Supplemental data for: Jounal of Experimental Botany

Genome-wide identification and characterization of novel genes involved in terpenoid biosynthesis in *Salvia miltiorrhiza*

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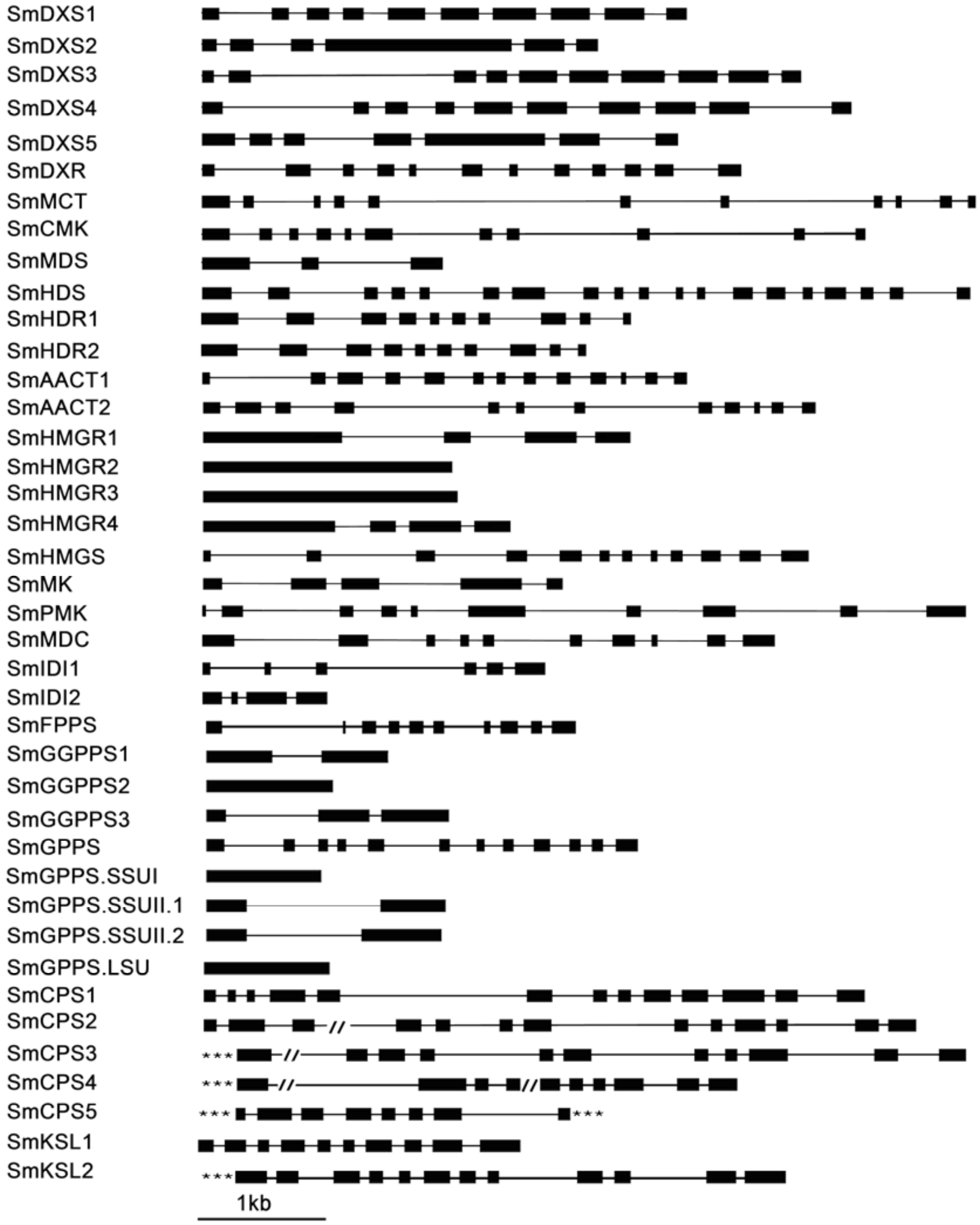
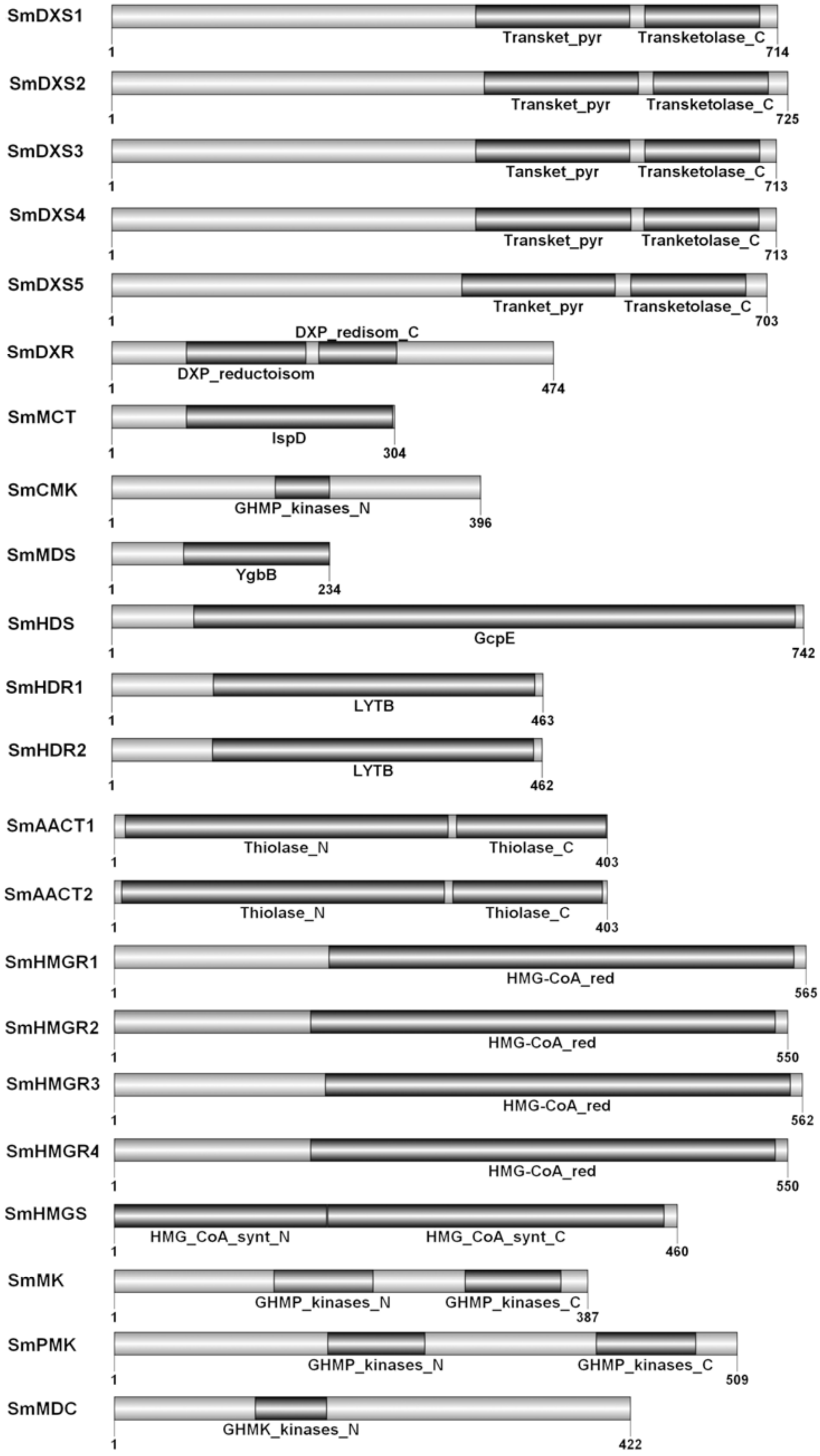


Figure S1. Exon/intron Structures of forty terpenoid biosynthesis-related genes. Heavy black lines represent exons. Thin black lines represent introns. Unknown sequences in the 5' or 3' regions of *SmCPS3*, *SmCPS4*, *SmCPS5* and *SmKSL2* are indicated by ‘***’, whereas unknown sequences in introns are indicated by ‘//’.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Transket_pyr
Transketolase_C
1
714
SmDXS2
Transket_pyr
Transketolase_C
1
725
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Tansket_pyr
Transketolase_C
1
713
SmDXS4
Transket_pyr
Tranketolase_C
1
713
SmDXS5
Tranket_pyr
Transketolase_C
1
703
DXP_redisom_C
SmDXR
DXP_reductoisom
1
474
SmMCT
IspD
1
304
SmCMK
GHMP_kinases_N
1
396
SmMDS
YgbB
1
234
SmHDS
GcpE
1
742
SmHDR1
LYTB
1
463
SmHDR2
LYTB
1
462
SmAACT1
Thiolase_N
Thiolase_C
1
403
SmAACT2
Thiolase_N
Thiolase_C
1
403
SmHMGR1
HMG-CoA_red
1
565
SmHMGR2
HMG-CoA_red
1
550
SmHMGR3
HMG-CoA_red
1
562
SmHMGR4
HMG-CoA_red
1
550
SmHMGS
HMG_CoA_synt_N
HMG_CoA_synt_C
1
460
SmMK
GHMP_kinases_N
GHMP_kinases_C
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1
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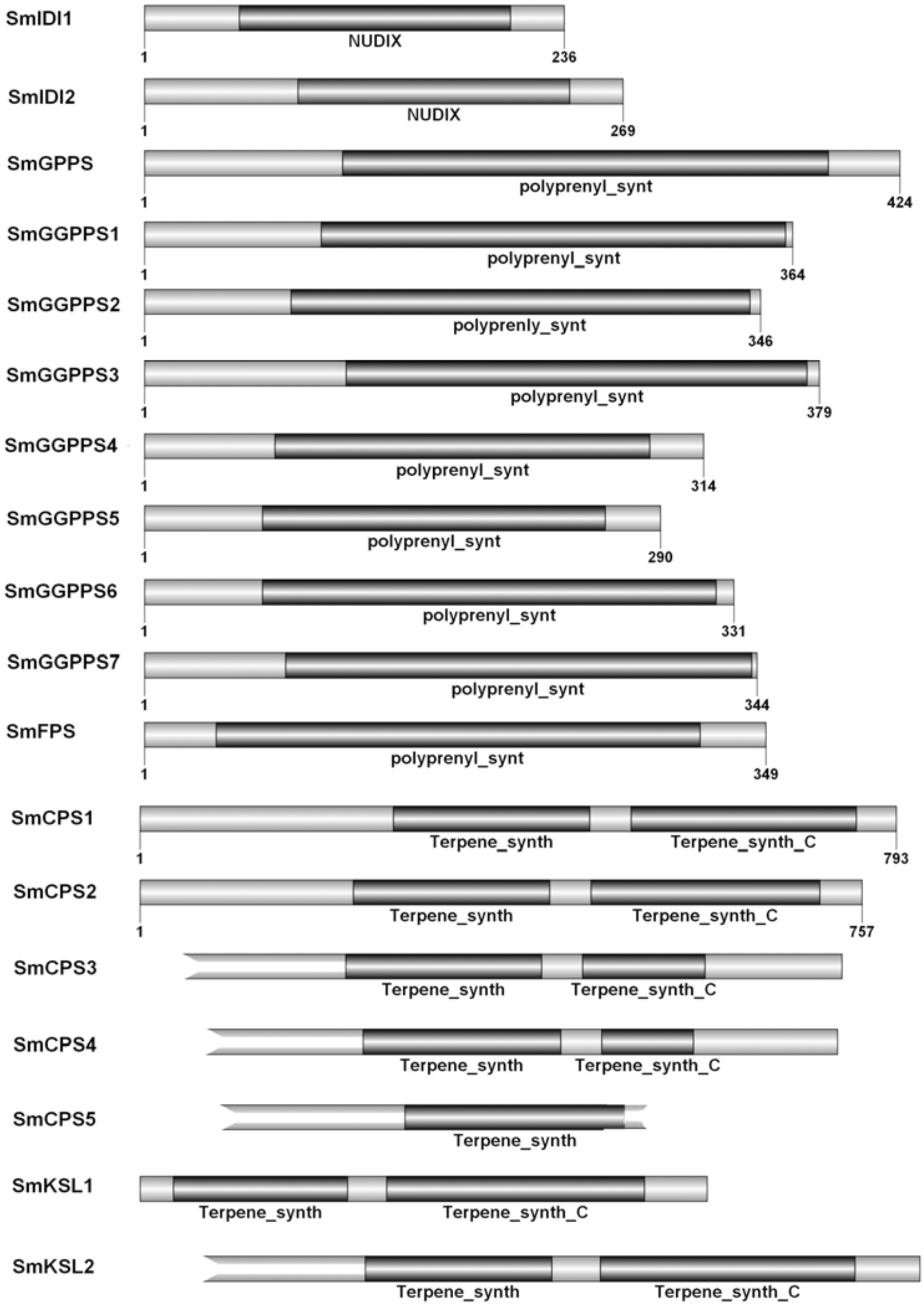
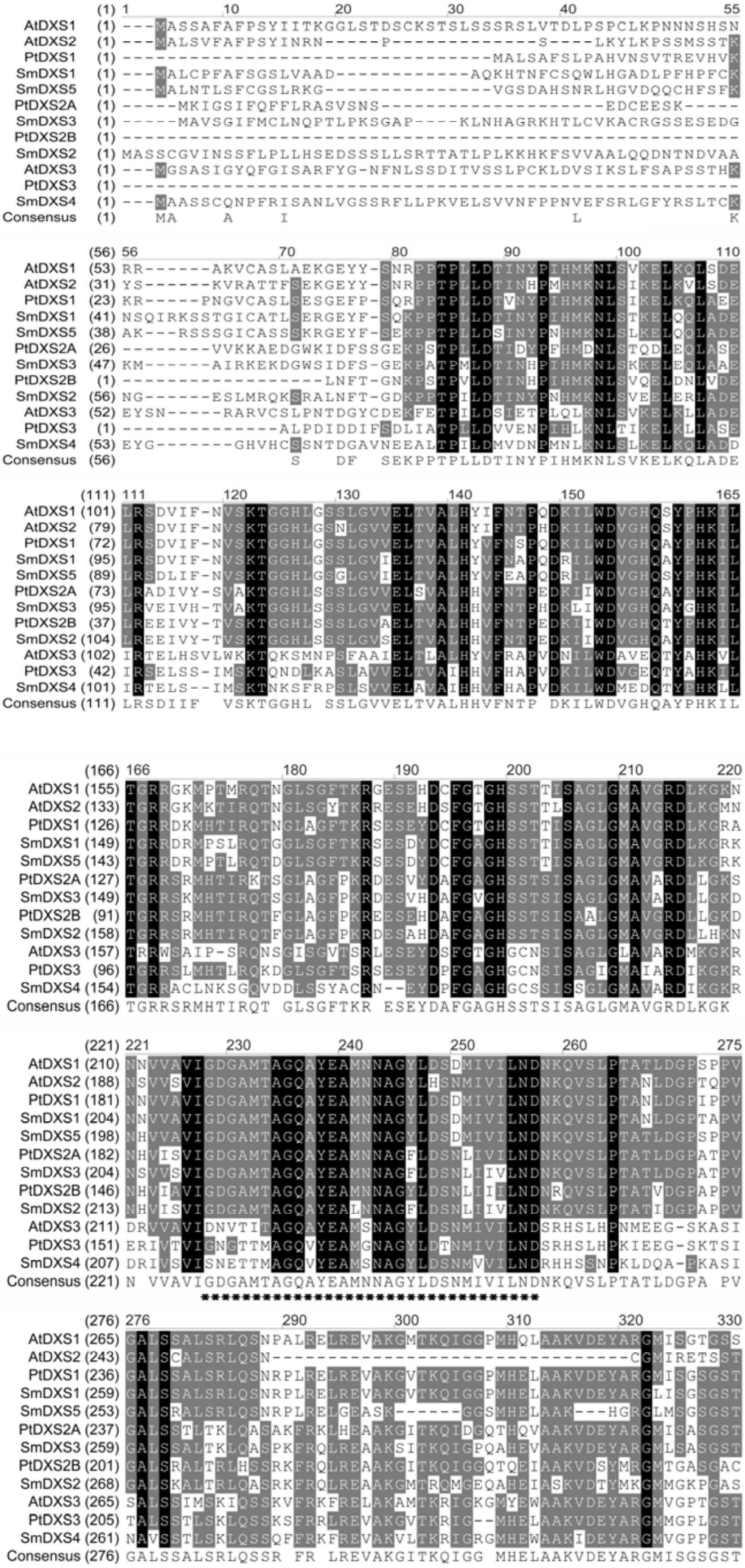


Figure S2. Conserved domains (black boxes) of enzymes involved in terpenoid biosynthesis in *S. miltiorrhiza*. Conserved domains were predicated by searching Pfam HMMs. Names of conserved domains are shown below the black boxes.


(1) 1 10 20 30 40 55
AtDXS1 (1) ---MASSAFAFPSYIITKGGLSTDSCKSTSLSSSRSLVTDLPSPCLKPNNNSHSN
AtDXS2 (1) ---MALSVFAFPSYINRN-----P-------------S----LKYLKPSSMSSTK
PtDXS1 (1) ----------------------------------MALSAFSLPAHVNSVTREVHVK
SmDXS1 (1) ---MALCPFAFSGSLVAAD------------AQKHTNFCSQWLHGADLPFHPFCK
SmDXS5 (1) ---MALNTLSFCGSLRKG---------------VGSDAHSNRLHGVDQQCHFSFK
PtDXS2A (1) -----MKIGSIFQFFLRASVSNS--------------------EDCEESK-----
SmDXS3 (1) -----MAVSGIFMCLNQPTLPKSGAP----KLNHAGRKHTLCVKACRGSSESEDG
PtDXS2B (1) ---
SmDXS2 (1) MASSCGVINSSFLPLLHSEDSSSLLSRTTATLPLKKHKFSVVAALQQDNTNDVAA
AtDXS3 (1) ---MGSASIGYQFGISARFYG-NFNLSSDITVSSLPCKLDVSIKSLFSAPSSTHK
PtDXS3 (1) ---
SmDXS4 (1) ---MAASSCQNPFRISANLVGSSRFLLPKVELSVVNFPPNVEFSRLGFYRSLTCK
Consensus (1) MA A I L K
(56) 56 70 80 90 100 110
AtDXS1 (53) RR------AKVCASLAEKGEYY-SNRPPTPLLDTINYPIHMKNLSVKELKQLSDE
AtDXS2 (31) YS------KVRATTFSEKGEYY-SNRPPTPLLDTINHPMHMKNLSIKELKVLSDE
PtDXS1 (23) KR-----PNGVCASLSESGEFP-SQRPPTPLLDTVNYPIHMKNLSIKELKQLAEE
SmDXS1 (41) NSQIRKSSTGICATLSERGEYF-SQKPPTPLLDTINYPIHMKNLSTKELQQLADE
SmDXS5 (38) AK---RSSSGICASSSKRGEYF-SEKPPTPLLDSINYPNHMKNLSLKELQQLADE
PtDXS2A (26) --------VVKKAEDGWKIDFSSGEKPSTPLLDTIDYPFHMDNLSTQDLEQLASE
SmDXS3 (47) KM------AIRKEKDGWSIDFS-GEKPATPMLDTINHPIHMKNLSKKELEQLAAE
PtDXS2B (1) -------------------LNFT-GNKPSTPVLDTINHPIHMKNLSVQELDNLVDE
SmDXS2 (56) NG------ESLMRQKSRALNFT-GDKPPTPILDTINYPNHMKNLSVEELERLADE
AtDXS3 (52) EYSN-----RARVCSLPNTDGYCDEKFETPILDSIETPLQLKNLSVKELKLLADE
PtDXS3 (1) ---------------ALPDIDDIFSDLIATPLLDVVENPIHLKNLTIKELKLLASE
SmDXS4 (53) EYG-------GHVHCSSNTDGAVNEEALTPILDMVDNPMNLKNLSLKELKQLADD
Consensus (56) S DF SEKPPTPLLDTINYPIHMKNLSVKELKQLADE
(111) 111 120 130 140 150 165
AtDXS1 (101) LRSDVIF-NVSKTGGHLGSSLGVVELTVALHYIFNTPQDKILWDVGHQSYPHKIL
AtDXS2 (79) LRSDVIF-NVSKTGGHLGSNLGVVELTVALHYIFNTPHDKILWDVGHQSYPHKIL
PtDXS1 (72) LRSDVIF-NVSKTGGHLGSSLGVVELTVALHYVFNSPQDKILWDVGHQAYPHKIL
SmDXS1 (95) LRSDVIF-NVSKTGGHLGSSLGVIELTVALHYVFNAPQDRILWDVGHQAYPHKIL
SmDXS5 (89) LRSDLIF-NVSKTGGHLGSGLGVIELTVALHYVFEAPQDRILWDVGHQSYPHKIL
PtDXS2A (73) LRADIVY-SVAKTGGHLSSSLGVVELSVALHHVFNTPEDKIIWDVGHQAYPHKIL
SmDXS3 (95) LRVEIVH-TVAKTGGHLSSSLGVVELTVALHHVFNTPHDKLIWDVGHQAYGHKIL
PtDXS2B (37) LREEIVY-TVSKTGGHLSSSLGVAELTVALHHVFNTPEDKIIWDVGHQTYPHKIL
SmDXS2 (104) LREEIVY-TVSKTGGHLSSSLGVSELTVALHHVFNTPEDKIIWDVGHQAYPHKIL
AtDXS3 (102) IRTELHSVLWKKTQKSMNPSFAAIELTLALHYVFRAPVDNILWDAVEQTYAHKVL
PtDXS3 (42) IRSELSS-IMSKTQNDLKASLAVVELTVAIHHVFHAPVDKILWDVGEQTYAHKIL
SmDXS4 (101) IRTELS--IMSKTNKSFRPSLSVVELAVAIHHVFHAPVDKILWDMEDQTYPHKLL
Consensus (111) LRSDIIF VSKTGGHL SSLGVVELTVALHHVFNTP DKILWDVGHQAYPHKIL
(166) 166 180 190 200 210 220
AtDXS1 (155) TGRRGKMPTMRQTNGLSGFTKRGESEHDCFGTGHSSTTISAGLGMAVGRDLKGKN
AtDXS2 (133) TGRRGKMKTIRQTNGLSGYTKRRESEHDSFGTGHSSTTLSAGLGMAVGRDLKGMN
PtDXS1 (126) TGRRDKMHTIRQTNGLAGFTKRSESEYDCFGTGHSSTTISAGLGMAVGRDLKGRA
SmDXS1 (149) TGRRDRMPSLRQTGGLSGFTKRSESDYDCFGAGHSSTTISAGLGMAVGRDLKGRK
SmDXS5 (143) TGRRDRMPTLRQTDGLSGFTKRSESDYDCFGAGHSSTTISAGLGMAVGRDLKGRK
PtDXS2A (127) TGRRSRMHTIRKTSGLAGFPKRDESVYDAFGAGHSSTSISAGLGMAVARDLLGKS
SmDXS3 (149) TGRRSKMHTIRQTSGLAGFPKRDESVHDAFGVGHSSTSISAGLGMAVARDLLGKD
PtDXS2B (91) TGRRSRMHTIRQTFGLAGFPKREESEHDAFGAGHSSTSISAALGMAVGRDLLGKD
SmDXS2 (158) TGRRSRMHTIRQTFGLAGFPKRDESAHDAFGAGHSSTSISAGLGMAVGRDLLHKN
AtDXS3 (157) TRRWSAIP-SRQNSGISGVTSRLESEYDSFGTGHGCNSISAGLGLAVARDMKGKR
PtDXS3 (96) TGRRSLMHTLRQKDGLSGFTSRSESEYDPFGAGHGCNSISAGIGMAIARDIKGKR
SmDXS4 (154) TGRRACLNKSGQVDDLSSYACRN--EYDPFGAGHGCSSISSGLGMAVARDIKGKR
Consensus (166) TGRRSRMHTIRQT GLSGFTKR ESEYDAFGAGHSSTSISAGLGMAVGRDLKGK
(221) 221 230 240 250 260 275
AtDXS1 (210) NNVVAVIGDGAMTAGQAYEAMNNAGYLDSDMIVILNDNKQVSLPTATLDGPSPPV
AtDXS2 (188) NSVVSVIGDGAMTAGQAYEAMNNAGYLHSNMIVILNDNKQVSLPTANLDGPTQPV
PtDXS1 (181) NNVVAVIGDGAMTAGQAYEAMNNAGYLDSDMIVILNDNKQVSLPTANLDGPIPPV
SmDXS1 (204) NNVVAVIGDGAMTAGQAYEAMNNAGYLDSDMIVILNDNKQVSLPTANLDGPTAPV
SmDXS5 (198) NHVVAVIGDGAMTAGQAYEAMNNAGYLDSDMIVILNDNKQVSLPTATLDGPSPPV
PtDXS2A (182) NHVISVIGDGAMTAGQAYEAMNNAGFLDSNLIVILNDNKQVSLPTATLDGPATPV
SmDXS3 (204) NSVVSVIGDGAMTAGQAYEAMNNAGFLDSNLIIVLNDNKQVSLPTATLDGPATPV
PtDXS2B (146) NHVIAVIGDGAMTAGQAYEAMNNAGYLDSNLIIILNDNRQVSLPTATVDGPAPPV
SmDXS2 (213) NHVISVIGDGAMTAGQAYEALNNAGFLDSNLIIVLNDNKQVSLPTATIDGPAPPV
AtDXS3 (211) DRVVAVIDNVTITAGQAYEAMSNAGYLDSNMIVILNDSRHSLHPNMEEG-SKASI
PtDXS3 (151) ERIVTVIGNGTTMAGQVYEAMGNAGYLDTNMIVILNDSRHSLHPKIEEG-SKTSI
SmDXS4 (207) DRIVSVISNETTMAGQVYEAMSNAGYLDSNMVVILNDRHHSSNPKLDQA-PKASI
Consensus (221) N VVAVIGDGAMTAGQAYEAMNNAGYLDSNMIVILNDNKQVSLPTATLDGPA PV
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(276) 276 290 300 310 320 330
AtDXS1 (265) GALSSALSRLQSNPALRELREVAKGMTKQIGGPMHQLAAKVDEYARGMISGTGSS
AtDXS2 (243) GALSCALSRLQSN-------------------------------CGMIRETSST
PtDXS1 (236) GALSSALSRLQSNRPLRELREVAKGVTKQIGGPMHELAAKVDEYARGMISGSGST
SmDXS1 (259) GALSSALSRLQSNRPLRELREVAKGVTKQIGGPMHELAAKVDEYARGLISGSGST
SmDXS5 (253) GALSRALSRLQSNRPLRELGEASK------GGSMHELAAK---HGRGLMSGSGST
PtDXS2A (237) GALSSTLTKLQASAKFRKLHEAAKGITKQIDGQTHQVAAKVDEYARGMISASGST
SmDXS3 (259) GALSSALTKLQASPKFRQLREAAKSITKQIGPQAHEVAAKVDEYARGMLSASGST
PtDXS2B (201) GALSRALTRLHSSRKFRQLREAAKGITKQIGGQTQEIAAKVDSYMRGMTGASGAC
SmDXS2 (268) GALSKALTRLQASRKFRQLREAAKGMTRQMGEQAHEIASKVDTYMKGMMGKPGAS
AtDXS3 (265) SALSSIMSKIQSSKVFRKFRELAKAMTKRIGKGMYEWAAKVDEYARGMVGPTGST
PtDXS3 (205) TALSSTLSKLQSSKSFRRLREVAKGVTKRIG--MHELAAKVDEYARGMMGPLGST
SmDXS4 (261) NAVSSTLSKLQSSQFFRKFREVAKVLTKRIGRGMHEWAAKIDEYARGMVGPPGST
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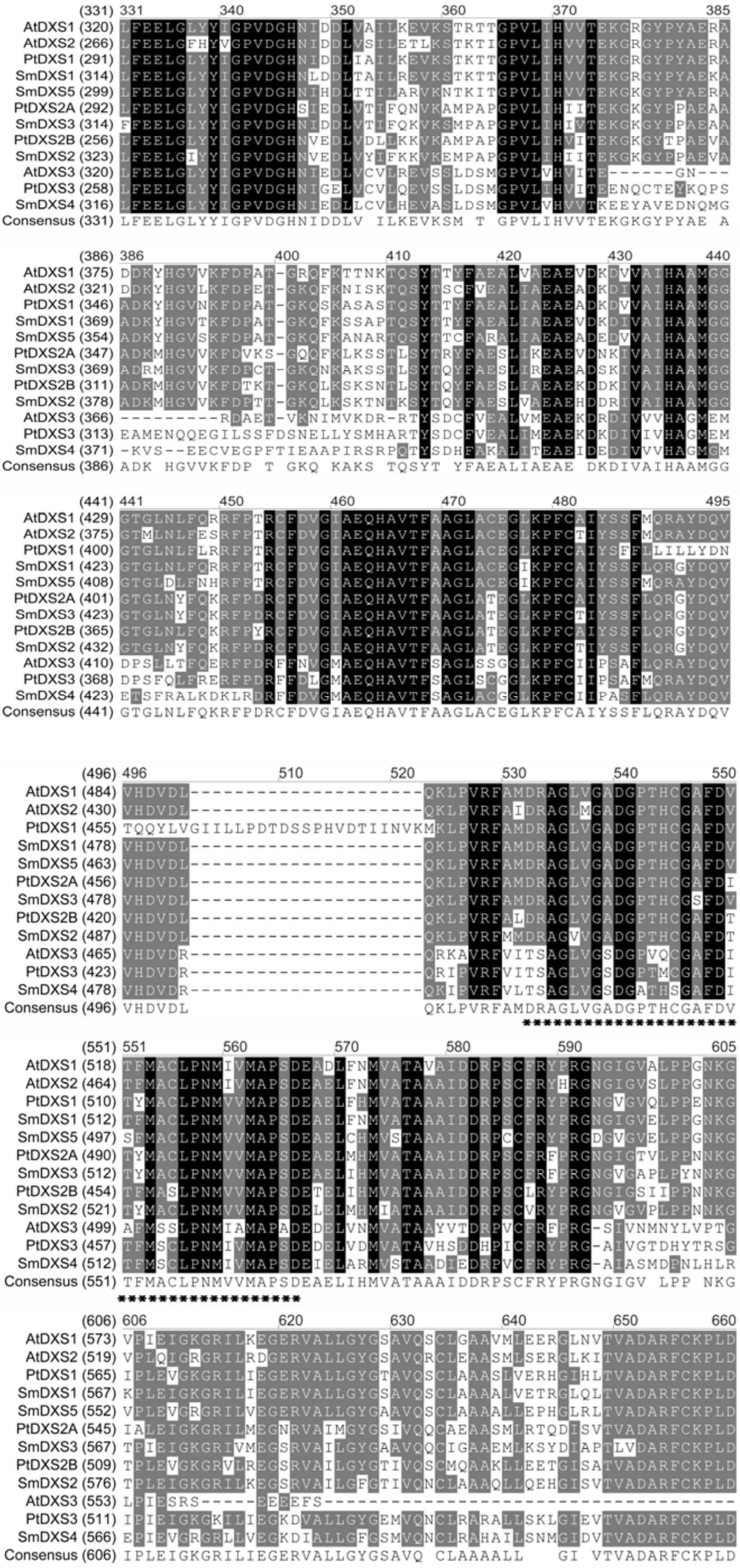

