

Sc-Pob3 --MSTDFDRIYLN--QSKFSGRFR IADSGLGWKISTSGGSAANQARKPFLLPATELSTVQ 56
Sm-SSRP1 MGDHQAQFNILLGGRGGANPGQLKISSKGFWRKSGGGKV-----VDVAKDDVKSVS 52
Pp-SSRP1 ----HQFNSILLGGRGGTNPGLKINSGGFQWRKAGGGKV-----VEVSTSDIASLS 48
Hv-SSRP1 MTDGHHFNILLGGRAGTNLQGFVHSGGLAWKRQGGGKT-----IEIDKADLTSVT 52
Os-SSRP1 MTDGHLFNILLGGRAGSNPGQFVKVYSGGLAWKRQGGGKT-----IEIEKSDLTSVT 52
Zm-SSRP1 MTDGHHFNILLGGRGGTNPQGFVHSGGLAWKRQGGGKT-----IEIDKADVAVT 52
Sb-SSRP1 MTGGHHFNILLGGRGGTNPQGFVYSGGLAWKRQGGGKT-----IEIDKADVAVT 52
At-SSRP1 MADGHSFNNISLGRGGKNPGLKINSGGIQWKKQGGGKA-----VEVDRSDIVSVS 52
Pt-SSRP1 MTDGHLFNILLGGRGGTNPGLKISPGGILWKKQGGGKA-----VEVDRADILGVT 52
Vv-SSRP1 MSEGHLFNNISLGRGGTNPQQLRVHPGGILWKKQGGGKA-----VEVDKSDIVGVT 52
Gm-SSRP1 MTDGHLFNNILTLGGRGGTNPQGIKIYPGGIIWKRQGGGKL-----IEVDKSDIMGVT 52
Dm-SSRP1 MTDLSLEYNDINAEVRGVLCSGRLKMTQNIIFKNKTGTGV-----EQISAEDIDLIN 52
Hs-SSRP1 MAETLEFNDVYQEVKGSMDNDRRLRSRQGIIFKNSKTGV-----DNIQAGELTEGI 52
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Sc-Pob3 WSRGCRGYDLKINTKNQGVILQDGFSDDDYLNLIKNDHFRRFNIQVEQREHSLRGWNWGT 116
Sm-SSRP1 WTRVRSYQMSIRLKAGSNVKTGFREQDVSSLNTFITSNIGVTPQDKPLAVSGRNWGEA 112
Pp-SSRP1 WTRVPKGFQGLVGLKAGRDVKNFNGFRESDMANLGSFFTTNMGITSEEKPLAISGRNWGDV 108
Hv-SSRP1 WMKVPRAYQLGVRVKDGLSYTFIGFREQDVSSLNFMQKNMGISPDEKQLSVGGHNWGM 112
Os-SSRP1 WMKVPRAYQLGVRTKDGLFYKFIGFREQDVSSLNFMQKNMGLSPDEKQLSVSGQNWGGI 112
Zm-SSRP1 WMKVPRAYQLGVRKAGLFYRFIGFREQDVSSLNFIQKNMGVTPDEKQLSVSGQNWGGI 112
Sb-SSRP1 WMKVPRAYQLGVRKIDGLFYRFIGFREQDVSSLNFIQKNMGVTPDEKQLSVSGHNWGGI 112
At-SSRP1 WTKVTKSNQLGVKTKDGLYKFIGFRDQDVPSSLSSFFQSSYGKTPDEKQLSVSGRNWGEV 112
Pt-SSRP1 WMKVPRTNQLSVLIIKGGPWYKFIGFRDQDLSTLTNFFQ-SHGITPEEKQLSVSGRNWGEV 111
Vv-SSRP1 WMKVPRTNQLGVRVKDGLYKFIGFREQDVTLNFFQHSCLNPEEKQLSVSGRNWGEV 112
Gm-SSRP1 WMKVPRSNQLGVQIKDGLYKFIGFRDQDVVSSLNFFQNTCGISVEEKQLSVSGRNWGEV 112
Dm-SSRP1 SQKFVGTWGLRVFTKGGVLRHRTGFRDSEHEKLGKFIKAAYSQEMVEKEMCVKGNWGT 112
