

Sc-SPT16	-----MEELNIDFDVFKKRIELLYSKYNEFEFGS--	28
At-SPT16	-----MADSRNGNARAPPSGVPPKAGNTYSIDVKNFISRARALYEHWKKHSA---	47
Ta-SPT16	-----MTDNGKAK-SG-----SGAAYTINLETFSKRLKVFYDHWNGNKS---	38
Os-SPT16	-----MADNGNAK-PGG----GGSGAYTINLDNFSKRLKVFYDHWKEHNS---	40
Sb-SPT16	-----MADNGNA-----K----GGSGAYTINLENFSKRLKVFYDHWKEHKS---	37
Zm-Spt16	MVALVNVSLLTNMADNGDA---K----GGSGAYAINIENFSKRLKVFYDHWKEHKS---	49
Gm-SPT16	-----MADHRNGSAQ-AANGKASAAGTAYSIDLNAFQTRLRSFYKHWDAHKT---	46
Pt-SPT16	-----MADQRNGTGQ-PSN----AARNAYADVEKFKTRLKALYSNWNENKA---	42
Vv-SPT16	-----MAEHRNGNAK-PSDGKASGAASPYAINLDNFTKRLKTLYSHWKEHSS---	46
Sm-SPT16	-----MADSRNGGDA-----KSKANDSGYDINIDDFVKRLNIFYKCWADEKN---	42
Pp-SPT16	-----MAE-RNG-----DGKGGRVQINLELYGKRLKLLNNKWKHEHKK---	36
Hs-SPT16	-----MAVTLDKDAYYRRVKRLYSNWRKG-----E	25
Dm-SPT16	-----MSSFVLDKEAFVRRVKRLYTEWRAPSIGHD	30
	: : . : * . : :	
Sc-SPT16	-----PNSLLFVL--GSSNAENPYQKTTILHNWLLSYEFPATLIALVPGKVIIITSSAKA	81
At-SPT16	DLWGSADALAIATPPAS--DDLRYLKSSALNIWLLGYEFPDTIMVFTKKQIHFLCSRKA	105
Ta-SPT16	DLWASSDAIAIATPPPS--EDLRYLKSTALDVWLLGYEFPETIIVFMQKQIHFLCSQKKA	96
Os-SPT16	DLWGSSNAIAIATPPPS--EDLRYLKSSALDVWLLGYEFPETIIVFMHKQIHFLCSQKKA	98
Sb-SPT16	DLWSSSDAIAIATPPPS--DDLRYLKSSALDIWLLGYEFPETIIVFMHKQIHVLCSSQKKA	95
Zm-Spt16	DLWGSSDAIAIATPPPS--DDLRYLKSSALDIWLLGYEFPETIIVFMHKQIHVLCSSQKKA	107
Gm-SPT16	DLWGSSDAIAVACPPPS--EDLRYLKSTALNLWLLGYEFPETIMVFSKKQIHILCSQKKA	104
Pt-SPT16	DLWGSSDVVAIATPPPS--EDLRYLKSSALNIWLLGYEFPETVMVFMKKQIHFLCSQKKA	100
Vv-SPT16	DLWGSSDALAIATPPAS--DDLRYLKSSALNIWLLGYEFPETIMVFMKKQIHFLCSQKKA	104
Sm-SPT16	ELWGGADAVAVFTPPRAEASELRYLKSSALNIWMLGYEFPDTLMVVFQALHFLCSQKKV	102
Pp-SPT16	EMWGGADAIIVTTPPAS--EDLRYLKSTALHIWLLGYEFPETVMVFMGALHFVCSKKA	94
Hs-SPT16	DEYANVDIAIVVS---VGVDIEIVYAKSTALQTLWLFGEYELTDTIMVFCDDKIIFMASKKKV	82
Dm-SPT16	DALRNLDCIMSI---VGVEEDVMYKSMALQLWLLGYELTDTISVFCSDAVYFLTSKKKI	87
	: : . : * * : * . * : : * : * : : * *	
Sc-SPT16	KHLQKAIDLFK----DPESKITLELWQRNNKEPELNKKLFDDVIALIN---SAGTKVGP	134
At-SPT16	SLLLEVKKPA---HDELKLDVIMHVKPKGDDGTGLMDAIFRAIRDLSRGGDNDQVVGHI	162
Ta-SPT16	NLIGTLKDA---SEAVGSDIILHVSKNGDGDIDLMDILRAVSAQSK---SDTPVVGHI	150
Os-SPT16	NLIGTLKKA---NDAVGADIIVLHVKAKNDSVGLMEDIVRAVCAQSK---SDDPIVGHI	152
Sb-SPT16	NLIGTLKKA---NESVGVDIIVLHVKTNGDGDADMHDIVQAARNQSK---SDKPIVGHI	149
Zm-Spt16	NLIGTLKKA---NEAVGVDIIVLHVKTNSDGDADMHDIVHAARNQSK---SDKPIVGHI	161
Gm-SPT16	SILESVKKA---REAVDADLVLHVKPRNDGTALMDAIFRALS---KSDGRDTPVVGHI	158
Pt-SPT16	SLLLEVKKPA---REVVGVDVVMHVKAKTNDGTGLMDAIFHAIYAQSSADGKDTPIVGHI	157
Vv-SPT16	SLLLEVVRKSA---KEAVGVEVVMHVKAASDDGTGLMDAIFRAVRANSS---SHDTPVVGHI	159