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   AtDXS2 (266) LFEELGFHYVGPVDGHNIDDLVSILETLKSTKTIGPVLIHVVTEKGRGYPYAERA
   PtDXS1 (291) LFEELGLYYIGPVDGHNIDDLIAILKEVKSTKTTGPVLIHVVTEKGRGYPYAERA
   SmDXS1 (314) LFEELGLYYIGPVDGHNLDDLTAILREVKSTKTTGPVLIHVVTEKGRGYPYAEKA
   SmDXS5 (299) LFEELGLYYIGPVDGHNIHDLTTILARVKNTKITGPVLIHVVTEKGKGYPYAERA
  PtDXS2A (292) LFEELGLYYIGPVDGHSIEDLVTIFQNVKAMPAPGPVLIHIITEKGKGYPPAEAA
   SmDXS3 (314) FFEELGLYYIGPVDGHNIDDLVTIFQKVKSMPAPGPVLIHIVTEKGKGYPPAEAA
  PtDXS2B (256) LFEELGLYYIGPVDGHNVEDLVDLLKKVKAMPAPGPVLIHVITEKGKGYTPAEVA
   SmDXS2 (323) LFEELGIYYIGPVDGHNVEDLVYIFKKVKEMPAPGPVLIHIITEKGKGYPPAEVA
   AtDXS3 (320) LFEELGLYYIGPVDGHNIEDLVCVLREVSSLDSMGPVLVHVITE------GN---
   PtDXS3 (258) LFEELGLYYIGPVDGHNIGELVCVLQEVSSLDSMGPVLIHVITEENQCTEYKQPS
   SmDXS4 (316) LFEELGLYYIGPVDGHNIEDLLCVLHEVASLDSMGPVLVHVVTKEEYAVEDNQMG
Consensus (331) LFEELGLYYIGPVDGHNIDDLV ILKEVKSM T GPVLIHVVTEKGKGYPYAE A

          (386) 386           400       410       420       430      440
   AtDXS1 (375) DDKYHGVVKFDPAT-GRQFKTTNKTQSYTTYFAEALVAEAEVDKDVVAIHAAMGG
   AtDXS2 (321) DDKYHGVLKFDPET-GKQFKNISKTQSYTSCFVEALIAEAEADKDIVAIHAAMGG
   PtDXS1 (346) ADKYHGVNKFDPAT-GKQSKASASTQSYTTYFAEALIAEAEADKDVVAIHAAMGG
   SmDXS1 (369) ADKYHGVTKFDPAT-GKQFKSSAPTQSYTTYFAEALIAEAEVDKDIVAIHAAMGG
   SmDXS5 (354) ADKYHGVSKFDPAT-GKQFKANARTQSYTTCFARALIAEAEADEDVVAIHAAMGG
  PtDXS2A (347) ADKMHGVVKFDVKS-GQQFKLKSSTLSYTRYFAESLIKEAEVDNKIVAIHAAMGG
   SmDXS3 (369) ADRMHGVVKFDPCT-GKQNKAKSSTLSYTQYFAESLIREAEADSKIVAIHAAMGG
  PtDXS2B (311) ADKMHGVVKFDTKT-GKQLKSKSNTLSYTQYFAESLIAEAEKDDKIVAIHAAMGG
   SmDXS2 (378) ADKMHGVVKFDPTT-GKQLKSKTNTKSYTQYFAESLVAEAEHDDRIVAIHAAMGG
   AtDXS3 (366) ---------RDAET-VKNIMVKDR-RTYSDCFVEALVMEAEKDRDIVVVHAGMEM
   PtDXS3 (313) EAMENQQEGILSSFDSNELLYSMHARTYSDCFVEALIMEAEKDKDIVIVHAGMEM
   SmDXS4 (371) -KVS--EECVEGPFTIEAAPIRSRPQTYSDHFAKALITEAEIDEDIVVVHAGMGM
Consensus (386) ADK HGVVKFDP T GKQ KAKS TQSYT YFAEALIAEAE DKDIVAIHAAMGG

          (441) 441      450       460       470       480            495
   AtDXS1 (429) GTGLNLFQRRFPTRCFDVGIAEQHAVTFAAGLACEGLKPFCAIYSSFMQRAYDQV
   AtDXS2 (375) GTMLNLFESRFPTRCFDVGIAEQHAVTFAAGLACEGLKPFCTIYSSFMQRAYDQV
   PtDXS1 (400) GTGLNLFLRRFPTRCFDVGIAEQHAVTFAAGLACEGLKPFCAIYSFFLLILLYDN
   SmDXS1 (423) GTGLNLFQRRFPTRCFDVGIAEQHAVTFAAGLACEGIKPFCAIYSSFLQRGYDQV
   SmDXS5 (408) GTGLDLFNHRFPTRCFDVGIAEQHAVTFAAGLACEGIKPFCAIYSSFMQRAYDQV
  PtDXS2A (401) GTGLNYFQKRFPDRCFDVGIAEQHAVTFAAGLATEGLKPFCAIYSSFLQRGYDQV
   SmDXS3 (423) GTGLNYFQKRFPDRCFDVGIAEQHAVTFAAGLATEGLKPFCTIYSSFLQRGYDQV
  PtDXS2B (365) GTGLNLFQKRFPYRCFDVGIAEQHAVTFAAGLATEGLKPFCAIYSSFLQRGYDQV
   SmDXS2 (432) GTGLNYFQKRFPDRCFDVGIAEQHAVTFAAGLATEGLKPFCTIYSSFLQRGYDQV
   AtDXS3 (410) DPSLLTFQERFPDRFFNVGMAEQHAVTFSAGLSSGGLKPFCIIPSAFLQRAYDQV
   PtDXS3 (368) DPSFQLFRERFPDRFFDLGMAEQHAVTFSAGLSCGGLKPFCIIPSAFMQRAYDQV
   SmDXS4 (423) ETSFRALKDKLRDRFFDVGMAEQHAVTFSAGLACGGLKPFCIIPASFLQRAYDQV
Consensus (441) GTGLNLFQKRFPDRCFDVGIAEQHAVTFAAGLACEGLKPFCAIYSSFLQRAYDQV

          (496) 496           510       520       530       540      550
   AtDXS1 (484) VHDVDL---------------------QKLPVRFAMDRAGLVGADGPTHCGAFDV
   AtDXS2 (430) VHDVDL---------------------QKLPVRFAIDRAGLMGADGPTHCGAFDV
   PtDXS1 (455) TQQYLVGIILLPDTDSSPHVDTIINVKMKLPVRFAMDRAGLVGADGPTHCGAFDV
   SmDXS1 (478) VHDVDL---------------------QKLPVRFAMDRAGLVGADGPTHCGAFDV
   SmDXS5 (463) VHDVDL---------------------QKLPVRFAMDRAGLVGADGPTHCGAFDV
  PtDXS2A (456) VHDVDL---------------------QKLPVRFAMDRAGLVGADGPTHCGAFDI
   SmDXS3 (478) VHDVDL---------------------QKLPVRFAMDRAGLVGADGPTHCGSFDV
  PtDXS2B (420) VHDVDL---------------------QKLPVRFALDRAGLVGADGPTHCGAFDT
   SmDXS2 (487) VHDVDL---------------------QKLPVRFMMDRAGVVGADGPTHCGAFDT
   AtDXS3 (465) VHDVDR---------------------QRKAVRFVITSAGLVGSDGPVQCGAFDI
   PtDXS3 (423) VHDVDR---------------------QRIPVRFVITSAGLVGSDGPTMCGAFDI
   SmDXS4 (478) VHDVDR---------------------QKIPVRFVLTSAGLVGSDGATHSGAFDI
Consensus (496) VHDVDL                     QKLPVRFAMDRAGLVGADGPTHCGAFDV
                                                  **********************

          (551) 551      560       570       580       590            605
   AtDXS1 (518) TFMACLPNMIVMAPSDEADLFNMVATAVAIDDRPSCFRYPRGNGIGVALPPGNKG
   AtDXS2 (464) TFMACLPNMIVMAPSDEAELFNMVATAAAIDDRPSCFRYHRGNGIGVSLPPGNKG
   PtDXS1 (510) TYMACLPNMVVMAPSDEAELFHMVATAAAIDDRPSCFRYPRGNGVGVQLPPENKG
   SmDXS1 (512) TFMACLPNMVVMAPSDEAELFNMVATAAAIDDRPSCFRYPRGNGIGVELPPGNKG
   SmDXS5 (497) SFMACLPNMVVMAPSDEAELCHMVSTAAAIDDRPCCFRYPRGDGVGVELPPGNKG
  PtDXS2A (490) TYMACLPNMVVMAPSDEAELMHMVATAAAIDDRPSCFRFPRGNGIGTVLPPNNKG
   SmDXS3 (512) TYMACLPNMVVMAPSDEAELIHMVATAAAIDDRPSCFRFPRGNGVGAPLPYNNKG
  PtDXS2B (454) TFMASLPNMVVMAPSDETELIHMVATAAAIDDRPSCLRYPRGNGIGSIIPPNNKG
   SmDXS2 (521) TYMACLPNMVVMAPSDELELMHMIATAAAIDDRPSCVRYPRGNGVGVPLPPNNKG
   AtDXS3 (499) AFMSSLPNMIAMAPADEDELVNMVATAAYVTDRPVCFRFPRG-SIVNMNYLVPTG
   PtDXS3 (457) TFMSCLPNMIVMAPSDEDELVDMVATAVHSDDHPICFRYPRG-AIVGTDHYTRSG
   SmDXS4 (512) TFMSCLPNMIVMAPSDEIELARMVSTAADIEDRPVCFRYPRG-AIASMDPNLHLR
Consensus (551) TFMACLPNMVVMAPSDEAELIHMVATAAAIDDRPSCFRYPRGNGIGV LPP NKG
               ******************

          (606) 606           620       630       640       650      660
   AtDXS1 (573) VPIEIGKGRILKEGERVALLGYGSAVQSCLGAAVMLEERGLNVTVADARFCKPLD
   AtDXS2 (519) VPLQIGRGRILRDGERVALLGYGSAVQRCLEAASMLSERGLKITVADARFCKPLD
   PtDXS1 (565) IPLEVGKGRILIEGERVALLGYGTAVQSCLAAASLVERHGIHLTVADARFCKPLD
   SmDXS1 (567) KPLEIGKGRILIEGERVALLGYGSAVQSCLAAAALVETRGLQLTVADARFCKPLD
   SmDXS5 (552) VPLEVGRGRILVEGERVALLGYGAAVQSCLAAAALLEPHGLRLTVADARFCKPLD
  PtDXS2A (545) IALEIGKGRILMEGNRVAIMGYGSIVQQCAEAASMLRTQDISVTVADARFCKPLD
   SmDXS3 (567) TPIEIGKGRIVMEGSRVAILGYGAAVQQCIGAAEMLKSYDIAPTLVDARFCKPLD
  PtDXS2B (509) TPLEVGKGRVLREGSRVAILGYGTIVQSCMQAAKLLEETGISATVADARFCKPLD
   SmDXS2 (576) TPLEIGKGRILKEGSRVAILGFGTIVQNCLAAAQLLQEHGISVTVADARFCKPLD
   AtDXS3 (553) LPIESRS-----EEEEFS-------------------------------------
   PtDXS3 (511) IPIEIGKGKILIEGKDVALLGYGEMVQNCLRARALLSKLGIEVTVADARFCKPLD
   SmDXS4 (566) EPIEVGRGRLLVEGKDIALLGFGSMVQNCLRAHAILSNMGIDVTVADARFCKPLD
Consensus (606) IPLEIGKGRILIEGERVALLGYGSAVQ CLAAAALL    GI VTVADARFCKPLD
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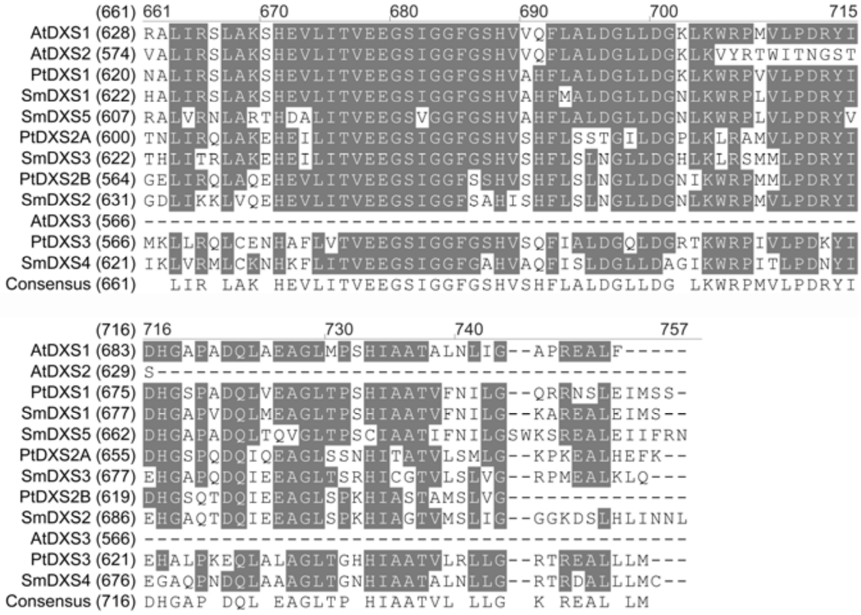
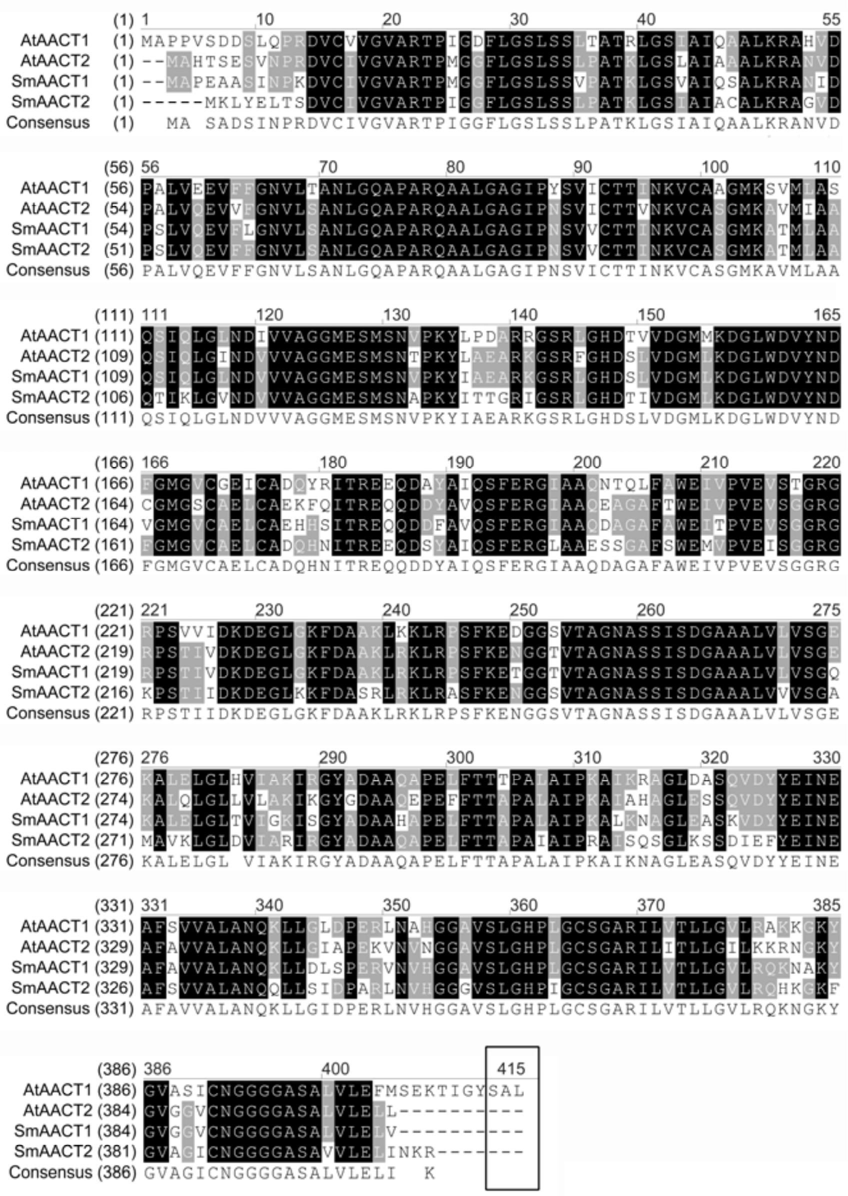


Figure S3. Sequence alignment of DXS proteins from *Salvia miltiorrhiza*, *Arabidopsis thaliana* and *Populus trichocarpa*. DXSs included are *A. thaliana* AtDXS1 (At4g15560), AtDXS2 (At3g21500), AtDXS3 (At 5G11380), *P. trichocarpa* PtDXS1(XP_002312717), PtDXS2A (XP_002303416), PtDXS2B (XP_002331678), PtDXS3 (XP_002308644), *S. miltiorrhiza* SmDXS1 (ACF21004), SmDXS2 (ACQ66107), SmDXS3 (JN831116), SmDXS4 (JN831117), SmDXS5 (JN831118). The consensus thiamine pyrophosphatase - binding motif (GDGAMTAG……VILND) and the pyridine binding domain (DRAGLVGAD……VMAPSD) was indicated by '***'.