Hs-SSRP1 WRRVALGHGLKLLTKNGHVYKDFRESEFEKLSDFFKTHYRLELMKDKLVCVGNWGT 112
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Sc-Pob3 DLARNEMVFALNGKPTFEIPYARINNTNLTSKNEVGIEFNIQDEEYQP--AGDELVEMR 173
Sm-SSRP1 ELEGNTLSFVVGKPAFEICVADI SNTQVQKNDVQMEFHVDD-----TANEKDTLMEMS 167
Pp-SSRP1 TLEGSSLAFSVGGKHAFDVSIADVSQTQMQGKNEVMLEFHVDD---TTGASEKDTLMELS 165
Hv-SSRP1 DIDGSSLTFMVGSKQAFEFSLADVSTQTLQKTDVLEFHVDD---TTGANEKDSLMDMS 169
Os-SSRP1 DINGNMLTFMVGSKQAFEVSLADVSTQTLQMQGKTDVLEFHVDD---TTGGNEKDSLMDLS 169
Zm-SSRP1 DIDGNMLTFMVGSKQAFEVSLPDVAQTQMQGKTDVLELHVDD---TTGANEKDSLMDLS 169
Sb-SSRP1 DIDGNMLTFMVGSKQAFEVSLADVAQTQMQGKTDVLELHVDD---TTGANEKDSLMDLS 169
At-SSRP1 DLHGNTLTLFVVGSKQAFEVSLADVSTQTLQKNDVTFEFHVDD---TAGANEKDSLMEIS 169
Pt-SSRP1 DLNGNMLTLFVVGSKQAFEVSLADVSTQTLQKNDVILEIDAIISNYILLCLQKDSLMEIS 171
Vv-SSRP1 DLNGNMLTLFVVGSKQAFEVSLADVSTQTLQKNDVILEFHVDD---TTGANEKDSLMEIS 169
Gm-SSRP1 DLNGNMLAFTVVGSKQAFEVSLADVSTQTLQKNDVILEFHVDD---TTGANEKDSLMEIS 169
Dm-SSRP1 RFMGSVLSFDKESKTI FEVPLSHVQC-VTGKNEVTLEFHQND-----DAPVGLLEMR 164
Hs-SSRP1 KFGGQLLSFDIGDQPVFEIPLSNVQC-TTGKNEVTLEFHQND-----DAEVSLEMEVR 164
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Sc-Pob3 FYIPGVIQTNVDENMTKKEESSNEVVPKEDGAEGEDVQMAVEEKSMAEAFYEELKEKAD 233
Sm-SSRP1 FHVPTNTTFVG-----DEERASAQVFCDKILSMAD 198
Pp-SSRP1 FHIPTNTTYIG-----DEERPPAQIFREKILSMGD 196
Hv-SSRP1 FHVPTSNTQFPG-----NENRTSAQILLEAILERAD 200
Os-SSRP1 FHVPTSNTQFLG-----DENRTAAQVLWETIMGVAD 200
Zm-SSRP1 FHVPTSNTQFVG-----DESRRPAHILWETILKFAD 200
Sb-SSRP1 FHVPTSNTQFVG-----DENRPPAHILWETILKFAD 200
Pt-SSRP1 FHIPNSNTQFVG-----DENRPPSQVFNFTIVAMAD 200
At-SSRP1 FHIPNNNTQYIG-----DENHPPAQVFRDLIVQKAD 202
Vv-SSRP1 FHIPNSNTQFVG-----DENRPPAQVFRDKIMSMAD 200
Gm-SSRP1 FHIPNSNTQFVG-----DENRPPAQVFRDKIMSMAD 200
Dm-SSRP1 FHIPAVES-----AEEDPVDFKHQNVMSKAS 190
Hs-SSRP1 FYVPPTQE-----DGVPVEAFAQNVLSKAD 190
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Sc-Pob3 IGEV-AGDAIVSFQDVFFTTPRGRYDIDIYKNSIRLRGKTYEYKLQHRQIQRIVSLPKAD 292
