

426311 1 MEEKI-----NSGDGPEK--RRAAFKHKTKGGQWAKRVLVGSSAMTGLGATILIGGAAKHPVRAFALPVTINFAAGSFLSGMTVTRAMLRTEHGSYNTTIGGG
Phpat.022G050400 1 MIVDGGPGRRRWRREFDGR--LMEFGGRPLDYRGSQWGYRILSKSLAAGGFGAGGAGLVGAVRGPALRLGLVGCNELLVAAGCYGAGNIGSRELRKAEPENLLDAVGG
Bra032686 1 MBS-----E-WFLKLSBAID---LPTSTIROPPLSERDLIPTLLAGVAGCAGTGLLSKRRKSLGLANVAASVYANFAIVTCYCGAREFVTAIRKTCGPDLLWSSAIGG
Bra015100 1 MAS---G--GKFAKRIIDH--VSPFTFVOP-TTTRKRLIPTLLAGVAGCAGTGLLSKRRKSLGLANVAASVYANFAIVTCYCGAREFVTAIRKTCGPDLLWSSAIGG
AT3G25120 1 MAL---G--DRKSEPKTQNA--LPPFPFIVQENGTPTKRVLLPSLLAGVIGGGAGLVSKHRAH--PNTPTYYANFAIVAGCYCGAREFVTAIRKTCGPDLLWSSAIGG
Carubv10014714 1 MAS-----G-DRKSEPKTQNA--LPPFPFIVQENGTPTKRVLLPSLLAGVIGGGAGLVSKHRAH--PNTPTYYANFAIVAGCYCGAREFVTAIRKTCGPDLLWSSAIGG
GRMZM2G076351 1 -----MNSVGG
LOC_Os04g30740 1 MA-----TPASEPAG--AGTPEPAAPFSAADWKEKILLDPAAVAGVGGAGFGLLSRRHARLGAARANATYANFAIVAGCYCGARELARDARASTPDDPMNSVGG
Medtr8g012725.1 1 MGS-----SENRENDEEV--VNTTFHSSSSSSSRHDWKNRIPIPTLLAGVAGCAGTGLLSKRRKSLGLANVAASVYANFAIVTCYCGAREFVTAIRKTCGPDLLWSSAIGG
Glyma17g16170 1 MG-----SENREAFQES--LNN---SPFSSSSSRHWKSRILPIPTLLAGVAGCAGTGLLSKRRKSLGLANVAASVYANFAIVTCYCGAREFVTAIRKTCGPDLLWSSAIGG
Cucsa.077990 1 MD-----G-DKAFHSDTFPFS--SSSDYGGKRRALVPTLLAGVGGGAGLSSKRRKRVHGLANISATYANFAIVTCYCGAREFVTAIRKTCGPDLLWSSAIGG
PGSC0003DMG400022033|PGSC0003DMT40005665 1 MD-----G-DKAFHSDTFPFS--SSSDYGGKRRALVPTLLAGVGGGAGLSSKRRKRVHGLANISATYANFAIVTCYCGAREFVTAIRKTCGPDLLWSSAIGG
Eucgr.K02137 1 MAS-----NRMPKFSQAEFFPFP--SSSSSSSSSDWKKRVEFEPALLAGVGGGAGLVSKRRKRVHGLANISATYANFAIVTCYCGAREFVTAIRKTCGPDLLWSSAIGG
GSVIVG01003251001 1 ---MASNEKMLE-SSSSSSSSSDWKKRVEFEPALLAGVGGGAGLVSKRRKRVHGLANISATYANFAIVTCYCGAREFVTAIRKTCGPDLLWSSAIGG
30217.t000006|30217.m000255 1 ---MASKPLQGEATHP-PPFPSSSSSSSDWKKRVEFEPALLAGVGGGAGLVSKRRKRVHGLANISATYANFAIVTCYCGAREFVTAIRKTCGPDLLWSSAIGG
Potri.002G246000 1 MG-----SSGMKPLQENAKAP-PPFP--SSSSSSSDWKKRVEFEPALLAGVGGGAGLVSKRRKRVHGLANISATYANFAIVTCYCGAREFVTAIRKTCGPDLLWSSAIGG