Sm-SPT16	KILEELQRP---RTSCGVVVLHVKLKRSDEGGPQMLEILDTVKAQ---SRSPVLGVL	154
Pp-SPT16	AHLEELQKSS---KMLTGVDIHHMKERKQDGSVQMNSVLDVAVKGFSK---GKTPVGV	148
Hs-SPT16	EFLKQIANTKGNENANGAPAITLLIREKNESNKSFFDKMIEAIKES----KNGKIGVF	137
Dm-SPT16	EFLKQTQNI---TEEGFPEINLLVRDRDTDKDQGNFEKLIKALQNS----KKGKRLGVF	138
	: : : : . : : *	
Sc-SPT16	EKDSYQGKFMTEWNPVWEAAVKENEFNVIDISLGLSKVWEVKDVNEQAFLSVSS-KGSDK	193
At-SPT16	AREAPEGKLETWTE---RLKNaNFQFVDITGGLSDLFAVKDDTEVMSVKKAAAYLAYS	218
Ta-SPT16	AREAPEGKLETWAE---KLAGGSVQLADVTHGFSELFVAVKDATEIICVKKAAAYLTSSV	206
Os-SPT16	AREAPEGKLEAWAD---KLSSSSVQLTDITNGFSELFAMKDTSEITCVKKASYLTSSV	208
Sb-SPT16	AREAPEGKLETWTE---KLSGSGVRLTDVTHGFSELFVAVKDTTEVTVCVKKAAAYLTSSV	205
Zm-Spt16	AREAPEGKLETWIK---KLSGSGRLVDVTHGFSELFVAVKDTTEITCVKKAAAYLTSSV	217
Gm-SPT16	SREAPEGKLEMWTE---KLKNTKFLQNDVANGLSLFAAKNNEELTSIKRAAYLTTSV	214
Pt-SPT16	AREAPEGIILETWAE---KLKGEFELADVTSGLSDLIAVKDADELINVKKAAFLTFVSV	213
Vv-SPT16	GREAPEGKLEMWTE---KLKNADFQLSDITNGFSDLFAMKDTSTELTNVKKAAFLTSSV	215
Sm-SPT16	AREAPEGTFMEKWDE---LLSSSRLEKVDVAAGLCEMFVAVKDESEINNKKAAAYLSATA	210
Pp-SPT16	SREATEGSVMKWA---CLEASGAATVDVSGGFSEIFAVKDEEIEISNIKNASHLSAAI	204
Hs-SPT16	SKDKFPGEFMKSWND---CLNKEGFDKIDISAVVAYTIAVKEDGELNLMKKAASITSEV	193
Dm-SPT16	AKDAYPGEFSEAWK---SLTASKFEHVDISTIIAYLMCPKDESEINNIRKASLVSMIDI	194
	: : * . * : : * : : * : * : : *	
Sc-SPT16	FMDLLSNEMVRAVDEELKITNAKLSDKIENKIDVVKFLKQLSPDLSALCPPNYKFNFDLL	253
At-SPT16	MKNVVVFNLESAIDEEKDVTHSALMDLTEKAILLEPTK-----ASVKLKPENV	265
Ta-SPT16	MKNFVVPKLEKVIDEERKVSHTSLMDDETEKAILDPLK-----AKVKLKPENI	253
Os-SPT16	MKNFVVPKLEKVIDEERKVSHTSLMDETEKAILDPLK-----VKVKLKAENV	255
Sb-SPT16	LKNFVVPKLEKVIDEERKVSHTSLMDDETEKAILDPLK-----VKVKLKPENV	252
Zm-Spt16	LKNFVVPKLEKVIDEERKVSHTSLMDDETEKAILDPLK-----VKVKLKPENV	264
Gm-SPT16	MKNFVVPKLENVIDEERKVSHTSLMDETEKAILLEPSK-----VNCKLKAENV	261
Pt-SPT16	MNNVVPKLENVIDEERKVSHTSLMDETEKAILDPTK-----AKAKLKAENV	260
Vv-SPT16	MKHVFPKLEKVIDEERKVSHTSLMDDETEKAILLEPAR-----VKVKLKAENV	262
Sm-SPT16	MKTFVVPKLEHVIDEERKVSHTSLMDETEKAILLEPPGK-----LKMKLAEGA	258
Pp-SPT16	LKSFVVPKLEVIDEERKVSHTSLMDETEKAILLEPPGK-----VKLKAEDV	250
Hs-SPT16	FNKFFKERVMEIVDADEKVRHSHKLAESVEKAIIEKK-----YLAGADPSTV	239
Dm-SPT16	FNKYLKDEIMDIDSDRKVKHKNLSDGCEAAIGEKK-----YTSGLDPRLL	240
	: : : : * : : * : : *	

Sc-SPT16 DWTYSPIIQSGGKFDLRVSARSTNDQLYGN--GCILASCGRYNNYCSNITRFLIDPSE 311
At-SPT16 DICYPPIFQSGGKFDLKPASAASNDPELLTYDPASIIICAVGARYNSYCSNVARTYLIDATS 325
Ta-SPT16 DICYPPVFQSGGKFDLRPGASSNDDYLYYDPASIIICAIGRYSYCSNVARTFLIDATP 313
Os-SPT16 DICYPPVFQSGGKFDLKPASSNDDYLYYDSASVIIICAIGARVYNYCSNMARTFLIDATP 315
