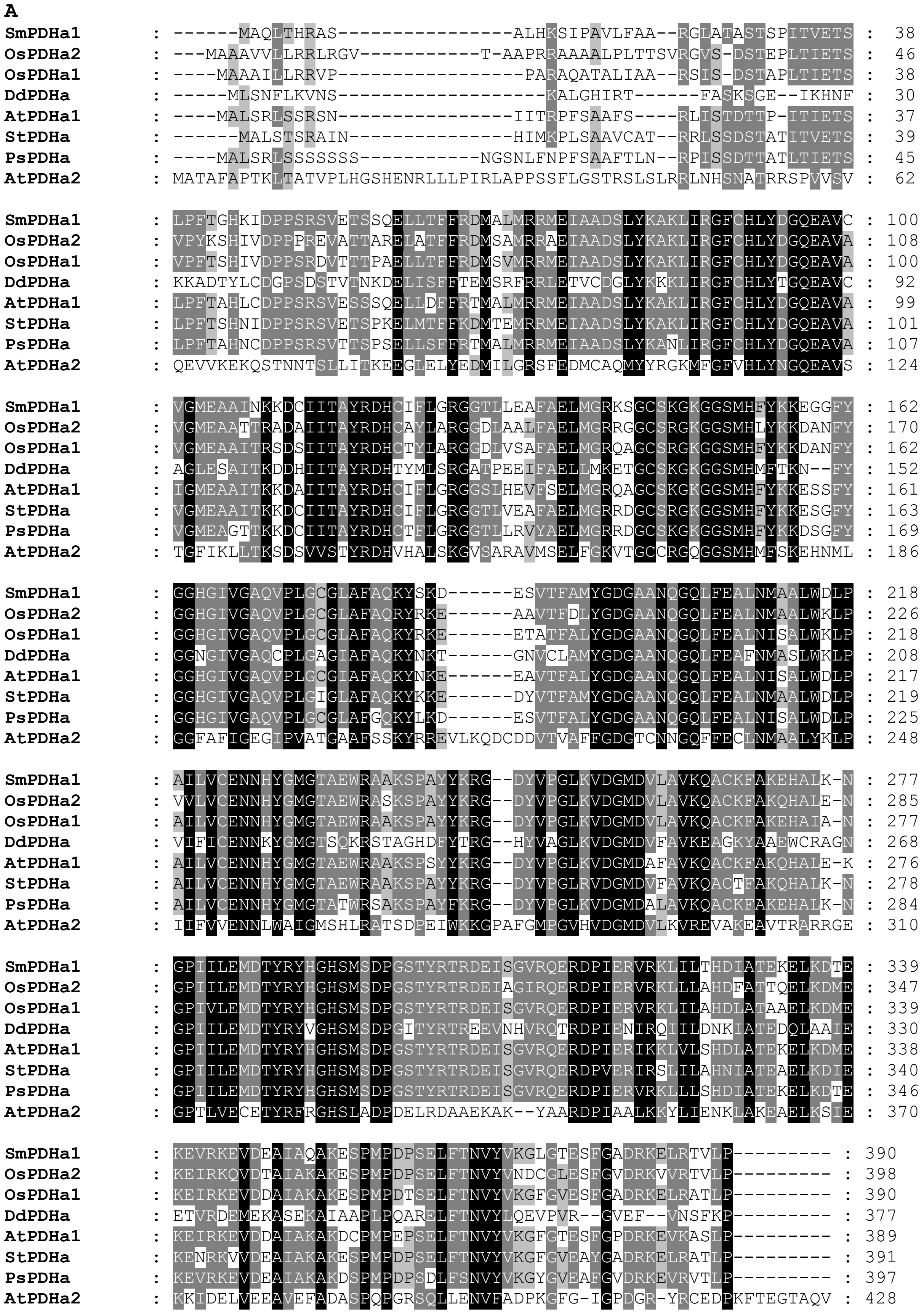
Supplementary Figures

Note: Figures S1-S28 show the multiple sequences alignment and phylogenetic analysis for each protein families identified in this study. The alignments were generated using the Clustal W program with default parameters. Black shading indicates that amino acids in this column are identical across all sequences; dark grey and light grey shadings indicate that the amino acids in the corresponding columns are 80% and 60% identical across all sequences. The Neighbor-Joining trees were constructed using the MEGA6 package. Details can be found in the legend for each figure.



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SmPDHa1   : ------MAQLTHRAS----------------ALHKSIPAVLFAA--RGLATASTSPITVETS :  38
OsPDHa2   : ---MAAAVVLLRRLRGV-----------T-AAPRRAAAALPLTTSVRGVS-DSTEPLTIETS :  46
OsPDHa1   : ----MAAAILLRRVP-----------------PARAQATALIAA--RSIS-DSTAPLTIETS :  38
DdPDHa    : -----MLSNFLKVNS------------------KALGHIRT------FASKSGE--IKHNF :  30
AtPDHa1   : ----MALSRLSSRSN----------------IITRPFSAAFS----RLISTDTTP-ITIETS :  37
StPDHa    : ------MALSTSRAIN---------------HIMKPLSAAVCAT--RRLSSDSTATITVETS :  39
PsPDHa    : ----MALSRLSSSSSSS-----------NGSNLFNPFSAAFTLN--RPISSDTTATLTIETS :  45
AtPDHa2   : MATAFAPTKLTATVPLHGSHENRLLLPIRLAPPSSFLGSTRSLSLRRLNHSNATRRSPVVSV :  62

SmPDHa1   : LPFTGHKIDPPSRSVETSSQELLTFFRDMALMRRMEIAADSLYKAKLIRGFCHLYDGQEAVC : 100
OsPDHa2   : VPYKSHIVDPPPREVATTARELATFFRDMSAMRRAEIAADSLYKAKLIRGFCHLYDGQEAVA : 108
OsPDHa1   : VPFTSHIVDPPSRDVTTTPAELLTFFRDMSVMRRMEIAADSLYKAKLIRGFCHLYDGQEAVA : 100
DdPDHa    : KKADTYLCDGPSDSTVTNKDELISFFTEMSRFRRLETVCDGLYKKKLIRGFCHLYTGQEAVC :  92
AtPDHa1   : LPFTAHLCDPPSRSVESSSQELLDFFRTMALMRRMEIAADSLYKAKLIRGFCHLYDGQEAVA :  99
StPDHa    : LPFTSHNIDPPSRSVETSPKELMTFFKDMTEMRRMEIAADSLYKAKLIRGFCHLYDGQEAVA : 101
PsPDHa    : LPFTAHNCDPPSRSVTTSPSELLSFFRTMALMRRMEIAADSLYKANLIRGFCHLYDGQEAVA : 107
AtPDHa2   : QEVVKEKQSTNNTSLLITKEEGLELYEDMILGRSFEDMCAQMYYRGKMFGFVHLYNGQEAVS : 124

SmPDHa1   : VGMEAAINKKDCIITAYRDHCIFLGRGGTLLEAFAELMGRKSGCSKGKGGSMHFYKKEGGFY : 162
OsPDHa2   : VGMEAATTRADAIITAYRDHCAYLARGGDLAALFAELMGRRGGCSRGKGGSMHLYKKDANFY : 170
OsPDHa1   : VGMEAAITRSDSIITAYRDHCTYLARGGDLVSAFAELMGRQAGCSRGKGGSMHFYKKDANFY : 162
DdPDHa    : AGLESAITKDDHIITAYRDHTYMLSRGATPEEIFAELLMKETGCSKGKGGSMHMFTKN--FY : 152
AtPDHa1   : IGMEAAITKKDAIITAYRDHCIFLGRGGSLHEVFSELMGRQAGCSKGKGGSMHFYKKESSFY : 161
StPDHa    : VGMEAAITKKDCIITAYRDHCIFLGRGGTLVEAFAELMGRRDGCSRGKGGSMHFYKKESGFY : 163
PsPDHa    : VGMEAGTTKKDCIITAYRDHCTFLGRGGTLLRVYAELMGRRDGCSKGKGGSMHFYKKDSGFY : 169
AtPDHa2   : TGFIKLLTKSDSVVSTYRDHVHALSKGVSARAVMSELFGKVTGCCRGQGGSMHMFSKEHNML : 186

SmPDHa1   : GGHGIVGAQVPLGCGLAFAQKYSKD------ESVTFAMYGDGAANQGQLFEALNMAALWDLP : 218
OsPDHa2   : GGHGIVGAQVPLGCGLAFAQRYRKE------AAVTFDLYGDGAANQGQLFEALNMAALWKLP : 226
OsPDHa1   : GGHGIVGAQVPLGCGLAFAQKYRKE------ETATFALYGDGAANQGQLFEALNISALWKLP : 218
DdPDHa    : GGNGIVGAQCPLGAGIAFAQKYNKT------GNVCLAMYGDGAANQGQLFEAFNMASLWKLP : 208
AtPDHa1   : GGHGIVGAQVPLGCGIAFAQKYNKE------EAVTFALYGDGAANQGQLFEALNISALWDLP : 217
StPDHa    : GGHGIVGAQVPLGIGLAFAQKYKKE------DYVTFAMYGDGAANQGQLFEALNMAALWDLP : 219
PsPDHa    : GGHGIVGAQVPLGCGLAFGQKYLKD------ESVTFALYGDGAANQGQLFEALNISALWDLP : 225
AtPDHa2   : GGFAFIGEGIPVATGAAFSSKYRREVLKQDCDDVTVAFFGDGTCNNGQFFECLNMAALYKLP : 248

SmPDHa1   : AILVCENNHYGMGTAEWRAAKSPAYYKRG--DYVPGLKVDGMDVLAVKQACKFAKEHALK-N : 277
OsPDHa2   : VVLVCENNHYGMGTAEWRASKSPAYYKRG--DYVPGLKVDGMDVLAVKQACKFAKQHALE-N : 285
OsPDHa1   : AILVCENNHYGMGTAEWRAAKSPAYYKRG--DYVPGLKVDGMDVLAVKQACKFAKEHAIA-N : 277
DdPDHa    : VIFICENNKYGMGTSQKRSTAGHDFYTRG--HYVAGLKVDGMDVFAVKEAGKYAAEWCRAGN : 268
AtPDHa1   : AILVCENNHYGMGTAEWRAAKSPSYYKRG--DYVPGLKVDGMDAFAVKQACKFAKQHALE-K : 276
StPDHa    : AILVCENNHYGMGTAEWRAAKSPAYYKRG--DYVPGLRVDGMDVFAVKQACTFAKQHALK-N : 278
PsPDHa    : AILVCENNHYGMGTATWRSAKSPAYFKRG--DYVPGLKVDGMDALAVKQACKFAKEHALK-N : 284
AtPDHa2   : IIFVVENNLWAIGMSHLRATSDPEIWKKGPAFGMPGVHVDGMDVLKVREVAKEAVTRARRGE : 310

SmPDHa1   : GPIILEMDTYRYHGHSMSDPGSTYRTRDEISGVRQERDPIERVRKLILTHDIATEKELKDTE : 339
OsPDHa2   : GPIILEMDTYRYHGHSMSDPGSTYRTRDEIAGIRQERDPIERVRKLLLAHDFATTQELKDME : 347
OsPDHa1   : GPIVLEMDTYRYHGHSMSDPGSTYRTRDEISGVRQERDPIERVRKLILAHDLATAAELKDME : 339
DdPDHa    : GPIILEMDTYRYVGHSMSDPGITYRTREEVNHVRQTRDPIENIRQIILDNKIATEDQLAAIE : 330
AtPDHa1   : GPIILEMDTYRYHGHSMSDPGSTYRTRDEISGVRQERDPIERIKKLVLSHDLATEKELKDME : 338
StPDHa    : GPIILEMDTYRYHGHSMSDPGSTYRTRDEISGVRQERDPVERIRSLILAHNIATEAELKDIE : 340
PsPDHa    : GPIILEMDTYRYHGHSMSDPGSTYRTRDEISGVRQERDPIERVRKLLLSHDIATEKELKDTE : 346
AtPDHa2   : GPTLVECETYRFRGHSLADPDELRDAAEKAK--YAARDPIAALKKYLIENKLAKEAELKSIE : 370

SmPDHa1   : KEVRKEVDEAIAQAKESPMPDPSELFTNVYVKGLGTESFGADRKELRTVLP--------- : 390
OsPDHa2   : KEIRKQVDTAIAKAKESPMPDPSELFTNVYVNDCGLESFGVDRKVVRTVLP--------- : 398
OsPDHa1   : KEIRKEVDDAIAKAKESPMPDTSELFTNVYVKGFGVESFGADRKELRATLP--------- : 390
DdPDHa    : ETVRDEMEKASEKAIAAPLPQARELFTNVYLQEVPVR--GVEF--VNSFKP--------- : 377
AtPDHa1   : KEIRKEVDDAIAKAKDCPMPEPSELFTNVYVKGFGTESFGPDRKEVKASLP--------- : 389
StPDHa    : KENRKVVDEAIAKAKESPMPDPSELFTNVYVKGFGVEAYGADRKELRATLP--------- : 391
PsPDHa    : KEVRKEVDEAIAKAKDSPMPDPSDLFSNVYVKGYGVEAFGVDRKEVRVTLP--------- : 397
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B

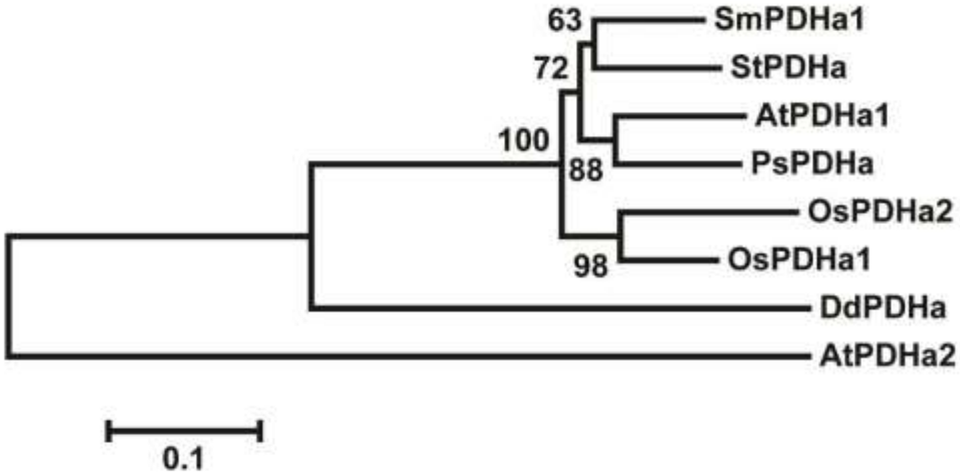

Fig S1. Multiple sequence alignment and phylogenetic tree for PDHa proteins from *S. miltiorrhiza* and its homologs from various other species.

(A) Multiple sequence alignment of PDHas. The species and accession number for each PDHa are shown in the parenthesis: SmPDHa1 (*S. miltiorrhiza*, KF887934); OsPDHa1 (*O. sativa* , Q6Z5N4); OsPDHa2 (Q654V6); AtPDHa1 (*A. thaliana*, AT1G59900); AtPDHa2 (AT1G01090.1); DdPDHa (*Dictyostelium discoideum*, Q54C70); StPDHa (*Solanum tuberosum*, P52903); PsPDHa (*Pisum sativum* , P52902).

(B) Phylogenetic relationships of PDHas from *S. miltiorrhiza* and various other species. PDHa proteins included are SmPDHa1 (*S. miltiorrhiza*, KF887934); OsPDHa1 (*O. sativa* , Q6Z5N4); OsPDHa2 (Q654V6); AtPDHa1 (*A. thaliana*, AT1G59900); AtPDHa2 (AT1G01090.1); DdPDHa (*D. discoideum*, Q54C70); StPDHa (*S. tuberosum*, P52903); PsPDHa (*P. sativum* , P52902).

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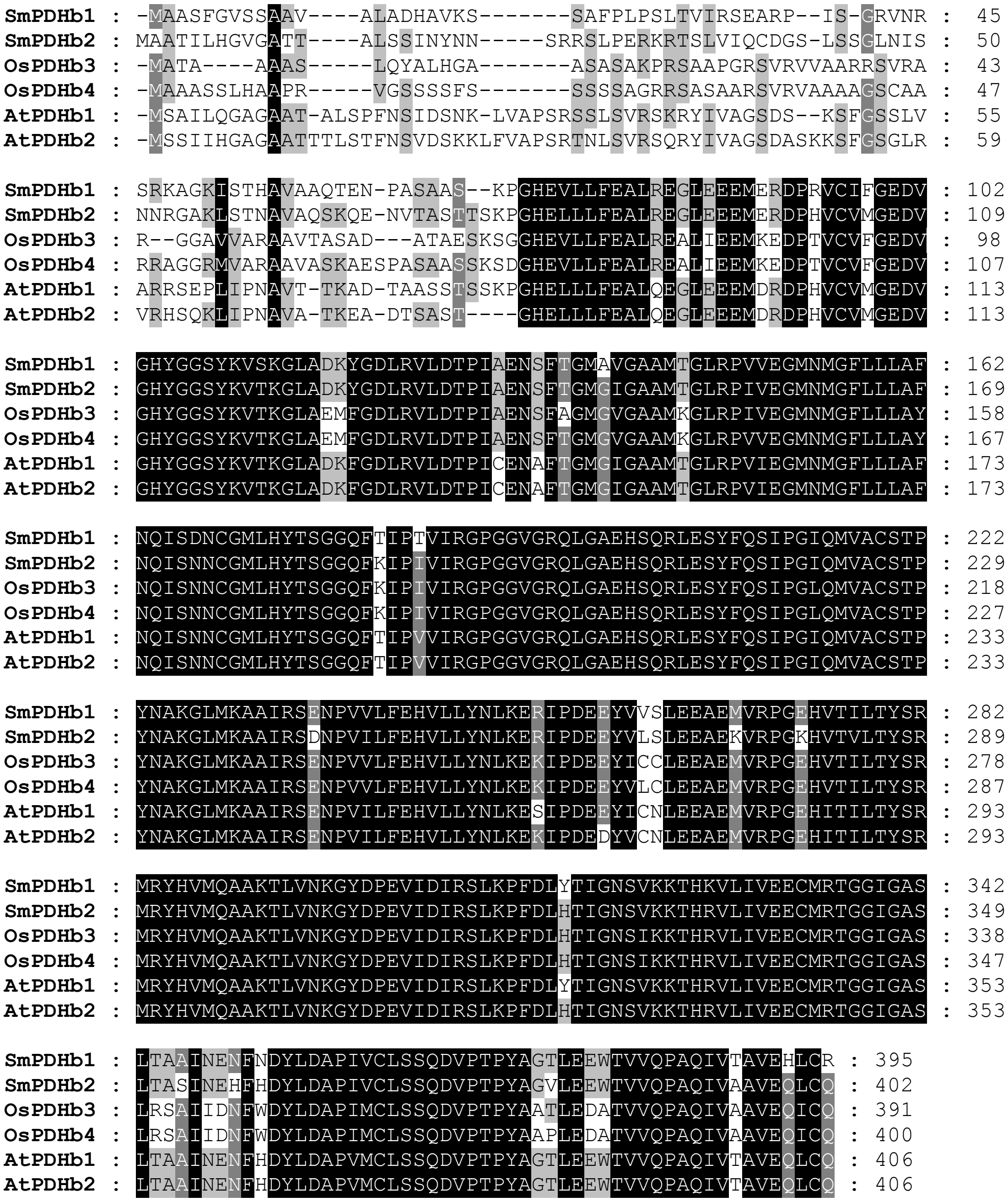

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SmPDHb2 : MAATILHGVGATT----ALSSINYNN-----SRRSLPERKRTSLVIQCDGS-LSSGLNIS :  50
OsPDHb3 : -MATA----AAAS-----LQYALHGA-------ASASAKPRSAAPGRSVRVVAARRSVRA :  43
OsPDHb4 : -MAAASSLHAAPR-----VGSSSSFS-------SSSSAGRRSASAARSVRVAAAAGSCAA :  47
AtPDHb1 : -MSAILQGAGAAT-ALSPFNSIDSNK-LVAPSRSSLSVRSKRYIVAGSDS--KSFGSSLV :  55
AtPDHb2 : -MSSIIHGAGAATTTLSTFNSVDSKKLFVAPSRTNLSVRSQRYIVAGSDASKKSFGSGLR :  59

SmPDHb1 : SRKAGKISTHAVAAQTEN-PASAAS--KPGHEVLLFEALREGLEEEMERDPRVCIFGEDV : 102
SmPDHb2 : NNRGAKLSTNAVAQSKQE-NVTASTTSKPGHELLLFEALREGLEEEMERDPHVCVMGEDV : 109
OsPDHb3 : R--GGAVVARAAVTASAD---ATAESKSGGHEVLLFEALREALIEEMKEDPTVCVFGEDV :  98
OsPDHb4 : RRAGGRMVARAAVASKAESPASAASSKSDGHEVLLFEALREALIEEMKEDPTVCVFGEDV : 107
AtPDHb1 : ARRSEPLIPNAVT-TKAD-TAASSTSSKPGHELLLFEALQEGLEEEMDRDPHVCVMGEDV : 113
AtPDHb2 : VRHSQKLIPNAVA-TKEA-DTSAST----GHELLLFEALQEGLEEEMDRDPHVCVMGEDV : 113

SmPDHb1 : GHYGGSYKVSKGLADKYGDLRVLDTPIAENSFTGMAVGAAMTGLRPVVEGMNMGFLLLAF : 162
SmPDHb2 : GHYGGSYKVTKGLADKYGDLRVLDTPIAENSFTGMGIGAAMTGLRPIVEGMNMGFLLLAF : 169
OsPDHb3 : GHYGGSYKVTKGLAEMFGDLRVLDTPIAENSFAGMGVGAAMKGLRPIVEGMNMGFLLLAY : 158
OsPDHb4 : GHYGGSYKVTKGLAEMFGDLRVLDTPIAENSFTGMGVGAAMKGLRPVVEGMNMGFLLLAY : 167
AtPDHb1 : GHYGGSYKVTKGLADKFGDLRVLDTPICENAFTGMGIGAAMTGLRPVIEGMNMGFLLLAF : 173
AtPDHb2 : GHYGGSYKVTKGLADKFGDLRVLDTPICENAFTGMGIGAAMTGLRPVIEGMNMGFLLLAF : 173

SmPDHb1 : NQISDNCGMLHYTSGGQFTIPTVIRGPGGVGRQLGAEHSQRLESYFQSIPGIQMVACSTP : 222
SmPDHb2 : NQISNNCGMLHYTSGGQFKIPIVIRGPGGVGRQLGAEHSQRLESYFQSIPGIQMVACSTP : 229
OsPDHb3 : NQISNNCGMLHYTSGGQFKIPIVIRGPGGVGRQLGAEHSQRLESYFQSIPGLQMVACSTP : 218
OsPDHb4 : NQISNNCGMLHYTSGGQFKIPIVIRGPGGVGRQLGAEHSQRLESYFQSIPGLQMVACSTP : 227
AtPDHb1 : NQISNNCGMLHYTSGGQFTIPVVIRGPGGVGRQLGAEHSQRLESYFQSIPGIQMVACSTP : 233
AtPDHb2 : NQISNNCGMLHYTSGGQFTIPVVIRGPGGVGRQLGAEHSQRLESYFQSIPGIQMVACSTP : 233

SmPDHb1 : YNAKGLMKAAIRSENPVVLFEHVLLYNLKERIPDEEYVVSLEEAEMVRPGEHVTILTYSR : 282
SmPDHb2 : YNAKGLMKAAIRSDNPVILFEHVLLYNLKERIPDEEYVLSLEEAEKVRPGKHVTVLTYSR : 289
OsPDHb3 : YNAKGLMKAAIRSENPVVLFEHVLLYNLKEKIPDEEYICCLEEAEMVRPGEHVTILTYSR : 278
OsPDHb4 : YNAKGLMKAAIRSENPVVLFEHVLLYNLKEKIPDEEYVLCLEEAEMVRPGEHVTILTYSR : 287
AtPDHb1 : YNAKGLMKAAIRSENPVILFEHVLLYNLKESIPDEEYICNLEEAEMVRPGEHITILTYSR : 293
AtPDHb2 : YNAKGLMKAAIRSENPVILFEHVLLYNLKEKIPDEDYVCNLEEAEMVRPGEHITILTYSR : 293

SmPDHb1 : MRYHVMQAAKTLVNKGYDPEVIDIRSLKPFDLYTIGNSVKKTHKVLIVEECMRTGGIGAS : 342
SmPDHb2 : MRYHVMQAAKTLVNKGYDPEVIDIRSLKPFDLHTIGNSVKKTHRVLIVEECMRTGGIGAS : 349
OsPDHb3 : MRYHVMQAAKTLVNKGYDPEVIDIRSLKPFDLHTIGNSIKKTHRVLIVEECMRTGGIGAS : 338
OsPDHb4 : MRYHVMQAAKTLVNKGYDPEVIDIRSLKPFDLHTIGNSIKKTHRVLIVEECMRTGGIGAS : 347
AtPDHb1 : MRYHVMQAAKTLVNKGYDPEVIDIRSLKPFDLYTIGNSVKKTHRVLIVEECMRTGGIGAS : 353
AtPDHb2 : MRYHVMQAAKTLVNKGYDPEVIDIRSLKPFDLHTIGNSVKKTHRVLIVEECMRTGGIGAS : 353

SmPDHb1 : LTAAINENFNDYLDAPIVCLSSQDVPTPYAGTLEEWTVVQPAQIVTAVEHLCR : 395
SmPDHb2 : LTASINEHFHDYLDAPIVCLSSQDVPTPYAGVLEEWTVVQPAQIVAAVEQLCQ : 402
OsPDHb3 : LRSAIIDNFWDYLDAPIMCLSSQDVPTPYAATLEDATVVQPAQIVAAVEQICQ : 391
OsPDHb4 : LRSAIIDNFWDYLDAPIMCLSSQDVPTPYAAPLEDATVVQPAQIVAAVEQICQ : 400
AtPDHb1 : LTAAINENFHDYLDAPVMCLSSQDVPTPYAGTLEEWTVVQPAQIVTAVEQLCQ : 406
AtPDHb2 : LTAAINENFHDYLDAPVMCLSSQDVPTPYAGTLEEWTVVQPAQIVTAVEQLCQ : 406
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B

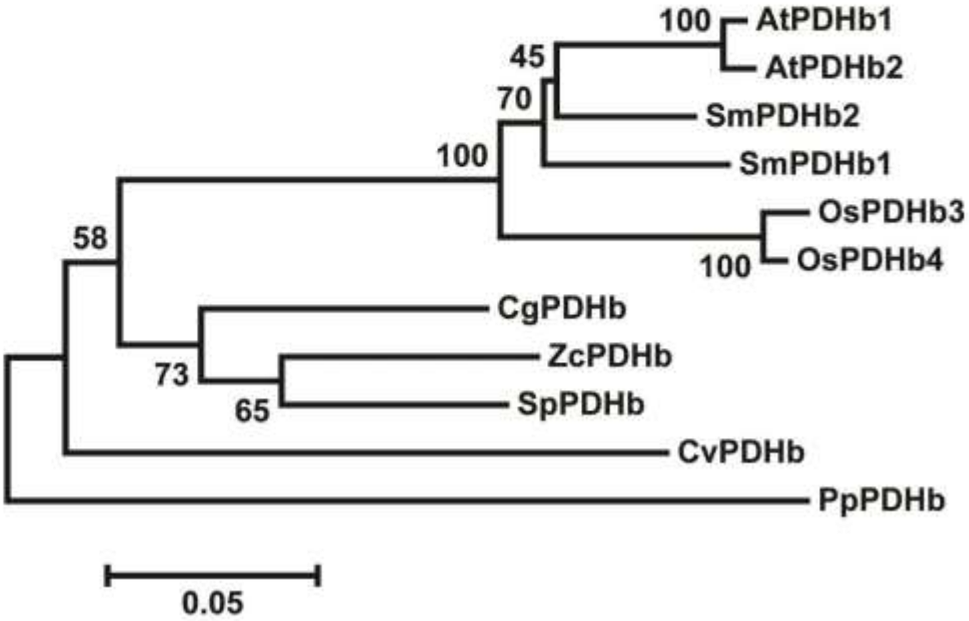
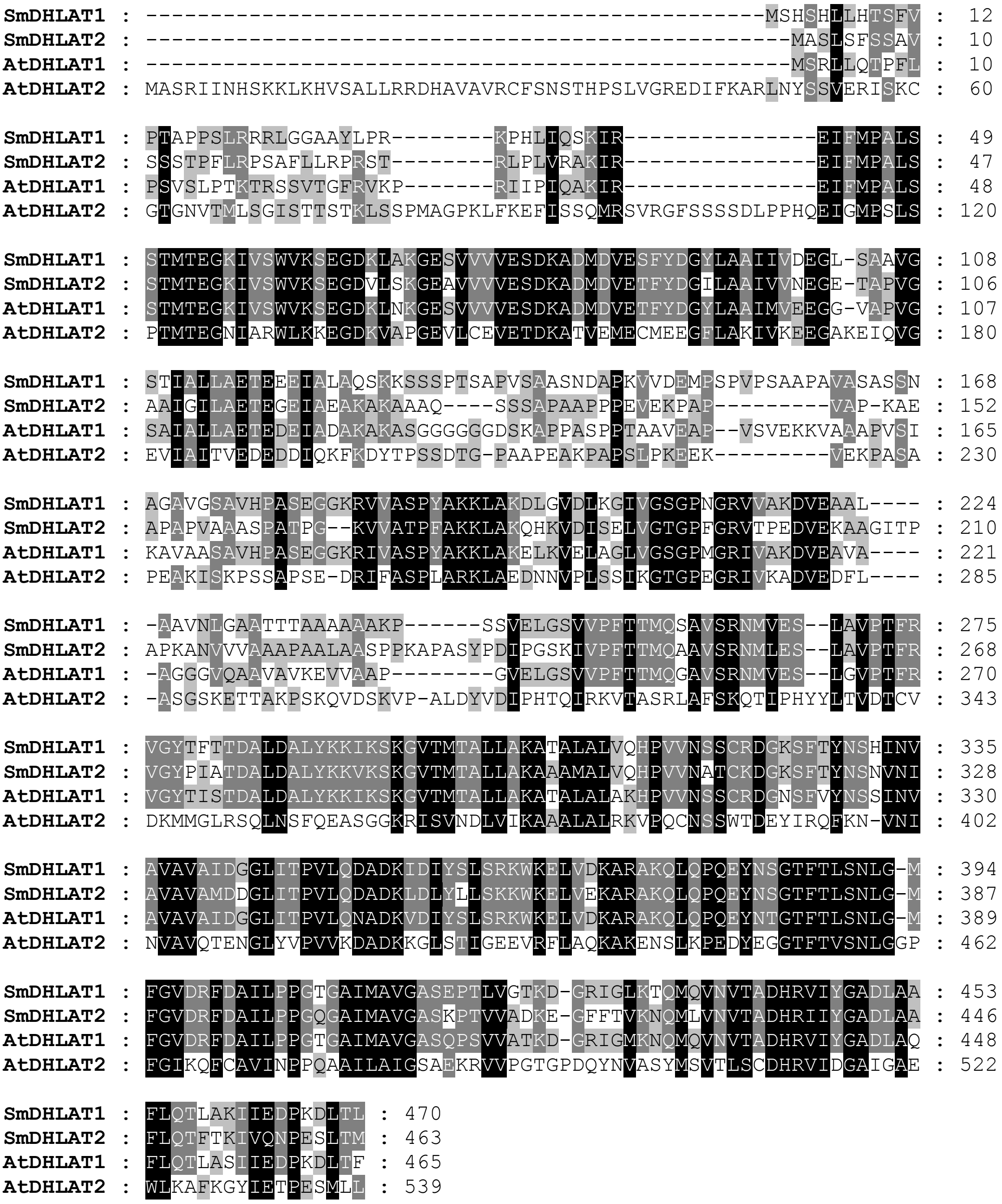


Fig S2. Multiple sequence alignment and phylogenetic tree for PDHb proteins from *S. miltiorrhiza* and its homologs from various other species.

(A) Multiple sequence alignment of PDHbs. The species and accession number for each PDHb are shown in the parenthesis: SmPDHb1 (*S. miltiorrhiza*, KF887928); SmPDHb2 (KJ784450); OsPDHb3 (*O. sativa* Q2QM55); OsPDHb4 (Q10G39); AtPDHb1 (*A. thaliana*, AT2G34590.1); AtPDHb2 (AT1G30120.1).

(B) Phylogenetic relationships of PDHbs from *S. miltiorrhiza* and various other species. PDHb proteins included are SmPDHb1 (*S. miltiorrhiza*, KF887928); SmPDHb2 (KJ784450); OsPDHb3 (*O. sativa* Q2QM55); OsPDHb4 (Q10G39); AtPDHb1 (*A. thaliana*, AT2G34590.1); AtPDHb2 (AT1G30120.1) , ZcPDHb (*Zygnema circumcarinatum* , Q32RM2); CvPDHb (*Chara vulgaris*, Q1ACL0); SpPDHb (*Staurastrum punctulatum*, Q32RS0); CgPDHb (*Chaetosphaeridium globosum*, Q8MA03); PpPDHb (*Porphyra purpurea*, P51266).

A



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SmDHLAT1 : ------------------------------------------------MSHSHLLHTSFV :  12
SmDHLAT2 : --------------------------------------------------MASLSFSSAV :  10
AtDHLAT1 : --------------------------------------------------MSRLLQTPFL :  10
AtDHLAT2 : MASRIINHSKKLKHVSALLRRDHAVAVRCFSNSTHPSLVGREDIFKARLNYSSVERISKC :  60

SmDHLAT1 : PTAPPSLRRRLGGAAYLPR--------KPHLIQSKIR---------------EIFMPALS :  49
SmDHLAT2 : SSSTPFLRPSAFLLRPRST--------RLPLVRAKIR---------------EIFMPALS :  47
AtDHLAT1 : PSVSLPTKTRSSVTGFRVKP-------RIIPIQAKIR---------------EIFMPALS :  48
AtDHLAT2 : GTGNVTMLSGISTTSTKLSSPMAGPKLFKEFISSQMRSVRGFSSSSDLPPHQEIGMPSLS : 120

SmDHLAT1 : STMTEGKIVSWVKSEGDKLAKGESVVVVESDKADMDVESFYDGYLAAIIVDEGL-SAAVG : 108
SmDHLAT2 : STMTEGKIVSWVKSEGDVLSKGEAVVVVESDKADMDVETFYDGILAAIVVNEGE-TAPVG : 106
AtDHLAT1 : STMTEGKIVSWVKSEGDKLNKGESVVVVESDKADMDVETFYDGYLAAIMVEEGG-VAPVG : 107
AtDHLAT2 : PTMTEGNIARWLKKEGDKVAPGEVLCEVETDKATVEMECMEEGFLAKIVKEEGAKEIQVG : 180

SmDHLAT1 : STIALLAETEEEIALAQSKKSSSPTSAPVSAASNDAPKVVDEMPSPVPSAAPAVASASSN : 168
SmDHLAT2 : AAIGILAETEGEIAEAKAKAAAQ----SSSAPAAPPPEVEKPAP---------VAP-KAE : 152
AtDHLAT1 : SAIALLAETEDEIADAKAKASGGGGGGDSKAPPASPPTAAVEAP--VSVEKKVAAAPVSI : 165
AtDHLAT2 : EVIAITVEDEDDIQKFKDYTPSSDTG-PAAPEAKPAPSLPKEEK---------VEKPASA : 230

SmDHLAT1 : AGAVGSAVHPASEGGKRVVASPYAKKLAKDLGVDLKGIVGSGPNGRVVAKDVEAAL---- : 224
SmDHLAT2 : APAPVAAASPATPG--KVVATPFAKKLAKQHKVDISELVGTGPFGRVTPEDVEKAAGITP : 210
AtDHLAT1 : KAVAASAVHPASEGGKRIVASPYAKKLAKELKVELAGLVGSGPMGRIVAKDVEAVA---- : 221
AtDHLAT2 : PEAKISKPSSAPSE-DRIFASPLARKLAEDNNVPLSSIKGTGPEGRIVKADVEDFL---- : 285

SmDHLAT1 : -AAVNLGAATTTAAAAAAKP------SSVELGSVVPFTTMQSAVSRNMVES--LAVPTFR : 275
SmDHLAT2 : APKANVVVAAAPAALAASPPKAPASYPDIPGSKIVPFTTMQAAVSRNMLES--LAVPTFR : 268
AtDHLAT1 : -AGGGVQAAVAVKEVVAAP--------GVELGSVVPFTTMQGAVSRNMVES--LGVPTFR : 270
AtDHLAT2 : -ASGSKETTAKPSKQVDSKVP-ALDYVDIPHTQIRKVTASRLAFSKQTIPHYYLTVDTCV : 343

SmDHLAT1 : VGYTFTTDALDALYKKIKSKGVTMTALLAKATALALVQHPVVNSSCRDGKSFTYNSHINV : 335
SmDHLAT2 : VGYPIATDALDALYKKVKSKGVTMTALLAKAAAMALVQHPVVNATCKDGKSFTYNSNVNI : 328
AtDHLAT1 : VGYTISTDALDALYKKIKSKGVTMTALLAKATALALAKHPVVNSSCRDGNSFVYNSSINV : 330
AtDHLAT2 : DKMMGLRSQLNSFQEASGGKRISVNDLVIKAAALALRKVPQCNSSWTDEYIRQFKN-VNI : 402

SmDHLAT1 : AVAVAIDGGLITPVLQDADKIDIYSLSRKWKELVDKARAKQLQPQEYNSGTFTLSNLG-M : 394
SmDHLAT2 : AVAVAMDDGLITPVLQDADKLDLYLLSKKWKELVEKARAKQLQPQEYNSGTFTLSNLG-M : 387
AtDHLAT1 : AVAVAIDGGLITPVLQNADKVDIYSLSRKWKELVDKARAKQLQPQEYNTGTFTLSNLG-M : 389
AtDHLAT2 : NVAVQTENGLYVPVVKDADKKGLSTIGEEVRFLAQKAKENSLKPEDYEGGTFTVSNLGGP : 462

SmDHLAT1 : FGVDRFDAILPPGTGAIMAVGASEPTLVGTKD-GRIGLKTQMQVNVTADHRVIYGADLAA : 453
SmDHLAT2 : FGVDRFDAILPPGQGAIMAVGASKPTVVADKE-GFFTVKNQMLVNVTADHRIIYGADLAA : 446
AtDHLAT1 : FGVDRFDAILPPGTGAIMAVGASQPSVVATKD-GRIGMKNQMQVNVTADHRVIYGADLAQ : 448
AtDHLAT2 : FGIKQFCAVINPPQAAILAIGSAEKRVVPGTGPDQYNVASYMSVTLSCDHRVIDGAIGAE : 522

SmDHLAT1 : FLQTLAKIIEDPKDLTL : 470
SmDHLAT2 : FLQTFTKIVQNPESLTM : 463
AtDHLAT1 : FLQTLASIIEDPKDLTF : 465
AtDHLAT2 : WLKAFKGYIETPESMLL : 539
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B

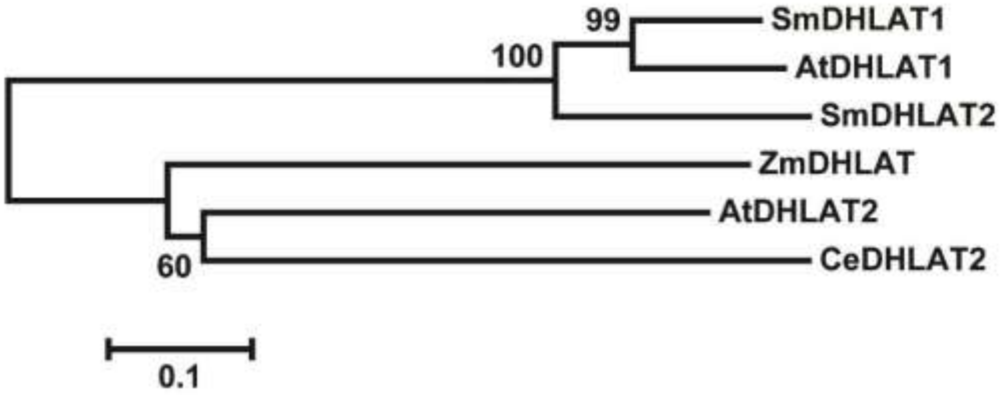

Fig S3. Multiple sequence alignment and phylogenetic tree for DHLAT proteins from *S. miltiorrhiza* and its homologs from various other species.

(A) Multiple sequence alignment of DHLATs. The species and accession number for each DHLAT are shown in the parenthesis: SmDHLAT1 (*S. miltiorrhiza*, KF887922); SmDHLAT2 (KJ784428);AtDHLAT1 (*A. thaliana*, AT1G34430.1); AtDHLAT2 (AT3G25860.1).

(B) Phylogenetic relationships of DHLATs from *S. miltiorrhiza* and various other species. DHLAT proteins included are SmDHLAT1 (*S. miltiorrhiza*, KF887922); SmDHLAT2 (KJ784428);AtDHLAT1 (*A. thaliana*, AT1G34430.1); AtDHLAT2 (AT3G25860.1); CePDCE2 (*Caenorhabditis elegans*, Q19749); ZmPdhC (*Zymomonas mobilis*, O66119).

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SmLPD1     : MHASISPLSTSN---------P--PHSTLQPYSSSRLCGLRREAFGFHSPSQFRNRGIGV :  49
SmLPD4     : MHSAIS-LSLSS-----PSPITRSSAASSTAPRSLRFCGLRREAFGAGASP--DASSLRL :  52
cpAtLPD2   : MQSVLS-LSFSQASLPLANRTLCSSNAAPSTPRNLRFCGLRREAFCFSPS---KQLT--S :  54
cpAtLPD1   : MQSAMA-LSFSQTSFTRPNHVLGSSGSVFSTPRSLRFCGLRREAFGFSTS---NQLAIRS :  56

SmLPD1     : VSAKTHSWRRSVFSASNSASDNGTSAPASFDYDLVIIGAGVGGHGAALHAVEKGLKTAII : 109
SmLPD4     : ARFNSRSQHFNLNGVLAALKGNGAPSSGGFDYDLVIIGAGVGGHGAALHAVEKGLKTAII : 112
cpAtLPD2   : CRFHIQSRRIEVSAAASSSAGNGAPSKS-FDYDLIIIGAGVGGHGAALHAVEKGLKTAII : 113
cpAtLPD1   : NRIQFLSRKSFQVSASASSNGNGAPPKS-FDYDLIIIGAGVGGHGAALHAVEKGLKTAII : 115

SmLPD1     : EGDVMGGTCVNRGCVPSKALLAVSGRMRELQDEHHLKALGLQVAAAGYDRQAVADHANNL : 169
SmLPD4     : EGDVVGGTCVNRGCVPSKALLAVSGRMRELQNEQHMKSFGLQVAAAGYDRQKVADHANNL : 172
cpAtLPD2   : EGDVVGGTCVNRGCVPSKALLAVSGRMRELQNEHHMKAFGLQVSAAGYDRQGVADHASNL : 173
cpAtLPD1   : EGDVVGGTCVNRGCVPSKALLAVSGRMRELQNEHHMKSFGLQVSAAGYDRQGVADHANNL : 175

SmLPD1     : ASRIRGNLTNSLTALGVDILTGFGTIVGPQKVKYGKIGSSDNVVTAKDIIIATGSIPFVP : 229
SmLPD4     : ASKIRGNLTNSMKALGVDILTGFGTILGPQKLKFGKGDSGDKIITAKDIIVATGSVPLVP : 232
cpAtLPD2   : ATKIRNNLTNSMKALGVDILTGFGAVLGPQKVKYG-----DNIITGKDIIIATGSVPFVP : 228
cpAtLPD1   : ATKIRNNLTNSMKAIGVDILTGFGSVLGPQKVKYGK----DNIITAKDIIIATGSVPFVP : 231

SmLPD1     : RGIEVDGKTVITSDHALKLEFVPDWIAIVGSGYIGLEFSDVYTALGSEVTFIEAMDQLMP : 289
SmLPD4     : KGIEVDGKTVITSDHALKLEFVPQWIAIVGSGYIGLEFSDVYTALGSEVTFVEALDQIMP : 292
cpAtLPD2   : KGIEVDGKTVITSDHALKLESVPDWIAIVGSGYIGLEFSDVYTALGSEVTFIEALDQLMP : 288
cpAtLPD1   : KGIEVDGKTVITSDHALKLESVPEWIAIVGSGYIGLEFSDVYTALGSEVTFIEALDQLMP : 291

SmLPD1     : GFDPEIGKLAQRVLINPRRIDYHTGVFATKITPAKDGKPVIIELIDAKTKEPKDTLEVDA : 349
SmLPD4     : GFDPEIGKLAQRVLVNPRKIDSYTGVFASKITPAKDGKPVQIELIDAKTKEPKETLEVDA : 352
CpAtLPD2   : GFDPEISKLAQRVLINTRKIDYHTGVFASKITPAKDGKPVLIELIDAKTKEPKDTLEVDA : 348
CpAtLPD1   : GFDPEISKLAQRVLINPRKIDYHTGVFASKITPARDGKPVLIELIDAKTKEPKDTLEVDA : 351

SmLPD1     : ALIATGRAPFTTGLGLENINVETQRGFVPVDERMRVIDADGNLIPHLYCIGDANGKLMLA : 409
SmLPD4     : ALIATGRAPFTKGLGLENINVQTQRGFVPVDERMRVIDANGKLVPHLYCIGDANGKMMLA : 412
cpAtLPD2   : ALIATGRAPFTNGLGLENINVTTQRGFIPVDERMRVIDGNGKLVPHLYCIGDANGKLMLA : 408
cpAtLPD1   : ALIATGRAPFTNGLGLENVNVVTQRGFIPVDERMRVIDGKGTLVPNLYCIGDANGKLMLA : 411

SmLPD1     : HTASAQGISVVEQLTGNDHVLNHLSIPAACFTHPEISMVGLTEPQAREKAENEGFEISIA : 469
SmLPD4     : HAASAQGISVVEQVTGNDHVLNHLSIPAACFTHPEISMVGLTEPQAREKAEKEGFEVSIA : 472
cpAtLPD2   : HAASAQGISVVEQVTGRDHVLNHLSIPAACFTHPEISMVGLTEPQAREKAEKEGFKVSIA : 468
cpAtLPD1   : HAASAQGISVVEQVSGRDHVLNHLSIPAACFTHPEISMVGLTEPQAKEKGEKEGFKVSVV : 471

SmLPD1     : KTSFKANTKALAENEGEGLAKLIYRPDNGEILGVHIFGMHAADLIHEASNAIALGTRVQD : 529
SmLPD4     : KTSFKANTKALAENEGEGMAKLIYRPDNGEILGVHIFGLHAADLIHEASNAIAMGTRIQD : 532
cpAtLPD2   : KTSFKANTKALAENEGEGLAKMIYRPDNGEILGVHIFGLHAADLIHEASNAIALGTRIQD : 528
cpAtLPD1   : KTSFKANTKALAENEGEGIAKMIYRPDNGEILGVHIFGLHAADLIHEASNAIALGTRIQD : 531

SmLPD1     : IKFAVHAHPTLSEVLDELYKSTKVNSHNTKPVSEPVTV---------------------- : 567
SmLPD4     : IKFAVHAHPTLSEVLDELFKSAKVKLSASKTVAEPVPV---------------------- : 570
cpAtLPD2   : IKLAVHAHPTLSEVVDELFKAAKVDSPASVTAQSVKVTV--------------------- : 567
cpAtLPD1   : IKLAVHAHPTLSEVLDELFKAAKVESHATTRTGDAKIKLNTNQEDRKGRRRGGDDEKQPS : 591

SmLPD1     : -------------------------------- :   -
SmLPD4     : -------------------------------- :   -
cpAtLPD2   : -------------------------------- :   -
cpAtLPD1   : VSKDLKDISTRPSSFFENISVGVLSLLSLIFV : 623
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B

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mtAtLPD1   : MAMAS-LARRKAYFLTRNLSNSPTDALRFSFSLSRGFASSGSDENDVVIIGGGPGGYVAA :  59
SmLPD2     : MAMAATLARRRAAALFSPSSKHLFSGTKYSWILSRGFAT-GSDENDVVIIGGGPGGYVAA :  59
mtAtLPD2   : MAMAS-LARRKAYFLTRNISNSPTDAFRFSFSLTRGFASSGSDDNDVVIIGGGPGGYVAA :  59
PsLPD      : MAMAN-LARRKGYSLLS------SETLRYSFSLRSRAFASGSDENDVVIGGGPGGYVAA :  53

mtAtLPD1   : IKASQLGLKTTCIEKRGALGGTCLNVGCIPSKALLHSSHMYHEAKHSFANHGIKVSSVEV : 119
SmLPD2     : IKAAQLGLKTTCIEKRGALGGTCLNVGCIPSKALLHSSHMYHEAKNSFAHHGIKVSSVEV : 119
mtAtLPD2   : IKAAQLGLKTTCIEKRGALGGTCLNVGCIPSKALLHSSHMYHEAKHVFANHGVKVSSVEV : 119
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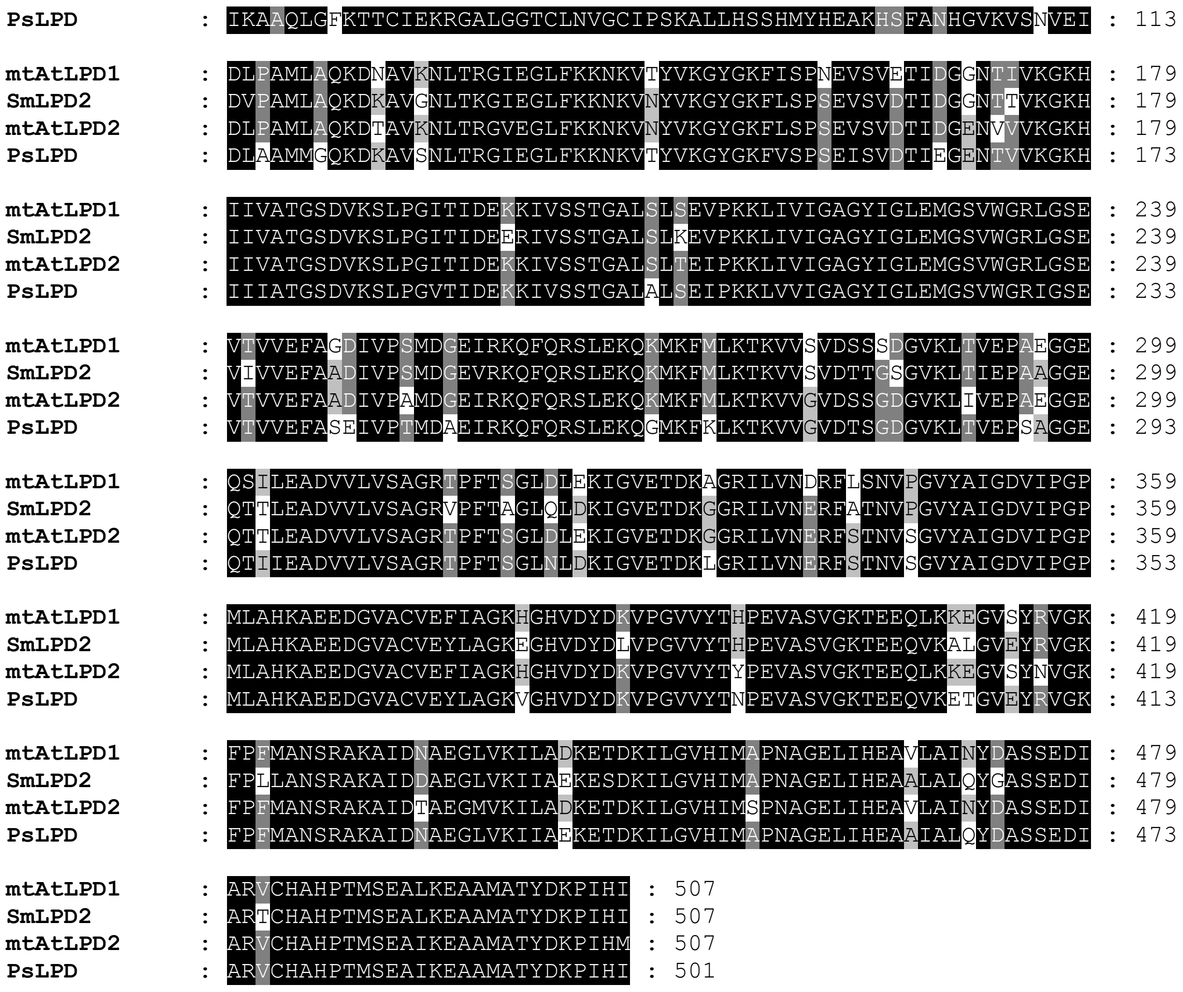

