

Additional file 6. Multiple sequence alignments used for generating the phylogenetic trees in this study.

Multiple sequence alignment of *Arabidopsis thaliana* and *Arabidopsis lyrata* PWWP-domain containing sequences. The multiple sequence alignment was used to reconstruct the maximum likelihood (Fig. 3) phylogeny.

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NP_190402_ATMlike_At_AT3G48190      -----GNLVVWMTKY-KKWWPGEVVDV--KADAKES-----
EFH52141_Alyrata                    -----GNLVVWMTKY-KKWWPGEVVDV--KADAKES-----
NP_195915_At_AT5G02950              -----DLVWAKLRS-YPWWPGLVFDK--SVASKAAMRHF
EFH47262_Alyrata                    -----DLVWAKIRS-YPWWPGQVIDA--SVASKAAKKHF
BAF01554_At_At3g09670              --ISDSDLVWAKVRS-HPWWPGQVFDV--SAATDKAKKHF
NP_187194_At_AT3G05430              --FEVGDMVWGVKVS-HPWWPGQIFNE--AFASPSVRRVK
XP_002882413_Alyrata                --FEVGDMVWGVKVS-HPWWPGQIFNE--AFASPSVRRMK
NP_198117_At_AT5G27650              --FEVGDVWGVKVS-HPWWPGHIFNE--AFASPSVRRMR
NP_189424_At_AT3G27860              --FHVGDVWGVKEANSQQWWPGQIYDS--LDASDLALKTM
XP_002875407_Alyrata                --FHVGDVWGVKEVNSQQWWPGQIYDS--LDASDLALKTM
NP_198850_At_AT5G40340              -----GDFVWGKIKN-HPWWPGQIYDP--SDASDLALKIK
XP_002878396_firstPWWP_Alyrata      -----PAWPAMVVDV--ISQAPDGVLLKH
XP_002878396_secondPWWP_Alyrat      -----RSQAPTAVLLKH
XP_002878409_Alyrata                --FTVGDVWAKCGKRFPWPAVVIDP--ISQAPDGVLLKH
NP_191733_ATX3_WHCS1r_AT3G6174      --FTVGDVWAKCGKRFPWPAVVIDP--ISQAPDGVLLKH
NP_194520_ATX4_WHCS1r_AT4G2791      --FYSGDLVWAKSGRNEPFWPAIVIDP--MTQAPELVLR
XP_002869532_Alyrata                --FYSGDLVWAKSGRNEPFWPAIVIDP--MTQAPELVLR
NP_200155_ATX5_At_AT5G53430         --FYSGDLVWKGSGRNEPFWPAIVIDP--MTQAPELVLR
XP_002864242_Alyrata                --FYSGDLVWKGSGRKEPFWPAIVIDP--MTQAPELVLR
NP_850170_ATX1_At2g31650            --FEPGDIVWAKLAG-HAMWPAVIVDESIVGERKGLNNKV
XP_002881186_Alyrata                --FETGDIVWAKLAG-HAMWPAVIVDESIVGERKGLNNKV
NP_172074_ATX2_AT1G05830            --FEPRDIWAKLTG-HAMWPAIVDESIVVKKRGLNNKI
XP_002889570_Alyrata                --FEPRDIWAKLTG-HAMWPAIVDESIVVKKRGLNNKA
NP_191866_At_HDGFr_AT3G63070        -EWKVGDVVLAKVKG-FPAWPVVDEP-----EKWG-HS
NP_850485_At_HDGFr_At2g48160        -----GDLVLAKVKG-FPAWPVVSEP-----EKWD-AS
XP_002880345_Alyrata                -KWKVGDVVLAKVKG-FPAWPAVSEP-----EKWG-AL
XP_002876705_Alyrata                ---KVGDLVLAKVKG-FPAWPAVVSQP-----EKWG-YS
NP_197706_HUA2_At_HDGFr_AT5G23      -QLVLGDLVLAKVKG-FPAWPAKISR-----EDWD-RA
XP_002872040_Alyrata                GQLILGDLVLAKVKG-FPAWPAKISR-----EDWD-RA
NP_196440_At_AT5G08230              GEMRLGDLVLAKVKG-FPAWPAKIGQP-----EDWN-QA
XP_002873347_Alyrata                --LRLGDLVLAKVKG-FPAWPAKIGQP-----EDWN-QA

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NP_190402_ATMlike_At_AT3G48190      -----FMVRSIG-----QSHLVSWFASSKLPFKESFEQ
EFH52141_Alyrata                    -----FMVRYIG-----QSHLVSWFAPLKLKPFKESFEQ
NP_195915_At_AT5G02950              KK-GNVLVAYFG-----DCTFA-WNNASQIKPFHQNFSQ
EFH47262_Alyrata                    KKKGNLLVAYFG-----DCTFA-WNNASQVQKPFHQNFSQ
BAF01554_At_At3g09670              KK-GSFLVTYFG-----DCTFA-WNEASRIKPFHQHFSQ
NP_187194_At_AT3G05430              KM-GYVLVAFFG-----DNSYG-WFDPAELIPFEPHVKE
XP_002882413_Alyrata                KM-GYVLVAFFG-----DNSYG-WFDPAELLPFEPHVAE
NP_198117_At_AT5G27650              RI-DHVLVAFFG-----DSSYG-WFDPAELIPFEPNLEE
NP_189424_At_AT3G27860              QK-GKLLVAYFG-----DGSFFGWCNPLELKPFLFNFK
XP_002875407_Alyrata                QK-GKLLVAYFG-----DGKFC-WCNPLELKPFLFNFK
NP_198850_At_AT5G40340              QK-GKLLVACFG-----DGTFA-WCGASQLKPFPAESFKE
XP_002878396_firstPWWP_Alyrata      CVPGAICVMFFGYSKNGTQRDYA-WVRQGMVYPFTEFMDK

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XP_002878396_secondPWWP_Alyrat
XP_002878409_Alyrata
NP_191733_ATX3_WHCS1r_AT3G6174
NP_194520_ATX4_WHCS1r_AT4G2791
XP_002869532_Alyrata
NP_200155_ATX5_At_AT5G53430
XP_002864242_Alyrata
NP_850170_ATX1_At2g31650
XP_002881186_Alyrata
NP_172074_ATX2_AT1G05830
XP_002889570_Alyrata
NP_191866_At_HDGFr_AT3G63070
NP_850485_At_HDGFr_At2g48160
XP_002880345_Alyrata
XP_002876705_Alyrata
NP_197706_HUA2_At_HDGFr_AT5G23
XP_002872040_Alyrata
NP_196440_At_AT5G08230
XP_002873347_Alyrata

CVPGAICVMFFGYLKNGTQSDYA-RVRQGMMPFTEFMDK
CVPGAICVMFFGYSKDGTQRDYA-WVRQGMMPFTEFMDK
CVPGAICVMFFGYSKDGTQRDYA-WVRQGMVYPFTEFMDK
CIPDAACVVFVFGHSGNENERDYA-WVRRGMIFPFVDYVAR
CIPDAACVVFVFGHSGNENERDYA-WVRRGMIFPFVDYVAR
CIPDAACVVFVFGHSGTENERDYA-WVRRGMIFPFVDYVER
CIPDAACVVFVFGHSGTENERDYA-WVRRGMIFPFVDYVDR
SGGGSLLVQFFG-----THDFA-RIKVKQAISFIKGLLS
SGGGSLLVQFFG-----THDFA-RIKEKQAISFIKGLLS
SGGRSVLVQFFG-----THDFA-RIQVKQAVSFLKGLLS
SGGRSVLVQFFG-----THDFA-R-----
ADSKKVTVHFFG-----TQQIA-FCNHGDVESFTEEKQ
PDSKKVFVHFFG-----TQQIA-FCNPGDVEAFTEERKQ
TDLKKVFVHFFG-----TQQIA-FCNHTDVEAFDERKQ
ADSKKVLVHFFG-----TQQIA-LCNPADVESFTEEKQ
PDPKKYFVQFFG-----TEEIA-FVAPPDIQAFITSEAKS
PDPKKYFVQFFG-----TEEIA-FVAPPDIQAFITSEAKS
PDPKKHFVQFYG-----TGEIG-FVTPPDIQPFITSETKK
PDPKKHFVQFFG-----TQEIG-FVAPPDIQPFITSEAKN

NP_190402_ATMlike_At_AT3G48190
EFH52141_Alyrata
NP_195915_At_AT5G02950
EFH47262_Alyrata
BAF01554_At_At3g09670
NP_187194_At_AT3G05430
XP_002882413_Alyrata
NP_198117_At_AT5G27650
NP_189424_At_AT3G27860
XP_002875407_Alyrata
NP_198850_At_AT5G40340
XP_002878396_firstPWWP_Alyrata
XP_002878396_secondPWWP_Alyrat
XP_002878409_Alyrata
NP_191733_ATX3_WHCS1r_AT3G6174
NP_194520_ATX4_WHCS1r_AT4G2791
XP_002869532_Alyrata
NP_200155_ATX5_At_AT5G53430
XP_002864242_Alyrata
NP_850170_ATX1_At2g31650
XP_002881186_Alyrata
NP_172074_ATX2_AT1G05830
XP_002889570_Alyrata
NP_191866_At_HDGFr_AT3G63070
NP_850485_At_HDGFr_At2g48160
XP_002880345_Alyrata
XP_002876705_Alyrata
NP_197706_HUA2_At_HDGFr_AT5G23
XP_002872040_Alyrata
NP_196440_At_AT5G08230
XP_002873347_Alyrata

VLNQ-----RNDNGFFDALQKA-----
VLNQ-----RNDKGGFFDAVEKA-----
MQEQ-----SNSAEFRDAIDCALDE-----
MQEQ-----SNLAEFRDAIDCALDE-----
MAKQ-----SSLPDFIDAIDFALEE-----
KSQQ-----TSSDHFAKAVEEAMNE-----
NSQQ-----TSSGHFAKAVEEAMDE-----
KSQQQ-----TVSKHFVRAVEEAKDE-----
FSKM-----SDSRRFLLAVEDA-----
FSKM-----SESKRFLSAVEEA-----
CSKV-----SNSRSFLGAVEEAVEE-----
FQDKTNLYNYKPSEFFKKALDEAVLAENG-----

FQDQTNLYNYKPSEFFKKALEEAVLAENG-----
FQDQTNLNFNYKASEFNKALEEAVLAENGN-----
FQEQPELQGCCKPGNFQMALEEAFLADQGF-----
FQEQSELQGCCKPGNFQMALEEAFLADQGF-----
LQEQSELRGCNPRDFQMALEEAFLADQGF-----
FQEQSELRGCNPREFQMALEEAFLADQGF-----
PSHLK-CKQ--PR-FEEGMQEA-----
PSHLK-CKQ--PR-FEEGMQEA-----
RSPLK-CKQ--PR-FEEAMEEA-----

SLLTR-RHAKGSD-FVRVAVKEITES-----
SLLTR-RHAKGSD-FVRVAVKEIIES-----
SLLTK-RHAKGSD-FLRAVKEIIES-----
LLLTK-RHAKGSD-FVRVAVKEITES-----
KLLAR-CQGKTVKYFAQAVEQICTA-----
KLLAR-CQGKTVKYFAQAVEQICTA-----
KLSAR-CQGKTVKYFSQAVEEIE-----
KLLAR-CQGKTVKYFSQAVEEIE-----

Multiple sequence alignment of plant PWWP-domain containing sequences. The multiple sequence alignment was used to reconstruct the neighbor joining (Fig. 4) phylogeny.