Sb-SPT16 DICYPPVFQSGGKFDLKPASSNDEYLYYDSASVIIICAIISKYSSYCSNVARTYLIDATP 312
Zm-Spt16 DICYPPVFQSGGKFDLKPASSNDEYLYYDSASIIICAIISKYSSYCSNVARTYLIDATP 324
Gm-SPT16 DICYPPIFQSGGEFDLRPSAASNDPELLHYDSASVILCAIGARYKSYCSNIARTFLIDADP 321
Pt-SPT16 DICYPPIFQSGGEFDLRPSAASNDPELLYDSASVIIICAVGARYNSYCSNVARTFLIDATP 320
Vv-SPT16 DICYPPIFQSGGEFDLRPSAASNDENLYYDSTSVIIICAIGRYSYCSNVARTFLIDANA 322
Sm-SPT16 DVCYPPIFQSGGVFDLKASASQSNEDPLYYDATAVIIICALGGRYNMYCSNVARTYLIDADT 318
Pp-SPT16 DICYPPVFQSGGVFDLKPSAVSNEEPLYDYLTLGVILCAIGARFRSYCSNVARSIMIDADK 310
Hs-SPT16 EMCYPPIIQSGGNYNLKFSVSDKNHMHF---GAITCAMGIRFKSYCSNLVRTLMDVPSQ 296
Dm-SPT16 DMAYPPIIQSGGAYSLKFSAVADKNPLHF---GVIVCSLGARYKSYCSNISRTFLVNPTE 297
: * *::*** :.*: .. : : : . * : * : : ***** : * : : :

Sc-SPT16 EMANNYDFLLTLQKEIVTNILKPGRTPKVEVYESVIEYIEKTKPELVPNFTKNIGSLIGLE 371
At-SPT16 LQSKAYEVLLKAHEAAI-DALRSRGRKINTVYQAALSVVEKNAPEFVDKLTKSAGTGIGLE 384
Ta-SPT16 AQSKAYETLLKAQEAAI-AACKPGNQMSAVFKAADVAVFEKNAPELLPNLTKSAGTGIGLE 372
Os-SPT16 TQIKAYETLLKAHEAAL-EALKPGNRMSAVYQAAVDVIEKNAPELLRNLTKSAGTGIGLE 374
Sb-SPT16 KQSKAYETLLKAHEAAV-QEVKPGNQMSAVYQAAVAVIEKDAPELLPNLTKSAGTGIGLE 371
Zm-Spt16 TQNKAYETLRKAHEAAI-QQVKPGNQMSAVYQAAVAVIEKDAPELLPNLTKSAGTGIGLE 383
Gm-SPT16 LQSRAYGVLLKAHEAVI-GSLKPGNRLSATYQAAVSVVENEAPDLISYLTKSAGTGIGIE 380
Pt-SPT16 LQSKAYAVLLKAHEAAI-GALKPGNKVSAAYQAALSVVEEAEPELVPNLSKSAGTGIGLE 379
Vv-SPT16 MQSKAYEVLLKAHEAAI-GALKPGNKVSAAYQAALAVVEKDAPELVSNLTKSAGTGIGLE 381
Sm-SPT16 SQEKAYKALLKAQEAAI-NALRPGNLSAVYKAAATTLEREAPELSSFLTRSAGAGIGIE 377
Pp-SPT16 TQEKAYKILLKAHEAAI-AALRPGNAMSVAYKAAAYAVVESGGPEFLPYFTKNAGTGIGIE 369
Hs-SPT16 EVQENYFLLQLQEELL-KELRHGVKICDVYNAVMDVVKKQKPELLNKITKNLFGFMGIE 355
Dm-SPT16 AMQENYTFVSVQEELL-KLLVPTKLCVDYKTLDFVKKKPKSMVDNLPKSGFGFANGLE 356
. * * : : : * : : : . : : * : : : : * : : : * : : :

Sc-SPT16 FRDSNFILNVKNDYRKIQRGDCFNISFGFNLLKDSQS---ANNYALQLADTVQIPLDET 427
At-SPT16 FRESGLNINAKNDK-VLRPKMAFVNSLGFQNLCESESRSKNNKFSLLLADTVLVDQ-- 441
Ta-SPT16 FRESGLNINAKNDR-LIKEGMI FVNLGLSNIQAETN-NEKTKQF SLLLADTALVNDK-- 428
Os-SPT16 FRESGLNINAKNDR-I IKAGMVFNVS LGLHNLQAEKK-SEKTKQY SLLLADTCLVPL--- 429
Sb-SPT16 FRESGLNINAKNDR-KIKQGMVFNVS LGLHNVQAETT-SEKTKQF SLLLADTVLVNER-- 427
Zm-Spt16 FRESGLNINAKNDR-RIKKGMVFNVS LGLHNIQAETT-SEKTKQF SLLLADTVLVNER-- 439
Gm-SPT16 FRESGLNINAKNEQ-IVKEGMVFNVS LGFQNVQREST-KSKSKHF SLLLADTVI INKD-- 436
Pt-SPT16 FRESGLNINAKNDR-VVKAKMVFNVS LGFQNLQNLQID-NPKIRNF SLLLADTVI VGDQ-- 435
Vv-SPT16 FRESGLNINAKNDR-VLKPGMVFNVS LGFQNLQTDN-NPKTKQF SVLLADSVI VGEK-- 437
Sm-SPT16 YRESGLSLNPRNEK-VIKAGMVFNVNI GLQNL EIKSS-NPKTRTYG LLLADTI VVRDK-- 433