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SmLPD2       : DVPAMLAQKDKAVGNLTKGIEGLFKKNKVNYVKGYGKFLSPSEVSVDTIDGGNTTVKGKH : 179
mtAtLPD2     : DLPAMLAQKDTAVKNLTRGVEGLFKKNKVNYVKGYGKFLSPSEVSVDTIDGENVVVKGKH : 179
PsLPD        : DLAAMMGQKDKAVSNLTRGIEGLFKKNKVTYVKGYGKFVSPSEISVDTIEGENTVVKGKH : 173

mtAtLPD1     : IIVATGSDVKSLPGITIDEKKIVSSTGALSLSEVPKKLIVIGAGYIGLEMGSVWGRLGSE : 239
SmLPD2       : IIVATGSDVKSLPGITIDEERIVSSTGALSLKEVPKKLIVIGAGYIGLEMGSVWGRLGSE : 239
mtAtLPD2     : IIVATGSDVKSLPGITIDEKKIVSSTGALSLTEIPKKLIVIGAGYIGLEMGSVWGRLGSE : 239
PsLPD        : IIIATGSDVKSLPGVTIDEKKIVSSTGALALSEIPKKLVVIGAGYIGLEMGSVWGRIGSE : 233

mtAtLPD1     : VTVVEFAGDIVPSMDGEIRKQFQRSLEKQKMKFMLKTKVVSVDSSSDGVKLTVEPAEGGE : 299
SmLPD2       : VIVVEFAADIVPSMDGEVRKQFQRSLEKQKMKFMLKTKVVSVDTTGSGVKLTIEPAAGGE : 299
mtAtLPD2     : VTVVEFAADIVPAMDGEIRKQFQRSLEKQKMKFMLKTKVVGVDSSGDGVKLIVEPAEGGE : 299
PsLPD        : VTVVEFASEIVPTMDAEIRKQFQRSLEKQGMKFKLKTKVVGVDTSGDGVKLTVEPSAGGE : 293

mtAtLPD1     : QSILEADVVLVSAGRTPFTSGLDLEKIGVETDKAGRILVNDRFLSNVPGVYAIGDVIPGP : 359
SmLPD2       : QTTLEADVVLVSAGRVPFTAGLQLDKIGVETDKGGRILVNERFATNVPGVYAIGDVIPGP : 359
mtAtLPD2     : QTTLEADVVLVSAGRTPFTSGLDLEKIGVETDKGGRILVNERFSTNVSGVYAIGDVIPGP : 359
PsLPD        : QTIIEADVVLVSAGRTPFTSGLNLDKIGVETDKLGRILVNERFSTNVSGVYAIGDVIPGP : 353

mtAtLPD1     : MLAHKAEEDGVACVEFIAGKHGHVDYDKVPGVVYTHPEVASVGKTEEQLKKEGVSYRVGK : 419
SmLPD2       : MLAHKAEEDGVACVEYLAGKEGHVDYDLVPGVVYTHPEVASVGKTEEQVKALGVEYRVGK : 419
mtAtLPD2     : MLAHKAEEDGVACVEFIAGKHGHVDYDKVPGVVYTYPEVASVGKTEEQLKKEGVSYNVGK : 419
PsLPD        : MLAHKAEEDGVACVEYLAGKVGHVDYDKVPGVVYTNPEVASVGKTEEQVKETGVEYRVGK : 413

mtAtLPD1     : FPFMANSRAKAIDNAEGLVKILADKETDKILGVHIMAPNAGELIHEAVLAINYDASSEDI : 479
SmLPD2       : FPLLANSRAKAIDDAEGLVKIIAEKESDKILGVHIMAPNAGELIHEAALALQYGASSEDI : 479
mtAtLPD2     : FPFMANSRAKAIDTAEGMVKILADKETDKILGVHIMSPNAGELIHEAVLAINYDASSEDI : 479
PsLPD        : FPFMANSRAKAIDNAEGLVKIIAEKETDKILGVHIMAPNAGELIHEAAIALQYDASSEDI : 473

mtAtLPD1     : ARVCHAHPTMSEALKEAAMATYDKPIHI : 507
SmLPD2       : ARTCHAHPTMSEALKEAAMATYDKPIHI : 507
mtAtLPD2     : ARVCHAHPTMSEAIKEAAMATYDKPIHM : 507
PsLPD        : ARVCHAHPTMSEAIKEAAMATYDKPIHI : 501
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C

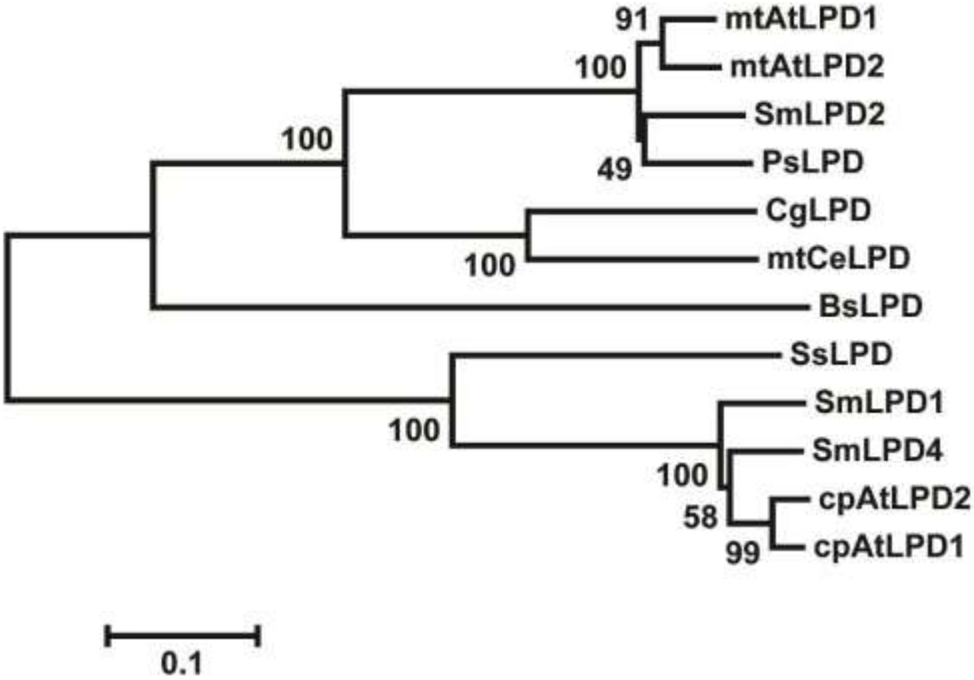
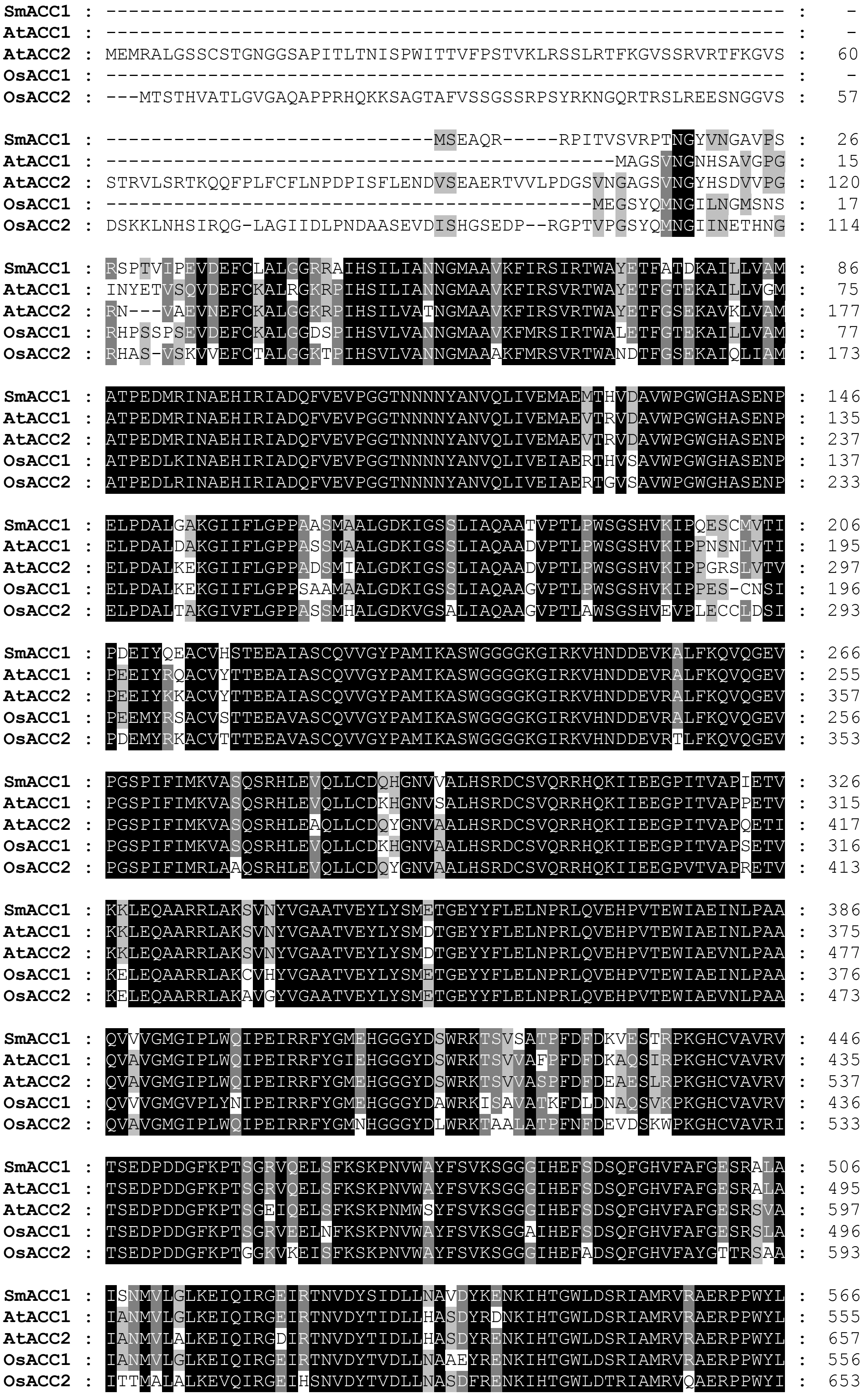


Fig S4. Multiple sequence alignment and phylogenetic tree for LPD proteins from *S. miltiorrhiza* and its homologs from various other species.
The subcellular locations of proteins were hint cp (chloroplast) or mt (mitochondrion) before the abbreviation of species name.
(A) Multiple sequence alignment of LPDs. The species and accession number for each LPD are shown in the parenthesis: SmLPD1 (*S. miltiorrhiza* , KF887936); SmLPD4 (KJ784433); cpAtLPD1 (*A. thaliana*, AT3G16950); cpAtLPD2 (AT4G16155).
(B) Multiple sequence alignment of LPDs. The species and accession number for each LPD are shown in the parenthesis: SmLPD2 (*S. miltiorrhiza* , KJ784431); mt AtLPD1 (*A. thaliana*, AT1G48030); mtAtLPD2 (AT3G17240); PsLPD (*Pisum sativum*, P31023).
(C) Phylogenetic relationships of LPDs from *S. miltiorrhiza* and various other species. LPD proteins included are SmLPD1 (*S. miltiorrhiza* , KF887936); SmLPD2 (KJ784431); SmLPD4 (KJ784433);cpAtLPD1 (*A. thaliana*, AT3G16950); cpAtLPD2 (AT4G16155); mtAtLPD1 (AT1G48030); mt AtLPD2 (AT3G17240); PsLPD (*P. sativum*, P31023); CgDLD(*Cricetulus griseus*, Q8CIZ7); mtCeLPD (*Caenorhabditis elegans*, O17953); SsLPD (*Synechocystis sp.* PCC 6803, P72740); BsLPD (*Bacillus subtilis*, P21880).

A



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AtACC1 : ------------------------------------------------------------ :   -
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OsACC1 : ------------------------------------------------------------ :   -
OsACC2 : ---MTSTHVATLGVGAQAPPRHQKKSAGTAFVSSGSSRPSYRKNGQRTRSLREESNGGVS :  57

SmACC1 : -----------------------------MSEAQR-----RPITVSVRPTNGYVNGAVPS :  26
AtACC1 : ---------------------------------------------MAGSVNGNHSAVGPG :  15
AtACC2 : STRVLSRTKQQFPLFCFLNPDPISFLENDVSEAERTVVLPDGSVNGAGSVNGYHSDVVPG : 120
OsACC1 : -------------------------------------------MEGSYQMNGILNGMSNS :  17
OsACC2 : DSKKLNHSIRQG-LAGIIDLPNDAASEVDISHGSEDP--RGPTVPGSYQMNGIINETHNG : 114

SmACC1 : RSPTVIPEVDEFCLALGGRRAIHSILIANNGMAAVKFIRSIRTWAYETFATDKAILLVAM :  86
AtACC1 : INYETVSQVDEFCKALRGKRPIHSILIANNGMAAVKFIRSVRTWAYETFGTEKAILLVGM :  75
AtACC2 : RN---VAEVNEFCKALGGKRPIHSILVATNGMAAVKFIRSVRTWAYETFGSEKAVKLVAM : 177
OsACC1 : RHPSSPSEVDEFCKALGGDSPIHSVLVANNGMAAVKFMRSIRTWALETFGTEKAILLVAM :  77
OsACC2 : RHAS-VSKVVEFCTALGGKTPIHSVLVANNGMAAAKFMRSVRTWANDTFGSEKAIQLIAM : 173

SmACC1 : ATPEDMRINAEHIRIADQFVEVPGGTNNNNYANVQLIVEMAEMTHVDAVWPGWGHASENP : 146
AtACC1 : ATPEDMRINAEHIRIADQFVEVPGGTNNNNYANVQLIVEMAEVTRVDAVWPGWGHASENP : 135
AtACC2 : ATPEDMRINAEHIRIADQFVEVPGGTNNNNYANVQLIVEMAEVTRVDAVWPGWGHASENP : 237
OsACC1 : ATPEDLKINAEHIRIADQFVEVPGGTNNNNYANVQLIVEIAERTHVSAVWPGWGHASENP : 137
OsACC2 : ATPEDLRINAEHIRIADQFVEVPGGTNNNNYANVQLIVEIAERTGVSAVWPGWGHASENP : 233

SmACC1 : ELPDALGAKGIIFLGPPAASMAALGDKIGSSLIAQAATVPTLPWSGSHVKIPQESCMVTI : 206
AtACC1 : ELPDALDAKGIIFLGPPASSMAALGDKIGSSLIAQAADVPTLPWSGSHVKIPPNSNLVTI : 195
AtACC2 : ELPDALKEKGIIFLGPPADSMIALGDKIGSSLIAQAADVPTLPWSGSHVKIPPGRSLVTV : 297
OsACC1 : ELPDALKEKGIIFLGPPSAAMAALGDKIGSSLIAQAAGVPTLPWSGSHVKIPPES-CNSI : 196
OsACC2 : ELPDALTAKGIVFLGPPASSMHALGDKVGSALIAQAAGVPTLAWSGSHVEVPLECCLDSI : 293

SmACC1 : PDEIYQEACVHSTEEAIASCQVVGYPAMIKASWGGGGKGIRKVHNDDEVKALFKQVQGEV : 266
AtACC1 : PEEIYRQACVYTTEEAIASCQVVGYPAMIKASWGGGGKGIRKVHNDDEVRALFKQVQGEV : 255
AtACC2 : PEEIYKKACVYTTEEAIASCQVVGYPAMIKASWGGGGKGIRKVHNDDEVRALFKQVQGEV : 357
OsACC1 : PEEMYRSACVSTTEEAVASCQVVGYPAMIKASWGGGGKGIRKVHNDDEVRALFKQVQGEV : 256
OsACC2 : PDEMYRKACVTTTEEAVASCQVVGYPAMIKASWGGGGKGIRKVHNDDEVRTLFKQVQGEV : 353

SmACC1 : PGSPIFIMKVASQSRHLEVQLLCDQHGNVVALHSRDCSVQRRHQKIIEEGPITVAPIETV : 326
AtACC1 : PGSPIFIMKVASQSRHLEVQLLCDKHGNVSALHSRDCSVQRRHQKIIEEGPITVAPPETV : 315
AtACC2 : PGSPIFIMKVASQSRHLEAQLLCDQYGNVAALHSRDCSVQRRHQKIIEEGPITVAPQETI : 417
OsACC1 : PGSPIFIMKVASQSRHLEVQLLCDKHGNVAALHSRDCSVQRRHQKIIEEGPITVAPSETV : 316
OsACC2 : PGSPIFIMRLAAQSRHLEVQLLCDQYGNVAALHSRDCSVQRRHQKIIEEGPVTVAPRETV : 413

SmACC1 : KKLEQAARRLAKSVNYVGAATVEYLYSMETGEYYFLELNPRLQVEHPVTEWIAEINLPAA : 386
AtACC1 : KKLEQAARRLAKSVNYVGAATVEYLYSMDTGEYYFLELNPRLQVEHPVTEWIAEINLPAA : 375
AtACC2 : KKLEQAARRLAKSVNYVGAATVEYLYSMDTGEYYFLELNPRLQVEHPVTEWIAEVNLPAA : 477
OsACC1 : KELEQAARRLAKCVHYVGAATVEYLYSMETGEYYFLELNPRLQVEHPVTEWIAEINLPAA : 376
OsACC2 : KELEQAARRLAKAVGYVGAATVEYLYSMETGEYYFLELNPRLQVEHPVTEWIAEVNLPAA : 473

SmACC1 : QVVVGMGIPLWQIPEIRRFYGMEHGGGYDSWRKTSVSATPFDFDKVESTRPKGHCVAVRV : 446
AtACC1 : QVAVGMGIPLWQIPEIRRFYGIEHGGGYDSWRKTSVVAFPFDFDKAQSIRPKGHCVAVRV : 435
AtACC2 : QVAVGMGIPLWQIPEIRRFYGMEHGGGYDSWRKTSVVASPFDFDEAESLRPKGHCVAVRV : 537
OsACC1 : QVVVGMGVPLYNIPEIRRFYGMEHGGGYDAWRKISAVATKFDLDNAQSVKPKGHCVAVRV : 436
OsACC2 : QVAVGMGIPLWQIPEIRRFYGMNHGGGYDLWRKTAALATPFNFDEVDSKWPKGHCVAVRI : 533

SmACC1 : TSEDPDDGFKPTSGRVQELSFKSKPNVWAYFSVKSGGGIHEFSDSQFGHVFAFGESRALA : 506
AtACC1 : TSEDPDDGFKPTSGRVQELSFKSKPNVWAYFSVKSGGGIHEFSDSQFGHVFAFGESRALA : 495
AtACC2 : TSEDPDDGFKPTSGEIQELSFKSKPNMWSYFSVKSGGGIHEFSDSQFGHVFAFGESRSVA : 597
OsACC1 : TSEDPDDGFKPTSGRVEELNFKSKPNVWAYFSVKSGGAIHEFSDSQFGHVFAFGESRSLA : 496
OsACC2 : TSEDPDDGFKPTGGKVKEISFKSKPNVWAYFSVKSGGGIHEFADSQFGHVFAYGTTRSAA : 593

SmACC1 : ISNMVLGLKEIQIRGEIRTNVDYSIDLLNAVDYKENKIHTGWLDSRIAMRVRAERPPWYL : 566
AtACC1 : IANMVLGLKEIQIRGEIRTNVDYTIDLLHASDYRDNKIHTGWLDSRIAMRVRAERPPWYL : 555
AtACC2 : IANMVLALKEIQIRGDIRTNVDYTIDLLHASDYRENKIHTGWLDSRIAMRVRAERPPWYL : 657
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OsACC2 : ITTMALALKEVQIRGEIHSNVDYTVDLLNASDFRENKIHTGWLDTRIAMRVQAERPPWYI : 653
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SmACC1 : SVVGGALYKASASSAATVSEYVGYLEKGQIPPKHISLVNSQVSLNIEGSKYTINMVRGGP :  626
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AtACC2 : SVVGGALYKASTTSSAVVSDYVGYLEKGQIPPKHISLVHSQVSLNIEGSKYTIDVVRGGS :  717
OsACC1 : SVVGGALYEASSRSSSVVTDYVGYLSKGQIPPKHISLVNLTVTLNIEGSKYTIETVRRGP :  616
OsACC2 : SVVGGALYKTVTANTATVSDYVGYLTKGQIPPKHISLVYTTVALNIDGKKYTIDTVRSGH :  713

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AtACC1 : GTYRLRMNKSEVVAEIHTLRDGGLLMQLDGKSHVIYAEEEAAGTRLLIDGRTCLLQNDHD :  675
AtACC2 : GTYRLRMSNSEVVAEIHTLRDGGLLMQLDGKSHVIYAKEEATGTRLLIDGRTCLLQNDHD :  777
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OsACC2 : GSYRLRMNGSTVDANVQILCDGGLLMQLDGNSHVIYAEEEASGTRLLIDGKTCMLQNDHD :  773

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AtACC1 : PSKLMAETPCKLMRYLISDNSNIDADTPYAEVEVMKMCMPLLSPASGVIHFKMSEGQAMQ :  735
AtACC2 : PSKLMAETPCKLLRYLVSDNSSIDTDTPYAEVEVMKMCMPLISPASGVIHFKLSEGQAMQ :  837
OsACC1 : PSKLLADTPCKLLRFLVADGSHVDADTPYAEVEVMKMCMPLLLPASGVIHFVMPEGQAMQ :  736
OsACC2 : PSKLLAETPCKLLRFLVADGAHVDADVPYAEVEVMKMCMPLLSPASGVIHVVMSEGQAMQ :  833

SmACC1 : AGELIARLDLDDPSAVRKAEPFHGSFPVLGPPTAISGKVHQRCAASLNAARMILAGYEHK :  806
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AtACC2 : AGELIAKLDLDDPSAVRKAKPFRGSFPRLGLPTAISGKVHQRCAATLNAARMILAGYDHK :  897
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OsACC2 : AGDLIARLDLDDPSAVKRAEPFEDTFPQMGLPIAASGQVHKLCAASLNACRMILAGYEHD :  893

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AtACC2 : VDEVLQDLLNCLDSPELPFLQWQECFAVLATRLPKDLRNMLELKYKEFEIISKTSLTPDF :  957
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OsACC2 : IDKVVPELVYCLDTPELPFLQWEELMSVLATRLPRNLKSELEGKYEEYKVKFDSGIINDF :  953

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AtACC1 : PAKLLKGILEAHLSSCDEKERGALERLIEPLMSLAKSYEGGRESHARVIVHSLFEEYLSV :  915
AtACC2 : PAKLLKGILEAHLSSCDEKERGSLERLIEPLMSLVKSYEGGRESHARLIVHSLFEEYLSV : 1017
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AtACC2 : SGVIASWEFL-EHFERKNTGPDDHEISEKGIVAKSSKRKRGTMVIIKSLQFLPSIINASL : 1256
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OsACC2 : SGVIALWEFPEGHFDARNGG------AVLG------DKRWGAMVIVKSLESLSMAIRFAL : 1241

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AtACC2 : RETNHSHCEYAR-------APLSGNMMHIAVVGINNQMSLLQDSGDEDQTQERVNKLAKI : 1309
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OsACC2 : KETSHYTSSE-------------GNMMHIALLGADNKMHIIQESGDD---ADRIAKLPLI : 1285

SmACC1 : LKEKEVSSSLRKAGVGVVSCIIQRDEGRGPMRHSFHWADEKLYYEEEPLLRHLEPPLSIY : 1276
AtACC1 : LKEEEVSSSLCSAGVGVISCIIQRDEGRTPMRHSFHWSLEKQYYVEEPLLRHLEPPLSIY : 1268
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AtACC2 : LKEEEVSLTLCSAGVGVISCIIQRDEGRTPMRHSFHWLMEKQYYVEEPLLRHVEPPLSVY : 1369
OsACC1 : LKDSTVTSHLNGAGVRVVSCIIQRDEGRPPMRHSFQWSVDKIYYEEDPMLRHVEPPLSTF : 1273
OsACC2 : LKDN--VTDLHASGVKTISFIVQRDEARMTMRRTFLWSDEKLSYEEEPILRHVEPPLSAL : 1343

SmACC1 : LELDKL--KDYENIRYTPSRDRQWHLYTVT----DKPRPIQRMFLRTLVRQPISNEGLTV : 1330
AtACC1 : LELDKL--KGYSNIQYTPSRDRQWHLYTVT----DKPVPIKRMFLRSLVRQATMNDGFIL : 1322
AtACC2 : LELDKL--KGYSNIQYSPSRDRQWHMYSVT----DRPVPIKRMFLRSLVRQTTMNDGFLL : 1423
OsACC1 : LELNKVNLDGYNEVKYTPSRDRQWHIYTLIKNKKDQRSNDQRLFLRTIVRQPGVTNGFLS : 1333
OsACC2 : LELDKLKVKGYNEMKYTPSRDRQWHIYTLRN--TENPKMLHRVFFRTLVRQPSVSNKFSS : 1401

SmACC1 : L---DQVTTLSLWTLSFTSRSILRSIISAMEELELNAHNSAIKPDHAHMYLYILREQQID : 1387
AtACC1 : QQGQDKQLSQTLISMAFTSKCVLRSLMDAMEELELNAHNAAMKPDHAHMFLCILREQQID : 1382
AtACC2 : QQGQDYQLSQTVLSMAFTSKCILRSLMNAMEELELNAHNAAMKPDHAHMFLCILREQQID : 1483
OsACC1 : GN-VDNEVGRAQASSSYTSSSILRSLMAALEEIELHAHNETVRSSYSHMYLCILRVQQLF : 1392
OsACC2 : GQIGDMEVGSAEEPLSFTSTSILRSLMTAIEELELHA----IRTGHSHMYLHVLKEQKLL : 1457

SmACC1 : DLLPYQKRADIATGQEEAAVEKILDELAHEINASVGVKMHRLGVCEWEVKLWITSNGEAN : 1447
AtACC1 : DLVPFPRRVEVNAEDEETTVEMILEEAAREIHRSVGVRMHRLGVCEWEVRLWLVSSGLAC : 1442
AtACC2 : DLVPYPRRFEVNAEDEETTVETILEEATQEIHRSVGVRMHALGVCEWEVRLWLVSSGLAN : 1543
OsACC1 : DLIPFSRTIDN-VGQDEATACTLLKNMALNIYEHVGVRMHRLSVCQWEVKLWLDCDGQAS : 1451
OsACC2 : DLVPVSGNTVLDVGQDEATAYSLLKEMAMKIHELVGARMHHLSVCQWEVKLKLDCDGPAS : 1517

SmACC1 : GAWRVVVTNVTGHTCIVHIYREVEDSATDRVVYTSAS-GQGPLHGLPVTAPYKPLGVLDQ : 1506
AtACC1 : GAWRVVVANVTGRTCTVHIYREVETPGRNSLIYHSIT-KKGPLHETPISDQYKPLGYLDR : 1501
AtACC2 : GAWRVVVANVTGRTCTVHIYREVEATGRNSLIYHSIT-KKGPLHGTLINGQYKPLNNLDR : 1602
OsACC1 : GAWRVVVTNVTGHTCTVDIYREVEDSNTHKLFYHSVTPSLGPLHGIVLDEPYKPLDAIDL : 1511
OsACC2 : GTWRIVTTNVTSHTCTVDIYREMEDKESRKLVYHPATPAAGPLHGVALNNPYQPLSVIDL : 1577

SmACC  : KRLLARKSSTTYCYDFPLAFQAALNKSWAEQSR-ISKP--IDKALIKVTELTFADKQGSW : 1563
AtACC1 : QRLAARRSNTTYCYDFPLAFGTALELLWASQHPGVKKP--YKDTLINVKELVFSKPEGSS : 1559
AtACC2 : KRLAARRSNTTYCYDFPLAFETALELNWASQHSGVRKP--CKNRLINVKELVFSNTEGSL : 1660
OsACC1 : KRYSARKNETTYCYDFPLAFETALKRSWKSTLSVVAEANEHNKSYAKVTELMFADSTGSW : 1571
OsACC2 : KRCSARNNRTTYCYDFPLAFETAVRKSWSSSTSGASKGVENAQCYVKATELVFADKHGSW : 1637

SmACC1 : GTPLVEEERPPGLNEIGMVAWRMEMSTPEFPDGRTIFIVSNDVTFKNGSFGPGEDAFFKA : 1623
AtACC1 : GTSLDLVERPPGLNDFGMVAWCLDMSTPEFPMGRKLLVIANDVTFKAGSFGPREDAFFLA : 1619
AtACC2 : GTSLIPVERPAGLNDIGMVAWILEMSTPEFPMGRKLLIVANDVTFKAGSFGPREDAFFLA : 1720
OsACC1 : GTPLVPVERSPGINDIGIVAWIMKLSTPEFPSGREIIVVSNDVTFKAGSFGPREDAFFDA : 1631
OsACC2 : GTPLVQMDRPAGLNDIGMVAWTLKMSTPEFPSGREIIVVANDITFRAGSFGPREDAFFEA : 1697

SmACC1 : VAEVACSQRLPLIYLAVNSGARIGVAEEVKSCFKVGWSDETNPERGFQYIYLTPEDHARI : 1683
AtACC1 : VTELACAKKLPLIYLAANSGARLGVAEEVKACFKVGWSDEISPENGFQYIYLSPEDHERI : 1679
AtACC2 : VTELACTKKLPLIYLAANSGARLGVAEEVKACFKVGWSDEVSPGNDFQYIYLSSEDYARI : 1780
OsACC1 : VTNLACERKLPLIYLSATAGARLGVAEEIKACFNVGWSDDESPERGFHYIYLTEQDYSRL : 1691
OsACC2 : VTNLACEKKLPLIYLAANSGARIGIADEVKSCFRVGWSDDGSPERGFQYIYLSEEDYARI : 1757

SmACC1 : GASVIAHELKLLSGETRWVIDTIVGKEDALGVENLTGSGAIASAYSKAYHETFTVTYVTG : 1743
AtACC1 : GSSVIAHEVKLSSGETRWVIDTIVGKEDGIGVENLTGSGAIAGAYSKAYNETFTLTFVSG : 1739
AtACC2 : GSSVIAHEVKLPSGETRWVIDTIVGKEDGLGVENLTGSGAIAGAYSRAYNETFTLTFVSG : 1840
OsACC1 : SSSVIAHELKLESGETRWVVDTIVGKEDGLGCENLHGSGAIASAYSKAYKETFTLTFVTG : 1751
OsACC2 : GTSVIAHKMQLDSGEIRWVIDSVVGKEDGLGVENIHGSAAIASAYSRAYKETFTLTFVTG : 1817

SmACC1 : RTVGIGAYLARLGMRCIQRLDQPIILTGFSALNKLLGREVYSSHMQLGGPKIMATNGVVH : 1803
AtACC1 : RTVGIGAYLARLGMRCIQRLDQPIILTGFSTLNKLLGREVYSSHMQLGGPKIMGTNGVVH : 1799
AtACC2 : RSVGIGAYLARLGMRCIQRLDQPIILTGFSTLNKLLGREVYSSHMQLGGPKIMGTNGVVH : 1900
OsACC1 : RAVGIGAYLARLGMRCIQRLDQPIILTGFSALNKLLGREVYSSHMQLGGPKIMATNGVVH : 1811
OsACC2 : RTVGIGAYLARLGIRCIQRLDQPIILTGYSALNKLLGREVYSSHMQLGGPKIMATNGVVH : 1877

SmACC1 : LTVSNDLEGISAILKWLSFVPPYSGGPLPILSPSDPPERLVEYLPETSCDPRAAICGTVD : 1863
AtACC1 : LTVSDDLEGVSAILNWLSYIPAYVGGPLPVLAPLDPPERIVEYVPENSCDPRAAIAGVKD : 1859
AtACC2 : LTVSDDLEGVSAILNWLSYIPAYVGGPLPVLAPLDPPERTVEYIPENSCDPRAAIAGIND : 1960
OsACC1 : LTVSDDLEGVSAILKWLSYVPPYVGGPLPIMKPLDPPDRPVTYFPENSCDARAAICGVQD : 1871
OsACC2 : LTVSDDLEGVSNILRWLSYVPAYIGGPLPVTTPLDPPDRPVAYIPENSCDPRAAIRGVDD : 1937

SmACC1 : GAGKWLGGMFDRDSFIETLEGWARTVVTGRAKLGGIPVGIIAVETQTMMQVIPADPGQLD : 1923
AtACC1 : NTGKWLGGIFDKNSFIETLEGWARTVVTGRAKLGGIPVGVVAVETQTVMQIIPADPGQLD : 1919
AtACC2 : NTGKWLGGIFDKNSFVETLEGWARTVVTGRAKLGGIPIGVVAVETQTVMHVIPADPGQLD : 2020
OsACC1 : SQGKWMGGMFDRESFVETLEGWAKTVVTGRAKLGGIPVGVIAVETQTMMQVIPADPGQLD : 1931
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OsACC2 : SQGKWLGGMFDKDSFVETFEGWAKTVVTGRAKLGGIPVGVIAVETQTMMQTIPADPGQLD : 1997

SmACC1 : SHERVVPQAGQVWFPDSATKTAQALMDFNKEELPLFILANWRGFSGGQRDLFEGILQAGS : 1983
AtACC1 : SHERVVPQAGQVWFPDSAAKTAQALMDFNREELPLFILANWRGFSGGQRDLFEGILQAGS : 1979
AtACC2 : SHERVVPQAGQVWFPDSAAKTAQALMDFNREQLPLFIIANWRGFSGGQRDLFEGILQAGS : 2080
OsACC1 : SAERVVPQAGQVWFPDSATKTAQALLDFNREELPLFILANWRGFSGGQRDLFEGILQAGS : 1991
OsACC2 : SREQSVPRAGQVWFPDSATKTAQALLDFNREGLPLFILANWRGFSGGQRDLFEGILQAGS : 2057

SmACC1 : TIVENLRTYGQPVFIYIPMMGELRGGAWVVVDSRINPDHIEMYAERTARGNVLEPEGLIE : 2043
AtACC1 : TIVENLRTYRQPVFVYIPMMGELRGGAWVVVDSQINSDYVEMYADETARGNVLEPEGTIE : 2039
AtACC2 : AIVENLRTYRQPVFVYIPMMGELRGGAWVVVDSQINSDYIEMYADETARGNVLEPEGMIE : 2140
OsACC1 : NIVENLRTYNQPAFVYIPMGGELRGGAWVVVDSKINPEHIEMYAERTAKGNVLEPEGLVE : 2051
OsACC2 : TIVENLRTYNQPAFVYIPMAAELRGGAWVVVDSKINPDRIECYAERTAKGNVLEPQGLIE : 2117

SmACC1 : IKFRTRELLECMSRLDPVLINLKSRLQEVRN-SGTPGMAEEIQIQIKTREKKLLPIYTQI : 2102
AtACC1 : IKFRTKELLECMGRLDQKLISLKAKLQDAKQ-SEAYANIELLQQQIKAREKQLLPVYIQI : 2098
AtACC2 : IKFRRKELLECMGRLDQTLINLKANIQDAKR-NKAYANIELLQKQIKTREKQLLPVYTQI : 2199
OsACC1 : IKFRPKELEECMLRLDPELIKLSTRLREMKKENAGLSEMDTTRRSIIARMKQLMPIYTQV : 2111
OsACC2 : IKFRSEELQDCMSRLDPTLIDLKAKLEVANK--NGSADTKSLQENIEARTKQLMPLYTQI : 2175

SmACC1 : ATKFAELHDTSLRMAAKGVIKQVVDWPKSRSFFYRRLHRRVVEDELVKTLRDAAGRRLEY : 2162
AtACC1 : ATKFAELHDTSMRMAAKGVIKSVVEWSGSRSFFYKKLNRRIAESSLVKNVREASGDNLAY : 2158
AtACC2 : ATKFAELHDTSMRMAAKGVIKSVVEWSGSRSFFYKKLYRRIAESSLVRNIRKASGDILSY : 2259
OsACC1 : ATRFAELHDTSARMAAKGVIGKVVDWEESRSFFYRRLRRRVTEDALAKEIREAAGEQLSQ : 2171
OsACC2 : AIRFAELHDTSLRMAAKGVIKKVVDWEESRSFFYKRLRRRISEDVLAKEIRAVAGEQFSH : 2235

SmACC1 : GSARDMIKEWFMSSEIAGGQESAWADDEAFFSWKDDMRSYNEKLQNLRVQKMLLQLSKLE : 2222
AtACC1 : KSSMRLIQDWFCNSDIAKGKEEAWTDDQVFFTWKDNVSNYELKLSELRAQKLLNQLAEIG : 2218
AtACC2 : KSAMGLIQDWFRKSEIAKGKEEAWTDDQLFFTWKDNVSNYEQKLSELRTQKLLNQLAEIG : 2319
OsACC1 : KSALDYIKKWYLSSNGSDGNSEKWNNDEAFFAWKDDPTNYENQLEELKAERVSKWLSRLA : 2231
OsACC2 : QPAIELIKKWYSAS-----HAAEWDDDDAFVAWMDNPENYKDYIQYLKAQRVSQSLSSLS : 2290

SmACC1 : SSTEDLQALPQALAALLAKMDLSTRDKLRDELRKVLD : 2259
AtACC1 : NS-SDLQALPQGLANLLNKVEPSKREELVAAIRKVLG : 2254
AtACC2 : NS-SDLQALPQGLANLLNKVDLSRREELVDAIRKVLG : 2355
OsACC1 : ES-PDVKALPNGLSIVLNKMNPSKREQVIDGLRQLLG : 2267
OsACC2 : DSSSDLQALPQGLSMLLDKMDPSRRAQLVEEIRKVLG : 2327
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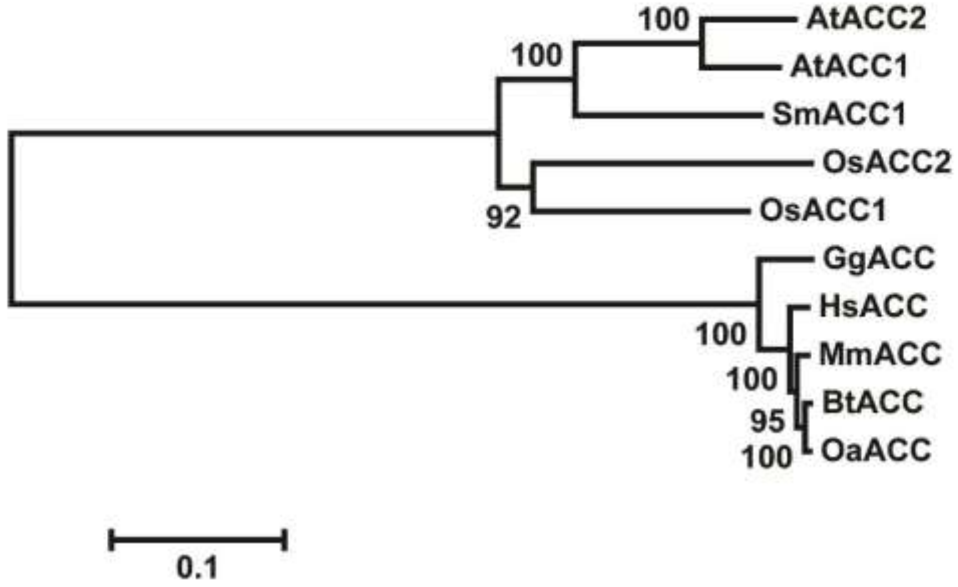
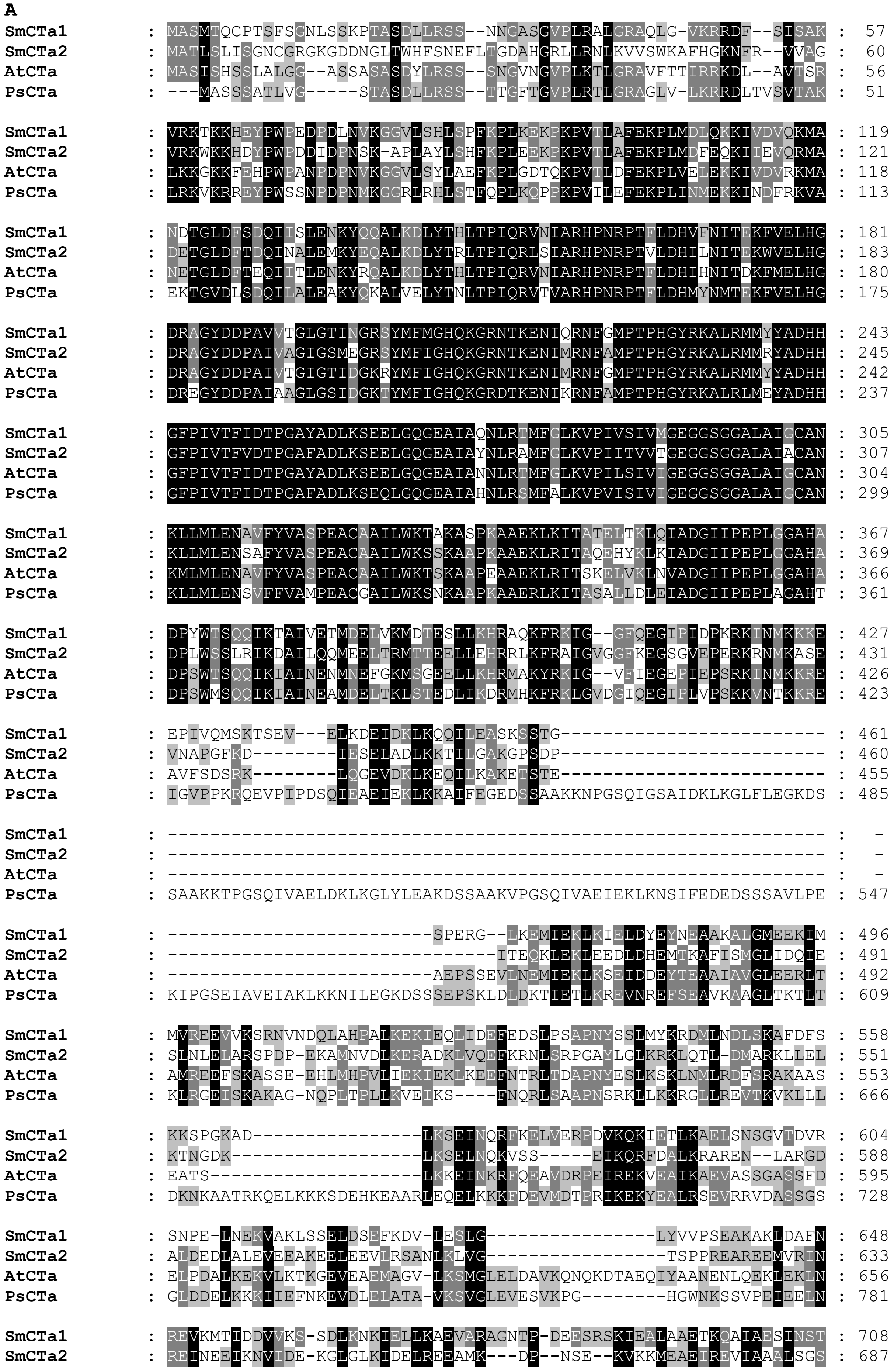


Fig S5. Multiple sequence alignment and phylogenetic tree for ACC proteins from *S. miltiorrhiza* and its homologs from various other species.

(A) Multiple sequence alignment of ACCs. The species and accession number for each ACC are shown in the parenthesis: SmACC1 (*S. miltiorrhiza*, KF876015); AtACC1 (*A. thaliana*, AT1G36160); OsACC1 (*O. sativa*, Q8S6N5); OsACC2 (B9FK36).

(B) Phylogenetic relationships of ACCs from *S. miltiorrhiza* and various other species. ACC proteins included are SmACC1 (*S. miltiorrhiza*, KF876015); AtACC1 (*A. thaliana*, AT1G36160) ; AtACC2 (F4I1L3); OsACC1 (*O. sativa*, Q8S6N5); OsACC2 (B9FK36).



