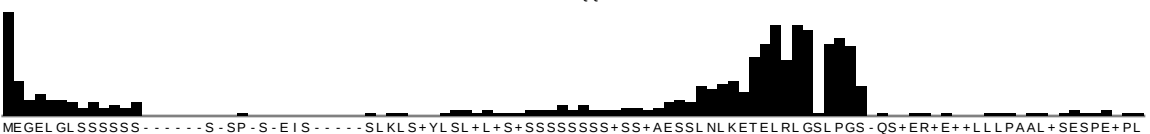


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LOC_Os01g09450.1 11667.m00901.altSplice/1-237	MAW	R	R	G	F	G	R	E	-	-	-
LOC_Os01g13030.1 11667.m01279/1-267	MSP	P	L	E	L	D	Y	I	G	L	S
LOC_Os01g18360.1 11667.m01799/1-204	MEE	C	K	G	G	G	M	S	P	S	S
LOC_Os01g48450.1 11667.m04699/1-272	MSP	P	L	E	P	H	D	Y	I	G	L
LOC_Os01g53880.1 11667.m05292/1-262	MEE	G	S	N	K	R	E	G	L	P	P
LOC_Os02g13520.1 11668.m01248.altSplice/1-308	MGE	A	S	E	S	M	K	K	I	S	R
LOC_Os02g49160.1 11668.m04779/1-206	MEC	M	A	-	-	-	-	-	-	-	-
LOC_Os02g56120.1 11668.m05537/1-183	MEL	E	L	G	L	-	-	-	-	-	-
LOC_Os02g57250.1 11668.m05658/1-282	M	R	G	V	A	G	P	T	A	G	E
LOC_Os05g08570.1 11682.m00824.altSplice/1-213	MSV	E	T	E	R	S	S	T	E	S	S
LOC_Os05g09480.1 11682.m00921/1-229	MAW	N	G	R	F	G	-	-	-	-	-
LOC_Os05g14180.1 11682.m01308/1-258	MSP	P	L	E	L	D	Y	I	G	L	S
LOC_Os05g44810.1 11682.m04283/1-328	MEE	F	K	D	K	L	P	P	T	-	-
LOC_Os05g48590.1 11682.m04652/1-282	MPP	P	L	E	A	R	D	Y	I	G	L
LOC_Os06g07040.1 11680.m00651/1-184	MEL	E	L	G	L	R	L	A	L	P	S
LOC_Os06g22870.1 11680.m02247/1-267	M	A	P	P	Q	E	R	D	Y	I	G
LOC_Os06g24850.1 11680.m02452/1-150	M	F	R	E	-	-	-	-	-	-	-
LOC_Os06g39590.1 11680.m03858/1-194	M	S	T	S	G	A	D	S	S	P	P
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PoptrIAA33.1/1-149	M	S	Q	Y	-	-	-	-	-	-	-
PoptrIAA33.2/1-117	M	-	-	-	-	-	-	-	-	-	-
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PoptrIAA3.4/1-199	M	E	R	S	M	A	Y	-	-	-	-
PoptrIAA29.2/1-233	M	E	L	Q	L	G	L	P	S	E	K
PoptrIAA12.2/1-258	M	S	K	V	E	V	-	-	-	-	-
PoptrIAA3.2/1-203	M	E	F	E	-	-	-	-	-	-	-
PoptrIAA20.2/1-175	M	G	R	G	A	T	S	S	S	S	S
PoptrIAA7.2/1-248	M	T	T	S	V	L	G	-	-	-	-
PoptrIAA34/1-194	M	D	S	N	-	-	-	-	-	-	-
PoptrIAA3.3/1-199	M	E	R	S	M	A	Y	-	-	-	-
PoptrIAA3.1/1-201	M	E	F	E	-	-	-	-	-	-	-
PoptrIAA27.1/1-307	M	S	M	P	L	E	H	D	Y	I	G
PoptrIAA7.1/1-267	M	A	-	-	-	-	-	-	-	-	-
PoptrIAA29.1/1-229	M	E	L	Q	L	G	L	P	T	Y	N
PoptrIAA27.2/1-349	M	S	S	I	P	K	E	H	D	Y	I