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            (1) 1        10        20        30        40            55
AtAACT1     (1) MAPPVSDDSLQPRDVCVVGVARTPIGDFLGSLSSLTATRLGSIAIQAALKRAHVD
AtAACT2     (1) --MAHTSESVNPRDVCIVGVARTPMGGFLGSLSSLPATKLGSLAIAAALKRANVD
SmAACT1     (1) --MAPEAASINPKDVCIVGVARTPMGGFLGSLSSVPATKLGSVAIQSALKRANID
SmAACT2     (1) -----MKLYELTSDVCIVGVARTPIGGFLGSLSSLPATKLGSIAIACALKRAGVD
Consensus   (1)   MA SADSINPRDVCIVGVARTPIGGFLGSLSSLPATKLGSIAIQAALKRANVD

           (56) 56            70        80        90        100     110
AtAACT1    (56) PALVEEVFFGNVLTANLGQAPARQAALGAGIPYSVICTTINKVCAAGMKSVMLAS
AtAACT2    (54) PALVQEVVFGNVLSANLGQAPARQAALGAGIPNSVICTTVNKVCASGMKAVMIAA
SmAACT1    (54) PSLVQEVFLGNVLSANLGQAPARQAALGAGIPNSVVCTTINKVCASGMKATMLAA
SmAACT2    (51) PSLVQEVFFGNVLSANLGQAPARQAALGAGIPNSVVCTTINKVCASGMKATMLAA
Consensus  (56) PALVQEVFFGNVLSANLGQAPARQAALGAGIPNSVICTTINKVCASGMKAVMLAA

          (111) 111      120       130       140       150          165
AtAACT1   (111) QSIQLGLNDIVVAGGMESMSNVPKYLPDARRGSRLGHDTVVDGMMKDGLWDVYND
AtAACT2   (109) QSIQLGINDVVVAGGMESMSNTPKYLAEARKGSRFGHDSLVDGMLKDGLWDVYND
SmAACT1   (109) QSIQLGLNDVVVAGGMESMSNVPKYIAEARKGSRLGHDSLVDGMLKDGLWDVYND
SmAACT2   (106) QTIKLGVNDVVVAGGMESMSNAPKYITTGRIGSRLGHDTIVDGMLKDGLWDVYND
Consensus (111) QSIQLGLNDVVVAGGMESMSNVPKYIAEARKGSRLGHDSLVDGMLKDGLWDVYND

          (166) 166           180       190       200       210     220
AtAACT1   (166) FGMGVCGEICADQYRITREEQDAYAIQSFERGIAAQNTQLFAWEIVPVEVSTGRG
AtAACT2   (164) CGMGSCAELCAEKFQITREQQDDYAVQSFERGIAAQEAGAFTWEIVPVEVSGGRG
SmAACT1   (164) VGMGVCAELCAEHHSITREQQDDFAVQSFERGIAAQDAGAFAWEITPVEVSGGRG
SmAACT2   (161) FGMGVCAELCADQHNITREEQDSYAIQSFERGLAAESSGAFSWEMVPVEISGGRG
Consensus (166) FGMGVCAELCADQHNITREQQDDYAIQSFERGIAAQDAGAFAWEIVPVEVSGGRG

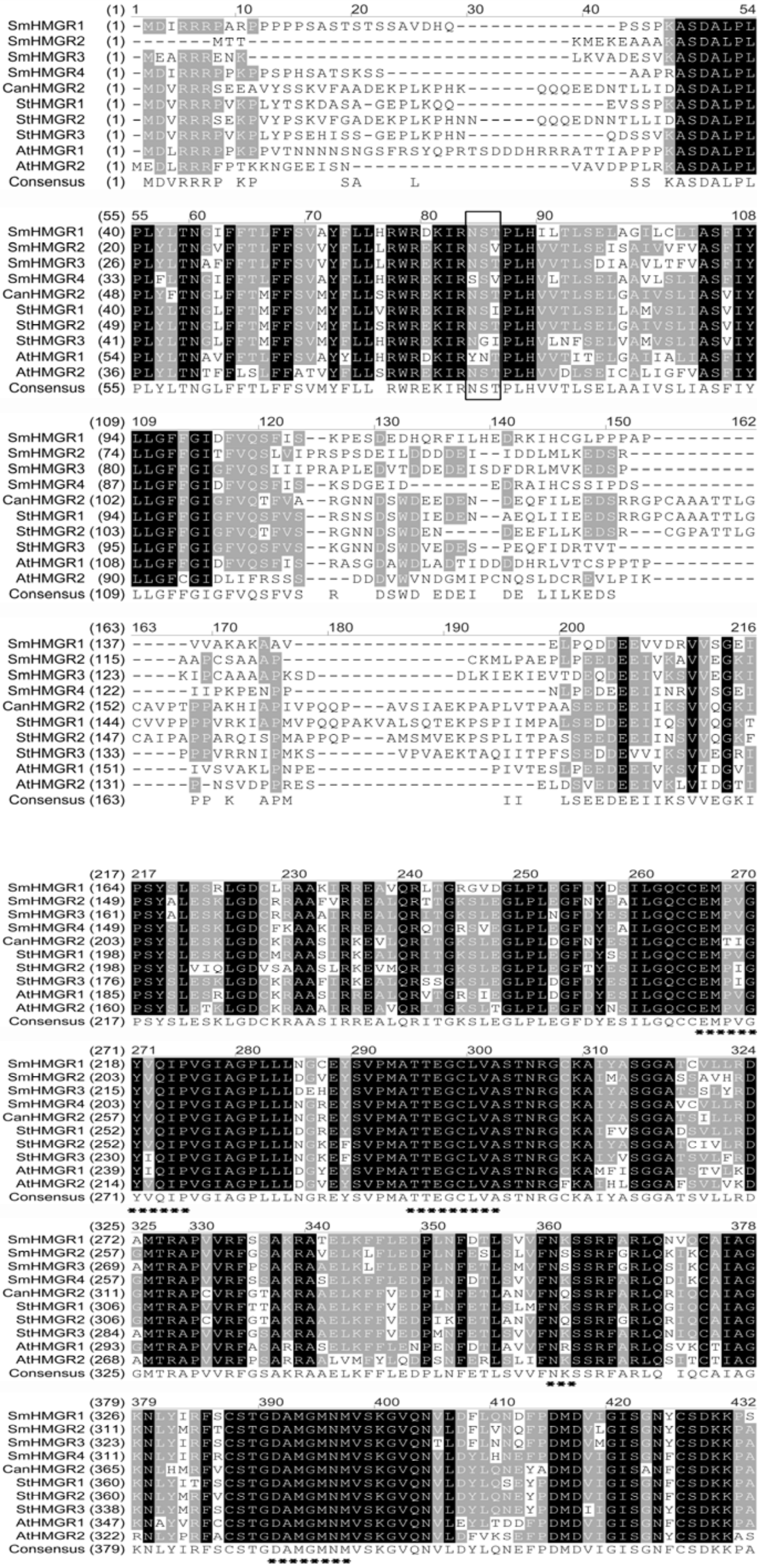
          (221) 221      230       240       250       260          275
AtAACT1   (221) RPSVVIDKDEGLGKFDAAKLKKLRPSFKEDGGSVTAGNASSISDGAAALVLVSGE
AtAACT2   (219) RPSTIVDKDEGLGKFDAAKLRKLRPSFKENGGTVTAGNASSISDGAAALVLVSGE
SmAACT1   (219) RPSTIVDKDEGLGKFDAAKLRKLRPSFKETGGTVTAGNASSISDGAAALVLVSGQ
SmAACT2   (216) KPSTIIDKDEGLKKFDASRLRKLRASFKENGGSVTAGNASSISDGAAALVVVSGA
Consensus (221) RPSTIIDKDEGLGKFDAAKLRKLRPSFKENGGSVTAGNASSISDGAAALVLVSGE

          (276) 276           290       300       310       320     330
AtAACT1   (276) KALELGLHVIAKIRGYADAAQAPELFTTTPALAIPKAIKRAGLDASQVDYYEINE
AtAACT2   (274) KALQLGLLVLAKIKGYGDAAQEPEFFTTAPALAIPKAIAHAGLESSQVDYYEINE
SmAACT1   (274) KALELGLTVIGKISGYADAAHAPELFTTAPALAIPKALKNAGLEASKVDYYEINE
SmAACT2   (271) MAVKLGLDVIARIRGYADAAQAPELFTTAPAIAIPRAISQSGLKSSDIEFYEINE
Consensus (276) KALELGL VIAKIRGYADAAQAPELFTTAPALAIPKAIKNAGLEASQVDYYEINE

          (331) 331      340       350       360       370          385
AtAACT1   (331) AFSVVALANQKLLGLDPERLNAHGGAVSLGHPLGCSGARILVTLLGVLRAKKGKY
AtAACT2   (329) AFAVVALANQKLLGIAPEKVNVNGGAVSLGHPLGCSGARILITLLGILKKRNGKY
SmAACT1   (329) AFAVVALANQKLLDLSPERVNVHGGAVSLGHPLGCSGARILVTLLGVLRQKNAKY
SmAACT2   (326) AFSVVALANQQLLSIDPARLNVHGGGVSLGHPIGCSGARILVTLLGVLRQHKGKF
Consensus (331) AFAVVALANQKLLGIDPERLNVHGGAVSLGHPLGCSGARILVTLLGVLRQKNGKY