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SmCTa1    : MASMTQCPTSFSGNLSSKPTASDLLRSS--NNGASGVPLRALGRAQLG-VKRRDF--SISAK :  57
SmCTa2    : MATLSLISGNCGRGKGDDNGLTWHFSNEFLTGDAHGRLLRNLKVVSWKAFHGKNFR--VVAG :  60
AtCTa     : MASISHSSLALGG--ASSASASDYLRSS--SNGVNGVPLKTLGRAVFTTIRRKDL--AVTSR :  56
PsCTa     : ---MASSSATLVG-----STASDLLRSS--TTGFTGVPLRTLGRAGLV-LKRRDLTVSVTAK :  51

SmCTa1    : VRKTKKHEYPWPEDPDLNVKGGVLSHLSPFKPLKEKPKPVTLAFEKPLMDLQKKIVDVQKMA : 119
SmCTa2    : VRKWKKHDYPWPDDIDPNSK-APLAYLSHFKPLEEKPKPVTLAFEKPLMDFEQKIIEVQRMA : 121
AtCTa     : LKKGKKFEHPWPANPDPNVKGGVLSYLAEFKPLGDTQKPVTLDFEKPLVELEKKIVDVRKMA : 118
PsCTa     : LRKVKRREYPWSSNPDPNMKGGRLRHLSTFQPLKQPPKPVILEFEKPLINMEKKINDFRKVA : 113

SmCTa1    : NDTGLDFSDQIISLENKYQQALKDLYTHLTPIQRVNIARHPNRPTFLDHVFNITEKFVELHG : 181
SmCTa2    : DETGLDFTDQINALEMKYEQALKDLYTRLTPIQRLSIARHPNRPTVLDHILNITEKWVELHG : 183
AtCTa     : NETGLDFTEQIITLENKYRQALKDLYTHLTPIQRVNIARHPNRPTFLDHIHNITDKFMELHG : 180
PsCTa     : EKTGVDLSDQILALEAKYQKALVELYTNLTPIQRVTVARHPNRPTFLDHMYNMTEKFVELHG : 175

SmCTa1    : DRAGYDDPAVVTGLGTINGRSYMFMGHQKGRNTKENIQRNFGMPTPHGYRKALRMMYYADHH : 243
SmCTa2    : DRAGYDDPAIVAGIGSMEGRSYMFIGHQKGRNTKENIMRNFAMPTPHGYRKALRMMRYADHH : 245
AtCTa     : DRAGYDDPAIVTGIGTIDGKRYMFIGHQKGRNTKENIMRNFGMPTPHGYRKALRMMYYADHH : 242
PsCTa     : DREGYDDPAIAAGLGSIDGKTYMFIGHQKGRDTKENIKRNFAMPTPHGYRKALRLMEYADHH : 237

SmCTa1    : GFPIVTFIDTPGAYADLKSEELGQGEAIAQNLRTMFGLKVPIVSIVMGEGGSGGALAIGCAN : 305
SmCTa2    : GFPIVTFVDTPGAFADLKSEELGQGEAIAYNLRAMFGLKVPIITVVTGEGGSGGALAIACAN : 307
AtCTa     : GFPIVTFIDTPGAYADLKSEELGQGEAIANNLRTMFGLKVPILSIVIGEGGSGGALAIGCAN : 304
PsCTa     : GFPIVTFIDTPGAFADLKSEQLGQGEAIAHNLRSMFALKVPVISIVIGEGGSGGALAIGCAN : 299

SmCTa1    : KLLMLENAVFYVASPEACAAILWKTAKASPKAAEKLKITATELTKLQIADGIIPEPLGGAHA : 367
SmCTa2    : KLLMLENSAFYVASPEACAAILWKSSKAAPKAAEKLRITAQEHYKLKIADGIIPEPLGGAHA : 369
AtCTa     : KMLMLENAVFYVASPEACAAILWKTSKAAPEAAEKLRITSKELVKLNVADGIIPEPLGGAHA : 366
PsCTa     : KLLMLENSVFFVAMPEACGAILWKSNKAAPKAAERLKITASALLDLEIADGIIPEPLAGAHT : 361

SmCTa1    : DPYWTSQQIKTAIVETMDELVKMDTESLLKHRAQKFRKIG--GFQEGIPIDPKRKINMKKKE : 427
SmCTa2    : DPLWSSLRIKDAILQQMEELTRMTTEELLEHRRLKFRAIGVGGFKEGSGVEPERKRNMKASE : 431
AtCTa     : DPSWTSQQIKIAINENMNEFGKMSGEELLKHRMAKYRKIG--VFIEGEPIEPSRKINMKKRE : 426
PsCTa     : DPSWMSQQIKIAINEAMDELTKLSTEDLIKDRMHKFRKLGVDGIQEGIPLVPSKKVNTKKRE : 423

SmCTa1    : EPIVQMSKTSEV---ELKDEIDKLKQQILEASKSSTG------------------------- : 461
SmCTa2    : VNAPGFKD--------IESELADLKKTILGAKGPSDP------------------------- : 460
AtCTa     : AVFSDSRK--------LQGEVDKLKEQILKAKETSTE------------------------- : 455
PsCTa     : IGVPPKRQEVPIPDSQIEAEIEKLKKAIFEGEDSSAAKKNPGSQIGSAIDKLKGLFLEGKDS : 485

SmCTa1    : -------------------------------------------------------------- :   -
SmCTa2    : -------------------------------------------------------------- :   -
AtCTa     : -------------------------------------------------------------- :   -
PsCTa     : SAAKKTPGSQIVAELDKLKGLYLEAKDSSAAKVPGSQIVAEIEKLKNSIFEDEDSSSAVLPE : 547

SmCTa1    : -------------------------SPERG--LKEMIEKLKIELDYEYNEAAKALGMEEKIM : 496
SmCTa2    : -------------------------------ITEQKLEKLEEDLDHEMTKAFISMGLIDQIE : 491
AtCTa     : -------------------------AEPSSEVLNEMIEKLKSEIDDEYTEAAIAVGLEERLT : 492
PsCTa     : KIPGSEIAVEIAKLKKNILEGKDSSSEPSKLDLDKTIETLKREVNREFSEAVKAAGLTKTLT : 609

SmCTa1    : MVREEVVKSRNVNDQLAHPALKEKIEQLIDEFEDSLPSAPNYSSLMYKRDMLNDLSKAFDFS : 558
SmCTa2    : SLNLELARSPDP-EKAMNVDLKERADKLVQEFKRNLSRPGAYLGLKRKLQTL-DMARKLLEL : 551
AtCTa     : AMREEFSKASSE-EHLMHPVLIEKIEKLKEEFNTRLTDAPNYESLKSKLNMLRDFSRAKAAS : 553
PsCTa     : KLRGEISKAKAG-NQPLTPLLKVEIKS----FNQRLSAAPNSRKLLKKRGLLREVTKVKLLL : 666

SmCTa1    : KKSPGKAD----------------LKSEINQRFKELVERPDVKQKIETLKAELSNSGVTDVR : 604
SmCTa2    : KTNGDK------------------LKSELNQKVSS-----EIKQRFDALKRAREN--LARGD : 588
AtCTa     : EATS--------------------LKKEINKRFQEAVDRPEIREKVEAIKAEVASSGASSFD : 595
PsCTa     : DKNKAATRKQELKKKSDEHKEAARLEQELKKKFDEVMDTPRIKEKYEALRSEVRRVDASSGS : 728

SmCTa1    : SNPE-LNEKVAKLSSELDSEFKDV-LESLG----------------LYVVPSEAKAKLDAFN : 648
SmCTa2    : ALDEDLALEVEEAKEELEEVLRSANLKLVG-----------------TSPPREAREEMVRIN : 633
AtCTa     : ELPDALKEKVLKTKGEVEAEMAGV-LKSMGLELDAVKQNQKDTAEQIYAANENLQEKLEKLN : 656
PsCTa     : GLDDELKKKIIEFNKEVDLELATA-VKSVGLEVESVKPG--------HGWNKSSVPEIEELN : 781

SmCTa1    : REVKMTIDDVVKS-SDLKNKIELLKAEVARAGNTP-DEESRSKIEALAAETKQAIAESINST : 708
SmCTa2    : REINEEIKNVIDE-KGLGLKIDELREEAMK---DP--NSE--KVKKMEAEIREVIAAALSGS : 687
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AtCTa       : QEITSKIEEVVRT-PEIKSMVELLKVETAKASKTPGVTEAYQKIEALEQQIKQKIAEALNTS : 717
PsCTa       : KDVQKEIEIVANSSPNVKRLIEQLKLEVAKSGGKP-DSESKSRIDALTQQIKKSLAEAVDSP : 842

SmCTa1      : ELKEKHEMLVAEMIEA----ATES-----EDDQSKLHDSQVNVNLETNRSFT : 751
SmCTa2      : PIKERLESLRLQDAGVVQENVG----------VDNGSTARVESSWWSERS-- : 727
AtCTa       : GLQEKQDELEKELAAARELAAEESDGSVKEDDDDDEDSSESGKSEMVNPSFA : 769
PsCTa       : SLKEKYENLTRPAGDT-------------------LTDDKLREKVGVNRNFS : 875
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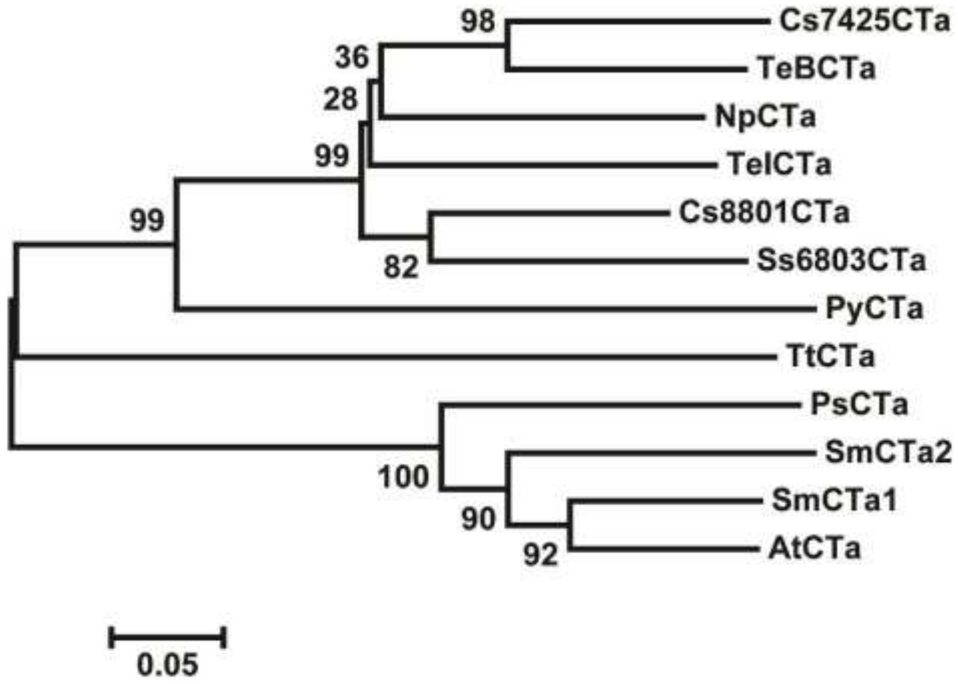
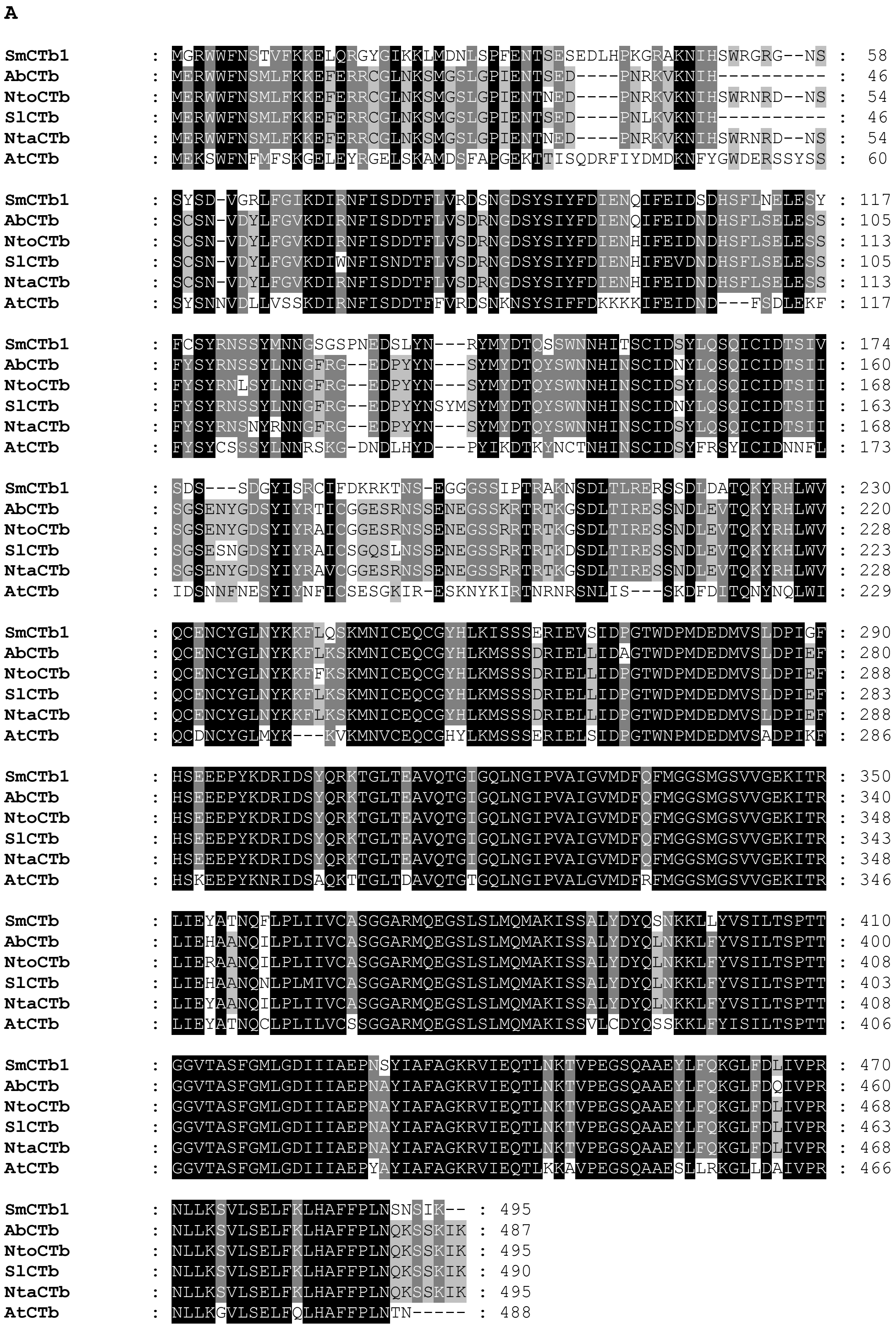


Fig S6. Multiple sequence alignment and phylogenetic tree for CTa proteins from *S. miltiorrhiza* and its homologs from various other species.

(A) Multiple sequence alignment of CTas. The species and accession number for each CTa are shown in the parenthesis: SmCTa1 (*S. miltiorrhiza*, KF887929); SmCTa2 (KJ784419); AtCTa (*A. thaliana*, AT2G38040.1); PsCTa (*Pisum sativum*, Q41008).

(B) Phylogenetic relationships of CTas from *S. miltiorrhiza* and various other species. CTa proteins included are SmCTa1 (*S. miltiorrhiza*, KF887929); SmCTa2 (KJ784419); AtCTa (*A. thaliana*, AT2G38040.1); PsCTa (*Pisum sativum*, Q41008); Cs7425CTa (*Cyanothece sp*. PCC 7425, B8HSZ5); TeBCTa (*Thermosynechococcus elongatus* BP-1, Q8DJB6); TeICTa (*Trichodesmium erythraeum* IMS101); Cs8801CTa (*Cyanothece sp*. PCC 8801, B7JZP4); Ss6803CTa (*Synechocystis sp*. PCC 6803, P74638); PyCTa (*Pyropia yezoensis*, Q1XDB6); TtCTa (*Thermus thermophilus* HB8, Q5SHG3).



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SmCTb1   : MGRWWFNSTVFKKELQRGYGIKKLMDNLSPFENTSESEDLHPKGRAKNIHSWRGRG--NS :  58
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NtoCTb   : MERWWFNSMLFKKEFERRCGLNKSMGSLGPIENTNED----PNRKVKNIHSWRNRD--NS :  54
SlCTb    : MERWWFNSMLFKKEFERRCGLNKSMGSLGPIENTSED----PNLKVKNIH---------- :  46
NtaCTb   : MERWWFNSMLFKKEFERRCGLNKSMGSLGPIENTNED----PNRKVKNIHSWRNRD--NS :  54
AtCTb    : MEKSWFNFMFSKGELEYRGELSKAMDSFAPGEKTTISQDRFIYDMDKNFYGWDERSSYSS :  60

SmCTb1   : SYSD-VGRLFGIKDIRNFISDDTFLVRDSNGDSYSIYFDIENQIFEIDSDHSFLNELESY : 117
AbCTb    : SCSN-VDYLFGVKDIRNFISDDTFLVSDRNGDSYSIYFDIENQIFEIDNDHSFLSELESS : 105
NtoCTb   : SCSN-VDYLFGVKDIRNFISDDTFLVSDRNGDSYSIYFDIENHIFEIDNDHSFLSELESS : 113
SlCTb    : SCSN-VDYLFGVKDIWNFISNDTFLVSDRNGDSYSIYFDIENHIFEVDNDHSFLSELESS : 105
NtaCTb   : SCSN-VDYLFGVKDIRNFISDDTFLVSDRNGDSYSIYFDIENHIFEIDNDHSFLSELESS : 113
AtCTb    : SYSNNVDLLVSSKDIRNFISDDTFFVRDSNKNSYSIFFDKKKKIFEIDND---FSDLEKF : 117

SmCTb1   : FCSYRNSSYMNNGSGSPNEDSLYN---RYMYDTQSSWNNHITSCIDSYLQSQICIDTSIV : 174
AbCTb    : FYSYRNSSYLNNGFRG--EDPYYN---SYMYDTQYSWNNHINSCIDNYLQSQICIDTSII : 160
NtoCTb   : FYSYRNLSYLNNGFRG--EDPYYN---SYMYDTQYSWNNHINSCIDSYLQSQICIDTSII : 168
SlCTb    : FYSYRNSSYLNNGFRG--EDPYYNSYMSYMYDTQYSWNNHINSCIDNYLQSQICIDTSII : 163
NtaCTb   : FYSYRNSNYRNNGFRG--EDPYYN---SYMYDTQYSWNNHINSCIDSYLQSQICIDTSII : 168
AtCTb    : FYSYCSSSYLNNRSKG-DNDLHYD---PYIKDTKYNCTNHINSCIDSYFRSYICIDNNFL : 173

SmCTb1   : SDS---SDGYISRCIFDKRKTNS-EGGGSSIPTRAKNSDLTLRERSSDLDATQKYRHLWV : 230
AbCTb    : SGSENYGDSYIYRTICGGESRNSSENEGSSKRTRTKGSDLTIRESSNDLEVTQKYRHLWV : 220
NtoCTb   : SGSENYGDSYIYRAICGGESRNSSENEGSSRRTRTKGSDLTIRESSNDLEVTQKYRHLWV : 228
SlCTb    : SGSESNGDSYIYRAICSGQSLNSSENEGSSRRTRTKDSDLTIRESSNDLEVTQKYKHLWV : 223
NtaCTb   : SGSENYGDSYIYRAVCGGESRNSSENEGSSRRTRTKGSDLTIRESSNDLEVTQKYRHLWV : 228
AtCTb    : IDSNNFNESYIYNFICSESGKIR-ESKNYKIRTNRNRSNLIS---SKDFDITQNYNQLWI : 229

SmCTb1   : QCENCYGLNYKKFLQSKMNICEQCGYHLKISSSERIEVSIDPGTWDPMDEDMVSLDPIGF : 290
AbCTb    : QCENCYGLNYKKFLKSKMNICEQCGYHLKMSSSDRIELLIDAGTWDPMDEDMVSLDPIEF : 280
NtoCTb   : QCENCYGLNYKKFFKSKMNICEQCGYHLKMSSSDRIELLIDPGTWDPMDEDMVSLDPIEF : 288
SlCTb    : QCENCYGLNYKKFLKSKMNICEQCGYHLKMSSSDRIELLIDPGTWDPMDEDMVSLDPIEF : 283
NtaCTb   : QCENCYGLNYKKFLKSKMNICEQCGYHLKMSSSDRIELLIDPGTWDPMDEDMVSLDPIEF : 288
AtCTb    : QCDNCYGLMYK---KVKMNVCEQCGHYLKMSSSERIELSIDPGTWNPMDEDMVSADPIKF : 286

SmCTb1   : HSEEEPYKDRIDSYQRKTGLTEAVQTGIGQLNGIPVAIGVMDFQFMGGSMGSVVGEKITR : 350
AbCTb    : HSEEEPYKDRIDSYQRKTGLTEAVQTGIGQLNGIPVAIGVMDFQFMGGSMGSVVGEKITR : 340
NtoCTb   : HSEEEPYKDRIDSYQRKTGLTEAVQTGIGQLNGIPVAIGVMDFQFMGGSMGSVVGEKITR : 348
SlCTb    : HSEEEPYKDRIDSYQRKTGLTEAVQTGIGQLNGIPVAIGVMDFQFMGGSMGSVVGEKITR : 343
NtaCTb   : HSEEEPYKDRIDSYQRKTGLTEAVQTGIGQLNGIPVAIGVMDFQFMGGSMGSVVGEKITR : 348
AtCTb    : HSKEEPYKNRIDSAQKTTGLTDAVQTGTGQLNGIPVALGVMDFRFMGGSMGSVVGEKITR : 346

SmCTb    : LIEYATNQFLPLIIVCASGGARMQEGSLSLMQMAKISSALYDYQSNKKLLYVSILTSPTT : 410
AbCTb    : LIEHAANQILPLIIVCASGGARMQEGSLSLMQMAKISSALYDYQLNKKLFYVSILTSPTT : 400
NtoCTb   : LIERAANQILPLIIVCASGGARMQEGSLSLMQMAKISSALYDYQLNKKLFYVSILTSPTT : 408
SlCTb    : LIEHAANQNLPLMIVCASGGARMQEGSLSLMQMAKISSALYDYQLNKKLFYVSILTSPTT : 403
NtaCTb   : LIEYAANQILPLIIVCASGGARMQEGSLSLMQMAKISSALYDYQLNKKLFYVSILTSPTT : 408
AtCTb    : LIEYATNQCLPLILVCSSGGARMQEGSLSLMQMAKISSVLCDYQSSKKLFYISILTSPTT : 406

SmCTb1   : GGVTASFGMLGDIIIAEPNSYIAFAGKRVIEQTLNKTVPEGSQAAEYLFQKGLFDLIVPR : 470
AbCTb    : GGVTASFGMLGDIIIAEPNAYIAFAGKRVIEQTLNKTVPEGSQAAEYLFQKGLFDQIVPR : 460
NtoCTb   : GGVTASFGMLGDIIIAEPNAYIAFAGKRVIEQTLNKTVPEGSQAAEYLFQKGLFDLIVPR : 468
SlCTb    : GGVTASFGMLGDIIIAEPNAYIAFAGKRVIEQTLNKTVPEGSQAAEYLFQKGLFDLIVPR : 463
NtaCTb   : GGVTASFGMLGDIIIAEPNAYIAFAGKRVIEQTLNKTVPEGSQAAEYLFQKGLFDLIVPR : 468
AtCTb    : GGVTASFGMLGDIIIAEPYAYIAFAGKRVIEQTLKKAVPEGSQAAESLLRKGLLDAIVPR : 466

SmCTb1   : NLLKSVLSELFKLHAFFPLNSNSIK-- : 495
AbCTb    : NLLKSVLSELFKLHAFFPLNQKSSKIK : 487
NtoCTb   : NLLKSVLSELFKLHAFFPLNQKSSKIK : 495
SlCTb    : NLLKSVLSELFKLHAFFPLNQKSSKIK : 490
NtaCTb   : NLLKSVLSELFKLHAFFPLNQKSSKIK : 495
AtCTb    : NLLKGVLSELFQLHAFFPLNTN----- : 488
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B

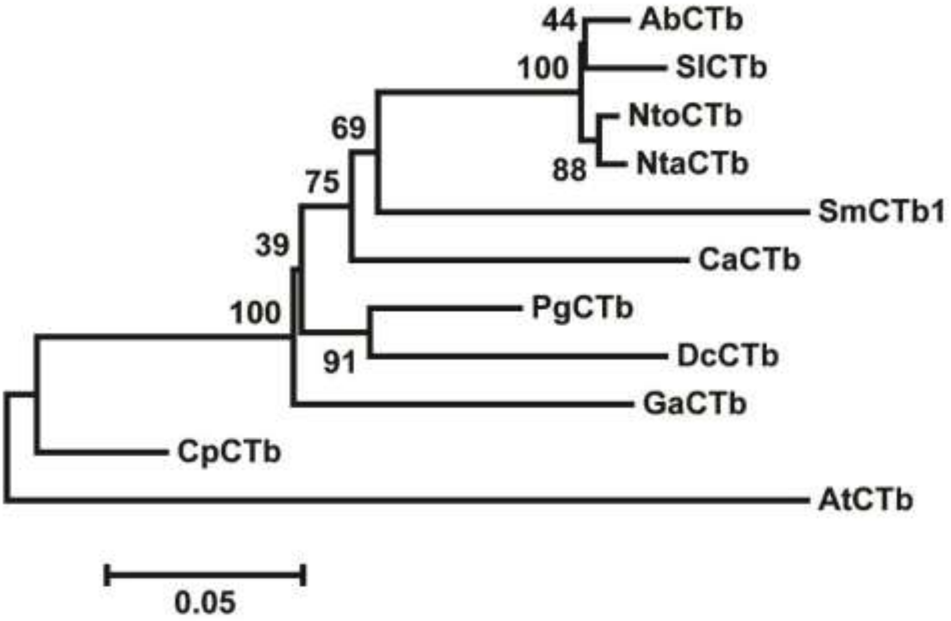
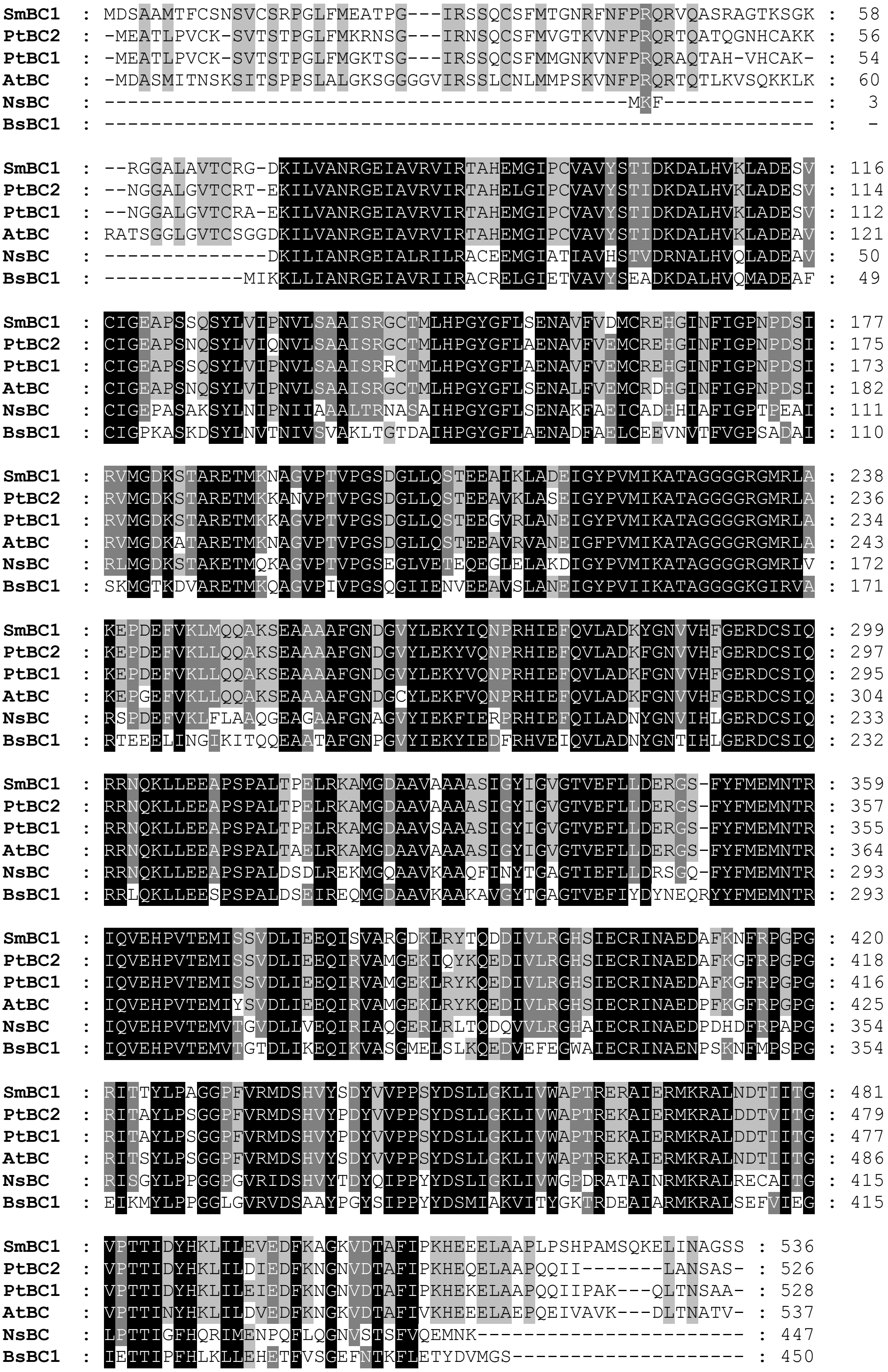


Fig S7. Multiple sequence alignment and phylogenetic tree for CTb proteins from *S. miltiorrhiza* and its homologs from various other species.

(A) Multiple sequence alignment of CTbs. The species and accession number for each CTb are shown in the parenthesis: SmCTb1 (*S. miltiorrhiza*, KF887943); AtCTb (*A. thaliana*, ATCG00500.1); AbCTb (*Atropa belladonna*, Q8S8W7); NtoCTb (*Nicotiana tomentosiformis*, Q33C25); PgCTb (*Panax ginseng*, Q68RZ7); SlCTb (*Solanum lycopersicum* , Q2MI91); NtCTb (*Nicotiana tabacum* , P12219).

(B) Phylogenetic relationships of CTbs from *S. miltiorrhiza* and various other species. CTb proteins included are SmCTb1 (KF887943); AtCTb (ATCG00500.1); AbCTb (*Atropa belladonna* , Q8S8W7); NtoCTb (*Nicotiana tomentosiformis*, Q33C25); PgCTb (*Panax ginseng* , Q68RZ7); SlCTb (*Solanum lycopersicum* , Q2MI91); NtCTb (*Nicotiana tabacum*, P12219); CaCTb (*Coffea Arabica*, A0A344); GaCTb(*Guizotia abyssinica*, B2LMK2); CpCTb(*Carica papaya*, B1A944); DcCTb(*Daucus carota*, Q0G9V3).

A



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SmBC1  : MDSAAMTFCSNSVCSRPGLFMEATPG---IRSSQCSFMTGNRFNFPRQRVQASRAGTKSGK :  58
PtBC2  : -MEATLPVCK-SVTSTPGLFMKRNSG---IRNSQCSFMVGTKVNFPRQRTQATQGNHCAKK :  56
PtBC1  : -MEATLPVCK-SVTSTPGLFMGKTSG---IRSSQCSFMMGNKVNFPRQRAQTAH-VHCAK- :  54
AtBC   : -MDASMITNSKSITSPPSLALGKSGGGGVIRSSLCNLMMPSKVNFPRQRTQTLKVSQKKLK :  60
NsBC   : ---------------------------------------------MKF------------- :   3
BsBC1  : ------------------------------------------------------------- :   -

SmBC1  : --RGGALAVTCRG-DKILVANRGEIAVRVIRTAHEMGIPCVAVYSTIDKDALHVKLADESV : 116
PtBC2  : --NGGALGVTCRT-EKILVANRGEIAVRVIRTAHELGIPCVAVYSTIDKDALHVKLADESV : 114
PtBC1  : --NGGALGVTCRA-EKILVANRGEIAVRVIRTAHEMGIPCVAVYSTIDKDALHVKLADESV : 112
AtBC   : RATSGGLGVTCSGGDKILVANRGEIAVRVIRTAHEMGIPCVAVYSTIDKDALHVKLADEAV : 121
NsBC   : --------------DKILIANRGEIALRILRACEEMGIATIAVHSTVDRNALHVQLADEAV :  50
BsBC1  : ------------MIKKLLIANRGEIAVRIIRACRELGIETVAVYSEADKDALHVQMADEAF :  49

SmBC1  : CIGEAPSSQSYLVIPNVLSAAISRGCTMLHPGYGFLSENAVFVDMCREHGINFIGPNPDSI : 177
PtBC2  : CIGEAPSNQSYLVIQNVLSAAISRGCTMLHPGYGFLAENAVFVEMCREHGINFIGPNPDSI : 175
PtBC1  : CIGEAPSSQSYLVIPNVLSAAISRRCTMLHPGYGFLAENAVFVEMCREHGINFIGPNPDSI : 173
AtBC   : CIGEAPSNQSYLVIPNVLSAAISRGCTMLHPGYGFLSENALFVEMCRDHGINFIGPNPDSI : 182
NsBC   : CIGEPASAKSYLNIPNIIAAALTRNASAIHPGYGFLSENAKFAEICADHHIAFIGPTPEAI : 111
BsBC1  : CIGPKASKDSYLNVTNIVSVAKLTGTDAIHPGYGFLAENADFAELCEEVNVTFVGPSADAI : 110

SmBC1  : RVMGDKSTARETMKNAGVPTVPGSDGLLQSTEEAIKLADEIGYPVMIKATAGGGGRGMRLA : 238
PtBC2  : RVMGDKSTARETMKKANVPTVPGSDGLLQSTEEAVKLASEIGYPVMIKATAGGGGRGMRLA : 236
PtBC1  : RVMGDKSTARETMKKAGVPTVPGSDGLLQSTEEGVRLANEIGYPVMIKATAGGGGRGMRLA : 234
AtBC   : RVMGDKATARETMKNAGVPTVPGSDGLLQSTEEAVRVANEIGFPVMIKATAGGGGRGMRLA : 243
NsBC   : RLMGDKSTAKETMQKAGVPTVPGSEGLVETEQEGLELAKDIGYPVMIKATAGGGGRGMRLV : 172
BsBC1  : SKMGTKDVARETMKQAGVPIVPGSQGIIENVEEAVSLANEIGYPVIIKATAGGGGKGIRVA : 171

SmBC1  : KEPDEFVKLMQQAKSEAAAAFGNDGVYLEKYIQNPRHIEFQVLADKYGNVVHFGERDCSIQ : 299
PtBC2  : KEPDEFVKLLQQAKSEAAAAFGNDGVYLEKYVQNPRHIEFQVLADKFGNVVHFGERDCSIQ : 297
PtBC1  : KEPDEFVKLLQQAKSEAAAAFGNDGVYLEKYVQNPRHIEFQVLADKFGNVVHFGERDCSIQ : 295
AtBC   : KEPGEFVKLLQQAKSEAAAAFGNDGCYLEKFVQNPRHIEFQVLADKFGNVVHFGERDCSIQ : 304
NsBC   : RSPDEFVKLFLAAQGEAGAAFGNAGVYIEKFIERPRHIEFQILADNYGNVIHLGERDCSIQ : 233
BsBC1  : RTEEELINGIKITQQEAATAFGNPGVYIEKYIEDFRHVEIQVLADNYGNTIHLGERDCSIQ : 232

SmBC1  : RRNQKLLEEAPSPALTPELRKAMGDAAVAAAASIGYIGVGTVEFLLDERGS-FYFMEMNTR : 359
PtBC2  : RRNQKLLEEAPSPALTPELRKAMGDAAVAAAASIGYIGVGTVEFLLDERGS-FYFMEMNTR : 357
PtBC1  : RRNQKLLEEAPSPALTPELRKAMGDAAVSAAASIGYIGVGTVEFLLDERGS-FYFMEMNTR : 355
AtBC   : RRNQKLLEEAPSPALTAELRKAMGDAAVAAAASIGYIGVGTVEFLLDERGS-FYFMEMNTR : 364
NsBC   : RRNQKLLEEAPSPALDSDLREKMGQAAVKAAQFINYTGAGTIEFLLDRSGQ-FYFMEMNTR : 293
BsBC1  : RRLQKLLEESPSPALDSEIREQMGDAAVKAAKAVGYTGAGTVEFIYDYNEQRYYFMEMNTR : 293

SmBC1  : IQVEHPVTEMISSVDLIEEQISVARGDKLRYTQDDIVLRGHSIECRINAEDAFKNFRPGPG : 420
PtBC2  : IQVEHPVTEMISSVDLIEEQIRVAMGEKIQYKQEDIVLRGHSIECRINAEDAFKGFRPGPG : 418
PtBC1  : IQVEHPVTEMISSVDLIEEQIRVAMGEKLRYKQEDIVLRGHSIECRINAEDAFKGFRPGPG : 416
AtBC   : IQVEHPVTEMIYSVDLIEEQIRVAMGEKLRYKQEDIVLRGHSIECRINAEDPFKGFRPGPG : 425
NsBC   : IQVEHPVTEMVTGVDLLVEQIRIAQGERLRLTQDQVVLRGHAIECRINAEDPDHDFRPAPG : 354
BsBC1  : IQVEHPVTEMVTGTDLIKEQIKVASGMELSLKQEDVEFEGWAIECRINAENPSKNFMPSPG : 354

SmBC1  : RITTYLPAGGPFVRMDSHVYSDYVVPPSYDSLLGKLIVWAPTRERAIERMKRALNDTIITG : 481
PtBC2  : RITAYLPSGGPFVRMDSHVYPDYVVPPSYDSLLGKLIVWAPTREKAIERMKRALDDTVITG : 479
PtBC1  : RITAYLPSGGPFVRMDSHVYPDYVVPPSYDSLLGKLIVWAPTREKAIERMKRALDDTIITG : 477
AtBC   : RITSYLPSGGPFVRMDSHVYSDYVVPPSYDSLLGKLIVWAPTREKAIERMKRALNDTIITG : 486
NsBC   : RISGYLPPGGPGVRIDSHVYTDYQIPPYYDSLIGKLIVWGPDRATAINRMKRALRECAITG : 415
BsBC1  : EIKMYLPPGGLGVRVDSAAYPGYSIPPYYDSMIAKVITYGKTRDEAIARMKRALSEFVIEG : 415

SmBC1  : VPTTIDYHKLILEVEDFKAGKVDTAFIPKHEEELAAPLPSHPAMSQKELINAGSS : 536
PtBC2  : VPTTIDYHKLILDIEDFKNGNVDTAFIPKHEQELAAPQQII-------LANSAS- : 526
PtBC1  : VPTTIDYHKLILEIEDFKNGNVDTAFIPKHEKELAAPQQIIPAK---QLTNSAA- : 528
AtBC   : VPTTINYHKLILDVEDFKNGKVDTAFIVKHEEELAEPQEIVAVK---DLTNATV- : 537
NsBC   : LPTTIGFHQRIMENPQFLQGNVSTSFVQEMNK----------------------- : 447
BsBC1  : IETTIPFHLKLLEHETFVSGEFNTKFLETYDVMGS-------------------- : 450
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B

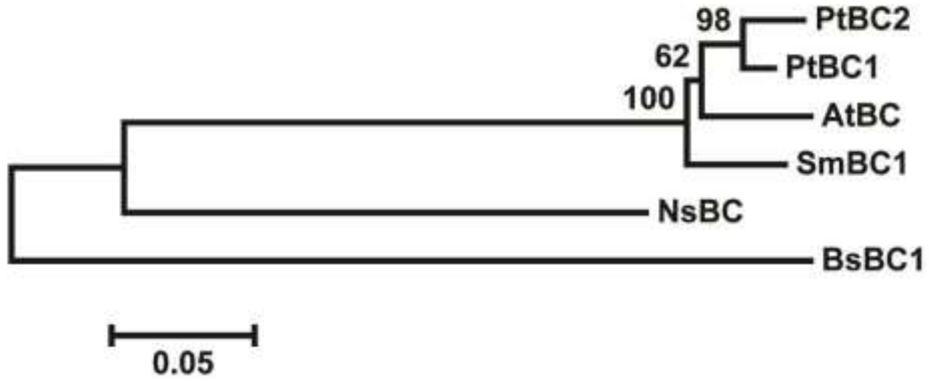

Fig S8. Multiple sequence alignment and phylogenetic tree for BC proteins from *S. miltiorrhiza* and its homologs from various other species.
(A) Multiple sequence alignment of BCs. The species and accession number for each BC are shown in the parenthesis: SmBC1 (*S. miltiorrhiza*, KF887921); AtBC1 (*A. thaliana*, AT5G35360.3); PtBC1 (*Populus trichocarpa*, B9HBA8); PtBC2 (B9N843); BsAccC1 (*Bacillus subtilis*, P49787); NsBC (*Nostoc sp. PCC7120*, Q06862).
(B) Phylogenetic relationships of BCs from *S. miltiorrhiza* and various other species. BC proteins included are SmBC1 (*S. miltiorrhiza*, KF887921); AtBC1 (*A. thaliana*, AT5G35360.3); PtBC1 (*Populus trichocarpa*, B9HBA8); PtBC2 (B9N843); BsAccC1 (*Bacillus subtilis*, P49787); NsBC (*Nostoc sp. PCC7120*, Q06862).

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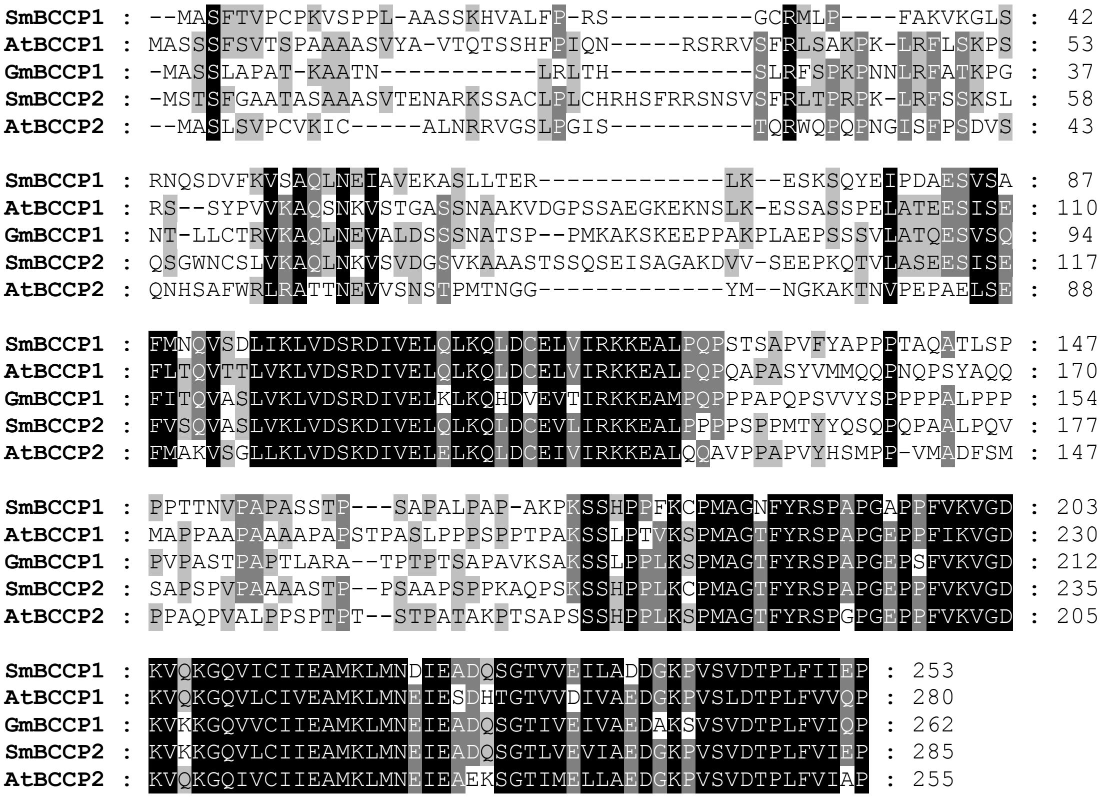

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SmBCCP1 : --MASFTVPCPKVSPPL-AASSKHVALFP-RS----------GCRMLP----FAKVKGLS :  42
AtBCCP1 : MASSSFSVTSPAAAASVYA-VTQTSSHFPIQN-----RSRRVSFRLSAKPK-LRFLSKPS :  53
GmBCCP1 : -MASSLAPAT-KAATN-----------LRLTH----------SLRFSPKPNNLRFATKPG :  37
SmBCCP2 : -MSTSFGAATASAAASVTENARKSSACLPLCHRHSFRRSNSVSFRLTPRPK-LRFSSKSL :  58
AtBCCP2 : --MASLSVPCVKIC-----ALNRRVGSLPGIS----------TQRWQPQPNGISFPSDVS :  43

SmBCCP1 : RNQSDVFKVSAQLNEIAVEKASLLTER-------------LK--ESKSQYEIPDAESVSA :  87
AtBCCP1 : RS--SYPVVKAQSNKVSTGASSNAAKVDGPSSAEGKEKNSLK-ESSASSPELATEESISE : 110
GmBCCP1 : NT-LLCTRVKAQLNEVALDSSSNATSP--PMKAKSKEEPPAKPLAEPSSSVLATQESVSQ :  94
SmBCCP2 : QSGWNCSLVKAQLNKVSVDGSVKAAASTSSQSEISAGAKDVV-SEEPKQTVLASEESISE : 117
AtBCCP2 : QNHSAFWRLRATTNEVVSNSTPMTNGG-------------YM--NGKAKTNVPEPAELSE :  88

SmBCCP1 : FMNQVSDLIKLVDSRDIVELQLKQLDCELVIRKKEALPQPSTSAPVFYAPPPTAQATLSP : 147
AtBCCP1 : FLTQVTTLVKLVDSRDIVELQLKQLDCELVIRKKEALPQPQAPASYVMMQQPNQPSYAQQ : 170
GmBCCP1 : FITQVASLVKLVDSRDIVELKLKQHDVEVTIRKKEAMPQPPPAPQPSVVYSPPPPALPPP : 154
SmBCCP2 : FVSQVASLVKLVDSKDIVELQLKQLDCEVLIRKKEALPPPPSPPMTYYQSQPQPAALPQV : 177
AtBCCP2 : FMAKVSGLLKLVDSKDIVELELKQLDCEIVIRKKEALQQAVPPAPVYHSMPP-VMADFSM : 147

SmBCCP1 : PPTTNVPAPASSTP---SAPALPAP-AKPKSSHPPFKCPMAGNFYRSPAPGAPPFVKVGD : 203
AtBCCP1 : MAPPAAPAAAAPAPSTPASLPPPSPPTPAKSSLPTVKSPMAGTFYRSPAPGEPPFIKVGD : 230
GmBCCP1 : PVPASTPAPTLARA--TPTPTSAPAVKSAKSSLPPLKSPMAGTFYRSPAPGEPSFVKVGD : 212
SmBCCP2 : SAPSPVPAAAASTP--PSAAPSPPKAQPSKSSHPPLKCPMAGTFYRSPAPGEPPFVKVGD : 235
AtBCCP2 : PPAQPVALPPSPTPT--STPATAKPTSAPSSSHPPLKSPMAGTFYRSPGPGEPPFVKVGD : 205

SmBCCP1 : KVQKGQVICIIEAMKLMNDIEADQSGTVVEILADDGKPVSVDTPLFIIEP : 253
AtBCCP1 : KVQKGQVLCIVEAMKLMNEIESDHTGTVVDIVAEDGKPVSLDTPLFVVQP : 280
GmBCCP1 : KVKKGQVVCIIEAMKLMNEIEADQSGTIVEIVAEDAKSVSVDTPLFVIQP : 262
SmBCCP2 : KVKKGQVLCIIEAMKLMNEIEADQSGTLVEVIAEDGKPVSVDTPLFVIEP : 285
AtBCCP2 : KVQKGQIVCIIEAMKLMNEIEAEKSGTIMELLAEDGKPVSVDTPLFVIAP : 255
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B

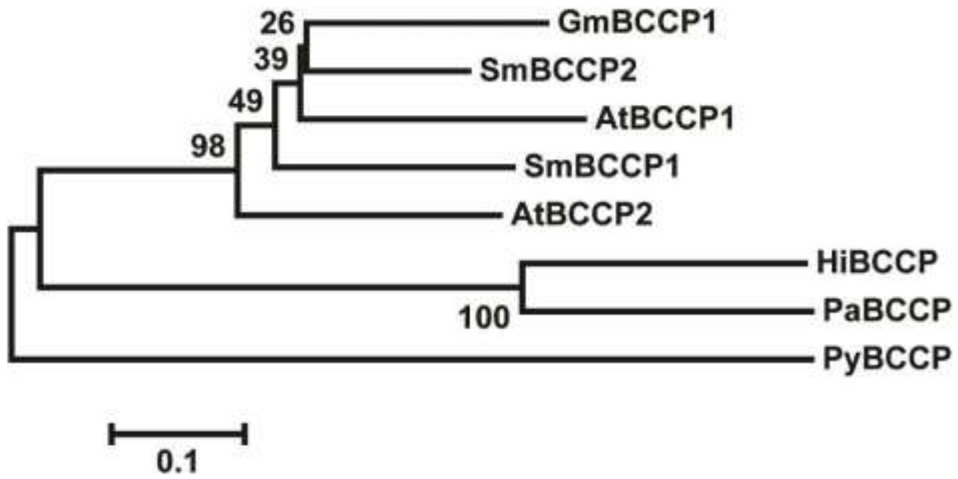

Fig S9. Multiple sequence alignment and phylogenetic tree for BCCP proteins from *S. miltiorrhiza* and its homologs from various other species.

(A) Multiple sequence alignment of BCCPs. The species and accession number for each BCCP are shown in the parenthesis: SmBCCP1 (*S. miltiorrhiza*, KF887920); SmBCCP2 (); AtBCCP1 (*A. thaliana*, AT5G15530.1); AtBCCP2 (AT5G16390.1); GmBCCP1 (*Glycine max*, Q42783).

(B) Phylogenetic relationships of BCCPs from *S. miltiorrhiza* and various other species. BCCP proteins included are SmBCCP1 (*S. miltiorrhiza*, KF887920); SmBCCP2 (KJ784427); AtBCCP1 (*A. thaliana*, AT5G15530.1); AtBCCP2 (AT5G16390.1); GmBCCP1 (*Glycine max*, Q42783); PyBCCP *(Pyropia yezoensis*, Q1XDK5); HiBCCP (*Haemophilus influenzae* Rd KW20, P43874); PaBCCP (*Pseudomonas aeruginosa* , P37799).

A

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SmHACPS1     : MRRGFSRMKLHCLDRTLFRSSHSLNGVHLPAPMETHLWYVKPSEVKSESLLKQYFDILSP :  60
SsHACPS      : ----------------MLPQP--------------QIWLCPTD----RPLIPGYQALLSS :  26
NsHACPS      : -----------MLQHTWLPKPPNLTLLSD----EVHLWRIPLD--QPESQLQDLAATLSS :  43
AtHACPS      : MR----IRVMSQLQRSLSIELPSLVPLQLPSRMETHLWFIRPDEVKSTSLLKHYSQLLSP :  56

SmHACPS1     : CERENVLRLQGEELRKSALLARALVRTTIAKYQMNSPVDPRSLKFRKNMHGKPEVCWPSM : 120
SsHACPS      : EEMARGERYQRPQDKQRFLTMRLALRILLARQLD---CLPQQLQFTYGPQGKPE-----L :  78
NsHACPS      : DELARANRFYFPEHRRRFTAGRGILRSILGGYLG---VEPGQVKFDYESRGKP--ILG-- :  96
AtHACPS      : TEKEKVLQMRGDELKKNALLARTLVRTTIARCMTNNEVDPKALMFKKNMYGKPEVDWQNY : 116

SmHACPS1     : DDWDPPPLHFNLSHTSSLIACGVTVNSQIGIDVEEKQRSTKHDILSFARRYFSKYEVQLL : 180
SsHACPS      : VDRERRSPWFNVAHSGNYGLIGLSTEGEIGVDLQIML--PKPHYLKLAKRFFAPQEVQQL : 136
NsHACPS      : DRFAESGLLFNLSHSQNLALCAVNYTRQIGIDLEYLR--PTSDLESLAKRFFLPREYELL : 154
AtHACPS      : TNCNNPPLHFNISHTDSLIACGVTVHVPVGIDVEDKERKIKHDILAFAERFYSADEVKFL : 176

SmHACPS1     : AAVSDPQAQQREFIKLWTLKEAYVKALGKGFSGAPFKTFTIRFRAVMEGGFKALDESSTK : 240
SsHACPS      : ESLEG-EKRTKLFYQLWTAKEAFLKATGKGISGGLNQVIPDENLAKYQY----------- : 184
NsHACPS      : RSLPD-EQKQKIFFRYWTCKEAYLKATGDGIAKLEEIEIALTPTEPAK------------ : 201
AtHACPS      : STLPDPEVQRKEFIKLWTLKEAYVKALGKGFSAAPFNTFTIQSKVGTKG-----EYNLCK : 231

SmHACPS1     : GYEIIVDSVDDPTNVTTSWQFLLLELGGSHYAAICTEKHSALDGKRNAPGKLMVWKTIPF : 300
SsHACPS      : LPD---SGDTNHWRLSSQPLLADQGSNDNYWMAIAWCTNEVN---------QVESNYLPN : 232
NsHACPS      : ------------LQTAPAWSLLELVPDDNCVAAVAVAG--FG-------WQPKFWHY--- : 237
AtHACPS      : MTEMTASSLEETNKCDGEWKFSLLELDDSHYAAICIEDDEASGG---APMRVIVRKTIPF : 288

SmHACPS1     : LEDEYVSGTDAVKMICGLQ : 319
SsHACPS      : IQPFQWPRNLDSLP----- : 246
NsHACPS      : ------------------- :   -
AtHACPS      : VEDELIS---ESKLL---- : 300
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B

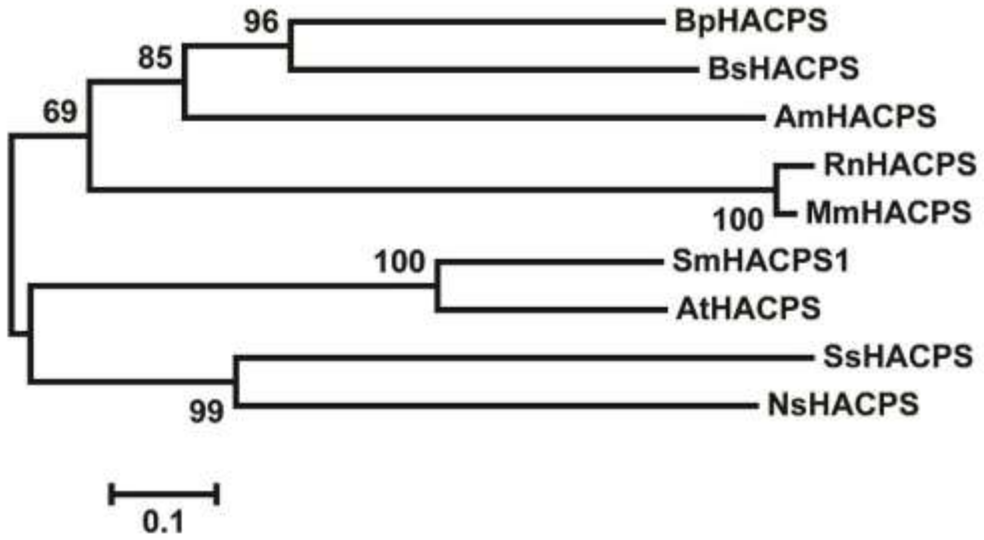
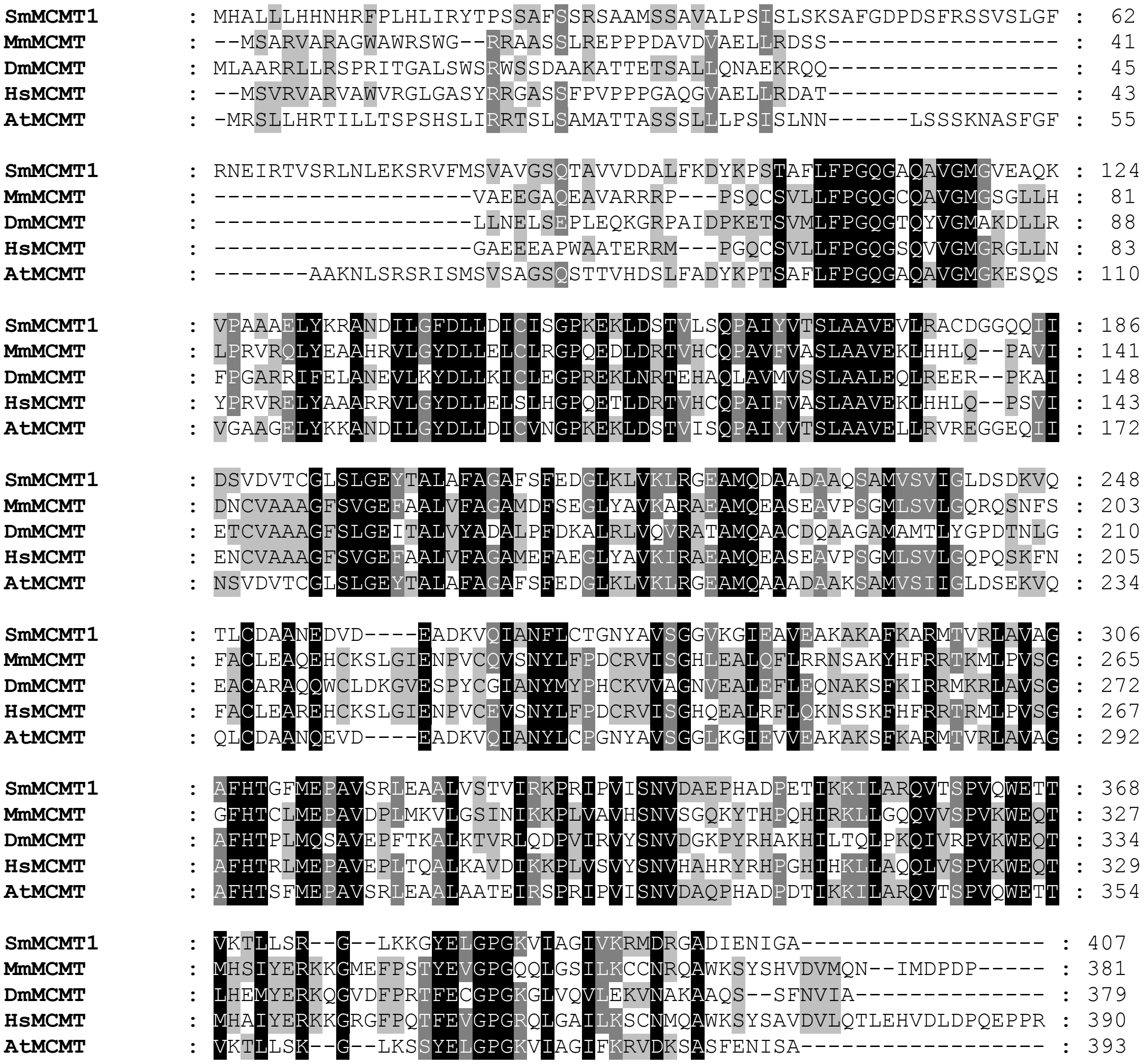


Fig S10. Multiple sequence alignment and phylogenetic tree for HACPS proteins from *S. miltiorrhiza* and its homologs from various other species.