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NP_850170_ATX1_At2g31650      -----FEPGDIVWAKLAG--HAMWPAVIV
XP_002881186_Alyrata          -----FETGDIVWAKLAG--HAMWPAVIV
NP_172074_ATX2_AT1G05830     -----FEPRDIWAKLTG--HAMWPAIIV
XP_002301643_Populus         -----LEPGDIWAKLTG--HAMWPAIVV
XP_002320433_Populus         -----PGDIWAKVTG--HAMWPAIVV
XP_002889570_Alyrata         -----FEPRDIWAKLTG--HAMWPAIIV
XP_002459927_Sorghum        -----PGDLVWAKITG--HAMWPAVVV
XP_002992195_Selaginella     -----GTVVWAKVKG--WPMWPAVLV
XP_002982095_Selaginella     DELALLANEMESFEEQISHGTVVWAKVKG--WPMWPAVLV
XP_001767466_Physcomitrella   -----GDLVWAKVKG--WPMWPAFVM
XP_001780587_Physcomitrella   -----GDLVWAKVKG--WPMWPAFVM
XP_002975241_Selaginella     -----FQHGDIVWAEETPG--YPMWPAFVM
XP_001760849_Physcomitrella   -----FKHGQLVWAKFAR--FPWWPAEII
XP_001751216_Physcomitrella   -----GQLVWAKFAR--FPWWPAEII
XP_002961091_Selaginella     -----SAGQLVWAKFSR--SPWWPAQVA
XP_002966918_Selaginella     -----SAGQLVWAKFSR--SPWWPAQVA
XP_002444527_Sorghum        -----FRLGDIWVKCSG--SSWWPAQVI
NP_189424_At_AT3G27860       -----FHVGFDFVWGEEANS--QQWWPGQIY
XP_002875407_Alyrata         -----FHVGFDFVWGKEVNS--QQWWPGQIY
NP_198850_At_AT5G40340       -----GDFVWGKIKN--HPWWPGQIY
XP_002305994_Populus         -----FRVGDFVWGKIKS--HPWWPGRVY
NP_195915_At_AT5G02950       -----DLVWAKLRS--YPMWPGLVF
XP_002871003_Alyrata         -----DLVWAKIRS--YPMWPGQVI
NP_187578_At_At3g09670       -----ISDSDLVWAKVRS--HPWWPGQVF
XP_002882633_Alyrata         -----ISDSDLVWAKVRS--HPWWPGQVF
XP_002326168_Populus         -----LSVGDVWVKVRS--HPWWPGQVF
XP_002322856_Populus         -----GDLVWVKVRS--HPWWPGQLF
XP_002315275_Populus         -----FVSVDVWVKVRS--HPWWPGQIF
XP_002439929_Sorghum        -----DLVWVKVRS--HPWWPGEIF
XP_002440507_Sorghum        -----PGRVWVKVRS--HPWWPAQVF
XP_002318650_Populus         -----FHVGDIVWVKTKN--QSWWPGKIF
XP_002461281_Sorghum        -----FAPGDMVWVKKLN--HAAWPGLIY
NP_187194_At_AT3G05430       -----FEVGDVWVKVRS--HPWWPGQIF
XP_002882413_Alyrata         -----FEVGDVWVKVRS--HPWWPGQIF
XP_002319529_Populus         -----FEVGDVWVKVRS--HPRWPGHIF
XP_002330150_Populus         -----FEVGDVWVKVRS--HPWWPGHIF
NP_198117_At_AT5G27650       -----FEVGDVWVKVRS--HPWWPGHIF
XP_002330341_Populus         -----
XP_002439285_Sorghum        -----PRFGDMVWVKVRS--HPWWPGHIY
NP_191866_At_HDGFr_AT3G63070 -----EWKVGDLVLAQVKG--FPAWPAVVD
NP_850485_At_HDGFr_At2g48160 -----GDLVLAQVKG--FPAWPAVVS
XP_002880345_Alyrata         -----KWKVGDLVLAQVKG--FPAWPAVVS
XP_002876705_Alyrata         -----KVGDLVLAQVKG--FPAWPAVVS
XP_002465241_Sorghum        -----WKVGDLVLAQVKG--FPAWPAVVS
XP_002463300_Sorghum        -----QWKVGDLVLAQVKG--FPAWPAVVS
XP_002974023_Selaginella     -----QWKIGDLVLAQVKG--FPAWPAVVS
XP_002983468_Selaginella     -----QWKIGDLVLAQVKG--FPAWPAVVS
XP_002962776_Selaginella     -----EWSVGDVLAQVKG--FPAWPAVVS
NP_197706_HUA2_At_HDGFr_AT5G23 -----QLVLGDLVLAQVKG--FPAWPAKIS
XP_002872040_Alyrata         -----GQLILGDLVLAQVKG--FPAWPAKIS
NP_196440_At_AT5G08230       -----GEMRLGDLVLAQVKG--FPAWPAKIG
XP_002873347_Alyrata         -----LRLGDLVLAQVKG--FPAWPAKIG

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XP_002310078_Populus -----QLRLGDLVLAKVKG--YPSWPAKIS
XP_002306384_Populus -----QLRLGDLVLAKVKG--YPSWPAKIS
XP_002443678_Sorghum -----REFQLGDLVLAKIKG--YPPWPAKIS
XP_001753837_Physcomitrella -----REFNEGDLVLAKVKG--WPAWPAQAE
XP_001765392_Physcomitrella -----REFNVGDLVLAKVKG--WPAWPAQ--
XP_002878409_Alyrata -----FTVGDLVWAKCGKR-FPAWPAVVI
XP_002878396_Alyrata -----PWPAMVV
NP_191733_ATX3_WHCS1r_AT3G6174 -----FTVGDLVWAKCGKR-FPAWPAVVI
XP_002302629_Populus -----FALGDIVWAKCGKR-YPWWPAIVI
NP_194520_ATX4_WHCS1r_AT4G2791 -----FYSGDLVWAKSGRN-EPFWPAIVI
XP_002869532_Alyrata -----FYSGDLVWAKSGRN-EPFWPAIVI
NP_200155_ATX5_At_AT5G53430 -----FYSGDLVWAKSGRN-EPFWPAIVI
XP_002864242_Alyrata -----FYSGDLVWAKSGRN-EPFWPAIVI
XP_002318412_Populus -----FYSGDLVWAKSGMK-YPFWPAIVI
XP_002321418_Populus -----FYSGDIVWAKSGNK-YPFWPAIVI
XP_002454931_Sorghum -----FVLGDVWARSQK-SPTWPALVI
XP_002961390_Selaginella -----FDIGDIVWAKSGKKDPVWPAKV
XP_002980880_Selaginella -----FDIGDIVWAKSGKKDPVWPAKV
XP_001777592_Physcomitrella -----FDLGEIVWAKSGKRNDPVWPARVI
XP_002456070_Sorghum -----LVYGDIVWAKLGKR-QPMWPGVLI

NP_850170_ATX1_At2g31650 DESIIGERKGLNKNVSGGSLLVQFFGTH-DFARI-----
XP_002881186_Alyrata DESVIGERKGLNKNVSGGSLLVQFFGTH-DFARI-----
NP_172074_ATX2_AT1G05830 DESVIVKRKGLNKNISGGRSVLVQFFGTH-DFARI-----
XP_002301643_Populus DGALIGDHKGISKNI-GGGSISVQFFGTH-DFARI-----
XP_002320433_Populus DEALIGNHKGISKNI-GGRSVSVQFFGTH-DFARI-----
XP_002889570_Alyrata DESVIVKRKGLNKNKASGGRSVLVQFFGTH-DFARI-----
XP_002459927_Sorghum DESNVPATRAL-KSIRLDQSIILVQFFGTH-DFARE-----
XP_002992195_Selaginella DEE-HAEKCGLERPLKKST-FAVQFFGSC-DFARL-----
XP_002982095_Selaginella DEE-HAEKCGLERPLKKST-FAVQFFGSC-DFARL-----
XP_001767466_Physcomitrella DED-HAAACGME-PGKKGM-VPLQFFGSY-DHCRF-----
XP_001780587_Physcomitrella DED-HAAACGMD-PGKKGM-VPLQFFGSY-DHCRF-----
XP_002975241_Selaginella DDQ-HARLCNLE--ISTGE-LPVHYFGTY-ESA-----
XP_001760849_Physcomitrella NERAFQPGTGGN--RRSNTDVLVRFVFGTY-DYG-----
XP_001751216_Physcomitrella NEKAVIPGTGGN--KRINADVLSKCF-IY-GLGSDGKCSG
XP_002961091_Selaginella DEKMSERT-----RQSKNHVLRVRFVFGNY-NYG-----
XP_002966918_Selaginella DEKMSERT-----RQSKNHVLRVRFVFGNY-NYG-----
XP_002444527_Sorghum DELCVGSKP--K--KKDKYDCLVRLYGTC-QYL-----
NP_189424_At_AT3G27860 DSL--DASDLALKTMQK-GKLLVAYFGDG-SFFG-----
XP_002875407_Alyrata DSL--DASDLALKTMQK-GKLLVAYFGDG-KFC-----
NP_198850_At_AT5G40340 DPS--DASDLALKIKQK-GKLLVACFGDG-TFA-----
XP_002305994_Populus DPS--NASDYAKKVKQR-DKILVAYFGDS-TFA-----
NP_195915_At_AT5G02950 DKS--VASKAAMRHFKK-GNVLVAYFGDC-TFA-----
XP_002871003_Alyrata DAS--VASKAAKKHFKKGNLLVAYFGDC-TFA-----
NP_187578_At_At3g09670 DAS--AATDKAKKHFKK-GSFLVTYFGDC-TFA-----
XP_002882633_Alyrata DAS--AATDKAKKHFKK-GSFLVTYFGDC-TFA-----
XP_002326168_Populus GRS--DASKKAKKHFKK-NSYLIAYFGDQ-TFA-----
XP_002322856_Populus GCA--DASKKAKKHFKK-DSYLIAYLGDQ-TFA-----
XP_002315275_Populus DPS--DASEKAMRYHKK-DCYLVAIFGDR-TFA-----
XP_002439929_Sorghum DPS--DASELALKHQK-GSHLVAYFGDN-TFA-----
XP_002440507_Sorghum DAA--DASADARALRRPRGAVLVAYFWDK-TFA-----
XP_002318650_Populus DPL--GVTKYAVQSDQR-NGLLVGYLGSC-HIA-----
XP_002461281_Sorghum SAG--GNGTGHE-----GQFLVSYFGDK-AFA-----
NP_187194_At_AT3G05430 NEA--FAS-PSVRRVKKMGYVLVAFFGDN-SYG-----
XP_002882413_Alyrata NEA--FAS-PSVRRMKKMGYVLVAFFGDN-SYG-----
XP_002319529_Populus NEA--FAS-SSVRRTRREGHVLVAFFGDS-SYG-----

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XP_002330341_Populus
XP_002439285_Sorghum
NP_191866_At_HDGFr_AT3G63070
NP_850485_At_HDGFr_At2g48160
XP_002880345_Alyrata
XP_002876705_Alyrata
XP_002465241_Sorghum
XP_002463300_Sorghum
XP_002974023_Selaginella
XP_002983468_Selaginella
XP_002962776_Selaginella
NP_197706_HUA2_At_HDGFr_AT5G23
XP_002872040_Alyrata
NP_196440_At_AT5G08230
XP_002873347_Alyrata
XP_002310078_Populus
XP_002306384_Populus
XP_002443678_Sorghum
XP_001753837_Physcomitrella
XP_001765392_Physcomitrella
XP_002878409_Alyrata
XP_002878396_Alyrata
NP_191733_ATX3_WHCS1r_AT3G6174
XP_002302629_Populus
NP_194520_ATX4_WHCS1r_AT4G2791
XP_002869532_Alyrata
NP_200155_ATX5_At_AT5G53430
XP_002864242_Alyrata
XP_002318412_Populus
XP_002321418_Populus
XP_002454931_Sorghum
XP_002961390_Selaginella
XP_002980880_Selaginella
XP_001777592_Physcomitrella
XP_002456070_Sorghum