          (386) 386           400          415
AtAACT1   (386) GVASICNGGGGASALVLEFMSEKTIGYSAL
AtAACT2   (384) GVGGVCNGGGGASALVLELL----------
SmAACT1   (384) GVGGVCNGGGGASALVLELV----------
SmAACT2   (381) GVAGICNGGGGASAVVLELINKR-------
Consensus (386) GVAGICNGGGGASALVLELI   K
```

Figure S4. Sequence alignment of AACT proteins from *S. miltiorrhiza* and *A. thaliana*. AACTs included are *A. thaliana* AtAACT1 (At5g47720), AtAACT2 (At5g48230), *S. miltiorrhiza* SmAACT1 (ABV08820), SmAACT2 (JN831101). The peroxisomal targeting signal 1 (PTS1) related motif (SAL) presented in the carboxy terminus of AtAACT1 is boxed.


(1) 1 10 20 30 40 54
SmHMGR1 (1) -MDIRRRPARPPPPPSASTSTSSAVDHQ--------------PSSPKASDALPL
SmHMGR2 (1) -------MTT----------------------------KMEKEAAAKASDALPL
SmHMGR3 (1) -MEARRRENK----------------------------LKVADESVKASDALPL
SmHMGR4 (1) -MDIRRRPPKPPSPHSATSKSS---------------------AAPRASDALPL
CanHMGR2 (1) -MDVRRRSEEAVYSSKVFAADEKPLKPHK------QQQEEDNTLLIDASDALPL
StHMGR1 (1) -MDVRRRPVKPLYTSKDASA-GEPLKQQ-------------EVSSPKASDALPL
StHMGR2 (1) -MDVRRRSEKPVYPSKVFGADEKPLKPHNN-----QQQEDNNTLLIDASDALPL
StHMGR3 (1) -MDVRRRPVKPLYPSEHISS-GEPLKPHN------------QDSSVKASDALPL
AtHMGR1 (1) -MDLRRRPPKPPVTNNNNSNGSFRSYQPRTSDDDHRRRATTIAPPPKASDALPL
AtHMGR2 (1) MEDLRRRFPTKKNGEEISN-------------------VAVDPPLRKASDALPL
Consensus (1) MDVRRRP KP SA L SS KASDALPL
(55) 55 60 70 80 90 108
SmHMGR1 (40) PLYLTNGIFFTLFFSVAYFLLHRWRDKIRNSTPLHILTLSELAGILCLIASFIY
SmHMGR2 (20) PLYLTNGVFFTLFFSVVYFLLLRWREKIRNSVPLHVVTLSEISAIVVFVASFIY
SmHMGR3 (26) PLYLTNAFFFTLFFSVVYFLLLRWREKIRNSTPLHVVTLSDIAAVLTFVASFIY
SmHMGR4 (33) PLFLTNGIFFTLFFSVAYFLLHRWREKIRSSVPLHVLTLSELAAVLSLIASFIY
CanHMGR2 (48) PLYFTNGLFFTMFFSVMYFLLSRWREKIRNSTPLHVVTLSELGAIVSLIASVIY
StHMGR1 (40) PLYLTNGLFFTMFFSVMYFLLVRWREKIRNSIPLHVVTLSELLAMVSLIASVIY
StHMGR2 (49) PLYLTNGLFFTMFFSVMYFLLSRWREKIRNSTPLHVVTLSELGAIVSLIASVIY
StHMGR3 (41) PLYLTNGLFFTMFFSVMYFLLHRWREKIRNGIPLHVLNFSELVAMVSLIASVIY
AtHMGR1 (54) PLYLTNAVFFTLFFSVAYYLLHRWRDKIRYNTPLHVVTITELGAIIALIASFIY
AtHMGR2 (36) PLYLTNTFFLSLFFATVYFLLSRWREKIRNSTPLHVVDLSEICALIGFVASFIY
Consensus (55) PLYLTNGLFFTLFFSVMYFLL RWREKIRNSTPLHVVTLSELAAIVSLIASFIY
(109) 109 120 130 140 150 162
SmHMGR1 (94) LLGFFGIDFVQSFIS--KPESDEDHQRFILHEDRKIHCGLPPPAP---------
SmHMGR2 (74) LLGFFGITFVQSLVIPRSPSDEILDDDDEI--IDDLMLKEDSR-----------
SmHMGR3 (80) LLGFFGIGFVQSIIIPRAPLEDVTDDEDEISDFDRLMVKEDSP-----------
SmHMGR4 (87) LLGFFGIDFVQSFIS--KSDGEID-------EDRAIHCSSIPDS----------
CanHMGR2 (102) LLGFFGIGFVQTFVA--RGNNDSWDEEDEN--DEQFILEEDSRRGPCAAATTLG
StHMGR1 (94) LLGFFGIGFVQSFVS--RSNSDSWDIEDEN--AEQLIIEEDSRRGPCAAATTLG
StHMGR2 (103) LLGFFGIGFVQTFVS--RGNNDSWDEN-----DEEFLLKEDSR---CGPATTLG
StHMGR3 (95) LLGFFGIGFVQSFVS--KGNNDSWDVEDES--PEQFIDRTVT------------
AtHMGR1 (108) LLGFFGIDFVQSFIS--RASGDAWDLADTIDDDDHRLVTCSPPTP---------
AtHMGR2 (90) LLGFCGIDLIFRSSS----DDDVWVNDGMIPCNQSLDCREVLPIK---------
Consensus (109) LLGFFGIGFVQSFVS R DSWD EDEI DE LILKEDS
(163) 163 170 180 190 200 216
SmHMGR1 (137) -----VVAKAKAAV----------------------ELPQDDEEVVDRVVSGEI
SmHMGR2 (115) ----AAPCSAAAP----------------CKMLPAEPLPEEDEEIVKAVVEGKI
SmHMGR3 (123) ----KIPCAAAAPKSD------------DLKIEKIEVTDEQDEEIVKSVVEGKI
SmHMGR4 (122) -----IIPKPENPP----------------------NLPEDEEEIINRVVSGEI
CanHMGR2 (152) CAVPTPPAKHIAPIVPQQP---AVSIAEKPAPLVTPAASEEDEEIIKSVVQGKI
StHMGR1 (144) CVVPPPPVRKIAPMVPQQPAKVALSQTEKPSPIIMPALSEDDEEIIQSVVQGKT
StHMGR2 (147) CAIPAPPARQISPMAPPQP---AMSMVEKPSPLITPASSEEDEEIINSVVQGKF
StHMGR3 (133) ----PPPVRRNIPMKS-------VPVAEKTAQIITPFSSEDDEVVIKSVVEGRI
AtHMGR1 (151) -----IVSVAKLPNPE---------------PIVTESLPEEDEEIVKSVIDGVI
AtHMGR2 (131) -----P-NSVDPPRES-------------------ELDSVEDEEIVKLVIDGTI
Consensus (163) PP K APM II LSEEDEEIIKSVVEGKI
(217) 217 230 240 250 260 270
SmHMGR1 (164) PSYSLESRLGDCLRAAKIRREAVQRLTGRGVDGLPLEGFDYDSILGQCCEMPVG
SmHMGR2 (149) PSYALESKLGDCRRAAFVRREALQRTTGKSLEGLPLEGFNYEAILGQCCEMPVG
SmHMGR3 (161) PSYALESKLGDCRRAAAIRREALQRITGKSLEGLPLNGFDYESILGQCCEMPVG
SmHMGR4 (149) PSYSLESKLGDCFKAAKIRREALQRQTGRSVEGLPLEGFDYEAILGQCCEMPVG
CanHMGR2 (203) PSYSLESKLGDCKRAASIRKEVLQRITGKSLEGLPLDGFNYESILGQCCEMTIG
StHMGR1 (198) PSYSLESKLGDCMRAASIRKEALQRITGKSLEGLPLEGFDYSSILGQCCEMPVG
StHMGR2 (198) PSYSLVIQLGDVSAAASLRKEVMQRITGKSLEGLPLEGFTYESILGQCCEMPIG
StHMGR3 (176) PSYSLESKLGDCKRAAFIRKEALQRSSGKSLEGLPLDGFDYESILGQCCEMPIG
AtHMGR1 (185) PSYSLESRLGDCKRAASIRREALQRVTGRSIEGLPLDGFDYESILGQCCEMPVG
AtHMGR2 (160) PSYSLETKLGDCKRAAAIRREAVQRITGKSLTGLPLEGFDYNSILGQCCEMPVG
Consensus (217) PSYSLESKLGDCKRAASIRREALQRITGKSLEGLPLEGFDYESILGQCCEMPVG
******
(271) 271 280 290 300 310 324
SmHMGR1 (218) YVQIPVGIAGPLLLNGCEYSVPMATTEGCLVASTNRGCKAIYASGGATCVLLRD
SmHMGR2 (203) YVQIPVGIAGPLLLDGVEYSVPMATTEGCLVASTNRGCKAIMASGGASSAVHRD
SmHMGR3 (215) YVQIPVGIAGPLLLDEHEYSVPMATTEGCLVASTNRGCKAIYASGGATSSLYRD
SmHMGR4 (203) YVQIPVGIAGPLLLNGREYSVPMATTEGCLVASTNRGCKAIYASGGAVCVLLRD
CanHMGR2 (257) YVQIPVGIAGPLLLNGREYSVPMATTEGCLVASTNRGCKAIYASGGATSILLRD
StHMGR1 (252) YVQIPVGIAGPLLLDGREYSVPMATTEGCLVASTNRGCKAIFVSGGADSVLLRD
StHMGR2 (252) YVQIPVGIAGPLLLNGKEFSVPMATTEGCLVASTNRGCKAIYASGGATCIVLRD
StHMGR3 (230) YIQIPVGIAGPLLLNGKEFSVPMATTEGCLVASTNRGCKAIYVSGGATSVLFRD
AtHMGR1 (239) YIQIPVGIAGPLLLDGYEYSVPMATTEGCLVASTNRGCKAMFISGGATSTVLKD
AtHMGR2 (214) YVQIPVGIAGPLLLDGVEYSVPMATTEGCLVASTNRGFKAIHLSGGAFSVLVKD
Consensus (271) YVQIPVGIAGPLLLNGREYSVPMATTEGCLVASTNRGCKAIYASGGATSVLLRD
****** *********
(325) 325 330 340 350 360 378
SmHMGR1 (272) AMTRAPVVRFSSAKRATELKFFLEDPLNFDTLSVVFNKSSRFARLQNVQCAIAG
SmHMGR2 (257) GMTRAPVVRFGSAKRAVELKLFLEDPLNFESLSLVFNSSSRFGRLQKIKCAIAG
SmHMGR3 (269) AMTRAPVVRFPSAKRAAELKLFLEDPLNFETLSMVFNSSSRFGRLQSIKCAIAG
SmHMGR4 (257) GMTRAPVVRFSSAKRASELKFFLEDPLNFDTLSVVFNKSSRFARLQDIKCAIAG
CanHMGR2 (311) GMTRAPCVRFGTAKRAAELKFFVEDPINFETLANVFNQSSRFARLQRIQCAIAG
StHMGR1 (306) GMTRAPVVRFTTAKRAAELKFFVEDPLNFETLSLMFNKSSRFARLQGIQCAIAG
StHMGR2 (306) GMTRAPCVRFGTAKRAAELKFFVEDPIKFETLANVFNQSSRFGRLQRIQCAIAG
StHMGR3 (284) AMTRAPVVRFGSAKRAAELKFFVEDPMNFETLSVVFNKSSRFARLQNIQCAIAG
AtHMGR1 (293) GMTRAPVVRFASARRASELKFFLENPENFDTLAVVFNRSSRFARLQSVKCTIAG
AtHMGR2 (268) AMTRAPVVRFPSARRAALVMFYLQDPSNFERLSLIFNKSSRFARLQSITCTIAG
Consensus (325) GMTRAPVVRFGSAKRAAELKFFLEDPLNFETLSVVFNKSSRFARLQ IQCAIAG
***
(379) 379 390 400 410 420 432
SmHMGR1 (326) KNLYIRFSCSTGDAMGMNMVSKGVQNVLDFLQNDFPDMDVIGISGNYCSDKKPS
SmHMGR2 (311) KNLYMRFTCSTGDAMGMNMVSKGVQNVLDFLVNQFPDMDVLGISGNYCSDKKPA
SmHMGR3 (323) KNLYIRFSCSTGDAMGMNMVSKGVQNTLDFLNNQFPDMDVMGISGNYCSDKKPA
SmHMGR4 (311) KNLYIRFRCSTGDAMGMNMVSKGVQNVLDYLHNEFPDMDVIGISGNFCSDKKPA
CanHMGR2 (365) KNLHMRFVCSTGDAMGMNMVSKGVQNVLDYLQNEYADMDVIGISANFCSDKKPA
StHMGR1 (360) KNLYITFSCSTGDAMGMNMVSKGVQNVLDYLQSEYPDMDVIGISGNFCSDKKPA
StHMGR2 (360) KNLYMRFVCSTGDAMGMNMVSKGVQNVLDYLQNEYPDMDVIGISGNFCSDKKPA
StHMGR3 (338) KNLYMRFSCSTGDAMGMNMVSKGVQNVLDYLQNEYPDMDIIGISGNYCSDKKPA
AtHMGR1 (347) KNAYVRFCCSTGDAMGMNMVSKGVQNVLEYLTDDFPDMDVIGISGNFCSDKKPA
AtHMGR2 (322) RNLYPRFACSTGDAMGMNMVSKGVQNVLDFVKSEFPDMDVIGISGNYCSDKKAS
Consensus (379) KNLYIRFSCSTGDAMGMNMVSKGVQNVLDYLQNEFPDMDVIGISGNFCSDKKPA
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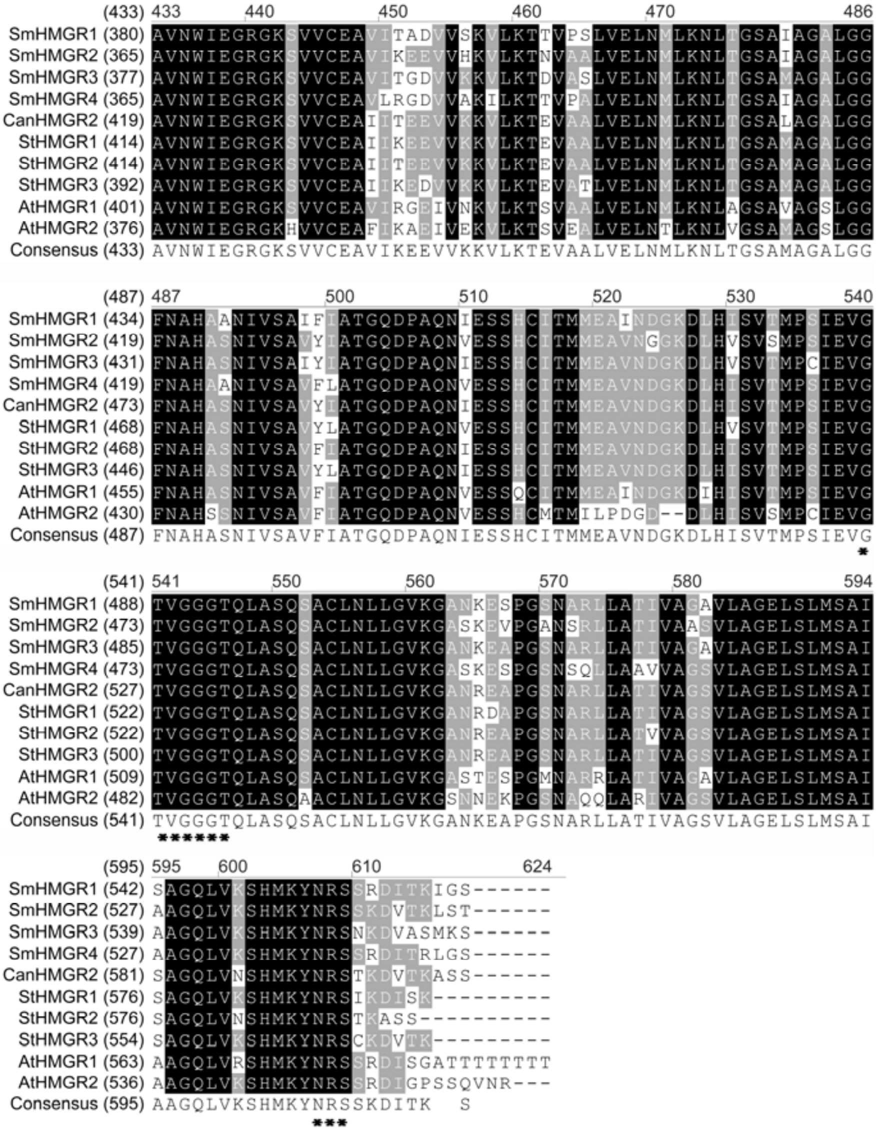

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          (433) 433    440       450       460       470           486
  SmHMGR1 (380) AVNWIEGRGKSVVCEAVITADVVSKVLKTTVPSLVELNMLKNLTGSAIAGALGG
  SmHMGR2 (365) AVNWIEGRGKSVVCEAVIKEEVVHKVLKTNVAALVELNMLKNLTGSAIAGALGG
  SmHMGR3 (377) AVNWIEGRGKSVVCEAVITGDVVKKVLKTDVASLVELNMLKNLTGSAMAGALGG
  SmHMGR4 (365) AVNWIEGRGKSVVCEAVLRGDVVAKILKTTVPALVELNMLKNLTGSAIAGALGG
 CanHMGR2 (419) AVNWIEGRGKSVVCEAIITEEVVKKVLKTEVAALVELNMLKNLTGSALAGALGG
  StHMGR1 (414) AVNWIEGRGKSVVCEAIIKEEVVKKVLKTEVAALVELNMLKNLTGSAMAGALGG
  StHMGR2 (414) AVNWIEGRGKSVVCEAIITEEVVKKVLKTEVAALVELNMLKNLTGSAMAGALGG
  StHMGR3 (392) AVNWIEGRGKSVVCEAIIKEDVVKKVLKTEVATLVELNMLKNLTGSAMAGALGG
  AtHMGR1 (401) AVNWIEGRGKSVVCEAVIRGEIVNKVLKTSVAALVELNMLKNLAGSAVAGSLGG
  AtHMGR2 (376) AVNWIEGRGKHVVCEAFIKAEIVEKVLKTSVEALVELNTLKNLVGSAMAGSLGG
Consensus (433) AVNWIEGRGKSVVCEAVIKEEVVKKVLKTEVAALVELNMLKNLTGSAMAGALGG

          (487) 487          500       510       520       530     540
  SmHMGR1 (434) FNAHAANIVSAIFIATGQDPAQNIESSHCITMMEAINDGKDLHISVTMPSIEVG
  SmHMGR2 (419) FNAHASNIVSAVYIATGQDPAQNVESSHCITMMEAVNGGKDLHVSVSMPSIEVG
  SmHMGR3 (431) FNAHASNIVSAIYIATGQDPAQNIESSHCITMMEAVNDGKDLHVSVTMPCIEVG
  SmHMGR4 (419) FNAHAANIVSAVFLATGQDPAQNVESSHCITMMEAVNDGKDLHISVTMPSIEVG
 CanHMGR2 (473) FNAHASNIVSAVYIATGQDPAQNIESSHCITMMEAVNDGKDLHISVTMPSIEVG
  StHMGR1 (468) FNAHASNIVSAVYLATGQDPAQNVESSHCITMMEAVNDGKDLHVSVTMPSIEVG
  StHMGR2 (468) FNAHASNIVSAVFIATGQDPAQNIESSHCITMMEAVNDGKDLHISVTMPSIEVG
  StHMGR3 (446) FNAHASNIVSAVYLATGQDPAQNIESSHCITMMEAVNDGKDLHISVTMPSIEVG
  AtHMGR1 (455) FNAHASNIVSAVFIATGQDPAQNVESSQCITMMEAINDGKDIHISVTMPSIEVG
  AtHMGR2 (430) FNAHSSNIVSAVFIATGQDPAQNVESSHCMTMILPDGD--DLHISVSMPCIEVG
Consensus (487) FNAHASNIVSAVFIATGQDPAQNIESSHCITMMEAVNDGKDLHISVTMPSIEVG
                                                                     *

          (541) 541      550       560       570       580         594
  SmHMGR1 (488) TVGGGTQLASQSACLNLLGVKGANKESPGSNARLLATIVAGAVLAGELSLMSAI
  SmHMGR2 (473) TVGGGTQLASQSACLNLLGVKGASKEVPGANSRLLATIVAASVLAGELSLMSAI
  SmHMGR3 (485) TVGGGTQLASQSACLNLLGVKGANKEAPGSNARLLATIVAGAVLAGELSLMSAI
  SmHMGR4 (473) TVGGGTQLASQSACLNLLGVKGASKESPGSNSQLLAAVVAGSVLAGELSLMSAI
 CanHMGR2 (527) TVGGGTQLASQSACLNLLGVKGANREAPGSNARLLATIVAGSVLAGELSLMSAI
  StHMGR1 (522) TVGGGTQLASQSACLNLLGVKGANRDAPGSNARLLATIVAGSVLAGELSLMSAI
  StHMGR2 (522) TVGGGTQLASQSACLNLLGVKGANREAPGSNARLLATVVAGSVLAGELSLMSAI
  StHMGR3 (500) TVGGGTQLASQSACLNLLGVKGANREAPGSNARLLATIVAGSVLAGELSLMSAI
  AtHMGR1 (509) TVGGGTQLASQSACLNLLGVKGASTESPGMNARRLATIVAGAVLAGELSLMSAI
  AtHMGR2 (482) TVGGGTQLASQAACLNLLGVKGSNNEKPGSNAQQLARIVAGSVLAGELSLMSAI
Consensus (541) TVGGGTQLASQSACLNLLGVKGANKEAPGSNARLLATIVAGSVLAGELSLMSAI
                *******

          (595) 595  600       610         624
  SmHMGR1 (542) SAGQLVKSHMKYNRSSRDITKIGS------
  SmHMGR2 (527) AAGQLVKSHMKYNRSSKDVTKLST------
  SmHMGR3 (539) AAGQLVKSHMKYNRSNKDVASMKS------
  SmHMGR4 (527) AAGQLVKSHMKYNRSSRDITRLGS------
 CanHMGR2 (581) SAGQLVNSHMKYNRSTKDVTKASS------
  StHMGR1 (576) SAGQLVKSHMKYNRSIKDISK---------
  StHMGR2 (576) SAGQLVNSHMKYNRSTKASS----------
  StHMGR3 (554) SAGQLVKSHMKYNRSCKDVTK---------
  AtHMGR1 (563) AAGQLVRSHMKYNRSSRDISGATTTTTTTT
  AtHMGR2 (536) AAGQLVKSHMKYNRSSRDIGPSSQVNR---
Consensus (595) AAGQLVKSHMKYNRSSKDITK  S
                            ***
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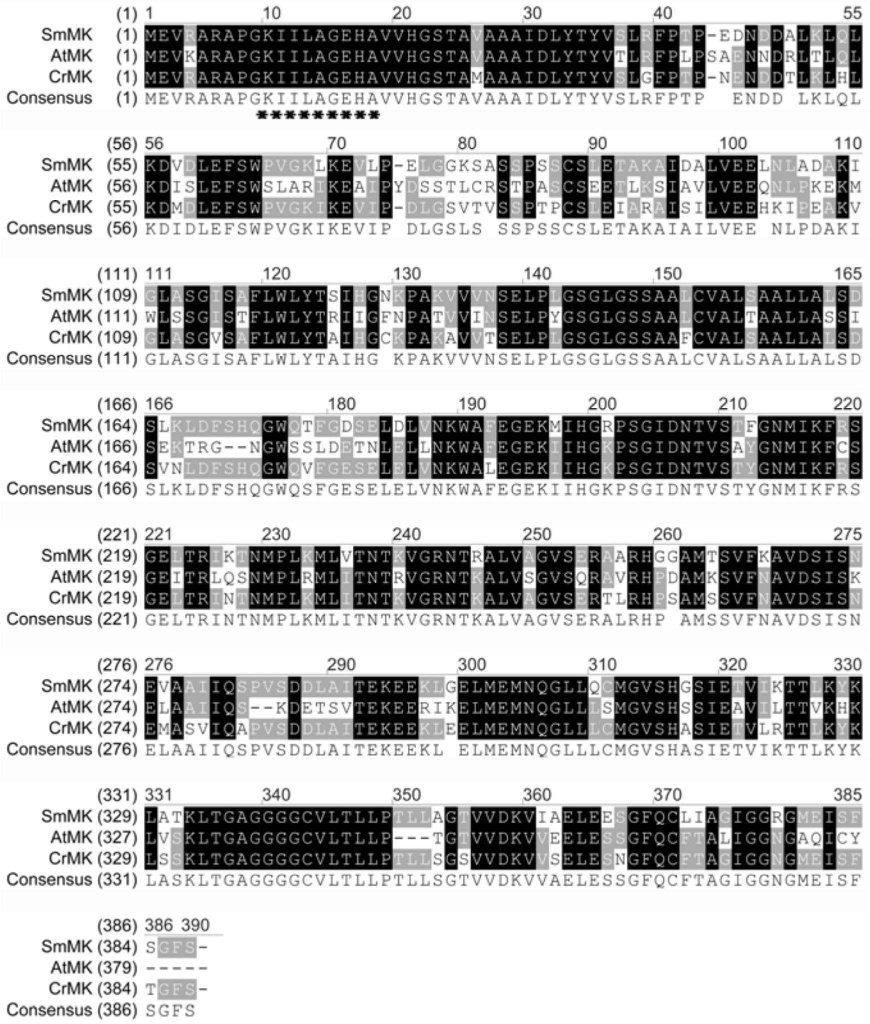
Figure S5. Sequence alignment of HMGR proteins from *S. miltiorrhiza* and various other plants. Proteins included are *Arabidopsis thaliana* AtHMGR1 (CAA33139), AtHMGR2 (AAA67317), *Solanum tuberosum* StHMGR1 (AAA93498), StHMGR2 (AAB52551), StHMGR3 (AAB52552), *Capsicum annuum* CanHMGR2 (AAD28179), and four *S. miltiorrhiza* SmHMGRs. The putative HMG-CoA-binding sites (EMPIGYVQIP and TTEGCLVA), NADP(H)-binding sites (DAMGMNM and GTVGGGT) and *N*-linked glycosylation sites (N-X-S/T) are indicated by '***'. The *N*-glycosylation site (NST) is boxed.



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            (1) 1        10        20        30        40            55
       SmMK (1) MEVRARAPGKIILAGEHAVVHGSTAVAAAIDLYTYVSLRFPTP-EDNDDALKLQL
       AtMK (1) MEVKARAPGKIILAGEHAVVHGSTAVAAAIDLYTYVTLRFPLPSAENNDRLTLQL
       CrMK (1) MEVRARAPGKIILAGEHAVVHGSTAMAAAIDLYTYVSLGFPTP-NENDDTLKLHL
  Consensus (1) MEVRARAPGKIILAGEHAVVHGSTAVAAAIDLYTYVSLRFPTP  ENDD LKLQL
                         *********

           (56) 56            70        80        90        100     110
      SmMK (55) KDVDLEFSWPVGKLKEVLP-ELGGKSASSPSSCSLETAKAIDALVEELNLADAKI
      AtMK (56) KDISLEFSWSLARIKEAIPYDSSTLCRSTPASCSEETLKSIAVLVEEQNLPKEKM
      CrMK (55) KDMDLEFSWPVGKIKEVIP-DLGSVTVSSPTPCSLEIARAISILVEEHKIPEAKV
 Consensus (56) KDIDLEFSWPVGKIKEVIP DLGSLS SSPSSCSLETAKAIAILVEE NLPDAKI

          (111) 111      120       130       140       150          165
     SmMK (109) GLASGISAFLWLYTSIHGNKPAKVVVNSELPLGSGLGSSAALCVALSAALLALSD
     AtMK (111) WLSSGISTFLWLYTRIIGFNPATVVINSELPYGSGLGSSAALCVALTAALLASSI
     CrMK (109) GLASGVSAFLWLYTAIHGCKPAKAVVTSELPLGSGLGSSAAFCVALSAALLALSD
Consensus (111) GLASGISAFLWLYTAIHG KPAKVVVNSELPLGSGLGSSAALCVALSAALLALSD

          (166) 166           180       190       200       210     220
     SmMK (164) SLKLDFSHQGWQTFGDSELDLVNKWAFEGEKMIHGRPSGIDNTVSTFGNMIKFRS
     AtMK (166) SEKTRG--NGWSSLDETNLELLNKWAFEGEKIIHGKPSGIDNTVSAYGNMIKFCS
     CrMK (164) SVNLDFSHQGWQVFGESELELVNKWALEGEKIIHGKPSGIDNTVSTYGNMIKFRS
Consensus (166) SLKLDFSHQGWQSFGESELELVNKWAFEGEKIIHGKPSGIDNTVSTYGNMIKFRS

          (221) 221      230       240       250       260          275
     SmMK (219) GELTRIKTNMPLKMLVTNTKVGRNTRALVAGVSERAARHGGAMTSVFKAVDSISN
     AtMK (219) GEITRLQSNMPLRMLITNTRVGRNTKALVSGVSQRAVRHPDAMKSVFNAVDSISK
     CrMK (219) GELTRINTNMPLKMLITNTKVGRNTKALVAGVSERTLRHPSAMSSVFNAVDSISN
Consensus (221) GELTRINTNMPLKMLITNTKVGRNTKALVAGVSERALRHP AMSSVFNAVDSISN

          (276) 276           290       300       310       320     330
     SmMK (274) EVAAIIQSPVSDDLAITEKEEKLGELMEMNQGLLQCMGVSHGSIETVIKTTLKYK
     AtMK (274) ELAAIIQS--KDETSVTEKEERIKELMEMNQGLLLSMGVSHSSIEAVILTTVKHK
     CrMK (274) EMASVIQAPVSDDLAITEKEEKLEELMEMNQGLLLCMGVSHASIETVLRTTLKYK
Consensus (276) ELAAIIQSPVSDDLAITEKEEKL ELMEMNQGLLLCMGVSHASIETVIKTTLKYK

          (331) 331      340       350       360       370          385
     SmMK (329) LATKLTGAGGGGCVLTLLPTLLAGTVVDKVIAELEESGFQCLIAGIGGRGMEISF
     AtMK (327) LVSKLTGAGGGGCVLTLLP---TGTVVDKVVEELESSGFQCFTALIGGNGAQICY
     CrMK (329) LSSKLTGAGGGGCVLTLLPTLLSGSVVDKVVSELESNGFQCFTAGIGGNGMEISF
Consensus (331) LASKLTGAGGGGCVLTLLPTLLSGTVVDKVVAELESSGFQCFTAGIGGNGMEISF

          (386) 386 390
     SmMK (384) SGFS-
     AtMK (379) -----
     CrMK (384) TGFS-
Consensus (386) SGFS
```

Figure S6. Sequence alignment of MK proteins from *S. miltiorrhiza*, *Arabidopsis thaliana* and *Catharanthus roseus*. Proteins included are *A. thaliana* AtMK (NP_198097), *C. roseus* CrMK (ADR65111), and *S. miltiorrhiza* SmMK (JN831104). The peroxisomal targeting signal 2 (PTS2) related nonapeptide (KIILAGEHA) is indicated by '***'.

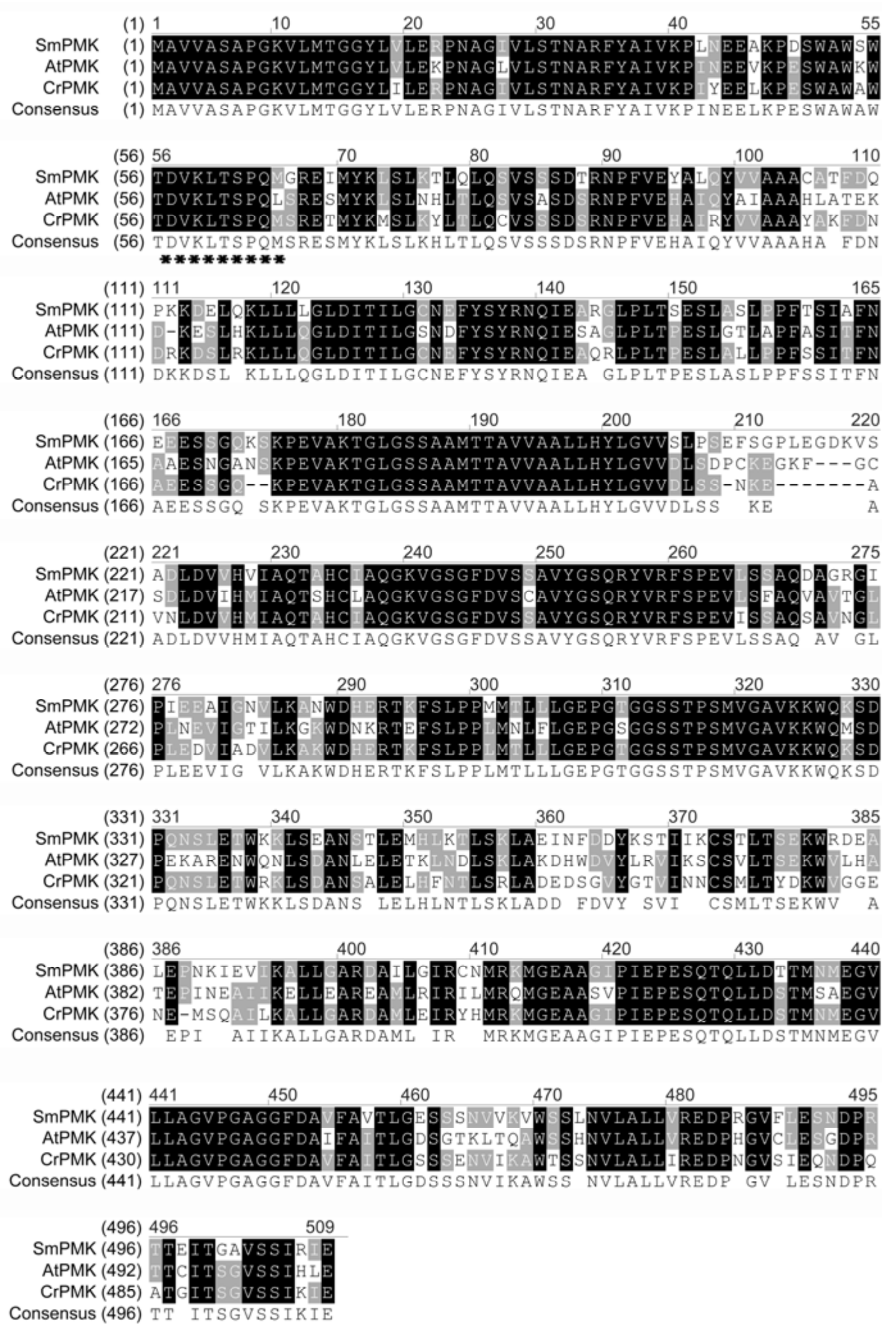


Figure S7. Sequence alignment of PMK proteins from *S. miltiorrhiza*, *Arabidopsis* thaliana and *Catharanthus roseus*. Proteins included are *A. thaliana* AtPMK (NP_174473), *C. roseus* CrPMK (ADR65112), and *S. miltiorrhiza* SmPMK (JN831095). The PTS2 related nonapeptide (DVKLTSPQL/M) is indicated by ‘***’.

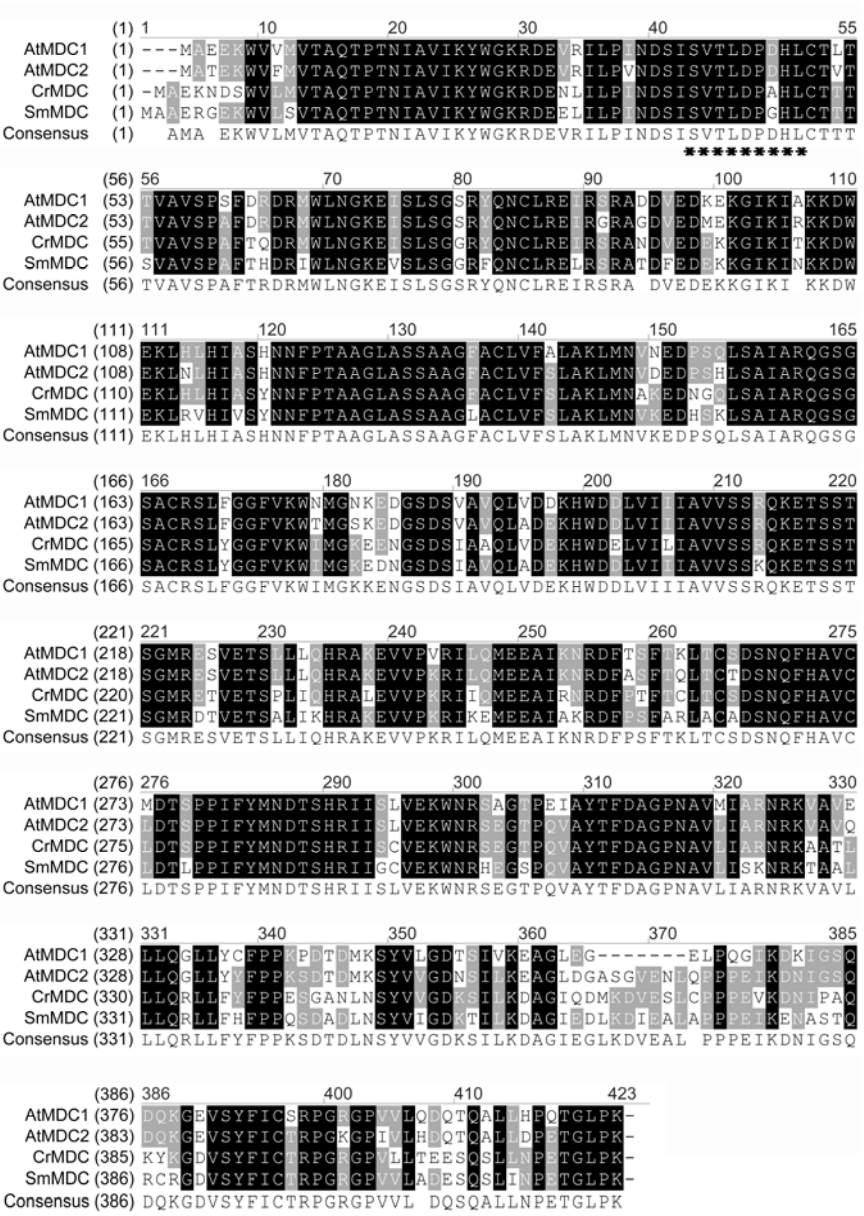


Figure S8. Sequence alignment of MDC proteins from *S. miltiorrhiza*, *Arabidopsis thaliana* and *Catharanthus roseus*. Proteins included are *A. thaliana* AtMDC (NP_174473), *C. roseus* CrMDC (ADR65113), and *S. miltiorrhiza* SmMDC (JN831105). The PTS2 related nonapeptide (SVTLDPXHL) is indicated by ‘***’.

