	Q	N	V	N	A	G	G	Y	V	N	G	M	K	E	L	D	R	A	N	R	M	-K	R	T	R	-----										
Solyc06g062360	197	I	G	E	V	N	E	I	F	K	D	L	A	V	L	V	H	E	Q	G	T	M	I	D	D	I	G	S	N	I	E	N	S	H	A	A	T	A	Q	G	R	S	Q	L	A	K	A	A	K	T	Q	R	S	N	S	-----						
Solyc11g066910	197	I	G	E	V	N	D	I	F	K	D	L	A	V	L	V	H	E	Q	G	T	M	I	D	D	I	G	S	N	I	E	N	S	H	A	A	T	A	Q	G	R	T	Q	L	A	K	A	A	K	T	Q	R	S	N	S	-----						
Solyc08g005200	197	I	G	E	V	N	E	I	F	K	D	L	A	V	L	V	H	E	Q	G	T	M	I	D	D	I	G	S	N	I	E	N	S	H	A	A	T	A	L	G	R	S	Q	L	A	K	A	A	K	T	Q	R	S	N	S	-----						
Solyc08g076540	197	I	G	E	V	N	E	I	F	K	D	L	A	V	L	V	H	E	Q	G	A	M	I	D	D	I	G	S	N	V	E	N	A	H	A	A	T	A	Q	G	R	S	Q	L	A	K	A	A	K	T	Q	R	S	N	S	-----						
AtSYP22	192	I	G	E	V	N	E	I	F	K	D	L	A	V	L	V	N	D	Q	G	V	M	I	D	D	I	G	T	H	I	D	N	S	R	A	A	T	S	Q	G	K	S	Q	L	V	Q	A	A	K	T	Q	K	S	N	S	-----						
AtSYP23	201	I	G	E	V	H	E	I	F	K	D	L	A	V	L	V	H	D	Q	G	N	M	I	D	D	I	G	T	H	I	D	N	S	Y	A	A	T	A	Q	G	K	S	H	L	V	---RH	Q	R	H	K	D	-----										
AtSYP21	203	I	R	D	V	N	G	M	F	K	D	L	A	L	M	V	N	H	Q	G	N	I	V	D	D	I	S	S	N	I	D	N	S	H	A	A	T	T	Q	A	T	V	Q	L	R	K	A	A	K	T	Q	R	S	N	S	-----						
Solyc06g072760	207	I	G	E	I	N	E	M	F	K	D	L	A	L	L	V	H	E	Q	G	T	M	I	D	D	I	S	S	N	I	G	S	S	H	D	A	T	A	Q	A	A	K	L	T	K	A	S	K	I	Q	Q	C	N	S	-----							
AtSYP41	243	V	N	D	I	A	Q	I	M	K	D	L	S	A	L	V	I	D	Q	G	T	I	V	D	R	I	D	Y	N	I	E	N	V	A	T	T	V	E	D	G	L	K	Q	L	Q	K	A	E	R	T	Q	R	H	G	G	-----						
AtSYP43	252	V	S	E	I	A	Q	I	M	K	D	L	S	A	L	V	I	D	Q	G	T	I	V	D	R	I	D	Y	N	I	Q	N	V	A	S	T	V	D	D	G	L	K	Q	L	Q	K	A	E	R	T	Q	R	Q	G	G	-----						
Solyc01g100170	245	V	N	D	I	A	Q	I	M	K	D	L	S	V	L	V	I	D	Q	G	T	I	V	D	R	I	D	H	N	I	Q	N	V	A	S	T	V	E	D	G	L	K	Q	L	K	K	A	E	R	S	Q	K	R	G	G	-----						
AtSYP42	244	V	N	D	I	A	Q	I	M	K	D	L	S	A	L	V	I	D	Q	G	T	I	V	D	R	I	D	Y	N	V	Q	N	V	S	T	S	V	E	E	G	Y	K	Q	L	Q	K	A	E	R	T	Q	R	E	G	A	-----						
Solyc09g075530	240	V	N	E	I	A	Q	I	M	K	D	L	S	V	L	V	I	D	Q	G	T	I	V	D	R	I	D	H	N	V	Q	S	V	S	A	S	V	E	E	G	F	K	Q	L	Q	K	A	E	R	S	Q	R	K	G	G	-----						
Solyc03g033850	206	M	V	E	M	S	A	L	N	H	L	M	S	T	H	V	L	Q	Q	A	Q	Q	I	E	L	L	Y	E	Q	A	V	E	A	T	Q	N	V	E	L	G	N	K	E	L	S	Q	A	I	Q	R	N	S	S	S	R	-----						
Solyc04g071730	243	M	V	E	M	S	A	L	N	H	L	M	S	T	H	V	L	Q	Q	A	Q	Q	I	E	L	L	Y	E	Q	A	V	E	A	T	Q	N	V	E	L	G	N	K	E	L	S	Q	A	I	Q	R	N	S	S	S	R	-----						
AtSYP81	236	M	V	E	M	S	A	L	N	H	L	M	A	T	H	V	L	Q	Q	A	Q	Q	I	E	F	L	Y	D	Q	A	V	E	A	T	K	N	V	E	L	G	N	K	E	L	S	Q	A	I	Q	R	N	S	S	S	R	-----						
AtSYP31	261	I	T	E	I	S	G	I	F	P	Q	L	A	T	M	V	T	Q	Q	G	E	L	A	I	R	I	D	D	N	M	D	E	S	L	V	N	V	E	G	A	R	S	A	L	L	Q	H	L	T	R	I	S	S	N	R	W	L	M	M	K	I	-----