NEA--FAS-SSVRRTRREGHVLVAFFGDS--SYG-----
NEA--FAS-PSVRRMRRIDHVLVAFFGDS--SYG-----
-----REGHVLVAFFGDG--SYG-----
SVN--LTDDEEVHRGYRDGLVLVAFFGDS--SYG-----
-----EPEKWGHSADSKKVTVHFFGT--QQIA-----
-----EPEKWDASPDSKKVVFVHFFGT--QQIA-----
-----EPEKWGALTDLKKVVFVHFFGT--QQIA-----
-----QPEKWGYSADSKKVLVHFFGT--QQIA-----
-----EPEQWKMPSTKKKPLVYFYGT--KQIA-----
-----FIKYSVHINIYRS--QDIV-----
-----RAEDFGRQRNPAKVVFVFFGT--KQIR-----
-----RAEDFGRQRNPAKVVFVFFGT--KQIR-----
-----KPEAFGQHHNPARVVFVFFGT--KQIR-----
-----RPEDWDRAPDPKKYFVQFFGT--EEIA-----
-----RPEDWDRAPDPKKYFVQFFGT--EEIA-----
-----QPEDWNQAPDPKKHFVQFFGT--GEIG-----
-----QPEDWNQAPDPKKHFVQFFGT--QEIG-----
-----RPEDWKRVAADAKKVFVYFFGT--QEIA-----
-----RPEDWKRAPDAKKVFVYFFGT--QEIA-----
-----RPEDWQHKTTPKKFFVYFYGT--EEIA-----
VSCFPQEIGKLETQGKHAGKYVVTYFGPG--QQIG-----
-----IGRLETQGKHAGKYVVTYFGPG--QQIG-----
DPISQAPDGVLL--KHCVPGAICVMFFGYS--KDG--TQRDYA
DPISQAPDGVLL--KHCVPGAICVMFFGYS--KNG--TQRDYA
DPISQAPDGVLL--KHCVPGAICVMFFGYS--KDG--TQRDYA
DPILQAPDAVL--SCCVPGAICIMFYGYS--KNG--TQRDYA
DPMTQAPDELVL--RSCIPDAACVVFVFGHS--GNE--NERDYA
DPMTQAPDELVL--RSCIPDAACVVFVFGHS--GNE--NERDYA
DPMTQAPDELVL--RSCIPDAACVMFFGHS--GTE--NERDYA
DPMTQAPDELVL--RSCIPDAACVMFFGHS--GTE--NERDYA
DPMTQAPDELVL--RSCIPDAACVMFFGHS--GTE--NERDYA
DPMTQAPDELVL--RSCIPDAACVMFFGCS--GNDGDQRDYA
DPMTQAPDELVL--RSCIPDAACVMFFGCS--GNDGNQRDYA
DPMQHAPDEVVL--NSCVPGALCVMFFGYS--ANG--HGRDYG
DPIKEVPESVR--RKCVPNRLCVMFYGESLARGVKRRDYA
DPIKEVPESVR--RKCVPNRLCVMFYGESLARGVKRRDYA
DPFREAPPVVR--ELSLPNSLCVMFYGPSSSKGKHSRDYA
DPTQQVAADAMPQPRRVAVLVCVMLFGWCTEFS--DEKKYV

NP_850170_ATX1_At2g31650
XP_002881186_Alyrata
NP_172074_ATX2_AT1G05830
XP_002301643_Populus
XP_002320433_Populus
XP_002889570_Alyrata
XP_002459927_Sorghum
XP_002992195_Selaginella
XP_002982095_Selaginella
XP_001767466_Physcomitrella
XP_001780587_Physcomitrella
XP_002975241_Selaginella
XP_001760849_Physcomitrella
XP_001751216_Physcomitrella
XP_002961091_Selaginella
XP_002966918_Selaginella
XP_002444527_Sorghum
NP_189424_At_AT3G27860

KVKQAISFIK--GLLSPSHLKCKQP-----RFEEG
KEKQAISFIK--GLLSPSHLKCKQP-----RFEEG
QVKQAVSFLK--GLLSRSPKCKQP-----RFEEA
KPKQAISFLK--GLLSSFHLKCKQP-----RFTRS
LSEQKLP-----
--EDCHDFEP--RDIWAKLTGHA-----

NNDKIVTFSK--GVQLKYHSKCKRP-----AFDQG
NNDKIVTFSK--GVQLKYHSKCKRP-----AFDQG
SYKKLVIFSK--GLMMKFHTKCKRV-----VFVQG
SYKKLVIFSK--GLMMKFHTKCKRV-----VFVQG

WVDPEVGLSEFDVKMQERSRIKKK-----AFQKG
WVDPKVGLSEFDVKLQERSKIKKK-----ALQKG
WVDPASDLKSFVDVDFDGRSQVPTK-----AFQKG
WVDPASDLKSFVDVDFDGRSQVPTK-----AFQKG
YVDPWKSNSEFEMMLKQENKSTME-----AFREV
WCNPLE--LKPFLNFKEFSKMSDS-----RRFLLA

XP_002875407_Alyrata WCNPLE-LKPFLENFKEFSKMSSES-----KRFLSA
NP_198850_At_AT5G40340 WCGASQ-LKPFSAESFKECSKVSNS-----RSFLGA
XP_002305994_Populus WCNPSQ-LSPFEENFVEMFKQSNS-----KSFVNA
NP_195915_At_AT5G02950 WNNASQ-IKPFHQNFSSQMFEQSNS-----AEFRDA
XP_002871003_Alyrata WNNASQ-VKPFHQNFSSQMFEQSNL-----AEFRDA
NP_187578_At_At3g09670 WNEASR-IKPFHQHFSQMAKQSSL-----PDFIDA
XP_002882633_Alyrata WNDASR-VKPFHQHFSQMAKQSSL-----PDFIDA
XP_002326168_Populus WNEVSK-IKPFRCNFSLLEKQSNL-----EDFHDA
XP_002322856_Populus WNEVSK-IKPFRCNFSLLEKQSNL-----EDFHDA
XP_002315275_Populus WNEASL-LKPFRRSHFSQVEKQSNL-----EVFQNA
XP_002439929_Sorghum WCDESQ-LKPFVITNYSQMEKQSTS-----DAFVGS
XP_002440507_Sorghum WNDAAA-LLPFRAF-----
XP_002318650_Populus WCLPSQ-LKPFHKDFEQMVVKNKA-----RSFLGA
XP_002461281_Sorghum WCDGAE-LRPYEPYFPVAELYDDGG-----EDFDAA
NP_187194_At_AT3G05430 WFDPAE-LIPFEPHVKEKSQQ-TSS-----DHFAKA
XP_002882413_Alyrata WFDPAE-LLPFEPHVAENSQQ-TSS-----GHFAKA
XP_002319529_Populus WFDPAE-LIQFDVNFAEKSQQ-TNS-----RTFIKA
XP_002330150_Populus WFDPAE-LIPFDANFAEKSQQ-TNS-----RTFIRA
NP_198117_At_AT5G27650 WFDPAE-LIPFEPNLEEKSSQQQTVS-----KHVRA
XP_002330341_Populus WLDPTE-LVQFDSHYVEKSKQTNAK-----VFLIKA
XP_002439285_Sorghum WFEPSE-LVPFEDHFTEK-----
NP_191866_At_HDGFr_AT3G63070 FCNHGD-VESFTEEEKQSLLTRRH-----AKGS--DFVRA
NP_850485_At_HDGFr_At2g48160 FCNPGD-VEAFTEERKQSLLTRRH-----AKGS--DFVRA
XP_002880345_Alyrata FCNHTD-VEAFTEERKQSLLTKRH-----AKGS--DFLRA
XP_002876705_Alyrata LCNPAD-VESFTEEEKQLLLTKRH-----AKGS--DFVRA
XP_002465241_Sorghum FCNYAD-LEAFTEEEKRSLAKRH-----GKGA--DFLRA
XP_002463300_Sorghum EITEPE-QWDLPAAKKKSIVAKK-----KLL--VYFYG
XP_002974023_Selaginella FCQHSE-ISAFTEARAALHARTL-----SKCVPSDLKRA
XP_002983468_Selaginella FCQHSE-ISAFTEARAALHARTL-----SKCVPSDLKRA
XP_002962776_Selaginella FCHHSE-ISKFTPEAKASLVAKAH-----SKCTPADLRLA
NP_197706_HUA2_At_HDGFr_AT5G23 FVAPPD-IQAFTSEAKSKLLARC-----QGKTV-KYFAQA
XP_002872040_Alyrata FVAPPD-IQAFTSEAKSKLLARC-----QGKTV-KYFAQA
NP_196440_At_AT5G08230 FVTTPD-IQPFTSETKKKLSARC-----QGKTV-KYFSQA
XP_002873347_Alyrata FVAPPD-IQPFTSEAKNKLLARC-----QGKTV-KYFSQA
XP_002310078_Populus FVAPSD-IQVFTNEVKNKLSARC-----QSKKD-RFFSQA
XP_002306384_Populus FVAPSD-IQVFTNEVKNKLSARC-----QSKKD-KFFSQA
XP_002443678_Sorghum FVPLAD-LEEFTEKTKNDLLDRAPNIKVQRKYV-QVFNDA
XP_001753837_Physcomitrella WCLPVE-LSEFDADQREASIQKSL-----KKTADKKFISA
XP_001765392_Physcomitrella WCLPVE-LSEFDADQREASVQKSL-----KKTADKKFIFA
XP_002878409_Alyrata WVRQGM-MYPFTEFMDKFQDQTNLYN-----YKPSEFKKA
XP_002878396_Alyrata WVRQGM-VYPFTEFMDKFQDQTNLYN-----YKPSEFKKA
NP_191733_ATX3_WHCS1r_AT3G6174 WVRQGM-VYPFTEFMDKFQDQTNLFN-----YKASEFNKA
XP_002302629_Populus WVKQGM-VFPFAEFMERFQVQSQMFK-----CKLSDFQVA
NP_194520_ATX4_WHCS1r_AT4G2791 WVRRGM-IFPFVDYVARFQEQLQ-----CKPGNFQMA
XP_002869532_Alyrata WVRRGM-IFPFVDYVARFQEQLQ-----CKPGNFQMA
NP_200155_ATX5_At_AT5G53430 WVRRGM-IFPFVDYVERLQEQLQ-----CNPRDFQMA
XP_002864242_Alyrata WVRRGM-IFPFVDYVDRFQEQLQ-----CNPREFQMA
XP_002318412_Populus WVQRGM-IFPFVDFVDRFQEQLQ-----CKPGDFQMA
XP_002321418_Populus WVQRGM-IFPFVDFVDRFQEQLQ-----FN-GDFQMA
XP_002454931_Sorghum WVKQGM-IFPFVDYLDRFQGGP-LYK-----LRPSKFRAA
XP_002961390_Selaginella WVRKGM-IFPFVDYLERFQSQTSEFNK-----SQPGDFWSA
XP_002980880_Selaginella WVRKGM-IFPFVDYLERFQSQTSEFNK-----SQPGDFWSA
XP_001777592_Physcomitrella WVKQGM-IFPFNAYLERFQSQTQLNR-----SRPVDFRQA
XP_002456070_Sorghum WVRQGL-IFPFSDYMDRFQGGTELSS-----CKPADFRRA

NP_850170_ATX1_At2g31650

MQEA-----

| | |
|--------------------------------|-------------|
| XP_002881186_Alyrata | MQEA----- |
| NP_172074_ATX2_AT1G05830 | MEEA----- |
| XP_002301643_Populus | LEEA----- |
| XP_002320433_Populus | ----- |
| XP_002889570_Alyrata | ----- |
| XP_002459927_Sorghum | ----- |
| XP_002992195_Selaginella | LRE----- |
| XP_002982095_Selaginella | LRE----- |
| XP_001767466_Physcomitrella | LEEVE----- |
| XP_001780587_Physcomitrella | LEEVE----- |
| XP_002975241_Selaginella | ----- |
| XP_001760849_Physcomitrella | IEEALEY---- |
| XP_001751216_Physcomitrella | IEEALEF---- |
| XP_002961091_Selaginella | LKEALEY---- |
| XP_002966918_Selaginella | LKEALEY---- |
| XP_002444527_Sorghum | LEK----- |
| NP_189424_At_AT3G27860 | VEDA----- |
| XP_002875407_Alyrata | VEEA----- |
| NP_198850_At_AT5G40340 | VEEAVEE---- |
| XP_002305994_Populus | VKEAVDE---- |
| NP_195915_At_AT5G02950 | IDCALDE---- |
| XP_002871003_Alyrata | IDCALDE---- |
| NP_187578_At_At3g09670 | IDFALEE---- |
| XP_002882633_Alyrata | IDFALEE---- |
| XP_002326168_Populus | VHCALDE---- |
| XP_002322856_Populus | VHCALDE---- |
| XP_002315275_Populus | VDCSLEE---- |
| XP_002439929_Sorghum | VNNALEE---- |
| XP_002440507_Sorghum | ----- |
| XP_002318650_Populus | VEKAVDE---- |
| XP_002461281_Sorghum | VEASLDE---- |
| NP_187194_At_AT3G05430 | VEEAMNE---- |
| XP_002882413_Alyrata | VEEAMDE---- |
| XP_002319529_Populus | VEEATDE---- |
| XP_002330150_Populus | VEEATDE---- |
| NP_198117_At_AT5G27650 | VEEAKDE---- |
| XP_002330341_Populus | VEEADD----- |
| XP_002439285_Sorghum | ----- |
| NP_191866_At_HDGFr_AT3G63070 | VKEITES---- |
| NP_850485_At_HDGFr_At2g48160 | VKEIIES---- |
| XP_002880345_Alyrata | VKEIIES---- |
| XP_002876705_Alyrata | VKEITES---- |
| XP_002465241_Sorghum | VDEIVE----- |
| XP_002463300_Sorghum | TKE----- |
| XP_002974023_Selaginella | VKEICE----- |
| XP_002983468_Selaginella | VKEICE----- |
| XP_002962776_Selaginella | VSEIC----- |
| NP_197706_HUA2_At_HDGFr_AT5G23 | VEQICTA---- |
| XP_002872040_Alyrata | VEQICTA---- |
| NP_196440_At_AT5G08230 | VEEI----- |
| XP_002873347_Alyrata | VEEI----- |
| XP_002310078_Populus | VKEICAA---- |
| XP_002306384_Populus | VKEICAA---- |
| XP_002443678_Sorghum | VEQICKA---- |
| XP_001753837_Physcomitrella | VKEIC----- |
| XP_001765392_Physcomitrella | VKEIC----- |
| XP_002878409_Alyrata | LEEAVLAENG- |

| | |
|--------------------------------|--------------|
| XP_002878396_Alyrata | LDEAVLAENG- |
| NP_191733_ATX3_WHCS1r_AT3G6174 | LEEAVLAENGN |
| XP_002302629_Populus | LEEAILAESGF |
| NP_194520_ATX4_WHCS1r_AT4G2791 | LEEAFLLADQGF |
| XP_002869532_Alyrata | LEEAFLLADQGF |
| NP_200155_ATX5_At_AT5G53430 | LEEALLADQGF |
| XP_002864242_Alyrata | LEEALLADQGF |
| XP_002318412_Populus | VEEAFLLAEQGF |
| XP_002321418_Populus | FEEAFLLAEQGF |
| XP_002454931_Sorghum | IEEAFLLAERGF |
| XP_002961390_Selaginella | IEEATLLAEAG- |
| XP_002980880_Selaginella | IEEATLLAEAG- |
| XP_001777592_Physcomitrella | ISEAKLAD--- |
| XP_002456070_Sorghum | VEEAFLLADQGF |