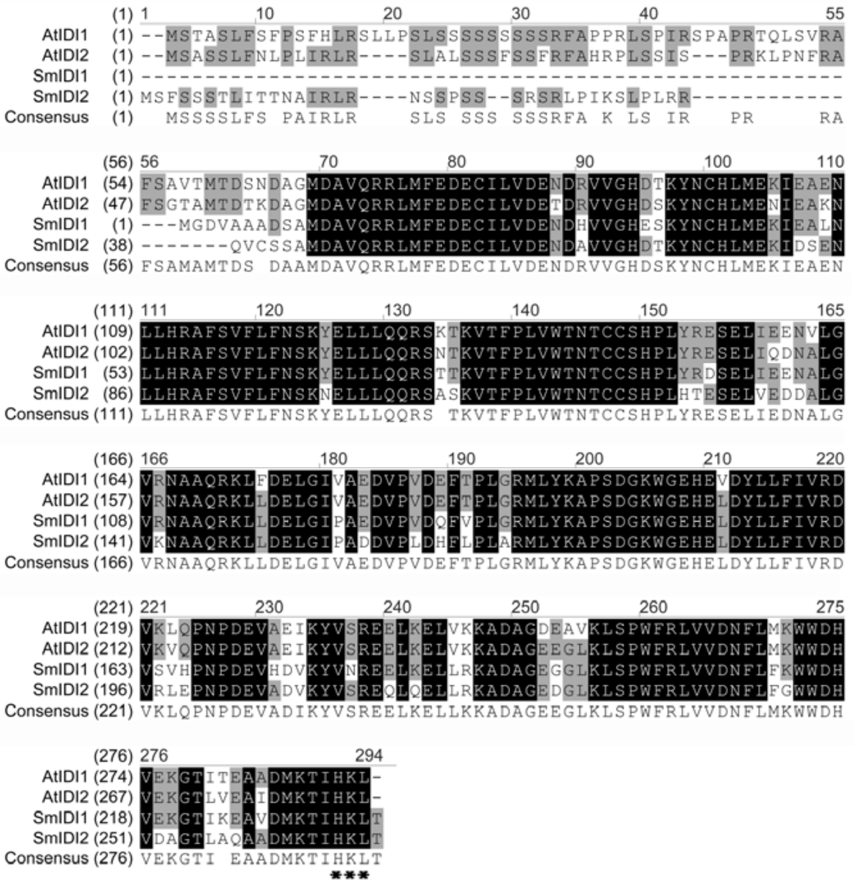
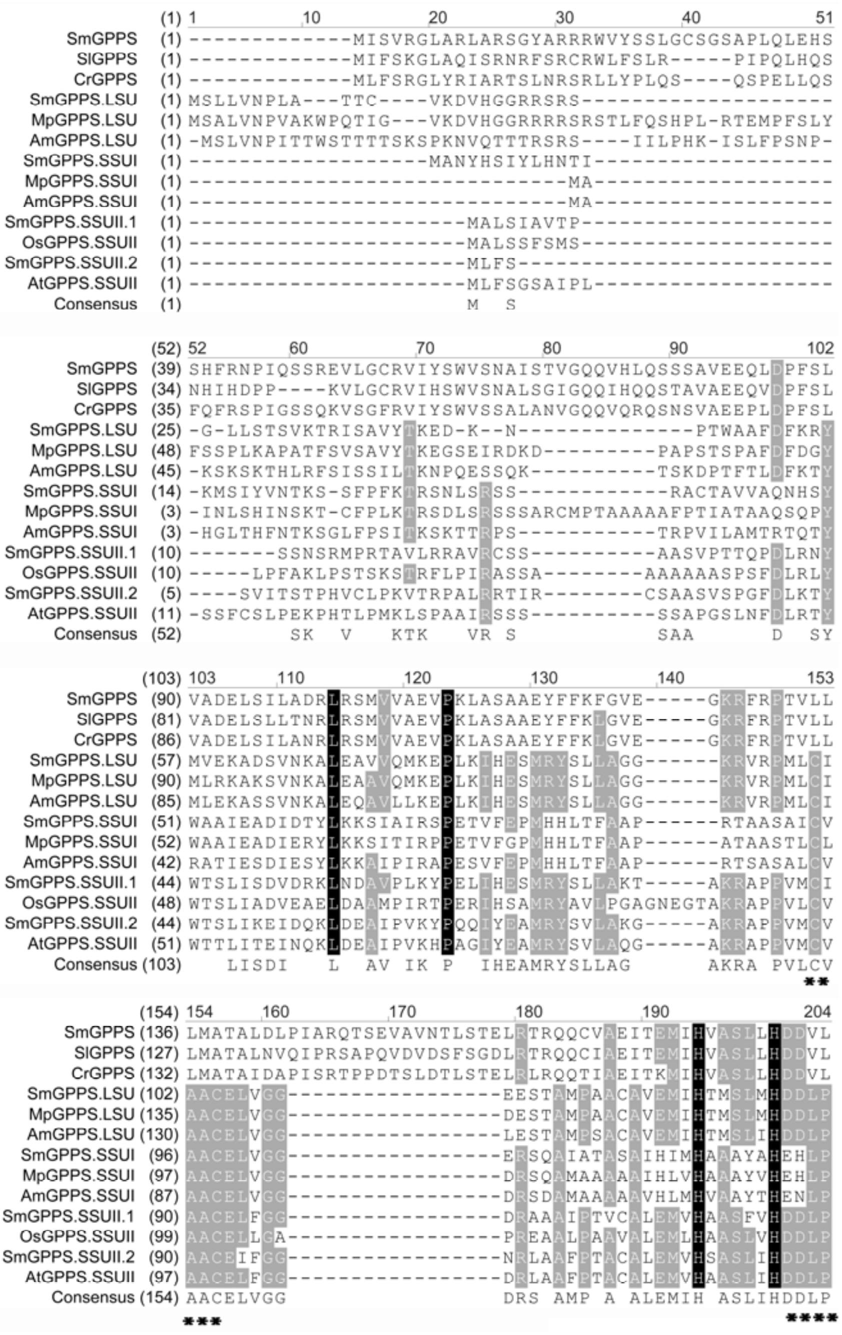


Figure S9. Sequence alignment of IDI proteins from *S. miltiorrhiza* and *Arabidopsis thaliana*. Proteins included are *A. thaliana* AtIDI1 (NP_197148), AtIDI2 (NP_186927), and two *S. miltiorrhiza* SmIDIs.The PTS1 related motif (HKL) is indicated by '***'.



```
                  (1) 1        10        20        30        40         51
SmGPPS            (1) -------------MISVRGLARLARSGYARRRWVYSSLGCSGSAPLQLEHS
SlGPPS            (1) -------------MIFSKGLAQISRNRFSRCRWLFSLR-----PIPQLHQS
CrGPPS            (1) -------------MLFSRGLYRIARTSLNRSRLLYPLQS----QSPELLQS
SmGPPS.LSU        (1) MSLLVNPLA---TTC----VKDVHGGRRSRS--------------------
MpGPPS.LSU        (1) MSALVNPVAKWPQTIG---VKDVHGGRRRRSRSTLFQSHPL-RTEMPFSLY
AmGPPS.LSU        (1) -MSLVNPITTWSTTTTSKSPKNVQTTTRSRS----IILPHK-ISLFPSNP-
SmGPPS.SSUI       (1) -------------------MANYHSIYLHNTI-------------------
MpGPPS.SSUI       (1) ------------------------------MA-------------------
AmGPPS.SSUI       (1) ------------------------------MA-------------------
SmGPPS.SSUII.1    (1) ----------------------MALSIAVTP--------------------
OsGPPS.SSUII      (1) ----------------------MALSSFSMS--------------------
SmGPPS.SSUII.2    (1) ----------------------MLFS-------------------------
AtGPPS.SSUII      (1) ----------------------MLFSGSAIPL-------------------
Consensus         (1)                       M  S

                 (52) 52      60        70        80        90          102
SmGPPS           (39) SHFRNPIQSSREVLGCRVIYSWVSNAISTVGQQVHLQSSSAVEEQLDPFSL
SlGPPS           (34) NHIHDPP----KVLGCRVIHSWVSNALSGIGQQIHQQSTAVAEEQVDPFSL
CrGPPS           (35) FQFRSPIGSSQKVSGFRVIYSWVSSALANVGQQVQRQSNSVAEEPLDPFSL
SmGPPS.LSU       (25) -G-LLSTSVKTRISAVYTKED-K--N--------------PTWAAFDFKRY
MpGPPS.LSU       (48) FSSPLKAPATFSVSAVYTKEGSEIRDKD---------PAPSTSPAFDFDGY
AmGPPS.LSU       (45) -KSKSKTHLRFSISSILTKNPQESSQK----------TSKDPTFTLDFKTY
SmGPPS.SSUI      (14) -KMSIYVNTKS-SFPFKTRSNLSRSS------------RACTAVVAQNHSY
MpGPPS.SSUI       (3) -INLSHINSKT-CFPLKTRSDLSRSSSARCMPTAAAAAFPTIATAAQSQPY
AmGPPS.SSUI       (3) -HGLTHFNTKSGLFPSITKSKTTRPS-----------TRPVILAMTRTQTY
SmGPPS.SSUII.1   (10) -------SSNSRMPRTAVLRRAVRCSS----------AASVPTTQPDLRNY
OsGPPS.SSUII     (10) -----LPFAKLPSTSKSTRFLPIRASSA--------AAAAAASPSFDLRLY
SmGPPS.SSUII.2    (5) ----SVITSTPHVCLPKVTRPALRRTIR--------CSAASVSPGFDLKTY
AtGPPS.SSUII     (11) -SSFCSLPEKPHTLPMKLSPAAIRSSS----------SSAPGSLNFDLRTY
Consensus        (52)         SK  V   KTK   VR S           SAA      D  SY

                (103) 103    110       120       130       140          153
SmGPPS           (90) VADELSILADRLRSMVVAEVPKLASAAEYFFKFGVE-----GKRFRPTVLL
SlGPPS           (81) VADELSLLTNRLRSMVVAEVPKLASAAEYFFKLGVE-----GKRFRPTVLL
CrGPPS           (86) VADELSILANRLRSMVVAEVPKLASAAEYFFKLGVE-----GKRFRPTVLL
SmGPPS.LSU       (57) MVEKADSVNKALEAVVQMKEPLKIHESMRYSLLAGG------KRVRPMLCI
MpGPPS.LSU       (90) MLRKAKSVNKALEAAVQMKEPLKIHESMRYSLLAGG------KRVRPMLCI
AmGPPS.LSU       (85) MLEKASSVNKALEQAVLLKEPLKIHESMRYSLLAGG------KRVRPMLCI
SmGPPS.SSUI      (51) WAAIEADIDTYLKKSIAIRSPETVFEPMHHLTFAAP------RTAASAICV
MpGPPS.SSUI      (52) WAAIEADIERYLKKSITIRPPETVFGPMHHLTFAAP------ATAASTLCL
AmGPPS.SSUI      (42) RATIESDIESYLKKAIPIRAPESVFEPMHHLTFAAP------RTSASALCV
SmGPPS.SSUII.1   (44) WTSLISDVDRKLNDAVPLKYPELIHESMRYSLLAKT-----AKRAPPVMCI
OsGPPS.SSUII     (48) WTSLIADVEAELDAAMPIRTPERIHSAMRYAVLPGAGNEGTAKRAPPVLCV
SmGPPS.SSUII.2   (44) WTSLIKEIDQKLDEAIPVKYPQQIYEAMRYSVLAKG-----AKRAPPVMCV
AtGPPS.SSUII     (51) WTTLITEINQKLDEAIPVKHPAGIYEAMRYSVLAQG-----AKRAPPVMCV
Consensus       (103)    LISDI   L  AV IK P  IHEAMRYSLLAG      AKRA PVLCV
                                                                     **

                (154) 154   160       170       180       190          204
SmGPPS          (136) LMATALDLPIARQTSEVAVNTLSTELRTRQQCVAEITEMIHVASLLHDDVL
SlGPPS          (127) LMATALNVQIPRSAPQVDVDSFSGDLRTRQQCIAEITEMIHVASLLHDDVL
CrGPPS          (132) LMATAIDAPISRTPPDTSLDTLSTELRLRQQTIAEITKMIHVASLLHDDVL
SmGPPS.LSU      (102) AACELVGG-----------------EESTAMPAACAVEMIHTMSLMHDDLP
MpGPPS.LSU      (135) AACELVGG-----------------DESTAMPAACAVEMIHTMSLMHDDLP
AmGPPS.LSU      (130) AACELVGG-----------------LESTAMPSACAVEMIHTMSLIHDDLP
SmGPPS.SSUI      (96) AACELVGG-----------------ERSQAIATASAIHIMHAAAYAHEHLP
MpGPPS.SSUI      (97) AACELVGG-----------------DRSQAMAAAAAIHLVHAAAYVHEHLP
AmGPPS.SSUI      (87) AACELVGG-----------------DRSDAMAAAAAVHLMHVAAYTHENLP
SmGPPS.SSUII.1   (90) AACELFGG-----------------DRAAAIPTVCALEMVHAASFVHDDLP
OsGPPS.SSUII     (99) AACELLGA-----------------PREAALPAAVALEMLHAASLVHDDLP
SmGPPS.SSUII.2   (90) AACEIFGG-----------------NRLAAFPTACALEMVHSASLIHDDLP
AtGPPS.SSUII     (97) AACELFGG-----------------DRLAAFPTACALEMVHAASLIHDDLP
Consensus       (154) AACELVGG                 DRS AMP A ALEMIH ASLIHDDLP
                      ***                                            ****
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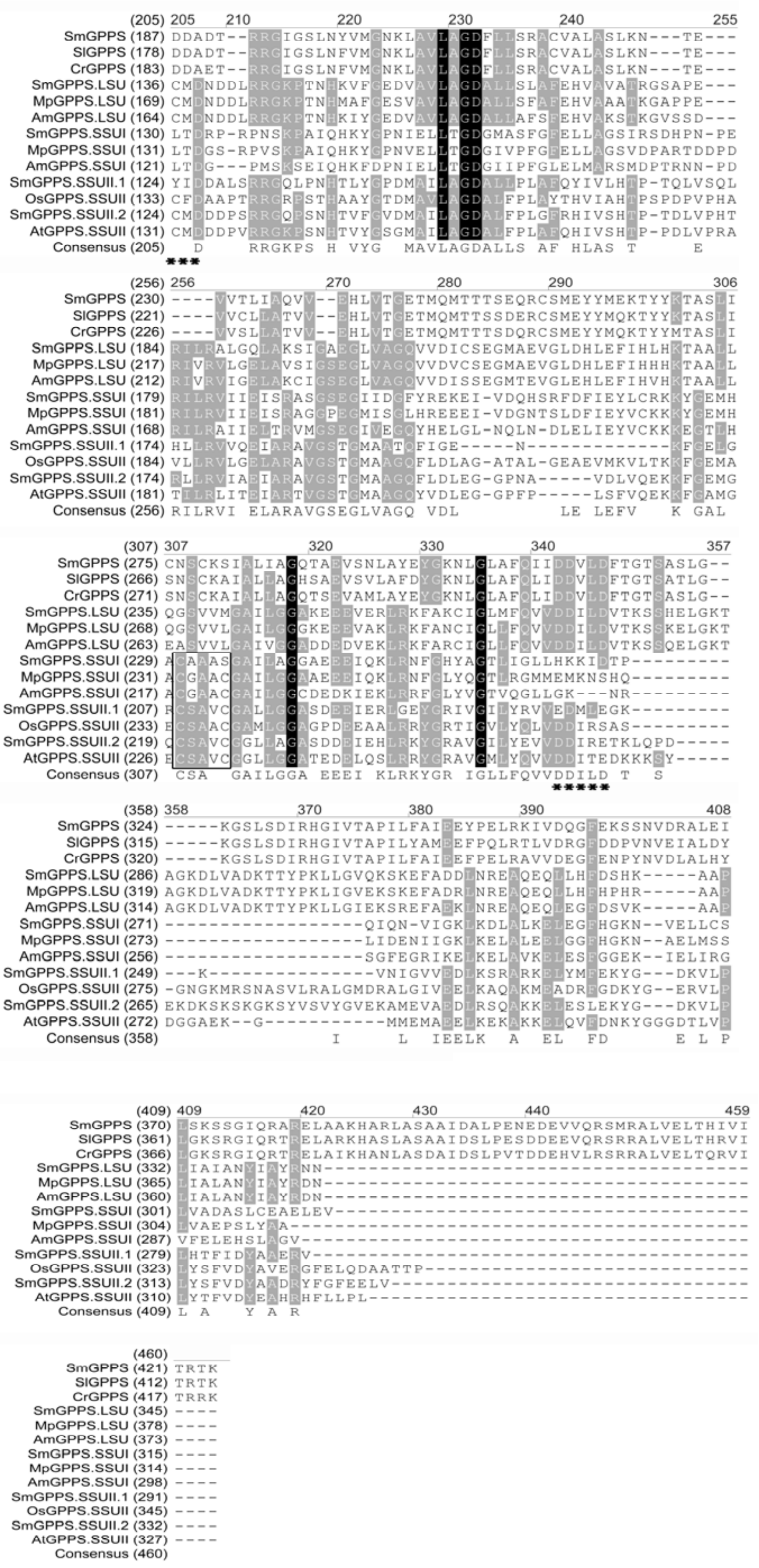


```
               (205) 205  210       220       230       240            255
       SmGPPS (187) DDADT--RRGIGSLNYVMGNKLAVLAGDFLLSRACVALASLKN---TE---
       SlGPPS (178) DDADT--RRGIGSLNFVMGNKLAVLAGDFLLSRACVALASLKN---TE---
       CrGPPS (183) DDAET--RRGIGSLNFVMGNKLAVLAGDFLLSRACVALASLKN---TE---
   SmGPPS.LSU (136) CMDNDDLRRGKPTNHKVFGEDVAVLAGDALLSLAFEHVAVATRGSAPE---
   MpGPPS.LSU (169) CMDNDDLRRGKPTNHMAFGESVAVLAGDALLSFAFEHVAAATKGAPPE---
   AmGPPS.LSU (164) CMDNDDLRRGKPTNHKIYGEDVAVLAGDALLAFSFEHVAKSTKGVSSD---
  SmGPPS.SSUI (130) LTDRP-RPNSKPAIQHKYGPNIELLTGDGMASFGFELLAGSIRSDHPN-PE
  MpGPPS.SSUI (131) LTDGS-RPVSKPAIQHKYGPNVELLTGDGIVPFGFELLAGSVDPARTDDPD
  AmGPPS.SSUI (121) LTDG---PMSKSEIQHKFDPNIELLTGDGIIPFGLELMARSMDPTRNN-PD
SmGPPS.SSUII.1 (124) YIDDALSRRGQLPNHTLYGPDMAILAGDALLPLAFQYIVLHTP-TQLVSQL
  OsGPPS.SSUII (133) CFDAAPTRRGRPSTHAAYGTDMAVLAGDALFPLAYTHVIAHTPSPDPVPHA
SmGPPS.SSUII.2 (124) CMDDDPSRRGQPSNHTVFGVDMAILAGDALFPLGFRHIVSHTP-TDLVPHT
  AtGPPS.SSUII (131) CMDDDPVRRGKPSNHTVYGSGMAILAGDALFPLAFQHIVSHTP-PDLVPRA
     Consensus (205)   D    RRGKPS H VYG  MAVLAGDALLS AF HLAS T     E
                    ***

               (256) 256           270       280       290            306
       SmGPPS (230) ----VVTLIAQVV--EHLVTGETMQMTTTSEQRCSMEYYMEKTYYKTASLI
       SlGPPS (221) ----VVCLLATVV--EHLVTGETMQMTTSSDERCSMEYYMQKTYYKTASLI
       CrGPPS (226) ----VVSLLATVV--EHLVTGETMQMTTTSDQRCSMEYYMQKTYYMTASLI
   SmGPPS.LSU (184) RILRALGQLAKSIGAEGLVAGQVVDICSEGMAEVGLDHLEFIHLHKTAALL
   MpGPPS.LSU (217) RIVRVLGELAVSIGSEGLVAGQVVDVCSEGMAEVGLDHLEFIHHHKTAALL
   AmGPPS.LSU (212) RIVRVIGELAKCIGSEGLVAGQVVDISSEGMTEVGLEHLEFIHVHKTAALL
  SmGPPS.SSUI (179) RILRVIIEISRASGSEGIIDGFYREKEI-VDQHSRFDFIEYLCRKKYGEMH
  MpGPPS.SSUI (181) RILRVIIEISRAGGPEGMISGLHREEEI-VDGNTSLDFIEYVCKKKYGEMH
  AmGPPS.SSUI (168) RILRAIIELTRVMGSEGIVEGQYHELGL-NQLN-DLELIEYVCKKKEGTLH
SmGPPS.SSUII.1 (174) HLLRVVQEIARAVGSTGMAATQFIGE-----N-------------KFGELG
  OsGPPS.SSUII (184) VLLRVLGELARAVGSTGMAAGQFLDLAG-ATAL-GEAEVMKVLTKKFGEMA
SmGPPS.SSUII.2 (174) RLLRVIAEIARAVGSTGMAAGQFLDLEG-GPNA-----VDLVQEKKFGEMG
  AtGPPS.SSUII (181) TILRLITEIARTVGSTGMAAGQYVDLEG-GPFP-----LSFVQEKKFGAMG
     Consensus (256) RILRVI ELARAVGSEGLVAGQ VDL        LE LEFV    K GAL

               (307) 307          320       330       340            357
       SmGPPS (275) CNSCKSIALIAGQTAEVSNLAYEYGKNLGLAFQIIDDVLDFTGTSASLG--
       SlGPPS (266) SNSCKAIALLAGHSAEVSVLAFDYGKNLGLAFQLIDDVLDFTGTSATLG--
       CrGPPS (271) SNSCKAIALLAGQTSEVAMLAYEYGKNLGLAFQLIDDVLDFTGTSASLG--
   SmGPPS.LSU (235) QGSVVMGAILGGAKEEEVERLRKFAKCIGLMFQVVDDILDVTKSSHELGKT
   MpGPPS.LSU (268) QGSVVLGAILGGGKEEEVAKLRKFANCIGLLFQVVDDILDVTKSSKELGKT
   AmGPPS.LSU (263) EASVVLGAIVGGADDEDVEKLRKFARCIGLLFQVVDDILDVTKSSQELGKT
  SmGPPS.SSUI (229) ACAAASGAILAGGAEEEIQKLRNFGHYAGTLIGLLHKKIDTP---------
  MpGPPS.SSUI (231) ACGAACGAILGGAAEEEIQKLRNFGLYQGTLRGMMEMKNSHQ---------
  AmGPPS.SSUI (217) ACGAACGAILGGCDEDKIEKLRRFGLYVGTVQGLLGK---NR---------
SmGPPS.SSUII.1 (207) RCSAVCGALLGGASDEEIERLGEYGRIVGILYRVVEDMLEGK---------
  OsGPPS.SSUII (233) ECSAACGAMLGGAGPDEEAALRRYGRTIGVLYQLVDDIRSAS---------
SmGPPS.SSUII.2 (219) QCSAVCGGLLAGASDDEIEHLRKYGRAVGILYEVVDDIRETKLQPD-----
  AtGPPS.SSUII (226) ECSAVCGGLLGGATEDELQSLRRYGRAVGMLYQVVDDITEDKKKSY-----
     Consensus (307)  CSA  GAILGGA EEEI KLRKYGR IGLLFQVVDDILD T  S
                                                       *****

               (358) 358         370       380       390             408
       SmGPPS (324) -----KGSLSDIRHGIVTAPILFAIEEYPELRKIVDQGFEKSSNVDRALEI
       SlGPPS (315) -----KGSLSDIRHGIVTAPILYAMEEFPQLRTLVDRGFDDPVNVEIALDY
       CrGPPS (320) -----KGSLSDIRHGIVTAPILFAIEEFPELRAVVDEGFENPYNVDLALHY
   SmGPPS.LSU (286) AGKDLVADKTTYPKLLGVQKSKEFADDLNREAQEQLLHFDSHK-----AAP
   MpGPPS.LSU (319) AGKDLVADKTTYPKLIGVEKSKEFADRLNREAQEQLLHFHPHR-----AAP
   AmGPPS.LSU (314) AGKDLVADKTTYPKLLGIEKSREFAEKLNREAQEQLEGFDSVK-----AAP
  SmGPPS.SSUI (271) ------------------QIQN-VIGKLKDLALKELEGFHGKN--VELLCS
  MpGPPS.SSUI (273) ------------------LIDENIIGKLKELALEELGGFHGKN--AELMSS
  AmGPPS.SSUI (256) ------------------SGFEGRIKELKELAVKELESFGGEK--IELIRG
SmGPPS.SSUII.1 (249) ---K---------------VNIGVVEDLKSRARKELYMFEKYG---DKVLP
  OsGPPS.SSUII (275) -GNGKMRSNASVLRALGMDRALGIVEELKAQAKMEADRFGDKYG--ERVLP
SmGPPS.SSUII.2 (265) EKDKSKSKGKSYVSVYGVEKAMEVAEDLRSQAKKELESLEKYG---DKVLP
  AtGPPS.SSUII (272) DGGAEK--G-----------MMEMAEELKEKAKKELQVFDNKYGGGDTLVP
     Consensus (358)                I     L  IEELK  A  EL  FD      E L P