Sm-SSRP1 VGPA-GGEAAVAFETVNVLTTPRGRYLVELHLSFLRLFG-ASDFKIQYTSVARLFLVLPKSA 256
Pp-SSRP1 VGPS-GAEAIALFEVHILTPRGRYNVELHASFLRLQGGANDFKIQYSSVVRFLILPKSN 255
Hv-SSRP1 TSSGSSGEAVVTFEGIAILTPRGRYAVDLHLSFLRLQGGANDFKIQYSSIVRFLFLPKSN 260
Os-SSRP1 V--DSSEEAVVTFEGIAILTPRGRYSVELHLSFLRLQGGANDFKIQYSSIVRFLFLPKSN 258
Zm-SSRP1 V--GSSEEPVVTTFEGIAILTPRGRYSVELHLSFLRLQGGANDFKIQYSSIVRFLFLPKSN 258
Sb-SSRP1 V--GSSEEPVVTDFEGIAILTPRGRYSVELHLSFLRLQGGANDFKIQYSSIVRFLFLPKSN 258
At-SSRP1 VSPG-VEDAVVTFESIAILTPRGRYNVELHLSFLRLQGGANDFKIQYSSVVRFLFLPKSN 259
Pt-SSRP1 VGAG-GEEAVVTFEGIAILTPRGRYSVELHLSFLRLQGGANDFKIQYSSVVRFLFLPKFN 261
Vv-SSRP1 VGAG-GEEAVVTFEGIAILTPRGRYSVELHLSFLRLQGGANDFKIQYSSVVRFLFLPKSN 259
Gm-SSRP1 VGAG-GEDAVVTFEGIAILTPRGRYSVELHMSFLRLQGGANDFKIQYSSVVRFLFLPKSN 259
Dm-SSRP1 VISA-SGESIAIFREIQILTTPRGRYDIKIFSTFFQLHGKTFDYKIPMDSVLRFLMLPHKD 249
Hs-SSRP1 VIQA-TGDAICIFRELQCLTPRGRYDIRIYPTFLHLHGKTFDYKIPYTTVLRFLFLPHKD 249
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Sc-Pob3 DIHLLLVLAIEPPLRQGGTTPYFVLVLFQKDEETEVLQNLLEDEDEYEENYKDKLKKQYDAK 352
Sm-SSRP1 QSSTYVVITLDDPPIRKGQTFYPHIVFQYQSEETELTPLISDELLNTKYKDRLAPQYKGL 316
Pp-SSRP1 QPHTFVVITLDDPPIRKGQTFYPHIVLQFPSEETIAECTLSIGEEELLNTKYKDRLQPAYKDL 315
Hv-SSRP1 NPHTIVVVITLDDPPIRKGQTLPHIVIQFETETVVQKNMKSRELLDEKYKDRLEESYQGL 320
Os-SSRP1 NPHTFVVVITLDDPPIRKGQTLPHIVIQFETEAVVERNLALTKVELLAEKYKDRLEESYKGL 318
Zm-SSRP1 NPHTFVVITLDDPPIRKGQTLPHIVIQFETEAVVERDLALSKELLVEKYKDRLEESYKGL 318
Sb-SSRP1 NPHTFVVITLDDPPIRKGQTLPHIVIQFETEAVVERDLALSKELLVDKYKDRLEESYKGL 318
At-SSRP1 QPHTFVVISLDDPPIRKGQTMYPHIVMQFETDTVVESELSISDELMTKFKDKLERSYKGL 319
Pt-SSRP1 QPHTFVVVITLDDPPIRKGQTLPHIVLQFDTDFVQSNLSMSEDLLYTKYKDKLEPSYKGL 321
Vv-SSRP1 QPHTFVVVITLDDPPIRKGQTLPHIVMQFETDYVQSELSLSEELLNSKYKDKLEPSYKGL 319
Gm-SSRP1 QPHTFVVIISLDDPPIRKGQTLPHIVMQFETDYVVESELAINEDLYNTKYKDKLDLSYKGL 319
Dm-SSRP1 SRQMFVFLSLDDPPIKQGQTRYHYLVLLFAPDEETIIELPFSEALRDKYEGKLEKESGP 309