Multiple sequence alignment of animal PWWP-domain containing sequences. The multiple sequence alignment was used to reconstruct the neighbor joining (Fig. 6) phylogeny.

```

3068_HDGF_NP_004485          -----KEYKCGDLVFAKMKGYPHWPARIDE---MPEAAVKS
50810_HDGFRP3_CCDS32314     -----REYKAGDLVFAKMKGYPHWPARIDE---LPEGAVKP
84717_HDGFRP2_UNQ785PRO1604 -----HAFKPGDLVFAKMKGYPHWPARIDD---IADGAVKP
154150_HDGFL1_NP_612641     -----YKSGDLVFAKLGKGYAHWPARIEH---MTQ-----
XP_001634069_Nv            -----MTYQPGDLIWAQMRGYPHWPARIDL---AAKDEVIP
84656_GLYR1_NM_032569       -----LRLGDLVWGKLGKRYPPWPGKIVN---PPKDLKKP
7468_a_WHSC1_NM_133330_WHSCr -----LHFQDIWVKLGNRWPAEIVCHPKNVPPNIQKM
64324_a_NSD1_NM_172349_WHSCr -----PHYREIVWVKVGRYRWPAEICHPRAVPSNIDKM
54904_a_WHSC1L1_NM_023034_WHSC -----LHYKQIVWVKLGNRWPAEICNPRSVPLNIQGL
XP_001635219_Nv            -----LLYGDIVWVKLGMWRWPAICNPRDVPPTNIQSM
114825_PWWP2Aisob_NP_001124336 -----ICVGDIVWAKIYGFPPWPARILT--ITVSRKDNG
170394_PWWP2B_NM_138499     -----VAVGDIVWVKIYGFPPWPARVLD--ISLGQKEDG
XP_001624451_Nv            -----INEGSIWVKVGHGPPWPGRVMA--ITEVVDQDQ
1788_DNMT3A_NM_022552       -----FGIGELVWVKLGRGFSWVPGRIVS--WMMTGRSRA
1789_DNMT3B_NM_006892       -----FGIGDLVWVKLGRGFSWVPAMVVS--WKATSKRQA
XP_001626231_Nv            -----GVLVWVKLGRGFSWVPGRVVT--YMEAGRPPP
54904_b_WHSC1L1_NM_023034_MSH6 -----KFQVGDVWVKVGTYPWVPCMVSSDPQLEVHTKIN
7468_b_WHSC1_NM_133330_MSH6L -----LKYNVGDVWVKVSGYPWVPCMVVSADPLLSYTKLK
64324_b_NSD1_NM_172349_MSH6L -----LKYEVGDVWVKVSGYPWVPCMVVSADPLINTHSKMK
152098_ZCWPW2_NP_001035522 -----PLGSLVWVKLQNWPSWPGIILCPDRFKGKYVITYD
XP_001633052_Nv            -----SPFPTGAIWVWAKLAGYPWVPCMVVSADPLINTHSKMK
10771_ZMYND11_NM_006624     WFCYPCIPNHELWVWAKMKGFGFWPAKVMQ----KEDNQVD
XP_001625954_Nv            WFCKPCFFPHELWVWAKMTGEPWPAKLLT----WSDDQTR
23613_ZMYND8_NM_183047     WFCEPCSNPHPLVWAKLKGFPWPAKALR----DKDGQVD
NP_116242                   -----FEVGMVLVWVHKHKYPFWPAVVKSVRQRDK-----
139221_MUM1L1_NM_152423     -----FETGMIVWFKYQKYPFWPAVVKSVRQRDK-----
728317_LOC728317_XP_001127165 -----IERGTMVWFKFQDHPFPAVVKSVSNTDK-----
728307_LOC728307_XP_001127139 -----IERGTMVWFKFQDHPFPAVVKSVSNTDK-----
27154_BRPF3_NM_015695       -----LEPLELVWAKCRGYPSYPALIIDPKMPREGLLHN
7862_BRPF1_NM_001003694     -----LDALDLVWAKCRGYPSYPALIIDPKMPREGMFHH
23774_BRD1_NM_014577        -----LEPLKVVWAKCSGYPSYPALIIDPKMPRVPGHHN
55063_ZCWPW1_NM_017984     ----ASYIPGSIWAKQYGYPPWPGMIESDPDLGEYFLFT
2956_MSH6_HSU54777         ----CDFSPGDLVWAKMEGYPWWPCLVYNHPFDGTFIREK

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:: * :*

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3068_HDGF_NP_004485          T-----ANKYQVFFFVGT-HETAFLGPKDLFPY-EESKEKEF
50810_HDGFRP3_CCDS32314     P-----ANKYPIFFFVGT-HETAFLGPKDLFPY-KEYKDKF
84717_HDGFRP2_UNQ785PRO1604 P-----PNKYPIFFFVGT-HETAFLGPKDLFPY-DKCKDKY
154150_HDGFL1_NP_612641     -----PNRYQVFFFVGT-HETAFLSPKRLFPY-KECKEKEF
XP_001634069_Nv            -----AKKYPIFFVGT-HETAVMPLPKDLFPY-EKHKHKF
84656_GLYR1_NM_032569       R---G-KKCFVVKFFVGT-EDHAWIKVEQLKPY-HAHKEEM
7468_a_WHSC1_NM_133330_WHSCr K---HEIGEFVFFFVGS-KDYWVTHQARVFPYMEGDRGSR
64324_a_NSD1_NM_172349_WHSCr R---HDVGEFPVFFFVGS-NDYLWVTHQARVFPYMEGDVSSK
54904_a_WHSC1L1_NM_023034_WHSC K---HDLGDFPFFFVGS-HDYVWVHQRVFPYVEGDGK-SF
XP_001635219_Nv            R---HQPGFVPMVFLGS-HDFYWIHKGRVFSYQDGDGKTE
114825_PWWP2Aisob_NP_001124336 L---LVRQEARISWFGS-PTTSFLALSQLSPFLENFQSRF
170394_PWWP2B_NM_138499     E---PSWREAKVSWFGS-PTTSFLSISKLSPFSEFFKLRF
XP_001624451_Nv            G----VDTFAHVTWFGS-NTSSEMPVQELQDFEPNFRRRY
1788_DNMT3A_NM_022552       A-----EGTRWVMWFGD-GKFSVVCVEKLMPLSS-FCSAF
1789_DNMT3B_NM_006892       M-----SGMRWVQWFGD-GKFSVVSADKLVALGL-FSQHF
XP_001626231_Nv            G-----PGNHVWVWFGD-NKFSQVYDVTLPFAE-FKSNF
54904_b_WHSC1L1_NM_023034_MSH6 ---TRGAREYHVQFFSNQPERAWVHEKRVREYKGHKQYEE

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7468_b_WHSC1_NM_133330_MSH61
64324_b_NSD1_NM_172349_MSH61
152098_ZCWPW2_NP_001035522
XP_001633052_Nv
10771_ZMYND11_NM_006624
XP_001625954_Nv
23613_ZMYND8_NM_183047
NP_116242
139221_MUM1L1_NM_152423
728317_LOC728317_XP_001127165
728307_LOC728307_XP_001127139
27154_BRPF3_NM_015695
7862_BRPF1_NM_001003694
23774_BRD1_NM_014577
55063_ZCWPW1_NM_017984
2956_MSH6_HSU54777

G-QKKSARQYHVQFFGDAPERAWIFEKSLVAFEGEGQFEK
VSNRRPYRQYVVEAFGDPSERAWVAGKAIVMFEGRHQFEE
P-DGNV-EEYHIEFLGDPHSRSWIKATFVGHYSITLKPEK
L-DDRIPISYHVVFVGKDVSRRAWNSFSVRELTADEEPEP
-----VRFFGHHHQRAWIPSENIQDITVNIHRLH
A-----LVREFFGSAHQ-----
-----ARFFG-QHDRAWVPINNCYLMSKEIPFSV
-----KASVLYIEGHMNPCKMG---FTVSLKSLKHFD
-----KASVLFVEANMNSEKKG---IRVNFRLKKFD
-----TARVLLLEANLHHGKRG---IQVPLRRLKHL
-----TARVLLLEANLHHGKRG---IQVPLRRLKHL
G-VPIPVPPPLDVLKLGQKQAEAGEKLFVLVFFDNKRTWQ
G-VPIPVPPLEVLKLGQMTQEAREHLYLVLFFDNKRTWQ
G-VTIPAPPLDVLKIGEHMQTKSDEKLFVLVFFDNKRSWQ
SHLDSLPSKYHVTFFGETVSRAWIPVNMMLKNFQELSLELS
G----KSVRVHVQFFDDSPTRGWVSKRLLKPYTGSKSKEA

3068_HDGF_NP_004485
50810_HDGFRP3_CCDS32314
84717_HDGFRP2_UNQ785PRO1604
154150_HDGFL1_NP_612641
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84656_GLYR1_NM_032569
7468_a_WHSC1_NM_133330_WHSCr
64324_a_NSD1_NM_172349_WHSCr
54904_a_WHSC1L1_NM_023034_WHSC
XP_001635219_Nv
114825_PWWP2Aisob_NP_001124336
170394_PWWP2B_NM_138499
XP_001624451_Nv
1788_DNMT3A_NM_022552
1789_DNMT3B_NM_006892
XP_001626231_Nv
54904_b_WHSC1L1_NM_023034_MSH6
7468_b_WHSC1_NM_133330_MSH61
64324_b_NSD1_NM_172349_MSH61
152098_ZCWPW2_NP_001035522
XP_001633052_Nv
10771_ZMYND11_NM_006624
XP_001625954_Nv
23613_ZMYND8_NM_183047
NP_116242
139221_MUM1L1_NM_152423
728317_LOC728317_XP_001127165
728307_LOC728307_XP_001127139
27154_BRPF3_NM_015695
7862_BRPF1_NM_001003694
23774_BRD1_NM_014577
55063_ZCWPW1_NM_017984
2956_MSH6_HSU54777

GKPN-----K--RKGFSGLWEIENN-----
GKSN-----K--RKGFNGLWEIENN-----
GKPN-----K--RKGFNGLWEIQNN-----
GKPN-----K--RRGFSAGLWEIENN-----
AKPC-----K--RKGFMEEALEEIVKN-----
IKIN-----K--GKRFQQAQVDAVEEFL-----
YQGV-----RGIGRVFKNALQEAARFREI----
DKMG-----KGVDTYKKAQEAARFEEL-----
AEGQ-----TSINKTFKKALEEAARFQEL----
SGNN-----KYLAKVFKKALVEAEKYDEW----
NK-----KRGKLYRKAITEAAKAA-----
NR-----KKGMYRKAITEAANAA-----
KK-----DKKGCYRRAVRQAQETL-----
HQAT-----YNKQPMYRKAIYEVLQVA-----
NLAT-----FNKLVSYRKAMYHALEKA-----
LVTK-----MKG--LYKKAVLDALEVL-----
LLAE-----ATKQASNHSEKQKIRKPRPQREARQ
LCQE-----SAKQAPTKAEEKIKLLKPISGKLRAQ
LP-----VLRRRGKQKEK-GYRHKVPQKILSK
CKN-----KKKWYKSALQEA-----
IGNI-----VVRKKNYKQLDDANGQARQALSPL
VKR-----SMGWKKACDELELH-----

KKT-----KSIFNSAMQEMEVEY-----
CK-----EKQTLNQAQREDFNQDIGWC----
CK-----EKQMLVDKAREDYSESIDWC----
CK-----EKEKLLKRAQKAYKQSVNWC----
CK-----EKEKLLKRAQKAYKQSVNWC----
WLPRDKVLPLGVEDTVDKLKMLEGRKTSIRKSVQVAYDRA
WLPRTKLVPLGVNQDLDEKMLEGRKSNIRKSVQIAYHRA
WLPKSKMVPLGIDETIDKLMMEGRNSSIRKAVRIAFDRA
VMKK-----RRNDCSQKLGVALMMAQEAQIS
QKGG-----HFYSAPPEILRAMQRADEALNKDKIKR

3068_HDGF_NP_004485
50810_HDGFRP3_CCDS32314
84717_HDGFRP2_UNQ785PRO1604
154150_HDGFL1_NP_612641

| | |
|--------------------------------|------------------|
| XP_001634069_Nv | ----- |
| 84656_GLYR1_NM_032569 | ----- |
| 7468_a_WHSC1_NM_133330_WHSCr | ----- |
| 64324_a_NSD1_NM_172349_WHSCr | ----- |
| 54904_a_WHSC1L1_NM_023034_WHSC | ----- |
| XP_001635219_Nv | ----- |
| 114825_PWWP2Aisob_NP_001124336 | ----- |
| 170394_PWWP2B_NM_138499 | ----- |
| XP_001624451_Nv | ----- |
| 1788_DNMT3A_NM_022552 | ----- |
| 1789_DNMT3B_NM_006892 | ----- |
| XP_001626231_Nv | ----- |
| 54904_b_WHSC1L1_NM_023034_MSH6 | WDIGIAHAEKALKMTR |
| 7468_b_WHSC1_NM_133330_MSH6l | WEMGIVQAEAAASMSV |
| 64324_b_NSD1_NM_172349_MSH6l | WEASVGLAE----- |
| 152098_ZCWPW2_NP_001035522 | ----- |
| XP_001633052_Nv | VQERLAV----- |
| 10771_ZMYND1l_NM_006624 | ----- |
| XP_001625954_Nv | ----- |
| 23613_ZMYND8_NM_183047 | ----- |
| NP_116242 | ----- |
| 139221_MUM1L1_NM_152423 | ----- |
| 728317_LOC728317_XP_001127165 | ----- |
| 728307_LOC728307_XP_001127139 | ----- |
| 27154_BRPF3_NM_015695 | MIH----- |
| 7862_BRPF1_NM_001003694 | LQH----- |
| 23774_BRD1_NM_014577 | MNH----- |
| 55063_ZCWPW1_NM_017984 | I----- |
| 2956_MSH6_HSU54777 | LELAV----- |

Multiple sequence alignment of *Arabidopsis thaliana* PWWP-domain containing sequences. The multiple sequence alignment was used to reconstruct the maximum likelihood (AF4) and neighbor joining (AF5) phylogenies.