PoptrIAA16.4/1-237	M	E	V	E	K	G	-	-	-	-	-
PoptrIAA9/1-366	M	S	P	P	L	G	V	V	E	E	G
PoptrIAA19.3/1-184	M	A	Q	P	-	-	-	-	-	-	-
PoptrIAA28.2/1-332	M	E	E	N	T	R	C	F	N	M	T
PoptrIAA12.1/1-276	M	E	G	G	L	L	G	G	G	G	S
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PoptrIAA27.3/1-335	M	Y	S	I	P	K	E	H	D	Y	I
PoptrIAA26.1/1-338	M	E	G	C	S	K	N	V	E	A	C
PoptrIAA16.2/1-246	M	T	S	I	M	G	A	E	-	-	-
PoptrIAA3.5/1-207	M	E	G	G	V	A	Y	-	-	-	-
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PoptrIAA15/1-220	M	S	P	E	N	G	S	N	L	-	-
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IAA2/1-174	M	A	Y	E	K	-	-	-	-	-	-
IAA3/1-189	M	D	E	F	-	-	-	-	-	-	-
IAA4/1-186	M	E	K	V	D	V	Y	-	-	-	-
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IAA6/1-189	M	A	K	E	-	-	-	-	-	-	-
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IAA9/1-338	M	S	P	E	E	L	Q	S	N	V	S
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IAA27/1-305	M	S	V	S	V	A	E	A	H	D	Y
IAA28/1-175	M	E	E	-	-	-	-	-	-	-	-
IAA29/1-251	M	E	L	D	L	G	L	S	L	P	-
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IAA31/1-158	M	E	V	S	N	S	C	S	S	F	S
IAA32/1-143	M	D	P	N	T	P	A	-	-	-	-
IAA33/1-171	M	N	S	F	-	-	-	-	-	-	-
IAA34/1-185	M	Y	C	S	D	P	P	H	L	V	-

Consensus



MEGELGLSSSSSSS-S-S-P-S-E-I-S-SLKL S+YLSL+S+SSSSSSSS+SS+AESSLNLKETELRLGSLPGS-QS+ER+E+LLLPAAL+SESPE+PL

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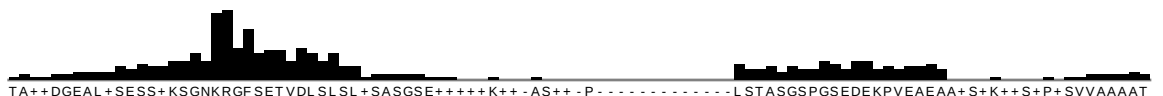
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Consensus

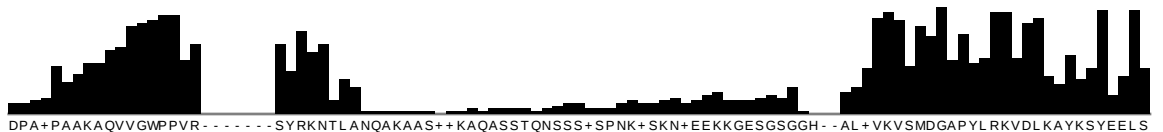


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- - - - -LTLSSVVH I DGNPN -STPRSLL -SLFVKVYMEGVP I GRKLDLLPLDGYKGLV
- - - - -RRRKT VVGWPPVS -SARRACG -ANYVKVKEGDA I GRKVDLALHSSYDELA
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- - - - -PEVKPAGLSPSR -FVKVFMHGEPEFERK I NLA I HNNYDLS
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- - - - -NGAASSQVVGWPP I R -SHRMH I MV -NQAKSQATEEFNSMNRKNAVEEKVGNKNI I NGNTKTRT -SLFVKVNMDSGTL I GRKVDLNAHCYETLA