Hs-SSRP1 QRQMFVVISLDDPPIKQGQTRYHFLILLFSKDEDISLTLNMNEEEVEKRFEGRLTKNMSG 309
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Sc-Pob3 THIVLSHVVLKGLTDRRIVIPG-EYKSKYDQCAVSCSFKANEGYLYPLDNAFFFLTKPTLY 411
Sm-SSRP1 SYEVFVEILRGLSGAGITKPGTKFRSSQEGYAVRAALKAEEGLLYPLEKSFFFLKPPTL 376
Pp-SSRP1 SHDVFTQILKGLSGAKVTRPG-KFRSAQDGYCVRTSLKAEEGLTYPLEKSFFFLKPPTL 374
Hv-SSRP1 VHEVFKVLRGLSGAKVTRPG-SFRSYKNGYAVKSSLKAEDGLLYPLEKGFFFLKPPTL 379
Os-SSRP1 IHEVFTKVLRLGLSGAKVTRPG-SFRSCQDGYAVKSSLKAEDGLLYPLEKGFFFLKPPTL 377
Zm-SSRP1 IHEVFTKVLRLGLSGAKVTRPG-SFRSCQDGYAVKSSLKAEDGLLYPLEKGFFFLKPPTL 377
Sb-SSRP1 IHEVFTKVLRLGLSGAKVTRPG-SFRSCQDGYAVKSSLKAEDGLLYPLEKGFFFLKPPTL 377
At-SSRP1 IHEVFTTVLRWLSGAKITKPG-KFRSSQDGFVAVKSSLKAEDGVLYPLEKGFFFLKPPTL 378
Pt-SSRP1 IHEVFTTILRGLSGAKVTRPG-KFRSCQDGYAVKSSLKAEDGVLYPLEKSFFFLKPPTL 380
Vv-SSRP1 IHEVFTLILRGLSGAKVTKPG-KFRSCQDGYAVKSSLKAEDGVLYPLEKSFFFLKPPTL 378
Gm-SSRP1 IHEVFTTILRGLSGAKVTKPG-KFRSCQDGYAVKSSLKAEDGILYPLEKSFFFLKPPTL 378
Dm-SSRP1 VYEVMGKVMKVLIGRKITGPG-NFIGHSGTAAVGC SFKAAAGYLYPLERGFYIYHKPPLH 368
Hs-SSRP1 LYEMVSRVMKALVNRKITVPG-NFQGHSGAQCITCSYKASSGLLYPLERGFYIYHKPPVH 368
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Sc-Pob3 IPFSDVSMVNISRAGQTS---TSRFTDLEVLRLSRNGSTTFANISKEEQQLLEQFLKSK 468
Sm-SSRP1 IVYEEIDYVEFERHGAAGTSSMSKNFDLILRLKTD-QEHLFRNISRNEYHSLFKFISEK 435
Pp-SSRP1 ILHDEIEYLEFERHGAAGTSSISSHYFDLLIRLKSE-QEHQFRNIQRNEYHNLNFNISGK 433
Hv-SSRP1 ILHEEIEFVEFERHGAGG-ASMSQYFDLLVKLKTND-QEHLFRNIQRSEYHNLNFNINGK 437
Os-SSRP1 ILHEEIEFVEFERHGAGG-ASISSHYFDLLVKLKTND-QEHLFRNIQRSEYHNLNFNINGK 435
Zm-SSRP1 ILHEEIEFVEFERHGAGG-ASISSHYFDLLVKLKTND-QEHLFRNIQRNEYHNLNFNINGK 435
Sb-SSRP1 ILHEEIEFVEFERHGAGG-ASISFHYFDLLVKLKTND-QEHLFRNIQRNEYHNLNFNINGK 435
At-SSRP1 ILHDEIDYVEFERHAAGG-ANM--HYFDLLIRLKT-HEHLFRNIQRNEYHNLNFTISSK 434
Pt-SSRP1 ILHEEIDYVEFERHAAGG-SNM--HYFDLLIRLKTE-QEHLFRNIQRNEYHNLNFDIFSGK 436