(A) Multiple sequence alignment of HACPSs. The species and accession number for each HACPS are shown in the parenthesis: SmHACPS1 (*S. miltiorrhiza*,KF887926); AtHACPS (*A. thaliana*, AT2G02770.1); SsHACPS (Synechocystis sp.PCC6803, Q55185); NsHACPS (Nostoc sp.PCC7120, P37695).

(B) Phylogenetic relationships of HACPSs from *S. miltiorrhiza* and various other species. HACPS proteins included are SmHACPS1 (*S. miltiorrhiza*, KF887926); AtHACPS (*A. thaliana*, AT2G02770.1); SsHACPS (Synechocystis sp.PCC6803, Q55185); NsHACPS (Nostoc sp.PCC7120, P37695); RnHACPS(*Rattus norvegicus*, B2RYJ4); BsHACPS(*Bacillus subtilis* subsp. subtilis str. 168, P39135); MmHACPS(*Mus musculus*, Q9CQF6); BpHACPS(*Bacillus pumilus*, P55810); AmHACPS(*Aneurinibacillus migulanus*, P40683).

A



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DmMCMT    : MLAARRLLRSPRITGALSWSRWSSDAAKATTETSALLQNAEKRQQ----------------- :  45
HsMCMT    : --MSVRVARVAWVRGLGASYRRGASSFPVPPPGAQGVAELLRDAT----------------- :  43
AtMCMT    : -MRSLLHRTILLTSPSHSLIRRTSLSAMATTASSSLLLPSISLNN------LSSSKNASFGF :  55

SmMCMT1   : RNEIRTVSRLNLEKSRVFMSVAVGSQTAVVDDALFKDYKPSTAFLFPGQGAQAVGMGVEAQK : 124
MmMCMT    : -------------------VAEEGAQEAVARRRP---PSQCSVLLFPGQGCQAVGMGSGLLH :  81
DmMCMT    : -------------------LLNELSEPLEQKGRPAIDPKETSVMLFPGQGTQYVGMAKDLLR :  88
HsMCMT    : -------------------GAEEEAPWAATERRM---PGQCSVLLFPGQGSQVVGMGRGLLN :  83
AtMCMT    : -------AAKNLSRSRISMSVSAGSQSTTVHDSLFADYKPTSAFLFPGQGAQAVGMGKESQS : 110

SmMCMT1   : VPAAAELYKRANDILGFDLLDICISGPKEKLDSTVLSQPAIYVTSLAAVEVLRACDGGQQII : 186
MmMCMT    : LPRVRQLYEAAHRVLGYDLLELCLRGPQEDLDRTVHCQPAVFVASLAAVEKLHHLQ--PAVI : 141
DmMCMT    : FPGARRIFELANEVLKYDLLKICLEGPREKLNRTEHAQLAVMVSSLAALEQLREER--PKAI : 148
HsMCMT    : YPRVRELYAAARRVLGYDLLELSLHGPQETLDRTVHCQPAIFVASLAAVEKLHHLQ--PSVI : 143
AtMCMT    : VGAAGELYKKANDILGYDLLDICVNGPKEKLDSTVISQPAIYVTSLAAVELLRVREGGEQII : 172

SmMCMT1   : DSVDVTCGLSLGEYTALAFAGAFSFEDGLKLVKLRGEAMQDAADAAQSAMVSVIGLDSDKVQ : 248
MmMCMT    : DNCVAAAGFSVGEFAALVFAGAMDFSEGLYAVKARAEAMQEASEAVPSGMLSVLGQRQSNFS : 203
DmMCMT    : ETCVAAAGFSLGEITALVYADALPFDKALRLVQVRATAMQAACDQAAGAMAMTLYGPDTNLG : 210
HsMCMT    : ENCVAAAGFSVGEFAALVFAGAMEFAEGLYAVKIRAEAMQEASEAVPSGMLSVLGQPQSKFN : 205
AtMCMT    : NSVDVTCGLSLGEYTALAFAGAFSFEDGLKLVKLRGEAMQAAADAAKSAMVSIIGLDSEKVQ : 234

SmMCMT1   : TLCDAANEDVD----EADKVQIANFLCTGNYAVSGGVKGIEAVEAKAKAFKARMTVRLAVAG : 306
MmMCMT    : FACLEAQEHCKSLGIENPVCQVSNYLFPDCRVISGHLEALQFLRRNSAKYHFRRTKMLPVSG : 265
DmMCMT    : EACARAQQWCLDKGVESPYCGIANYMYPHCKVVAGNVEALEFLEQNAKSFKIRRMKRLAVSG : 272
HsMCMT    : FACLEAREHCKSLGIENPVCEVSNYLFPDCRVISGHQEALRFLQKNSSKFHFRRTRMLPVSG : 267
AtMCMT    : QLCDAANQEVD----EADKVQIANYLCPGNYAVSGGLKGIEVVEAKAKSFKARMTVRLAVAG : 292

SmMCMT1   : AFHTGFMEPAVSRLEAALVSTVIRKPRIPVISNVDAEPHADPETIKKILARQVTSPVQWETT : 368
MmMCMT    : GFHTCLMEPAVDPLMKVLGSINIKKPLVAVHSNVSGQKYTHPQHIRKLLGQQVVSPVKWEQT : 327
DmMCMT    : AFHTPLMQSAVEPFTKALKTVRLQDPVIRVYSNVDGKPYRHAKHILTQLPKQIVRPVKWEQT : 334
HsMCMT    : AFHTRLMEPAVEPLTQALKAVDIKKPLVSVYSNVHAHRYRHPGHIHKLLAQQLVSPVKWEQT : 329
AtMCMT    : AFHTSFMEPAVSRLEAALAATEIRSPRIPVISNVDAQPHADPDTIKKILARQVTSPVQWETT : 354

SmMCMT1   : VKTLLSR--G--LKKGYELGPGKVIAGIVKRMDRGADIENIGA------------------ : 407
MmMCMT    : MHSIYERKKGMEFPSTYEVGPGQQLGSILKCCNRQAWKSYSHVDVMQN--IMDPDP----- : 381
DmMCMT    : LHEMYERKQGVDFPRTFECGPGKGLVQVLEKVNAKAAQS--SFNVIA-------------- : 379
HsMCMT    : MHAIYERKKGRGFPQTFEVGPGRQLGAILKSCNMQAWKSYSAVDVLQTLEHVDLDPQEPPR : 390
AtMCMT    : VKTLLSK--G--LKSSYELGPGKVIAGIFKRVDKSASFENISA------------------ : 393
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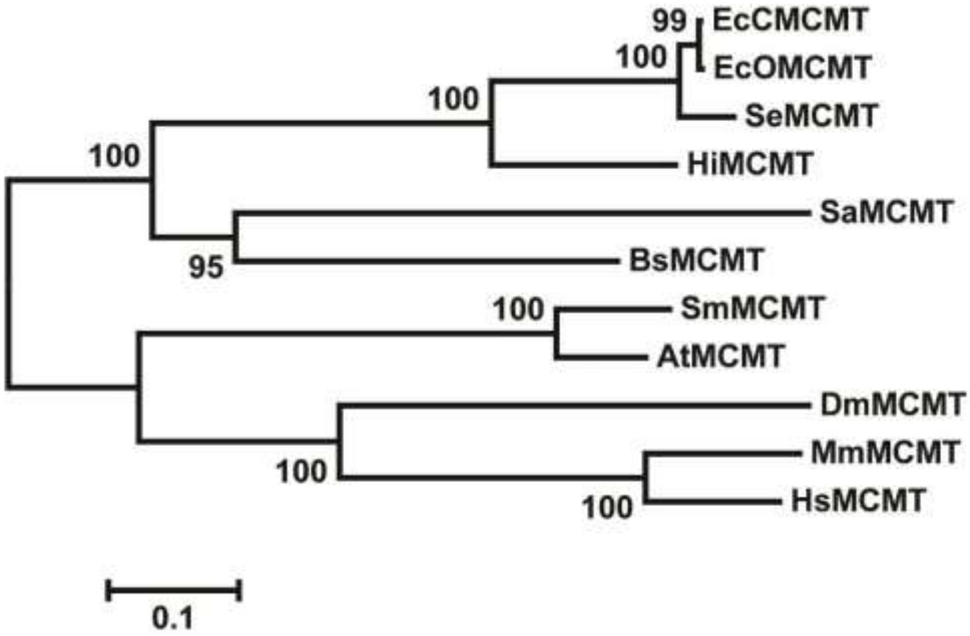

Fig S11. Multiple sequence alignment and phylogenetic tree for MCMT proteins from *S. miltiorrhiza* and its homologs from various other species.

(A) Multiple sequence alignment of MCMTs. The species and accession number for each MCMT are shown in the parenthesis: SmMCMT1 (*S. miltiorrhiza,* KF887939); AtMCMT (*A. thaliana,* AT2G30200.1). MmMCMT (*Mus musculus*, Q8R3F5); DmMCMT (*Drosophila melanogaster*, Q8T3L6); HsMCMT (*Homo sapiens*, Q8IVS2).

(B) Phylogenetic relationships of MCMTs from *S. miltiorrhiza* and various other species. MCMT proteins included are SmMCMT1 (KF887939); AtMCMT (AT2G30200.1); MmMCMT (Q8R3F5); DmMCMT (Q8T3L6); HsMCMT (Q8IVS2); SaMCMT(*Staphylococcus aureus* subsp. aureus MRSA252, Q6GHK5); EcCMCMT(*Escherichia coli* CFT073, P0AAJ0); EcOMCMT(*Escherichia coli* O157:H7, Q8X8I7);BsMCMT(*Bacillus subtilis* subsp. subtilis str. 168, P71019); SeMCMT (*Salmonella enterica* subsp. enterica serovar Typhimurium str. LT2, O85140); HiMCMT (*Haemophilus influenzae* Rd KW20, P43712).

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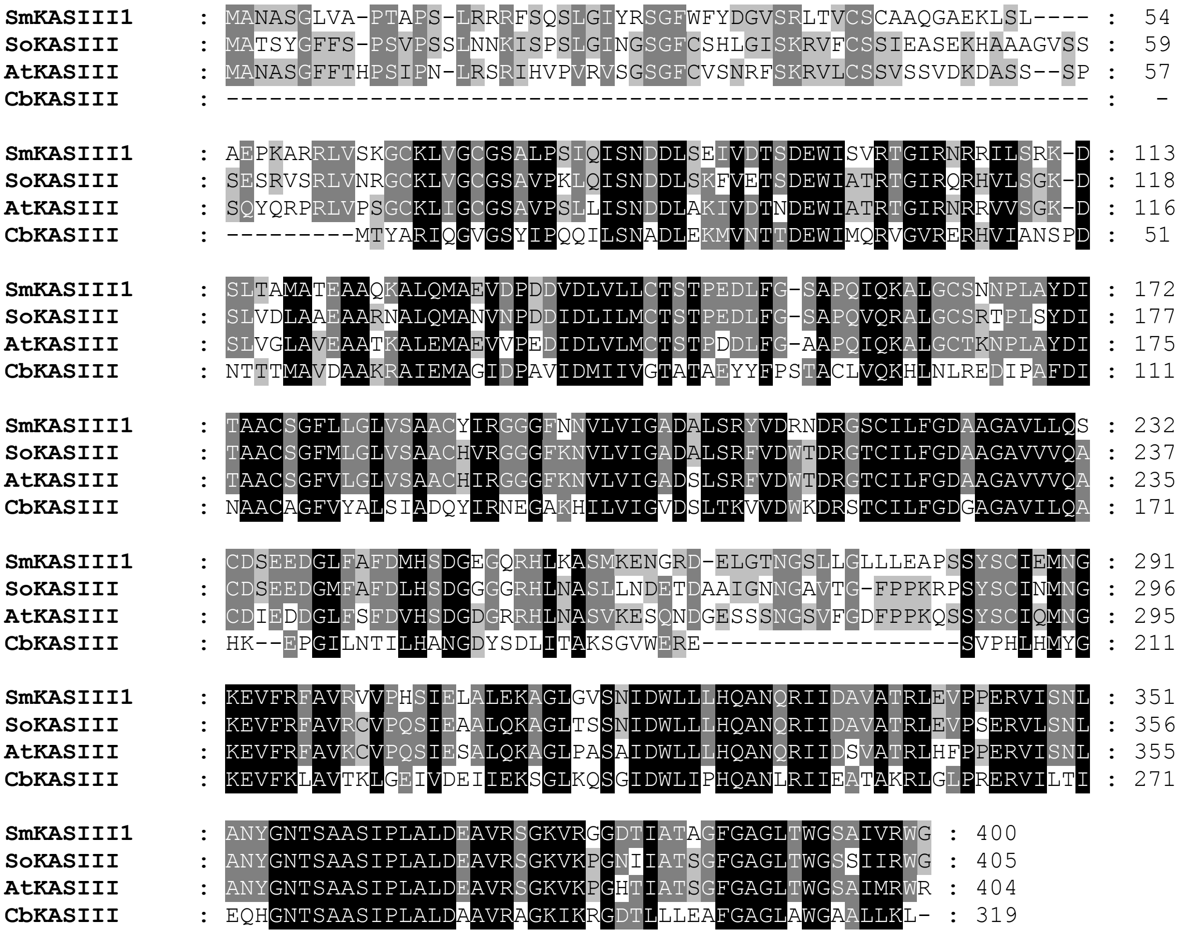

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SoKASIII   : MATSYGFFS-PSVPSSLNNKISPSLGINGSGFCSHLGISKRVFCSSIEASEKHAAAGVSS :  59
AtKASIII   : MANASGFFTHPSIPN-LRSRIHVPVRVSGSGFCVSNRFSKRVLCSSVSSVDKDASS--SP :  57
CbKASIII   : ------------------------------------------------------------ :   -

SmKASIII1  : AEPKARRLVSKGCKLVGCGSALPSIQISNDDLSEIVDTSDEWISVRTGIRNRRILSRK-D : 113
SoKASIII   : SESRVSRLVNRGCKLVGCGSAVPKLQISNDDLSKFVETSDEWIATRTGIRQRHVLSGK-D : 118
AtKASIII   : SQYQRPRLVPSGCKLIGCGSAVPSLLISNDDLAKIVDTNDEWIATRTGIRNRRVVSGK-D : 116
CbKASIII   : ---------MTYARIQGVGSYIPQQILSNADLEKMVNTTDEWIMQRVGVRERHVIANSPD :  51

SmKASIII1  : SLTAMATEAAQKALQMAEVDPDDVDLVLLCTSTPEDLFG-SAPQIQKALGCSNNPLAYDI : 172
SoKASIII   : SLVDLAAEAARNALQMANVNPDDIDLILMCTSTPEDLFG-SAPQVQRALGCSRTPLSYDI : 177
AtKASIII   : SLVGLAVEAATKALEMAEVVPEDIDLVLMCTSTPDDLFG-AAPQIQKALGCTKNPLAYDI : 175
CbKASIII   : NTTTMAVDAAKRAIEMAGIDPAVIDMIIVGTATAEYYFPSTACLVQKHLNLREDIPAFDI : 111

SmKASIII1  : TAACSGFLLGLVSAACYIRGGGFNNVLVIGADALSRYVDRNDRGSCILFGDAAGAVLLQS : 232
SoKASIII   : TAACSGFMLGLVSAACHVRGGGFKNVLVIGADALSRFVDWTDRGTCILFGDAAGAVVVQA : 237
AtKASIII   : TAACSGFVLGLVSAACHIRGGGFKNVLVIGADSLSRFVDWTDRGTCILFGDAAGAVVVQA : 235
CbKASIII   : NAACAGFVYALSIADQYIRNEGAKHILVIGVDSLTKVVDWKDRSTCILFGDGAGAVILQA : 171

SmKASIII1  : CDSEEDGLFAFDMHSDGEGQRHLKASMKENGRD-ELGTNGSLLGLLLEAPSSYSCIEMNG : 291
SoKASIII   : CDSEEDGMFAFDLHSDGGGRHLNASLLNDETDAAIGNNGAVTG-FPPKRPSYSCINMNG : 296
AtKASIII   : CDIEDDGLFSFDVHSDGDGRRHLNASVKESQNDGESSSNGSVFGDFPPKQSSYSCIQMNG : 295
CbKASIII   : HK--EPGILNTILHANGDYSDLITAKSGVWERE------------------SVPHLHMYG : 211

SmKASIII1  : KEVFRFAVRVVPHSIELALEKAGLGVSNIDWLLLHQANQRIIDAVATRLEVPPERVISNL : 351
SoKASIII   : KEVFRFAVRCVPQSIEAALQKAGLTSSNIDWLLLHQANQRIIDAVATRLEVPSERVLSNL : 356
AtKASIII   : KEVFRFAVKCVPQSIESALQKAGLPASAIDWLLLHQANQRIIDSVATRLHFPPERVISNL : 355
CbKASIII   : KEVFKLAVTKLGEIVDEIIEKSGLKQSGIDWLIPHQANLRIIEATAKRLGLPRERVILTI : 271

SmKASIII1  : ANYGNTSAASIPLALDEAVRSGKVRGGDTIATAGFGAGLTWGSAIVRWG : 400
SoKASIII   : ANYGNTSAASIPLALDEAVRSGKVKPGNIIATSGFGAGLTWGSSIIRWG : 405
AtKASIII   : ANYGNTSAASIPLALDEAVRSGKVKPGHTIATSGFGAGLTWGSAIMRWR : 404
CbKASIII   : EQHGNTSAASIPLALDAAVRAGKIKRGDTLLLEAFGAGLAWGAALLKL- : 319
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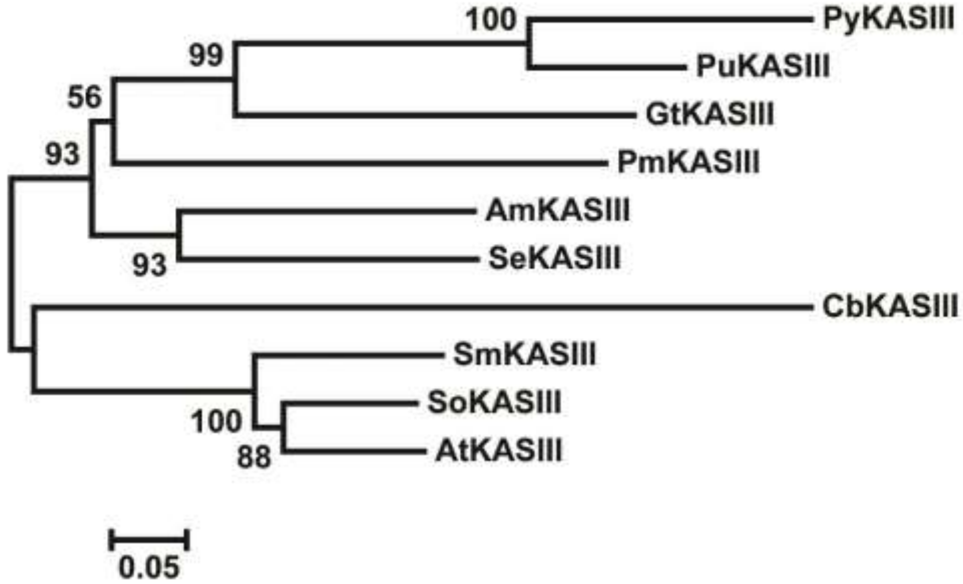

Fig S12. Multiple sequence alignment and phylogenetic tree for KASIII proteins from *S. miltiorrhiza* and its homologs from various other species.

(A) Multiple sequence alignment of KASIIIs. The species and accession number for each KASIII are shown in the parenthesis: SmKASIII1 (*S. miltiorrhiza*, KF887934); AtKAS (*A. thaliana*, AT1G62640.1); SoKASIII (Spinacia oleracea, Q07510); CbKASIII (Coxiella burnetii, A9NBY3).

(B) Phylogenetic relationships of KASIIIs from *S. miltiorrhiza* and various other species. KASIII proteins included are SmKASIII1 (*S. miltiorrhiza*, KF887934); AtKASIII (*A. thaliana*, AT1G62640.1); SoKASIII (*Spinacia oleracea*, Q07510); CbKASIII (*Coxiella burnetii*, A9NBY3);AmKASIII (*Acaryochloris marina* MBIC11017, B0CE67);PmKASIII (*Prochlorococcus marinus* str. MIT 9215, A8G2E1);PyKASIII (*Pyropia yezoensis*, Q1XDU1);SeKASIII (*Synechococcus elongatus* PCC 6301, Q5N5X5);GtKASIII (*Gracilaria tenuistipitata* var. liui, Q6B945);PmKASIII (*Prochlorococcus marinus* subsp. marinus str. CCMP1375, Q7VE55).

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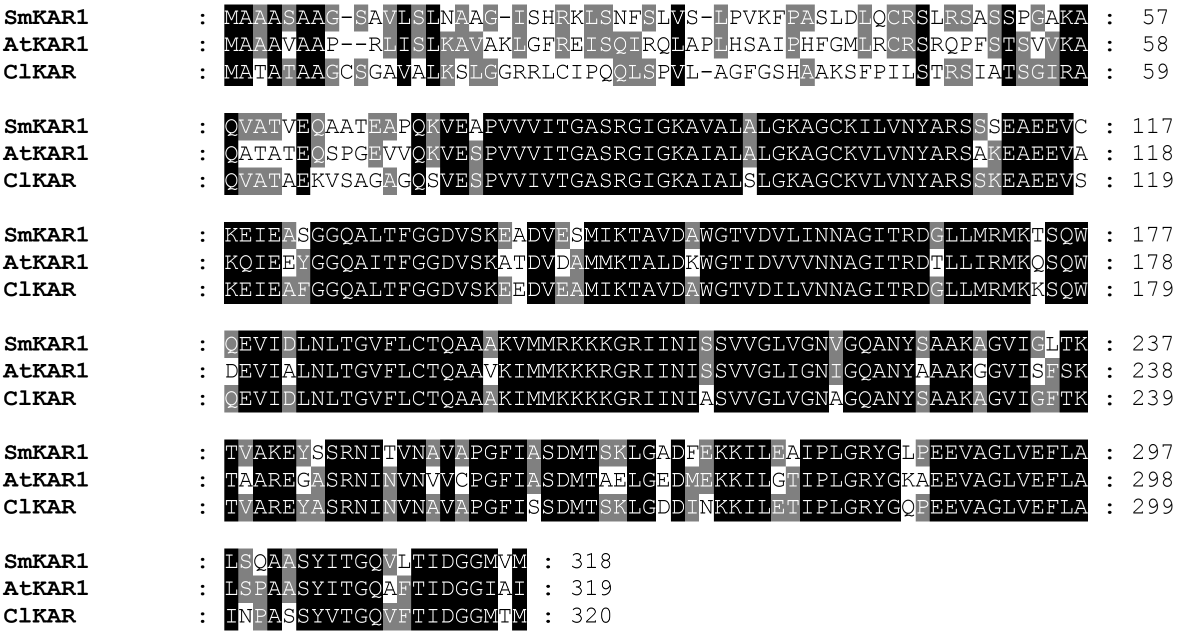

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SmKAR1    : MAAASAAG-SAVLSLNAAG-ISHRKLSNFSLVS-LPVKFPASLDLQCRSLRSASSPGAKA :  57
AtKAR1    : MAAAVAAP--RLISLKAVAKLGFREISQIRQLAPLHSAIPHFGMLRCRSRQPFSTSVVKA :  58
ClKAR     : MATATAAGCSGAVALKSLGGRRLCIPQQLSPVL-AGFGSHAAKSFPILSTRSIATSGIRA :  59

SmKAR1    : QVATVEQAATEAPQKVEAPVVVITGASRGIGKAVALALGKAGCKILVNYARSSSEAEEVC : 117
AtKAR1    : QATATEQSPGEVVQKVESPVVVITGASRGIGKAIALALGKAGCKVLVNYARSAKEAEEVA : 118
ClKAR     : QVATAEKVSAGAGQSVESPVVIVTGASRGIGKAIALSLGKAGCKVLVNYARSSKEAEEVS : 119

SmKAR1    : KEIEASGGQALTFGGDVSKEADVESMIKTAVDAWGTVDVLINNAGITRDGLLMRMKTSQW : 177
AtKAR1    : KQIEEYGGQAITFGGDVSKATDVDAMMKTALDKWGTIDVVVNNAGITRDTLLIRMKQSQW : 178
ClKAR     : KEIEAFGGQALTFGGDVSKEEDVEAMIKTAVDAWGTVDILVNNAGITRDGLLMRMKKSQW : 179

SmKAR1    : QEVIDLNLTGVFLCTQAAAKVMMRKKKGRIINISSVVGLVGNVGQANYSAAKAGVIGLTK : 237
AtKAR1    : DEVIALNLTGVFLCTQAAVKIMMKKKRGRIINISSVVGLIGNIGQANYAAAKGGVISFSK : 238
ClKAR     : QEVIDLNLTGVFLCTQAAAKIMMKKKKGRIINIASVVGLVGNAGQANYSAAKAGVIGFTK : 239

SmKAR1    : TVAKEYSSRNITVNAVAPGFIASDMTSKLGADFEKKILEAIPLGRYGLPEEVAGLVEFLA : 297
AtKAR1    : TAAREGASRNINVNVVCPGFIASDMTAELGEDMEKKILGTIPLGRYGKAEEVAGLVEFLA : 298
ClKAR     : TVAREYASRNINVNAVAPGFISSDMTSKLGDDINKKILETIPLGRYGQPEEVAGLVEFLA : 299

SmKAR1    : LSQAASYITGQVLTIDGGMVM : 318
AtKAR1    : LSPAASYITGQAFTIDGGIAI : 319
ClKAR     : INPASSYVTGQVFTIDGGMTM : 320
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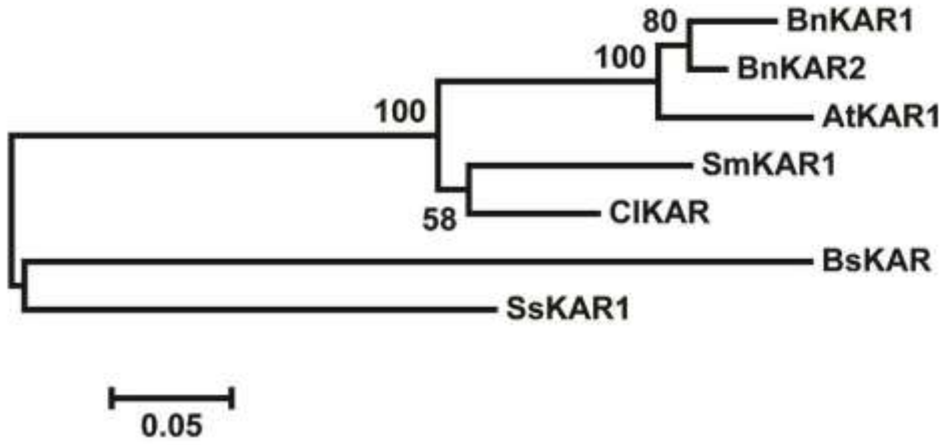

Fig S13. Multiple sequence alignment and phylogenetic tree for KAR proteins from *S. miltiorrhiza* and its homologs from various other species.

(A) Multiple sequence alignment of KARs. The species and accession number for each KAR are shown in the parenthesis: SmKAR1 (*S. miltiorrhiza,* KF887931); AtKAR1 (*A. thaliana*, AT1G24360.1); ClKAR (*Cuphea lanceolata*, P28643).

(B) Phylogenetic relationships of KARs from *S. miltiorrhiza* and various other species. KAR proteins included are SmKAR 1 (KF887931); AtKAR1 (AT1G24360.1); ClKAR (P28643); BnKAR(*Brassica napus*, Q93X62);BsKAR (*Bacillus subtilis* subsp. subtilis str. 168, P51831);SsKAR(*Synechocystis* sp. PCC 6803 substr. Kazusa, P73574).

A

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SmHAD1 : MASTVFSQSLFSVQSSSSSPISTKSIAGVSLPFKQPFVAPKSDIISRKIRMSSVVSSTST :  60
AtHAD  : MATTSNS-VLFLS--SDS-LIHHHHHQPLHLSSSRSHSVSLP--PNKRSNSLTLRCSTNG :  54
SsHAD  : ---------------------------------------------------MTEST-- :   5

SmHAD1 : AGSSHSADTPIELKFPAFPTVMDINQIRDILPHRFPFLLVDRVIEYTPGVSAVAIKNVTI : 120
AtHAD  : DSTSTEKETPIELKFPAFPTVMDINQIREILPHRFPFLLVDRVIEYTPGVSAVAIKNVTI : 114
SsHAD  : --TS-----D---------VVLTSEQIAGLLPHRYPFALVDRVIAHDPGVSATAIKNVTM :  49

SmHAD1 : NDNFFPGHFPERPIMPGVLMVEAMAQVGGLVMLQ-PEVGGSRDNFFFAGVDKVRFRKPVI : 179
AtHAD  : NDNFFPGHFPERPIMPGVLMIEAMAQVGGIVMLQ-PEVGGSQDNFFFAGIDKVRFRKPVI : 173
SsHAD  : NEPQFQGHFPERPLMPGVLIVEAMAQVGGLIVTQMPDLP--KGLFVFAGIDGVRFRRPVV : 107

SmHAD1 : AGDTLVMRMNLVKLQ-KRFGIAKMEGKAYVGGEVVCEGEFLMAMGSESSG : 228
AtHAD  : AGDTLVMRMTLLKFQ-KRFGLAKMEGKAYVGGALVCEGEFMMVSAGSS-- : 220
SsHAD  : PGDQLVIRCELLSLKRKRFG--KVKAEATVDGDLACSGELMFSLVD---- : 151
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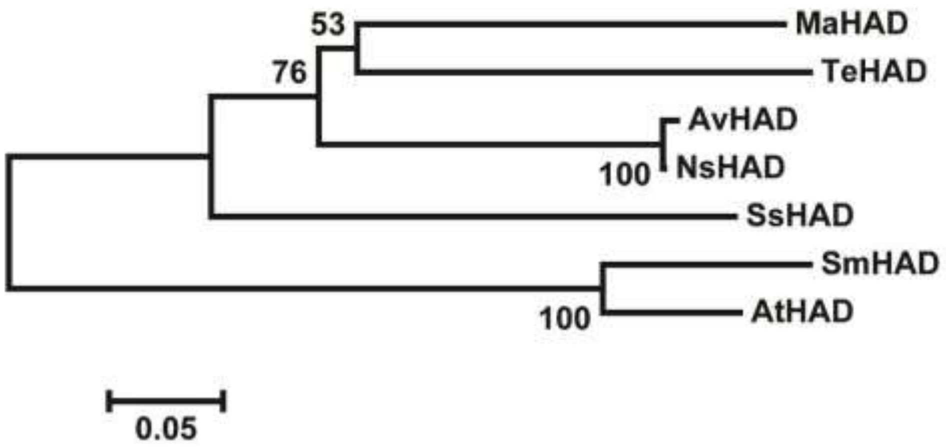

Fig S14. Multiple sequence alignment and phylogenetic tree for HAD proteins from *S. miltiorrhiza* and its homologs from various other species.

(A) Multiple sequence alignment of HADs. The species and accession number for each HAD are shown in the parenthesis: SmHAD1 (*S. miltiorrhiza*, KF887927); AtHAD1 (*A. thaliana*, AT2G22230.1); SsHAD (Synechocystis sp. PCC6803, P73848).

(B) Phylogenetic relationships of HADs from *S. miltiorrhiza* and various other species. HAD proteins included are SmHAD1 (KF887927); AtHAD1 (AT2G22230.1); SsHAD (P73848); MaHAD(*Microcystis aeruginosa* NIES-843, B0JIT3);AvHAD(*Anabaena variabilis* ATCC 29413, Q3MH14);TeHAD(*Thermosynechococcus elongatus* BP-1, Q8DI01);NsHAD(*Nostoc* sp. PCC 7120, Q8YUR4).

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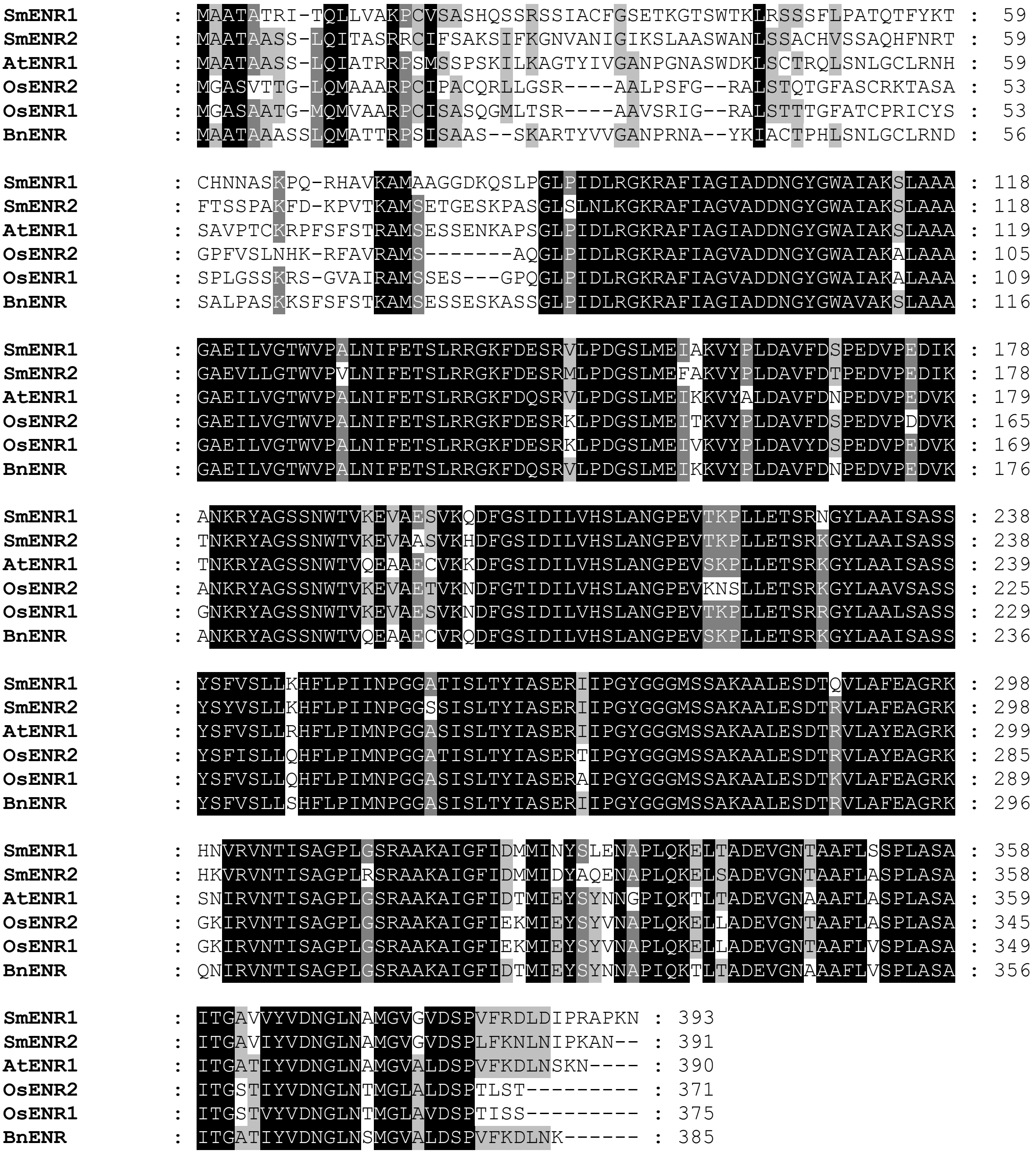

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SmENR2     : MAATAASS-LQITASRRCIFSAKSIFKGNVANIGIKSLAASWANLSSACHVSSAQHFNRT :  59
AtENR1     : MAATAASS-LQIATRRPSMSSPSKILKAGTYIVGANPGNASWDKLSCTRQLSNLGCLRNH :  59
OsENR2     : MGASVTTG-LQMAAARPCIPACQRLLGSR----AALPSFG--RALSTQTGFASCRKTASA :  53
OsENR1     : MGASAATG-MQMVAARPCISASQGMLTSR----AAVSRIG--RALSTTTGFATCPRICYS :  53
BnENR      : MAATAAASSLQMATTRPSISAAS--SKARTYVVGANPRNA--YKIACTPHLSNLGCLRND :  56

SmENR1     : CHNNASKPQ-RHAVKAMAAGGDKQSLPGLPIDLRGKRAFIAGIADDNGYGWAIAKSLAAA : 118
SmENR2     : FTSSPAKFD-KPVTKAMSETGESKPASGLSLNLKGKRAFIAGVADDNGYGWAIAKSLAAA : 118
AtENR1     : SAVPTCKRPFSFSTRAMSESSENKAPSGLPIDLRGKRAFIAGIADDNGYGWAIAKSLAAA : 119
OsENR2     : GPFVSLNHK-RFAVRAMS-------AQGLPIDLRGKRAFIAGVADDNGYGWAIAKALAAA : 105
OsENR1     : SPLGSSKRS-GVAIRAMSSES---GPQGLPIDLRGKRAFIAGVADDNGYGWAIAKALAAA : 109
BnENR      : SALPASKKSFSFSTKAMSESSESKASSGLPIDLRGKRAFIAGIADDNGYGWAVAKSLAAA : 116

SmENR1     : GAEILVGTWVPALNIFETSLRRGKFDESRVLPDGSLMEIAKVYPLDAVFDSPEDVPEDIK : 178
SmENR2     : GAEVLLGTWVPVLNIFETSLRRGKFDESRMLPDGSLMEFAKVYPLDAVFDTPEDVPEDIK : 178
AtENR1     : GAEILVGTWVPALNIFETSLRRGKFDQSRVLPDGSLMEIKKVYALDAVFDNPEDVPEDVK : 179
OsENR2     : GAEILVGTWVPALNIFETSLRRGKFDESRKLPDGSLMEITKVYPLDAVFDSPEDVPDDVK : 165
OsENR1     : GAEILVGTWVPALNIFETSLRRGKFDESRKLPDGSLMEIVKVYPLDAVYDSPEDVPEDVK : 169
BnENR      : GAEILVGTWVPALNIFETSLRRGKFDQSRVLPDGSLMEIKKVYPLDAVFDNPEDVPEDVK : 176

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AtENR1     : TNKRYAGSSNWTVQEAAECVKKDFGSIDILVHSLANGPEVSKPLLETSRKGYLAAISASS : 239
OsENR2     : ANKRYAGSSNWTVKEVAETVKNDFGTIDILVHSLANGPEVKNSLLETSRKGYLAAVSASS : 225
OsENR1     : GNKRYAGSSNWTVKEVAESVKNDFGSIDILVHSLANGPEVTKPLLETSRRGYLAALSASS : 229
BnENR      : ANKRYAGSSNWTVQEAAECVRQDFGSIDILVHSLANGPEVSKPLLETSRKGYLAAISASS : 236

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BnENR      : YSFVSLLSHFLPIMNPGGASISLTYIASERIIPGYGGGMSSAKAALESDTRVLAFEAGRK : 296

SmENR1     : HNVRVNTISAGPLGSRAAKAIGFIDMMINYSLENAPLQKELTADEVGNTAAFLSSPLASA : 358
SmENR2     : HKVRVNTISAGPLRSRAAKAIGFIDMMIDYAQENAPLQKELSADEVGNTAAFLASPLASA : 358
AtENR1     : SNIRVNTISAGPLGSRAAKAIGFIDTMIEYSYNNGPIQKTLTADEVGNAAAFLASPLASA : 359
OsENR2     : GKIRVNTISAGPLGSRAAKAIGFIEKMIEYSYVNAPLQKELLADEVGNTAAFLASPLASA : 345
OsENR1     : GKIRVNTISAGPLGSRAAKAIGFIEKMIEYSYVNAPLQKELLADEVGNTAAFLVSPLASA : 349
BnENR      : QNIRVNTISAGPLGSRAAKAIGFIDTMIEYSYNNAPIQKTLTADEVGNAAAFLVSPLASA : 356

SmENR1     : ITGAVVYVDNGLNAMGVGVDSPVFRDLDIPRAPKN : 393
SmENR2     : ITGAVIYVDNGLNAMGVGVDSPLFKNLNIPKAN-- : 391
AtENR1     : ITGATIYVDNGLNAMGVALDSPVFKDLNSKN---- : 390
OsENR2     : ITGSTIYVDNGLNTMGLALDSPTLST--------- : 371
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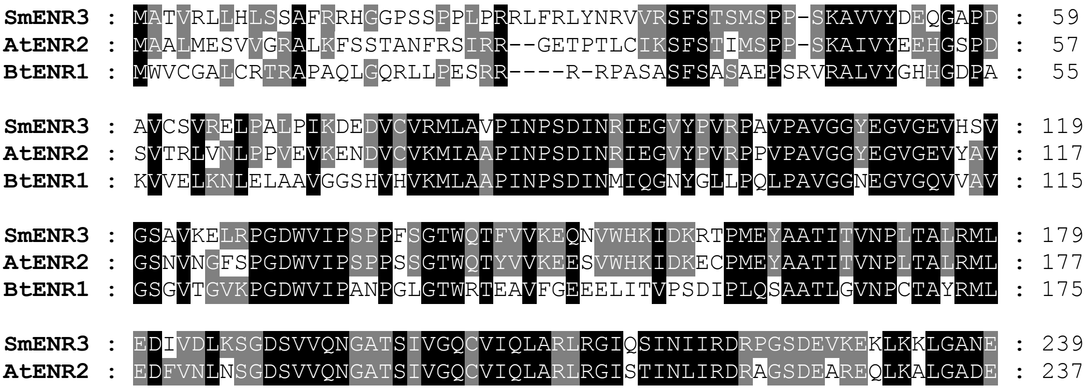

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BtENR1 : MWVCGALCRTRAPAQLGQRLLPESRR----R-RPASASFSASAEPSRVRALVYGHHGDPA :  55

SmENR3 : AVCSVRELPALPIKDEDVCVRMLAVPINPSDINRIEGVYPVRPAVPAVGGYEGVGEVHSV : 119
AtENR2 : SVTRLVNLPPVEVKENDVCVKMIAAPINPSDINRIEGVYPVRPPVPAVGGYEGVGEVYAV : 117
BtENR1 : KVVELKNLELAAVGGSHVHVKMLAAPINPSDINMIQGNYGLLPQLPAVGGNEGVGQVVAV : 115

SmENR3 : GSAVKELRPGDWVIPSPPFSGTWQTFVVKEQNVWHKIDKRTPMEYAATITVNPLTALRML : 179
AtENR2 : GSNVNGFSPGDWVIPSPPSSGTWQTYVVKEESVWHKIDKECPMEYAATITVNPLTALRML : 177
BtENR1 : GSGVTGVKPGDWVIPANPGLGTWRTEAVFGEEELITVPSDIPLQSAATLGVNPCTAYRML : 175

SmENR3 : EDIVDLKSGDSVVQNGATSIVGQCVIQLARLRGIQSINIIRDRPGSDEVKEKLKKLGANE : 239
AtENR2 : EDFVNLNSGDSVVQNGATSIVGQCVIQLARLRGISTINLIRDRAGSDEAREQLKALGADE : 237
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BtENR1 : VDFERLRPRDSIIQNASNSGVGQAVIQIAAARGLRTINVLRDTPDLQKLTDTLKNLGANH : 235

SmENR3 : VFTENQLAVKSVKHFLADIPEPALGFNCVGGNAASLVLKFLKQGGTMVTYGGMSKKPITV : 299
AtENR2 : VFSESQLNVKNVKSLLGNLPEPALGFNCVGGNAASLVLKYLREGGTMVTYGGMSKKPITV : 297
BtENR1 : VVTEEELRKPEMKSFFKDVPQPRLALNCVGGKSSTELLRHLAPGGTMVTYGGMAKQPVIA : 295

SmENR3 : STGSFIFKDLSLRGFWLQKWMGAEKAKESREMIDYLLSLTRSGELKY-DMELTPFDQFPT : 358
AtENR2 : STTSFIFKDLALRGFWLQSWLSMGKVKECREMIDYLLGLARDGKLKY-ETELVPFEEFPV : 356
BtENR1 : SVSQLIFKDLKLRGFWLSQWKKDHSPDQFKELILTLCDLIRRGQLTAPACSEVPLQDYLC : 355

SmENR3 : ALDKALGKLGSQPKQVIKF : 377
AtENR2 : ALDKALGKLGRQPKQVITF : 375
BtENR1 : ALEASTQPFVS-SKQILTM : 373
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C

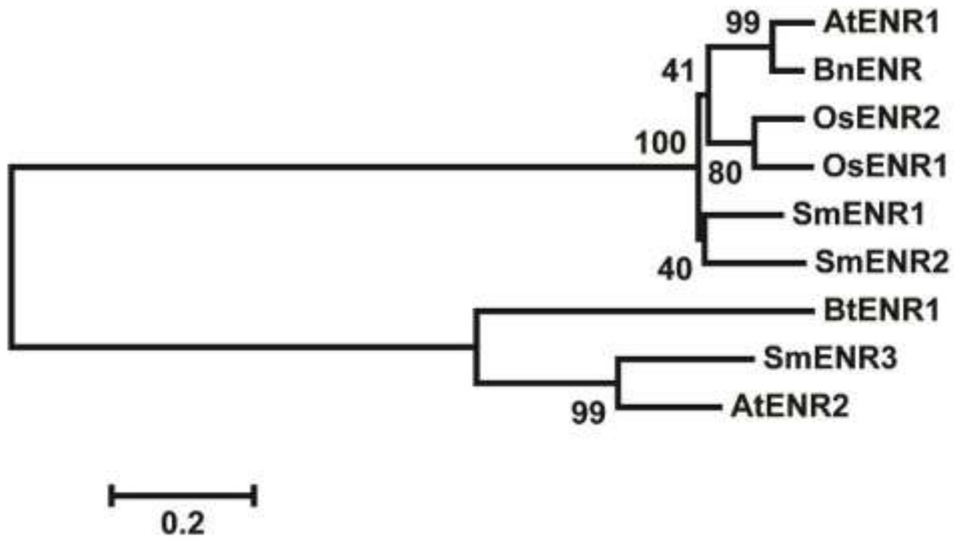
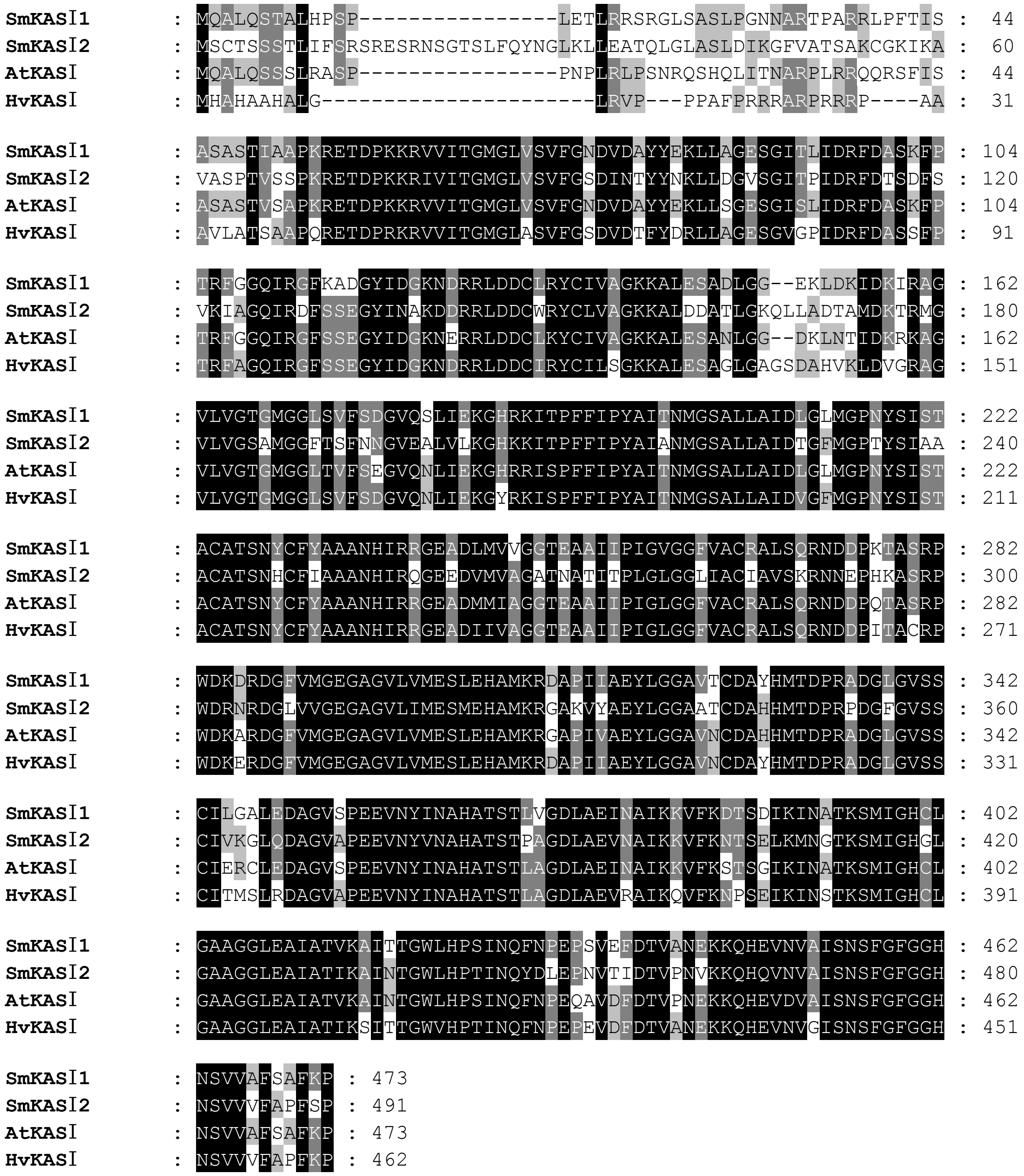


Fig S15. Multiple sequence alignment and phylogenetic tree for ENR proteins from *S. miltiorrhiza* and its homologs from various other species.