               (409) 409        420       430       440                459
       SmGPPS (370) LSKSSGIQRARELAAKHARLASAAIDALPENEDEVVQRSMRALVELTHIVI
       SlGPPS (361) LGKSRGIQRTRELARKHASLASAAIDSLPESDDEEVQRSRRALVELTHRVI
       CrGPPS (366) LGKSRGIQRTRELAIKHANLASDAIDSLPVTDDEHVLRSRRALVELTQRVI
   SmGPPS.LSU (332) LIAIANYIAYRNN--------------------------------------
   MpGPPS.LSU (365) LIALANYIAYRDN--------------------------------------
   AmGPPS.LSU (360) LIALANYIAYRDN--------------------------------------
  SmGPPS.SSUI (301) LVADASLCEAELEV-------------------------------------
  MpGPPS.SSUI (304) LVAEPSLYAA-----------------------------------------
  AmGPPS.SSUI (287) VFELEHSLAGV----------------------------------------
SmGPPS.SSUII.1 (279) LHTFIDYAAERV---------------------------------------
  OsGPPS.SSUII (323) LYSFVDYAVERGFELQDAATTP-----------------------------
SmGPPS.SSUII.2 (313) LYSFVDYAADRYFGFEELV--------------------------------
  AtGPPS.SSUII (310) LYTFVDYEAHRHFLLPL----------------------------------
     Consensus (409) L A   Y A R