Vv-SSRP1 ILHEEIDYVEFERHAAGG-SNM--HYFDLLIRLKTE-QEHLFRNIQRNEYHNLNFDIFSGK 434
Gm-SSRP1 ILHEEIDYVEFERHAAGG-SNM--HYFDLLIRLKSE-QEHLFRNIQRNEYHNLNFTISSK 434
Dm-SSRP1 IRFEEISSVNFARSGGST-----RSFDFEVTLKNQ-TVHIFSSIEKEEYAKLFDYITQK 421
Hs-SSRP1 IRFDEISFVNFARGTTTT-----RSFDFEIEETKQG-TQYTFSSIEREEYKGLDFVNAK 421
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Sc-Pob3 NLRVKNEEDREVQE---RLQTAGSDSDEEDIN--MG-----S-----AGEDDES 508
Sm-SSRP1 GLKILNFQTQG---SSAVAEALQ-GSDDEGVDPHLERIRIARATG-----DEGDSDEE 484
Pp-SSRP1 NLKIMNLDGAQG--TSGVAAALE-GSDDEGVDPHLNRIRSARESGAGL---GDESDDEE 487
Hv-SSRP1 GLKVMNLG-DGQGTG-GVTDVLR-DTDDVAVDPHLERIKNQA-----V---SSEASDEE 485
Os-SSRP1 HLKIMNLG-DGQGATGGVTAVLR-DTDDVAVDPHLERIKNQA-----G---D-EESDEE 483
Zm-SSRP1 NIKIMNLGGDGGQASGVVTDVLR-DTDDVAVDPHLERIKNQA-----G---D-EESDEE 484
Sb-SSRP1 NIKIMNLGGDGGQASGVVTDVLR-DTDDVAVDPHLERIKNQA-----G---D-DESDEE 484
At-SSRP1 GLKIMNLGGAG-T-ADGVAAVLGDNDDDVAVDPHLTRIRNQA-----A-----DESDEE 481
Pt-SSRP1 GMKIMNLGDMQ-T-AGGVAAVLQ-NDDDDVAVDPHLARIRNEA-----G---D-DESDEE 483
Vv-SSRP1 GLKIMNLGDVQ-T-ADGVAAVLQ-NDDDDVAVDPHLERIKNEA-----G---G-DESDEE 481
Gm-SSRP1 GLKILNLGDAQ-P-TVGIKKVL-NDDDDVAVDPHLERIKNEA-----G---G-DESDEE 481
Dm-SSRP1 KLHVSNMGKDKSGY---KDVDFGSDNENEPDAYLARLKAAREKEEDDD-DGDSDEEST 477
Hs-SSRP1 KLNKIKRNLKEGMN---PSYDEYADSDQHDAYLERMKEEGKIREENANDSSDDSGEET 478
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Sc-Pob3 DEDFQVSSDNDNAEVAEEFSDAA-----LSDAEGGSDEERPSPKPKVE----- 552
Sm-SSRP1 DEDFVADK---DDEGSPTDDSGEE----EEDASDSDSGEQQDERPVKDKKKVEASQK-- 535
Pp-SSRP1 DEDFVAEK---DDAGSPTDESDEG----EPDGSDDGGERPKKKREKREDVAPKSA--- 535
Hv-SSRP1 DEDFVLHK---DDGSPTDDSGGE----ESDASESGG--EKEKSSKKEARSSKPPVKRK 535
Os-SSRP1 DEDFVADK---DDSGSPTDDSGEE----DSDASESGG--EKEKLSKKEASSKPPVKRK 533
Zm-SSRP1 DEDFVADK---DDSGSPTDDSGDE----ESDASDGG--EKEKSSKKEASSKPPVKRK 534
Sb-SSRP1 DEDFVADK---DDSGSPTDDSGDE----DSDASDGG--EKEKSSKKEASSKPPVKRK 534