Solyc07g054140	256	I	S	E	I	G	G	I	F	T	H	L	A	T	M	V	A	Q	Q	G	E	L	A	I	R	I	D	D	N	V	D	E	S	L	T	N	V	E	G	A	Q	G	A	L	L	K	Y	L	N	R	I	S	S	N	S	---R	K	V	-----			
AtSYP32	286	I	H	E	I	S	S	I	F	T	Q	L	A	T	M	V	S	Q	Q	G	E	I	A	I	R	I	D	Q	N	M	E	D	T	L	A	N	V	E	G	A	Q	S	Q	L	A	R	Y	L	N	S	I	S	S	N	R	W	L	M	M	K	I	-----</

AtPEN1	285	-----	KWTCIA
VvPEN1	273	-----	KWTCYG
HvROR2	283	-----	KWTFIG
SlPEN1a	278	-----	KWTCIA
SlPEN1b	275	-----	KWTCFA
AtSYP122	284	-----	KWTCFA
AtSYP124	274	-----	KWTCYA
AtSYP123	277	-----	KWACIA
AtSYP111	283	-----	KWMCIG
AtSYP131	276	-----	KWMCIA
AtSYP125	269	-----	KWTCYA
AtSYP132	275	-----	KWMCIA
AtSYP112	281	-----	SWVLWV
Solyc12g005580	280	-----	KCACFA
Solyc10g008570	282	-----	KCTCIA
Solyc10g081580	280	-----	KWMCFA
Solyc01g056810	223	-----	KWMCIA
Solyc07g052470	279	-----	KCMMIA
Solyc06g053760	284	-----	RCMCIG
Solyc02g085090	276	-----	AWICWV
Solyc01g109750	258	-----	TWACWI
Solyc06g062360	251	-----	SLTC--
Solyc11g066910	251	-----	SLTC--
Solyc08g005200	251	-----	SLTC--
Solyc08g076540	251	-----	SLTC--
AtSYP22	246	-----	SLTC--
AtSYP23	252	-----	QI----
AtSYP21	257	-----	SLTC--
Solyc06g072760	261	-----	STSC--
AtSYP41	297	-----	MVKCAS
AtSYP43	306	-----	MVMCAS
Solyc01g100170	299	-----	MVMCAT
AtSYP42	298	-----	MVKCAT
Solyc09g075530	294	-----	MVKCAT
Solyc03g033850	260	-----	TF----
Solyc04g071730	297	-----	TF----
AtSYP81	290	-----	TF----
AtSYP31	321	F-----	
Solyc07g054140	313	SCTENYT	TAACTTCCTGCAAAGTTCATGAATAATATTCACTTTCTCACACCATACAGCGA
AtSYP32	346	F-----	
Solyc08g067910			

AtPEN1	291	IIILIIITTVVVLAVLKPWNNSSGGGG-----
VvPEN1	279	IIILIVIILLIVLFTVRPWENN-----
HvROR2	289	IGILLVVILIIVIPIVLKNTNKSNNNNNSQQ-----
SlPEN1a	284	IIILLIIIVLVVVL-SIQPWKK-----
SlPEN1b	281	IIILLIIILIVVL-SIQPWKK-----
AtSYP122	290	IIILLIIIVVLIVVFTVKPWESNGGGGG-----
AtSYP124	280	ILLFIVVFALLLI-----
AtSYP123	283	TILAIVVIVILF-----
AtSYP111	289	IIVLLIIILIVVIPIITSFSSS-----
AtSYP131	282	ILILLIIIIITVISVLKPWTQKNG-----
AtSYP125	275	IILFIVIFILLLI-----
AtSYP132	281	IIILLIVVAVIVVGVLKPW-KNKS-----
AtSYP112	287	SILGVLILLVCVISML-----
Solyc12g005580	286	VFLIIILLIILL-----TF-----
Solyc10g008570	288	ILLIIILLIIKLHLQIVSMFLKLLGHRHYSSVTFFTNPPSKESEIIHLCRSDLLSQAIKLL
Solyc10g081580	286	IMILLIIVAIIIVGVLPWQSNKG-----
Solyc01g056810	229	IIILLIIVAVIVVGVLKPWNSNKG-----
Solyc07g052470	285	IIILLIIAAIIVLSVIKPWKK-----
Solyc06g053760	290	AIILLILILVVIPIATSFTKS-----
Solyc02g085090	282	WAVLLIIILVVCLIA TL-----