Pp-SPT16 FRESGLTLNAKNER-VIRPGMAFVNS LGFHNL TTESS-NPKSKTF SLLLADTAI VVEK-- 425
Hs-SPT16 FREGSLVINSKNQY-KLKKGMVFS INLGFSDL TNKEGKKPEEKTYALF IGDTVLVDED-- 412
Dm-SPT16 FRENSIVIGPKCQA-LLKKNMVFNLHVGISNL TNPEATDKEGKNYALF IGDTVLVGEQ-- 413
:* : : : : : : * : * : : : . : : : * : : :

Sc-SPT16 EPPRFLT-NYTKAKSQISFYFNNEEEDNKKKS-SPATKVPSKPDNRNISKILRTKL-RG-E 483
At-SPT16 KPELL-T-KCSKSVKDVAYSFKEDDEE---E---EKPRK---KARTSG-SE-NYITKTAL 487
Ta-SPT16 AAELIL-T-NCSKAVKDVAYSFNEDDEEVPK---PKRA---KVEPNG-VE-ALPSKATL 476
Os-SPT16 --ENLTA-SCSKLVKDVAYSFNDEDEVLPV---KK-----VEVNAK-EA-LPPTKATL 474
Sb-SPT16 GHDILTA-PCSKAVKDVAYSFNEDDEDV-A----EV-----KMESKT-ID-VMPKATL 473
Zm-Spt16 GHEVLTATA-PCSKAFKDVAYSFNEDDDAVAA---EV-----KIKSKT-ID-VMPKATL 486
Gm-SPT16 KTEVVTS-MSSKALKDIAYSFNEDDEE---E---ENPSA---KADANG-AE-PLMSKTTL 483
Pt-SPT16 NPDVVTS-KSSKAVKDVAYSFNEDDEE---EE---QPKA---RAEVNG-GE-NLMSKTTL 483
Vv-SPT16 GPEVVTS-ISSKAVKDVAYSFNEDDEE---ERPKV---KPEANG-GE-AVSSKATL 487
Sm-SPT16 GPDVVTS-LSSKAFQDIAYSFKDDEEPEERPRS-----KPASNG-AE-PVYVKATL 482
Pp-SPT16 GPPEVPTLKCSKTYTDIAYSFKDDEEDEVKVEAKPKV---KSESNGSNE-PAVRMATL 480
Hs-SPT16 GPATVLT-SVKKKVKNVGIFLKNEDDEEEEEE-----KDEAEDLLGRGSRAALL 460
Dm-SPT16 SPASVMT-PSKKIKNVGIFIKDSDDEEDVDDK--KTA---KEDQGTEILGRSKRNAVL 466
. : . * : : : : :

Sc-SPT16 ARGGAEDAQKEQIRKENQKKLHEKLEKNGLLRFSAAD-ANGPDSEPRQYFKKYESYVRDS 542
At-SPT16 -RSDDHVVSKEELRKHQAELARQKNEETARRLAGDSSGAGDSRSTAKTSADVAYKNVN 546
Ta-SPT16 -RSDNQEMSKEELRKHQAELARQKNEETARRLAGGGSGNGDGRGPRNSNELVAYKNVN 535
Os-SPT16 -RSDNQEMSKEELRKHQAELARQKNEETARRLAGVSGSGDGRGPRSSNELVAYKNVN 533
Sb-SPT16 -RSDNQEMSKEELRKHQAELARQKNEETARRLAGVSGSGDGRGPARASNELVAYKNVN 532
Zm-Spt16 -RSDNQEMSKEELRKHQAELARQKNEETARRLAGVGTGSGDGRGPARASNELVAYKNVN 545
Gm-SPT16 -RSDNHEMSKEELRKHQAELARQKNEETARRLAGGNETGDNRSSRSTSAELVAYKNIN 542
Pt-SPT16 -RSDNGEISKEELRKHQAELARQKNEETARRLAGGSAKGDNRRAASKTSTDLVAYKNVN 542
Vv-SPT16 -RSDNQEMSKEELRKHQAELARQKNEETARRLAGGGSGAGDNRGAVKATGDLIAYKNVN 546
Sm-SPT16 -RSDNQEMTKEDQRRQMQAELALKNEETARRLAGAFGHGEGHNMVKSSEGMTAYRNVD 541
Pp-SPT16 -RSDNQEMTKEDQRRQMQAELARQKNEETARRLAGGGLSGDGGQPNKTTGDI IAYRNVD 539
Hs-SPT16 TERTRNEMTAEKRRAHQKELAAQLNEEAKRRLTEQKGE---QQIQKARKSNVSYKNPS 516
Dm-SPT16 ESKLRNEINTEEKRKEHQRELAQQLNERAKDRLARQGNS---KEVEKVRKNTVSYKISIS 522
* : * : * : * : : : : * : : : : : : * : : :

Sc-SPT16 QLP--TNIRDLR IHVDWKSQTI ILLPIYGRVPPFHINSYKNGSKNEEG-EYTYLRLNFNSP 599
At-SPT16 DM---PH-KELMIQVDTRNEAVLLPIYGLVPPFHVATIRTVSGNQDTNRNCYIRIIFNV 602
Ta-SPT16 DV---PYSRELVIQVDQRNEAVLLPIYGSMPVPHVSTVKSVTSHQD-NRTCTIRIFFNV 591