- - - - -PPVT -VAL EGRS I CQR I SLHKHYSYSLA
- - - - -IPPV T -VVL EGRS I CQR I SLHKHYSYSLA
- - - - -LAPVVGWPP I R -SFRKNLAG -SSTPKLVSESRNKPKEGSSLKPDSEFRN -DLFVKIINMEGVP I GRK I NLAAYDSYKEL S
- - - - -APPAKAQVVGWPP I R -SYRKNCLQ -PKKNDQVDA -GMVVKVSDGAPYLRK I DLKVYKSYPEL L
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- - - - -GSPTAGSQVVGWPP I R -AYRMNSLVNQAKAARAEEDKGI GEKDI SKDNLKK I CNGNKTSAPSNEKGH -LGFVKVNMDSG I P I GRKVDLNAHACYETLA
- - - - -APP I KAQVVGWPP I R -SYRKNCLQ -AKKLEAEAA -GLYVKVSMDSGAPYLRK I DLKVYKGYPELL
- - - - -PSDQQLSDWPP I K -SENECCSA -TFFVKVYMEG I P I GRKLDLHADHGYDL I
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- - - - -YGDLMWVRAN -SPLKHSTS -WAYVKVNMDSGVP I VGRK I CMLDHGYSYSLA
- - - - -PPAKAQVVGWPP I R -SYRKNCLQ -PKKNDRVDGA -GMVVKVSDGAPYLRK I DLKVYSYPEL L
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- - - - -YGEL I DWSQS -YNS I TQLK -SEDTGHQRLAQGYNNNEGSRGK -YAYVKVNL DGLVVGKVLVDQGAETLA
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Consensus



DPA+PAAKAQVVGWPPVR - - - - -SYRKNTLANQAKAAS++KAQASSTQNSSS+SPNK+SKN+EEKKGESGSGGH- -AL+YKVSMDGAPYLRKVDLKA YKSYEELS

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LOC_Os02g56120.1|11668.m05537/1-183
LOC_Os02g57250.1|11668.m05658/1-282
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LOC_Os06g39590.1|11680.m03858/1-194
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LAL EKMFSCFITGRSS-SHKTSKRDLRTDGSRADAL-----KDQEYVLTIEDKDGDDWMLVGDLPWDLFTTSCRKLIRMGSDEAAGMAPRSL EQTGQNKX-
DTLHMF PSTNQEDGH-----DRRRRHYPVATYEDDEGDDWMLVGDVPWEMFVSSVKRLKILVX-
LAL EKMFSCTFVGHE-----SNGKSGRDGLSDCRLMDLK-NGTELVTYIEDKDGDDWMLVGDVPWMMFTDSCRRLRMKGSDAVGLAPRATDKSKNRX-
QALQSMFHGFLSDGIA-----TRDNELQRME-EGSKRYVLTVYEDNEGDRMLVGDVPWEYVCLLX-
RALHGMFASCLAVRGG-----GGDGEGTKLVDLVT-GAEYVPTYEDKDGDDWMLVGDVPWKMVFESCKRLRMKSSSEAVN LAPRSRRX-
EALDLLFTFKCF SATAS-----DGC-----SDGQFAIAYEDKDGDLMLVGDVPWEMFISSCKKLRMKGSSEARX-