Solyc01g109750	264	GALVLVFLLCILIAIL-----
Solyc06g062360	255	-LLLVIFGIVLLIVII-----
Solyc11g066910	255	-LLLVIFGIVLLIVII-----
Solyc08g005200	255	-LLLVIFGIIILLIVII-----
Solyc08g076540	255	-LLLVIFGIVLLIVIV-----
AtSYP22	250	-LLLVIFGIVLLIVII-----
AtSYP23	254	-----LLCLI-----
AtSYP21	261	-LLILIFGIVLLIVII-----
Solyc06g072760	265	-LLLVIFGVILLIIIV-----
AtSYP41	303	VLVILCFIMLLLLILK-----
AtSYP43	312	VLVILCFIMLVLLILK-----
Solyc01g100170	305	VLVIMCFIMLVLLILK-----
AtSYP42	304	ILLVLCLIMIVLLILK-----
Solyc09g075530	300	ILVIMCFVMLVLLVLK-----
Solyc03g033850	262	-LLLFLVLTFSILFLDWYS-----
Solyc04g071730	299	-LLLFLVLTFSILFLDWYS-----
AtSYP81	292	-LLFFFVLTFSVLFLDWYS-----
AtSYP31	322	-AVIILFLIVFLFFVA-----
Solyc07g054140	373	GACTACGATGAAGATA-----
AtSYP32	347	-FVLIAFLMIFLFFVA-----
Solyc08g067910		

AtPEN1		-----
VvPEN1		-----
HvROR2		-----
SlPEN1a		-----
SlPEN1b		-----
AtSYP122		-----
AtSYP124	293	-----PAL-----
AtSYP123	296	-----PILFNTLLRP-----
AtSYP111		-----
AtSYP131		-----
AtSYP125	288	-----PLL-----
AtSYP132		-----
AtSYP112		-----
Solyc12g005580	299	-----PL-----
Solyc10g008570	348	KSTEKISSKPIVYATLIQTCTKSHSFNHGVQFHTHVIKTGIETDRFVGNSLLALYFKLGS
Solyc10g081580		-----
Solyc01g056810		-----
Solyc07g052470		-----
Solyc06g053760		-----
Solyc02g085090		-----
Solyc01g109750		-----
Solyc06g062360		-----
Solyc11g066910		-----
Solyc08g005200		-----
Solyc08g076540		-----
AtSYP22		-----
AtSYP23		-----
AtSYP21		-----
Solyc06g072760		-----
AtSYP41		-----
AtSYP43		-----
Solyc01g100170		-----
AtSYP42		-----
Solyc09g075530		-----
Solyc03g033850		-----
Solyc04g071730		-----
AtSYP81		-----
AtSYP31		-----
Solyc07g054140		-----
AtSYP32		-----
Solyc08g067910		-----

AtPEN1		-----
VvPEN1		-----
HvROR2		-----
SlPEN1a		-----
SlPEN1b		-----
AtSYP122		-----
AtSYP124		-----
AtSYP123		-----
AtSYP111		-----
AtSYP131		-----
AtSYP125		-----
AtSYP132		-----
AtSYP112		-----
Solyc12g005580	301	-----W-----
Solyc10g008570	408	NFLETRRFFDGMVYKDVVAWSSMITGYVRIGKPKISLELYGEMIDLGFEPNGFTLSAVIK
Solyc10g081580		-----
Solyc01g056810		-----
Solyc07g052470		-----
Solyc06g053760		-----
Solyc02g085090		-----
Solyc01g109750		-----
Solyc06g062360		-----
Solyc11g066910		-----
Solyc08g005200		-----
Solyc08g076540		-----
AtSYP22		-----
AtSYP23		-----
AtSYP21		-----
Solyc06g072760		-----
AtSYP41		-----
AtSYP43		-----
Solyc01g100170		-----
AtSYP42		-----
Solyc09g075530		-----
Solyc03g033850		-----
Solyc04g071730		-----