Os-SPT16 DV---PYARELVIQVDQKNEAVLLPIYGSMPVPHVSTVKSVTSHQD-NRTCTIRIFFNV 589
Sb-SPT16 DV---PFVRDLVIQVDQKNEAVLLPIYGSMPVPHVSTVKSVTSHQD-NRTCTIRIFFNV 588
Zm-Spt16 DV---PFVRDLVIQVDQKNEAVLLPIYGSMPVPHVSTVKSVTSHQD-NRTCTIRIFFNV 601
Gm-SPT16 DL---PPPREAMIQIDQKSEAVLLPIGSMVPFHVAFIRTVSSQQDTNRNCYIRIIFNV 599
Pt-SPT16 DI---PPARDLMIQIDQKNEAVLLPIYGNMVPFHVSTIRTVSSQQDTNRCTYIRIIFNV 599
Vv-SPT16 DL---PPKELMIQVDQKNEAILLPIYGSMPVPHVATVKS SVSSQQDTNRCTYIRIIFNV 603
Sm-SPT16 EL---PFSRELMIQVDQKNEAVLLPIYGI M VPFHIATVRTINNHQDL-NSSIIRIIFNV 597
Pp-SPT16 DI---PA-RELKIHVDQKNEAVLLPVYGLLVPFHATVKS SVSSQQDG-GHSYIRIIFNV 594
Hs-SPT16 LMPKEPHIREMKIYIDKKYETVIMPVFGIATPFIATIKNISMSVEG-DYTYLRINFCY 575
Dm-SPT16 QMPREPEVKELKLVYDVKKYETVIMPVFGIQVPFHISTIKNISQSVEG-EYTYLRINFHP 581
: : : : * : : : : * * : : : : * * :

Sc-SPT16 GSSGGISKVVEELPYEESADNQFVRSITLRSKDGDRMSET-----FKQIADLKKE 649
At-SPT16 GTPFNP-----DSNLSKNQGAIYLKEVFRKDSRHSSEV-----TQQIKTLRRQ 648
Ta-SPT16 GMPFSND-----KDLKSQGAIYLKEITFRSKDPRHSSEV-----VQQIKTLRRQ 635
Os-SPT16 GMPFSND-----SNLKSQGAIYLKEITFRSKDPRHSSEV-----VQQIKTLRRQ 633
Sb-SPT16 GMPFSND-----SKLNSQGAIYLKEITFRSKDPRHSSEV-----VQQIKTLRRQ 632
Zm-Spt16 GMPFSND-----SKFNSQGAIYLKEITFRSKDPRHSSEV-----VQQIKTLRRQ 645
Gm-SPT16 GTPFSPH----DSNSMKFQGS IYLKEASFRSKDSRHISEV-----VQSIKTLRRQ 645
Pt-SPT16 GAAPNP-----DSNLSKHQGAIYLKEVFRSKDPRHISEV-----VQLIKTLRRH 645
Vv-SPT16 GTPFSPH----DSNSMKFQGS IYLKEVFRSKDPRHISEV-----VQMIKTLRRQ 649
Sm-SPT16 GAGFTTN----DVPFQKFPHMIYLKEISFRSTDIKHSTQI-----VQMMKTLKRQ 643
Pp-SPT16 GAGFGPN----DVPTQKFPFRSIYVKEVFRSNDTRHSYQV-----VQLIKTLRRQ 640
Hs-SPT16 GSALGRN----EGNIFPNPEATFVKIETYRASNIKAPGEQTVPALNLQNAFRIKEVQKR 631
Dm-SPT16 GATMGRN----EGGLYPQPEATFVKEVITYRSSNVKEHGVGAPSANLNNAFRIKEVQKR 637
* : : : : * : : : : * : : : : *

Sc-SPT16 ATKREQERKALADVQQDKLIENK-TGRTRKLDQIFVRPNPDT--KRPSTVFIHENGIR 706
At-SPT16 VMARESERAERATLVTQEKLQLAGNKFKPLRLSELWIRPPFSGR-KKIPGTLEAHANGFR 707
Ta-SPT16 VASRESERAERATLVTQEKLQASNKTKQMLNDVWIRPPFGGRGRKLTGTLEAHVNGFR 695
Os-SPT16 VASRESERAERATLVTQEKLQLTSNRKMPVRLSDVWIRPAFGGGRGRKLTGTLESHVNGFR 693
Sb-SPT16 VASRESERAERATLVTQEKLQIGNRMKMLRLSDVWIRPAFGGGRGRKLTGNLEAHVNGFR 692
Zm-Spt16 VASRESERAERATLVTQEKLQIGSNRMKMMRLSDVWIRPAFGGGRGRKLTGNLEAHVNGFR 705
Gm-SPT16 VVARESERAERATLVTQEKLQLANRFRKPIRLSDLWIRPAFGGGRGRKIPGTLEAHVNGFR 705
Pt-SPT16 VVARESERAERATLVTQEKLQLAGNRFRKPIRLTDLWIRPVFTGRGRKLPGALEAHVNGFR 705
Vv-SPT16 VASRESERAERATLVTQEKLQLAGTRFRKPIRLSDLWIRPSFGGGRGRKLTGSLESHTNGFR 709
Sm-SPT16 VSQRESEKAERATLVTQEKLQISK--GKAIRLSDLWIRPPFAGRKR--RGTLEAHVNGFR 700
Pp-SPT16 VAQRESERAERATLVTQERLQIGK--GRPIRLSDLWIRPAFGGGRGRKMSGTLEAHVNGFR 698