(A) Multiple sequence alignment of ENRs. The species and accession number for each ENR are shown in the parenthesis: SmENR1 (*S. miltiorrhiza,* KF887923); SmENR2 (KJ784429);AtENR1 (*A. thaliana* , AT2G05990.1); *O. sativa* OsENR1 (Q6Z0I4); OsENR1 (Q6H5J0); BnENR (*Brassica napus* , P80030).

(B) Multiple sequence alignment of ENRs. The species and accession number for each ENR are shown in the parenthesis: SmENR3 (KJ784430); AtENR2 (AT3G45770); BtENR1 (*Bos taurus* , Q7YS70). (C) Phylogenetic relationships of ENRs from *S. miltiorrhiza* and various other species. ENR proteins included are SmENR1 (KF887923); SmENR2 (KJ784429);SmENR3 (KJ784430); AtENR1 (AT2G05990.1); AtENR2 (AT3G45770); OsENR1 (Q6Z0I4); OsENR1 (Q6H5J0); BnENR (P80030); BtENR1 (Q7YS70).

A



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SmKASI1  : MQALQSTALHPSP----------------LETLRRSRGLSASLPGNNARTPARRLPFTIS :  44
SmKASI2  : MSCTSSSTLIFSRSRESRNSGTSLFQYNGLKLLEATQLGLASLDIKGFVATSAKCGKIKA :  60
AtKASI   : MQALQSSSLRASP----------------PNPLRLPSNRQSHQLITNARPLRRQQRSFIS :  44
HvKASI   : MHAHAAHALG----------------------LRVP---PPAFPRRRARPRRRP----AA :  31

SmKASI1  : ASASTIAAPKRETDPKKRVVITGMGLVSVFGNDVDAYYEKLLAGESGITLIDRFDASKFP : 104
SmKASI2  : VASPTVSSPKRETDPKKRIVITGMGLVSVFGSDINTYYNKLLDGVSGITPIDRFDTSDFS : 120
AtKASI   : ASASTVSAPKRETDPKKRVVITGMGLVSVFGNDVDAYYEKLLSGESGISLIDRFDASKFP : 104
HvKASI   : AVLATSAAPQRETDPRKRVVITGMGLASVFGSDVDTFYDRLLAGESGVGPIDRFDASSFP :  91

SmKASI1  : TRFGGQIRGFKADGYIDGKNDRRLDDCLRYCIVAGKKALESADLGG--EKLDKIDKIRAG : 162
SmKASI2  : VKIAGQIRDFSSEGYINAKDDRRLDDCWRYCLVAGKKALDDATLGKQLLADTAMDKTRMG : 180
AtKASI   : TRFGGQIRGFSSEGYIDGKNERRLDDCLKYCIVAGKKALESANLGG--DKLNTIDKRKAG : 162
HvKASI   : TRFAGQIRGFSSEGYIDGKNDRRLDDCIRYCILSGKKALESAGLGAGSDAHVKLDVGRAG : 151

SmKASI1  : VLVGTGMGGLSVFSDGVQSLIEKGHRKITPFFIPYAITNMGSALLAIDLGLMGPNYSIST : 222
SmKASI2  : VLVGSAMGGFTSFNNGVEALVLKGHKKITPFFIPYAIANMGSALLAIDTGFMGPTYSIAA : 240
AtKASI   : VLVGTGMGGLTVFSEGVQNLIEKGHRRISPFFIPYAITNMGSALLAIDLGLMGPNYSIST : 222
HvKASI   : VLVGTGMGGLSVFSDGVQNLIEKGYRKISPFFIPYAITNMGSALLAIDVGFMGPNYSIST : 211

SmKASI1  : ACATSNYCFYAAANHIRRGEADLMVVGGTEAAIIPIGVGGFVACRALSQRNDDPKTASRP : 282
SmKASI2  : ACATSNHCFIAAANHIRQGEEDVMVAGATNATITPLGLGGLIACIAVSKRNNEPHKASRP : 300
AtKASI   : ACATSNYCFYAAANHIRRGEADMMIAGGTEAAIIPIGLGGFVACRALSQRNDDPQTASRP : 282
HvKASI   : ACATSNYCFYAAANHIRRGEADIIVAGGTEAAIIPIGLGGFVACRALSQRNDDPITACRP : 271

SmKASI1  : WDKDRDGFVMGEGAGVLVMESLEHAMKRDAPIIAEYLGGAVTCDAYHMTDPRADGLGVSS : 342
SmKASI2  : WDRNRDGLVVGEGAGVLIMESMEHAMKRGAKVYAEYLGGAATCDAHHMTDPRPDGFGVSS : 360
AtKASI   : WDKARDGFVMGEGAGVLVMESLEHAMKRGAPIVAEYLGGAVNCDAHHMTDPRADGLGVSS : 342
HvKASI   : WDKERDGFVMGEGAGVLVMESLEHAMKRDAPIIAEYLGGAVNCDAYHMTDPRADGLGVSS : 331

SmKASI1  : CILGALEDAGVSPEEVNYINAHATSTLVGDLAEINAIKKVFKDTSDIKINATKSMIGHCL : 402
SmKASI2  : CIVKGLQDAGVAPEEVNYVNAHATSTPAGDLAEVNAIKKVFKNTSELKMNGTKSMIGHGL : 420
AtKASI   : CIERCLEDAGVSPEEVNYINAHATSTLAGDLAEINAIKKVFKSTSGIKINATKSMIGHCL : 402
HvKASI   : CITMSLRDAGVAPEEVNYINAHATSTLAGDLAEVRAIKQVFKNPSEIKINSTKSMIGHCL : 391

SmKASI1  : GAAGGLEAIATVKAITTGWLHPSINQFNPEPSVEFDTVANEKKQHEVNVAISNSFGFGGH : 462
SmKASI2  : GAAGGLEAIATIKAINTGWLHPTINQYDLEPNVTIDTVPNVKKQHQVNVAISNSFGFGGH : 480
AtKASI   : GAAGGLEAIATVKAINTGWLHPSINQFNPEQAVDFDTVPNEKKQHEVDVAISNSFGFGGH : 462
HvKASI   : GAAGGLEAIATIKSITTGWVHPTINQFNPEPEVDFDTVANEKKQHEVNVGISNSFGFGGH : 451

SmKASI1  : NSVVAFSAFKP : 473
SmKASI2  : NSVVVFAPFSP : 491
AtKASI   : NSVVAFSAFKP : 473
HvKASI   : NSVVVFAPFKP : 462
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B

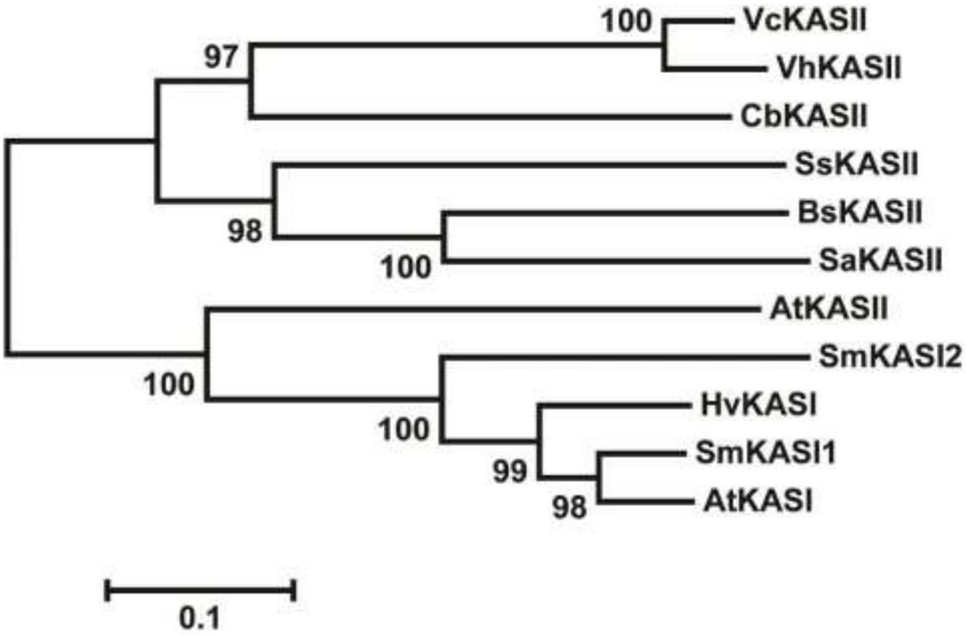
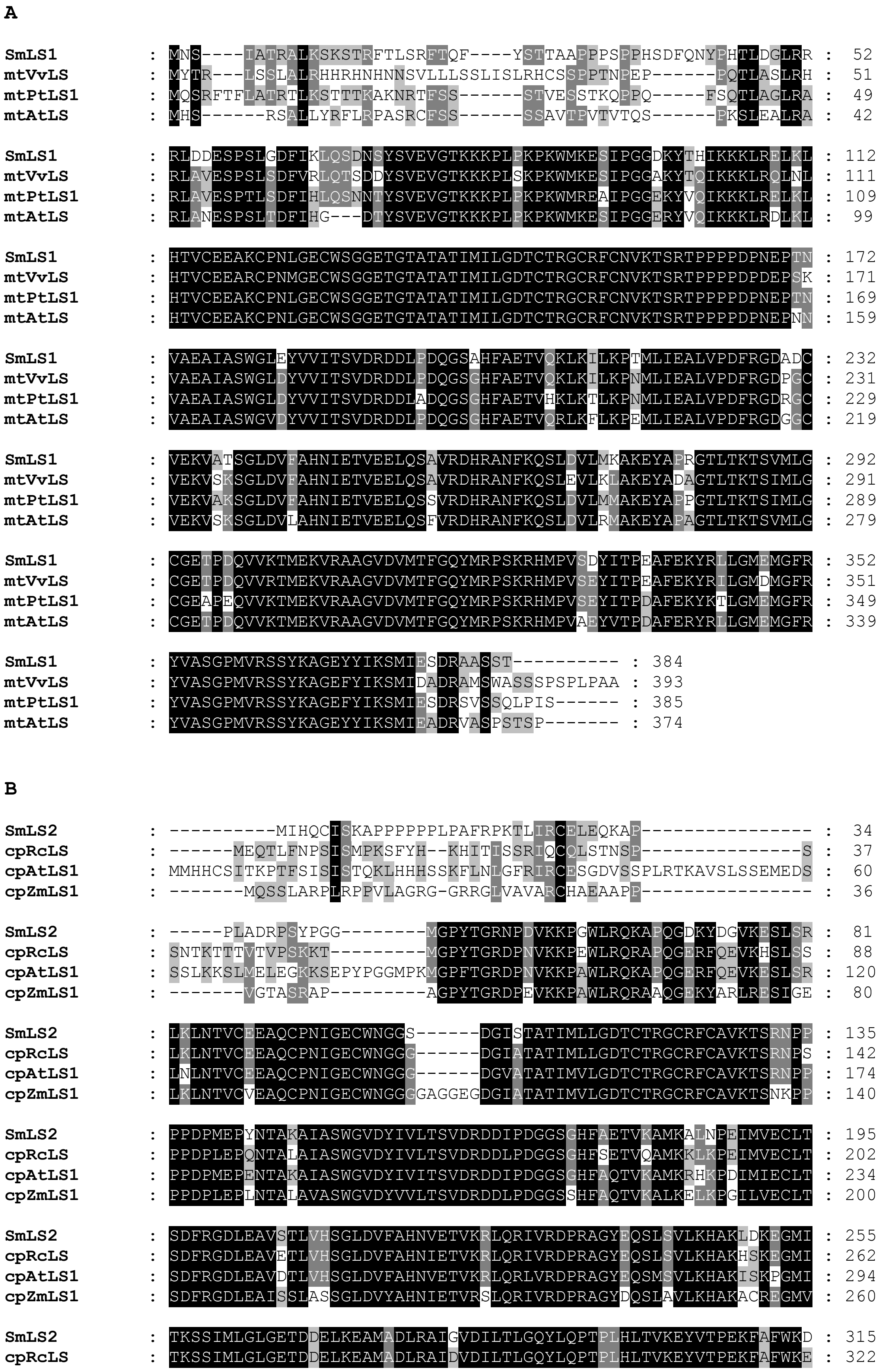


Fig S16. Multiple sequence alignment and phylogenetic tree for KASI proteins from *S. miltiorrhiza* and its homologs from various other species.

(A) Multiple sequence alignment of KASIs. The species and accession number for each KASI are shown in the parenthesis: SmKASI1 (*S. miltiorrhiza* ,KF887932); Sm KASI2 (KJ784434);At KASI (*A. thaliana* , AT5G46290.3); HvKASI (*Hordeum vulgare*, P23902).

(B) Phylogenetic relationships of KASIs from *S. miltiorrhiza* and various other species. KASI proteins included are SmKASI1 (KF887932); SmKASI2 (KJ784434);AtKASI1 (AT5G46290.3); HvKASI (*Hordeum vulgare*, P23902);CbKASII (*Coxiella burnetii*, Q83E37);SaKASII (*Staphylococcus aureus*, Q7A6F8); SsKASII (*Synechocystis* sp. PCC 6803, P73283) ; VcKASII(*Vibrio cholera*, Q9KQH9);VhKASII (*Vibrio harveyi*, P55338).



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A

SmLS1      : MNS----IATRALKSKSTRFTLSRFTQF----YSTTAAPPPSPPHSDFQNYPHTLDGLRR :  52
mtVvLS     : MYTR---LSSLALRHHRHNHNNSVLLLSSLISLRHCSSPPTNPEP------PQTLASLRH :  51
mtPtLS1    : MQSRFTFLATRTLKSTTTKAKNRTFSS------STVESSTKQPPQ-----FSQTLAGLRA :  49
mtAtLS     : MHS------RSALLYRFLRPASRCFSS------SSAVTPVTVTQS------PKSLEALRA :  42

SmLS1      : RLDDESPSLGDFIKLQSDNSYSVEVGTKKKPLPKPKWMKESIPGGDKYTHIKKKLRELKL : 112
mtVvLS     : RLAVESPSLSDFVRLQTSDDYSVEVGTKKKPLSKPKWMKESIPGGAKYTQIKKKLRQLNL : 111
mtPtLS1    : RLAVESPTLSDFIHLQSNNTYSVEVGTKKKPLPKPKWMREAIPGGEKYVQIKKKLRELKL : 109
mtAtLS     : RLANESPSLTDFIHG---DTYSVEVGTKKKPLPKPKWMKESIPGGERYVQIKKKLRDLKL :  99

SmLS1      : HTVCEEAKCPNLGECWSGGETGTATATIMILGDTCTRGCRFCNVKTSRTPPPPDPNEPTN : 172
mtVvLS     : HTVCEEARCPNMGECWSGGETGTATATIMILGDTCTRGCRFCNVKTSRTPPPPDPDEPSK : 171
mtPtLS1    : HTVCEEAKCPNLGECWSGGETGTATATIMILGDTCTRGCRFCNVKTSRTPPPPDPNEPTN : 169
mtAtLS     : HTVCEEAKCPNLGECWSGGETGTATATIMILGDTCTRGCRFCNVKTSRTPPPPDPNEPNN : 159

SmLS1      : VAEAIASWGLEYVVITSVDRDDLPDQGSAHFAETVQKLKILKPTMLIEALVPDFRGDADC : 232
mtVvLS     : VAEAIASWGLDYVVITSVDRDDLPDQGSGHFAETVQKLKILKPNMLIEALVPDFRGDPGC : 231
mtPtLS1    : VAEAIASWGLDYVVITSVDRDDLADQGSGHFAETVHKLKTLKPNMLIEALVPDFRGDRGC : 229
mtAtLS     : VAEAIASWGVDYVVITSVDRDDLPDQGSGHFAETVQRLKFLKPEMLIEALVPDFRGDGGC : 219

SmLS1      : VEKVATSGLDVFAHNIETVEELQSAVRDHRANFKQSLDVLMKAKEYAPRGTLTKTSVMLG : 292
mtVvLS     : VEKVSKSGLDVFAHNIETVEELQSAVRDHRANFKQSLEVLKLAKEYADAGTLTKTSIMLG : 291
mtPtLS1    : VEKVAKSGLDVFAHNIETVEELQSSVRDHRANFKQSLDVLMMAKEYAPPGTLTKTSIMLG : 289
mtAtLS     : VEKVSKSGLDVLAHNIETVEELQSFVRDHRANFKQSLDVLRMAKEYAPAGTLTKTSVMLG : 279

SmLS1      : CGETPDQVVKTMEKVRAAGVDVMTFGQYMRPSKRHMPVSDYITPEAFEKYRLLGMEMGFR : 352
mtVvLS     : CGETPDQVVRTMEKVRAAGVDVMTFGQYMRPSKRHMPVSEYITPEAFEKYRILGMDMGFR : 351
mtPtLS1    : CGEAPEQVVKTMEKVRAAGVDVMTFGQYMRPSKRHMPVSEYITPDAFEKYKTLGMEMGFR : 349
mtAtLS     : CGETPDQVVKTMEKVRAAGVDVMTFGQYMRPSKRHMPVAEYVTPDAFERYRLLGMEMGFR : 339

SmLS1      : YVASGPMVRSSYKAGEYYIKSMIESDRAASST---------- : 384
mtVvLS     : YVASGPMVRSSYKAGEFYIKSMIDADRAMSWASSSPSPLPAA : 393
mtPtLS1    : YVASGPMVRSSYKAGEFYIKSMIESDRSVSSQLPIS------ : 385
mtAtLS     : YVASGPMVRSSYKAGEYYIKSMIEADRVASPSTSP------- : 374


B

SmLS2      : ----------MIHQCISKAPPPPPPLPAFRPKTLIRCELEQKAP---------------- :  34
cpRcLS     : ------MEQTLFNPSISMPKSFYH--KHITISSRIQCQLSTNSP---------------S :  37
cpAtLS1    : MMHHCSITKPTFSISISTQKLHHHSSKFLNLGFRIRCESGDVSSPLRTKAVSLSSEMEDS :  60
cpZmLS1    : -------MQSSLARPLRPPVLAGRG-GRRGLVAVARCHAEAAPP---------------- :  36

SmLS2      : -----PLADRPSYPGG--------MGPYTGRNPDVKKPGWLRQKAPQGDKYDGVKESLSR :  81
cpRcLS     : SNTKTTTVTVPSKKT---------MGPYTGRDPNVKKPEWLRQRAPQGERFQEVKHSLSS :  88
cpAtLS1    : SSLKKSLMELEGKKSEPYPGGMPKMGPFTGRDPNVKKPAWLRQKAPQGERFQEVKESLSR : 120
cpZmLS1    : -------VGTASRAP---------AGPYTGRDPEVKKPAWLRQRAAQGEKYARLRESIGE :  80

SmLS2      : LKLNTVCEEAQCPNIGECWNGGS------DGISTATIMLLGDTCTRGCRFCAVKTSRNPP : 135
cpRcLS     : LKLNTVCEEAQCPNIGECWNGGG------DGIATATIMLLGDTCTRGCRFCAVKTSRNPS : 142
cpAtLS1    : LNLNTVCEEAQCPNIGECWNGGG------DGVATATIMVLGDTCTRGCRFCAVKTSRNPP : 174
cpZmLS1    : LKLNTVCVEAQCPNIGECWNGGGGAGGEGDGIATATIMVLGDTCTRGCRFCAVKTSNKPP : 140

SmLS2      : PPDPMEPYNTAKAIASWGVDYIVLTSVDRDDIPDGGSGHFAETVKAMKALNPEIMVECLT : 195
cpRcLS     : PPDPLEPQNTALAIASWGVDYIVLTSVDRDDLPDGGSGHFSETVQAMKKLKPEIMVECLT : 202
cpAtLS1    : PPDPMEPENTAKAIASWGVDYIVITSVDRDDIPDGGSGHFAQTVKAMKRHKPDIMIECLT : 234
cpZmLS1    : PPDPLEPLNTALAVASWGVDYVVLTSVDRDDLPDGGSSHFAQTVKALKELKPGILVECLT : 200

SmLS2      : SDFRGDLEAVSTLVHSGLDVFAHNVETVKRLQRIVRDPRAGYEQSLSVLKHAKLDKEGMI : 255
cpRcLS     : SDFRGDLEAVETLVHSGLDVFAHNIETVKRLQRIVRDPRAGYEQSLSVLKHAKHSKEGMI : 262
cpAtLS1    : SDFRGDLEAVDTLVHSGLDVFAHNVETVKRLQRLVRDPRAGYEQSMSVLKHAKISKPGMI : 294
cpZmLS1    : SDFRGDLEAISSLASSGLDVYAHNIETVRSLQRIVRDPRAGYDQSLAVLKHAKACREGMV : 260

SmLS2      : TKSSIMLGLGETDDELKEAMADLRAIGVDILTLGQYLQPTPLHLTVKEYVTPEKFAFWKD : 315
cpRcLS     : TKSSIMLGLGETDDELKEAMADLRAIDVDILTLGQYLQPTPLHLTVKEYVTPEKFAFWKE : 322
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cpAtLS1       : TKTSIMLGLGETDEELKEAMADLRAIDVDILTLGQYLQPTPLHLTVKEYVTPEKFDFWKT : 354
cpZmLS1       : TKSSIMLGLGETDEEVKQAMMDLRAIGVDILTLGQYLQPTERHLTVREYVTPEKFQFWKE : 320

SmLS2         : YGESIGFRYVASGPLVRSSYRAGELFIKTMVKEEKTKNGSA- : 356
cpRcLS        : YGESIGFRYVASGPMVRSSYRAGELFVKTMVKERSSNSAAKP : 364
cpAtLS1       : YGESIGFRYVASGPLVRSSYRAGELFVKTMVKESYSKSLS-- : 394
cpZmLS1       : YGESVGFRYVASGPLVRSSYRAGELFVQNLVRNNKTGSSSS- : 361
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C

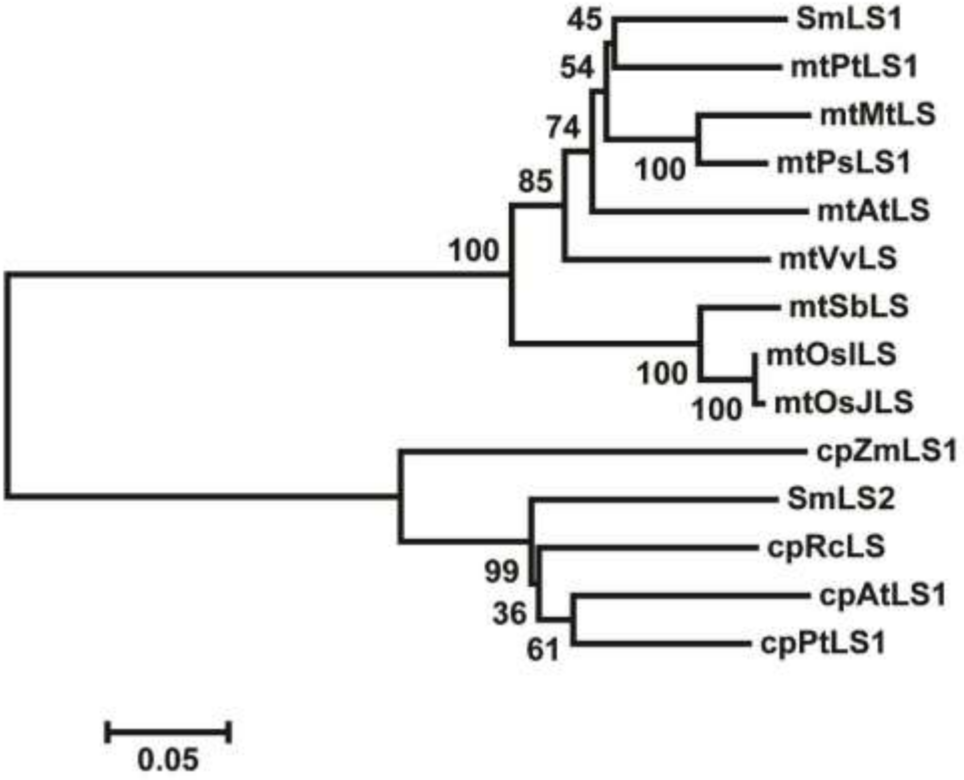
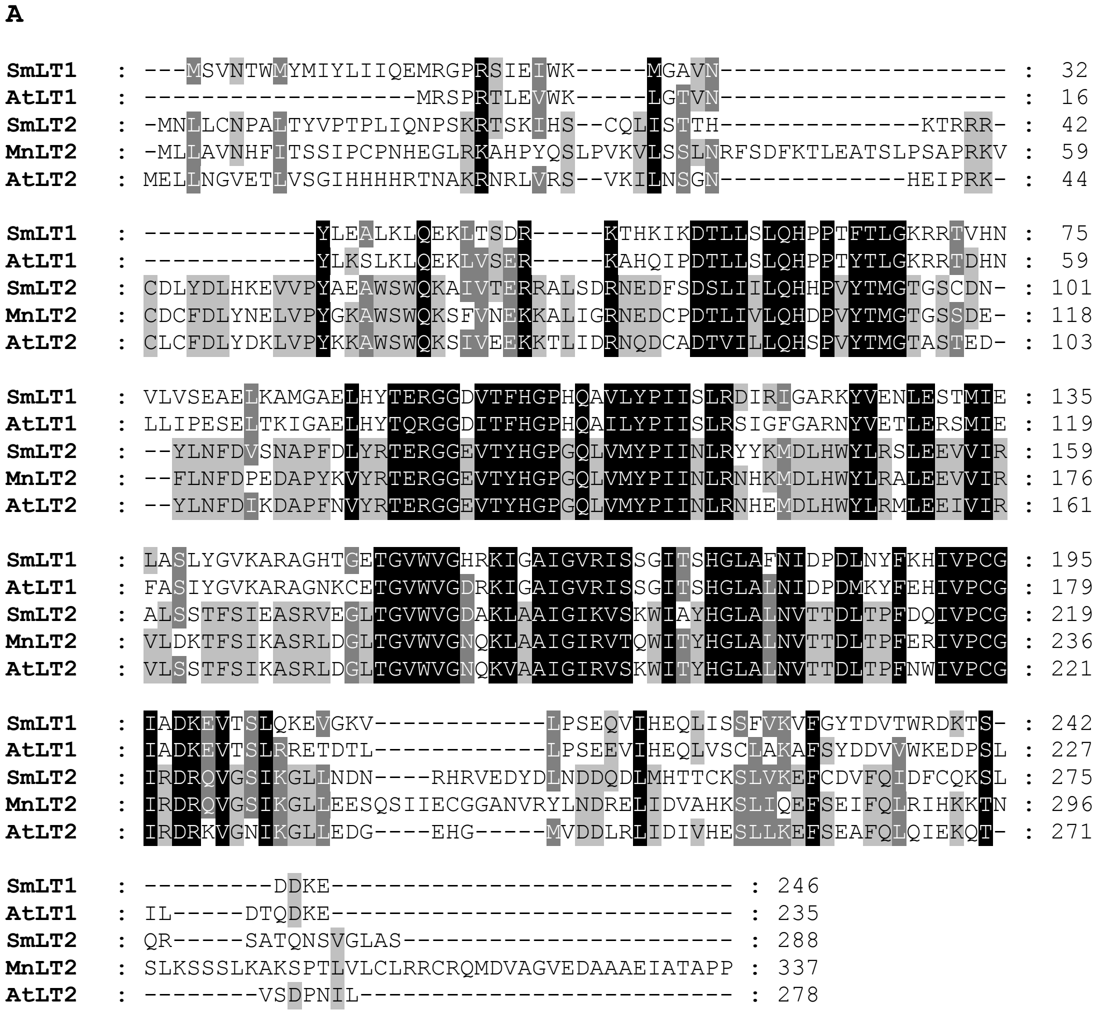


Fig S17. Multiple sequence alignment and phylogenetic tree for LS proteins from *S. miltiorrhiza* and its homologs from various other species.
The subcellular locations of proteins were hint cp (chloroplast) or mt (mitochondrion) before the abbreviation of species name.
(A) Multiple sequence alignment of LSs. The species and accession number for each LS are shown in the parenthesis: SmLS1 (*S. miltiorrhiza*, KF887937); mtAtLS1 (*A. thaliana*, At2g20860); mtPtLS (*Populus trichocarpa*, B9H5L9); mtVvLS (*Vitis vinifera* ,A5CB81).
(B) Multiple sequence alignment of LSs. The species and accession number for each LS are shown in the parenthesis: SmLS2 (KJ784448) ;cpAtLS1 (At5g08415); cpZmLS1 (*Zea mays*, B6TN12); cpRcLS (*Ricinus communis*, B9RX57) (C) Phylogenetic relationships of LSs from *S. miltiorrhiza* and various other species. LS proteins included are SmLS1 (KF887937); mtAtLS1 (At2g20860); cpAtLS1 (At5g08415); mtPtLS (B9H5L9); mtVvLS (VA5CB81); cpZmLS1 (B6TN12); cpRcLS (B9RX57); mtOsILS (*Oryza sativa* Indica Group, A2XU53); mtSbLS(*Sorghum bicolor*, C5Y9R0); mtMtLS (*Medicago truncatula*, B7FM45); mtPsLS1 (*Pisum sativum*, Q3LSN5); mtOsJLS (*Oryza sativa* Japonica Group, Q7XRF1); cpPtLS1(*Populus trichocarpa* , B9I666).



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SmLT1 : ---MSVNTWMYMIYLIIQEMRGPRSIEIWK-----MGAVN-------------------- :  32
AtLT1 : -------------------MRSPRTLEVWK-----LGTVN-------------------- :  16
SmLT2 : -MNLLCNPALTYVPTPLIQNPSKRTSKIHS--CQLISTTH--------------KTRRR- :  42
MnLT2 : -MLLAVNHFITSSIPCPNHEGLRKAHPYQSLPVKVLSSLNRFSDFKTLEATSLPSAPRKV :  59
AtLT2 : MELLNGVETLVSGIHHHHRTNAKRNRLVRS--VKILNSGN-------------HEIPRK- :  44

SmLT1 : ------------YLEALKLQEKLTSDR-----KTHKIKDTLLSLQHPPTFTLGKRRTVHN :  75
AtLT1 : ------------YLKSLKLQEKLVSER-----KAHQIPDTLLSLQHPPTYTLGKRRTDHN :  59
SmLT2 : CDLYDLHKEVVPYAEAWSWQKAIVTERRALSDRNEDFSDSLIILQHHPVYTMGTGSCDN- : 101
MnLT2 : CDCFDLYNELVPYGKAWSWQKSFVNEKKALIGRNEDCPDTLIVLQHDPVYTMGTGSSDE- : 118
AtLT2 : CLCFDLYDKLVPYKKAWSWQKSIVEEKKTLIDRNQDCADTVILLQHSPVYTMGTASTED- : 103

SmLT1 : VLVSEAELKAMGAELHYTERGGDVTFHGPHQAVLYPIISLRDIRIGARKYVENLESTMIE : 135
AtLT1 : LLIPESELTKIGAELHYTQRGGDITFHGPHQAILYPIISLRSIGFGARNYVETLERSMIE : 119
SmLT2 : --YLNFDVSNAPFDLYRTERGGEVTYHGPGQLVMYPIINLRYYKMDLHWYLRSLEEVVIR : 159
MnLT2 : --FLNFDPEDAPYKVYRTERGGEVTYHGPGQLVMYPIINLRNHKMDLHWYLRALEEVVIR : 176
AtLT2 : --YLNFDIKDAPFNVYRTERGGEVTYHGPGQLVMYPIINLRNHEMDLHWYLRMLEEIVIR : 161

SmLT1 : LASLYGVKARAGHTGETGVWVGHRKIGAIGVRISSGITSHGLAFNIDPDLNYFKHIVPCG : 195
AtLT1 : FASIYGVKARAGNKCETGVWVGDRKIGAIGVRISSGITSHGLALNIDPDMKYFEHIVPCG : 179
SmLT2 : ALSSTFSIEASRVEGLTGVWVGDAKLAAIGIKVSKWIAYHGLALNVTTDLTPFDQIVPCG : 219
MnLT2 : VLDKTFSIKASRLDGLTGVWVGNQKLAAIGIRVTQWITYHGLALNVTTDLTPFERIVPCG : 236
AtLT2 : VLSSTFSIKASRLDGLTGVWVGNQKVAAIGIRVSKWITYHGLALNVTTDLTPFNWIVPCG : 221

SmLT1 : IADKEVTSLQKEVGKV------------LPSEQVIHEQLISSFVKVFGYTDVTWRDKTS- : 242
AtLT1 : IADKEVTSLRRETDTL------------LPSEEVIHEQLVSCLAKAFSYDDVVWKEDPSL : 227
SmLT2 : IRDRQVGSIKGLLNDN----RHRVEDYDLNDDQDLMHTTCKSLVKEFCDVFQIDFCQKSL : 275
MnLT2 : IRDRQVGSIKGLLEESQSIIECGGANVRYLNDRELIDVAHKSLIQEFSEIFQLRIHKKTN : 296
AtLT2 : IRDRKVGNIKGLLEDG----EHG-----MVDDLRLIDIVHESLLKEFSEAFQLQIEKQT- : 271

SmLT1 : ---------DDKE---------------------------- : 246
AtLT1 : IL-----DTQDKE---------------------------- : 235
SmLT2 : QR-----SATQNSVGLAS----------------------- : 288
MnLT2 : SLKSSSLKAKSPTLVLCLRRCRQMDVAGVEDAAAEIATAPP : 337
AtLT2 : --------VSDPNIL-------------------------- : 278
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B

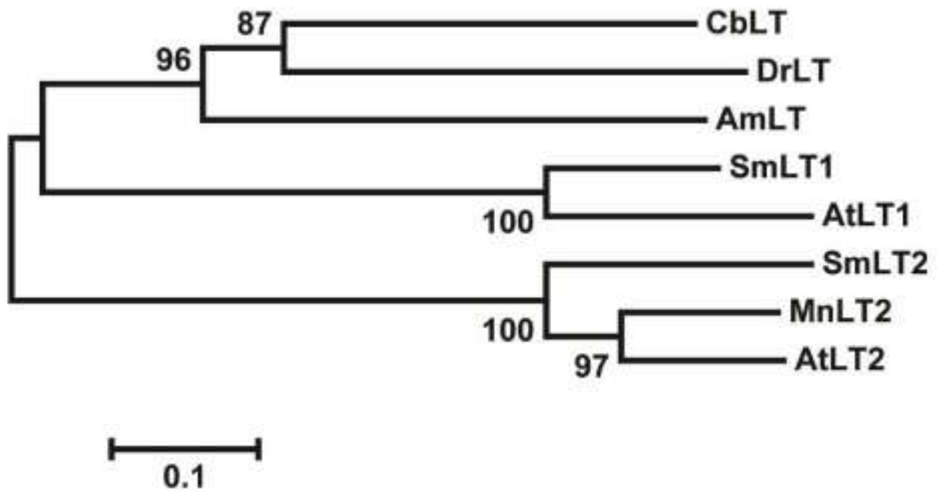
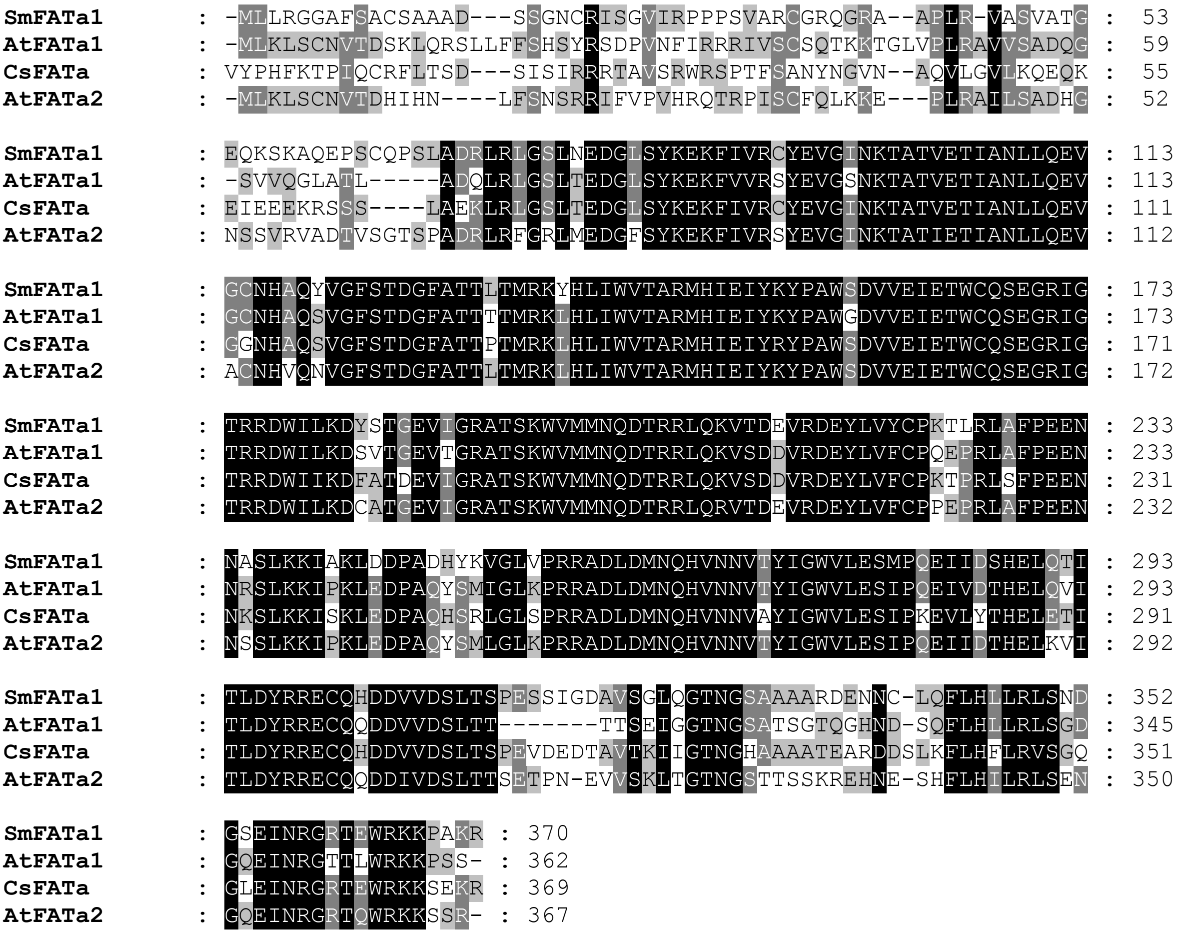


Fig S18. Multiple sequence alignment and phylogenetic tree for LT proteins from *S. miltiorrhiza* and its homologs from various other species.

(A) Multiple sequence alignment of LTs. The species and accession number for each LT are shown in the parenthesis: SmLT1 (*S. miltiorrhiza* ,KF887938); SmLT2 (KJ784449); AtLT1 (*A. thaliana* ,At1g04640); AtLT2 (At4g31050); MnLT2 (*Morus notabilis*, EXB51235).

(B) Phylogenetic relationships of LTs from *S. miltiorrhiza* and various other species. LT proteins included are *a* SmLT1 (KF887938); SmLT2 (KJ784449); AtLT1 (At1g04640); AtLT2 (At4g31050); MnLT2 (EXB51235);CbLT (*Caldicellulosiruptor bescii* DSM 6725, B9MQ23); DrLT (*Desulfotomaculum reducens* MI-1, A4J246); AmLT (*Alkaliphilus metalliredigens* QYMF, A6TWD0).

A



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SmFATa1      : -MLLRGGAFSACSAAAD---SSGNCRISGVIRPPPSVARCGRQGRA--APLR-VASVATG :  53
AtFATa1      : -MLKLSCNVTDSKLQRSLLFFSHSYRSDPVNFIRRRIVSCSQTKKTGLVPLRAVVSADQG :  59
CsFATa       : VYPHFKTPIQCRFLTSD---SISIRRRTAVSRWRSPTFSANYNGVN--AQVLGVLKQEQK :  55
AtFATa2      : -MLKLSCNVTDHIHN----LFSNSRRIFVPVHRQTRPISCFQLKKE---PLRAILSADHG :  52

SmFATa1      : EQKSKAQEPSCQPSLADRLRLGSLNEDGLSYKEKFIVRCYEVGINKTATVETIANLLQEV : 113
AtFATa1      : -SVVQGLATL-----ADQLRLGSLTEDGLSYKEKFVVRSYEVGSNKTATVETIANLLQEV : 113
CsFATa       : EIEEEKRSSS----LAEKLRLGSLTEDGLSYKEKFIVRCYEVGINKTATVETIANLLQEV : 111
AtFATa2      : NSSVRVADTVSGTSPADRLRFGRLMEDGFSYKEKFIVRSYEVGINKTATIETIANLLQEV : 112

SmFATa1      : GCNHAQYVGFSTDGFATTLTMRKYHLIWVTARMHIEIYKYPAWSDVVEIETWCQSEGRIG : 173
AtFATa1      : GCNHAQSVGFSTDGFATTTTMRKLHLIWVTARMHIEIYKYPAWGDVVEIETWCQSEGRIG : 173
CsFATa       : GGNHAQSVGFSTDGFATTPTMRKLHLIWVTARMHIEIYRYPAWSDVVEIETWCQSEGRIG : 171
AtFATa2      : ACNHVQNVGFSTDGFATTLTMRKLHLIWVTARMHIEIYKYPAWSDVVEIETWCQSEGRIG : 172

SmFATa1      : TRRDWILKDYSTGEVIGRATSKWVMMNQDTRRLQKVTDEVRDEYLVYCPKTLRLAFPEEN : 233
AtFATa1      : TRRDWILKDSVTGEVTGRATSKWVMMNQDTRRLQKVSDDVRDEYLVFCPQEPRLAFPEEN : 233
CsFATa       : TRRDWIIKDFATDEVIGRATSKWVMMNQDTRRLQKVSDDVRDEYLVFCPKTPRLSFPEEN : 231
AtFATa2      : TRRDWILKDCATGEVIGRATSKWVMMNQDTRRLQRVTDEVRDEYLVFCPPEPRLAFPEEN : 232

SmFATa1      : NASLKKIAKLDDPADHYKVGLVPRRADLDMNQHVNNVTYIGWVLESMPQEIIDSHELQTI : 293
AtFATa1      : NRSLKKIPKLEDPAQYSMIGLKPRRADLDMNQHVNNVTYIGWVLESIPQEIVDTHELQVI : 293
CsFATa       : NKSLKKISKLEDPAQHSRLGLSPRRADLDMNQHVNNVAYIGWVLESIPKEVLYTHELETI : 291
AtFATa2      : NSSLKKIPKLEDPAQYSMLGLKPRRADLDMNQHVNNVTYIGWVLESIPQEIIDTHELKVI : 292

SmFATa1      : TLDYRRECQHDDVVDSLTSPESSIGDAVSGLQGTNGSAAAARDENNC-LQFLHLLRLSND : 352
AtFATa1      : TLDYRRECQQDDVVDSLTT-------TTSEIGGTNGSATSGTQGHND-SQFLHLLRLSGD : 345
CsFATa       : TLDYRRECQHDDVVDSLTSPEVDEDTAVTKIIGTNGHAAAATEARDDSLKFLHFLRVSGQ : 351
AtFATa2      : TLDYRRECQQDDIVDSLTTSETPN-EVVSKLTGTNGSTTSSKREHNE-SHFLHILRLSEN : 350

SmFATa1      : GSEINRGRTEWRKKPAKR : 370
AtFATa1      : GQEINRGTTLWRKKPSS- : 362
CsFATa       : GLEINRGRTEWRKKSEKR : 369
AtFATa2      : GQEINRGRTQWRKKSSR- : 367
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B

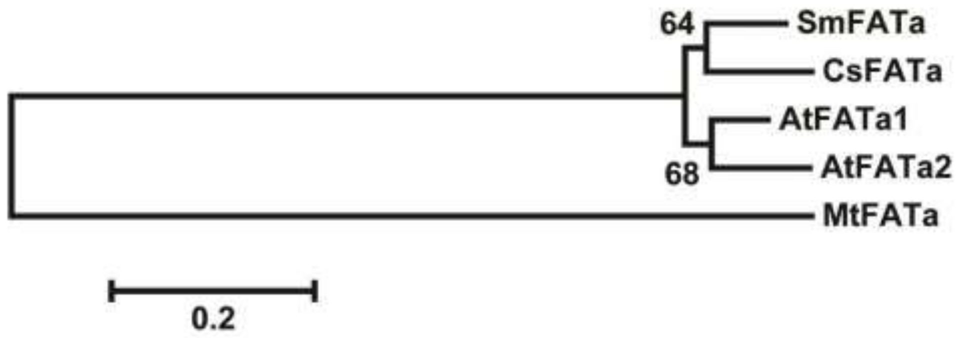
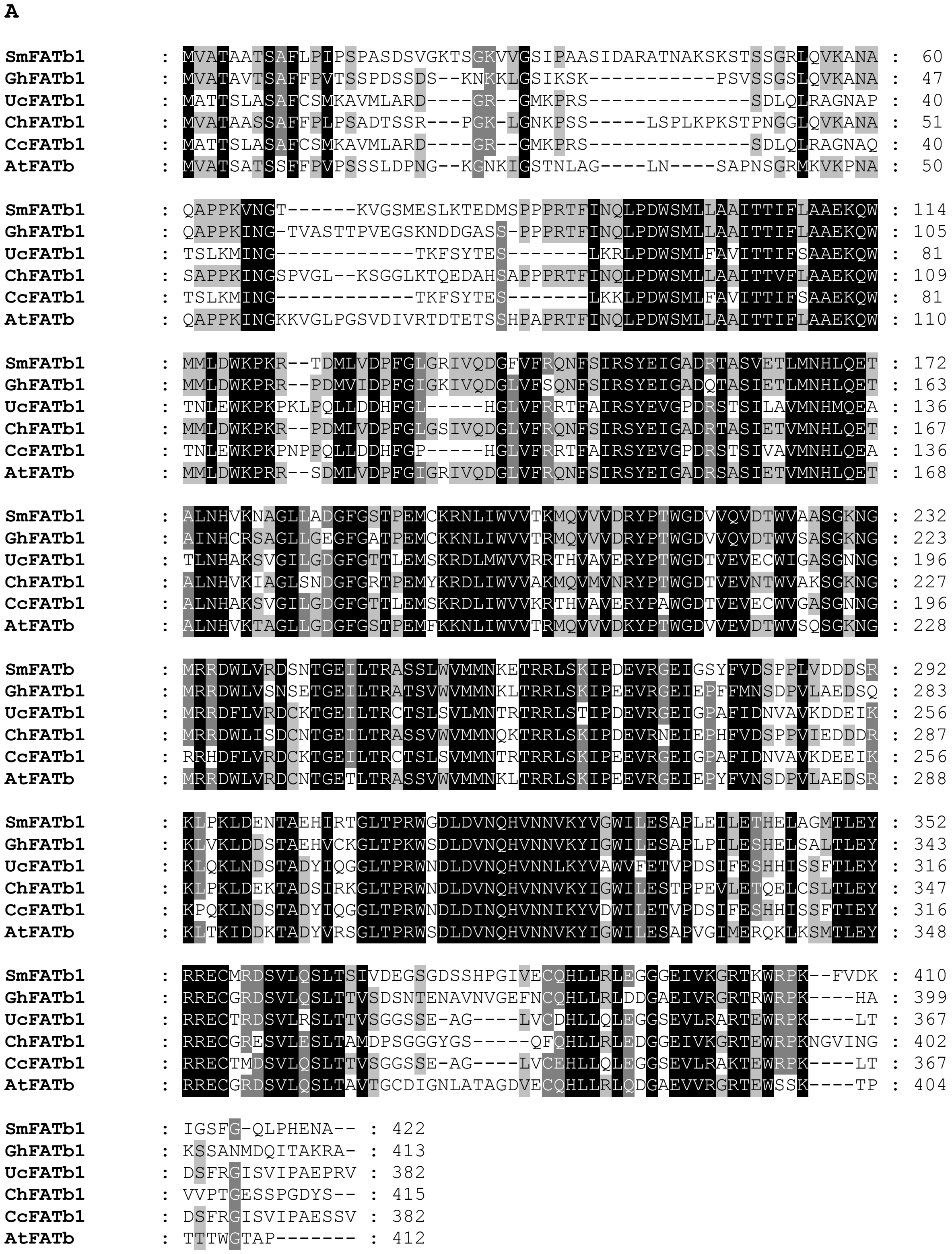


Fig S19. Multiple sequence alignment and phylogenetic tree for FATa proteins from *S. miltiorrhiza* and its homologs from various other species.

(A) Multiple sequence alignment of FATas. The species and accession number for each FATa are shown in the parenthesis: Sm FATa1 (*S. miltiorrhiza* ,KF887924); AtFATa1 (*A. thaliana*, At3g25110); AtFATa2 (At4g13050); CsFATa (*Coriandrum sativum* ,Q42712).

(B) Phylogenetic relationships of FATas from *S. miltiorrhiza* and various other species. FATa proteins included are Sm FATa1 (KF887924); AtFATa1 (At3g25110); AtFATa2 (At4g13050); CsFATa (*Coriandrum sativum* , Q42712); MtFAta (*Mycobacterium tuberculosis*, Q10856).