```

NP_850170_ATX1_At2g31650      --FEPGDIVWAKLAG-HAMWPAVIVDESIIGERKGLNNKV
NP_172074_ATX2_AT1G05830     --FEPRDIIWAKLTG-HAMWPAIVDESIVKRRKGLNNKI
NP_195915_At_AT5G02950      -----DLVWAKLRS-YPWWPGLVFD-KSVASKAAMRHFK
NP_187578_At_At3g09670      --ISDSDLVWAKVRS-HPWWPGQVFD-ASAATDKAKKHFK
NP_190402_ATMlike_AT3G48190  -----GNLVVWMTKY-KKWWPGEVVD-FKADAKES-----
NP_187194_At_AT3G05430      --FEVGDMMVWGKVKVS-HPWWPGQIFN-EAFASPSVRRVKK
NP_198117_At_AT5G27650      --FEVGDMLVWGKVKVS-HPWWPGHIFN-EAFASPSVRRMRR
NP_198850_At_AT5G40340      -----GDFVWGKIKN-HPWWPGQIYD-PSDASDLALKIKQ
NP_189424_At_AT3G27860      --FHVGDFVWGEEANSQQWWPGQIYD-SLDASDLALKTMQ
NP_194520_ATX4_WHCS1r_AT4G2791 --FYSGDLVWAKSGRNEPFWPAIVIDPMTQAPELVLRSCI
NP_200155_ATX5_At_AT5G53430  --FYSGDLVWGKSGRNEPFWPAIVIDPMTQAPELVLRSCI
NP_191733_ATX3_WHCS1r_AT3G6174 --FTVGDVWAKCGKRFPAWPAVIDPISQAPDGVLKHCV
NP_191866_At_HDGFr_AT3G63070 -EWKVGDLVLAKVKG-FPAWPAVVEPEKWHGSADSK---
NP_850485_At_HDGFr_At2g48160 -----GDLVLAKVKG-FPAWPAVSEPEKWDASPDSK---
NP_197706_HUA2_At_HDGFr_AT5G23  -QLVLGDLVLAKVKG-FPAWPAKISRPEWDRAPDPK---
NP_196440_At_AT5G08230      -GEMRLGDLVLAKVKG-FPAWPAKIGQPEDWNQAPDPK---

NP_850170_ATX1_At2g31650      SGGGSLLVQFFGTHD-----FARIKVKQAI SFIKGLLS P
NP_172074_ATX2_AT1G05830     SGGRSVLVQFFGTHD-----FARIQVKQAVSFLKGLLSR
NP_195915_At_AT5G02950      KG--NVLVAYFGDCT-----FA-WNNASQIKPFHQNF SQM
NP_187578_At_At3g09670      KG--SFLVTYFGDCT-----FA-WNEASRIKPFHQNF SQM
NP_190402_ATMlike_AT3G48190  -----FMVRSIGQSH-----LVSWFASSKLKPFKESFEQV
NP_187194_At_AT3G05430      MG--YVLVAFFGDN-----SYGWFDPAELIPPEPHVKEK
NP_198117_At_AT5G27650      ID--HVLVAFFGDS-----SYGWFDPAELIPPEPNLEEK
NP_198850_At_AT5G40340      KG--KLLVACFGDG-----TFAWCGASQLKPF AESFKEC
NP_189424_At_AT3G27860      KG--KLLVAYFGDGS-----FFGWCNPLELKPFL ENFKEF
NP_194520_ATX4_WHCS1r_AT4G2791 PD--AACVVFFGHSGNENERDYAWVRRGMIFFPFVDYVARF
NP_200155_ATX5_At_AT5G53430  PD--AACVMFFGHSGTENERDYAWVRRGMIFFPFVDYVERL
NP_191733_ATX3_WHCS1r_AT3G6174 PG--AICVMFFGYSKDGTQRDYAWVRQGMVYPFTEFMDKF
NP_191866_At_HDGFr_AT3G63070 ----KVTVHFFGTQQ-----IAFCNHGDVESFTEEEKQS
NP_850485_At_HDGFr_At2g48160 ----KVFVHFFGTQQ-----IAFCNPGDVEAFTEERKQS
NP_197706_HUA2_At_HDGFr_AT5G23 ----KYFVQFFGTEE-----IAFVAPPDIQAF TSEAKSK
NP_196440_At_AT5G08230      ----KHFVQFYGTGE-----IGFVTPPDIQPF TSETKKK

NP_850170_ATX1_At2g31650      SHLK----CKQPRFEEGMQEA-----
NP_172074_ATX2_AT1G05830     SPLK----CKQPRFEEAMEEA-----
NP_195915_At_AT5G02950      QEQ-----SNSAEFRDAIDCALDE----
NP_187578_At_At3g09670      AKQ-----SSLPDFIDAIDFALEE----
NP_190402_ATMlike_AT3G48190  LNQ-----RNDNGFFDALQKA-----
NP_187194_At_AT3G05430      SQQ-----TSSDHFAKAVEEAMNE----
NP_198117_At_AT5G27650      SQQQ----TVSKHFVRAVEEAKDE----
NP_198850_At_AT5G40340      SKV-----SNSRSFLGAVEEAVEE----
NP_189424_At_AT3G27860      SKM-----SDSRRFLLAVEDA-----
NP_194520_ATX4_WHCS1r_AT4G2791 QEQP ELQGCKPGNFQMALEEAFLADQGF
NP_200155_ATX5_At_AT5G53430  QEQSELRGCNPRDFQMALEEA LLADQGF
NP_191733_ATX3_WHCS1r_AT3G6174 QDQTNL FNYKASEFNKALEEA VLAENGN
NP_191866_At_HDGFr_AT3G63070 LLTR-RHAKGSD-FVRAVKEI TES----
NP_850485_At_HDGFr_At2g48160 LLTR-RHAKGSD-FVRAVKEI IES----
NP_197706_HUA2_At_HDGFr_AT5G23 LLAR-CQGKTVKYFAQAVEQICTA----
NP_196440_At_AT5G08230      LSAR-CQGKTVKYFSQAVEEI-----

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Multiple sequence alignment of plant and algae PWWP-domain containing sequences. The multiple sequence alignment was used to reconstruct the neighbor joining (AF8) phylogeny.

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XP_002318650_Populus      -----FHVGDIVVVKTKN---QSWWPGKI
XP_002461281_Sorghum     -----FAPGDMVWGKKLN---HAAWPGLI
NP_189424_At_AT3G27860   -----FHVGDFVWGEEANS--QQWWPGQI
XP_002875407_Alyrata     -----FHVGDFVWGKEVNS--QQWWPGQI
NP_198850_At_AT5G40340   -----GDFVWGKIKN---HPWWPGQI
XP_002305994_Populus     -----FRVGDFVWGKIKS---HPWWPGRV
NP_195915_At_AT5G02950   -----DLVWAKLRS---YPWWPGLV
XP_002871003_Alyrata     -----DLVWAKIRS---YPWWPGQV
NP_187578_At_At3g09670   -----ISDSDLVWAKVRS---HPWWPGQV
XP_002882633_Alyrata     -----ISDSDLVWAKVRS---HPWWPGQV
XP_002326168_Populus     -----LSVGDVWVGKIRS---HPWWPGQV
XP_002322856_Populus     -----GDLVWGKIRS---HPWWPGQI
XP_002315275_Populus     -----FVSVDLVWGVKRS---HPWWPGQI
XP_002439929_Sorghum     -----DLVWGKIVKS---HPWWPGEI
XP_002440507_Sorghum     -----PGRLVWGVKVRD---HPWWPAQV
NP_187194_At_AT3G05430   -----FEVGDMVWGVKRS---HPWWPGQI
XP_002882413_Alyrata     -----FEVGDMVWGVKRS---HPWWPGQI
XP_002319529_Populus     -----FEVGDMVWGVKRS---HPRWPGHI
XP_002330150_Populus     -----FEVGDMVWGVKRS---HPWWPGHI
NP_198117_At_AT5G27650   -----FEVGDVWGVKRS---HPWWPGHI
XP_002330341_Populus     -----
XP_002439285_Sorghum     -----PRFGDMVWAKVKS---HPWWPGHI
XP_002878409_Alyrata     -----FTVGDVWAKCGKR--FPAWPAVV
XP_002878396_Alyrata     -----
NP_191733_ATX3_WHCS1r_AT3G6174 -----FTVGDVWAKCGKR--FPAWPAVV
XP_002302629_Populus     -----FALGDVWAKCGKR--YPWWPAIV
NP_194520_ATX4_WHCS1r_AT4G2791 -----FYSGDLVWAKSGRN--EPFWPAIV
XP_002869532_Alyrata     -----FYSGDLVWAKSGRN--EPFWPAIV
NP_200155_ATX5_At_AT5G53430 -----FYSGDLVWAKSGRN--EPFWPAIV
XP_002864242_Alyrata     -----FYSGDLVWAKSGRK--EPFWPAIV
XP_002318412_Populus     -----FYSGDLVWAKSGMK--YFPWPAIV
XP_002321418_Populus     -----FYSGDVWAKSGNK--SPTWPAIV
XP_002454931_Sorghum     -----FVLGDVWARSGKK--SPTWPAIV
XP_002961390_Selaginella -----FDIGDIVWAKSGKKK--DPVWPAKV
XP_002980880_Selaginella -----FDIGDIVWAKSGKKK--DPVWPAKV
XP_001777592_Physcomitrella -----FDLGEIVWAKSGKRN--DPVWPARV
XP_002456070_Sorghum     -----LVYGDVWAKLGKR--QPMWPGVL
XP_003078017_O_tauri     -----VHGDVVFARASSRATEPLWPAVV
NP_191866_At_HDGFr_AT3G63070 -----EWKVGDLVLAKVKG---FPAWPAVV
NP_850485_At_HDGFr_At2g48160 -----GDLVLAKVKG---FPAWPAVV
XP_002880345_Alyrata     -----KWKVGDLVLAKVKG---FPAWPAVV
XP_002876705_Alyrata     -----KVGDLVLAKVKG---FPAWPAVV
XP_002465241_Sorghum     -----WKVGDLVLAKMKG---FPAWPAIV
XP_002463300_Sorghum     -----QWKVGDLVLAKMKG---FPAWPAIV
NP_197706_HUA2_At_HDGFr_AT5G23 -----QLVLGDLVLAKVKG---FPAWPAIV
XP_002872040_Alyrata     -----GQLILGDLVLAKVKG---FPAWPAIV
NP_196440_At_AT5G08230   -----GEMRLGDLVLAKVKG---FPAWPAIV
XP_002873347_Alyrata     -----LRLGDLVLAKVKG---FPAWPAIV
XP_002310078_Populus     -----QLRLGDLVLAKVKG---YPSWPAIV
XP_002306384_Populus     -----QLRLGDLVLAKVKG---YPSWPAIV
XP_002443678_Sorghum     -----REPQLGDLVLAKIKG---YPPWPAIV
XP_002974023_Selaginella -----QWKIGDLVLAKVKG---FPAWPAIV