Hs-SPT16 YKTREAEKEKEGIVKQDSLVINLNRSNP-KLKDLYIRPNIAQ--KRMQGSLEAHVNGFR 688
Dm-SPT16 FKTREAEEREKEDLVKQDQTLILSQNGNP-KLKDLYIRPNIVT--KRMTGSLEAHVNGFR 694
** * : * * : * : * : : : * : : * * * :

Sc-SPT16 FQSPLRTDSRIDILFNSIKNLIFQSCKGELIVVIHHLKNPILMGKKKIQDVQFYREASD 766
At-SPT16 YST-TRPDERVDLRFANIKHAFFQPAEKEMITLLHFHLHNNIMVGTKKTKDVQFYVEVMD 766
Ta-SPT16 YST-SRADERVDIMYGNIKHAFQPAEKEMITLLHFHLHNNIMVGNKTKDVQFYVEVMD 754
Os-SPT16 YST-SRADERVDIMYGNVKAFFQPAEKEMITLLHFHLHNNIMVGNKTKDVQFYVEVMD 752
Sb-SPT16 YST-SRSDERVDIMFGNIKHAFQPAEKEMITLLHFHLHNNIMVGNKTKDVQFYVEVMD 751
Zm-Spt16 YST-SRSDERVDIMFGNIKHAFQPAEKEMITLLHFHLHNNIMVGNKTKDVQFYVEVMD 764
Gm-SPT16 YST-TRQDERVDIMFGNIKHSFFQPAENEMITLLHFHLHNNIMVGNKTKDVQFYVEVMD 764
Pt-SPT16 FST-SRSEERVDIMFNSIKHAFFQPAEKEMITLLHFHLHNNIMVGNKTKDVQFYVEVMD 764
Vv-SPT16 YST-SRSPERVDIMYGNIKHAFQPAEKEMITLLHFHLHNNIMVGNKTKDVQFYVEVMD 768
Sm-SPT16 YST-MKAETVVDILYRNIRHAFFQPAEKEMITLLHFHLHNNIMVGNKTKDVQFYVEVMD 759
Pp-SPT16 YST-MRQEEKVDIMYRNIKHAFFQPAEKEMITLVHFHLHNNIMVGTKKTKDVQFYVEVME 757
Hs-SPT16 FTS-VRG-DKVDILYNNIKHALFQPCDGEIIVLHFHLKNAIMFGKKRHTDVQFYTEVGE 746
Dm-SPT16 YIS-VRG-DKVDILYNNIKSAFFQPCDGEIIVLHFHLKYAIMFGKKKHVDVQFYTEVGE 752
: : : : * : : : * * : : * * : : * * : : * * : * * * : * * :

Sc-SPT16 MSVDETGGGRRGQSRFRYRQDEDELEQEERKRRAALDKEFKYFADAIAEA-----SN 820
At-SPT16 VVQSL-GGGR-----SAYDPDEIDEEQRERDRKNINMDFNHFANRVNDMWSQPQFAS 819
Ta-SPT16 VVQTV-GGSRR-----SALDPDEIDEEQRERDRKNINMEFQNYINKVNDHWSQPQFKG 807
Os-SPT16 VVQTL-GGNRR-----SALDPDEIDEEQRERDRKNINMDFQNFVNKVNDSHWSQPQFKG 805
Sb-SPT16 VVQTV-GGSRR-----SALDPDEIDEEQRERDRKNINMDFQNFVNKVNDSHWSQPQFKG 804
Zm-Spt16 VVQTL-GGSRR-----SALDPDEIDEEQRERDRKNINMDFQNFVNKVNDSHWSQPQFKG 817
Gm-SPT16 MVQNV-GGGR-----SAYDPDELEEEQRERDRKNINVEFQTFVNRNLNDLWGQPQFNG 817
Pt-SPT16 VVQTV-GGGR-----SAYDPDEIDEEQRERDRKNINMDFQSFVNRVNDLWSQPQFSG 817
Vv-SPT16 VVQTV-GGGR-----SAYDPDEIDEEQRERDRKNINMDFQNFVNKVNDSHWSQPQFKG 821
Sm-SPT16 GVQNV-GGSRR-----SHFDPDEIDEEQAERERKNKLNKEFEVFKVTDLWEPALRN 812
Pp-SPT16 VVQTV-GGSRR-----SMDPDEIDEEQERDRKNINKEFEAFVVRMAELWDQPWRE 810
Hs-SPT16 ITTDL-GKH-Q-----HMHDRDDLAEQEMERMRHKLKTAFAKNIEKVEAL-----TK 792
Dm-SPT16 ITTDL-GKH-Q-----HMHDRDDLAEQAELELRHKLKTAFAKSFCEKVETM-----TK 798
* : * : * : * * : : * : * : : :

Sc-SPT16	GLLTVENTFRDLGFQGVPNRSVAVFCMPTTDCVLQLEPPFLVINLEEEVICILERVQFGL	880
At-SPT16	LDLEFDQPLRELGFHGVPHKTSAFI IPTSSCLVELIEYPPFLVSVLSEIEIVNLERVGFQ	879
Ta-SPT16	LDLEFDIPLRELGFHGVVYKASAFI IPTSTCLVELIETPFLVVTLGEIEIVNLERVGFQ	867
Os-SPT16	LDLEFDVPLRELGFHGVVYKASAFI IPTSTCLVELIETPFLVVTLSEIEIVNLERVGFQ	865