QALQSMFHGFLSDGIA-----TRDNELQQME-EGSKRYVLTVYEDNEGDRMLVGDVPWELFIASVKRLYIAQDPPRVHAKLRX-
RVLTKMTHFFCPADY-----SSTNKGEEDC-AKSD EFI FLVYEDGDRMLVGDVPWELFIASVKRLYIAKNPAPRNKEHAEIAKRKETEDAIDN
FTLKRLGNNYSMPFE-----LEGFVNNEEDGAI DNDFDLLYDDMNGVRYLLGEVPWEVFTITVKRIYIPVAEQQNESEYEEEEEDNAAAAATAD
FTLKRLGNNYSMPFE-----LEGLVNKEEDGAI DSDFDLLYDDMDGVRYFLGDVPWMMFTVTKRIYIPVAEQQNESEYEEEEEDNAAAAATAD
EAL EAMFLCFSGGAA-----DAA-----VNPDSFVATYEDKDGDLMLVGDVPFEMFI STCKRLRMKGSSEARGLGATRGX-
KALEKMFSSFTIGNCG-----SHGVNGMNEKSIDALL-NGSEYVPTYEDKDGDDWMLVGDVPWEMFVESCCKRLRMKGSSEAI GLAPRAVEKCKNRSX-
MAFQNMFTSFTIGKCG-----SHQQLKESNKL-RDDL EYVPTYEDKDGDDWMLVGDVPWEMFVESCCKRLRMKGSSEAI GLAPRAVEKCKSX-
EAL EAMFVCFSGAADG-----ANPSEFAITYQDKDGDLMLVGDVPFDMFTSTCKRLRMKKSSEATGLGSPRQMKIX-
LALQKMFGTFTATGNN-----MNEV-----NGSDAVTITYEDKDGDDWMLVGDVPWMMFVESCCKRLRMKGSSEAI GLAPRAKDKYKNKXS-
DALDALFGCF SADASA-----SAAHFAYAYEDKDGDLMLAGDVPWDMFISSCKKLRMKGSSEARX-
EALNDMFYCYSTIGLMD-----GYGEHAHVYEDGDGDDWMLVGDVPWEMFISSCKMRVMRACEARGLSSNAX-
KALENMFKLTIGEYSE-----REGY-----KGSEYAPTYEDKDGDDWMLIGDVPWDMFLSSCKKLRLIKGSEATG-
QALENMFRLTITTLNMRALSTPEHKIMIDAKRHSQLL-----GGSSEFVLTYEDKDGDDWMLVGDVPWGMFISSVKRLRMKKSSEATGLGK-
KALRQMFVDGAGSDSG-----QNTSSASDSVSDLDLDS-NAIPGHLIAYEDIENDLLAGDLTWKDFVRVAKRIILIPAKGNSRKATGAV-
KALRQMFVDGAGSDSG-----STASSASESVSDHDLDTL-NAVPGHLIAYEDIESDLLAGDLNKKDFVRVAKRIILIPAKGNSRK-
VALIDELFRGLLAARRE-TADPRNDKKYKKEANANAGSV-----SGSEYTLVYEDNEGDRILVGDVPWMMFVSTAKRLRVLKTSEISTPQRAFTFKL-
KALENMFKLTIGEYSE-----NEGY-----NGSEFAPTYEDKDGDDWMLVGDVPWDMFISSCKKLRLMKGSSEARGLGC-
QTL LDMF-----GICQ-----ENSSNYRLTYQDRGDDWMLAEDVPWRNFLGTVQLKLKLMRSSN-
QALEEMFFRSATTINS-----IGGEKRVQTKPSKLL-DGLSEFLLTYEDKEGDDWMLVGDVPWGMFLNSVKRLRMRTSEANGLAPRFQDRNEKQRIKPV-
KALEEMFKSKVGEYSE-----REGY-----NGSEHYPTYEDKDGDDWMLVGDVPWDMFINSCCKRLIMKSESEARGLGCAV-
QTLQDMNTSILWPEM-----DIE-----HSGQCHVLTYEDKEGDDWMLIGDVPWEMFLPSVRLRLK ITRADSL-
DALAKMFSSTMGNYG-----AQGMDFMNESKLMDDL-NSSEYVPSYEDKDGDDWMLVGDVPWEMFVNSCKRLRMKGSSEAI GLAPRAVEKCKSRT-