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SmFATb1   : MVATAATSAFLPIPSPASDSVGKTSGKVVGSIPAASIDARATNAKSKSTSSGRLQVKANA :  60
GhFATb1   : MVATAVTSAFFPVTSSPDSSDS--KNKKLGSIKSK-----------PSVSSGSLQVKANA :  47
UcFATb1   : MATTSLASAFCSMKAVMLARD----GR--GMKPRS--------------SDLQLRAGNAP :  40
ChFATb1   : MVATAASSAFFPLPSADTSSR---PGK-LGNKPSS-----LSPLKPKSTPNGGLQVKANA :  51
CcFATb1   : MATTSLASAFCSMKAVMLARD----GR--GMKPRS--------------SDLQLRAGNAQ :  40
AtFATb    : MVATSATSSFFPVPSSSLDPNG--KGNKIGSTNLAG----LN----SAPNSGRMKVKPNA :  50

SmFATb1   : QAPPKVNGT------KVGSMESLKTEDMSPPPRTFINQLPDWSMLLAAITTIFLAAEKQW : 114
GhFATb1   : QAPPKING-TVASTTPVEGSKNDDGASS-PPPRTFINQLPDWSMLLAAITTIFLAAEKQW : 105
UcFATb1   : TSLKMING------------TKFSYTES-------LKRLPDWSMLFAVITTIFSAAEKQW :  81
ChFATb1   : SAPPKINGSPVGL--KSGGLKTQEDAHSAPPPRTFINQLPDWSMLLAAITTVFLAAEKQW : 109
CcFATb1   : TSLKMING------------TKFSYTES-------LKKLPDWSMLFAVITTIFSAAEKQW :  81
AtFATb    : QAPPKINGKKVGLPGSVDIVRTDTETSSHPAPRTFINQLPDWSMLLAAITTIFLAAEKQW : 110

SmFATb1   : MMLDWKPKR--TDMLVDPFGLGRIVQDGFVFRQNFSIRSYEIGADRTASVETLMNHLQET : 172
GhFATb1   : MMLDWKPRR--PDMVIDPFGIGKIVQDGLVFSQNFSIRSYEIGADQTASIETLMNHLQET : 163
UcFATb1   : TNLEWKPKPKLPQLLDDHFGL-----HGLVFRRTFAIRSYEVGPDRSTSILAVMNHMQEA : 136
ChFATb1   : MMLDWKPKR--PDMLVDPFGLGSIVQDGLVFRQNFSIRSYEIGADRTASIETVMNHLQET : 167
CcFATb1   : TNLEWKPKPNPPQLLDDHFGP-----HGLVFRRTFAIRSYEVGPDRSTSIVAVMNHLQEA : 136
AtFATb    : MMLDWKPRR--SDMLVDPFGIGRIVQDGLVFRQNFSIRSYEIGADRSASIETVMNHLQET : 168

SmFATb1   : ALNHVKNAGLLADGFGSTPEMCKRNLIWVVTKMQVVVDRYPTWGDVVQVDTWVAASGKNG : 232
GhFATb1   : AINHCRSAGLLGEGFGATPEMCKKNLIWVVTRMQVVVDRYPTWGDVVQVDTWVSASGKNG : 223
UcFATb1   : TLNHAKSVGILGDGFGTTLEMSKRDLMWVVRRTHVAVERYPTWGDTVEVECWIGASGNNG : 196
ChFATb1   : ALNHVKIAGLSNDGFGRTPEMYKRDLIWVVAKMQVMVNRYPTWGDTVEVNTWVAKSGKNG : 227
CcFATb1   : ALNHAKSVGILGDGFGTTLEMSKRDLIWVVKRTHVAVERYPAWGDTVEVECWVGASGNNG : 196
AtFATb    : ALNHVKTAGLLGDGFGSTPEMFKKNLIWVVTRMQVVVDKYPTWGDVVEVDTWVSQSGKNG : 228

SmFATb    : MRRDWLVRDSNTGEILTRASSLWVMMNKETRRLSKIPDEVRGEIGSYFVDSPPLVDDDSR : 292
GhFATb1   : MRRDWLVSNSETGEILTRATSVWVMMNKLTRRLSKIPEEVRGEIEPFFMNSDPVLAEDSQ : 283
UcFATb1   : MRRDFLVRDCKTGEILTRCTSLSVLMNTRTRRLSTIPDEVRGEIGPAFIDNVAVKDDEIK : 256
ChFATb1   : MRRDWLISDCNTGEILTRASSVWVMMNQKTRRLSKIPDEVRNEIEPHFVDSPPVIEDDDR : 287
CcFATb1   : RRHDFLVRDCKTGEILTRCTSLSVMMNTRTRRLSKIPEEVRGEIGPAFIDNVAVKDEEIK : 256
AtFATb    : MRRDWLVRDCNTGETLTRASSVWVMMNKLTRRLSKIPEEVRGEIEPYFVNSDPVLAEDSR : 288

SmFATb1   : KLPKLDENTAEHIRTGLTPRWGDLDVNQHVNNVKYVGWILESAPLEILETHELAGMTLEY : 352
GhFATb1   : KLVKLDDSTAEHVCKGLTPKWSDLDVNQHVNNVKYIGWILESAPLPILESHELSALTLEY : 343
UcFATb1   : KLQKLNDSTADYIQGGLTPRWNDLDVNQHVNNLKYVAWVFETVPDSIFESHHISSFTLEY : 316
ChFATb1   : KLPKLDEKTADSIRKGLTPRWNDLDVNQHVNNVKYIGWILESTPPEVLETQELCSLTLEY : 347
CcFATb1   : KPQKLNDSTADYIQGGLTPRWNDLDINQHVNNIKYVDWILETVPDSIFESHHISSFTIEY : 316
AtFATb    : KLTKIDDKTADYVRSGLTPRWSDLDVNQHVNNVKYIGWILESAPVGIMERQKLKSMTLEY : 348

SmFATb1   : RRECMRDSVLQSLTSIVDEGSGDSSHPGIVECQHLLRLEGGGEIVKGRTKWRPK--FVDK : 410
GhFATb1   : RRECGRDSVLQSLTTVSDSNTENAVNVGEFNCQHLLRLDDGAEIVRGRTRWRPK----HA : 399
UcFATb1   : RRECTRDSVLRSLTTVSGGSSE-AG----LVCDHLLQLEGGSEVLRARTEWRPK----LT : 367
ChFATb1   : RRECGRESVLESLTAMDPSGGGYGS-----QFQHLLRLEDGGEIVKGRTEWRPKNGVING : 402
CcFATb1   : RRECTMDSVLQSLTTVSGGSSE-AG----LVCEHLLQLEGGSEVLRAKTEWRPK----LT : 367
AtFATb    : RRECGRDSVLQSLTAVTGCDIGNLATAGDVECQHLLRLQDGAEVVRGRTEWSSK----TP : 404

SmFATb1   : IGSFG-QLPHENA-- : 422
GhFATb1   : KSSANMDQITAKRA- : 413
UcFATb1   : DSFRGISVIPAEPRV : 382
ChFATb1   : VVPTGESSPGDYS-- : 415
CcFATb1   : DSFRGISVIPAESSV : 382
AtFATb    : TTTWGTAP------- : 412
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B

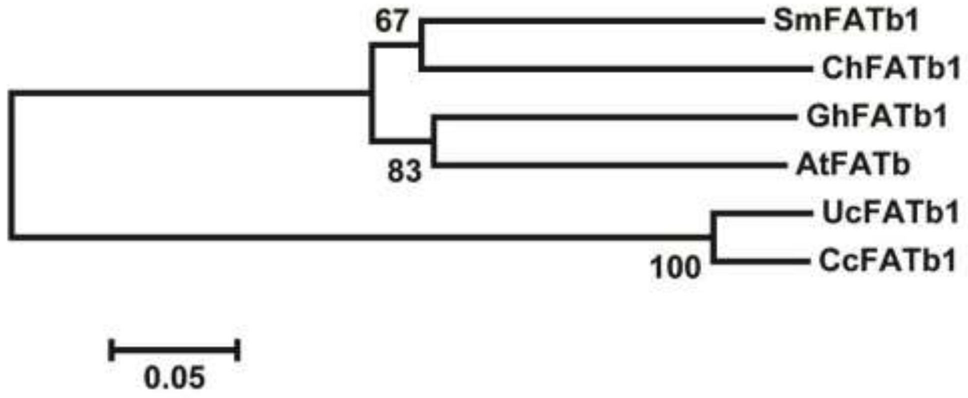

Fig S20. Multiple sequence alignment and phylogenetic tree for FATb proteins from *S. miltiorrhiza* and its homologs from various other species.

(A) Multiple sequence alignment of FATbs. The species and accession number for each FATb are shown in the parenthesis: SmFATb1 (*S. miltiorrhiza* ,KF887925); AtFATb (*A. thaliana* ,At1g08510); GhFATb1(*Gossypium hirsutum* ,Q9SQI3); UcFATb1(*Umbellularia californica* ,Q41635); ChFATb1(*Cuphea hookeriana* ,Q39513); CcFATb1(*Cinnamomum camphora*, Q39473).

(B) Phylogenetic relationships of FATbs from *S. miltiorrhiza* and various other species. FATb proteins included are SmFATb1 (KF887925); AtFATb (At1g08510); GhFATb1(Q9SQI3); UcFATb1(Q41635); ChFATb1(Q39513); CcFATb1(Q39473).

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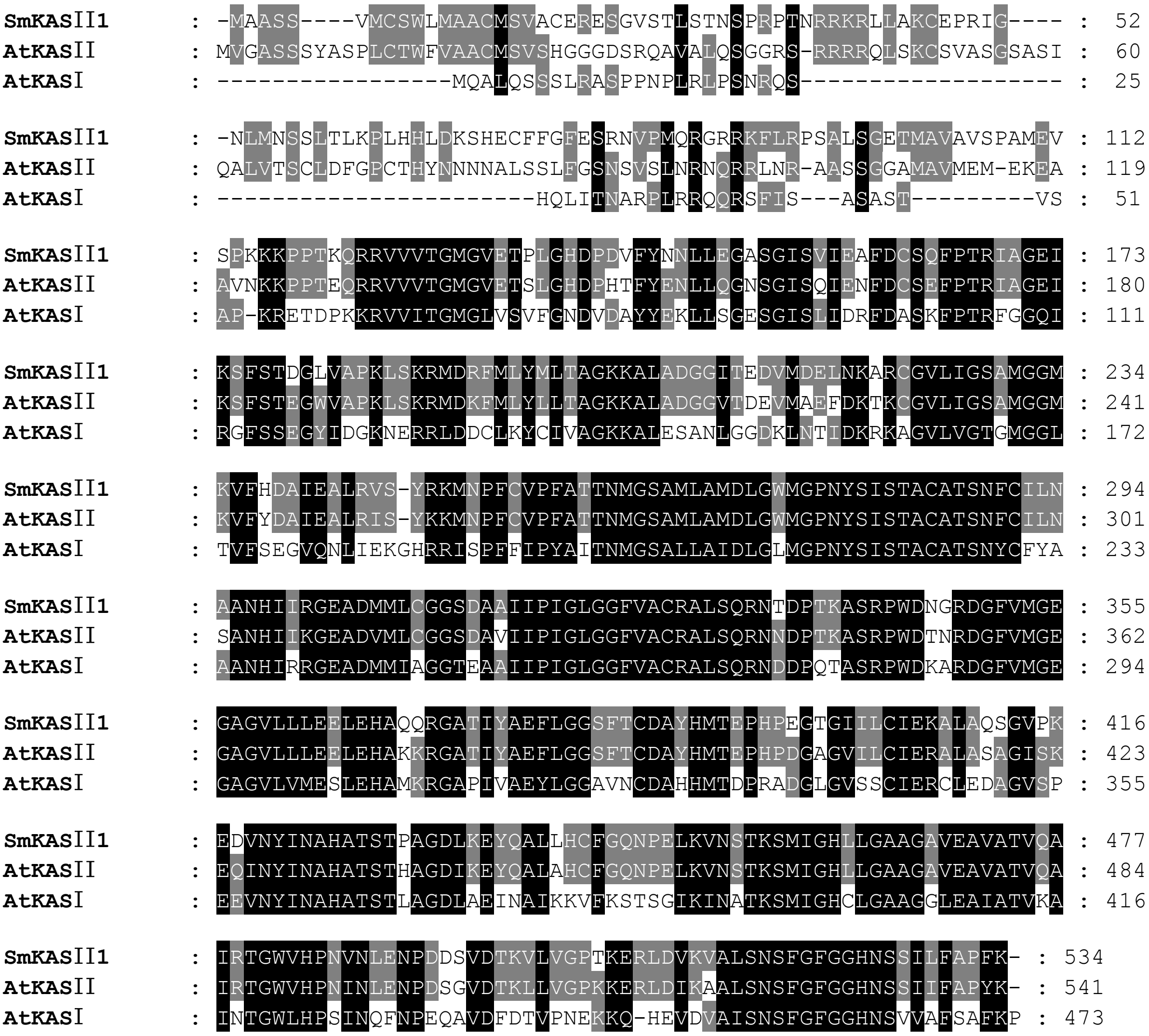

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SmKASII1  : -MAASS----VMCSWLMAACMSVACERESGVSTLSTNSPRPTNRRKRLLAKCEPRIG---- :  52
AtKASII   : MVGASSSYASPLCTWFVAACMSVSHGGGDSRQAVALQSGGRS-RRRRQLSKCSVASGSASI :  60
AtKASI    : -----------------MQALQSSSLRASPPNPLRLPSNRQS------------------- :  25

SmKASII1  : -NLMNSSLTLKPLHHLDKSHECFFGFESRNVPMQRGRRKFLRPSALSGETMAVAVSPAMEV : 112
AtKASII   : QALVTSCLDFGPCTHYNNNNALSSLFGSNSVSLNRNQRRLNR-AASSGGAMAVMEM-EKEA : 119
AtKASI    : -----------------------HQLITNARPLRRQQRSFIS---ASAST---------VS :  51

SmKASII1  : SPKKKPPTKQRRVVVTGMGVETPLGHDPDVFYNNLLEGASGISVIEAFDCSQFPTRIAGEI : 173
AtKASII   : AVNKKPPTEQRRVVVTGMGVETSLGHDPHTFYENLLQGNSGISQIENFDCSEFPTRIAGEI : 180
AtKASI    : AP-KRETDPKKRVVITGMGLVSVFGNDVDAYYEKLLSGESGISLIDRFDASKFPTRFGGQI : 111

SmKASII1  : KSFSTDGLVAPKLSKRMDRFMLYMLTAGKKALADGGITEDVMDELNKARCGVLIGSAMGGM : 234
AtKASII   : KSFSTEGWVAPKLSKRMDKFMLYLLTAGKKALADGGVTDEVMAEFDKTKCGVLIGSAMGGM : 241
AtKASI    : RGFSSEGYIDGKNERRLDDCLKYCIVAGKKALESANLGGDKLNTIDKRKAGVLVGTGMGGL : 172

SmKASII1  : KVFHDAIEALRVS-YRKMNPFCVPFATTNMGSAMLAMDLGWMGPNYSISTACATSNFCILN : 294
AtKASII   : KVFYDAIEALRIS-YKKMNPFCVPFATTNMGSAMLAMDLGWMGPNYSISTACATSNFCILN : 301
AtKASI    : TVFSEGVQNLIEKGHRRISPFFIPYAITNMGSALLAIDLGLMGPNYSISTACATSNYCFYA : 233

SmKASII1  : AANHIIRGEADMMLCGGSDAAIIPIGLGGFVACRALSQRNTDPTKASRPWDNGRDGFVMGE : 355
AtKASII   : SANHIIKGEADVMLCGGSDAVIIPIGLGGFVACRALSQRNNDPTKASRPWDTNRDGFVMGE : 362
AtKASI    : AANHIRRGEADMMIAGGTEAAIIPIGLGGFVACRALSQRNDDPQTASRPWDKARDGFVMGE : 294

SmKASII1  : GAGVLLLEELEHAQQRGATIYAEFLGGSFTCDAYHMTEPHPEGTGIILCIEKALAQSGVPK : 416
AtKASII   : GAGVLLLEELEHAKKRGATIYAEFLGGSFTCDAYHMTEPHPDGAGVILCIERALASAGISK : 423
AtKASI    : GAGVLVMESLEHAMKRGAPIVAEYLGGAVNCDAHHMTDPRADGLGVSSCIERCLEDAGVSP : 355

SmKASII1  : EDVNYINAHATSTPAGDLKEYQALLHCFGQNPELKVNSTKSMIGHLLGAAGAVEAVATVQA : 477
AtKASII   : EQINYINAHATSTHAGDIKEYQALAHCFGQNPELKVNSTKSMIGHLLGAAGAVEAVATVQA : 484
AtKASI    : EEVNYINAHATSTLAGDLAEINAIKKVFKSTSGIKINATKSMIGHCLGAAGGLEAIATVKA : 416

SmKASII1  : IRTGWVHPNVNLENPDDSVDTKVLVGPTKERLDVKVALSNSFGFGGHNSSILFAPFK- : 534
AtKASII   : IRTGWVHPNINLENPDSGVDTKLLVGPKKERLDIKAALSNSFGFGGHNSSIIFAPYK- : 541
AtKASI    : INTGWLHPSINQFNPEQAVDFDTVPNEKKQ-HEVDVALSNSFGFGGHNSVVAFSAFKP : 473
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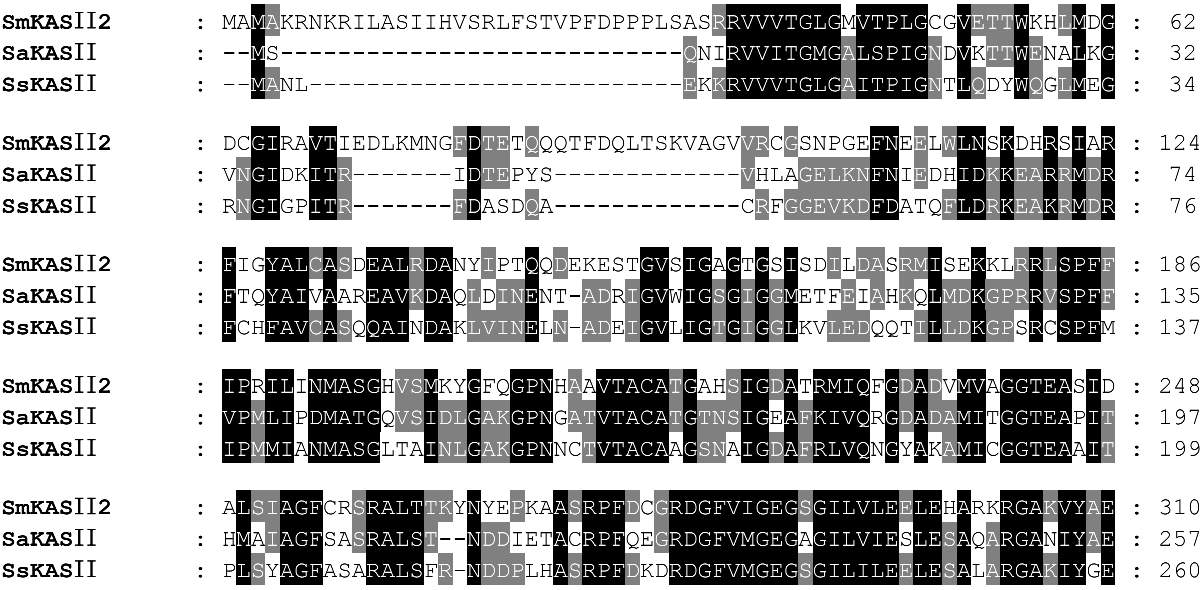

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SmKASII2  : MAMAKRNKRILASIIHVSRLFSTVPFDPPPLSASRRVVVTGLGMVTPLGCGVETTWKHLMDG :  62
SaKASII   : --MS----------------------------QNIRVVITGMGALSPIGNDVKTTWENALKG :  32
SsKASII   : --MANL--------------------------EKKRVVVTGLGAITPIGNTLQDYWQGLMEG :  34

SmKASII2  : DCGIRAVTIEDLKMNGFDTETQQQTFDQLTSKVAGVVRCGSNPGEFNEELWLNSKDHRSIAR : 124
SaKASII   : VNGIDKITR-------IDTEPYS-------------VHLAGELKNFNIEDHIDKKEARRMDR :  74
SsKASII   : RNGIGPITR-------FDASDQA-------------CRFGGEVKDFDATQFLDRKEAKRMDR :  76

SmKASII2  : FIGYALCASDEALRDANYIPTQQDEKESTGVSIGAGTGSISDILDASRMISEKKLRRLSPFF : 186
SaKASII   : FTQYAIVAAREAVKDAQLDINENT-ADRIGVWIGSGIGGMETFEIAHKQLMDKGPRRVSPFF : 135
SsKASII   : FCHFAVCASQQAINDAKLVINELN-ADEIGVLIGTGIGGLKVLEDQQTILLDKGPSRCSPFM : 137

SmKASII2  : IPRILINMASGHVSMKYGFQGPNHAAVTACATGAHSIGDATRMIQFGDADVMVAGGTEASID : 248
SaKASII   : VPMLIPDMATGQVSIDLGAKGPNGATVTACATGTNSIGEAFKIVQRGDADAMITGGTEAPIT : 197
SsKASII   : IPMMIANMASGLTAINLGAKGPNNCTVTACAAGSNAIGDAFRLVQNGYAKAMICGGTEAAIT : 199

SmKASII2  : ALSIAGFCRSRALTTKYNYEPKAASRPFDCGRDGFVIGEGSGILVLEELEHARKRGAKVYAE : 310
SaKASII   : HMAIAGFSASRALST--NDDIETACRPFQEGRDGFVMGEGAGILVIESLESAQARGANIYAE : 257
SsKASII   : PLSYAGFASARALSFR-NDDPLHASRPFDKDRDGFVMGEGSGILILEELESALARGAKIYGE : 260
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SmKASII2   : VRGYGMSGDAYHITQPHGDGRGAVLAMSRALKQVLDSYFLIIIRSLIYVPCPFCGWQSGLNP : 372
SaKASII    : IVGYGTTGDAYHITAPAPEGEGGSRAMQAAMD------------------------DAGIEP : 295
SsKASII    : MVGYAMTCDAYHITAPVPDGRGATRAIAWALK------------------------DSGLKP : 298

SmKASII2   : NEVDYINAHATSTPLGDAVEAKAIQSLFCYHAASGNLAFSSTKGATGHLLGAAGAVEAIFSI : 434
SaKASII    : KDVQYLNAHGTSTPVGDLNEVKAIKNTFGEAAK--HLKVSSTKSMTGHLLGATGGIEAIFSA : 355
SsKASII    : EMVSYINAHGTSTPANDVTETRAIKQALGNHAY--NIAVSSTKSMTGHLLGGSGGIEAVATV : 358

SmKASII2   : LSIHHGIAPLTLNLTKPDPIFNGDFMPLSASKMMSIRAAMSNSFGFGGTNSSLLFAALD- : 493
SaKASII    : LSIKDSKVAPTIHAVTPDPECDLDIVP-NEAQDLDITYAMSNSLGFGGHNAVLVFKKFEA : 414
SsKASII    : MAIAEDKVPPTINLENPDPECDLDYVP-GQSRALIVDVALSNSFGFGGHNVTLAFKKYQ- : 416
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C

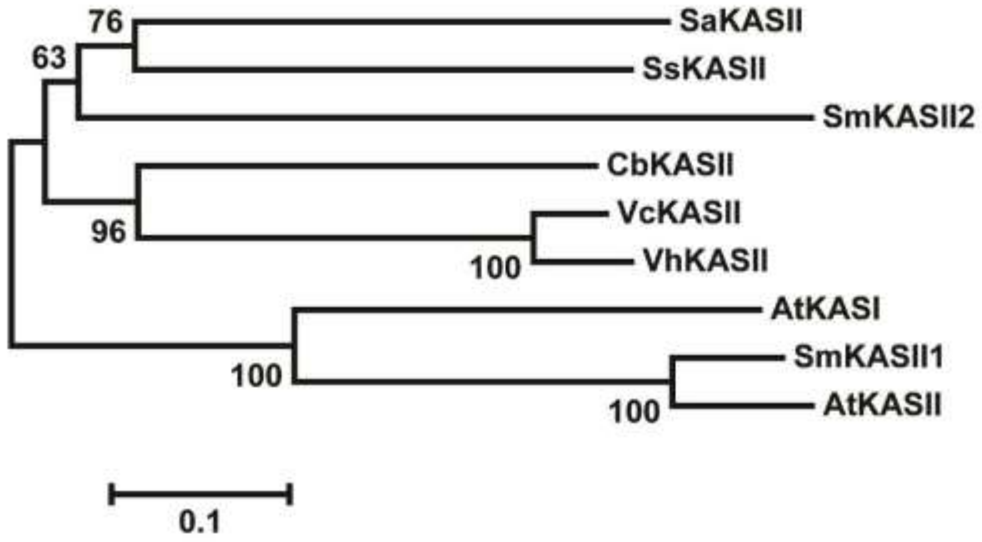
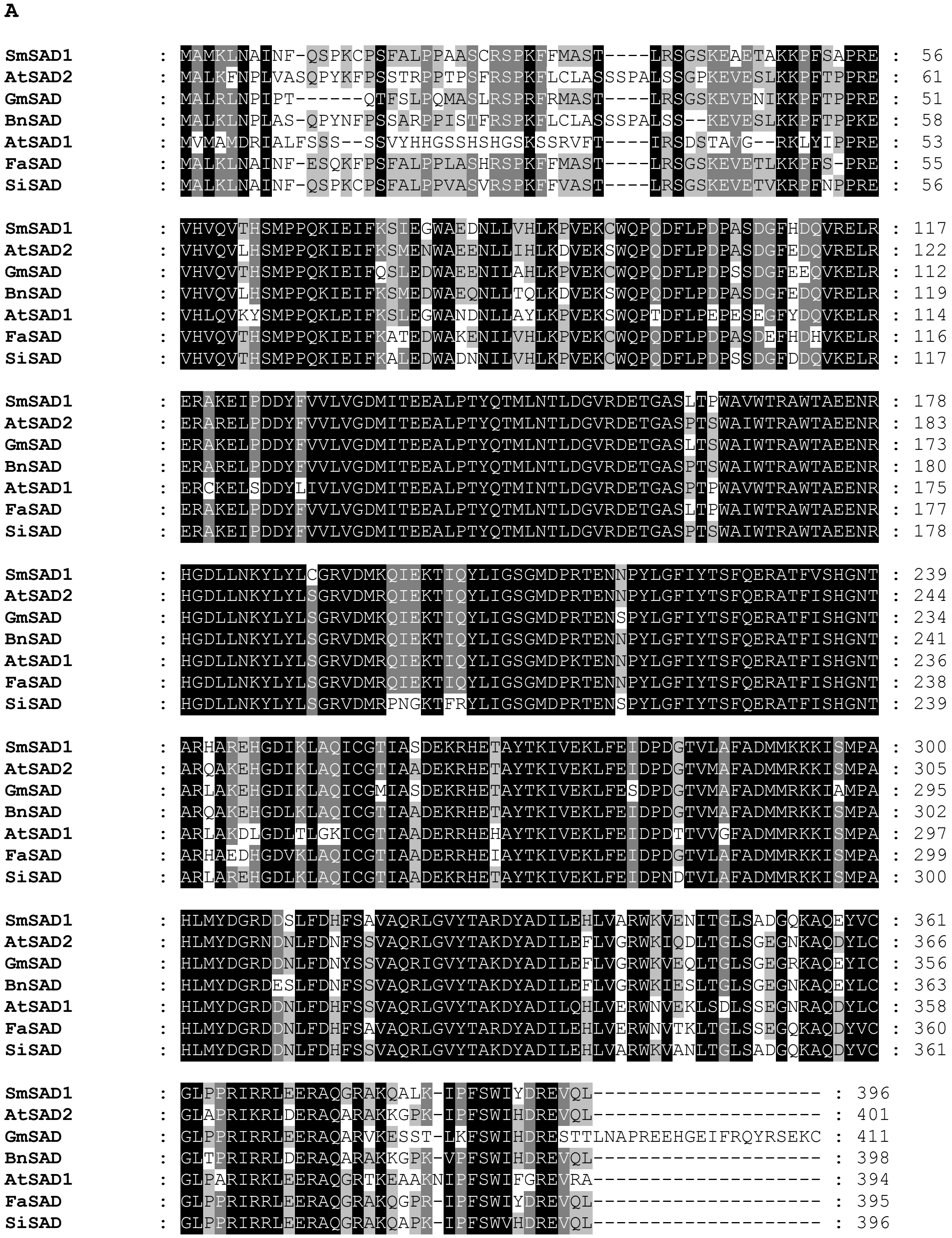


Fig S21. Multiple sequence alignment and phylogenetic tree for KASII proteins from *S. miltiorrhiza* and its homologs from various other species.
(A) Multiple sequence alignment of KASIIs. The species and accession number for each KASII are shown in the parenthesis: SmKASII1 (*S. miltiorrhiza* ,KF887933); AtKASII (*A. thaliana* , AT1G74960.2); AtKASI (AT5G46290.3).
(B) Multiple sequence alignment of KASIIs. The species and accession number for each KASII are shown in the parenthesis: SmKASII2 (KJ784437); SaKASII (*Staphylococcus aureus* ,Q7A6F8); SsKASII (*Synechocystis* sp.PCC6803 ,P73283). (C) Phylogenetic relationships of KASIIs from *S. miltiorrhiza* and various other species. KASII proteins included are SmKASII1 (KF887933); SmKASII2 (KJ784437); SaKASII (Q7A6F8); SsKASII (P73283); AtKASII (AT1G74960.2); AtKASI (AT5G46290.3); CbKASII(*Coxiella burnetii* RSA 493, Q83E37); VcKASII (*Vibrio cholera*, Q9KQH9);VhKASII(*Vibrio harveyi*, P55338).



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AtSAD2   : MALKFNPLVASQPYKFPSSTRPPTPSFRSPKFLCLASSSPALSSGPKEVESLKKPFTPPRE :  61
GmSAD    : MALRLNPIPT------QTFSLPQMASLRSPRFRMAST----LRSGSKEVENIKKPFTPPRE :  51
BnSAD    : MALKLNPLAS-QPYNFPSSARPPISTFRSPKFLCLASSSPALSS--KEVESLKKPFTPPKE :  58
AtSAD1   : MVMAMDRIALFSSS--SSVYHHGSSHSHGSKSSRVFT----IRSDSTAVG--RKLYIPPRE :  53
FaSAD    : MALKLNAINF-ESQKFPSFALPPLASHRSPKFFMAST----LRSGSKEVETLKKPFS-PRE :  55
SiSAD    : MALKLNAINF-QSPKCPSFALPPVASVRSPKFFVAST----LRSGSKEVETVKRPFNPPRE :  56

SmSAD1   : VHVQVTHSMPPQKIEIFKSIEGWAEDNLLVHLKPVEKCWQPQDFLPDPASDGFHDQVRELR : 117
AtSAD2   : VHVQVLHSMPPQKIEIFKSMENWAEENLLIHLKDVEKSWQPQDFLPDPASDGFEDQVRELR : 122
GmSAD    : VHVQVTHSMPPQKIEIFQSLEDWAEENILAHLKPVEKCWQPQDFLPDPSSDGFEEQVKELR : 112
BnSAD    : VHVQVLHSMPPQKIEIFKSMEDWAEQNLLTQLKDVEKSWQPQDFLPDPASDGFEDQVRELR : 119
AtSAD1   : VHLQVKYSMPPQKLEIFKSLEGWANDNLLAYLKPVEKSWQPTDFLPEPESEGFYDQVKELR : 114
FaSAD    : VHVQVTHSMPPQKIEIFKATEDWAKENILVHLKPVEKCWQPQDFLPDPASDEFHDHVKELR : 116
SiSAD    : VHVQVTHSMPPQKIEIFKALEDWADNNILVHLKPVEKCWQPQDFLPDPSSDGFDDQVKELR : 117

SmSAD1   : ERAKEIPDDYFVVLVGDMITEEALPTYQTMLNTLDGVRDETGASLTPWAVWTRAWTAEENR : 178
AtSAD2   : ERARELPDDYFVVLVGDMITEEALPTYQTMLNTLDGVRDETGASPTSWAIWTRAWTAEENR : 183
GmSAD    : ERAKELPDDYFVVLVGDMITEEALPTYQTMLNTLDGVRDETGASLTSWAIWTRAWTAEENR : 173
BnSAD    : ERARELPDDYFVVLVGDMITEEALPTYQTMLNTLDGVRDETGASPTSWAIWTRAWTAEENR : 180
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FaSAD    : ERAKELPDDYFVVLVGDMITEEALPTYQTMLNTLDGVRDETGASLTPWAIWTRAWTAEENR : 177
SiSAD    : ERAKEIPDDYFVVLVGDMITEEALPTYQTMLNTLDGVRDETGASPTSWAIWTRAWTAEENR : 178

SmSAD1   : HGDLLNKYLYLCGRVDMKQIEKTIQYLIGSGMDPRTENNPYLGFIYTSFQERATFVSHGNT : 239
AtSAD2   : HGDLLNKYLYLSGRVDMRQIEKTIQYLIGSGMDPRTENNPYLGFIYTSFQERATFISHGNT : 244
GmSAD    : HGDLLNKYLYLSGRVDMKQIEKTIQYLIGSGMDPRTENSPYLGFIYTSFQERATFISHGNT : 234
BnSAD    : HGDLLNKYLYLSGRVDMRQIEKTIQYLIGSGMDPRTENNPYLGFIYTSFQERATFISHGNT : 241
AtSAD1   : HGDLLNKYLYLSGRVDMRQIEKTIQYLIGSGMDPKTENNPYLGFIYTSFQERATFISHGNT : 236
FaSAD    : HGDLLNKYLYLSGRVDMRQIEKTIQYLIGSGMDPRTENNPYLGFIYTSFQERATFISHGNT : 238
SiSAD    : HGDLLNKYLYLSGRVDMRPNGKTFRYLIGSGMDPRTENSPYLGFIYTSFQERATFISHGNT : 239

SmSAD1   : ARHAREHGDIKLAQICGTIASDEKRHETAYTKIVEKLFEIDPDGTVLAFADMMKKKISMPA : 300
AtSAD2   : ARQAKEHGDIKLAQICGTIAADEKRHETAYTKIVEKLFEIDPDGTVMAFADMMRKKISMPA : 305
GmSAD    : ARLAKEHGDIKLAQICGMIASDEKRHETAYTKIVEKLFESDPDGTVMAFADMMRKKIAMPA : 295
BnSAD    : ARQAKEHGDLKLAQICGTIAADEKRHETAYTKIVEKLFEIDPDGTVMAFADMMRKKISMPA : 302
AtSAD1   : ARLAKDLGDLTLGKICGTIAADERRHEHAYTKIVEKLFEIDPDTTVVGFADMMRKKISMPA : 297
FaSAD    : ARHAEDHGDVKLAQICGTIAADERRHEIAYTKIVEKLFEIDPDGTVLAFADMMRKKISMPA : 299
SiSAD    : ARLAREHGDLKLAQICGTIAADEKRHETAYTKIVEKLFEIDPNDTVLAFADMMRKKISMPA : 300

SmSAD1   : HLMYDGRDDSLFDHFSAVAQRLGVYTARDYADILEHLVARWKVENITGLSADGQKAQEYVC : 361
AtSAD2   : HLMYDGRNDNLFDNFSSVAQRLGVYTAKDYADILEFLVGRWKIQDLTGLSGEGNKAQDYLC : 366
GmSAD    : HLMYDGRDDNLFDNYSSVAQRIGVYTAKDYADILEFLVGRWKVEQLTGLSGEGRKAQEYIC : 356
BnSAD    : HLMYDGRDESLFDNFSSVAQRLGVYTAKDYADILEFLVGRWKIESLTGLSGEGNKAQEYLC : 363
AtSAD1   : HLMYDGRDDNLFDHFSSVAQRLGVYTAKDYADILQHLVERWNVEKLSDLSSEGNRAQDYLC : 358
FaSAD    : HLMYDGRDDNLFDHFSAVAQRLGVYTARDYADILEHLVERWNVTKLTGLSSEGQKAQDYVC : 360
SiSAD    : HLMYDGRDDNLFDHFSSVAQRLGVYTAKDYADILEHLVARWKVANLTGLSADGQKAQDYVC : 361

SmSAD1   : GLPPRIRRLEERAQGRAKQALK-IPFSWIYDREVQL--------------------- : 396
AtSAD2   : GLAPRIKRLDERAQARAKKGPK-IPFSWIHDREVQL--------------------- : 401
GmSAD    : GLPPRIRRLEERAQARVKESST-LKFSWIHDRESTTLNAPREEHGEIFRQYRSEKC : 411
BnSAD    : GLTPRIRRLDERAQARAKKGPK-VPFSWIHDREVQL--------------------- : 398
AtSAD1   : GLPARIRKLEERAQGRTKEAAKNIPFSWIFGREVRA--------------------- : 394
FaSAD    : GLPPRIRRLEERAQGRAKQGPR-IPFSWIYDREVQL--------------------- : 395
SiSAD    : GLPPRIRRLEERAQGRAKQAPK-IPFSWVHDREVQL--------------------- : 396
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B

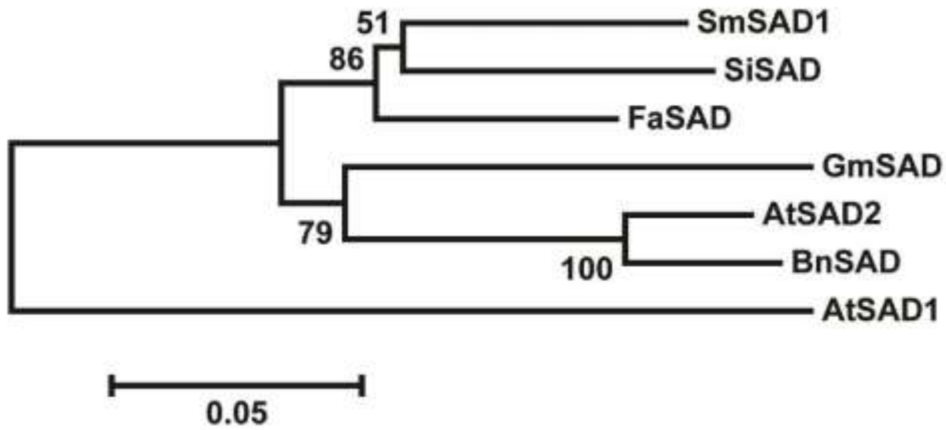
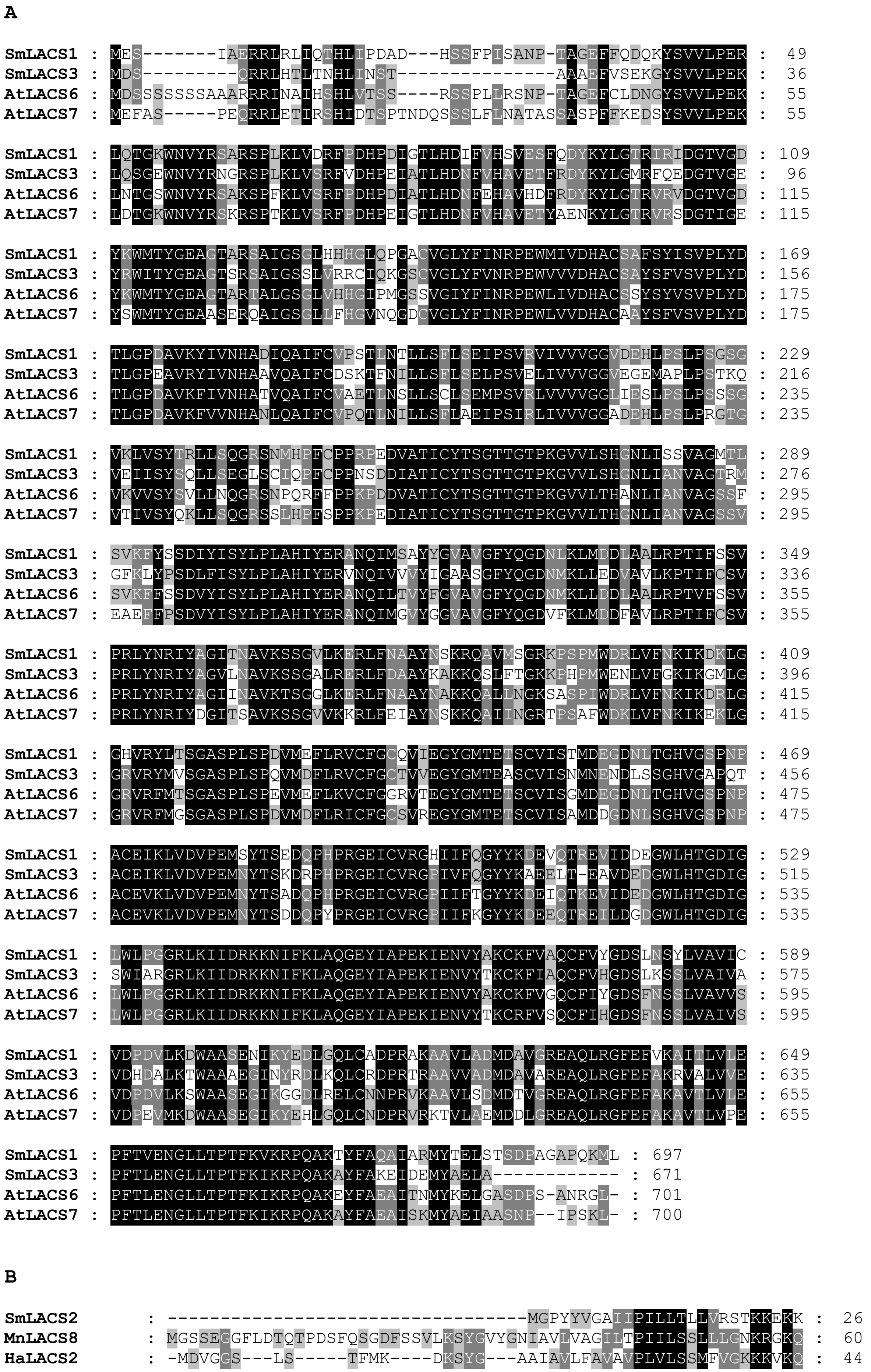


Fig S22. Multiple sequence alignment and phylogenetic tree for SAD proteins from *S. miltiorrhiza* and its homologs from various other species. (A) Multiple sequence alignment of SADs. The species and accession number for each SAD are shown in the parenthesis: SmSAD1 (*S. miltiorrhiza* ,KF887940); AtSAD1 (*A. thaliana*, AT5G16240); AtSAD2 (At2g43710); SiSAD (*Sesamum indicum* ,CAC44792); FaSAD (*Fraxinus americana* ,ADZ95599); GmSAD(*Glycine max* ,Q42807); BnSAD (*Brassica napus*, P29108).

(B) Phylogenetic relationships of SADs from *S. miltiorrhiza* and various other species. SAD proteins included are SmSAD1 (KF887940); AtSAD1 (AT5G16240); AtSAD2 (At2g43710); SiSAD (CAC44792); FaSAD (ADZ95599); GmSAD(Q42807); BnSAD (P29108).



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SmLACS3 : MDS---------QRRLHTLTNHLINST---------------AAAEFVSEKGYSVVLPEK :  36
AtLACS6 : MDSSSSSSSAAARRRINAIHSHLVTSS----RSSPLLRSNP-TAGEFCLDNGYSVVLPEK :  55
AtLACS7 : MEFAS-----PEQRRLETIRSHIDTSPTNDQSSSLFLNATASSASPFFKEDSYSVVLPEK :  55

SmLACS1 : LQTGKWNVYRSARSPLKLVDRFPDHPDIGTLHDIFVHSVESFQDYKYLGTRIRIDGTVGD : 109
SmLACS3 : LQSGEWNVYRNGRSPLKLVSRFVDHPEIATLHDNFVHAVETFRDYKYLGMRFQEDGTVGE :  96
AtLACS6 : LNTGSWNVYRSAKSPFKLVSRFPDHPDIATLHDNFEHAVHDFRDYKYLGTRVRVDGTVGD : 115
AtLACS7 : LDTGKWNVYRSKRSPTKLVSRFPDHPEIGTLHDNFVHAVETYAENKYLGTRVRSDGTIGE : 115

SmLACS1 : YKWMTYGEAGTARSAIGSGLHHHGLQPGACVGLYFINRPEWMIVDHACSAFSYISVPLYD : 169
SmLACS3 : YRWITYGEAGTSRSAIGSSLVRRCIQKGSCVGLYFVNRPEWVVVDHACSAYSFVSVPLYD : 156
AtLACS6 : YKWMTYGEAGTARTALGSGLVHHGIPMGSSVGIYFINRPEWLIVDHACSSYSYVSVPLYD : 175
AtLACS7 : YSWMTYGEAASERQAIGSGLLFHGVNQGDCVGLYFINRPEWLVVDHACAAYSFVSVPLYD : 175

SmLACS1 : TLGPDAVKYIVNHADIQAIFCVPSTLNTLLSFLSEIPSVRVIVVVGGVDEHLPSLPSGSG : 229
SmLACS3 : TLGPEAVRYIVNHAAVQAIFCDSKTFNILLSFLSELPSVELIVVVGGVEGEMAPLPSTKQ : 216
AtLACS6 : TLGPDAVKFIVNHATVQAIFCVAETLNSLLSCLSEMPSVRLVVVVGGLIESLPSLPSSSG : 235
AtLACS7 : TLGPDAVKFVVNHANLQAIFCVPQTLNILLSFLAEIPSIRLIVVVGGADEHLPSLPRGTG : 235

SmLACS1 : VKLVSYTRLLSQGRSNMHPFCPPRPEDVATICYTSGTTGTPKGVVLSHGNLISSVAGMTL : 289
SmLACS3 : VEIISYSQLLSEGLSCIQPFCPPNSDDIATICYTSGTTGTPKGVVLSHGNLIANVAGTRM : 276
AtLACS6 : VKVVSYSVLLNQGRSNPQRFFPPKPDDVATICYTSGTTGTPKGVVLTHANLIANVAGSSF : 295
AtLACS7 : VTIVSYQKLLSQGRSSLHPFSPPKPEDIATICYTSGTTGTPKGVVLTHGNLIANVAGSSV : 295

SmLACS1 : SVKFYSSDIYISYLPLAHIYERANQIMSAYYGVAVGFYQGDNLKLMDDLAALRPTIFSSV : 349
SmLACS3 : GFKLYPSDLFISYLPLAHIYERVNQIVVVYIGAASGFYQGDNMKLLEDVAVLKPTIFCSV : 336
AtLACS6 : SVKFFSSDVYISYLPLAHIYERANQILTVYFGVAVGFYQGDNMKLLDDLAALRPTVFSSV : 355
AtLACS7 : EAEFFPSDVYISYLPLAHIYERANQIMGVYGGVAVGFYQGDVFKLMDDFAVLRPTIFCSV : 355

SmLACS1 : PRLYNRIYAGITNAVKSSGVLKERLFNAAYNSKRQAVMSGRKPSPMWDRLVFNKIKDKLG : 409
SmLACS3 : PRLYNRIYAGVLNAVKSSGALRERLFDAAYKAKKQSLFTGKKPHPMWENLVFGKIKGMLG : 396
AtLACS6 : PRLYNRIYAGIINAVKTSGGLKERLFNAAYNAKKQALLNGKSASPIWDRLVFNKIKDRLG : 415
AtLACS7 : PRLYNRIYDGITSAVKSSGVVKKRLFEIAYNSKKQAIINGRTPSAFWDKLVFNKIKEKLG : 415

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SmLACS3 : GRVRYMVSGASPLSPQVMDFLRVCFGCTVVEGYGMTEASCVISNMNENDLSSGHVGAPQT : 456
AtLACS6 : GRVRFMTSGASPLSPEVMEFLKVCFGGRVTEGYGMTETSCVISGMDEGDNLTGHVGSPNP : 475
AtLACS7 : GRVRFMGSGASPLSPDVMDFLRICFGCSVREGYGMTETSCVISAMDDGDNLSGHVGSPNP : 475

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SmLACS3 : ACEIKLVDVPEMNYTSKDRPHPRGEICVRGPIVFQGYYKAEELT-EAVDEDGWLHTGDIG : 515
AtLACS6 : ACEVKLVDVPEMNYTSADQPHPRGEICVRGPIIFTGYYKDEIQTKEVIDEDGWLHTGDIG : 535
AtLACS7 : ACEVKLVDVPEMNYTSDDQPYPRGEICVRGPIIFKGYYKDEEQTREILDGDGWLHTGDIG : 535

SmLACS1 : LWLPGGRLKIIDRKKNIFKLAQGEYIAPEKIENVYAKCKFVAQCFVYGDSLNSYLVAVIC : 589
SmLACS3 : SWIARGRLKIIDRKKNIFKLAQGEYIAPEKIENVYTKCKFIAQCFVHGDSLKSSLVAIVA : 575
AtLACS6 : LWLPGGRLKIIDRKKNIFKLAQGEYIAPEKIENVYAKCKFVGQCFIYGDSFNSSLVAVVS : 595
AtLACS7 : LWLPGGRLKIIDRKKNIFKLAQGEYIAPEKIENVYTKCRFVSQCFIHGDSFNSSLVAIVS : 595

SmLACS1 : VDPDVLKDWAASENIKYEDLGQLCADPRAKAAVLADMDAVGREAQLRGFEFVKAITLVLE : 649
SmLACS3 : VDHDALKTWAAAEGINYRDLKQLCRDPRTRAAVVADMDAVAREAQLRGFEFAKRVALVVE : 635
AtLACS6 : VDPDVLKSWAASEGIKGGDLRELCNNPRVKAAVLSDMDTVGREAQLRGFEFAKAVTLVLE : 655
AtLACS7 : VDPEVMKDWAASEGIKYEHLGQLCNDPRVRKTVLAEMDDLGREAQLRGFEFAKAVTLVPE : 655

SmLACS1 : PFTVENGLLTPTFKVKRPQAKTYFAQAIARMYTELSTSDPAGAPQKML : 697
SmLACS3 : PFTLENGLLTPTFKIKRPQAKAYFAKEIDEMYAELA------------ : 671
AtLACS6 : PFTLENGLLTPTFKIKRPQAKEYFAEAITNMYKELGASDPS-ANRGL- : 701
AtLACS7 : PFTLENGLLTPTFKIKRPQAKAYFAEAISKMYAEIAASNP--IPSKL- : 700


B

SmLACS2       : ----------------------------------MGPYYVGAIIPILLTLLVRSTKKEKK :  26
MnLACS8       : MGSSEGGFLDTQTPDSFQSGDFSSVLKSYGVYGNIAVLVAGILTPIILSSLLLGNKRGKQ :  60
HaLACS2       : -MDVGGS---LS-----TFMK----DKSYG---AAIAVLFAVAVPLVLSSMFVGKKKVKQ :  44
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CaLACS       : MEDSEGSNPYTSSVERLTSYDY--ISKNYGSSGVTGAVFIAIIMPIILSMLLMGKKKAKQ :  58

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HaLACS2      : RGVPVEVGGEPGFGMRNVRSKKLVDVPWEGATTMAALFEQSCKKHSQHRFLGTRKLIERS : 104
CaLACS       : RGVPVQVGGEAGLAMRNVKSARLVEVPWEGATTVPALFEQSCKKHSSDRCLGTRKLVSRD : 118

SmLACS2      : -VEISDGKSFEKLHLGEYEWLSYGQAFESVCHFSSGLVQLGHQKGERAAIFADTREEWFI : 145
MnLACS8      : FVTASDGRKFEKLHLGDYEWQTYGEVLDRASNFASGLVKLGHNVDTRAAIFSETRAEWLI : 180
HaLACS2      : FIDGSGGRKFEKLHLGEYEWETFGQVFERVCNFASGLIQLGHDPDTRIAIFSDTRAEWLI : 164
CaLACS       : FVTASDGRKFEKLHLGEYQWESYGQVFDRTCNFASGLIKFGHDVDTHAAICAETRPEWII : 178

SmLACS2      : ALQGCFRRNITVVTIYASLGEEALCHSFNETEVTTVICGHKELKKIANISGQLDTVKRII : 205
MnLACS8      : AFQGCFRQNVTVVTVYASLGEDALIHSLNETSATTLICDSKQLKKLAAIRTSLQTIQNVI : 240
HaLACS2      : AFEGCFRQNITVVTIYASLGDDALIHSLNETKVSTLICDSKLLKKVASVSSSLETVTNVI : 224
CaLACS       : AFQGCFRQNITVVTIYASLGDDALIHSLNETQVSTLICDAKQLKKVASVSSSLKTIKNVI : 238

SmLACS2      : CMDDEFQSDASLVSLVSGSSGWTVTSFLEVEKLGRENSVDPDLPLSADIAVIMYTSGSTG : 265
MnLACS8      : YIEDDGSSKDNGL--FESLSDWTVASFSEVERLGKTSPVPANLPSKNGIAVIMYTSGSTG : 298
HaLACS2      : YFESDNTEALS------KIGDWQISSFSEVEKMGRNSPVKARLPIKKDIAVIMYTSGSTG : 278
CaLACS       : YFEDDETAIDS-----TNIDSWRMSSFSAVEKLGKNSPIQPRLPIKEDIAVIMYTSGSTG : 293

SmLACS2      : MPKGVMMTHGNILATASAVMTIVPGLGHNDVYLAYLPLAHILELAAENIMPAIGSSIGYG : 325
MnLACS8      : LPKGVMVTHGNIVATAAAVMTVIPGIDSKDVYLAYLPLAHVFELAAESVMLAAGCRIGYG : 358
HaLACS2      : LPKGVMMTHGNVVATAAAVMTVIPGIGTSDVYMAYLPLAHIFELAAETVMITAGSSIGYG : 338
CaLACS       : LPKGVMITHGNIVATSAAVMTVIPNLGSSDVYLAYLPLAHVFELAAETVMLTAGACIGYG : 353

SmLACS2      : SPLTLTDTSNKIKRGTKGDATVLMPTLLASVPAILDRVRDGVRKKIDATGGLPKKLFDLA : 385
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CaLACS       : SALTLTDTSNKVMKGTKGDATVLKPTLMAAVPAILDRVRDGVMKKVEEKAGSAKKLFHIG : 413

SmLACS2      : YSRRLSAINGSWFGAWGLERFLWDLLVFRKVRAILGGRIRFILSGGAPLSGDTQRFINIC : 445
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HaLACS2      : YQRRLLAVDGSWLGAWGLEKLLWDAIVFKKIQSVLGGKMRFMLCGGAPLAADTQRFINVC : 458
CaLACS       : FNRRLAAMEGSWFGAWGLEKQLWDIIIFKKVRAVLGGDIRFMLCGGAPLSGDTQRFINIC : 473

