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                                         10        20        30        40        50        60        70        80        90       100
                                ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
AT3G06450.1-AtBOR3              ----------------------------------------MDEAESFVPFQGIKKDVKGRLNCYKQDWISGLRAGFRILAPTTYIFFASAIPVITFG 57
AT3G62270.1-AtBOR2              ----------------------------------------MEETFVPFEGIKNDLKGRLMCYKQDWTGGIKAGFRILAPTTYIFFASAIPVISFG 55
AT4G32510.1-AtBOR7              ----------------------------------------MEGVKFPFGGIINDFNGRRKCYKQDWLAAFNSGVRILAPTLYIFIASALPVIAFG 55
AT2G47160.1-AtBOR1              ----------------------------------------MEETFVPFEGIKNDLKGRLMCYKQDWTGGFKAGFRILAPTTYIFFASAIPVISFG 55
AT5G25430.1-AtBOR6              ------------------------------------------MKSEGESGPFQGILRDIEGRRKCYKQDWIRGIKTGIRILAPTCYIFFASSLPVVAFG 57
AT1G15460.1-AtBOR4              ------------------------------------MEEERVDSSKRLFRGIVADLRGRALCYKEDWVAGLRSGFGILAPTTYIFFASALPVIAFG 60
AT1G74810.1-AtBOR5              ------------------------------------MEEERVEGSKRPFQGIIRDVKGRALCYKQDWIAGLRSGFGILAPTTYYFFASALPVIAFG 60
Bradi4g04420.1.p-AtBOR2         ----------------------------------------MEESFVPLRGIKNDLRGRLTCYKQDWTGGFRAGIRILAPTTYIFFASAIPVISFG 55
Bradi2g34110.1.p-AtBOR4         ----------------------------------------MEHKKTLFKGVIEDFRGRAACYKQDWHNGFSSGFRILAPTLYIFFASALPVIAFG 55
Bradi2g04690.1.p-AtBOR4         ----------------------------------------MDLLRNPFKGVVADVKGRASWYKDDWVAGLRAGFRILAPTMYIFFASALPVIAFG 55
Brara.D00064.1.p-AtBOR2         ----------------------------------------MEETFVPFEGIKNDLKGRLRCYKKDWTGGFKAGFRILAPTTYIFFASAIPVISFG 55
Brara.A00544.1.p-AtBOR7         ----------------------------------------MEGANTPFAGIINDFNGRRKCYKQDWLAAFNSGVRILAPTLYIFIASALPVIAFG 55
Brara.C03154.1.p-AtBOR3         ------------------------------------------MAEAESFVPFQGIKNDIKGRLRCYKHDWISGFRAGFRILAPTTYIFFASAIPVITFG 57
Brara.F01062.1.p-AtBOR4         ------------------------------------MEKEIS--SKRPFRGIADLKGRALCYKQDWITGLRSDFGILAPTTYIFFASALPVIAFG 58
Brara.F02740.1.p-AtBOR6         ------------------------------------------MESEG--GPFKGILRDIEGRRKCYKQDWILGFKTGLRILAPTCYIFFASSLPVVAFG 55
Brara.B02140.1.p-AtBOR4         ------------------------------------MEEERVGSSKRPFRGIADLKGRALCYKHDWVAGLRSGFGILAPTTYYFFASALPVIAFG 60
Cre10.g443900.t1.1-AtBOR1       ------------------------------------MEATPRPPQRWPGSDIVFEARRRLEVYSADWRDGFRVRARILAPSTYIFLASLLPALAFG 60
Cucsa.192570.1-AtBOR2           ----------------------------------------MEETFVPLRGIKNDLKGRLVCYKQDWTGGLRAGYRILAPTTYIFFASAIPVISFG 55
Cucsa.300580.1-AtBOR4           ----------------------------------------MEILRTPFRGILNDIRRRAACYKQDWIDGRISGIGILAPTAYIFFASALPVIAFG 55
Cucsa.098470.1-AtBOR2           ----------------------------------------MEETFFPFRGIKNDIRGRLLCYRQDWTGGFRTGIRILAPTTYIFFASAIPVISFG 55
Eucgr.C02816.1-AtBOR4           ----------------------------------------MENLKTPFKGIVKDVRGRAACYKQDWACGFCSGYRILAPTAYIFFASALPVIAFG 55