At-SSRP1 DEDFVMGE--DDGGSPDDSGD-----DSDASEGGVGEIKEKSIKKEPKKEASS-- 531
Pt-SSRP1 DEDFVLGK---DDGSPTDDSGEE----ESDASESGD--EKENPGKDKFKREVSSS--- 530
Vv-SSRP1 DEDFVLDK---DDGSPTDDSGEE----ESDASESGG--EKEKPSKKEKKEPSVSVS--- 528
Gm-SSRP1 DSDFVADK---DDEGSPTDDSGAD-----DSDATDSDG--EKEKPAKKEKSKDLPSK--- 528
Dm-SSRP1 DEDFKPNE--NESDVAAEYDSNVESDSDSDSDASGGGG--DSDGAKKKKKEKSEKKE--- 530
Hs-SSRP1 DESFNPGE--EEDVAEEFSDNASASSSSN-----EG--DSDRDEKRRKQL----- 520
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Sc-Pob3	-----	552
Sm-SSRP1	P-----A-ATKTKKKKDEEGDGDGDKKKKRRK KDPNAPKRALSGFMYFSLAERENLKKS--T	586
Pp-SSRP1	P-----KRRKKKDEADGEDGGKRRKKK KDPNAPKRALSAFMRFQLEERKKMKADPGQ	589
Hv-SSRP1	PKGKDGESEKRRPKGKDGESEKRRPKKK KDPNAPKRPMMPFMYFSMAERAGVKDS--N	593
Os-SSRP1	PKGRDE-----EGSDKRKPKKK KDPNAPKRAMTPFMYFSMAERGNMKNN--N	578
Zm-SSRP1	HKARDD-----EGQEKKKPKKK KDPNAPKRAMTPFMYFSMAERGNMKSS--N	579
Sb-SSRP1	PKARDD-----EGHEKKKAKKK KDPNAPKRAMTPFMYFSMAERGNMKSS--N	579
At-SSRP1	-----KGLPPKRRKTVAADEGSKRKKPKKK KDPNAPKRAMSGFMFFSQMERDNIKKE--H	584
Pt-SSRP1	-----KAVTKRKS--RDGEESQKRRKPKKK KDPNAPKRKSKSAYVFFSQMERENVKKS--N	581
Vv-SSRP1	-----KASSSKKPKDGDGEDGSKRRKQKKK KDPNAPKRAMSGFMFFSQTERENIKKS--T	581
Gm-SSRP1	-----ASTSKK--SKDDEDGKRRKQKKR KDPNAPKRAMSGFMFFSKLERENLKKT--N	578
Dm-SSRP1	-----KKEKKHKEKERT--KKPSKKK KDSGKPKRATTAFMLWLNDRSREIKRE--N	577
Hs-SSRP1	-----KKAKMAKDRKSRKKPVEVKKG KDPNAPKRPMAYMLWLNASREIKSD--H	569
Sc-Pob3	-----	552
Sm-SSRP1	PGISFKDVAKTLGERWKAMSKDEKEPFESQARVDKERYTKQMGGYNKGNAGGSTADDESS	646
Pp-SSRP1	ASMSFGEFGKSLGEEKWRNMSASDKAPYEADAKVDQERYKKAMAGYK-----	635
Hv-SSRP1	PDLAPTDVAKKLGEMWQKMSTEDKQPYILOSQADKKRYEKESAAAYRA--AAPVDVDAGSG	651
Os-SSRP1	PDLPTTEIAKKLGEMWQKMTGEEKQPYIQSQVDKKRYEKESAVYRG--AAAMDVDSGSG	636
Zm-SSRP1	PDLPTTEIAKKLGEMWQKMSGEEKQPYIQQAQVDKKRYEKESAVYRG--EATVDVDSGNE	637
Sb-SSRP1	PDLPTTEIAKKLGEMWQKMSSEEKQPYIQQAQVDKKRYEKESAVYRG--EATADVDSGNE	637
At-SSRP1	PGIAFGEVGVKVLGDKWRQMSADDEKPYEAKAQVDKQRYKDEISDYK--NPQPMNVDSGND	642