               (460)
       SmGPPS (421) TRTK
       SlGPPS (412) TRTK
       CrGPPS (417) TRRK
   SmGPPS.LSU (345) ----
   MpGPPS.LSU (378) ----
   AmGPPS.LSU (373) ----
  SmGPPS.SSUI (315) ----
  MpGPPS.SSUI (314) ----
  AmGPPS.SSUI (298) ----
SmGPPS.SSUII.1 (291) ----
  OsGPPS.SSUII (345) ----
SmGPPS.SSUII.2 (332) ----
  AtGPPS.SSUII (327) ----
     Consensus (460)
```

Figure S10. Sequence alignment of GPPS proteins from *S. miltiorrhiza* and various other plants. GPPS proteins inlucled are *Solanum lycopersicum* SlGPPS (ABB88703), *Catharanthus roseus* CrGPPS (ACC77966), *Mentha x piperita* MpGPPS.LSU (AF182828), *Antirrhinum majus* AmGPPS.LSU (AAS82860), MpGPPS.SSUI (AF182827), AmGPPS.SSUI (AAS82859), rice OsGPPS.SSUII (EAY87007), *Arabidopsis thaliana* AtGPPS.SSUII (At4g38460), and five *S. miltiorrhiza* GPPSs. The FARM (the first aspartate-rich motif, DDLPCMD), SARM (the second aspartate-rich motif, DDXXD) and CXXXC motifs are indicated by '***'.

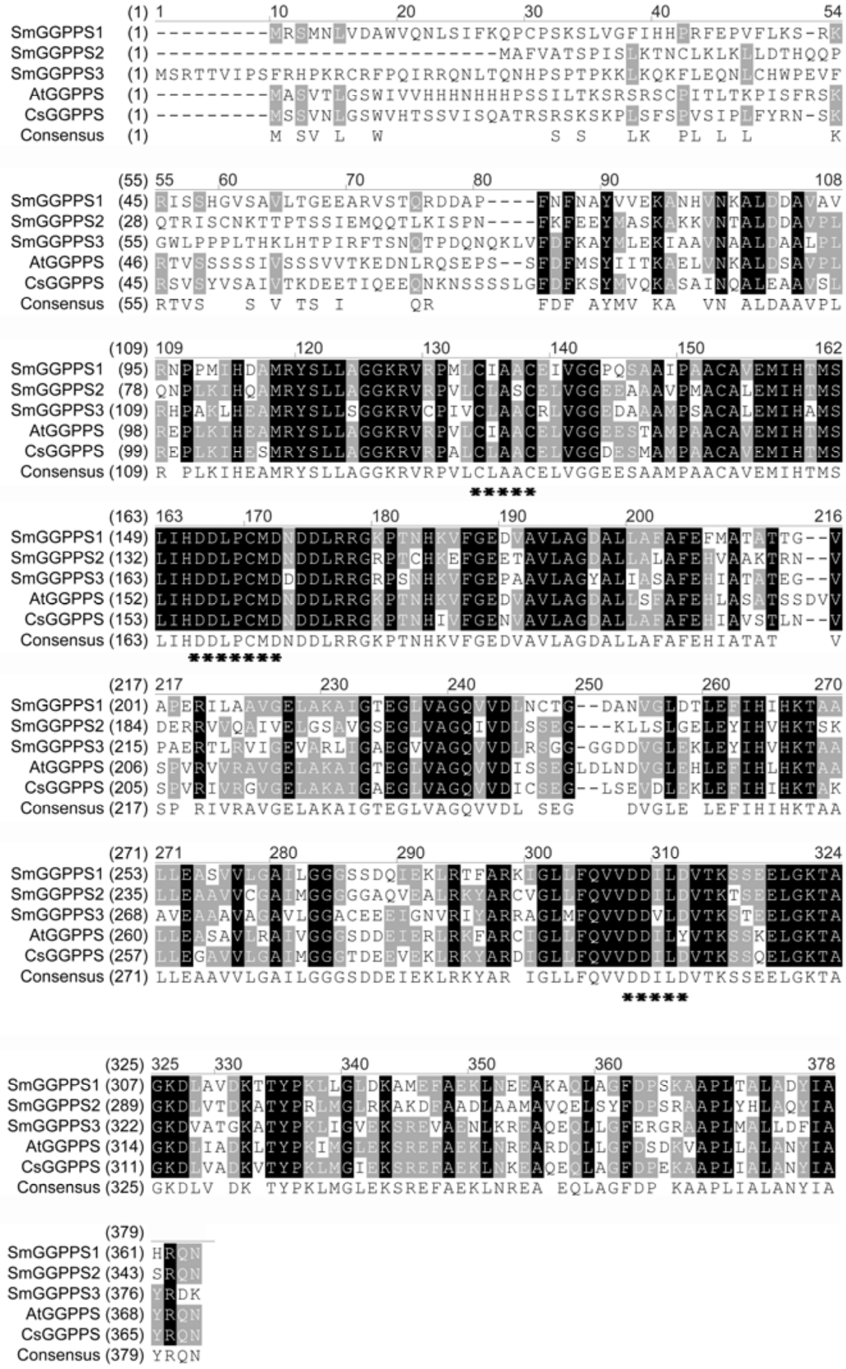


Figure S11. Sequence alignment of GGPPS proteins from *S. miltiorrhiza* and various other plants. GGPPS proteins included are *A. thaliana* AtGGPPS (AAM65107), *Croton sublyratus* CsGGPPS (BAA86284), and three *S. miltiorrhiza* SmGGPPSs. The FARM (the first aspartate-rich motif, DDLPCMD), SARM (the second aspartate-rich motif, DDXXD) and CXXXC motifs are indicated by '***'.

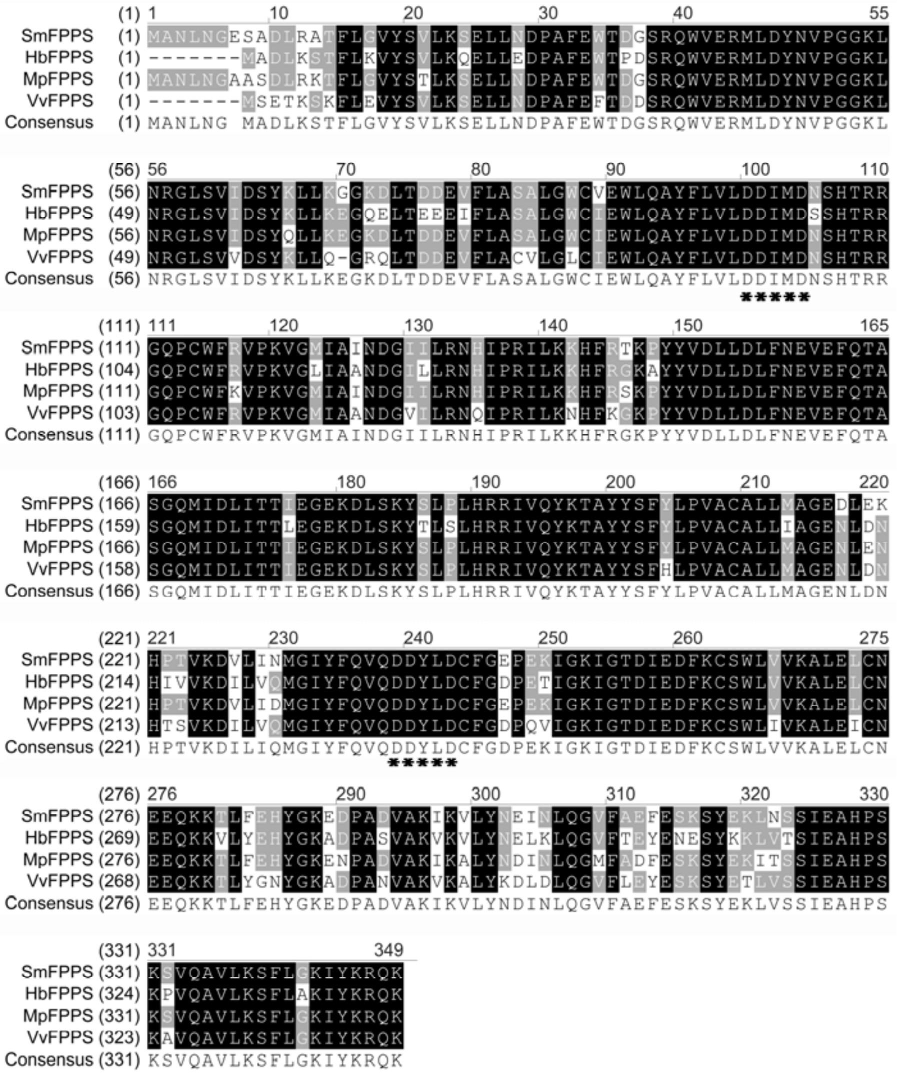


Figure S12. Sequence alignment of FPPS proteins from *S. miltiorrhiza* and various other plants. FPPS proteins included are *Hevea brasiliensis* HbFPPS (AAM98379), *Mentha x piperita* MpFPPS (AF384040), *Vitis vinifera* VvFPPS (AAX76910), and the *S. miltiorrhiza* SmFPPS. The FARM (the first aspartate-rich motif, DDIMD) and SARM motifs (the second aspartate-rich motif, DDXXD) are indicated by '***'.

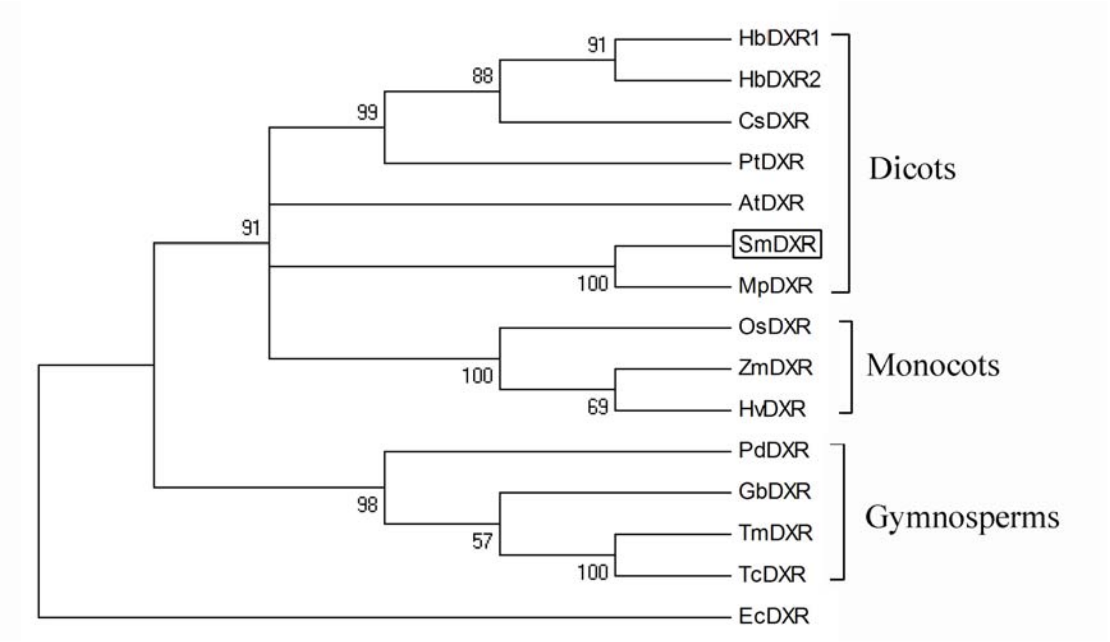


Figure S13. Phylogenetic relationships of DXRs form *S. miltiorrhiza* and various other plants. DXR proteins included are *S. miltiorrhiza* SmDXR (ABJ80680), *Hevea brasiliensis* HbDXR1 (AAS94121), HbDXR2 (ABF18928), *A. thaliana* AtDXR (AED97658), *Populus trichocarpa* PtDXR (XP_002318048), *Zea mays* ZmDXR (CAC03581), *Mentha* × *piperita* MpDXR (AF116825), rice OsDXR (AF367205), *H. vulgare* HvDXR (CAE47438), *C. stellatopilosus* CsDXR (ABO38177), *P. densiflora* PdDXR (ACC54558), *G. biloba* GbDXR (AAR95700), *Taxus x media* TmDXR (AAU87836), and *T. cuspidate* TcDXR (AAT47184). *E. coli* EcDXR (NP_414715) was used as an out group.

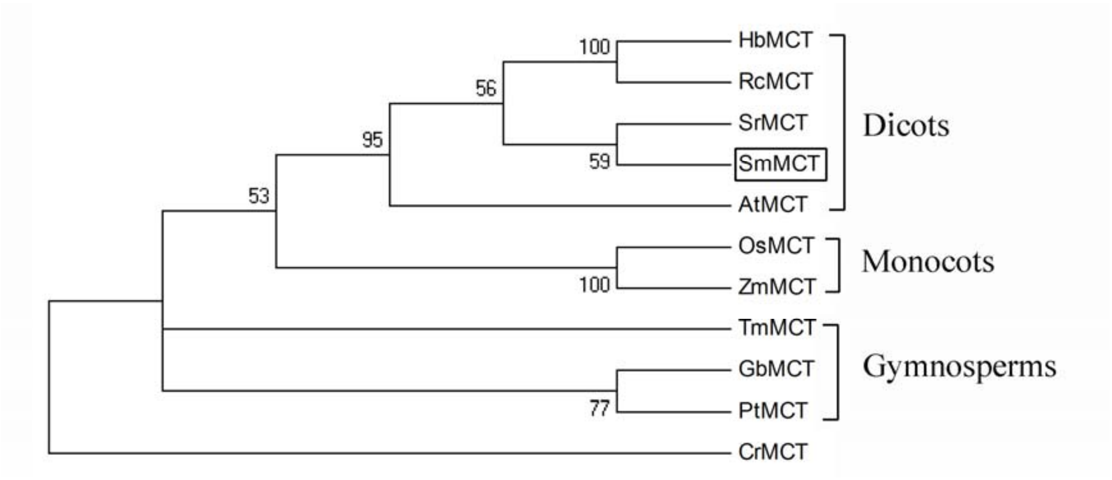


Figure S14. Phylogenetic relationships of MCTs form *S. miltiorrhiza* and various other plants. MCT proteins included are *S. rebaudiana* SrMCT (ABB88837), *S. miltiorrhiza* SmMCT (JN831096), *A. thaliana* AtMCT (NP_565286), *H. brasiliensis* HbMCT (BAF98291), *R. communis* RcMCT (XP_002519366), rice OsMCT (BAD82245), *Z. mays* ZmMCT (NP_001140440), *Taxus x media* TmMCT (ABU48538), *G. biloba* GbMCT (AAZ80386), and *P. sitchensis* PtMCT (ACN40114). *E. coli* EcMCT (XP_001698942) was used as an out group.

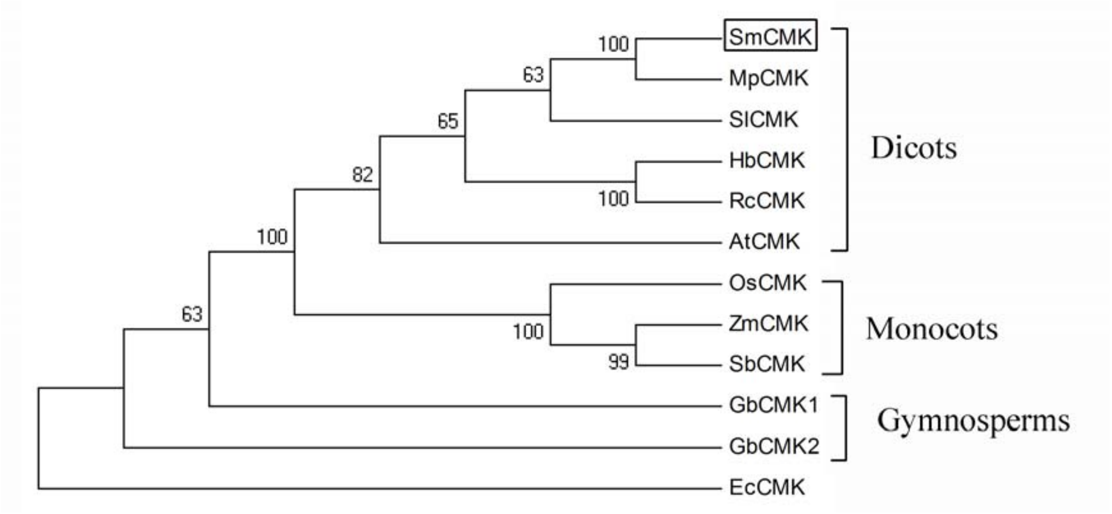


Figure S15. Phylogenetic relationships of CMKs form *S. miltiorrhiza* and various other plants. CMK proteins included are *G. biloba* GbCMK1 (AAZ80384), GbCMK2 (DQ102359), *A. thaliana* AtCMK (BT000208), *L. esculentum* LeCMK (AAB49936), *S. miltiorrhiza* SmCMK (ABP96842), rice OsCMK (NP_915832), *Z. mays* ZmCMK (NP_001149138), *S. bicolor* SbCMK (XP_002456497), *M. piperita* MpCMK (CAB65292), *H. brasiliensis* HbCMK (BAF98293), and *R. communis* RbCMK (XP_002523216). *E. coli* EcCMK (NP_415726) was used as an out group.

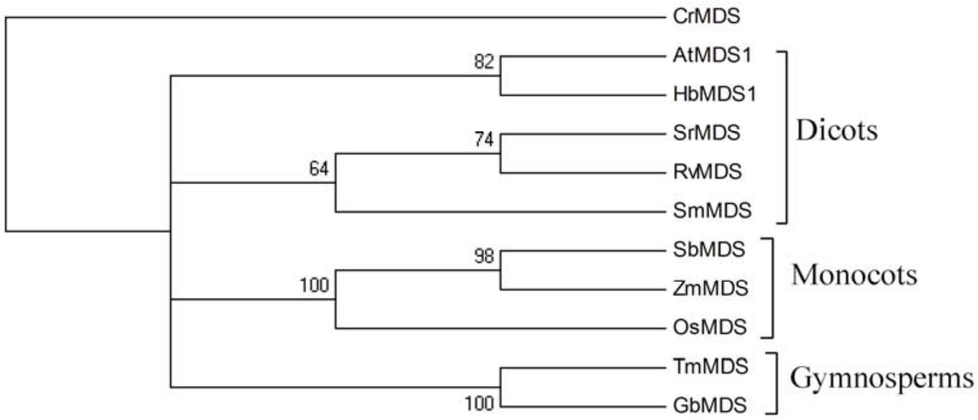


Figure S16. Phylogenetic relationships of MDSs form *S. miltiorrhiza* and various other plants. MDS proteins included are SrMDS (*S. rebaudiana*, ABG23395), RvMDS (*R. verticillata*, ABV89583), HbMDS1 (*H. brasiliensis*, BAF98294), AtMDS1 (*A. thaliana*, NP_850971), OsMDS (*O.sativa*, BAD29384), SbMDS (*S. bicolor*, XP_002452756), ZmMDS (*Z,mays*, NP_001150687), GbMDS (*G. biloba*, ABL77405), TmMDS (*Taxus x media*, ABU48537), and *S. miltiorrhiza* SmMDS (JN831097). CrMDS (*C. reinhardtii*, XP_001690985) was used as an out group.

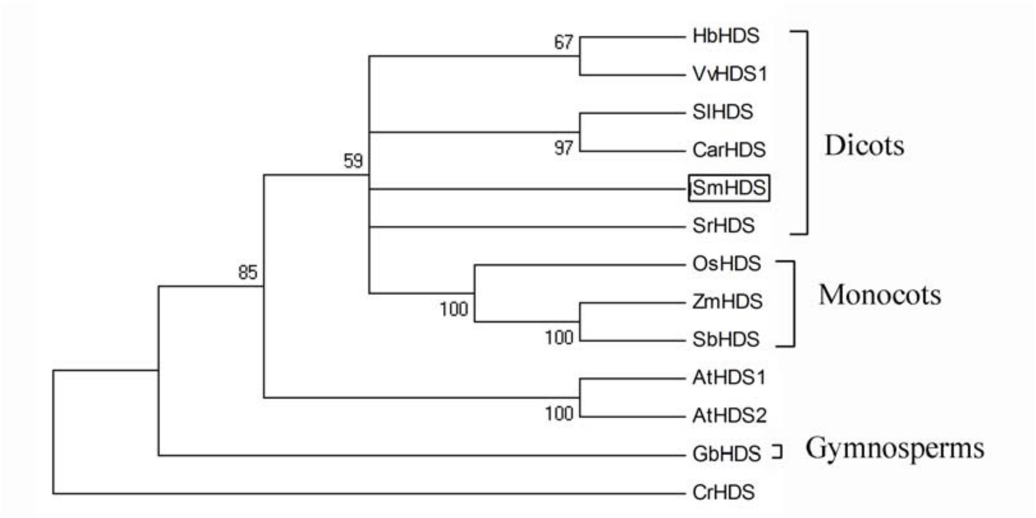


Figure S17. Phylogenetic relationships of HDSs form *S. miltiorrhiza* and various other plants. HDS proteins included are AtHDS1 (*A. thaliana*, NP_200868.2), HbHDS (*H. brasiliensis*, BAF98296), AtHDS2/GcpE protein (BAB09833), CarHDS (*C. roseus*, AAO24774), GbHDS (*G. biloba*, ABB78087), VvHDS1 (*V. vinifera*, XP_002285130), SlHDS (*S. lycopersicum*, AF435086), SrHDS (*S. rebaudiana*, ABG75916.2), OsHDS (*O. sativa*, AAO72576), ZmHDS (*Z. mays*, ACL53652), SbHDS (*S. bicolor*, XP_002454137), and *S. miltiorrhiza* SmHDS (JN831098). CrHDS (*C. reinhardtii*, XP_001690937) was used as an out group.

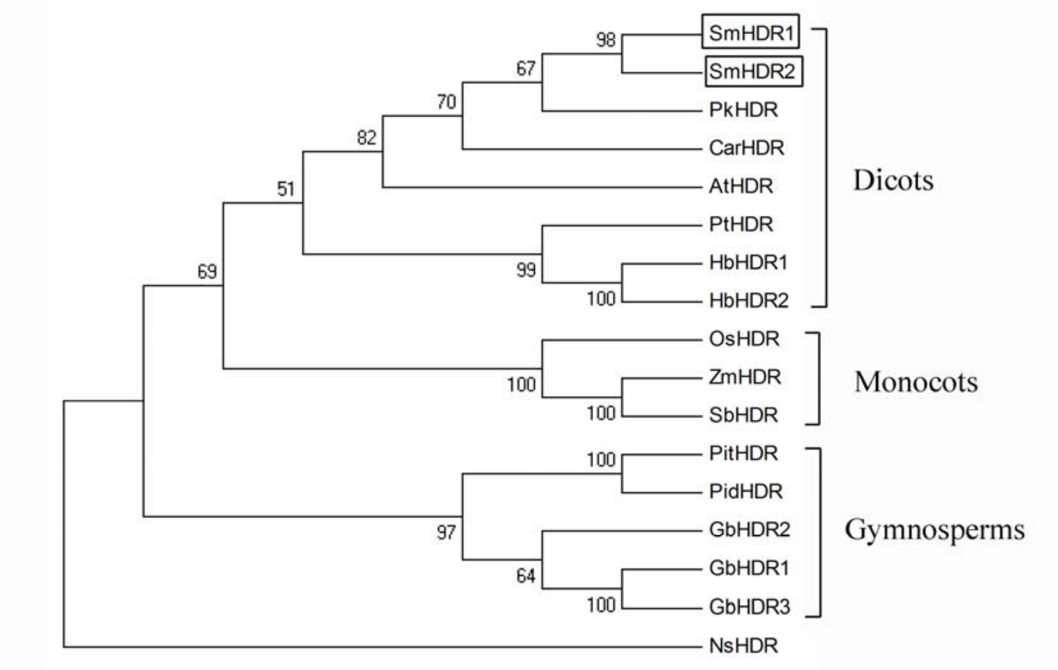


Figure S18. Phylogenetic relationships of HDRs form *S. miltiorrhiza* and various other plants. HDR proteins included are PtHDR (*P. trichocarpa*, XP_002305413), HbHDR1 (*H. brasiliensis*, ACG55683), HbHDR2 (*H. brasiliensis*, BAF98297), AtHDR (*A. thaliana*, NP_567965), CarHDR (*C. roseus*, ABI30631), PkHDR (*P. kurrooa*, ABM89226), PitHDR (*P. taeda*, ABO26588), PidHDR (*P. densiflora*, ACC54561), GbHDR1 (*G. biloba*, ABC84344), GbHDR2 (*G. biloba*, ABB78089), GbHDR3 (*G. biloba*, ABB78090), OsHDR (*O. sativa*, NP_001051167), ZmHDR (*Z. mays*, NP_001169300), SbHDR (*S. bicolor*, XP_002463933), and two *S. miltiorrhiza* SmHDRs. NsHDR (*Nostoc sp. PCC 7120*, NP_485028) was used as an out group.

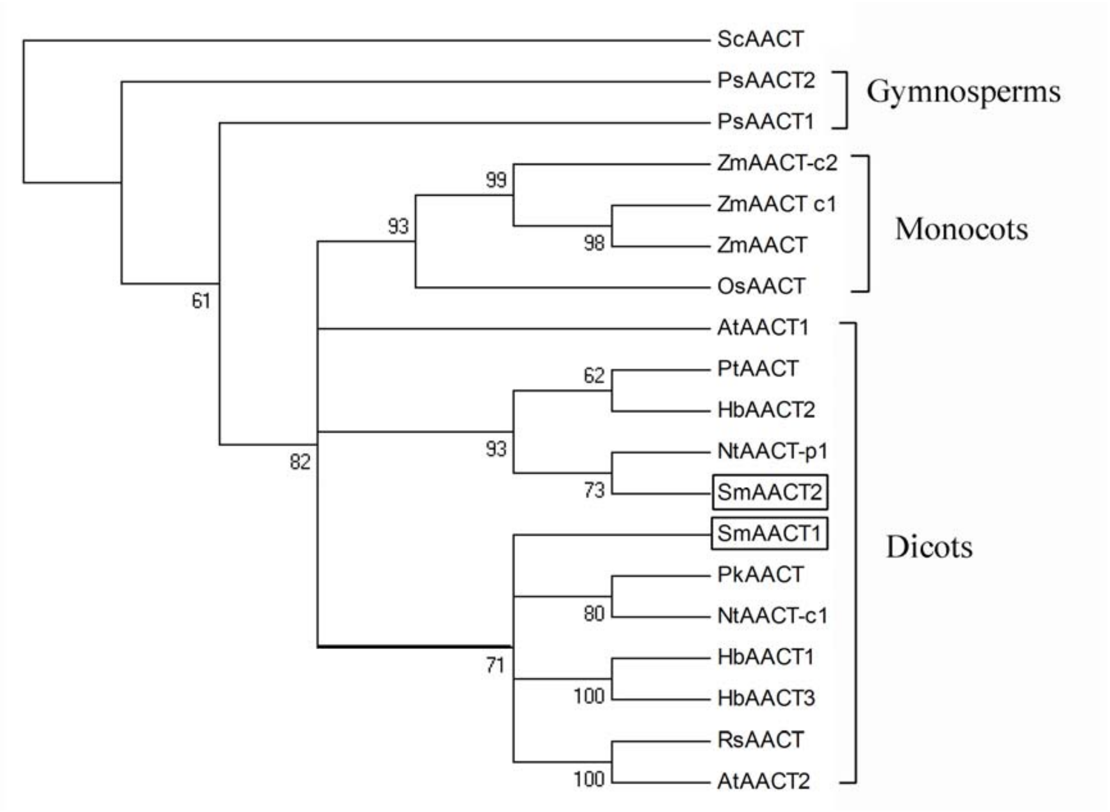


Figure S19. Phylogenetic relationships of AACTs form *S. miltiorrhiza* and various other plants. AACT proteins included are ZmAACT (*Z. mays*, ACF85124), ZmAACT-c1 (ACG34735), ZmAACT-c2 (NP_001148667), OsAACT (*O. sativa*, NP_001041797), AtAACT1 (*A. thaliana*, AT5G47720), AtAACT2 (AT5G48230), PtAACT (*P. sitchensis*, XP_002308755), HbAACT1 (*H. brasiliensis*, BAF98276), HbAACT2 (AF429383), HbAACT3 (BAF98277), RsAACT (*R. sativus*, CAA55006), PkAACT (*P. kurrooa*, ABC74567), PsAACT1 (*P. sitchensis*, ACN40771), PsAACT2 (ACN41149.1), NtAACT-c1 (*N. tabacum*, AAU95618), NtAACT-p1 (AAU95619), and two *S. miltiorrhiza* SmAACTs. ScAACT (*S. cerevisiae*, P41338.3) was used as an out group.

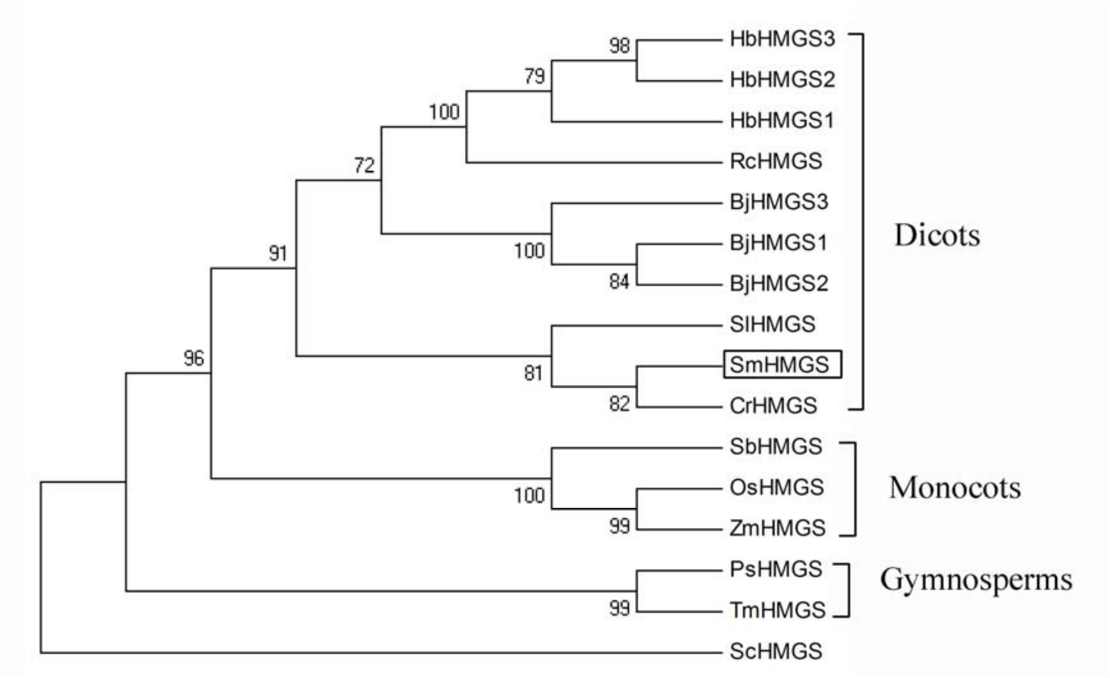


Figure S20. Phylogenetic relationships of HMGSs form *S. miltiorrhiza* and various other plants. HMGS proteins included are BjHMGS1 (*B. juncea*, AF188639), BjHMGS2 (AF188640), BJHMGS3 (AF148847_1), OsHMGS (*O. sativa*, Os08g0544900), SlHMGS (*S. lycopersicum*, ABX55778), HbHMGS1 (*H. brasiliensis*, AF429389), HbHMGS2 (AAS46245.1), HbHMGS3 (BAF98279), TmHMGS (*Taxus x media*, AAT73206), CrHMGS (*C. roseus*, AEC13715), PsHMGS (*P. sylvestris*, CAA65250), SmHMGS (*S. miltiorrhiza*, ACV65039), RcHMGS (*R. communis*, XP_002509692), SbHMGS (*S. bicolor*, XP_002468628), ZmHMGS (*Z. mays*, ACG33137). ScHMGS (*S. cerevisiae*, P54839) was used as an out group.

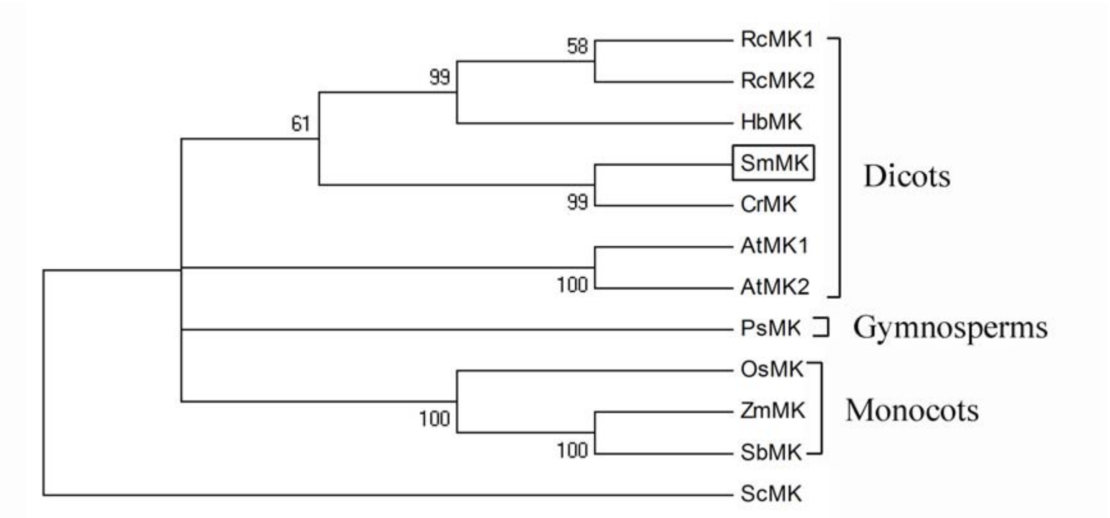


Figure S21. Phylogenetic relationships of MKs form *S. miltiorrhiza* and various other plants. MK proteins included are OsMK (*O. sativa*, Os10g0329300), AtMK1 (*A. thaliana*, NP_198097), AtMK2 (L77688), HbMK (*H. brasiliensis*, AF429384), ZmMK (*Z. mays*, ACG46416), PsMK (*P. sitchensis*, ACN40231), SbMK (*S. bicolor,* XP_002453181), RcMK1 (*R. communis*, XP_002512365), RcMK2 (XP_002529655), CrMK (*C. roseus*, ADR65111), and SmMK (*S. miltiorrhiza*, JN831104). ScMK (*S. cerevisiae*, P24521) was used as an outgroup.

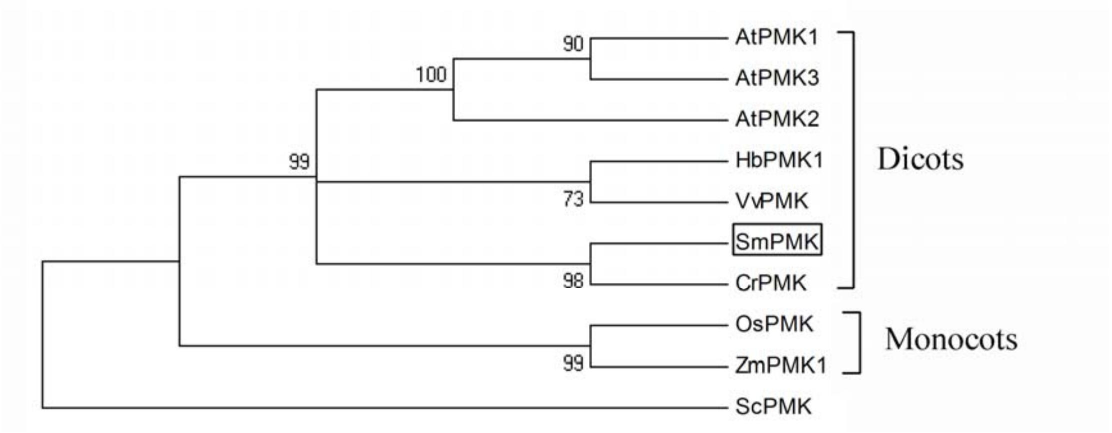


Figure S22. Phylogenetic relationships of PMKs form *S. miltiorrhiza* and various other plants. PMK proteins included are OsPMK (*O. sativa*, Os03g0253100), AtPMK1 (*A. thaliana*, NP_174473), AtPMK2 (NP_001185124), AtPMK3 (BAD43274), HbPMK1 (*H. brasiliensis*, AF429385), ZmPMK1 (Z. mays, ACG35008), VvPMK (V. vinifera, XP_002275808), CrPMK (C. roseus, ADR65112), and SmPMK (*S. miltiorrhiza*, JN831095). ScPMK (*S. cerevisiae* RM11-1a, EDV11711) was used as an out group.

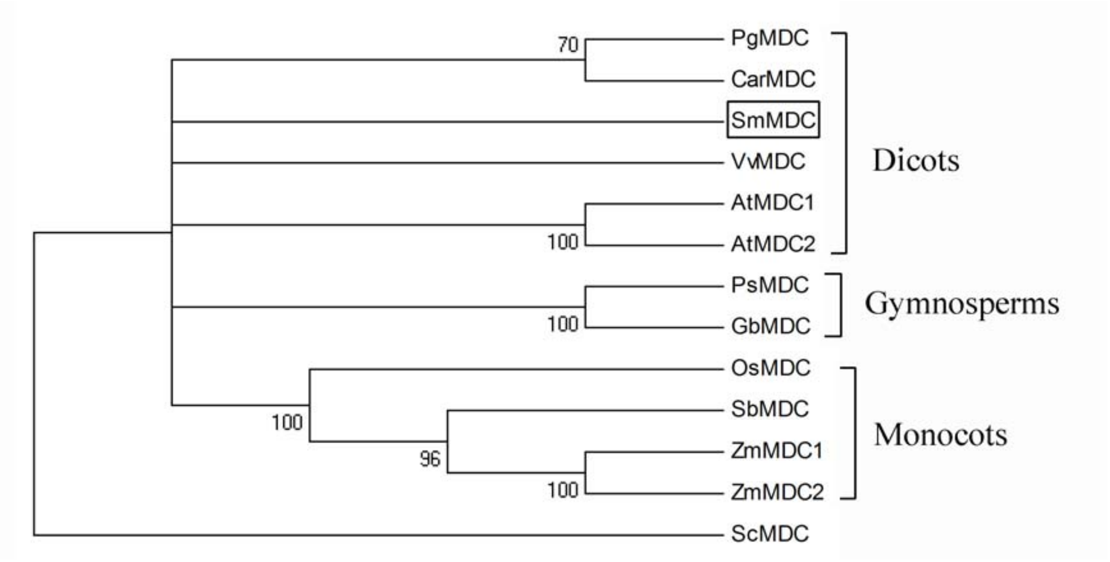