AtSYP81		-----
AtSYP31		-----
Solyc07g054140		-----
AtSYP32		-----
Solyc08g067910		-----

Fig. S1 Multialignment of plant syntaxins. The dataset includes all the Arabidopsis syntaxins (AtSYPs and AtPEN1), barley HvROR2, grapevine VvPEN1 and 21 putative syntaxins retrieved from the tomato proteome by this study (indicated by the SolGenomics Network database ID code). The black box includes the SYP1-clade syntaxins (in number of 21). The six syntaxins belonging to the SYP1b-subclade are highlighted in light red.

The position of characteristic domains of syntaxins (the three helix domain Ha, Hb and Hc, the Qa-SNARE domain and the membrane-spanning (MS) domain) are indicated. Gray color indicates residues physio-chemically conserved throughout the dataset; green color indicates residues physio-chemically conserved in SYP1 syntaxins. Yellow color highlights 24 residues specifically conserved in syntaxins of the SYP1b subclade described in this study.

		Ha																			
SlPEN1a	1	MNDLFSGSFSRFRNEEQSPNQESAG----	IOMRQ----	QTG----	GVNLDKFFEDVETIKD																
AtPEN1	1	MNDLFSSSFSRFRSGEPSPRRDVAGGGDGV	QMANPAGSTG----		GVNLDKFFEDVESVKE																
VvPEN1	1	MNDLFSGSFSRFRSEEPSPS-----	VENTS----	STA----	GVNLDKFFEDVESIKE																
HvROR2	1	MNNLFSSSWKRAGAGGDG----	DLESGGGGV	EMTAPPGAAA----	GASLDRFFEDVESIKD																
AtSYP122	1	MNDLLSGSFKTSVADGSSPPHS-----	HNIEMSKAKVSG	CSCHG	GNNLDTFFLDVEVVNE																
SlPEN1b	1	MNDLFSGSFSRYR--ENDHDQDSHG----	IEMGD----	TC----	GVNLDKFFEDVEAIKD																
		Hb																			
SlPEN1a	50	ELKELEKIHTQLHNSHEQSKTLHNAKNVKDLRKKMDNDVSLALKKAKFIKVRLEALDRSN																			
AtPEN1	57	ELKELDRLNETLSSCHEQSKTLHNAKAVKDLRKKMDGDVGVALKKAKMIKVKLEALDRAN																			
VvPEN1	45	ELREMESLQOKLHDAHEQSKTLHNANSVKELRSRMDSHVSLALKKAKLIKLRLEALDRSN																			
HvROR2	54	DLRELERIQRSLHDGNESEGKSLHDASAVRALRSRMDADVAAAIAKKAKVKLRLESLDRAN																			
AtSYP122	56	DLKELDRLCHNLRSSNEQSKTLHNANAVKELKKMDADVTAAKKTARRLKGNLEALDRAN																			
SlPEN1b	47	ELKNLEKIYAQLQSSNEKSKTLHNAKAVKDLRKKMDDVSLALKKAKFIKVRLEALDRSN																			
		Hc																			
SlPEN1a	110	AANRSVPGCGPGSSSDRTTRTSVVNGLRKKLQESMNQFNELRQRMASEYRETVQRRYFTVT																			
AtPEN1	117	AANRSLPGCGPGSSSDRTTRTSVINGLRKKLMDSMDSFNRLRELISSEYRETVQRRYFTVT																			
VvPEN1	105	AANRSLPGCGPGSSSDRTTRTSVVNGLRKKLRDSMDAFTSIRNQISSEYRETVQRRYFTVT																			