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XP_002983468_Selaginella -----QWKIGDLVLAKVKG---FPAWPAQV
 XP_002962776_Selaginella -----EWSVGDLVLAKVKG---FPAWPAQV
 XP_001753837_Physcomitrella -----REFNEGDLVLAKVKG---WPAWPAQA
 XP_001765392_Physcomitrella -----REFNVGDLVLAKVKG---WPAWPAQ-
 NP_850170_ATX1_At2g31650 -----FEPGDIVWAKLAG---HAMWPAVI
 XP_002881186_Alyrata -----FETGDIVWAKLAG---HAMWPAVI
 NP_172074_ATX2_AT1G05830 -----FEPRDI IWAKLTG---HAMWPAII
 XP_002889570_Alyrata -----FEPRDI IWAKLTG---HAMWPAII
 XP_002301643_Populus -----LEPGDI IWAKLTG---HAMWPAIV
 XP_002320433_Populus -----PGDI IWAKVTG---HAMWPAIV
 XP_002459927_Sorghum -----PGDLVWAKITG---HAMWPAVV
 XP_002992195_Selaginella -----GTVVWAKVKG---WPMWPAIV
 XP_002982095_Selaginella DELALLANEMESFEEQISHGTVVWAKVKG---WPMWPAIV
 XP_001767466_Physcomitrella -----GDLVWAKVKG---WPMWPAFV
 XP_001780587_Physcomitrella -----GDLVWAKVKG---WPMWPAFV
 XP_002975241_Selaginella -----FQHGDIVWAEETPG---YPMWPAFV
 XP_001693149_Chlamydomonas -----LRPGEVVWAQVRR---SAPWPAIV
 XP_001760849_Physcomitrella -----FKHGQLVWAKFAR---FPWWPAEI
 XP_001751216_Physcomitrella -----GQLVWAKFAR---FPWWPAEI
 XP_002961091_Selaginella -----SAGQLVWAKFSR---SPWWPAQV
 XP_002966918_Selaginella -----SAGQLVWAKFSR---SPWWPAQV
 XP_002444527_Sorghum -----FRLGDI TWVKCSG---SSWWPAQV

XP_002318650_Populus FDPLGVTKYAVQ--SDQR---NGLLVGYLGC-----
 XP_002461281_Sorghum YSAGGN-----G--TGHE---GQFLVSYFGDK-----
 NP_189424_At_AT3G27860 YDSL DADSLALK--TMQK---GKLLVAYFGDG-----
 XP_002875407_Alyrata YDSL DADSLALK--TMQK---GKLLVAYFGDG-----
 NP_198850_At_AT5G40340 YDPSDASDLALK--IKQK---GKLLVACFGDG-----
 XP_002305994_Populus YDPSNASDYAKK--VKQR---DKLLVAYFGDS-----
 NP_195915_At_AT5G02950 FDKSVASKAAMR--HFKK---GNVLVAYFGDC-----
 XP_002871003_Alyrata IDASVASKAAKK--HFKKK---GNLLVAYFGDC-----
 NP_187578_At_At3g09670 FDASAATDKAKK--HFKK---GSFLVTYFGDC-----
 XP_002882633_Alyrata FDASAATDKAKK--YFKK---GSFLVTYFGDC-----
 XP_002326168_Populus FGRSDASKKAKK--YFKK---NSYLIAYFGDQ-----
 XP_002322856_Populus FGCADASKKAKK--HFKK---DSYLIAYLGDQ-----
 XP_002315275_Populus FDPDASEKAMR--YHKK---DCYLVAYFGDR-----
 XP_002439929_Sorghum FDPDASELALK--HQKK---GSHLVAYFGDN-----
 XP_002440507_Sorghum FDAADASADARA--LRRPR--GAVLVAYFWDK-----
 NP_187194_At_AT3G05430 FNEAFAS-PSVR--RVKKM--GYVLVAFFGDN-----
 XP_002882413_Alyrata FNEAFAS-PSVR--RMKKM--GYVLVAFFGDN-----
 XP_002319529_Populus FNEAFAS-SSVR--RTRRE--GHVLVAFFGDS-----
 XP_002330150_Populus FNEAFAS-SSVR--RTRRE--GHVLVAFFGDS-----
 NP_198117_At_AT5G27650 FNEAFAS-PSVR--RMRI--DHVLVAFFGDS-----
 XP_002330341_Populus -----RE--GHVLVAFFGDG-----
 XP_002439285_Sorghum YSVNLT DDEEVH--RGYRD--GLVLVAFFGDS-----
 XP_002878409_Alyrata IDPISQAPDGLV--KHCVP--GAICVMFFGYS-KDG-TQR
 XP_002878396_Alyrata VDPISQAPDGLV--KHCVP--GAICVMFFGYS-KNG-TQR
 NP_191733_ATX3_WHCS1r_AT3G6174 IDPISQAPDGLV--KHCVP--GAICVMFFGYS-KDG-TQR
 XP_002302629_Populus IDPILQAPDAVL--SCCVP--GAICIMFYGYS-KNG-TQR
 NP_194520_ATX4_WHCS1r_AT4G2791 IDPMTQAPLVL--RSCIP--DAACVFFGHGS-GNE-NER
 XP_002869532_Alyrata IDPMTQAPLVL--RSCIP--DAACVFFGHGS-GNE-NER
 NP_200155_ATX5_At_AT5G53430 IDPMTQAPLVL--RSCIP--DAACVFFGHGS-GTE-NER
 XP_002864242_Alyrata IDPMTQAPLVL--RSCIP--DAACVFFGHGS-GTE-NER
 XP_002318412_Populus IDPMTQAPLVL--RSCIA--DAACVFFGCS-GNDGDQR
 XP_002321418_Populus IDPMTQAPLVL--RSCIA--DAACVFFGCS-GNDGNQR
 XP_002454931_Sorghum IDPMQHAPVVL--NSCVP--GALCVMFFGYS-ANG-HGR

XP_002961390_Selaginella VDPIKEVPESVR--RKCVP--NRLCVMFYGESLARGVKRR
XP_002980880_Selaginella VDPIKEVPESVR--RKCVP--NRLCVMFYGESLARGVKRR
XP_001777592_Physcomitrella IDPFREAPPMVR--ELSLP--NSLCVMFYGPSKSKGKHSR
XP_002456070_Sorghum IDPTQQVAADAMPQPRRV--AVLCVMLFGWCTEFS-DEK
XP_003078017_O_tauri VEPW-DAPEGVR--KQCEP--ESVCVMFLGPSATRGRAR
NP_191866_At_HDGFr_AT3G63070 D-----EPEKWGHSADS--KKVTVHFFGT-----
NP_850485_At_HDGFr_At2g48160 S-----EPEKWDASADS--KKVTVHFFGT-----
XP_002880345_Alyrata S-----EPEKWGALTDL--KKVTVHFFGT-----
XP_002876705_Alyrata S-----QPEKWGYSADS--KKVLVHFFGT-----
XP_002465241_Sorghum S-----EPEQWKMPSTK--KKPLVYFYGT-----
XP_002463300_Sorghum -----FIK--YSVHINIYRS-----
NP_197706_HUA2_At_HDGFr_AT5G23 S-----RPEDWDRAPDP--KKYFVQFFGT-----
XP_002872040_Alyrata S-----RPEDWDRAPDP--KKYFVQFFGT-----
NP_196440_At_AT5G08230 G-----QPEDWNQAPDP--KKHFVQFFGT-----
XP_002873347_Alyrata G-----QPEDWNQAPDP--KKHFVQFFGT-----
XP_002310078_Populus S-----RPEDWKRADA--KKVTVHFFGT-----
XP_002306384_Populus S-----RPEDWKRADA--KKVTVHFFGT-----
XP_002443678_Sorghum S-----RPEDWQHKPTP--KKFFVYFYGT-----
XP_002974023_Selaginella S-----RAEDFGRQNP--AKVTVHFFGT-----
XP_002983468_Selaginella S-----RAEDFGRQNP--AKVTVHFFGT-----
XP_002962776_Selaginella S-----KPEAFGQHHNP--ARVTVHFFGT-----
XP_001753837_Physcomitrella EVSCFPQEIGKLETQKHA--GKYVTVYFGPG-----
XP_001765392_Physcomitrella -----IGRLETQKHA--GKYVTVYFGPG-----
NP_850170_ATX1_At2g31650 VDESIIGERKGLNKNVSGGG--SLLVQFFGTH-----
XP_002881186_Alyrata VDESVIGERKGLNKNVSGGG--SLLVQFFGTH-----
NP_172074_ATX2_At1G05830 VDESIVIKRGLNKNKISGGR--SVLVQFFGTH-----
XP_002889570_Alyrata VDESIVIKRGLNKNKASGGR--SVLVQFFGTH-----
XP_002301643_Populus VDGalIGHKGLS-KNIGGG--SISVQFFGTH-----
XP_002320433_Populus VDEALIGHKGLS-KNIGGR--SVSVQFFGTH-----
XP_002459927_Sorghum VDESNVPATRALK-SIRLDQ--SILVQFFGTH-----
XP_002992195_Selaginella LDEE-HAEKCGLERPLKKS---TFAVQFFGSC-----
XP_002982095_Selaginella LDEE-HAEKCGLERPLKKS---TFAVQFFGSC-----
XP_001767466_Physcomitrella MDED-HAAACGME-PGKKG---MVPLQFFGYS-----
XP_001780587_Physcomitrella MDED-HAAACGMD-PGKKG---MVPLQFFGYS-----
XP_002975241_Selaginella MDDQ-HARLCNLE--ISTG---ELPVHYFGTY-----
XP_001693149_Chlamydomonas ITRE-EAEREGLVGGSRGLGHNHQVFRFFGDY-----
XP_001760849_Physcomitrella INERAFQPGTGGNRRSNTD----VLVRFVFGTY-----
XP_001751216_Physcomitrella INEKAVIPGTGGNKRINAD----VLSKCF-IY-----
XP_002961091_Selaginella ADEKSMSERT---RQSKNH----VLVRFVFGNY-----
XP_002966918_Selaginella ADEKSMSERT---RQSKNH----VLVRFVFGNY-----
XP_002444527_Sorghum IDELCVGSKP--KKKDKYD----CLVRLYGT-----