QLEDMFGRQASGLR-----LF-----QAGSEFCLFYKDRERNRTVGDVPWEMFVSSVKRLRIARKSEPLLPYSPAFS-
KALEDMFKLTIGEYSE-----KEGY-----NGSDFAPTYEDKDGDDWMLVGDVPWDMFI STCKRLRMKGSSEARGLGC-
EVVEEMFKFKVGEYSE-----REGY-----NGSEYVPTYEDKDGDDWMLVGDVPWEMFINSCCKRLIMKSESEARGLGCAV-
SAL EKMFSCTFIGQC-----SHVVPQGDGLSESRLLMDLL-HGSEYVLTIEDKDDWMLVGDVPWKMFTDSCRRLRMKGSSEAI GLAPRAVEKCKSRN-
DALAKMFSSTMGNYG-----AQGMDFMNESKLMDDL-NSSEYVPSYEDKDGDDWMLVGDVPWEMFVDSCKRLRMKGSSEAI GLAPRAVEKCKSRT-
KALSI SMFAKCKNLEKD-----AASRLTYQDKDGDDWMLAGDVPWQTFMESVQRLKIVRNAG-
SALEKMFSCFTIGQC-----SHGLRGQDGLTESRLKDILL-HGSEYVLTIEDKDGDDWMLVGDVPWDMFTDSCRRLRMKGSSEAI GLAPRAVEKCKNRN-
DAL GKMFSSFTIGNCG-----SHGLKDFL NESKLI DILL-NGTDVYPTYEDKDGDDWMLVGDVPWDMFVNSCKRLRMKGT EATGLAPRAVEKCKNRSYK-
SALEKMFSCFTIGQYG-----SHGAPGREMLSESKLDLL-HGSEYVLTIEDKDGDDWMLVGDVPWEMFIETCKRLRMKSSDAIGLAPRAVEKCKNRN-
VALERLFGCYGIGKAL-----KDEYVPITYEDKDGDDWMLVGDVPWEMFVESCCKRLRMKSSSEAKGFLQPRGALKGISKDERH-
VADIELFRGLLAAQRE-TCDPMGENKMDEAKENCVS-----SGSEYTLVYEDNEGDRILVGDVPWMMFVSTAKRLRVLKTSEKVSVGINKEQKTPSCAVALG-
QALEEMFFRSSTTINS-----IGGQKPLSKFSKLL-DGSSEFVLTYEDKEGDDWMLVGDVPWGMFLTSVKRLRMRTSEANGLAPRLQDRNEKQRSKPV-
DAL GKMFSSFTIGNCG-----SHGMKDFL NESKLI DILL-NGTDVYPTYEDKDGDDWMLVGDVPWDMFVESCCKRLRMKGT EATGLGNEYTA-
DAL GKMFSSFTIGNCG-----SGTKDFMNESKLI DILL-NSSEYVPTYEDKDGDDWMLVGDVPWGMFVDSCKRLRMKGSSEAI GLAPRAVEKCKNRS-
IAYDELFRGLLAAQRD-SSSNGIMDKQEEAKAITGVL-----DGSGEYTLVYEDNEGDMMLVGDVPWMMFVSTVKRLRVLKSSEVSAL SRE-
SAL EKMFGCFTIGQC-----SHGLAARDGLTESCLKDLH-GSEYVLTIEDKDGDDWMLVGDVPWDMFTDSCRRLRMKGSSEAI GLAPRAVEKCKNRN-
TAVDELFRGLLAAQRD-SSCNGIMNKQEGEKA I MGVL-----DGSGEYTLVYEDNEGDRMLVGDVPWMMFVSTVKRLRVLKSSEVSALLGSSKHEKVPV-
DAL GKMFSSFTIGNCG-----SQGMKDFMNESKLI DILL-NGSDYVPTYEDKDGDDWMLVGDVPWEMFVDSCKRLRMKGSSEAI GLAPRAVEKCKNR I-
KALENMFKLTIGEYSE-----REGY-----KGSEYAPTYEDKDGDDWMLVGDVPWDMFLSSCKKLRLMKGSSEAI GLGCGA-
VALEKFLGCFGIGKAL-----KDTDCEYVPIYEDKDGDDWMLVGDVPWEMFISSCKKLRMKRSSEAKGFLQPRGALQQGNISKDD-