Pt-SSRP1	PGIVFGEITKALADKWNAMSAAEKEPYEEMARDDKQRYKQVNDYKKNKPNQPMNVDSGYE	641
Vv-SSRP1	PGIAFTEVGRVVLGDKWKKMTAAEKEPYEAKAQADKKRYRDEISGYK--SNPQPMNVDSGNE	640
Gm-SSRP1	PGISFTDVSRLVGEKWKLLSVEEKEPYEAKAREDKRYKDEISGYK--NPQPMNIDSGNE	636
Dm-SSRP1	PGIKVTEIAKKGEMWKEKLD--KSKWEDAAAKDKQRYHDEMRYKPEAGGSDNEKGGK	635
Hs-SSRP1	PGISITDLSKKAGEIWKGMSKEKKEEWRKAEDARRDYEKAMKEYEGGRGESSKRDKSKK	629
Sc-Pob3	-----	552
Sm-SSRP1	D-----	647
Pp-SSRP1	-----	635
Hv-SSRP1	NGSD-----	655
Os-SSRP1	GNESD-----	641
Zm-SSRP1	SD-----	639
Sb-SSRP1	SD-----	639
At-SSRP1	SDSN-----	646
Pt-SSRP1	SDS-----	644
Vv-SSRP1	SDSE-----	644
Gm-SSRP1	SDSA-----	640
Dm-SSRP1	SSKK----RKTEPSPS----KKANTSGSGFKSKEYISDDDSTSSDDEKDNPAKSKP	686
Hs-SSRP1	KKKVVKMEKKSTPSRGSSSKSSRQLSESFKSKEFVSSDESSGENKSKKKRR----R	684
Sc-Pob3	-----	552
Sm-SSRP1	-----	647
Pp-SSRP1	-----	635
Hv-SSRP1	-----	655
Os-SSRP1	-----	641
Zm-SSRP1	-----	639
Sb-SSRP1	-----	639
At-SSRP1	-----	646
Pt-SSRP1	-----	644
Vv-SSRP1	-----	644
Gm-SSRP1	-----	640
Dm-SSRP1	PSDGDAKKKKAKSESEPEESEEDSNASDEDEDEEASD	723
Hs-SSRP1	SEDSE----EELASTPPSSEDSASGSDE-----	709

Figure S1. Amino acid sequence alignment of SSRP1 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-SSRP1 as query. The sequences were aligned using Clustal Omega (<https://www.ebi.ac.uk/Tools/msa/clustalo/>). The HMG-box domain present in SSRP1 proteins is highlighted in yellow, but it is absent from Sc-Pob3 (and other fungal Pob3 sequences; Pfab et al., 2018). Compared to their plant counterparts, metazoan SSRP1 proteins have a more extended domain C-terminal of the HMG-box. 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), *Hordeum vulgare* (Hv), *Oryza sativa* (Os), *Physcomitrella patens* (Pp), *Populus trichocarpa* (Pt), *Saccharomyces cerevisiae* (Sc), *Selaginella moellendorffii* (Sm), *Sorghum bicolor* (Sb), *Vitis vinifera* (Vv), *Zea mays* (Zm).