XP_002318650_Populus HIA-----WCLPSQLKPFHKDFEQMVVKN-----
XP_002461281_Sorghum AFA-----WCDGAEALRPYEPYFVAELYD-----D
NP_189424_At_AT3G27860 SFFG-----WCNPLELKPFLNFKKFSKMS-----
XP_002875407_Alyrata KFC-----WCNPLELKPFLNFKKFSKMS-----
NP_198850_At_AT5G40340 TFA-----WCGASQLKPFASFKECSKVS-----
XP_002305994_Populus TFA-----WCNPSQLSPFEENFVEMFKQS-----
NP_195915_At_AT5G02950 TFA-----WNNASQIKPFHQNFSSMQEQS-----
XP_002871003_Alyrata TFA-----WNNASQVQPFHQNFSSMQEQS-----
NP_187578_At_At3g09670 TFA-----WNEASRIKPFHQNFSSMAKQS-----
XP_002882633_Alyrata TFA-----WNDASRVKPFHQNFSSMAKQS-----
XP_002326168_Populus TFA-----WNEVSKIKPFRCNFSLLEKQS-----
XP_002322856_Populus TFA-----WNEVSKIKPFRCNFSLLEKQS-----
XP_002315275_Populus TFA-----WNEASLLKPFRRSHFSQVEKQS-----
XP_002439929_Sorghum TFA-----WCDESQKPFVNTNYSQMEKQS-----

| | |
|--------------------------------|--|
| XP_002440507_Sorghum | TFA-----WNDAALLPFRAGF----- |
| NP_187194_At_AT3G05430 | SYG-----WFDPAELIPFEPHVKEKSQQ-----T |
| XP_002882413_Alyrata | SYG-----WFDPAELLPFEPHVAENSQQ-----T |
| XP_002319529_Populus | SYG-----WFDPAELIQFDVNFAEKSQQ-----T |
| XP_002330150_Populus | SYG-----WFDPAELIPFDANFAEKSQQ-----T |
| NP_198117_At_AT5G27650 | SYG-----WFDPAELIPFEPNLEEKSQQ-----T |
| XP_002330341_Populus | SYG-----WLDPTELVQFDSHYVEKSKQT-----N |
| XP_002439285_Sorghum | SYG-----WFEPSELVPFEDHFTEK----- |
| XP_002878409_Alyrata | DYA-----WVRQGMYPFTEFMDKFQDQTNLY----NY |
| XP_002878396_Alyrata | DYA-----WVRQGMVYPFTEFMDKFQDKTNLY----NY |
| NP_191733_ATX3_WHCS1r_AT3G6174 | DYA-----WVRQGMVYPFTEFMDKFQDQTNLF----NY |
| XP_002302629_Populus | DYA-----WVKQGMVFPFAEFMERFQVQSQMF----KC |
| NP_194520_ATX4_WHCS1r_AT4G2791 | DYA-----WVRRGMIFPFVDYVARFQEQLQ----GC |
| XP_002869532_Alyrata | DYA-----WVRRGMIFPFVDYVARFQEQSELQ----GC |
| NP_200155_ATX5_At_AT5G53430 | DYA-----WVRRGMIFPFVDYVERLQEQSELR----GC |
| XP_002864242_Alyrata | DYA-----WVRRGMIFPFVDYVDRFQEQSELR----GC |
| XP_002318412_Populus | DYA-----WVQRGMIFPFDFVDRFQEQSELD----DC |
| XP_002321418_Populus | DYA-----WVQRGMIFPFMDFLDRFQEQSELD----DF |
| XP_002454931_Sorghum | DYG-----WVKQGMIFPFVDYLDRFQGGQP--LY----KL |
| XP_002961390_Selaginella | DYA-----WVRKGMIFPFVDYLERFQSQTSEFN----KS |
| XP_002980880_Selaginella | DYA-----WVRKGMIFPFVDYLERFQSQTSEFN----KS |
| XP_001777592_Physcomitrella | DYA-----WVKQGMIFPFNAYLERFQSQTQLN----RS |
| XP_002456070_Sorghum | KYV-----WVRQGLIFPFSDYMDRFQGGTELS----SC |
| XP_003078017_O_tauri | DYC-----WATEERLAPYAR-AEALFAQKQVAK----RM |
| NP_191866_At_HDGFr_AT3G63070 | QQIA-----FCNHGDVESFTEKKQSLLTRRH-----A |
| NP_850485_At_HDGFr_At2g48160 | QQIA-----FCNPGDVEAFTEERKQSLLTRRH-----A |
| XP_002880345_Alyrata | QQIA-----FCNHTDVEAFTEERKQSLLTKRH-----A |
| XP_002876705_Alyrata | QQIA-----LCNPADVESFTEKKQLLLTKRH-----A |
| XP_002465241_Sorghum | KQIA-----FCNYADLEAFTEKKRSLLAKRH-----G |
| XP_002463300_Sorghum | QDIV-----EITPEQWDLPAAKKKSIVAKK----- |
| NP_197706_HUA2_At_HDGFr_AT5G23 | EEIA-----FVAPPDIQAFTSEAKSKLLARC----QGK |
| XP_002872040_Alyrata | EEIA-----FVAPPDIQAFTSEAKSKLLARC----QGK |
| NP_196440_At_AT5G08230 | GEIG-----FVTPPDIQPFTSETKKKLSARC----QGK |
| XP_002873347_Alyrata | QEIG-----FVAPPDIQPFTSEAKNKLARC----QGK |
| XP_002310078_Populus | QEIA-----FVAPSDIQVFTNEVKNKLSARC----QSK |
| XP_002306384_Populus | QEIA-----FVAPSDIQVFTNEVKNKLSARC----QSK |
| XP_002443678_Sorghum | EEIA-----FVPLADLEEFTEKTKNDLLDRAPNIKVQRK |
| XP_002974023_Selaginella | KQIR-----FCQHSEISAFTVEARAALHARTLS----KC |
| XP_002983468_Selaginella | KQIR-----FCQHSEISAFTVEARAALHARTLS----KC |
| XP_002962776_Selaginella | KQIR-----FCHHSEISKFTPEAKASLVAKAHS----KC |
| XP_001753837_Physcomitrella | QQIG-----WCLPVELSEFDADQREASIQKSLK----KT |
| XP_001765392_Physcomitrella | QQIG-----WCLPVELSEFDADQREASVQKSLK----KT |
| NP_850170_ATX1_At2g31650 | DFAR-----IKVKQAISFIKGLLSPSHLKCKQP----- |
| XP_002881186_Alyrata | DFAR-----IKEKQAISFIKGLLSPSHLKCKQP----- |
| NP_172074_ATX2_At1G05830 | DFAR-----IQVKQAVSFLKGLLSRSPKCKQP----- |
| XP_002889570_Alyrata | DFAR-----EDCHDFEPRDIIWAKLTGHA----- |
| XP_002301643_Populus | DFAR-----IKPKQAISFLKGLLSSFHLKCKQP----- |
| XP_002320433_Populus | DFAR-----YLSEQKLP----- |
| XP_002459927_Sorghum | DFAR-----F----- |
| XP_002992195_Selaginella | DFAR-----LNNDKIVTFFSKGVQLKYHSKCKRP----- |
| XP_002982095_Selaginella | DFAR-----LNNDKIVTFFSKGVQLKYHSKCKRP----- |
| XP_001767466_Physcomitrella | DHCR-----FSYKLVIFFSKGLMMKFHTKCKRV----- |
| XP_001780587_Physcomitrella | DHCR-----FSYKLVIFFSKGLMMKFHTKCKRV----- |
| XP_002975241_Selaginella | ESA----- |
| XP_001693149_Chlamydomonas | TVFA-----LPAISAGRIPD-----RGAVV----- |
| XP_001760849_Physcomitrella | DYG-----WVDPEVGLSEFDVKMQERSRIKKK----- |
| XP_001751216_Physcomitrella | GLGSDGKCSGWVDPKVGLESEFDVKLQERSKIKKK----- |

XP_002961091_Selaginella
XP_002966918_Selaginella
XP_002444527_Sorghum

NYG-----WVDPASDLSKFDVDFDGRSQVPTK-----
NYG-----WVDPASDLSKFDVDFDGRSQVPTK-----
QYL-----YVDPWKSNSEFEMMLKQENKSTME-----

XP_002318650_Populus
XP_002461281_Sorghum
NP_189424_At_AT3G27860
XP_002875407_Alyrata
NP_198850_At_AT5G40340
XP_002305994_Populus
NP_195915_At_AT5G02950
XP_002871003_Alyrata
NP_187578_At_At3g09670
XP_002882633_Alyrata
XP_002326168_Populus
XP_002322856_Populus
XP_002315275_Populus
XP_002439929_Sorghum
XP_002440507_Sorghum
NP_187194_At_AT3G05430
XP_002882413_Alyrata
XP_002319529_Populus
XP_002330150_Populus
NP_198117_At_AT5G27650
XP_002330341_Populus
XP_002439285_Sorghum
XP_002878409_Alyrata
XP_002878396_Alyrata
NP_191733_ATX3_WHCS1r_AT3G6174
XP_002302629_Populus
NP_194520_ATX4_WHCS1r_AT4G2791
XP_002869532_Alyrata
NP_200155_ATX5_At_AT5G53430
XP_002864242_Alyrata
XP_002318412_Populus
XP_002321418_Populus
XP_002454931_Sorghum
XP_002961390_Selaginella
XP_002980880_Selaginella
XP_001777592_Physcomitrella
XP_002456070_Sorghum
XP_003078017_O_tauri
NP_191866_At_HDGFr_AT3G63070
NP_850485_At_HDGFr_At2g48160
XP_002880345_Alyrata
XP_002876705_Alyrata
XP_002465241_Sorghum
XP_002463300_Sorghum
NP_197706_HUA2_At_HDGFr_AT5G23
XP_002872040_Alyrata
NP_196440_At_AT5G08230
XP_002873347_Alyrata
XP_002310078_Populus
XP_002306384_Populus
XP_002443678_Sorghum
XP_002974023_Selaginella

KARSFLGAVEKAVDE----
GGEDFDAAVEASLDE----
DSRRFLLAVEDA-----
ESKRFLSAVEEA-----
NSRSFLGAVEEAVEE----
NSKSFVNAVKEAVDE----
NSAEFRDAIDCALDE----
NLAEFRDAIDCALDE----
SLPDFIDAIDFALEE----
SLPDFIDAIDFALEE----
NLEDFHDAVHCALDE----
NLEDFHDAVHCALDE----
NSEVFNQNAVDCSLEE----
TSDAFVGSVNNALEE----

SSDHFAKAVEEAMNE----
SSGHFAKAVEEAMDE----
NSRTFIKAVEEATDE----
NSRTFIRAVEEATDE----
VSKHFVRAVEEAKDE----
AKVFLIKAVEEADD-----

KPSEFKKALEEAVLAENG-
KPSEFKKALDEAVLAENG-
KASEFNKALEEAVLAENGN
KLSDFQVALEEEAILAESGF
KPGNFQMALEEAFLADQGF
KPGNFQMALEEAFLADQGF
NPRDFQMALEEALLADQGF
NPREFQMALEEALLADQGF
KPGDFQMAVEEAFLAEQGF
N-GDFQMAFEEAFLAEQGF
RPSKFRAAIEEAFLAERGF
QPGDFWSAIEEATLAEAG-
QPGDFWSAIEEATLAEAG-
RPVDFRQAISEAKLAD---
KPADFRRAVEEAFLADQGF
RPNAFNEACAEA-----
KGSDFVRVAVKEITES----
KGSDFVRVAVKEIIES----
KGSDFLRVAVKEIIES----
KGSDFVRVAVKEITES----
KGADFLRAVDEIVE-----
KLLVYFYGTKE-----
TVKYFAQAVEQICTA----
TVKYFAQAVEQICTA----
TVKYFSQAVEEII-----
TVKYFSQAVEEII-----
KDRFFSQAVKEICAA----
KDKFFSQAVKEICAA----
YVQVFNDAVEQICKA----
VPSDLKRAVKEICE-----

| | |
|-----------------------------|---------------------|
| XP_002983468_Selaginella | VPSDLKRAVKEICE----- |
| XP_002962776_Selaginella | TPADLRLAVSEIC----- |
| XP_001753837_Physcomitrella | ADKKFISAVKEIC----- |
| XP_001765392_Physcomitrella | ADKKFIFAVKEIC----- |
| NP_850170_ATX1_At2g31650 | ---RFEEGMQEA----- |
| XP_002881186_Alyrata | ---RFEEGMQEA----- |
| NP_172074_ATX2_AT1G05830 | ---RFEEAMEEA----- |
| XP_002889570_Alyrata | ----- |
| XP_002301643_Populus | ---RFTRSLEEA----- |
| XP_002320433_Populus | ----- |
| XP_002459927_Sorghum | ----- |
| XP_002992195_Selaginella | ---AFDQGLRE----- |
| XP_002982095_Selaginella | ---AFDQGLRE----- |
| XP_001767466_Physcomitrella | ---VFVQGLEEVE----- |
| XP_001780587_Physcomitrella | ---VFVQGLEEVE----- |
| XP_002975241_Selaginella | ----- |
| XP_001693149_Chlamydomonas | ---PFLSGL----- |
| XP_001760849_Physcomitrella | ---AFQKGIEEALEY---- |
| XP_001751216_Physcomitrella | ---ALQKGIEEALEF---- |
| XP_002961091_Selaginella | ---AFQKGLKEALEY---- |
| XP_002966918_Selaginella | ---AFQKGLKEALEY---- |
| XP_002444527_Sorghum | ---AFREVLEK----- |