HvROR2	114	AANRSVAGCGPGSSSDRTTRTSVVAGLRKKLRDAMESFSSLSRRTITSEYRETVARRYFTVT																			
AtSYP122	116	EVNRSLPESGPGSSSDRQRTSVVNGLRKKLKDEMEKTSRVRETITNEYKETVGRMCFVT																			
SlPEN1b	107	ASNRSVPGCGPGSSSDRTTRTSVVNGLRKKLQESMNQFNELRQRMASEYRETVQRRYFTVT																			
		Qa-SNARE																			
SlPEN1a	170	GENPDEGTLDTLISTGQSETFLQKAIQEQ--GRGQVMDTMEIOERHEAVKELERNLKELEH																			
AtPEN1	177	GENPDERTLDRLISTGESERFLQKAIQEQ--GRGRVLDTINEIOERHDAVKDIEKNLRELH																			
VvPEN1	165	GENPDEKTVDLLISTGESETFLQKAIQEQ--GRGRVLDTISEIRERHESVKELERNLKELEH																			
HvROR2	174	GSQPDEATLDTLAETGGERLLQRAIAEQQGRGEVIGVVAEIOERHGAVADLERSLLELQ																			
AtSYP122	176	GEYPDEATLERLISTGESETFLQKAIQEQ--GRGRILDITINEIOERHDAVKDIEKSLNELH																			
SlPEN1b	167	GENPDEAVLDTLISTGQSETFLQKAIQEQ--GRGQVMDTMEIOERHEAVKEIERNLKELEH																			
		MS																			
SlPEN1a	229	QVFMDMAVLVESQGAQLDDIESQVNRANSFVRGGAQQLQVARKHOKSSRKWTCIAIIILL																			
AtPEN1	236	QVFLDMAVLVEHQGAQLDDIESHVGRASSFIRGGTDQLQTARVYQKNTRKWTCIAIIILI																			
VvPEN1	224	QVFLDMAVLVQAQGEQLDDIESQVARANSFVTGGTQQLQTARKHQISSRKWTCYGIIILI																			
HvROR2	234	QVFNDMAVLVAAQGEQLDDIEGHVGRARSFVDRGREQLQVARKHOKSSRKWTFIGIGILL																			
AtSYP122	235	QVFLDMAVLVEHQGAQLDDIEGNVKRANSLVRSQADRLVKARFYQKNTRKWTCFAIIILL																			
SlPEN1b	226	QVFLDMAVLVESQGEQLDDIESQVNRANSFVRGGAQQLQVARKHOKNTRKWTCFAIIILL																			
SlPEN1a	289	IIVLVVVL-SIQPWKK-----																			
AtPEN1	296	IIITVVVLAVLKPWNNSSGGGGGGGGGTGGSGPNSGTTPPNPPQARRLLR																			
VvPEN1	284	VIIILLIVLFTVRPWENN-----GSSSSGSTSSTSPPPPPPPPPTQA																			
HvROR2	294	VVILIIIVIPIVLKNTNKSNNNNS-----QQ																			
AtSYP122	295	IIVVLIVVFTVKPWESNGGGGGGAPRQATPVQAQP----PPPPAVNRRLLR																			
SlPEN1b	286	IIILIVVL-SIQPWKK-----																			

Fig. S2 Syntaxins of the SYP1b-subclade multialignment. The protein dataset includes Arabidopsis AtPEN1 and AtSYP122, tomato SlPEN1a and SlPEN1b, barley HvROR2 and grapevine VvPEN1. The position of characteristic syntaxin domains (the three helix domain Ha, Hb and Hc, the Qa-SNARE domain and the membrane-spanning (MS) domain) are indicated. Red colour indicates amino acids differentially conserved in the syntaxins functionally characterized in plant-pathogen interaction.