NALQDMFSCFSFTIRN-----YLNERTIMEQEV-----NNGVEYVPTYEDKDGDDWMLVGDVPWKMVFESCCKRLRMKKSSEATGFAPRTPSKCSSS-
HTLLDMF-----GICQ-----ENSSNYRLTYQDRGDDWMLAEDVPWRNFLGTVQLKLKLMRSSN-
QTLQDMNTSILWPEM-----DVE-----HSGKCHVLTYEDKEGDDWMLIGDVPWEMFLPSVRLRLK ITRADSL-
VALEKFLGCFGIGKAL-----KDTDCEYVPIYEDKDGDDWMLVGDVPWEMFIESCCKRLIMKRSSEAKGFLQPRGALQQGNISKDD-
KALENMFKFTVGEYSE-----REGY-----KGSFVPTYEDKDGDDWMLVGDVPWDMFSSSCCKRLRMKGSSEAPTAL-
KALENMFKVMIGEYSE-----REGY-----KGSFVPTYEDKDGDDWMLVGDVPWDMFSSSCCKRLRMKGSSEAPTAL-
KALEVMFKFSVGEYFE-----RDGY-----KGSDFVPTYEDKDGDDWMLIGDVPWEMFICTCKRLRMKGSSEAKGLGCGV-
KSL ENMFKFSVGEYFE-----REGY-----KGSDFVPTYEDKDGDDWMLVGDVPWEMFVSCCKRLRMKGSSEAKGLGCGGL-
SALQILFGCYINFDOT-----LKESCEVPIYEDKDGDDWMLAGDVPWEMFLGSCCKRLRMKRSNCRNG-
TVLENLFGCLGIGVAK-----EGKKKECII IYEDKDRDMLVGDVPWQMFKESCCKRLIVKRS DATGFGLQDQ-
DALAKMFSSTMGNYG-----AQGMDFMNESKLMNLL-NSSEYVPSYEDKDGDDWMLVGDVPWEMFVESCCKRLRMKGSSEAVGLAPRAVEKCKNRS-
SAL EKMFSCTFLGQC-LHGAQGRERMS EIKLKDILL-HGSEFVLTIEDKDGDDWMLVGDVPWEMFIETCQKLRLMKGSSEAI GLAPGAVEKSKNERV-
SALEKMTFTFTLQQC-----SNGAAGKMDLSETKLDLL-NGKDYVLTIEDKDGDDWMLVGDVPWEMFIDVCKKLKIMKGCDAGLAAAPRAVEKCKMRA-
KTLDL MFFQIPSPVTR-----SNTQGYKTIKETCTSKLL-DGSSEYIITYQDKDGDDWMLVGDVPWQMF LGSVRLRLIMKTSI I GAGVGK-
NTLEEMFLKPKLGSRT-----LETDGHMETPVKILP-DGSSGLVLTYEDKEGDDWMLVGDVPWGMFISVYTRRLRMKTSEATGKAQMI L-
QTL EEMFGMTGLYCF-----QMRTL-----DGSSEFVLTYEDKEGDDWMLVGDVPWRMFI NSVKRLRVLMKTSEANGLAARNQEPNERQRPQV-
DALAKMFSSTMGSYG-----AQGMDFMNESKVMDDL-NSSEYVPSYEDKDGDDWMLVGDVPWMMFVESCCKRLRMKGSSEAI GLAPRAVEKCKNRS-
TAL ENMFQGIITICRV-----TELE-----RKGEFVATYEDKDGDLMLVGDVPWMMFVESCCKRMRLMKTGDAGL-
NALSKMFSSTIGNYG-----POGMKDFMNESKLI DILL-NGSDYVPTYEDKDGDDWMLVGDVPWEMFVDSCKRLRMKGSSEAI GLAPRALEKCKNRS-
NALSNMFSSTMGKHG-----GEEGMDFMNERKLMDLV-NSWDYVPSYEDKDGDDWMLVGDVPWMMFVDTCKRLRMKGSSEAI GLAPRAVEKCKSRA-
FTVDKFLFRGLLAAQRD-----FPSSI EDEKPI TGLL-DGNGEYTLTYEDNEGDKMLVGDVPWQMFVSSVKRLRVKTSEISSALT YGNGQKEMRR-
FALDKLFGFRGIGVAL-----KGDGNCSEYVITYEDKDGDDWMLAGDVPWGMFL ESCCKRLRMKRS DATGFGLQPRGVDE-