Multiple sequence alignment of PWWP-domain containing sequences. The multiple sequence alignment was used to reconstruct the neighbor joining (AF9) phylogeny.

```

3068_HDGF_NP_004485      KEYKCGDLVFAKMKGYPHWP-----ARI--D
50810_HDGF3P3_CCDS32314 REYKAGDLVFAKMKGYPHWP-----ARI--D
84717_HDGF2P2_UNQ785PRO1604 HAFKPGDLVFAKMKGYPHWP-----ARI--D
154150_HDGFL1_NP_612641  --YKSGDLVFAKLKGYAHWP-----ARI--E
XP_001634069_Nv         MTYQPGDLIWAKMRGYPHWP-----ARI--D
84656_GLYR1_NM_032569    --LRLGDLVWGKLGYPWP-----GKI--V
54904_b_WHSC1L1_NM_023034_MSH6 -KFQVGDVWVKVGTYPWWP-----CMVSSD
7468_b_WHSC1_NM_133330_MSH61 LKYNVGDVWVKVSGYPWWP-----CMVSAD
64324_b_NSD1_NM_172349_MSH61 LKYEVDLWAKFKRRPWWP-----CRICSD
152098_ZCWPW2_NP_001035522 ---PLGSLVLVKLQNWPSWP-----GILCPD
XP_001633052_Nv         SPFPTGAIWAKLAGYPWWP-----AMMEDD
7468_a_WHSC1_NM_133330_WHSCr --LHFQDIWVKLGNYRWWP-----AEVCHPKNV
64324_a_NSD1_NM_172349_WHSCr --PHYREIVWVKVGRYRWWP-----AEICHPRAV
54904_a_WHSC1L1_NM_023034_WHSC --LHYKQIVWVKLGNYRWWP-----AEICNPRSV
XP_001635219_Nv         --LLYGDIVWVKLGMYPWWP-----AMICNPRDV
XP_001747378_b_Mb       -----DVVWAKYGSYRWWP-----AVILSATEY
23613_ZMYND8_NM_183047   -----WF-C--EPCSN-----PHPLVWAKLKGf
10771_ZMYND11_NM_006624  -----WF-C--YPCIP-----NHELWAKMKGF
27154_BRPF3_NM_015695    --LEPLELVWAKCRGYPSYPALIIDPKMPREGLLHNGVPI
7862_BRPF1_NM_001003694 --LDALDLVWAKCRGYPSYPALIIDPKMPREGMFHHGVPi
23774_BRD1_NM_014577    --LEPLKVVWAKCSGYPSYPALIIDPKMPRVPGHHNGVTI
114825_PWWP2Aisob_NP_001124336 --ICVGDIVWAKIYGFPPWWP-----ARILTI
170394_PWWP2B_NM_138499  --VAVGDIVWVKIHGFPWWP-----ARVLDI
XP_001624451_Nv         --INEGSIWGVKHGHPWWP-----GRVMAI
1788_DNMT3A_NM_022552    --FGIGELVWVKLGFSSWWP-----GRIVSW
1789_DNMT3B_NM_006892    --FGIGDLVWVKIKGFSWWP-----AMVVSF
XP_001626231_Nv         -----GVLVWVKLKGYPWWP-----GRVVTY
NP_116242                --FEVGMLVWHKHKYPFWP-----AVVKSf
139221_MUM1L1_NM_152423  --FETGMIVWFKYQKYPFWP-----AVIKSI
728317_LOC728317_XP_001127165 --IERGTMVWFKFQDHPFWP-----AVVKSf
728307_LOC728307_XP_001127139 --IERGTMVWFKFQDHPFWP-----AVVKSf
55063_ZCWPW1_NM_017984   ASYIPGSIWAKQYGYPPWWP-----GMIESD
XP_001750279_Mb         --PQAWDFVWARMRGYPWYP-----AMLVNW
2956_MSH6_HSU54777       CDFSPPGDLVWAKMEGYPPWWP-----CLVYNH
XP_003084095_O_tauri    -----NQLVWAKLPGHPFWPG-----LRVNLET
XP_003079195_O_tauri    -----AVIP-----ESARTG

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3068_HDGF_NP_004485      EMPEAAVKST-----ANKYQVFFFG-THETA
50810_HDGF3P3_CCDS32314 ELPEGAVKPP-----ANKYPIFFFG-THETA
84717_HDGF2P2_UNQ785PRO1604 DIADGAVKPP-----PNKYPIFFFG-THETA
154150_HDGFL1_NP_612641  HMTQ-----PNRYQVFFFG-THETA
XP_001634069_Nv         LAAKDEVIP-----AKKYPIFFYG-THETA
84656_GLYR1_NM_032569    NPPKDLKKPRG-----KRCFFVKFFG-TEDHA
54904_b_WHSC1L1_NM_023034_MSH6 PQLEVHTKIN-----TRGAREYHVQFFSNQPERA
7468_b_WHSC1_NM_133330_MSH61 PLLHSYTKLKG-----QKKSARQYHVQFFGDAPERA
64324_b_NSD1_NM_172349_MSH61 PLINTHSMKMKVS-----NRRPYRQYVEAFGDPSERA
152098_ZCWPW2_NP_001035522 RFKKGKYVTYDP-----DGNV-EEYHIEFLGDPHSRS
XP_001633052_Nv         PDYGYYYETDL-----DDRIPISYHVVFVGKDVSR
7468_a_WHSC1_NM_133330_WHSCr ---PPNIQK-----MKHEIGEFVFFFG-SKDYY
64324_a_NSD1_NM_172349_WHSCr ---PSNIDK-----MRHDVGEFVFFFG-SNDYL
54904_a_WHSC1L1_NM_023034_WHSC ---PLNIQG-----LKHDLGDFVFFFG-SHDYY
XP_001635219_Nv         ---PTNIQS-----MRHQGEFVVMFLG-SHDFY

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10771_ZMYND11_NM_006624
27154_BRPF3_NM_015695
7862_BRPF1_NM_001003694
23774_BRD1_NM_014577
114825_PWWP2Aisob_NP_001124336
170394_PWWP2B_NM_138499
XP_001624451_Nv
1788_DNMT3A_NM_022552
1789_DNMT3B_NM_006892
XP_001626231_Nv
NP_116242
139221_MUM1L1_NM_152423
728317_LOC728317_XP_001127165
728307_LOC728307_XP_001127139
55063_ZCWPW1_NM_017984
XP_001750279_Mb
2956_MSH6_HSU54777
XP_003084095_O_tauri
XP_003079195_O_tauri

---PERCGQ-----SPAEGN-FLVKFLG-SNDVA
PFWPAKALRDKD-----G-QVDAR-----FFG-QHDRA
GFWPAKVMQKED-----N-QVDVR-----FFGHHHQRA
PVPPLDVLKLG-----QKQAEAGEKLFVLVFFDNKRTWQ
PVPPLDVLKLG-----QMTQEAREHLYLVVFFDNKRTWQ
PAPPLDVLKIGE-----HMQTKSDEKLFVLVFFDNKRSWQ
TVSRKDNGLL-----VRQEARISWFG-SPTTS
SLGQKEDGEP-----SWREAKVSWFG-SPTTS
TEVVDDQGG-----VDTFAHVTWFG-SNTSS
WMTGRSRAA-----EGTRVWVWFG-DGKFS
KATSKRQAM-----SGMRWVQWFG-DGKFS
MEAGRPPPG-----PGNHVVKWFG-DNKFS
RQRDKKASV-----LYIEGHMNPMMKGF
RRKERKASV-----LFVEANMNSEKKG
SNTDKTARV-----LLEANLHHGKRG
SNTDKTARV-----LLEANLHHGKRG
PDLGEYFLFTS-----HLDSLPSKYHVTFGETVSR
QTPRDDLAECPVSDAVLKSQPSQDESSLVRFDDKTGSWA
PFDGTFFIREKG-----KSVRVHVQFFDSDPTRG
DFIPE DARKMS-----RDGEVLVFFFG-ENSFG
GFASKVSD-----EHLRVVFFDDKHSFA

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50810_HDGF3_CCDS32314
84717_HDGF2_UNQ785PRO1604
154150_HDGFL1_NP_612641
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7468_b_WHSC1_NM_133330_MSH61
64324_b_NSD1_NM_172349_MSH61
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64324_a_NSD1_NM_172349_WHSCr
54904_a_WHSC1L1_NM_023034_WHSC
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27154_BRPF3_NM_015695
7862_BRPF1_NM_001003694
23774_BRD1_NM_014577
114825_PWWP2Aisob_NP_001124336
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XP_001624451_Nv
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XP_001626231_Nv
NP_116242
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728307_LOC728307_XP_001127139
55063_ZCWPW1_NM_017984
XP_001750279_Mb
2956_MSH6_HSU54777

FLGPKDLFPYEESK--EKFGK---PNKRKGFSEGLWEIEN
FLGPKDLFPYKEYK--DKFGK---SNKRKGFNEGLWEIEN
FLGPKDLFPYDKCK--DKYK---PNKRKGFNEGLWEIQN
FLSPKDLFPYKECK--EKFGK---PNKRKGFSAAGLWEIEN
VMLPKDLFPYKHK--HKFAK---PCKRKFMEALVEIIVK
WIKVEQLKPYHAHK--EEMIK---INKGRFQQAVDAVEE
WVHEKRVREYKGHKQYELLAE--ATKQASNHSEKQKIRK
WIFEKSLVAFEGEGQFEKLCQE--SAKQAPTAKAEKIKLLK
WVAGKAIVMFEGRHQFEELP----VLRRRGKQKEK-GYRH
WIKATFVGHYSITLKPEKCKN----KWKYKSALQEA--
WVNSFSVRELTADDEEPEDIGNI--VVRKKNYKQLDDANG
WTHQARVFPYMEGDRGSRYQGV--RGIGRVFKNALQEAEEA
WTHQARVFPYMEGDVSSKDKMG--KGVDGTYKKALQEAAA
WVHQGRVFPYVEGDK-SFAEQ--TSINKTFKALEEAAK
WIHKGRVFSYQDGDGKTESGNN--KYLAKVFKKALVEAKE
WVGHEIIPFNGDQ-----KNSYFTRNLKAAK
WVPINNCYLMSKEIP-FSVKKT--KSIFNSAMQEMEVEY--
WIPSENIQDITVNIHRLHVKRS--MG-WKKACDELELH--
WLPRDKVLPLGVEDTVDKLML--EGRKTSIRKSVQVAYD
WLPRTKLVPLGVNQDLDEKML--EGRKSNIRKSVQIAYH
WLPKSKMVPLGIDETIDKLKMM--EGRNSSIRKAVRIAFD
FLALSQLSPFLENFQSRFNK-----KRKGLYRKAITAAK
FLSISKLSPFSEFFKLRFNK-----KKGMYRKAITAAN
EMPVQELQDFEPNFRRRYK-----DKKGCYRRAVRQAQE
VVCVEKLMPLSS-FCSAFHQAT--YKQPMYRKAIYEVLQ
EVSADKLVALLGL-FSQHFNLAT--FNKLVSYRKAMYHALE
QVTYDITVLPFAE-FKSNFLVTK--MKG--LYKKAVALDALE
TVSLKSLKHFDCKEKQTLN-----AREDFNQDIGWC--
RVNFRRLKFKFDCKEKQMLVDK-----AREDYSESIDWC--
QVPLRRLKHLDCKEKEKLLK-----AQKAYKQSVNWC--
QVPLRRLKHLDCKEKEKLLK-----AQKAYKQSVNWC--
WIPVNMMLKNFQELSLELSVMKK--RRNDCSQKLGVALMMA
WVTSQVMRMFASAWVDAQMLS--QTSKHAKDVFRSLFE
WVSKRLLKPYTGSKSKEAQKGGHFYSAPPEILRAMQRADE

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XP_003079195_O_tauri

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N-----
N-----
N-----
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QARQALSPLVQERLAV-----
RFREI-----
RFEEL-----
RFQEL-----
KYDEW-----
SFQE-----

RAMIH-----
RALQH-----
RAMNH-----
AA-----
AA-----
TL-----
VA-----
KA-----
VL-----

QEAEQISI-----

ALNKDKIKRLELAV-----
E-----