Sb-SPT16	LDLEFDVPLRELGFYGVVYKASAFI IPTSTCLVELIENPFLVSVLSEIEIVNLERVGFQ	864
Zm-Spt16	LDLEFDVPLRELGFHGVVYKASAFI IPTSTCLVELIETPFLVSVLSEIEIVNLERVGFQ	877
Gm-SPT16	LDLEFDQPLRELGFPGVPHKSSVFIVPTSACLVELIETPFLVVTLSEIEIVNLERVGLGQ	877
Pt-SPT16	LDLEFDQPLRELGFHGVPHKVSFIVPTSACLVELIETPFLVVTLGEIEIVNLERVGLGQ	877
Vv-SPT16	LDLEFDQPLRELGFHGVPHKASAFI VPTSACLVELIETPFLVITLSEIEIVNLERVGLGQ	881
Sm-SPT16	YGLEFDIPFRELGFHGVPNKTSAFI VPTVKCLVELIEFPFLVTVEDIELVNLERVGFAQ	872
Pp-SPT16	LDLEFDIPFRELGFHGVPNKSSAFI VPTVNCLVELIETPFLVSVLNDIEIVNLERVGLGQ	870
Hs-SPT16	ELEFEVFPFRDLGFNGAPYRSTCLLQPTSSALVNATEWPPFVVTLDEVELIHFERVQFHL	852
Dm-SPT16	SVVEFDTPFRELGFPGAPFRSTVTLQPTSGSLVNLTEWPPFVITLDDVELVHFERVQFHL	858
	: .: :*:*** *. * : : ** .** : * * :*: : :*: :*** :	
Sc-SPT16	KNFDMVFVYKDFNKPVTHINTVPIESLDFLKQWLTDMDIPYTVSTINLNWATIMKSLQDD	940
At-SPT16	KNFDMAIIFKDFKDKDVLRVDSVPTSSLEGIKEWLDTTDIKYYESKLNLNWRQILKTIIDD	939
Ta-SPT16	KNFDMAIVFKDFKDKDVLRLIDSIPSTSLDAIKEWLDTTDLKYYESRLNLNWRPILKTIIDD	927
Os-SPT16	KNFDMAIVFKDFKDKDVLRLIDSIPSTSLDAIKEWLDTTDLKYYESRLNLNWRPILKTIIDD	925
Sb-SPT16	KNFDMAIVFKDFKDKDVLRLIDSIPASLDAIKEWLDTTDLKYYESRLNLNWRPILKTIIDD	924
Zm-Spt16	KNFDMAIVFKDFKDKDVLRLIDSIPASLDAIKEWLDTTDLKYYESRLNLNWRPILKTIIDD	937
Gm-SPT16	KNFDMTIVFKDFKRDVLRIDSIPSTSLDGKIKEWLDTTDIKYYESRLNLNWRQILKTIIDD	937
Pt-SPT16	KNFDMTIVFKDFKRDVLRIDSIPSTSLDGKIKEWLDTTDIKYYESRLNLNWRQILKTIIDD	937
Vv-SPT16	KNFDMTIVFKDFKRDVLRIDSIPSTSLDGKIKEWLDTTDLKYYESRLNLNWRPILKTIIDD	941
Sm-SPT16	KAFDMAIIFKDFKDKDVLRLIDAIPTSLDNKIKEWLNSMAIKYYESRMNLNWRPILKTIIDD	932
Pp-SPT16	KAFDMAIVFKDFKREVLRLIDAIPTSLDGKIKEWLNSMNIKYYESRMNLNWRPILKTIIDD	930
Hs-SPT16	KNFDMVIVYKDYSKKVTMINAIPVSLDPIKEWLNSCDLKYTEGVQSLNWTIMKTIIDD	912
Dm-SPT16	RNFDMIVFVKEYNKKVAMVNAIPMNLMDHVKEWLNSCDIRYSEGVQSLNWTIMKTIIDD	918
	: *** .:*** : * :*: * :*: * : * . *** *:* : *	
Sc-SPT16	PYQFFLDGGWNFLATGSDDEASD---ESEEVESEYEASEDDVSDSESAFSEDEEGSEVDD	996
At-SPT16	PQSFIDDDGGWEFLNLDGSDSESG---GSEESDKGYEPSDVEVESESEDEASESESLVES	995
Ta-SPT16	PQKFVDDGGWEFLNMEASDSEAE---ETEESDQGYEPSDAEPESESEEDSDSASLVES	983
Os-SPT16	PQKFIDDDGGWEFLNMEASDSETE---ETEESDQGYEPSDAEPESESEEDSDSASLVES	981
Sb-SPT16	PQKFIDDDGGWEFLNMEASDSETE---ETEESDQGYVPSDAEPESESEEDSDSASLVES	980
Zm-Spt16	PQKFIDDDGGWEFLNMEASDSETE---DTEESDQGYVPSDAEPESESEEDSDSASLVES	993
Gm-SPT16	PQSFIEGGGWEFLNLEATDSESE---NSEESDKGYEPSDVEPESEDEASDSESLVES	993
Pt-SPT16	PQSFIDDDGGWEFLNLEASDSDSD---NSEDSDQGYIPSDAEPESESEEDVSDSASLVES	993
Vv-SPT16	PEKFIEDGGWEFLNLEVSDDSDSE---NSQESDQGYEPSDVQSDTGSEEEGDDSESLVES	997
Sm-SPT16	PKKFIDDDGGWEFLNMEASDSESE---KSEESDKGYEPSDLEPSESEDEGSDSESVVES	988
Pp-SPT16	PKKFIEDGGWEFLNMEASDSESD---KSEESDEGYEPSDVEVSESEEDSDSDES SVVES	986