RTLDFMNASILWAE-----EDMC-----NEKSHVLT YADKEGDDWMMVGDVPWEMFLSTVRLRLKISRANHY-
FVVDKFLFRGLLAAQRD-----ISDQGGEKPI IGLL-DGKGEFTLT YEDNEGDKMLVGDVPWQMFVSSVKRLRVIKSSEISSALTFGCSKQEKMMH-
SAL EKMFSCTFIGQF-----SHGGCGRDGLNESRLTDL- RGSEYVPTYEDKDDWMLVGDVPWEMFISSCKKLRLMKSSSEAI GLAPRVMEKCRSRN-
HAVDKLFSSKDSWDLN-----ROYTLVYEDTEGDKVLVGDVPWEMFVSTVKRLHVLTSHAFSLSPRKHGE-
NSLITMFT EYEDCDRE-DTNYTFTFGKEGDDWLRGDVTKWIFAESVHRIS IIRDRPCA YTRCLF-
TTL DYMNASILWAE-----EDM-----CSEKSHVLT YADKEGDDWMMVGDVPWEMFLSSVRLRLKISRATHY-
ENL SHMFDTSICGNR-----DRKHVLT YEDKDGDDWMMVGDIPWDMFLETVRLRLK ITRPERY-
LQLNDMF-----DRVG-----IEVPDD-
SALRQMFVDGADSTDD-----LDLS-----NAIPGHLIAYEDMENDLLAGDLTWKDFVRVAKRIILIPVKGNTRQVKRNE-
HQL EDMFGMQSVSGLR-----LF-----QMESEFCLVYRDEGLVRNAGDVPWMEFI ESVERLIRTRNDAYLPF-

Consensus



	430	440	450	460
LOC_Os01g08320.1 11667.m00781/1-208	-	-	-	-
LOC_Os01g09450.1 11667.m00901_altSplice/1-237	-	-	-	-
LOC_Os01g13030.1 11667.m01279/1-267	-	-	-	-
LOC_Os01g18360.1 11667.m01799/1-204	-	-	-	-
LOC_Os01g48450.1 11667.m04699/1-272	-	-	-	-
LOC_Os01g53880.1 11667.m05292/1-262	-	-	-	-
LOC_Os02g13520.1 11668.m01248_altSplice/1-308	AL F X	-	-	-
LOC_Os02g49160.1 11668.m04779/1-206	-	-	-	-
LOC_Os02g56120.1 11668.m05537/1-183	-	-	-	-
LOC_Os02g57250.1 11668.m05658/1-282	SX	-	-	-
LOC_Os05g08570.1 11682.m00824_altSplice/1-213	-	-	-	-
LOC_Os05g09480.1 11682.m00921/1-229	-	-	-	-
LOC_Os05g14180.1 11682.m01308/1-258	-	-	-	-
LOC_Os05g44810.1 11682.m04283/1-328	-	-	-	-
LOC_Os05g48590.1 11682.m04652/1-282	-	-	-	-
LOC_Os06g07040.1 11680.m00651/1-184	-	-	-	-
LOC_Os06g22870.1 11680.m02247/1-267	-	-	-	-
LOC_Os06g24850.1 11680.m02452/1-150	-	-	-	-
LOC_Os06g39590.1 11680.m03858/1-194	-	-	-	-
LOC_Os07g08460.1 11673.m00782_altSplice/1-220	-	-	-	-
LOC_Os08g01780.1 11674.m00085/1-247	-	-	-	-
LOC_Os11g11410.1 11687.m01091/1-144	X	-	-	-
LOC_Os11g11420.1 11687.m01092/1-163	EDVDGNHWMRNHLWSVGPILQX	-	-	-