SmLACS2      : LGAPIGQGYGLTETCAGGTFSEYDDPSVGRVGAPLPCSVVKLVDWPEGGYLISDSPKPRG : 505
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MnLACS8      : EILVGGHSVTAGYFKNQEKTEEVYQVDENGMRWFYTGDIGRFHPDGCLEIIDRKKDIVKL : 598
HaLACS2      : EVVVGGYSVTAGYFNNEEKTKEVFKVDESGMRWFYTGDIGRFHPDGCLEIIDRKKDIVKL : 578
CaLACS       : EVVVGGCSITAGYFNNEDKTNEVYKVDERGMRWFYTGDIGRFHPDGCIEIIDRKKDIIKL : 593

SmLACS2      : QHGEYVSLGKVEAALIVSPYVENIMVHADSLYNYCVALVVASQHTLEAWATKQGIQYSDF : 625
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HaLACS2      : QHGEYISLGKVEAALASSKYVENVMLHADPFHSYCVALVVPPHQVLEQWAQSAGISYKDF : 638
CaLACS       : QHGEYISLGKVEAALLSSDYVESIMVYADPFHSYCVALVVPSRQVLEKWSQENSIQHKDF : 653

SmLACS2      : ADLCQKEETLKEVSNSLLKEAKAARLEKFEVPAKIKLLSEAWTPESGLVTAALKLKREVI : 685
MnLACS8      : HDLCEKAEAINEVQQSLSKVGKAAKLGKFELPAKIKLLADPWTPQSGLVTAALKIKREQL : 718
HaLACS2      : ADLCDKKESVSEVLQSLNKVAKDAKLDKFEIPAKIKLMPEPWTPESGLVTAALKLKREQL : 698
CaLACS       : SELCDKAESVNEIKQSISKVAKAARLEKFELPAKINLIPESWTPETGLVTAALKLKREPL : 713

SmLACS2      : RKTFSDDLSKLYSS------------------------------- : 699
MnLACS8      : KSKFKNELTKFIKAIFSRSYACKENRQALLPVALKPELGETMTWR : 763
HaLACS2      : KAKFKDDLQMLYG-------------------------------- : 711
CaLACS       : KARYKNELEKLYQ-------------------------------- : 726
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C

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RcLACS4 : MAQQRQRKYLIEVEKAKEAKDGKPSVGPVYRSLFAKDGFPPPIPGLDSCWDVFRMSVEKYP :  61
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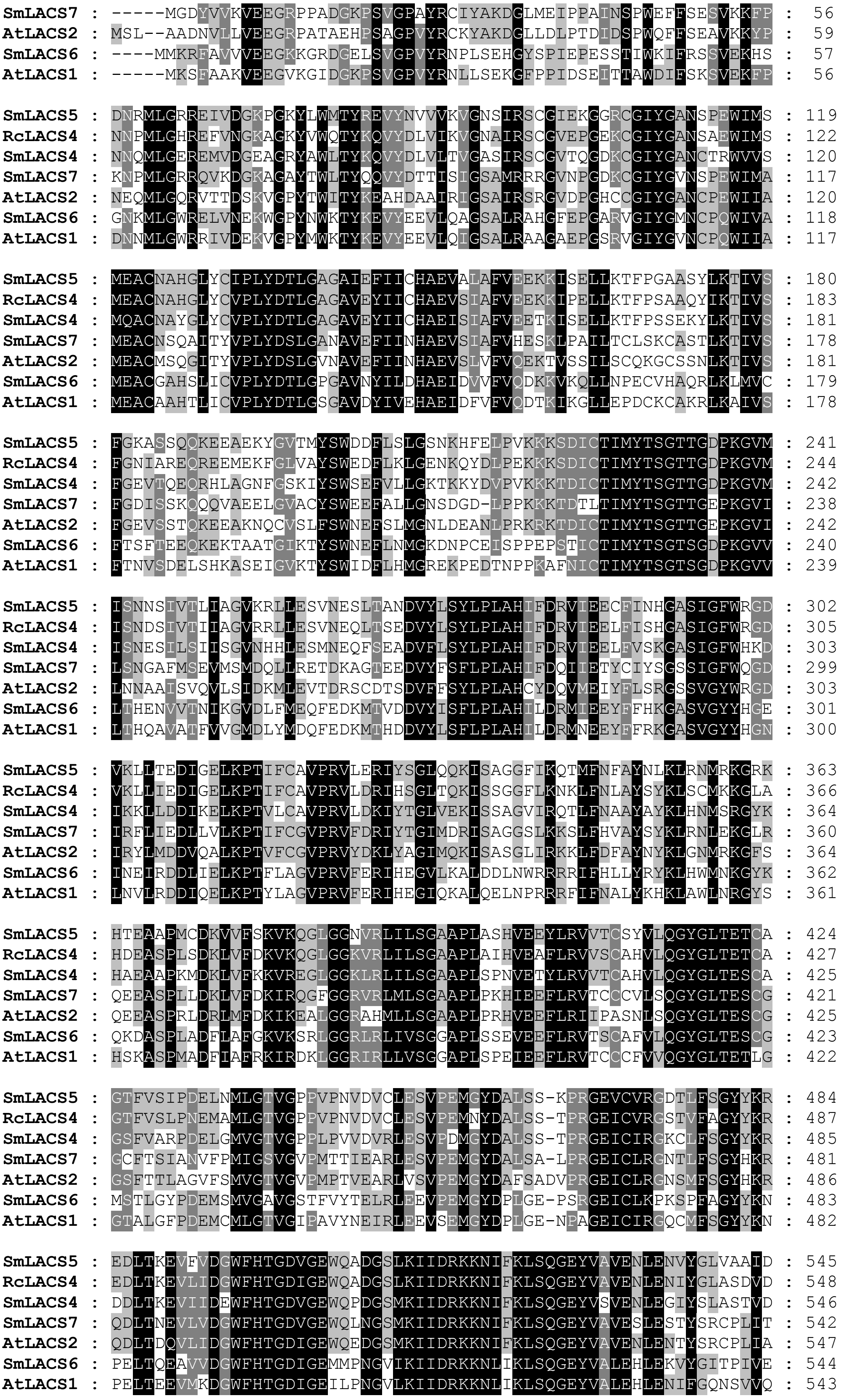

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SmLACS6 : ----MMKRFAVVVEEGKKGRDGELSVGPVYRNPLSEHGYSPIEPESSTIWKIFRSSVEKHS :  57
AtLACS1 : -----MKSFAAKVEEGVKGIDGKPSVGPVYRNLLSEKGFPPIDSEITTAWDIFSKSVEKFP :  56

SmLACS5 : DNRMLGRREIVDGKPGKYLWMTYREVYNVVVKVGNSIRSCGIEKGGRCGIYGANSPEWIMS : 119
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AtLACS2 : NEQMLGQRVTTDSKVGPYTWITYKEAHDAAIRIGSAIRSRGVDPGHCCGIYGANCPEWIIA : 120
SmLACS6 : GNKMLGWRELVNEKWGPYNWKTYKEVYEEVLQAGSALRAHGFEPGARVGIYGMNCPQWIVA : 118
AtLACS1 : DNNMLGWRRIVDEKVGPYMWKTYKEVYEEVLQIGSALRAAGAEPGSRVGIYGVNCPQWIIA : 117

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RcLACS4 : MEACNAHGLYCVPLYDTLGAGAVEYIICHAEVSIAFVEEKKIPELLKTFPSAAQYIKTIVS : 183
SmLACS4 : MQACNAYGLYCVPLYDTLGAGAVEYIICHAEISIAFVEETKISELLKTFPSSEKYLKTIVS : 181
SmLACS7 : MEACNSQAITYVPLYDSLGANAVEFIINHAEVSIAFVHESKLPAILTCLSKCASTLKTIVS : 178
AtLACS2 : MEACMSQGITYVPLYDSLGVNAVEFIINHAEVSLVFVQEKTVSSILSCQKGCSSNLKTIVS : 181
SmLACS6 : MEACGAHSLICVPLYDTLGPGAVNYILDHAEIDVVFVQDKKVKQLLNPECVHAQRLKLMVC : 179
AtLACS1 : MEACAAHTLICVPLYDTLGSGAVDYIVEHAEIDFVFVQDTKIKGLLEPDCKCAKRLKAIVS : 178

SmLACS5 : FGKASSQQKEEAEKYGVTMYSWDDFLSLGSNKHFELPVKKKSDICTIMYTSGTTGDPKGVM : 241
RcLACS4 : FGNIAREQREEMEKFGLVAYSWEDFLKLGENKQYDLPEKKKSDICTIMYTSGTTGDPKGVM : 244
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SmLACS7 : FGDISSKQQQVAEELGVACYSWEEFALLGNSDGD-LPPKKKTDTLTIMYTSGTTGEPKGVI : 238
AtLACS2 : FGEVSSTQKEEAKNQCVSLFSWNEFSLMGNLDEANLPRKRKTDICTIMYTSGTTGEPKGVI : 242
SmLACS6 : FTSFTEEQKEKTAATGIKTYSWNEFLNMGKDNPCEISPPEPSTICTIMYTSGTSGDPKGVV : 240
AtLACS1 : FTNVSDELSHKASEIGVKTYSWIDFLHMGREKPEDTNPPKAFNICTIMYTSGTSGDPKGVV : 239

SmLACS5 : ISNNSIVTLIAGVKRLLESVNESLTANDVYLSYLPLAHIFDRVIEECFINHGASIGFWRGD : 302
RcLACS4 : ISNDSIVTIIAGVRRLLESVNEQLTSEDVYLSYLPLAHIFDRVIEELFISHGASIGFWRGD : 305
SmLACS4 : ISNESILSIISGVNHHLESMNEQFSEADVFLSYLPLAHIFDRVIEELFVSKGASIGFWHKD : 303
SmLACS7 : LSNGAFMSEVMSMDQLLRETDKAGTEEDVYFSFLPLAHIFDQIIETYCIYSGSSIGFWQGD : 299
AtLACS2 : LNNAAISVQVLSIDKMLEVTDRSCDTSDVFFSYLPLAHCYDQVMEIYFLSRGSSVGYWRGD : 303
SmLACS6 : LTHENVVTNIKGVDLFMEQFEDKMTVDDVYISFLPLAHILDRMIEEYFFHKGASVGYYHGE : 301
AtLACS1 : LTHQAVATFVVGMDLYMDQFEDKMTHDDVYLSFLPLAHILDRMNEEYFFRKGASVGYYHGN : 300

SmLACS5 : VKLLTEDIGELKPTIFCAVPRVLERIYSGLQQKISAGGFIKQTMFNFAYNLKLRNMRKGRK : 363
RcLACS4 : VKLLIEDIGELKPTIFCAVPRVLDRIHSGLTQKISSGGFLKNKLFNLAYSYKLSCMKKGLA : 366
SmLACS4 : IKKLLDDIKELKPTVLCAVPRVLDKIYTGLVEKISSAGVIRQTLFNAAYAYKLHNMSRGYK : 364
SmLACS7 : IRFLIEDLLVLKPTIFCGVPRVFDRIYTGIMDRISAGGSLKKSLFHVAYSYKLRNLEKGLR : 360
AtLACS2 : IRYLMDDVQALKPTVFCGVPRVYDKLYAGIMQKISASGLIRKKLFDFAYNYKLGNMRKGFS : 364
SmLACS6 : INEIRDDLIELKPTFLAGVPRVFERIHEGVLKALDDLNWRRRRIFHLLYRYKLHWMNKGYK : 362
AtLACS1 : LNVLRDDIQELKPTYLAGVPRVFERIHEGIQKALQELNPRRRFIFNALYKHKLAWLNRGYS : 361

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SmLACS4 : HAEAAPKMDKLVFKKVREGLGGKLRLILSGAAPLSPNVETYLRVVTCAHVLQGYGLTESCA : 425
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SmLACS4 : GSFVARPDELGMVGTVGPPLPVVDVRLESVPDMGYDALSS-TPRGEICIRGKCLFSGYYKR : 485
SmLACS7 : GCFTSIANVFPMIGSVGVPMTTIEARLESVPEMGYDALSA-LPRGEICLRGNTLFSGYHKR : 481
AtLACS2 : GSFTTLAGVFSMVGTVGVPMPTVEARLVSVPEMGYDAFSADVPRGEICLRGNSMFSGYHKR : 486
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AtLACS1 : GTALGFPDEMCMLGTVGIPAVYNEIRLEEVSEMGYDPLGE-NPAGEICIRGQCMFSGYYKN : 482

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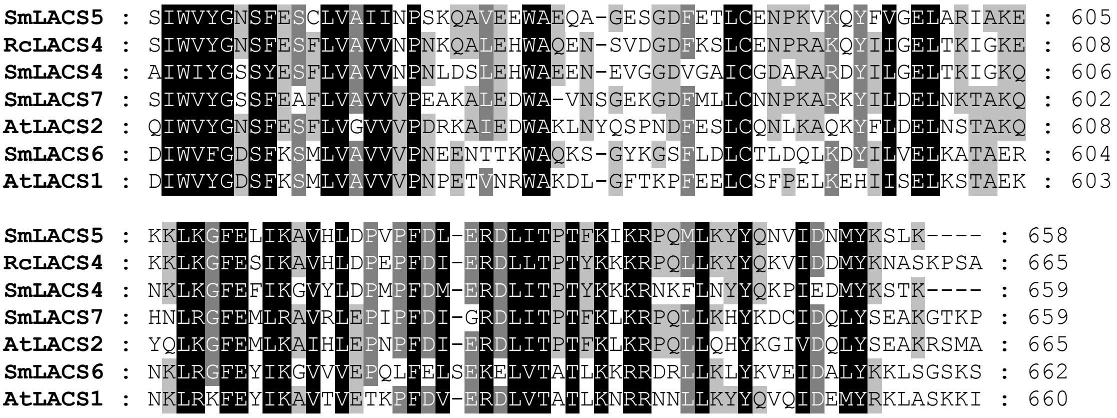

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RcLACS4 : SIWVYGNSFESFLVAVVNPNKQALEHWAQEN-SVDGDFKSLCENPRAKQYIIGELTKIGKE : 608
SmLACS4 : AIWIYGSSYESFLVAVVNPNLDSLEHWAEEN-EVGGDVGAICGDARARDYILGELTKIGKQ : 606
SmLACS7 : SIWVYGSSFEAFLVAVVVPEAKALEDWA-VNSGEKGDFMLLCNNPKARKYILDELNKTAKQ : 602
AtLACS2 : QIWVYGNSFESFLVGVVVPDRKAIEDWAKLNYQSPNDFESLCQNLKAQKYFLDELNSTAKQ : 608
SmLACS6 : DIWVFGDSFKSMLVAVVVPNEENTTKWAQKS-GYKGSFLDLCTLDQLKDYILVELKATAER : 604
AtLACS1 : DIWVYGDSFKSMLVAVVVPNPETVNRWAKDL-GFTKPFEELCSFPELKEHIISELKSTAEK : 603

SmLACS5 : KKLKGFELIKAVHLDPVPFDL-ERDLITPTFKIKRPQMLKYYQNVIDNMYKSLK---- : 658
RcLACS4 : KKLKGFESIKAVHLDPEPFDI-ERDLLTPTYKKKRPQLLKYYQKVIDDMYKNASKPSA : 665
SmLACS4 : NKLKGFEFIKGVYLDPMPFDM-ERDLITPTYKKKRNKFLNYYQKPIEDMYKSTK---- : 659
SmLACS7 : HNLRGFEMLRAVRLEPIPFDI-GRDLITPTFKLKRPQLLKHYKDCIDQLYSEAKGTKP : 659
AtLACS2 : YQLKGFEMLKAIHLEPNPFDI-ERDLITPTFKLKRPQLLQHYKGIVDQLYSEAKRSMA : 665
SmLACS6 : NKLRGFEYIKGVVVEPQLFELSEKELVTATLKKRRDRLLKLYKVEIDALYKKLSGSKS : 662
AtLACS1 : NKLRKFEYIKAVTVETKPFDV-ERDLVTATLKNRRNNLLKYYQVQIDEMYRKLASKKI : 660
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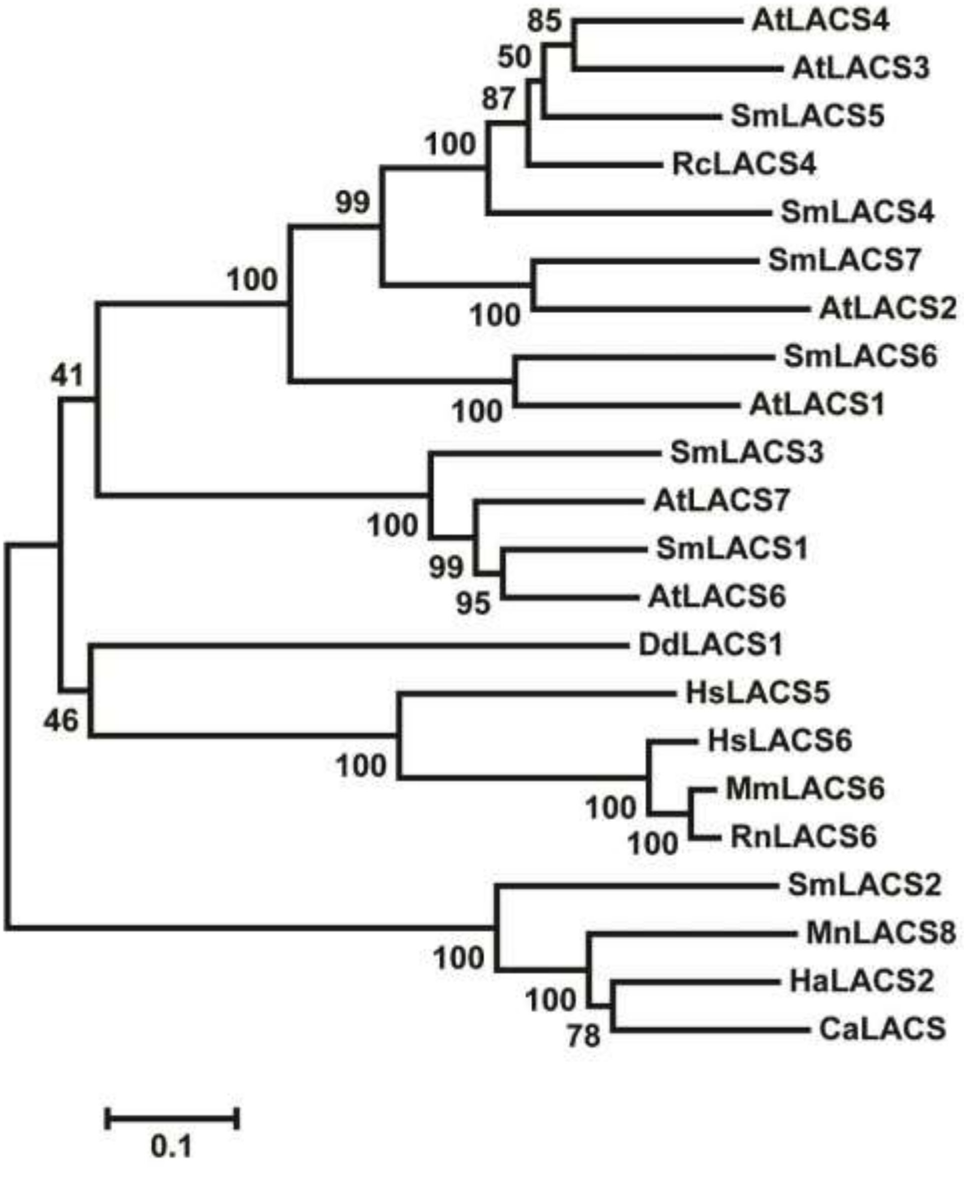
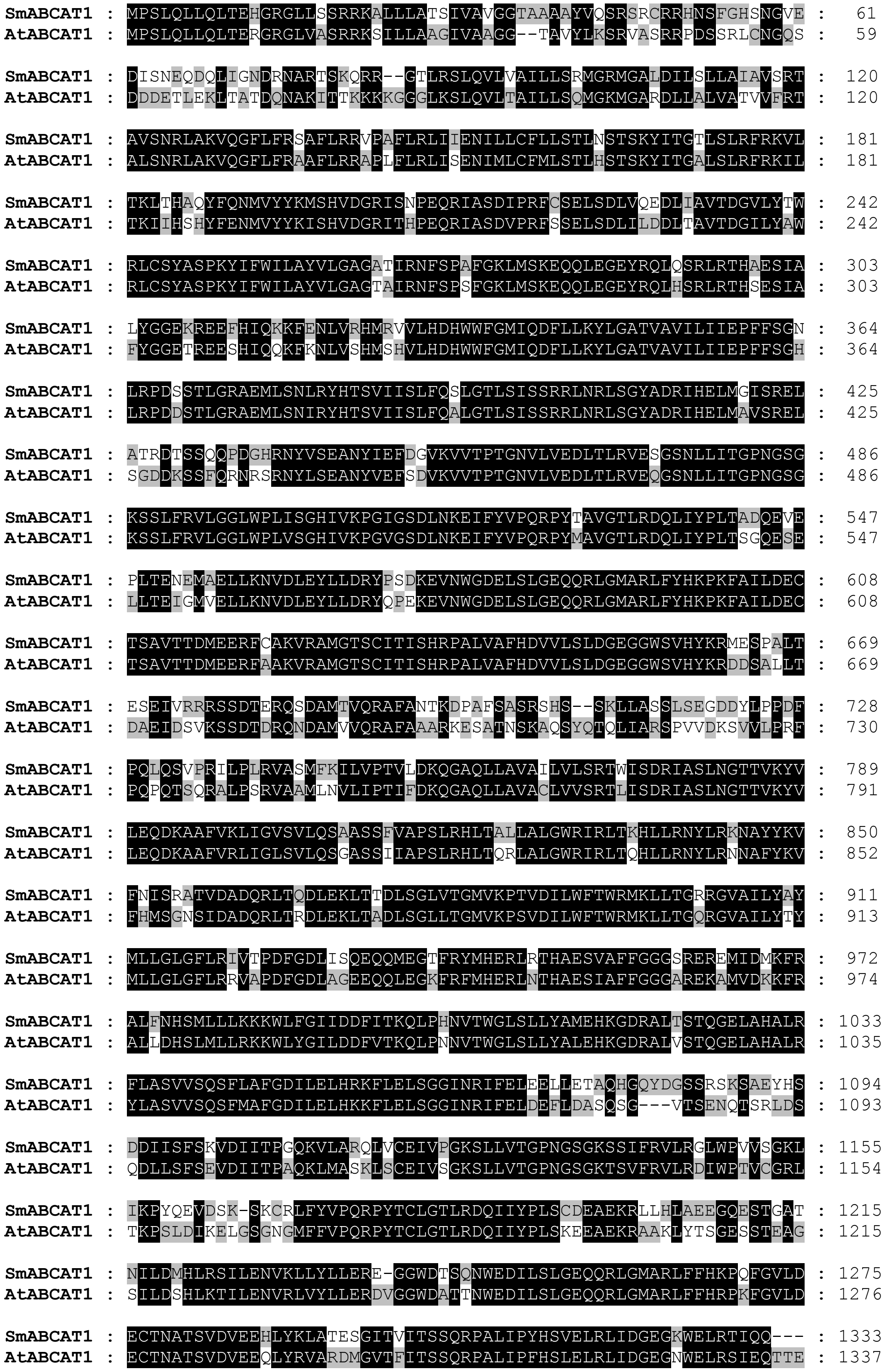


Fig S23. Multiple sequence alignment and phylogenetic tree for LACS proteins from *S. miltiorrhiza* and its homologs from various other species.

(A) Multiple sequence alignment of LACSs. The species and accession number for each LACS are shown in the parenthesis: SmLACS1 (*S. miltiorrhiza* ,KF887935); SmLACS8 (TBA);AtLACS6 (*A. thaliana* , At3g05970); AtLACS7 (At5g27600).
(B) Multiple sequence alignment of LACSs. The species and accession number for each LACS are shown in the parenthesis: SmLACS2 (KJ784439); SmLACS3 (KJ784440);MnLACS8 (*Morus notabilis* ,EXB34470); HaLACS2 (*Helianthus annuus*, ADV16379); CaLACS (*Capsicum annuum*, ACF17664).
(C) Multiple sequence alignment of LACSs. The species and accession number for each LACS are shown in the parenthesis: SmLACS4 (KJ784441); SmLACS5 (KJ784442);SmLACS6 (KJ784443); SmLACS7 (KJ784444);AtLACS1 (At2g47240); AtLACS2 (At1g49430).
(D) Phylogenetic relationships of LACSs from *S. miltiorrhiza* and various other species. LACS proteins included are SmLACS1 (KF887935); SmLACS2 (KJ784439); SmLACS3 (KJ784440); SmLACS4 (KJ784441); SmLACS5 (KJ784442);SmLACS6 (KJ784443); SmLACS7 (KJ784444);SmLACS8 (TBA); AtLACS1 (At2g47240); AtLACS2 (At1g49430); AtLACS6 (*A. thaliana* , At3g05970); AtLACS7 (At5g27600); MnLACS8 (EXB34470); HaLACS2 (ADV16379); CaLACS (ACF17664); HsLACS5(*Homo sapiens*,Q9ULC5); HsACSL6 (Q9UKU0); CpLACS1(*Cavia porcellus*, Q9JID6); RnLACS6(*Rattus norvegicus*, P33124); DdLACS1(*Dictyostelium discoideum*, Q55DR6); HaLACS2(*Helianthus annuus*, ADV16379).

A



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SmABCAT1 : MPSLQLLQLTEHGRGLLSSRRKALLLATSIVAVGGTAAAAYVQSRSRCRRHNSFGHSNGVE :   61
AtABCAT1 : MPSLQLLQLTERGRGLVASRRKSILLAAGIVAAGG--TAVYLKSRVASRRPDSSRLCNGQS :   59

SmABCAT1 : DISNEQDQLIGNDRNARTSKQRR--GTLRSLQVLVAILLSRMGRMGALDILSLLAIAVSRT :  120
AtABCAT1 : DDDETLEKLTATDQNAKITTKKKKGGGLKSLQVLTAILLSQMGKMGARDLLALVATVVFRT :  120

SmABCAT1 : AVSNRLAKVQGFLFRSAFLRRVPAFLRLIIENILLCFLLSTLNSTSKYITGTLSLRFRKVL :  181
AtABCAT1 : ALSNRLAKVQGFLFRAAFLRRAPLFLRLISENIMLCFMLSTLHSTSKYITGALSLRFRKIL :  181

SmABCAT1 : TKLTHAQYFQNMVYYKMSHVDGRISNPEQRIASDIPRFCSELSDLVQEDLIAVTDGVLYTW :  242
AtABCAT1 : TKIIHSHYFENMVYYKISHVDGRITHPEQRIASDVPRFSSELSDLILDDLTAVTDGILYAW :  242

SmABCAT1 : RLCSYASPKYIFWILAYVLGAGATIRNFSPAFGKLMSKEQQLEGEYRQLQSRLRTHAESIA :  303
AtABCAT1 : RLCSYASPKYIFWILAYVLGAGTAIRNFSPSFGKLMSKEQQLEGEYRQLHSRLRTHSESIA :  303

SmABCAT1 : LYGGEKREEFHIQKKFENLVRHMRVVLHDHWWFGMIQDFLLKYLGATVAVILIIEPFFSGN :  364
AtABCAT1 : FYGGETREESHIQQKFKNLVSHMSHVLHDHWWFGMIQDFLLKYLGATVAVILIIEPFFSGH :  364

SmABCAT1 : LRPDSSTLGRAEMLSNLRYHTSVIISLFQSLGTLSISSRRLNRLSGYADRIHELMGISREL :  425
AtABCAT1 : LRPDDSTLGRAEMLSNIRYHTSVIISLFQALGTLSISSRRLNRLSGYADRIHELMAVSREL :  425

SmABCAT1 : ATRDTSSQQPDGHRNYVSEANYIEFDGVKVVTPTGNVLVEDLTLRVESGSNLLITGPNGSG :  486
AtABCAT1 : SGDDKSSFQRNRSRNYLSEANYVEFSDVKVVTPTGNVLVEDLTLRVEQGSNLLITGPNGSG :  486

SmABCAT1 : KSSLFRVLGGLWPLISGHIVKPGIGSDLNKEIFYVPQRPYTAVGTLRDQLIYPLTADQEVE :  547
AtABCAT1 : KSSLFRVLGGLWPLVSGHIVKPGVGSDLNKEIFYVPQRPYMAVGTLRDQLIYPLTSGQESE :  547

SmABCAT1 : PLTENEMAELLKNVDLEYLLDRYPSDKEVNWGDELSLGEQQRLGMARLFYHKPKFAILDEC :  608
AtABCAT1 : LLTEIGMVELLKNVDLEYLLDRYQPEKEVNWGDELSLGEQQRLGMARLFYHKPKFAILDEC :  608

SmABCAT1 : TSAVTTDMEERFCAKVRAMGTSCITISHRPALVAFHDVVLSLDGEGGWSVHYKRMESPALT :  669
AtABCAT1 : TSAVTTDMEERFAAKVRAMGTSCITISHRPALVAFHDVVLSLDGEGGWSVHYKRDDSALLT :  669

SmABCAT1 : ESEIVRRRSSDTERQSDAMTVQRAFANTKDPAFSASRSHS--SKLLASSLSEGDDYLPPDF :  728
AtABCAT1 : DAEIDSVKSSDTDRQNDAMVVQRAFAAARKESATNSKAQSYQTQLIARSPVVDKSVVLPRF :  730

SmABCAT1 : PQLQSVPRILPLRVASMFKILVPTVLDKQGAQLLAVAILVLSRTWISDRIASLNGTTVKYV :  789
AtABCAT1 : PQPQTSQRALPSRVAAMLNVLIPTIFDKQGAQLLAVACLVVSRTLISDRIASLNGTTVKYV :  791

SmABCAT1 : LEQDKAAFVKLIGVSVLQSAASSFVAPSLRHLTALLALGWRIRLTKHLLRNYLRKNAYYKV :  850
AtABCAT1 : LEQDKAAFVRLIGLSVLQSGASSIIAPSLRHLTQRLALGWRIRLTQHLLRNYLRNNAFYKV :  852

SmABCAT1 : FNISRATVDADQRLTQDLEKLTTDLSGLVTGMVKPTVDILWFTWRMKLLTGRRGVAILYAY :  911
AtABCAT1 : FHMSGNSIDADQRLTRDLEKLTADLSGLLTGMVKPSVDILWFTWRMKLLTGQRGVAILYTY :  913

SmABCAT1 : MLLGLGFLRIVTPDFGDLISQEQQMEGTFRYMHERLRTHAESVAFFGGGSREREMIDMKFR :  972
AtABCAT1 : MLLGLGFLRRVAPDFGDLAGEEQQLEGKFRFMHERLNTHAESIAFFGGGAREKAMVDKKFR :  974

SmABCAT1 : ALFNHSMLLLKKKWLFGIIDDFITKQLPHNVTWGLSLLYAMEHKGDRALTSTQGELAHALR : 1033
AtABCAT1 : ALLDHSLMLLRKKWLYGILDDFVTKQLPNNVTWGLSLLYALEHKGDRALVSTQGELAHALR : 1035

SmABCAT1 : FLASVVSQSFLAFGDILELHRKFLELSGGINRIFELEELLETAQHGQYDGSSRSKSAEYHS : 1094
AtABCAT1 : YLASVVSQSFMAFGDILELHKKFLELSGGINRIFELDEFLDASQSG---VTSENQTSRLDS : 1093

SmABCAT1 : DDIISFSKVDIITPGQKVLARQLVCEIVPGKSLLVTGPNGSGKSSIFRVLRGLWPVVSGKL : 1155
AtABCAT1 : QDLLSFSEVDIITPAQKLMASKLSCEIVSGKSLLVTGPNGSGKTSVFRVLRDIWPTVCGRL : 1154

SmABCAT1 : IKPYQEVDSK-SKCRLFYVPQRPYTCLGTLRDQIIYPLSCDEAEKRLLHLAEEGQESTGAT : 1215
AtABCAT1 : TKPSLDIKELGSGNGMFFVPQRPYTCLGTLRDQIIYPLSKEEAEKRAAKLYTSGESSTEAG : 1215

SmABCAT1 : NILDMHLRSILENVKLLYLLERE-GGWDTSQNWEDILSLGEQQRLGMARLFFHKPQFGVLD : 1275
AtABCAT1 : SILDSHLKTILENVRLVYLLERDVGGWDATTNWEDILSLGEQQRLGMARLFFHRPKFGVLD : 1276

SmABCAT1 : ECTNATSVDVEEHLYKLATESGITVITSSQRPALIPYHSVELRLIDGEGKWELRTIQQ--- : 1333
AtABCAT1 : ECTNATSVDVEEQLYRVARDMGVTFITSSQRPALIPFHSLELRLIDGEGNWELRSIEQTTE : 1337
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B

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SmABCAT2   : MIGLEFPTYLPVQNFHGKSSFLRSGCYGYQLKHKKKLYHFTLKPNTSMLVALRRRKRNRTS :  61
MmABCD4    : ----------------------------------MAVPGPTARAGARPRLDLQLVQRFVRI :  27
AtABCAT4   : ----------------------------------MAVAGPAPGAGARPRLDLQFLQRFLQI :  27
EcABCD     : ------------------------------------------MITIPITLRMLIAKYLCLL :  19
SyABCD     : -----------MTQAQAKRFQFDRQLWHRFVETAQPYFYPVGQKQTRVFLGLILALMVVVV :  50

SmABCAT2   : FSVSVARSSLVPPEQPPGPQSNQEDPQRNPPDVQTLAKR---------FWKVAAPYWFSDD : 113
MmABCD4    : QKVFFPSWSS--------------------------------------------------- :  37
AtABCAT4   : LKVLFPSWSS--------------------------------------------------- :  37
EcABCD     : KPFWLRKNNK--------------------------------------------------- :  29
SyABCD     : ALTLFLSMGLTLWATAIFPDFFAKSGEGLVDGVQGLINSPAPWIGLVALAMAGAVFISQRQ : 111

SmABCAT2   : KATARWRLATVFALTLGTTGISVGFNFLGRDFFN----ALANKDQEQFTKQLVYYLAAFAG : 170
MmABCD4    : --QNVLMFMTLLCVTLLEQLVIYQVGLIPSQYY----GVLGNKDLDGFKALTLLAVTLIVL :  92
AtABCAT4   : --QNALMFLTLLCLTLLEQFVIYQVGLIPSQYY----GVLGNKDLEGFKTLTFLAVMLIVL :  92
EcABCD     : --TSVLLIIIILAMILGVVKIQVWLNDWNNDFFN----ALSQKETDKLWQLVLWFPALLGI :  84
SyABCD     : KLQQRWLQWLLLGVLLSLLFVVNGLNVILSFVFRFIDTALNGKDAEVFWQFLWIYGIVIVV : 172

SmABCAT2   : GIPVFVLRDYAKDTLSLRWRSWMTSFYMDRYLKNQTFYKIQ---SQSIIDNPDQRIVDDLS : 228
MmABCD4    : NSTLKSFDQFTCNLLYVSWRKDLTEHLHHLYFRARVYYTLN--VLRDDIDNPDQRISQDVE : 151
AtABCAT4   : NSTLKSFDQFTCNLLYVSWRKDLTEHLHRLYFRGRAYYTLN--VLRDDIDNPDQRISQDVE : 151
EcABCD     : FVLISVNKTWLIKLLTIRWREWLTDYYLNRWFADKNYYFTQIYGEHKNTDNPDQRIAEDIL : 145
SyABCD     : AIPIIVAYRYLRQKLGVLWRQWLTEHFLGRYFKGRSYYHLDSNSAYTLIDNPDQRITQDIQ : 233

SmABCAT2   : AFTGTALAFSLTLFNASVDLISFSNILYGIYPPLFVV---------------LLAYSLGGT : 274
MmABCD4    : RFCRQLSSVTSKLIISPFTLTYYTYQCFQSTGWLGPVS--------------IFGYFIVGT : 198
AtABCAT4   : RFCRQLSSMASKLIISPFTLVYYTYQCFQSTGWLGPVS--------------IFGYFILGT : 198
EcABCD     : LLISKTLSLSFGFIQSLSMLITFTVILWESAGTLSFTVGGTEWNIQGYMVYTVVLIVIGGT : 206
SyABCD     : SFTGVTLDFLLDILDSILTLISFTAILYTISQTLMWG---------------LIGYAVFGT : 279

SmABCAT2   : AISIFLGRDLVTLNFLQEKKEADFRYGLVRVRENAESIAFYGGEENEIQLLLQRFSSAFEN : 335
MmABCD4    : MVNKTLMGPIVTKLVQQEKLEGDFRFKHMQIRVNAEPAAFYRAGLVEHMRTDRRLQRLLQT : 259
AtABCAT4   : VVNKTLMGPIVMKLVHQEKLEGDFRFKHMQIRVNAEPAAFYRAGHVEHMRTDRRLQRLLQT : 259
EcABCD     : LFTHKVGKRIRPLNVEKQRSEATFRTNLVQHNKQAELIALSNAESLQRQELSDNFHTIKEN : 267
SyABCD     : VVAIAIGTRLIRINYEQLRLEANFRYGLVRVRDNAESIAFYRGEGLERKQVTDRLLGAIRN : 340

SmABCAT2   : LSKLLLSSRNLDFFTSGYRYLIQILPAAVVAPMYFSGKI-EFG--VINQSVS----AFNHI : 389
MmABCD4    : QRELMSRELWLYIGINTFDYLGSILSYVVIAIPIFSGVYGDLSPTELSTLVSKNAFVCIYL : 320
AtABCAT4   : QRELMSKELWLYIGINTFDYLGSILSYVVIAIPIFSGVYGDLSPAELSTLVSKNAFVCIYL : 320
EcABCD     : WHRLMNRQRWLDYWQNIYSRSLSVLPYFLLLPQFISGQI-NLG--GLMKSRQ----AFMLV : 321
SyABCD     : FNLLIIWQALISLFQLGYNYFTRLIPYIIIAPLYLAGDL-DFG--AIAQAS----LAFGMV : 394

SmABCAT2   : LGDVSLIIYQFQAISAFSAVIDRLGEFDDLLSKSETRSEADSTEEIVREFCNINDSSASNG : 450
MmABCD4    : ISCFTQLIDLSTTLSDVAGYTHRIGELQEALL--DMSRKSQDCEALGESEWDLDKTPGCPT : 379
AtABCAT4   : ISCFTQLIDLSTTLSDVAGYTHRIGQLRETLL--DMSLKSQDCEILGESEWGLDTPPGWPA : 379
EcABCD     : SNNLSWFIYKYDELAELAAVIDRLYEFHQLTEQ-RPTNKPKNCQHA--------VQ----- : 368
SyABCD     : LSALSLVTNQIQNITEFAASINRLGEFYESLN--GPSNELERPESTGFDHNVITTRIGATV : 453

SmABCAT2   : SILPGRGQELLVLENLTLLAP-SKATLIRDLSVKIFEKEHLLISGPSGSGKTSLLRAIAGL : 510
MmABCD4    : TEPSDTA---FLLDRVSILAPSSDKPLIKDLSLKICEGQSLLITGNTGTGKTSLLRVLGGL : 437
AtABCAT4   : AEPADTA---FLLERVSISAPSSDKPLIKDLSLKISEGQSLLITGNTGTGKTSLLRVLGGL : 437
EcABCD     : ------------VADASIRTP-DNKIILENLNFHVSPGKWLLLKGYSGAGKTTLLKTLSHC : 416
SyABCD     : A-----------LENVTLSPPNSSRILVRDLSIAVAPGNHLLIMGPSGSGKSSLLRAIAGL : 503

SmABCAT2   : WSFGKGTIKFYDRNAKDSAPCLSNDVASSEISIVDKMKPECNILEKRNARGVFFLPQKPYM : 571
MmABCD4    : WEGMKGSVQMLAD---------------------------------FGPHGVLFLPQKPFF : 465
AtABCAT4   : WTSTRGSVQMLTD---------------------------------FGPHGVLFLPQKPFF : 465
EcABCD     : WPWFKGDISS--------------------------------------PADSWYVSQTPLI : 439
SyABCD     : WDSGQGTIERPE------------------------------------LADLLFLPQRPYM : 528

SmABCAT2   : VLGTLRQQLLYPTWSDATTPNSDTANPNGSPPFLMLAQDMDARVEMPSTDDLIQVLEDVRL : 632
MmABCD4    : TDGTLREQVIYPLK--EIYPDSGSAD----------------------DERIVRFLELAGL : 502
AtABCAT4   : TDGTLREQVIYPLK--EVYPDSGSAD----------------------DERILRFLELAGL : 502
EcABCD     : KTGLLKEIICKALP--------LPVD----------------------DKSLSEVLHQVGL : 470
SyABCD     : ILGTLREQLIYPS-------AQSIAD----------------------DDFLLETLNKVNL : 560
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SmABCAT2      : GYILSRFS-LDSTYEWSS--VLSIGEQQRLAYARLLLSKPNLVLLDESTSALDEANEAHLY : 690
MmABCD4       : SSLVARTGGLDQQVDWNWYDVLSPGEMQRLSFARLFYLQPKYAVLDEATSALTEEAESELY : 563
AtABCAT4      : SNLVARTEGLDQQVDWNWYDVLSPGEMQRLSFARLFYLQPKYAVLDEATSALTEEVESELY : 563
EcABCD        : GKLAARIH--DHDR-WGD--ILSSGEKQRIALARLILRRPKWIFLDETTSHLEEQEAIRLL : 526
SyABCD        : PDLAERFGGLDSLENWSS--VLSLGEQQRIALARVFINQPRYAILDEATSALDVNNEAELY : 619

SmABCAT2      : QLIAASGIT--FVSVGHRRTLYEHHKNVLHISPLEPTDSGPNWRFEPLNKDSQYSLSKK : 747
MmABCD4       : RIGQQLGMT--FISVGHRPSLEKFHSWVLRLH------GGGSWELTRIKLE--------- : 606
AtABCAT4      : RIGQQLGMT--FISVGHRQSLEKFHSLVLKLC------GGGRWELMRIKVE--------- : 606
EcABCD        : RLVREKLPTSGVIMVTHQPGVWNLADDICDIS-------------AVL----------- : 561
SyABCD        : HALTDLGTT--FISVGHRPTLRNFHRQCLEVQ------AEGRWQISPINN--------- : 661
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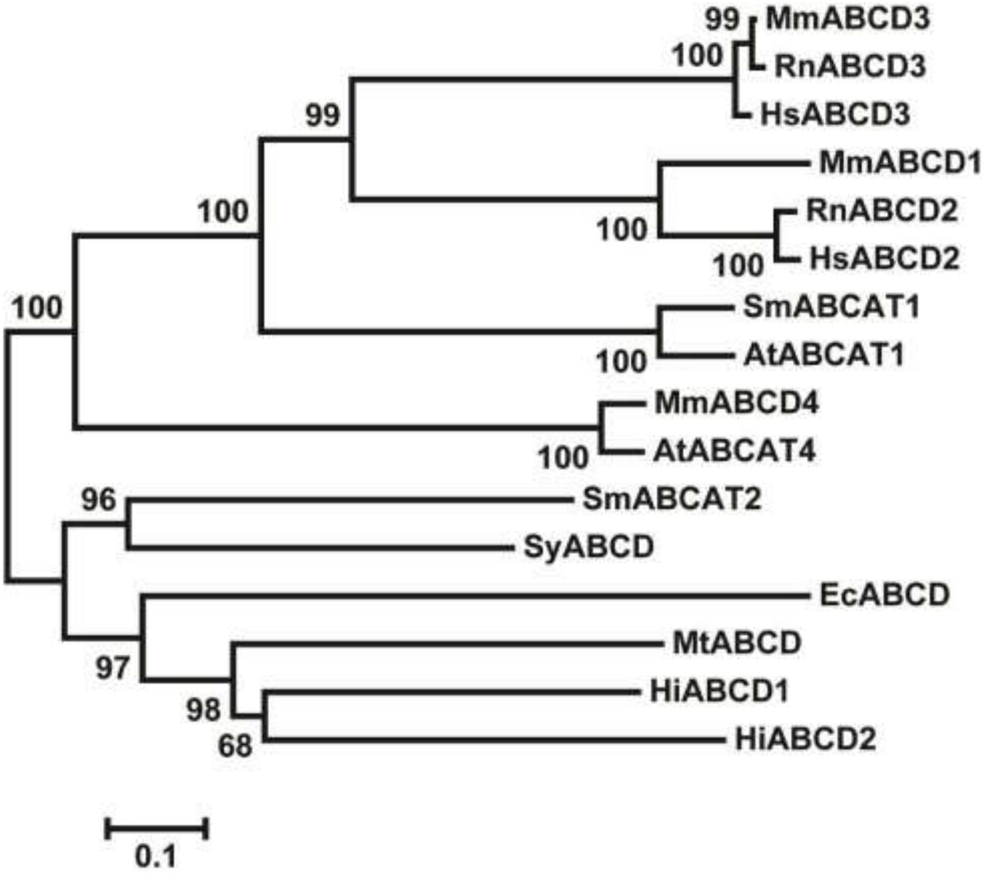
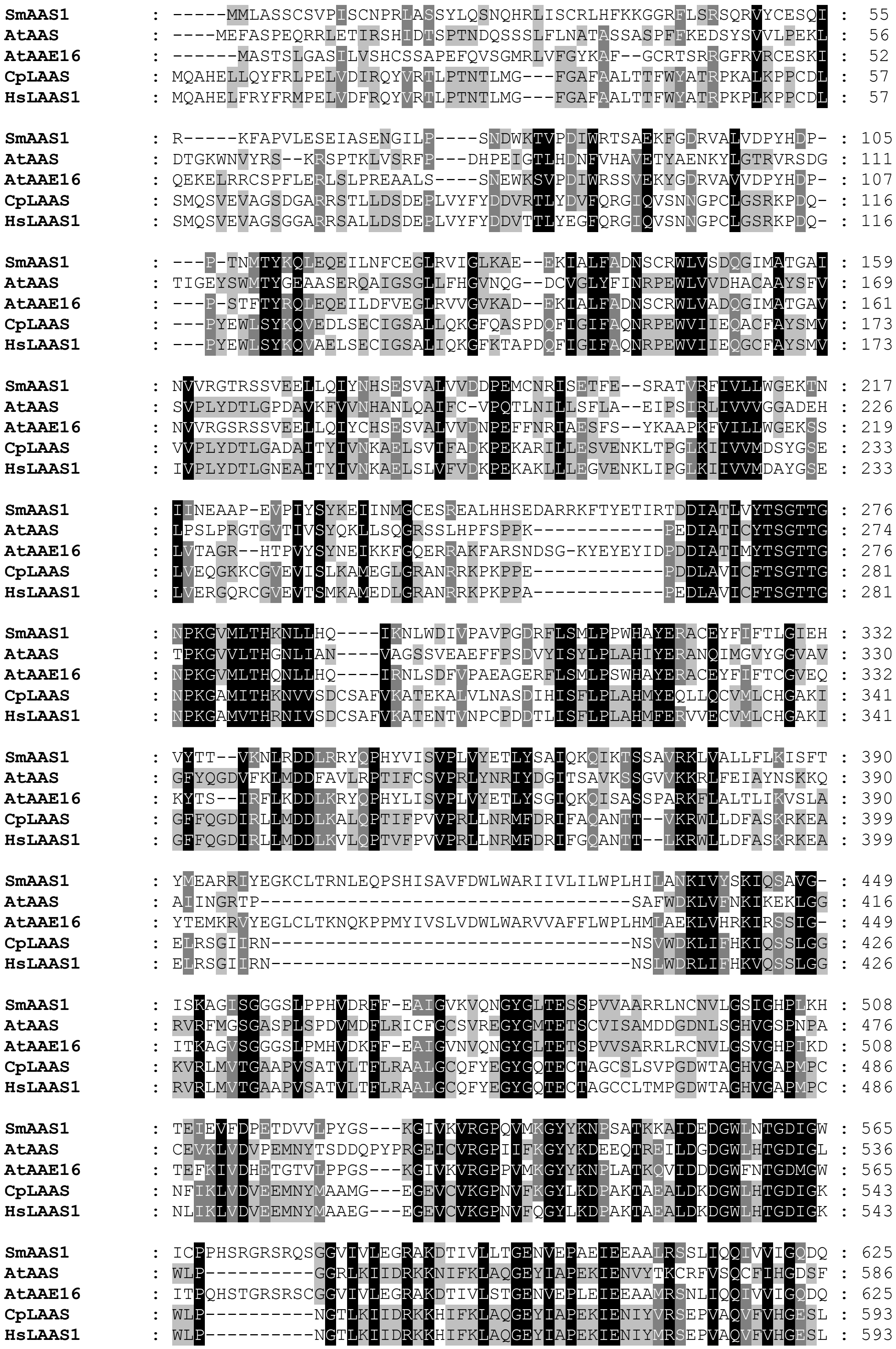


Fig S24. Multiple sequence alignment and phylogenetic tree for ABCAT proteins from *S. miltiorrhiza* and its homologs from various other species.

(A) Multiple sequence alignment of ABCATs. The species and accession number for each ABCAT are shown in the parenthesis: SmABCAT1(KF887918), SmABCAT2(KJ784418); MmABCD3 (*Mus musculus*, P55096); RnABCD2 (*Rattus norvegicus*, Q9QY44); AtABCAT1 (*Arabidopsis thaliana*, Q94FB9); HsABCD2 (*Homo sapiens*, Q9UBJ2); MmABCD1 (P48410); RnABCD3 (*Rattus norvegicus*, P16970); HsABCD3 (P28288).

(B) Phylogenetic relationships of ABCATs from *S. miltiorrhiza* and various other species. ABCAT proteins included are SmABCAT1(KF887918), SmABCAT2(KJ784418); AtABCAT1 (Q94FB9); EcABCD(*Escherichia coli*,WP_000628576.1); SyABCD(*Synechocystis sp.*,WP_010873651.1); MtABCD(*Mycobacterium tuberculosis*, WP_003899035.1); HiABCD1(*Haemophilus influenza*,WP_005668011.1); HiABCD2(WP_014326530.1); MmABCD1, (P48410);MmABCD3 (P55096); RnABCD3 (P16970); RnABCD2 (Q9QY44); HsABCD2 (Q9UBJ2); HsABCD3 (Homo sapiens, P28288).