Hs-SPT16	PEGFFEQQGWSFLEPEGEESDAEEGSDSESEIEDETFNPSEDDYEEEEED--SDEYSSEA	970
Dm-SPT16	PEGFFEQQGWTFLDPESGSEGENE--TAESEDEAYNPTDAES--DEESD--EDSEYSEAS	973
	* * . *** ** : : : . . :	
Sc-SPT16	DISGDESEDYTGDESEEGEDWDELEKKAARADRGANFRD-----	1035
At-SPT16	-DDDEEDSEQSEEEKGKTWDELEREATNADREHGVEDSEERKRRKMKAFGKSRPQT	1054
Ta-SPT16	-DEDEEEDSDESEEEKGKTWDELEREATNADRDHGAESDSEERRRRKVKTFKSGAPP	1042
Os-SPT16	-DEDEEDDSEEDSEEEKGKTWEELEREASNADRENGAESDSEERRRRKVKTFKSRPPP	1040
Sb-SPT16	-DDDE-ESDESEEEKGKTWEELEREASNADREHGAESDSEERRRRKAKTFKSKRAPE	1038
Zm-Spt16	-DDDDE-ESDESEEEKGKTWEELEREASNADREHGAESDSEERRRRKAKTFKSKRAPE	1051
Gm-SPT16	-EDDGEEDSEEDSEEEKGKTWEELEREASNADREKGNESDSEEDRKRKAKSFGKSRGAG	1052
Pt-SPT16	-EDDEEEDSEEDSEEEKGKTWEELEREASNADREKGDSDSEERNRRKVKTFKSKRAP	1052
Vv-SPT16	-EDDVEEDSDGDESEEQGKTWEELEREASNADREKREKGDSEERKRRKMKAFGKARVPE	1056
Sm-SPT16	-EDDEE--EEDSDEEEEGMSWDELEAKASKEDKEKGDSESEERRRRKAKMTGKTRASP	1045
Pp-SPT16	-DDDEA-EEEESEEEGLTWDQLEEAARKDDKMGDEEDSEDERHRNRKKAAGKGRMPD	1044
Hs-SPT16	-EESDYSKESLGSSEESGKDWDLEEEARKADRESRYEEEEEQSRMSRKR---KASVHS	1026
Dm-SPT16	-EDSEESDEDLGSDEESGKDWDLEREAEEEDRNHDYAADDKPRNGKFDKSKHGKSSKHS	1032
 :*. * * : ** * . * :	
Sc-SPT16	-----	1035
At-SPT16	SGGGSSSMKN-----M--PPSK-----RKHR	1074
Ta-SPT16	QRGPSSSKHAPLPQRGG---SSSGNKS--PPSSSK-----GPPSKPKFR	1085
Os-SPT16	ER-----SSFK-----G-GPSKPKFR	1056
Sb-SPT16	-R-----SSFK-----GAPPSKPKFR	1054
Zm-Spt16	-R-----SSFK-----GAPPSKPKFR	1067
Gm-SPT16	L-----S-----SSMTKRPKLR	1064
Pt-SPT16	RPAPRPAPR-----PAPR--PPRTVP-----GSMPKRPKFR	1082
Vv-SPT16	-----KRSTR-----GSLPKRPKLR	1071
Sm-SPT16	K-----APPKRFKTR	1056
Pp-SPT16	PR-----DAK-----RGQPNKRPKVR	1060
Hs-SPT16	SGRG-----SNRGRHSSA-----PPKRRK-----	1047
Dm-SPT16	PSKSSK--DKYNSRDKHHSSSSSGNKSSSKDKDRKRSRDRDNGHKS KSRH-	1083

Figure S2. Amino acid sequence alignment of SPT16 from different organisms. Sequences (plant, green; metazoan, red; fungal, blue) were retrieved by database searches using blastp (<https://blast.ncbi.nlm.nih.gov/>) using At-SPT16 as query. The sequences were aligned using Clustal Omega (<https://www.ebi.ac.uk/Tools/msa/clustalo/>). The species of which the protein sequences were retrieved are indicated as follows: *Arabidopsis thaliana* (At), *Drosophila melanogaster* (Dm), *Glycine max* (Gm), *Homo sapiens* (Hs), *Oryza sativa* (Os), *Physcomitrella patens* (Pp), *Populus trichocarpa* (Pt), *Saccharomyces cerevisiae* (Sc), *Selaginella moellendorffii* (Sm), *Sorghum bicolor* (Sb), *Triticum aestivum* (Ta), *Vitis vinifera* (Vv), *Zea mays* (Zm).