LOC_Os11g11430.1 11687.m01093/1-172	EDGDGAAADDGVAAAADDVDDVAGYTSNDDPSFDX	-	-	-
LOC_Os12g40900.1 11686.m04059/1-198	-	-	-	-
LOC_Os12g40890.1 11686.m04058/1-278	-	-	-	-
LOC_Os03g43400.1 11669.m04312/1-234	-	-	-	-
LOC_Os03g43410.1 11669.m04313/1-227	-	-	-	-
LOC_Os03g53150.1 11669.m05378_altSplice/1-237	-	-	-	-
LOC_Os03g58350.1 11669.m05916/1-198	-	-	-	-
LOC_Os09g35870.1 11681.m03177/1-141	-	-	-	-
PoptrIAA3.6/1-192	-	-	-	-
PoptrIAA11/1-290	-	-	-	-
PoptrIAA33.1/1-149	-	-	-	-
PoptrIAA33.2/1-117	-	-	-	-
PoptrIAA28.1/1-239	-	-	-	-
PoptrIAA3.4/1-199	-	-	-	-
PoptrIAA29.2/1-233	-	-	-	-
PoptrIAA12.2/1-258	-	-	-	-
PoptrIAA3.2/1-203	-	-	-	-
PoptrIAA20.2/1-175	-	-	-	-
PoptrIAA7.2/1-248	-	-	-	-
PoptrIAA34/1-194	-	-	-	-
PoptrIAA3.3/1-199	-	-	-	-
PoptrIAA3.1/1-201	-	-	-	-
PoptrIAA27.1/1-307	-	-	-	-
PoptrIAA7.1/1-267	-	-	-	-
PoptrIAA29.1/1-229	-	-	-	-
PoptrIAA27.2/1-349	-	-	-	-
PoptrIAA16.4/1-237	-	-	-	-
PoptrIAA9/1-366	-	-	-	-
PoptrIAA19.3/1-184	-	-	-	-
PoptrIAA28.2/1-332	R	-	-	-
PoptrIAA12.1/1-276	-	-	-	-
PoptrIAA16.3/1-229	-	-	-	-
PoptrIAA16.1/1-250	-	-	-	-
PoptrIAA26.2/1-249	-	-	-	-
PoptrIAA27.3/1-335	-	-	-	-
PoptrIAA26.1/1-338	-	-	-	-
PoptrIAA16.2/1-246	-	-	-	-
PoptrIAA3.5/1-207	-	-	-	-
PoptrIAA19.2/1-189	RD	-	-	-
PoptrIAA15/1-220	-	-	-	-
PoptrIAA29.3/1-233	-	-	-	-
PoptrIAA20.1/1-174	-	-	-	-
PoptrIAA19.1/1-189	RD	-	-	-
IAA1/1-168	-	-	-	-
IAA2/1-174	-	-	-	-
IAA3/1-189	-	-	-	-
IAA4/1-186	-	-	-	-
IAA5/1-163	-	-	-	-
IAA6/1-189	-	-	-	-
IAA7/1-243	-	-	-	-
IAA8/1-321	-	-	-	-
IAA9/1-338	-	-	-	-
IAA10/1-261	-	-	-	-
IAA11/1-246	-	-	-	-
IAA12/1-173	-	-	-	-
IAA13/1-246	-	-	-	-
IAA14/1-228	-	-	-	-
IAA15/1-179	-	-	-	-
IAA16/1-236	-	-	-	-
IAA17/1-229	-	-	-	-
IAA18/1-267	-	-	-	-
IAA19/1-197	-	-	-	-
IAA20/1-175	-	-	-	-
IAA26/1-269	-	-	-	-
IAA27/1-305	-	-	-	-
IAA28/1-175	-	-	-	-
IAA29/1-251	-	-	-	-
IAA30/1-172	-	-	-	-
IAA31/1-158	-	-	-	-
IAA32/1-143	-	-	-	-
IAA33/1-171	-	-	-	-
IAA34/1-185	-	-	-	-

Consensus

RD · DG · · · · ·