A



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SmAAS1      : -----MMLASSCSVPISCNPRLASSYLQSNQHRLISCRLHFKKGGRFLSRSQRVYCESQI :  55
AtAAS       : ----MEFASPEQRRLETIRSHIDTSPTNDQSSSLFLNATASSASPFFKEDSYSVVLPEKL :  56
AtAAE16     : ------MASTSLGASILVSHCSSAPEFQVSGMRLVFGYKAF--GCRTSRRGFRVRCESKI :  52
CpLAAS      : MQAHELLQYFRLPELVDIRQYVRTLPTNTLMG---FGAFAALTTFWYATRPKALKPPCDL :  57
HsLAAS1     : MQAHELFRYFRMPELVDFRQYVRTLPTNTLMG---FGAFAALTTFWYATRPKPLKPPCDL :  57

SmAAS1      : R-----KFAPVLESEIASENGILP----SNDWKTVPDIWRTSAEKFGDRVALVDPYHDP- : 105
AtAAS       : DTGKWNVYRS--KRSPTKLVSRFP---DHPEIGTLHDNFVHAVETYAENKYLGTRVRSDG : 111
AtAAE16     : QEKELRRCSPFLERLSLPREAALS----SNEWKSVPDIWRSSVEKYGDRVAVVDPYHDP- : 107
CpLAAS      : SMQSVEVAGSDGARRSTLLDSDEPLVYFYDDVRTLYDVFQRGIQVSNNGPCLGSRKPDQ- : 116
HsLAAS1     : SMQSVEVAGSGGARRSALLDSDEPLVYFYDDVTTLYEGFQRGIQVSNNGPCLGSRKPDQ- : 116

SmAAS1      : ---P-TNMTYKQLEQEILNFCEGLRVIGLKAE--EKIALFADNSCRWLVSDQGIMATGAI : 159
AtAAS       : TIGEYSWMTYGEAASERQAIGSGLLFHGVNQG--DCVGLYFINRPEWLVVDHACAAYSFV : 169
AtAAE16     : ---P-STFTYRQLEQEILDFVEGLRVVGVKAD--EKIALFADNSCRWLVADQGIMATGAV : 161
CpLAAS      : ---PYEWLSYKQVEDLSECIGSALLQKGFQASPDQFIGIFAQNRPEWVIIEQACFAYSMV : 173
HsLAAS1     : ---PYEWLSYKQVAELSECIGSALIQKGFKTAPDQFIGIFAQNRPEWVIIEQGCFAYSMV : 173

SmAAS1      : NVVRGTRSSVEELLQIYNHSESVALVVDDPEMCNRISETFE--SRATVRFIVLLWGEKTN : 217
AtAAS       : SVPLYDTLGPDAVKFVVNHANLQAIFC-VPQTLNILLSFLA--EIPSIRLIVVVGGADEH : 226
AtAAE16     : NVVRGSRSSVEELLQIYCHSESVALVVDNPEFFNRIAESFS--YKAAPKFVILLWGEKSS : 219
CpLAAS      : VVPLYDTLGADAITYIVNKAELSVIFADKPEKARILLESVENKLTPGLKIIVVMDSYGSE : 233
HsLAAS1     : IVPLYDTLGNEAITYIVNKAELSLVFVDKPEKAKLLLEGVENKLIPGLKIIVVMDAYGSE : 233

SmAAS1      : IINEAAP-EVPIYSYKEIINMGCESREALHHSEDARRKFTYETIRTDDIATLVYTSGTTG : 276
AtAAS       : LPSLPRGTGVTIVSYQKLLSQGRSSLHPFSPPK------------PEDIATICYTSGTTG : 274
AtAAE16     : LVTAGR--HTPVYSYNEIKKFGQERRAKFARSNDSG-KYEYEYIDPDDIATIMYTSGTTG : 276
CpLAAS      : LVEQGKKCGVEVISLKAMEGLGRANRRKPKPPE------------PDDLAVICFTSGTTG : 281
HsLAAS1     : LVERGQRCGVEVTSMKAMEDLGRANRRKPKPPA------------PEDLAVICFTSGTTG : 281

SmAAS1      : NPKGVMLTHKNLLHQ----IKNLWDIVPAVPGDRFLSMLPPWHAYERACEYFIFTLGIEH : 332
AtAAS       : TPKGVVLTHGNLIAN----VAGSSVEAEFFPSDVYISYLPLAHIYERANQIMGVYGGVAV : 330
AtAAE16     : NPKGVMLTHQNLLHQ----IRNLSDFVPAEAGERFLSMLPSWHAYERACEYFIFTCGVEQ : 332
CpLAAS      : NPKGAMITHKNVVSDCSAFVKATEKALVLNASDIHISFLPLAHMYEQLLQCVMLCHGAKI : 341
HsLAAS1     : NPKGAMVTHRNIVSDCSAFVKATENTVNPCPDDTLISFLPLAHMFERVVECVMLCHGAKI : 341

SmAAS1      : VYTT--VKNLRDDLRRYQPHYVISVPLVYETLYSAIQKQIKTSSAVRKLVALLFLKISFT : 390
AtAAS       : GFYQGDVFKLMDDFAVLRPTIFCSVPRLYNRIYDGITSAVKSSGVVKKRLFEIAYNSKKQ : 390
AtAAE16     : KYTS--IRFLKDDLKRYQPHYLISVPLVYETLYSGIQKQISASSPARKFLALTLIKVSLA : 390
CpLAAS      : GFFQGDIRLLMDDLKALQPTIFPVVPRLLNRMFDRIFAQANTT--VKRWLLDFASKRKEA : 399
HsLAAS1     : GFFQGDIRLLMDDLKVLQPTVFPVVPRLLNRMFDRIFGQANTT--LKRWLLDFASKRKEA : 399

SmAAS1      : YMEARRIYEGKCLTRNLEQPSHISAVFDWLWARIIVLILWPLHILANKIVYSKIQSAVG- : 449
AtAAS       : AIINGRTP---------------------------------SAFWDKLVFNKIKEKLGG : 416
AtAAE16     : YTEMKRVYEGLCLTKNQKPPMYIVSLVDWLWARVVAFFLWPLHMLAEKLVHRKIRSSIG- : 449
CpLAAS      : ELRSGIIRN---------------------------------NSVWDKLIFHKIQSSLGG : 426
HsLAAS1     : ELRSGIIRN---------------------------------NSLWDRLIFHKVQSSLGG : 426

SmAAS1      : ISKAGISGGGSLPPHVDRFF-EAIGVKVQNGYGLTESSPVVAARRLNCNVLGSIGHPLKH : 508
AtAAS       : RVRFMGSGASPLSPDVMDFLRICFGCSVREGYGMTETSCVISAMDDGDNLSGHVGSPNPA : 476
AtAAE16     : ITKAGVSGGGSLPMHVDKFF-EAIGVNVQNGYGLTETSPVVSARRLRCNVLGSVGHPIKD : 508
CpLAAS      : KVRLMVTGAAPVSATVLTFLRAALGCQFYEGYGQTECTAGCSLSVPGDWTAGHVGAPMPC : 486
HsLAAS1     : RVRLMVTGAAPVSATVLTFLRAALGCQFYEGYGQTECTAGCCLTMPGDWTAGHVGAPMPC : 486

SmAAS1      : TEIEVFDPETDVVLPYGS---KGIVKVRGPQVMKGYYKNPSATKKAIDEDGWLNTGDIGW : 565
AtAAS       : CEVKLVDVPEMNYTSDDQPYPRGEICVRGPIIFKGYYKDEEQTREILDGDGWLHTGDIGL : 536
AtAAE16     : TEFKIVDHETGTVLPPGS---KGIVKVRGPPVMKGYYKNPLATKQVIDDDGWFNTGDMGW : 565
CpLAAS      : NFIKLVDVEEMNYMAAMG---EGEVCVKGPNVFKGYLKDPAKTAEALDKDGWLHTGDIGK : 543
HsLAAS1     : NLIKLVDVEEMNYMAAEG---EGEVCVKGPNVFQGYLKDPAKTAEALDKDGWLHTGDIGK : 543

SmAAS1      : ICPPHSRGRSRQSGGVIVLEGRAKDTIVLLTGENVEPAEIEEAALRSSLIQQIVVIGQDQ : 625
AtAAS       : WLP----------GGRLKIIDRKKNIFKLAQGEYIAPEKIENVYTKCRFVSQCFIHGDSF : 586
AtAAE16     : ITPQHSTGRSRSCGGVIVLEGRAKDTIVLSTGENVEPLEIEEAAMRSNLIQQIVVIGQDQ : 625
CpLAAS      : WLP----------NGTLKIIDRKKHIFKLAQGEYIAPEKIENIYVRSEPVAQVFVHGESL : 593
HsLAAS1     : WLP----------NGTLKIIDRKKHIFKLAQGEYIAPEKIENIYMRSEPVAQVFVHGESL : 593
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SmAAS1       : RRLGAIIVPNKEEILSQAKR-LAMVEPDVAELSKQK-QTNLLHEELRKWTSDCSFQ--VG : 681
AtAAS        : NSSLVAIVSVDPEVMKDWAASEGIKYEHLGQLCNDPRVRKTVLAEMDDLGREAQLRGFEF : 646
AtAAE16      : RRLGAIVIPNKEAAEGAAKQKISPVDSEVNELSKET-ITSMVYEELRKWTSQCSFQ--VG : 682
CpLAAS       : QAFLIAIVVPDAESLASWARKRGFEGS-FEELCRNKDVKKAILEDMVRIGKDSGLKSFEQ : 652
HsLAAS1      : QAFLIAIVVPDVETLCSWAQKRGFEGS-FEELCRNKDVKKAILEDMVRLGKDSGLKPFEQ : 652

SmAAS1       : P--ILVVDDPFTIDSGLMTPTMKIRRDRVVSLYQEQIDNLYKGIV--------- : 724
AtAAS        : AKAVTLVPEPFTLENGLLTPTFKIKRPQAKAYFAEAISKMYAEIAASNPIPSKL : 700
AtAAE16      : P--VLIVDEPFTIDNGLMTPTMKIRRDKVVDQYKNEIERLYK------------ : 722
CpLAAS       : VRGIALHPELFSVDNGLLTPTMKAKRPELRNYFRSQIDELYSTIKV-------- : 698
HsLAAS1      : VKGITLHPELFSIDNGLLTPTMKAKRPELRNYFRSQIDDLYSTIKV-------- : 698
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B

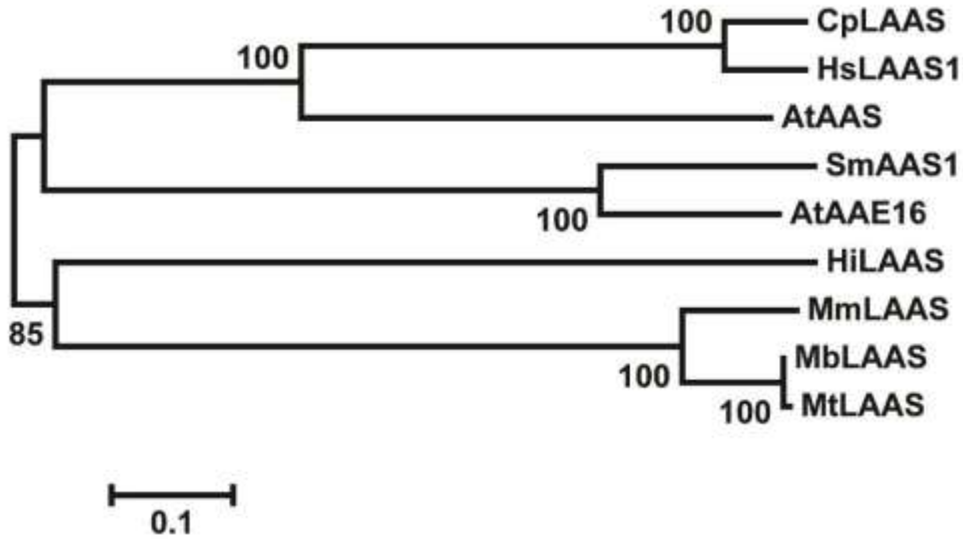
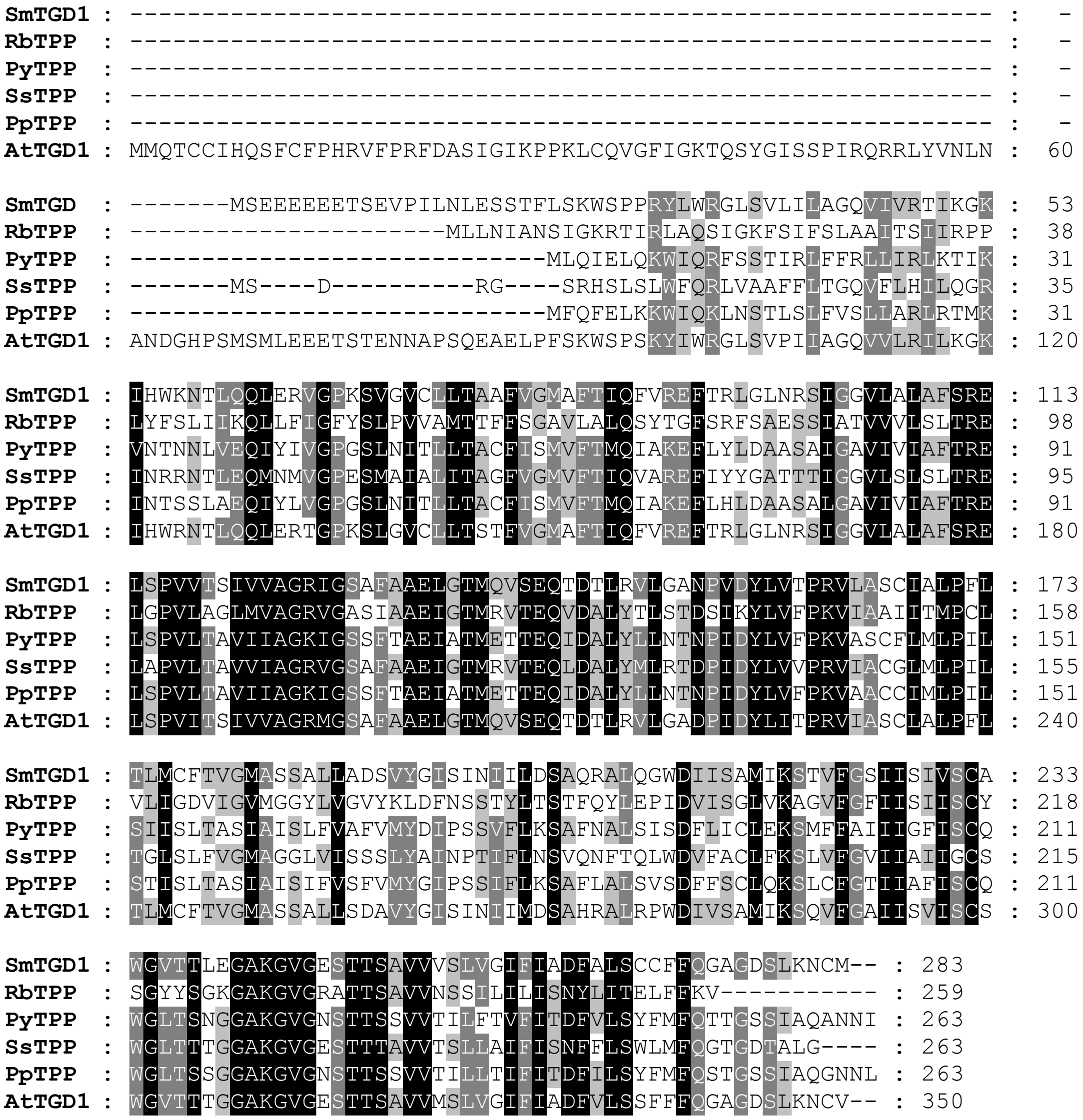


Fig S25. Multiple sequence alignment and phylogenetic tree for AAS proteins from *S. miltiorrhiza* and its homologs from various other species.

(A) Multiple sequence alignment of AASs. The species and accession number for each AAS are shown in the parenthesis: SmAAS1 (*S. miltiorrhiza,* KF887917); AtAAS1 (*A. thaliana* ,AT4G14070.1); AtAAE16 (At3g23790); CpLAAS (*Cavia porcellus* ,Q9JID6); HsLAAS1 (*Homo sapiens* ,P33121).

(B) Phylogenetic relationships of AASs from *S. miltiorrhiza* and various other species. AAS proteins included are SmAAS1 (KF887917); AtAAS1 (AT4G14070.1); AtAAE16 (At3g23790); CpLAAS (Q9JID6); HsLAAS1 (P33121);MbLAAS(*Mycobacterium bovis* , Q7TYX8); MmLAAS (*Mycobacterium marinum* , B2HGV4);MtLAAS(*Mycobacterium tuberculosis,* O53521).

A



```
SmTGD1 : ------------------------------------------------------------ :   -
RbTPP  : ------------------------------------------------------------ :   -
PyTPP  : ------------------------------------------------------------ :   -
SsTPP  : ------------------------------------------------------------ :   -
PpTPP  : ------------------------------------------------------------ :   -
AtTGD1 : MMQTCCIHQSFCFPHRVFPRFDASIGIKPPKLCQVGFIGKTQSYGISSPIRQRRLYVNLN :  60

SmTGD  : -------MSEEEEEETSEVPILNLESSTFLSKWSPPRYLWRGLSVLILAGQVIVRTIKGK :  53
RbTPP  : ----------------------MLLNIANSIGKRTIRLAQSIGKFSIFSLAAITSIIRPP :  38
PyTPP  : -----------------------------MLQIELQKWIQRFSSTIRLFFRLLIRLKTIK :  31
SsTPP  : -------MS----D----------RG----SRHSLSLWFQRLVAAFFLTGQVFLHILQGR :  35
PpTPP  : -----------------------------MFQFELKKWIQKLNSTLSLFVSLLARLRTMK :  31
AtTGD1 : ANDGHPSMSMLEEETSTENNAPSQEAELPFSKWSPSKYIWRGLSVPIIAGQVVLRILKGK : 120

SmTGD1 : IHWKNTLQQLERVGPKSVGVCLLTAAFVGMAFTIQFVREFTRLGLNRSIGGVLALAFSRE : 113
RbTPP  : LYFSLIIKQLLFIGFYSLPVVAMTTFFSGAVLALQSYTGFSRFSAESSIATVVVLSLTRE :  98
PyTPP  : VNTNNLVEQIYIVGPGSLNITLLTACFISMVFTMQIAKEFLYLDAASAIGAVIVIAFTRE :  91
SsTPP  : INRRNTLEQMNMVGPESMAIALITAGFVGMVFTIQVAREFIYYGATTTIGGVLSLSLTRE :  95
PpTPP  : INTSSLAEQIYLVGPGSLNITLLTACFISMVFTMQIAKEFLHLDAASALGAVIVIAFTRE :  91
AtTGD1 : IHWRNTLQQLERTGPKSLGVCLLTSTFVGMAFTIQFVREFTRLGLNRSIGGVLALAFSRE : 180

SmTGD1 : LSPVVTSIVVAGRIGSAFAAELGTMQVSEQTDTLRVLGANPVDYLVTPRVLASCIALPFL : 173
RbTPP  : LGPVLAGLMVAGRVGASIAAEIGTMRVTEQVDALYTLSTDSIKYLVFPKVIAAIITMPCL : 158
PyTPP  : LSPVLTAVIIAGKIGSSFTAEIATMETTEQIDALYLLNTNPIDYLVFPKVASCFLMLPIL : 151
SsTPP  : LAPVLTAVVIAGRVGSAFAAEIGTMRVTEQLDALYMLRTDPIDYLVVPRVIACGLMLPIL : 155
PpTPP  : LSPVLTAVIIAGKIGSSFTAEIATMETTEQIDALYLLNTNPIDYLVFPKVAACCIMLPIL : 151
AtTGD1 : LSPVITSIVVAGRMGSAFAAELGTMQVSEQTDTLRVLGADPIDYLITPRVIASCLALPFL : 240

SmTGD1 : TLMCFTVGMASSALLADSVYGISINIILDSAQRALQGWDIISAMIKSTVFGSIISIVSCA : 233
RbTPP  : VLIGDVIGVMGGYLVGVYKLDFNSSTYLTSTFQYLEPIDVISGLVKAGVFGFIISIISCY : 218
PyTPP  : SIISLTASIAISLFVAFVMYDIPSSVFLKSAFNALSISDFLICLEKSMFFAIIIGFISCQ : 211
SsTPP  : TGLSLFVGMAGGLVISSSLYAINPTIFLNSVQNFTQLWDVFACLFKSLVFGVIIAIIGCS : 215
PpTPP  : STISLTASIAISIFVSFVMYGIPSSIFLKSAFLALSVSDFFSCLQKSLCFGTIIAFISCQ : 211
AtTGD1 : TLMCFTVGMASSALLSDAVYGISINIIMDSAHRALRPWDIVSAMIKSQVFGAIISVISCS : 300

SmTGD1 : WGVTTLEGAKGVGESTTSAVVVSLVGIFIADFALSCCFFQGAGDSLKNCM-- : 283
RbTPP  : SGYYSGKGAKGVGRATTSAVVNSSILILISNYLITELFFKV----------- : 259
PyTPP  : WGLTSNGGAKGVGNSTTSSVVTILFTVFITDFVLSYFMFQTTGSSIAQANNI : 263
SsTPP  : WGLTTTGGAKGVGESTTTAVVTSLLAIFISNFFLSWLMFQGTGDTALG---- : 263
PpTPP  : WGLTSSGGAKGVGNSTTSSVVTILLTIFITDFILSYFMFQSTGSSIAQGNNL : 263
AtTGD1 : WGVTTTGGAKGVGESTTSAVVMSLVGIFIADFVLSSFFFQGAGDSLKNCV-- : 350
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B

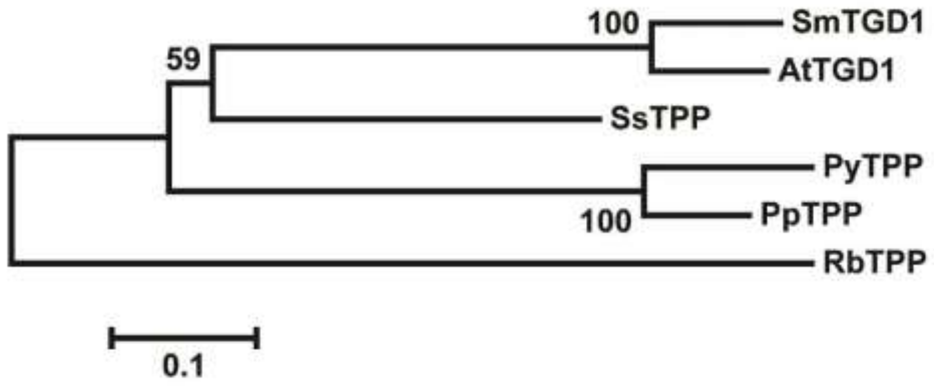
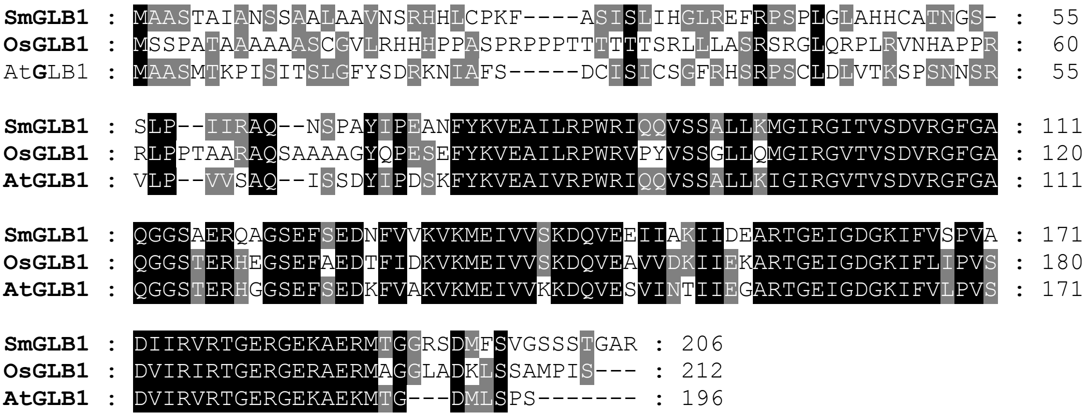


Fig S26. Multiple sequence alignment and phylogenetic tree for TGD proteins from *S. miltiorrhiza* and its homologs from various other species.

(A) Multiple sequence alignment of TGDs. The species and accession number for each TGD are shown in the parenthesis: SmTGD1 (*S. miltiorrhiza* ,KF887942); AtTGD1 (*A. thaliana* ,AT1G19800.2); RbTPP (*Rickettsia bellii*,Q1RGU3); PyTPP (*Pyropia yezoensis*, Q1XD94); SsTPP (*Synechocystis sp.*,P73009); PpTPP (*Porphyra purpurea* ,P51393).

(B) Phylogenetic relationships of TGDs from *S. miltiorrhiza* and various other species. TGD proteins included are SmTGD1 (KF887942); AtTGD1 (AT1G19800.2); RbTPP (Q1RGU3); PyTPP (Q1XD94); SsTPP (P73009); PpTPP (P51393).

A



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SmGLB1 : MAASTAIANSSAALAAVNSRHHLCPKF----ASISLIHGLREFRPSPLGLAHHCATNGS- :  55
OsGLB1 : MSSPATAAAAAASCGVLRHHHPPASPRPPPTTTTTSRLLLASRSRGLQRPLRVNHAPPR :  60
AtGLB1 : MAASMTKPISITSLGFYSDRKNIAFS-----DCISICSGFRHSRPSCLDLVTKSPSNNSR :  55

SmGLB1 : SLP--IIRAQ--NSPAYIPEANFYKVEAILRPWRIQQVSSALLKMGIRGITVSDVRGFGA : 111
OsGLB1 : RLPPTAARAQSAAAAGYQPESEFYKVEAILRPWRVPYVSSGLLQMGIRGVTVSDVRGFGA : 120
AtGLB1 : VLP--VVSAQ--ISSDYIPDSKFYKVEAIVRPWRIQQVSSALLKIGIRGVTVSDVRGFGA : 111

SmGLB1 : QGGSAERQAGSEFSEDNFVVKVKMEIVVSKDQVEEIIAKIIDEARTGEIGDGKIFVSPVA : 171
OsGLB1 : QGGSTERHEGSEFAEDTFIDKVKMEIVVSKDQVEAVVDKIIEKARTGEIGDGKIFLIPVS : 180
AtGLB1 : QGGSTERHGGSEFSEDKFVAKVKMEIVVKKDQVESVINTIIEGARTGEIGDGKIFVLPVS : 171

SmGLB1 : DIIRVRTGERGEKAERMTGGRSDMFSVGSSSTGAR : 206
OsGLB1 : DVIRIRTGERGERAERMAGGLADKLSSAMPIS--- : 212
AtGLB1 : DVIRVRTGERGEKAEKMTG---DMLSPS------- : 196
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B

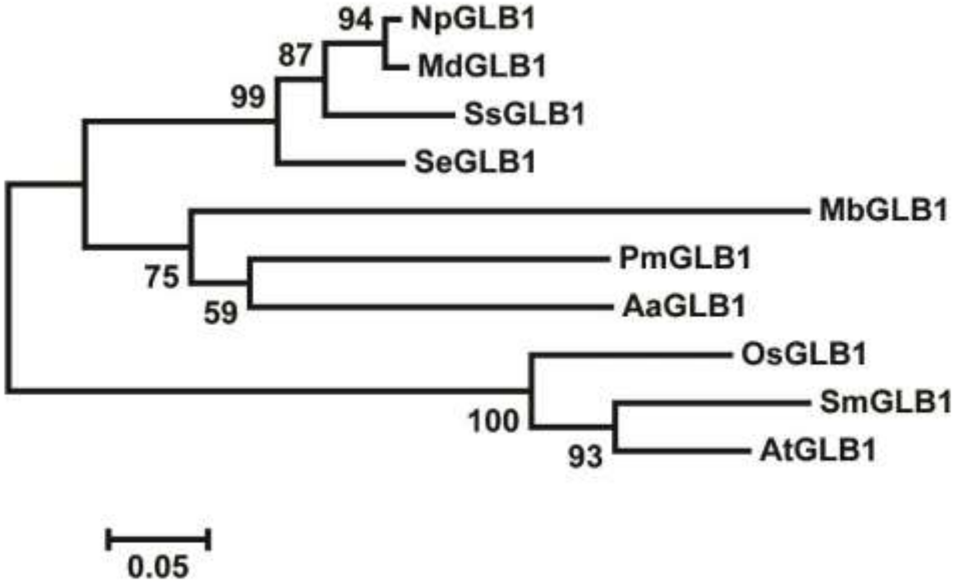

Fig S27. Multiple sequence alignment and phylogenetic tree for GLB proteins from *S. miltiorrhiza* and its homologs from various other species.

(A) Multiple sequence alignment of GLBs. The species and accession number for each GLB are shown in the parenthesis: *S. miltiorrhiza* and various other plants. GLB1s included are SmGLB1 (*S. miltiorrhiza* ,KF887941); AtGLB1 (*A. thaliana* ,AT4G01900.1); OsGLB1 (*O. sativa* ,Q6AUR2). (B) Phylogenetic relationships of GLBs from *S. miltiorrhiza* and various other species. GLB proteins included are form *S. miltiorrhiza* and various other plants. GLB1 proteins included are SmGLB1 (KF887941); AtGLB1 (AT4G01900.1); OsGLB1 (Q6AUR2);SeGLB1 (*Synechococcus elongates*, P0A3F4);MbGLB1 (*Mycobacterium bovis* ,P64250); PmGLB1 (*Pasteurella multocida sub sp.* Q9CJK1); AaGLB1(*Aquifex aeolicus*, O66513);NpGLB1 (*Nostoc punctiforme*, O30794);MdGLB1 (*Microchaete diplosiphon*, Q47894);SsGLB1 (*Synechocystis sp.* , Q55247).

A

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SmWRI1      : ------------------------------------------------------------ :   -
SmWRI2      : ------------------------------------------------------------ :   -
SmWRI4      : ------------------------------------------------------------ :   -
SmWRI5      : ------------------------------------------------------------ :   -
SmWRI9      : ------------------------------------------------------------ :   -
SmWRI10     : ------------------------------------------------------------ :   -
SmWRI12     : MKSMNDEESATTAADINNWLGFSLSP-HMKMEAN----FSQAPPTSSAAAAP---PNNFY :  52
AtAP2L4     : ------------------------------------------------------------ :   -
AtRTOE3     : ------------------------------------------------------------ :   -
AtAPETALA2  : ------------------------------------------------------------ :   -
AtANT       : MKSFCDND-DNNHSNTTNLLGFSLSSNMMKMGGRGGREAIYSSSTSSAATSSSSVPPQLV :  59
AtAP2L1     : ------------------------------------------------------------ :   -
AtWRI1      : ------------------------------------------------------------ :   -

SmWRI1      : ------------------------------------------------------------ :   -
SmWRI2      : ------------------------------------------------------------ :   -
SmWRI4      : -------------------------------------MLNLNLAIDPSSPTADRAETASD :  23
SmWRI5      : ------------------------------------------------------------ :   -
SmWRI9      : ------------------------------------------------------------ :   -
SmWRI10     : -------------------------------------MLDLNIDAVFSVDSAPSDDEVDC :  23
SmWRI12     : LANSAAMF-------AGDDFHPPLSVMPLKSDGSLCIMEALSR-SHSHAPPNSSPKLEDF : 104
AtAP2L4     : ------------------------------------------------------------ :   -
AtRTOE3     : -------------------------------------MWNLNDSPDHH---EESD----- :  15
AtAPETALA2  : -------------------------------------MWDLNDAPHQTQREEESEE---F :  20
AtANT       : VGDNTSNFGVCYGSNPNGGIYSHMSVMPLRSDGSLCLMEALNRSSHSNHHQDSSPKVEDF : 119
AtAP2L1     : ------------------------------------------------------------ :   -
AtWRI1      : ------------------------------------------------------------ :   -

SmWRI1      : ------------------------------------------------------------ :   -
SmWRI2      : ------------------------------------------------------------ :   -
SmWRI4      : RHFALSGDQMEYSGSSSSSVVNVETSSTAGDENSFSDHF-------------VGFNIWKS :  70
SmWRI5      : ------------------------------------------------------------ :   -
SmWRI9      : ------------------------------------------------------------ :   -
SmWRI10     : RKAATADSVASTTTSTTNNAAAAEVDCNSW---TMKKSV-------------STLNFSIL :  67
SmWRI12     : LGGATMAAAH-QAMGLTLDTSFYSQQQNQN---HYFSNYNFYQNEQHQIPQISEDEIPCL : 160
AtAP2L4     : ------------------------------------------------------------ :   -
AtRTOE3     : ---SRGNPVGHVSNGMSQSATW--------------------------------LPFVLP :  40
AtAPETALA2  : CYSSPSKRVGSFSNSSSSAVVIEDGSDD------------------------DELNRVRP :  56
AtANT       : FGTHHNNTSHKEAMDLSLDSLFYNTTHEPNTTTNFQEFFSFPQTRNHEEETRNYGNDPSL : 179
AtAP2L1     : ------------------------------------------------------------ :   -
AtWRI1      : ------------------------------------------------------------ :   -

SmWRI1      : -----------------------------MKRKSPSSSCSSSSSSC------CIESPSIA :  25
SmWRI2      : ---------------------------------------MGRSSK-------VAKKSSVS :  14
SmWRI4      : NG------------DCEESEKSSYGYVTK-----EFFPASGGEGR--------MQCLDLS : 105
SmWRI5      : ---------------------------------------MARSSKQKNRPLAAASAAEIS :  21
SmWRI9      : --------------------------------ASSSSEHAAKPEE-----TGGGESSEAR :  23
SmWRI10     : DK------------HVIEIEDDANNNVNSSGNELQLFPIGTSPPSPTPAMVRAKYWLNLS : 115
SmWRI12     : KTWMDHHHALQ-QHHINNNNSMAEDRSAAAMRSTEIQSLSLSMSPGSQ--SSCVTASRQI : 217
AtAP2L4     : ------------------------------MASVSSSDQGPKTEAGCSG-GGGGESSETV :  29
AtRTOE3     : --------------------------VTR-----NFFPAQSMEPG--------VRWSGFN :  61
AtAPETALA2  : N----------------------NPLVTH-----QFFPEMDSNGGGVASGFPRAHWFGVK :  89
AtANT       : THGGSFNVGVYGEFQQSLSLSMSPGSQSSCITGSHHHQQNQNQNHQSQNHQQISEALVET : 239
AtAP2L1     : --------------------------MFIAVEVSPVMEDITRQSKK------TSVENETG :  28
AtWRI1      : -----------------------------MKKRLTTSTCSSSPSSS------VSSSTTTS :  25

SmWRI1      : QPSAPESK-PKPKRVR-AKR--------NQSDNSATSAKSR-SSIYRGVTRHRWTGRYEA :  74
SmWRI2      : DDNNS-----KSRRTR--K---------------RESPHQR-SSVHRGVTRHRWTGRYEA :  51
SmWRI4      : ENHHELTEQRIISQEQQ-------QQKRQLVKKSRRGPRSR-SSQYRGVTFYRRTGRWES : 157
SmWRI5      : DNDRR-----EGKRKR--KS------------APRESPQQR-SSIHRGVTRHRWTGRFEA :  61
SmWRI9      : PPPDQLLLYRGLKKAKKERGCT---AKERISRMPPCTAGKR-SSIYRGVTRHRWTGRYEA :  79
SmWRI10     : VPEVSGGGSGVELGIYKAQLPANAPVQPPQAKKSRRGPRSR-SSQYRGVTFYRRTGRWES : 174
SmWRI12     : SPTQTTECAAMETKKRGAQKLG--QQKQTVHRKSIDTFGQR-TSQYRGVTRHRWTGRYEA : 274
AtAP2L4     : AASDQMLLYRGFKKAKKERGCT---AKERISKMPPCTAGKR-SSIYRGVTRHRWTGRYEA :  85
AtRTOE3     : SVGKSDP-SGSGRPEEP-------EISPP-IKKSRRGPRSR-SSQYRGVTFYRRTGRWES : 111
AtAPETALA2  : FCQSDLA-TGSSAGKATNVAAAVVEPAQP-LKKSRRGPRSR-SSQYRGVTFYRRTGRWES : 146
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AtANT       : SVGFETTTMAAAKKKRGQEDVVVVGQKQIVHRKSIDTFGQR-TSQYRGVTRHRWTGRYEA : 298
AtAP2L1     : DDQSATSVVLKAKRKR--RS------------QPRDAPPQR-SSVHRGVTRHRWTGRYEA :  73
AtWRI1      : SPIQSEA--PRPKRAKRAKKSS---PSGDKSHNPTSPASTRRSSIYRGVTRHRWTGRFEA :  80

SmWRI1      : HLWDKTTWNSIQNKRGRQIYLGAYDNEEDAARTYDLAALKYWGPATILNFPVEGYTKDVE : 134
SmWRI2      : HLWDKNCWNESQNKKGRQVYLGAYDDEEAAAHAYDLAALKYWGQDTVLNFPLSTYQKEFK : 111
SmWRI4      : HIWD----------CGKQVYLGGFDTAHAAARAYDRAAIKFRGLDADINFNVSDYDEDLK : 207
SmWRI5      : HLWDKDCWNESQNKKGRQVYLGAYNDEEAAARAYDLAALKYWGQDTTLNFPLPTYQKELQ : 121
SmWRI9      : HLWDKSTWNQNQNKKGKQVYLGAYDDEEAAARAYDLAALKYWGPGTLINFPVTDYARDLE : 139
SmWRI10     : HIWD----------CGKQVYLGGFDTAHAAARAYDRAAIKFRGVDADINFTIGDYDEEMK : 224
SmWRI12     : HLWDNSCKKEGQTRKGRQVYLGGYDMEDKAARAYDLAALKYWGPSTHINFGLENYHQELE : 334
AtAP2L4     : HLWDKSTWNQNQNKKGKQVYLGAYDDEEAAARAYDLAALKYWGPGTLINFPVTDYTRDLE : 145
AtRTOE3     : HIWD----------CGKQVYLGGFDTAHAAARAYDRAAIKFRGVDADINFDIEDYLDDLK : 161
AtAPETALA2  : HIWD----------CGKQVYLGGFDTAHAAARAYDRAAIKFRGVEADINFNIDDYDDDLK : 196
AtANT       : HLWDNSFKKEGHSRKGRQVYLGGYDMEEKAARAYDLAALKYWGPSTHTNFSAENYQKEIE : 358
AtAP2L1     : HLWDKNSWNETQTKKGRQVYLGAYDEEDAAARAYDLAALKYWGRDTILNFPLCNYEEDIK : 133
AtWRI1      : HLWDKSSWNSIQNKKGKQVYLGAYDSEEAAAHTYDLAALKYWGPDTILNFPAETYTKELE : 140

SmWRI1      : EMQKLSKEEYLASLR-----RRSSGFSRGVSKYRGVARHHHNGRWEARIGRVCGNKYLYL : 189
SmWRI2      : EMERQSKEEYIGSLR-----RKSSGFSRGVSKYRGVARHHHNGRWEARIGRVFGNKYLYL : 166
SmWRI4      : QMRNLTKEEFVHILR-----RQSTGFSRGSSKYRGVT-LHKCGRWEARMGQFLGKKYIYL : 261
SmWRI5      : EMEGQSKEEYISSLR-----RKSSGFSRGVSKYRGVARHHHNGRWEARIGRVFGNKYLYL : 176
SmWRI9      : EMQNVSREDYLASLR-----RKSSGFSRGISKYRPLS---S--RWDSQFGRTPGTDYNNN : 189
SmWRI10     : QMKSLTKEEFVHILR-----RQSNGFARGSSKYRGVT-LHKCGRWEARMGQFIGKKYMYL : 278
SmWRI12     : DMKNMSRQEYVAHLR-----RKSSGFSRGASIYRGVTRHHQHGRWQARIGRVAGNKDLYL : 389
AtAP2L4     : EMQNLSREEYLASLRRYPFGRKSSGFSRGIAKYRGLQ---S--RWDASASRMPGPEYFSN : 200
AtRTOE3     : QMGNLTKEEFMHVLR-----RQSTGFPRGSSKYRGVT-LHKCGRWESRLGQFLNKKYVYL : 215
AtAPETALA2  : QMTNLTKEEFVHVLR-----RQSTGFPRGSSKYRGVT-LHKCGRWEARMGQFLGKKYVYL : 250
AtANT       : DMKNMTRQEYVAHLR-----RKSSGFSRGASIYRGVTRHHQHGRWQARIGRVAGNKDLYL : 413
AtAP2L1     : EMESQSKEEYIGSLR-----RKSSGFSRGVSKYRGVAKHHHNGRWEARIGRVFGNKYLYL : 188
AtWRI1      : EMQRVTKEEYLASLR-----RQSSGFSRGVSKYRGVARHHHNGRWEARIGRVFGNKYLYL : 195

SmWRI1      : GTYSTQEEAAAAYDMA-------------AIEFRGPNAVTNFDISNYADKLKK------F : 230
SmWRI2      : GTFATQEEAATAYDMA-------------AIEYRGLNAVTNFDLSRYVKCLRP------- : 206
SmWRI4      : GLFDSEIEAARAYDKA-------------AIKCNGREAVTNFEPITYEEELSSEAPV--G : 306
SmWRI5      : GTYATQEEAAAAYDMA-------------AIKYRGNNAVTNFDLSRYINCN--------- : 214
SmWRI9      : ALY--GDEAATGSENAGVYNVERKIDLSNYIKWWGTSKSSLTDFQSKAVVDETN---PGG : 244
SmWRI10     : GLFGSEVEAARAYDKA-------------AIKSNGREAITNFELSNYDREMNFNSGN--G : 323
SmWRI12     : GTFSTQEEAAEAYDIA-------------AIKFRGVNAVTNFDISRYDVEK--------I : 428
AtAP2L4     : IHYGAGDDRGTEGDFLGSFCLERKIDLTGYIKWWGANKNRQPESSSKASEDAN------- : 253
AtRTOE3     : GLFDTEIEAARAYDKA-------------AIKCNGKDAVTNFDPKVYEEEEDLSS----- : 257
AtAPETALA2  : GLFDTEVEAARAYDKA-------------AIKCNGKDAVTNFDPSIYDEELNAESS---G : 294
AtANT       : GTFGTQEEAAEAYDVA-------------AIKFRGTNAVTNFDITRYDVDR--------I : 452
AtAP2L1     : GTYATQEEAAIAYDIA-------------AIEYRGLNAVTNFDISRYLKLP--------- : 226
AtWRI1      : GTYNTQEEAAAAYDMA-------------AIEYRGANAVTNFDISNYIDRLKKKGVFPFP : 242

SmWRI1      : IPEVQVEE---VHVKQETNS----------------TPPDEVQAD---EDPHPVAET--- : 265
SmWRI2      : HPDNPNNP--HPISNGNVESN------------SMQIPNQELGEL---DHHRPIETT--- : 246
SmWRI4      : AGDQHNLDLNLSIAPPEKSQ-----------WQIHNMEMESFHINYGSNNLPESELKGSA : 355
SmWRI5      : MDDNS------PIAR---ES-----------------PTAAEAEA---AASPP------- : 238
SmWRI9      : SDDVASELKALERSIQPTEP--------------YEMPRLGVSP----ERLNHKKIS--- : 283
SmWRI10     : G-NGSSLDLNLGISLSSDGPQGNDTTRNPHFPIQPSEFPDGKRLKVEPISAPQELMQKYP : 382
SmWRI12     : MASNTLPTGEVARRTKEGRP----------------AAEASVEEC---HASSQRGEA--- : 466
AtAP2L4     : VEDAGTELKTLEHTSHATEP--------------YKAPNLGVLCG---TQRKEKEISSPS : 296
AtRTOE3     : --ETTRNGHNLGLSLGESS-------------------SEEFRLKSDIASIRSRIRDEER : 296
AtAPETALA2  : N-PTTPQDHNLDLSLGNSAN--------------SKHKSQDMRLRMNQQQQDSLHSNEVL : 339
AtANT       : MSSNTLLSGELARRNNN----------------------SIVVR---NTEDQT------ : 480
AtAP2L1     : VPENP-----IDTANNLLES----------------PHSDLSPF---IKPNHES----- : 256
AtWRI1      : VNQANHQEGILVEAKQEVETRE-----------AKEEPREEVKQQYVEEPPQEEEEK--- : 288

SmWRI1      : ---SSPKPEPKDSN---------------ESEGMVTMEPIEEHG-HPWDLCLDTLFNIL- : 305
SmWRI2      : ---TLPSDHGGAAT---------------------------PSS--ALGLLLQSS----- : 269
SmWRI4      : SASAAAQLPHEPGNI------------------------------CQYPLMWRGADSCF : 384
SmWRI5      : ----LPIGSGGE---------------------------------ALGLLLQSS----- : 255
SmWRI9      : ---AMSTLLKSAAYKS------------LQERITKKQG--KDENDENENKSNIDK----- : 321
SmWRI10     : PMWAGIYAGFAPNSK------------------------------ELATRMSG------ : 405
SmWRI12     : ---CSSAQVEHVSNGCDW--K--M----VLHNNEAPAPAPGHQGVGSLDVKTLNLGNY-- : 513
AtAP2L4     : SSSALSILSQSPAFKS------------LEEKVLKIQESCNNENDENANRNIINME---- : 340
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AtRTOE3      : LLGSDLSLAMMTTT---------------------------------------------- : 310
AtAPETALA2   : GLGQTGMLNHTPNSN-------------------------------HQFPGSSN------ : 362
AtANT        : ---ALNAVVEGGSN---------------------------------------------- : 491
AtAP2L1      : ---DLSQSQSSSED---------------------------NDD--RKTKLLKSSP---- : 280
AtWRI1       : ---EEEKAEQQEAEIVGYSEEAAVVNCCIDSSTIMEMDRCGDNNELAWNFCMMDTGFSP- : 344

SmWRI1       : --PIPDMPLGKAS-----EVFDYKGFDDDIECIFDE------PLDD-NEILQYGGQIDAA : 351
SmWRI2       : ---KFKEMLKQTTA-F--NEPPRSSFPDDIQTSFE---------------IQDSS-SVAE : 307
SmWRI4       : RPVYKGTTIGKVV-----EVDPSANWTRDHYQPSPLFS------------TAASSGFATS : 427
SmWRI5       : ---KFKEMMEPN--------PPRSSFPDDIQTSFD---------------FQDSS-TYAD : 288
SmWRI9       : --IELGKTVEKSCHDG-ASERRDVAYGINGGLPIHR--YQLAPLLS-APLLTNYNSIDPL : 375
SmWRI10      : ----EAVPLPGYS-----SNWQWKMPSHGMVTPVPVMAS-----------SAASSGFSPA : 445
SmWRI12      : --QHPTFSVGLHDLMGLDSSQSQRVVDGSAATMAPHFSNASSLVTSLSSSREASPDRYGG : 571
AtAP2L4      : --KNNGKAIEKPVVS----HG--VALGGAAALSLQKSMYPLTSLLT-APLLTNYNTLDPL : 391
AtRTOE3      : -------------------VRSEKQQSDGGG--NRVVG------------MAASSGFSPQ : 337
AtAPETALA2   : ----IGSGGGFSL-----FPAAENHRFDGRASTNQVLTN-----------AAASSGFSPH : 402
AtANT        : --------------K--EVSTPERLLSFPAIFALPQVN------------QKMFGSNMGG : 523
AtAP2L1      : --LVAEEVIGPSTPPE--IAPPRRSFPEDIQTYFG---------------CQNSGKLTAE : 321
AtWRI1       : --FLTDQNLANENPIEYPELFNELAFEDNIDFMFDD------GKHE-CLNLENLDCCVVG : 395

SmWRI1       : DALVAQDLKGRDASASTSPSSSPLSSTTSACSNI----------- : 385
SmWRI2       : EHGIVFG-------EYDSFSSPMFECELQA--------------- : 330
SmWRI4       : ------SAA-----IHHQLPFTTAPPHHYLPPVATLNNRSNFYWT : 461
SmWRI5       : ENDIIFS-------DYDFLS--MFQCGLDE--------------- : 309
SmWRI9       : TDPLLWSSLVPVLPTGSSRMNEVTKNESS-SGYTFFQQGE----- : 414
SmWRI10      : --------------TSPYFSSVVPLTNRAQFPATAFHSLQ----- : 471
SmWRI12      : PNKFMSPSSNVGAWIPTAQLRPVPLTTAHLPVFAAWNDA------ : 610
AtAP2L4      : ADPILWT---PFLPSGSSLTSEVTKTETSCSTYSYLPQEK----- : 428
AtRTOE3      : --------------PSPYR---IPRTFHFSRP------------- : 352
AtAPETALA2   : HHNQIFNST-----STPHQN--WLQTNGFQPPLMRPS-------- : 432
AtANT        : N---MSPWTSN----PNAELKTVALTLPQMPVFAAWADS------ : 555
AtAP2L1      : EDDVIFG-------DLDSFLTPDFYSELNDC-------------- : 345
AtWRI1       : RESPPSSSSPLSCLSTDSASSTTTTTTSVSCNYLV---------- : 430
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B

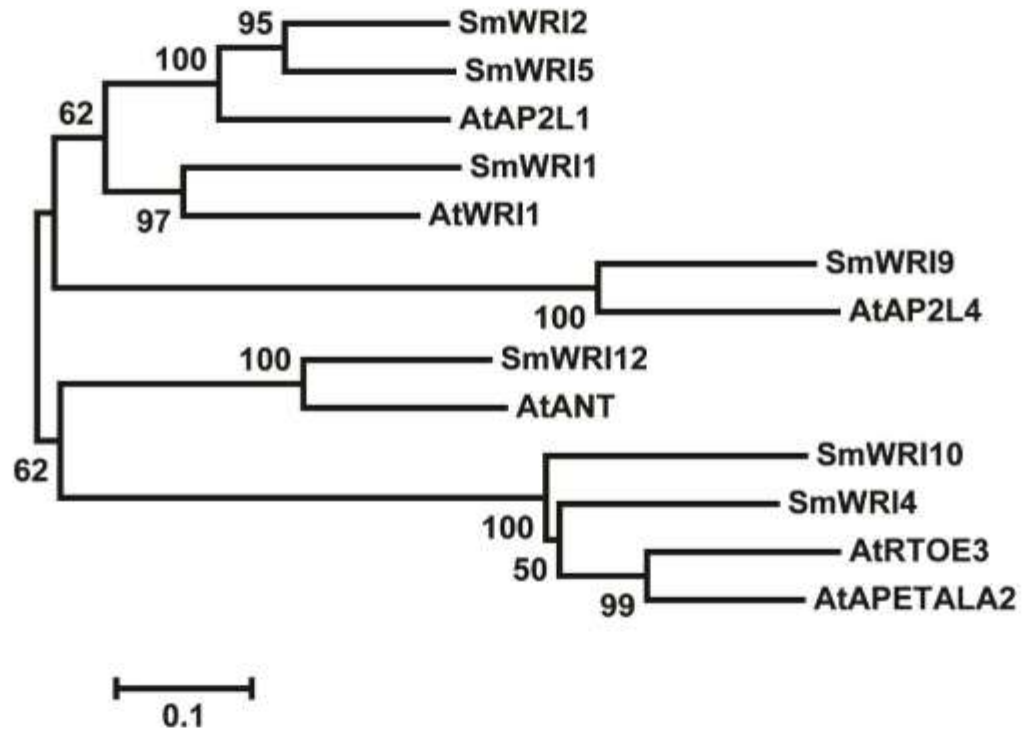

Fig S28. Multiple sequence alignment and phylogenetic tree for WRI proteins from *S. miltiorrhiza* and its homologs from various other species. (Some SmWRIs are partial and not shown in this Fig.)

(A) Multiple sequence alignment of WRIs. The species and accession number for each WRI are shown in the parenthesis: SmWRI1 (*S. miltiorrhiza*, KF887944); SmWRI2 (KJ784453);SmWRI4 (KJ784455); SmWRI5 (KJ784456); SmWRI9 (KJ784460); SmWRI10 (KJ784461); SmWRI12 (KJ784463); *A. thaliana* AtWRI (AT3G54320.1); AtAP2L4 (At2g41710); AtRTOE3 (At5g67180); AtAPETALA2 (At4g36920); AtANT (At4g37750); AtAP2L1 (At1g16060).

(B) Phylogenetic relationships of WRIs from *S. miltiorrhiza* and various other species. WRI proteins included are SmWRI1 (KF887944); SmWRI2 (KJ784453);SmWRI4 (KJ784455); SmWRI5 (KJ784456); SmWRI9 (KJ784460); SmWRI10 (KJ784461); SmWRI12 (KJ784463); AtWRI (AT3G54320.1); AtAP2L4 (At2g41710); AtRTOE3 (At5g67180); AtAPETALA2 (At4g36920); AtANT (At4g37750); AtAP2L1 (At1g16060).