426311 101 MISGIMLARLQCTAASPFSMGLLEAVGTCGCFMANQWDEYRLKKFVDTLPDDAFPEFRTRKIMVLEAMNERSN---HSLWLFPRKLSLEEFQHMALARRMKQENG--
Phpat.022G050400 109 FSGALLGHFHGGRARTEPLMGILFAVVGTLGQLGAAYEYRIRRHFNITLPSPLADANVEVVPVKSEETEESSMKLPDWPICMLSAEQAKKRAEQERKQKTVEN
Bra032686 98 LFSGALLGRLOGCPGAGRYSLAFAPFGTAFDYAGRRSKP-----P-----SRV-----RNMSTILPVMWPIQVLDDEALAKKAKBOKLTPR---
Bra015100 100 LFSGALLGRLOGCPGAGRYSLAFAPFGTAFDYAGRRSKP-----P-----SRV-----RNMSTILPVMWPIQVLDDEALAKKAKBOKLTPR---
AT3G25120 101 LFSGALLGRLOGCPGAGRYSLAFAPFGTAFDYAGRRSKP-----P-----SRV-----RNMSTILPVMWPIQVLDDEALAKKAKBOKLTPR---
Carubv10014714 101 LFSGALLGRLOGCPGAGRYSLAFAPFGTAFDYAGRRSKP-----P-----SRV-----RNMSTILPVMWPIQVLDDEALAKKAKBOKLTPR---
GRMZM2G076351 8 LASGAVLGRLOGGCHFGAVKVAVFFAAGTALDYALKLSP-----Q-----NGKWHALKS--HFSGDKDWFILPEWSPQVLDDEALAKKAKBOKLTPR---
LOC_Os04g30740 98 LASGAVLGRLOGGCHFGAVKVAVFFAAGTALDYALKLSP-----Q-----NGKWHALKS--HFSGDKDWFILPEWSPQVLDDEALAKKAKBOKLTPR---
Medtr8g012725.1 104 FSGALLGRLOGGCHFGAVKVAVFFAAGTALDYALKLSP-----Q-----NGKWHALKS--HFSGDKDWFILPEWSPQVLDDEALAKKAKBOKLTPR---
Glyma17g16170 100 FSGALLGRLOGGCHFGAVKVAVFFAAGTALDYALKLSP-----Q-----NGKWHALKS--HFSGDKDWFILPEWSPQVLDDEALAKKAKBOKLTPR---
Cucsa.077990 101 FSGALLGRLOGGCHFGAVKVAVFFAAGTALDYALKLSP-----Q-----NGKWHALKS--HFSGDKDWFILPEWSPQVLDDEALAKKAKBOKLTPR---
PGSC0003DMG400022033|PGSC0003DMT40005665 97 FSGALLGRLOGGCHFGAVKVAVFFAAGTALDYALKLSP-----Q-----NGKWHALKS--HFSGDKDWFILPEWSPQVLDDEALAKKAKBOKLTPR---
Eucgr.K02137 106 FSGALLGRLOGGCHFGAVKVAVFFAAGTALDYALKLSP-----Q-----NGKWHALKS--HFSGDKDWFILPEWSPQVLDDEALAKKAKBOKLTPR---
GSVIVG01003251001 97 FSGALLGRLOGGCHFGAVKVAVFFAAGTALDYALKLSP-----Q-----NGKWHALKS--HFSGDKDWFILPEWSPQVLDDEALAKKAKBOKLTPR---
30217.t000006|30217.m000255 101 FSGALLGRLOGGCHFGAVKVAVFFAAGTALDYALKLSP-----Q-----NGKWHALKS--HFSGDKDWFILPEWSPQVLDDEALAKKAKBOKLTPR---
Potri.002G246000 102 FSGALLGRLOGGCHFGAVKVAVFFAAGTALDYALKLSP-----Q-----NGKWHALKS--HFSGDKDWFILPEWSPQVLDDEALAKKAKBOKLTPR---

426311 206 ---SVDE-----
Phpat.022G050400 219 LQHGFVPLKQOKS*
Bra032686 178 ---LNKES*
Bra015100 181 -SFRNKED*
AT3G25120 182 -VLGKLNKE*
Carubv10014714 182 -VLGKLNKE*
GRMZM2G076351 94 -ALGKLNKE*
LOC_Os04g30740 188 -ALSKLKKEP*
Medtr8g012725.1 198 -RIRSRDKEDS*
Glyma17g16170 194 -RIRSRDKEDS*
Cucsa.077990 188 -ALGKLNKE*
PGSC0003DMG400022033|PGSC0003DMT40005665 185 ---LNKES*
Eucgr.K02137 184 -TLGKLNKE*
GSVIVG01003251001 184 -SLGKLNKE*
30217.t000006|30217.m000255 193 -RALKLNKE*
Potri.002G246000 191 -RALKLNKE*