Figure S23. Phylogenetic relationships of MDCs form *S. miltiorrhiza* and various other plants. MDC proteins included are VvMDC (*V. vinifera*, CAN82519), AtMDC1 (*A. thaliana*, NP_181404), AtMDC2 (NP_566995), ZmMDC1 (*Z. mays*, ACF86239), ZmMDC2 (NP_001149256), PsMDC (*P. sitchensis,* ACN41090), SbMDC (*S. bicolor*, XP_002452980), PgMDC (P. ginseng, ADI80345), CrMDC (*C. roseus*, ADR65113), OsMDC (*O.sativa*, BAD27942), GbMDC (*G. biloba*, AAV32433), and SmMDC (*S. miltiorrhiza*, JN831105). ScMDC (*S. cerevisiae*, P32377.2) was used as an out group.

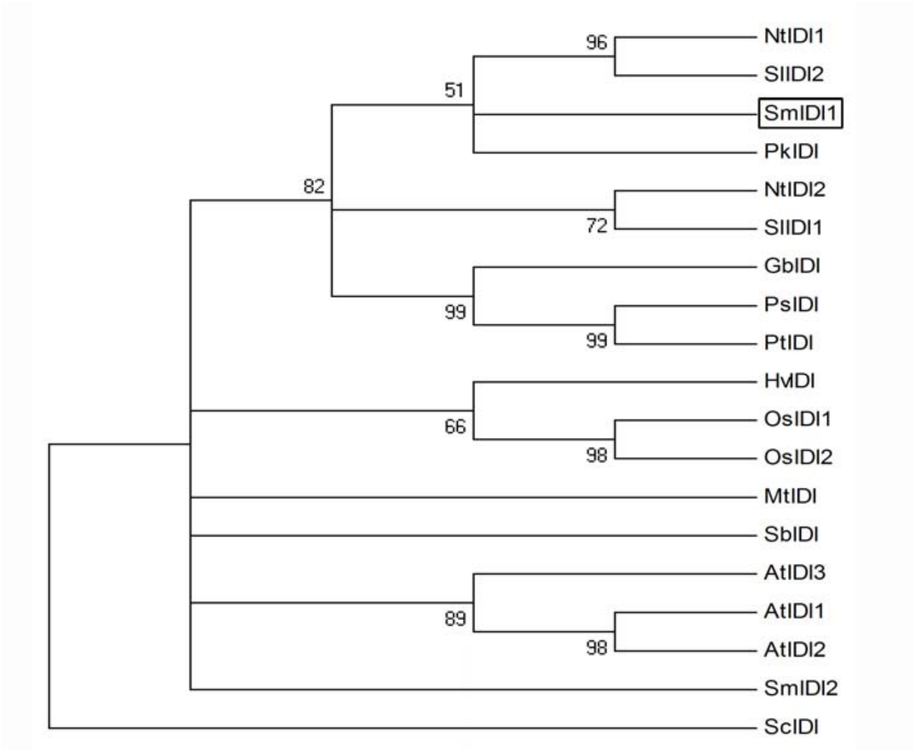


Figure S24. Phylogenetic relationships of IDIs form *S. miltiorrhiza* and various other plants. IDI proteins included are AtIDI1 (*A. thaliana*, AF188066), AtIDI2 (NP_186927), AtIDI3 (AF188067), GbIDI (*G. biloba*, ACU56979), MtIDI (*M. truncatula*, ACJ84381), NtIDI1 (N. tabacum, BAB40973), NtIDI2 (BAB40974), OsIDI1(O. sativa, ABR26078), OsIDI2 (AF188065), PkIDI (*P. kurrooa*, ABO14800), PsIDI (*P. sitchensis*, ACN41037), PtIDI (*P. taeda*, ACU56978), SbIDI (*S. bicolor*, XP_002439804), SlIDI1 (*S. lycopersicum*, ABX55779), SlIDI2 (ACS34993), HvIDI (H. vulgare, BAJ86792), SmIDI1 (*S. miltiorrhiza*, ABV08818) and SmIDI2 (JN831106). ScIDI (*S. cerevisiae*, AAB68245) was used as an out group.

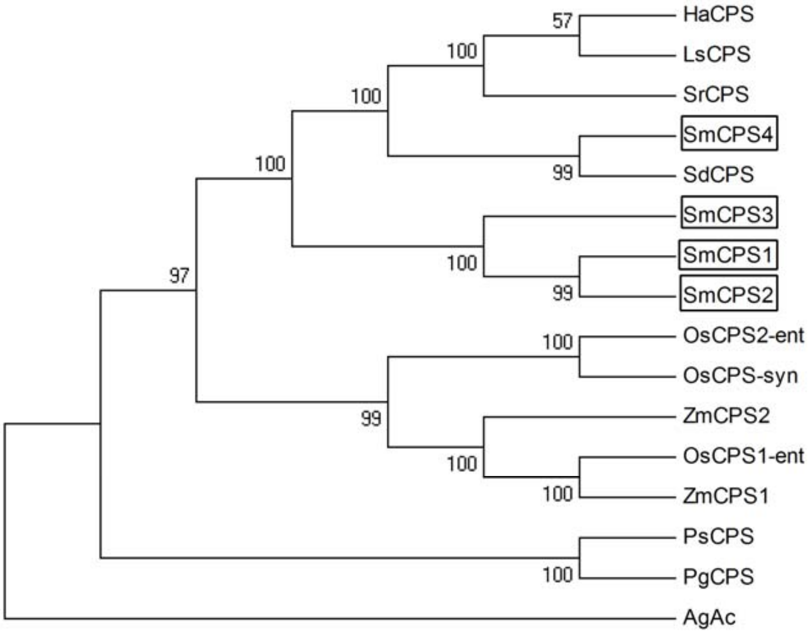


Figure S25. Phylogenetic relationships of CPSs form *S. miltiorrhiza* and various other plants. CPS proteins included are HaCPS (*H. annuus*, CBL42915), SrCPS (*S. rebaudiana*, AAB87091), LsCPS (*L. sativa*, BAB12440), SdCPS (*S. dulcis*, BAB03594), PsCPS (*P. sitchensis*, ADB55709), PgCPS (*P. glauca*, ADB55707), OsCPS1-ent (*O. sativa*, BAD42449.2), OsCPS2-ent/OsCyc2 (BAD42452), OsCPS-syn/OsCyc1 (BAD42451), ZmCPS1 (*Z. mays*, AAA73960), ZmCPS2 AAT70083), SmCPS1 (*S. miltiorrhiza*, ABV57835), SmCPS2 (JN831114), SmCPS3 (JN831115), and SmCPS4 (JN831120). AgAc (*A. grandis*, AAB05407) was used as an outgroup. Sequences in upstream of the partially conserved motif SPYDTAWVAL were trimmed.

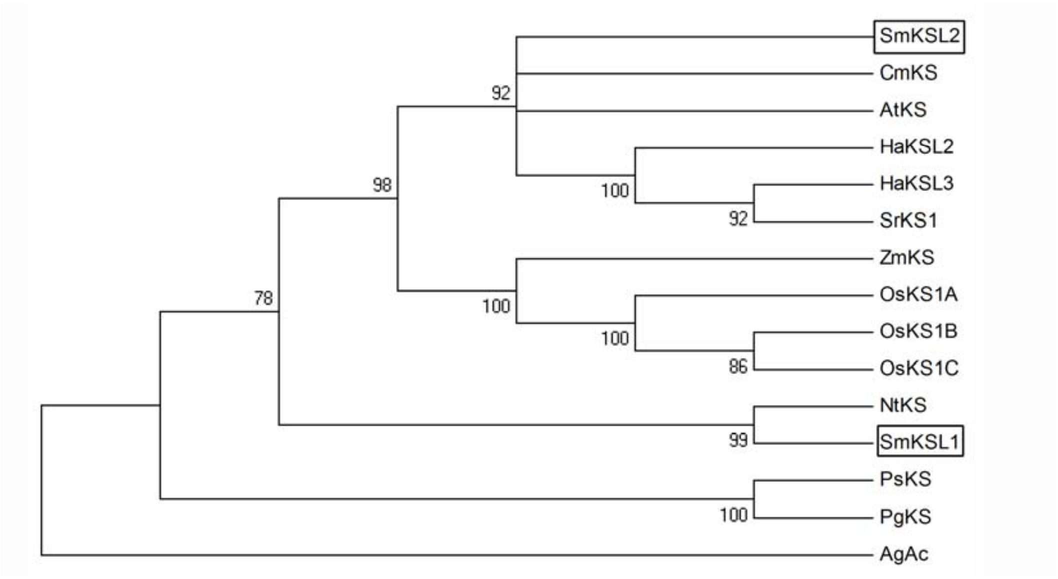
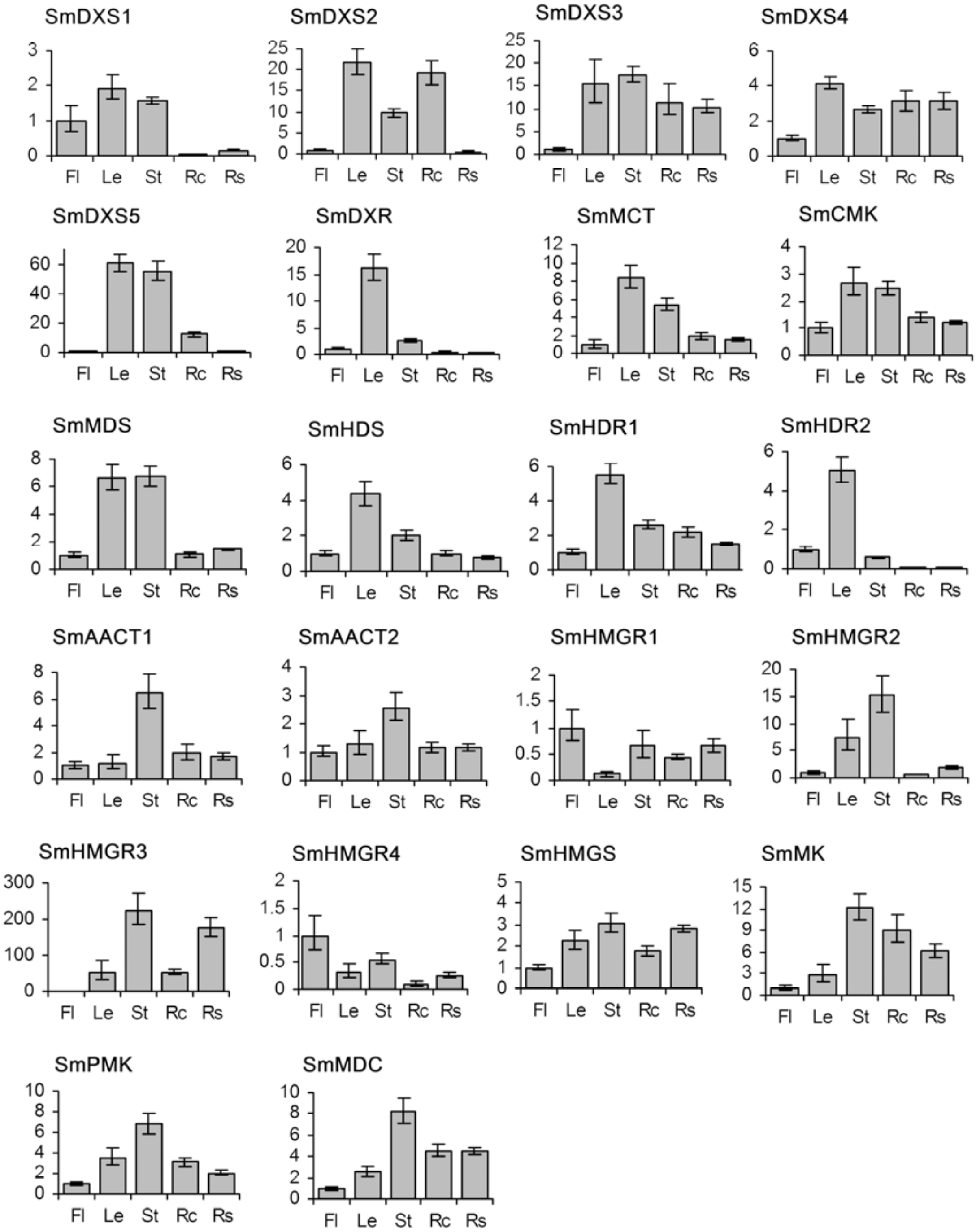


Figure S26. Phylogenetic relationships of KS and KSLs form *S. miltiorrhiza* and various other plants. Proteins included are NtKS (*N. tabacum*, AAS98912), SmKS1 (*S. miltiorrhiza*, ABV08817), SmKSL2 (JN831119), HaKSL2 (*H. annuus*, CBL42916), HaKSL3 (CBL42917), SrKS1 (*S. rebaudiana*, AF097310), CmKS (*C. mollissima*, AEF32083), AtKS (*A. thaliana*, AAC39443), PsKS (*P. sitchensis*, ADB55710), PgKs (*P. glauca*, ADB55708), OsKS1A (*O. sativa*, AAQ72559), OsKS1B (AAQ72560), OsKS1C (AAQ72561.1), and ZmKS (*Z. mays*, AF105149). AgAc (*A. grandis*, AAB05407) was used as an out group. About 200 amino acids in the N-terminal of most KS proteins were trimmed because SmKSL1 lacks those sequences.


SmDXS1
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0
SmDXS2
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15
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5
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SmDXS3
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5
0
SmDXS4
6
4
2
0
SmDXS5
60
40
20
0
SmDXR
20
15
10
5
0
SmMCT
12
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2
1
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SmMDS
8
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4
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6
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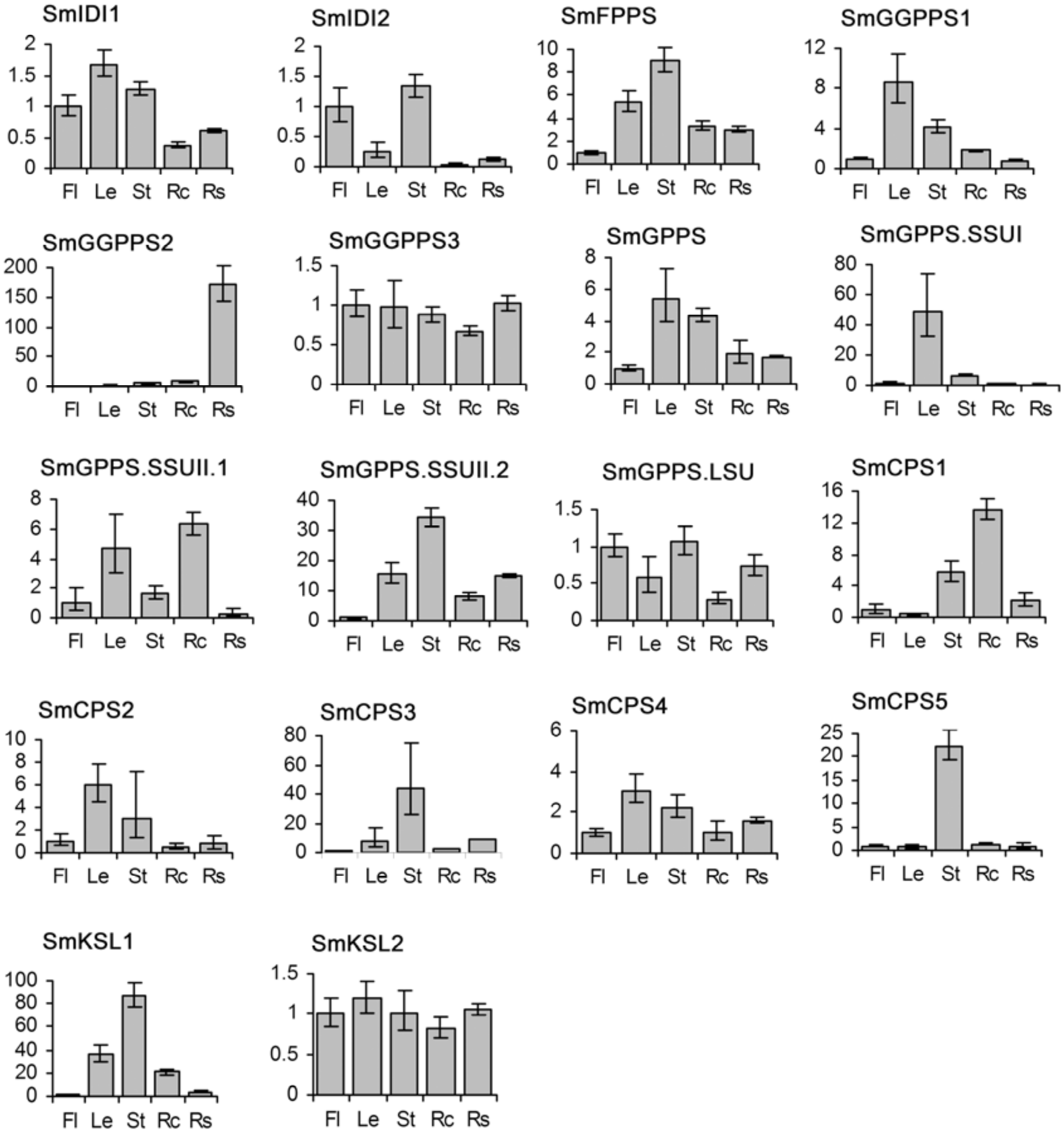
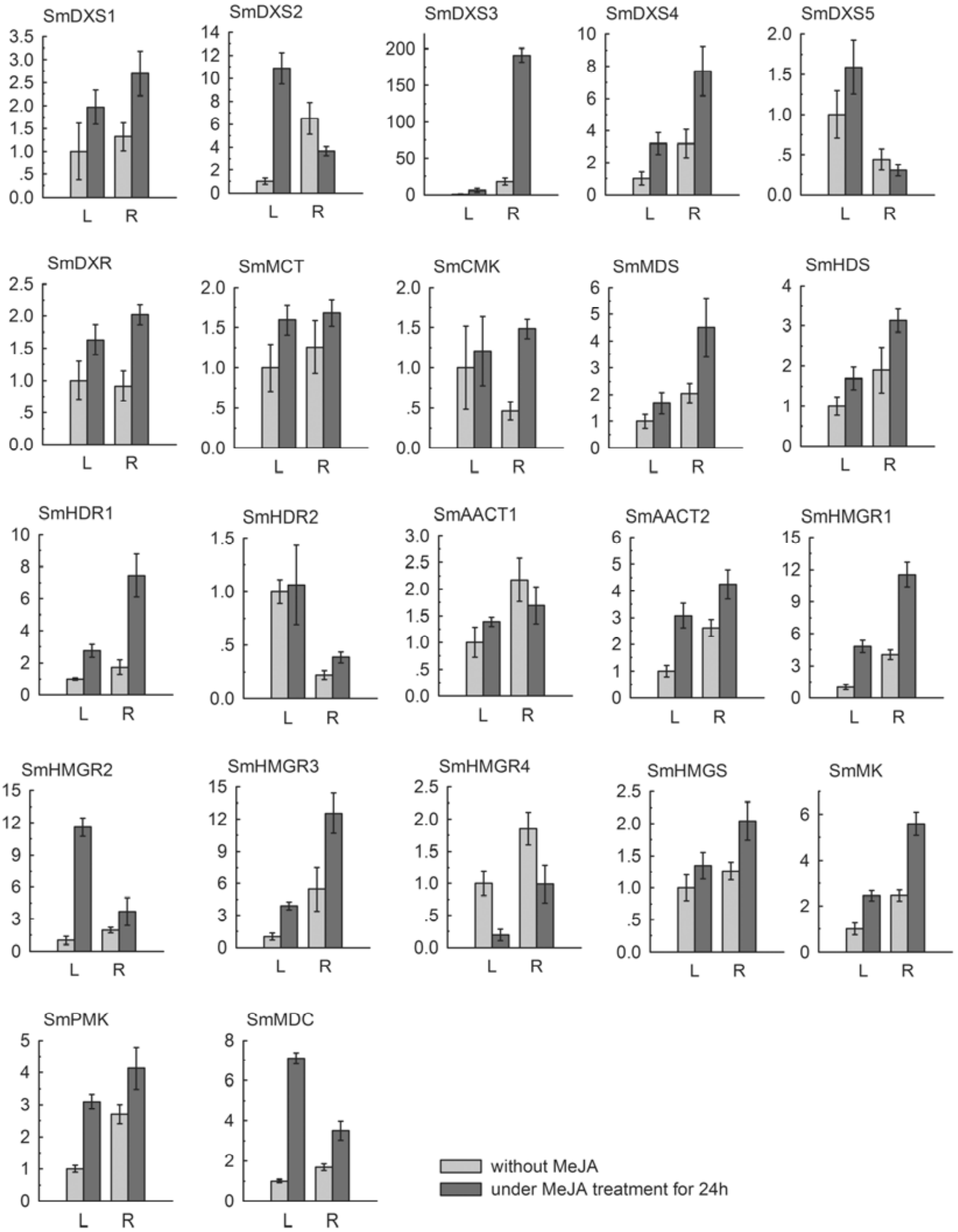


Figure S27. Expression patterns of forty terpenoid biosynthesis-related genes in various tissues of *S. miltiorrhiza* plants. Fold changes of transcript levels in flowers (Fl), leaves (Le), stems (St), root cortices (Rc) and root steles (Rs) of *S. miltiorrhiza* plants grown in soil are shown. Transcript levels in flowers were arbitrarily set to 1.


SmDXS1
SmDXS2
SmDXS3
SmDXS4
SmDXS5
SmDXR
SmMCT
SmCMK
SmMDS
SmHDS
SmHDR1
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SmAACT1
SmAACT2
SmHMGR1
SmHMGR2
SmHMGR3
SmHMGR4
SmHMGS
SmMK
SmPMK
SmMDC
L
R
without MeJA
under MeJA treatment for 24h

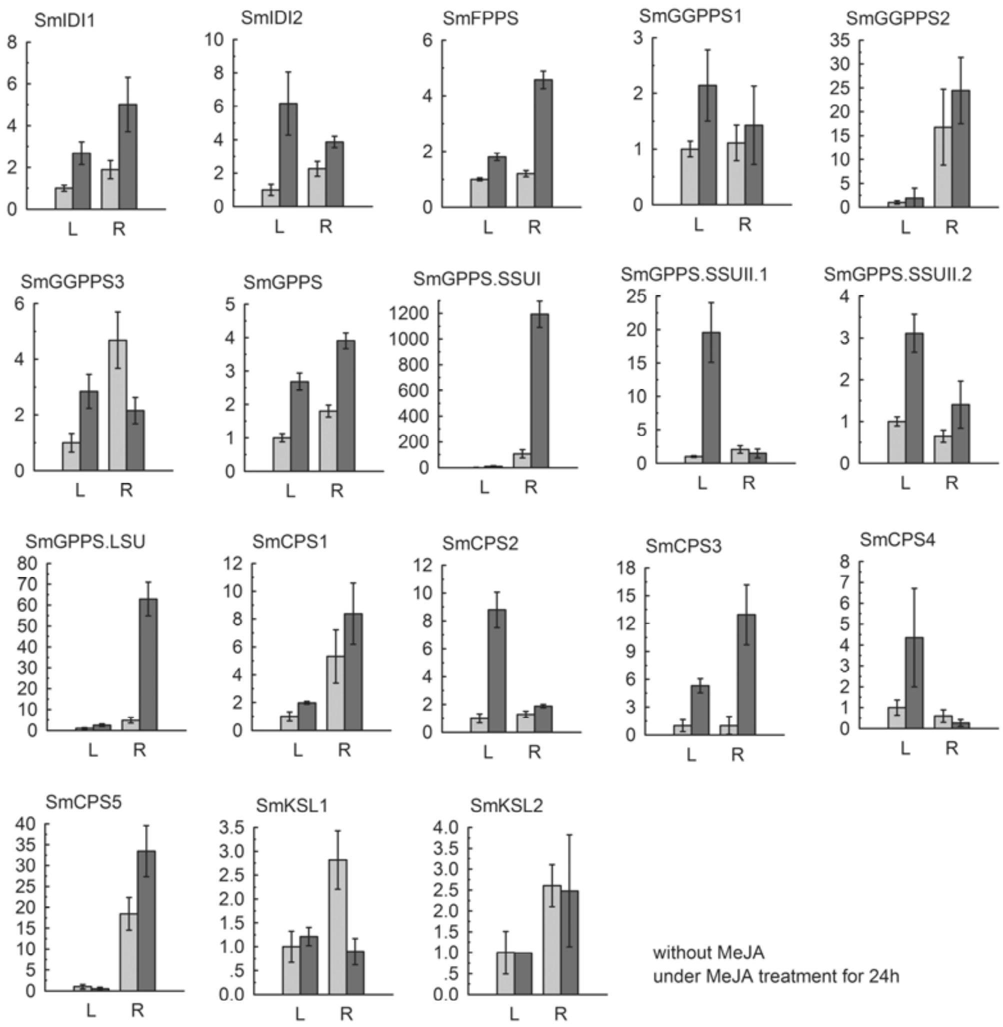

Figure S28. Expression patterns of forty pterpenoid biosynthesis-related genes in *S. miltiorrhiza* plantlets treated with MeJA. Fold changes of transcript levels in leaves (L) and roots (R) of *S. miltiorrhiza* plantlets treated with MeJA for 0 and 24 hours. Transcript levels in leaves of plantlets without treatment were arbitrarily set to 1.

Table S1. Primers used for quantitative real-time RT-PCR.

Gene name	Primer name	Sequence (5' to 3')
SmUBQ	UBQ-F	agatgggcggacacttgctgatta
	UBQ-R	actctccacctccaaagtgatggt
SmDXS1	DXS1-F	catgctcttatacggagcttggcca
	DXS1-R	ggcgtgagtcctgcttccatcagt
SmDXS2	DXS2-F	cagcgcccatatttctcatttcttat
	DXS2-R	gaagactgtcttttcccccaccaat
SmDXS3	DXS3-F	ggctccattgggggatttggttca
	DXS3-R	cactgaagtttgagagcttccatag
SmDXS4	DXS4-F	tctctcgacggccttctcgatgct
	DXS4-R	catcaagagaagagcgtcgcgggt
SmDXS5	DXS5-F	gttggtggctttggatcacacgtt
	DXS5-R	tctctaaagcttctctggatttccaa
SmDXR	DXR-F	tggaggcaccatgaccggagttct
	DXR-R	gggcccactggtcgtagtggatga
SmMCT	MCT-F	acctgaaatttgcattgcctgggaa
	MCT-R	tccttgattgtagccttagcaggaa
SmCMK	CMK-F	ccaagagtggtcgggtgagattgg
	CMK-R	ggggcatgcctcttgtggcttaat
SmMDS	MDS-F	ttggccacggatttgaccttcatc
	MDS-R	tgccctatatctgggagcccaagc
SmHDS	HDS-F	cgtggtgacgaaccccaagaagag
	HDS-R	gccagcaccgataaccaagtcgtc
SmHDR1	HDR1-F	ctcagaattgcgtggaattccatca
	HDR1-R	ttaagccgattgcaatacttctgctt
SmHDR2	HDR2-F	atcgtattgggttgacagcgagaaa
	HDR2-R	tatgccgtttgcaatacttcatcgc
SmAACT1	AACT1-F	aaagctctggagctcgggcttaca
	AACT1-R	tccaaaccagcattcttgagtgcct
SmAACT2	AACT2-F	gcaatggcagttaaacttggattgga
	AACT2-R	gagattgctctcggtatcgcaatg
SmHMGR1	HMGR1-F	caataaggaggctcccggatccaa
	HMGR1-R	acttcatgctcgcaacatccttatt
SmHMGR2	HMGR2-F	ctcaacctgctgggagtcaaggga
	HMGR2-R	ttgagagcttagtaacatctttggaa
SmHMGR3	HMGR3-F	caataaggaggctcccggatccaa
	HMGR3-R	acttcatgctcgcaacatccttatt
SmHMGR4	HMGR4-F	tagcatcacaatcggcttgcctca
	HMGR4-R	ctcgaccggttgtacttcatgtga
SmHMGS	HMGS-F	aggactgcagccttcttgcaccag

	HMGS-R	ttcgcaatggccttcttggcatag
SmMK	MK-F	ttcgtctgctgctctttgtgttgc
	MK-R	agatggcctcccatggatcatctt
SmPMK	PMK-F	tgcatgtcatcgctcaaactgctc
	PMK-R	tcaattggaatccctcgaccagca
SmMDC	MDC-F	agtgcttgccgcagcttgtatggt
	MDC-R	ctggtttcaaccgtgtcacgcatt
SmIDI1	IDI1-F	gcatccaaatccagacgaagtgca
	IDI1-R	tttctcgacgtggtcccaccactt
SmIDI2	IDI2-F	gtgaagtacgtgagccgcgagcaa
	IDI2-R	tttcatgtcagccgcttgggcga
SmGPPS	GPPS-F	atacaaggcggggtattggctcttt
	GPPS-R	tgcatggtctcaccagtgaccaga
SmGGPPS1	GGPPS1-F	ctgcattgttagaggcatctgtagttt
	GGPPS1-R	agcttgggatacgtggtcttgtcg
SmGGPPS2	GGPPS2-F	ccagattgtggacttgtcgagcga
	GGPPS2-R	caacacacctggcgtacttcctcaa
SmGGPPS3	GGPPS3-F	gcgtgcgaggaggagatcgggaat
	GGPPS3-R	cctggacttctccactccgatgagt
SmGPPS.SSUI	GPPS.SSUI-F	tcacgagcatctccctctgaccga
	GPPS.SSUI-R	gctggcccgactgatctctattata
SmGPPS.SSUII.1	GPPS.SSUII.1-F	cgaggccaactacccaaccacacat
	GPPS.SSUII.1-R	tctcctgcacgactcgaaggaggt
SmGPPS.SSUII.2	GPPS.SSUII.2-F	tgacttgccgtgcatggatgatgat
	GPPS.SSUII.2-R	cccactgcccttgctatctcagca
SmGPPS.LSU	GPPS.LSU-F	gttcgccaagtgcatcggcctca
	GPPS.LSU-R	agccttgtgagaatcgaagtgaagg
SmFPPS	FPPS-F	gcgggtgaggacctggagaaacat
	FPPS-R	cagggcctttacaaccagccaagaa
SmCPS1	CPS1-F	ccacatcgccttcagggaagaaat
	CPS1-R	tttatgctcgatttcgctgcgatct
SmCPS2	CPS2-F	ggtctcatcgccttcaacgaagat
	CPS2-R	tccttatcctttatgctcccatcca
SmCPS3	CPS3-F	ggagatgccaattcgaacatcaga
	CPS3-R	tcaaatatagttgcggcggccaaa
SmCPS4	CPS4-F	cggctgccttgggctacaacaata
	CPS4-R	tccctggtgacctcctccttccca
SmCPS5	CPS5-F	tagaagatgcagctactttctctgct
	CPS5-R	catcatcttcaccgccgtactgtt
SmKSL1	KSL1-F	tggaaacagtgtgacccttctgct
	KSL1-R	gcttgcatacaaataacacccaatcct
SmKSL2	KSL2-F	ttagttttggagggcaagaagagtgt
	KSL2-R	ctcctgtttggtcgttgagaagaata

Table S2. Conserved motifs of PTs in various plant species.

Different types of PTs	**The first CXXXC motif**	**FARM motif ($\mathbf{DDX_{2\text{-}4D}}$)**	**The second CXXXC motif**	**SARM motif (DDXXD)**
SmGPPS,SlGPPS,CrGPPS (subunits of homodimeric GPPSs)		DDVLD		DDVLD
SmGPPS.LSU, MpGPPS.LSU, AmGPPS.LSU (large subunits of heteromeric GPPSs)	CIAAC	DDLPCMD		DDILD
SmGPPS.SSUI, MpGPPS.SSUI, AmGPPS.SSUI (small subunits of heteromeric GPPSs, typeI)	CV/LAAC		CGAAC (except for SmGPPS.SSUI)	
SmGPPS.SSUII.1, OsGPPS.SSUII.1, SmGPPS.SSUII.2, AtGPPS.SSUII.2 (small subunits of heteromeric GPPSs, type II)	CV/IAAC	DDLPXXD	CSAV/AC	
SmGGPPS1, SmGGPPS2, SmGGPPS3, AtGGPPS, CsGGPPS	CLAAC	DDLPCMD		DDXXD
SmFPPS, HbFPPS, MpFPPS, VvFPPS		DDIMD		DDYLD