Eucgr.J03035.1-AtBOR4           ----------------------------------------MENIKSPFKGIREDLRGRTLCYKQDWVNGLRSGISILAPTAYIFFASALPVIAFG 55
Eucgr.H04094.1-AtBOR2           ----------------------------------------MEETFVPFRGIKNDLQGRLLCYKQDWTGGLRAGFRILAPTTYIFFASAIPVISFG 55
Eucgr.C04162.1-AtBOR4           ----------------------------------------MESIR-TPFRGIIQDLKGRKACYKQDWANGVCCGARILAPTTYYFFASALPVIAFG 55
Eucgr.H00896.1-AtBOR1           ----------------------------------------MEETFVPLEGIKNDLRGRLMCYRQDWSGGFRAGIRILAPTTYIFFASAIPVISFG 55
Eucgr.B00302.1-AtBOR2           ----------------------------------------MEETFVPFRGIKNDLRARLLCYKQDWTGGIKAGIRILAPTTYIFFASAIPVISFG 55
Glyma.06G181900.1.p-AtBOR2      ----------------------------------------MEETFVPLRGIKNDLKARIPCYRQDWTSGFQAGIRILAPTTYIFFASAIPVISFG 55
Glyma.15G011200.1.p-AtBOR4      ----------------------------------------MESLKTPLKGVINDLRGRAVYKDDWTSGLYSGTGILAPTTYIFFASALPVIAFG 55
Glyma.04G184000.1.p-AtBOR2      ----------------------------------------MEETFVPLRGIKNDLKARIPCYRQDWTSGFQAGIRILAPTTYIFFASAIPVISFG 55
Glyma.17G207700.1.p-AtBOR6      ------------------------------------MGPPRLASMGPFGGIIQDVKGRVECYKHDWASAICSGIRILAPTFYIFFASALPVIAFG 59
Glyma.04G069500.1.p-AtBOR7      ------------------------------------------MGAPFKGIIQDFKGRAQCYKQDWICALCSGVSILAPTFYIFFASALPVIAFG 52
Glyma.09G031400.1.p-AtBOR2      ----------------------------------------MEETFVPFRGIKNDLQGRLMCYKQDWIGGLTAGFRILAPTTYIFFASAIPVISFG 55
Glyma.19G219500.1.p-AtBOR2      ----------------------------------------MEETFVPFEGIKNDLRGRLMCYKQDWSGGIKAGLRIWAPTTYIFFASAIPVISFG 55
Glyma.03G222300.1.p-AtBOR2      ----------------------------------------MEETFVPFEGIKNDLRGRLMCYKQDWTGGIKAGLRIWAPTTYIFFASAIPVISFG 55
Gorai.005G135900.1-AtBOR2       ----------------------------------------MEETFVPFRGIKNDLKGRLLCYKQDWTGGLSAGIRILAPTTYIFFASAIPVISFG 55
Gorai.011G205300.1-AtBOR4       ----------------------------------------MGNMKSPFKGITKDIKGRSVCYKQDWVNGLCSGFRIFAPTFYIFFASALPVIAFG 55
Gorai.005G070200.1-AtBOR1       ----------------------------------------MEESFVPFRGIKNDLEGRLKCYKQDWTSGLRAGFRILAPTTYIFFASAIPVISFG 55
Gorai.006G266200.1-AtBOR2       ----------------------------------------MEESFVPFGGIKNDIKGRLKCYKQDWTSGLSAGFRILAPTTYIFFASAIPVISFG 55
Gorai.008G137000.1-AtBOR1       ----------------------------------------MEETFVPLRGIKNDLRGRLLCYKQDWTSGFKAGFRILAPTTYIFFASAIPVISFG 55
Gorai.004G146300.1-AtBOR2       ----------------------------------------MEETFVPLRGIKNDLRGRLMCYKQDWTGGFKAGFRILAPTTYIFFASAIPVISFG 55
Gorai.009G010600.1-AtBOR4       ----------------------------------------MENIS-PFKGIIKDVKGRSACYKQDWVSGFRSGYRILAPTTYIFFASALPVIAFG 54
Medtr2g032690.1-AtBOR1          ----------------------------------------MKDTFIPFRGIKNDVKKRLMCYKHDWIVGLTAGFRILAPTTYIFFASAIPVISFG 55
Medtr7g110000.1-AtBOR2          ----------------------------------------MEETFVPFEGIKNDLRGRLMCYKQDWTGGIKAGVRILAPTTYIFFASAIPVISFG 55
Medtr3g077670.1-AtBOR2          ----------------------------------------MEETFVPFRGIKNDFKARIVCYRQDWTSGFCAGARILAPTTYIFFASAIPVISFG 55
Medtr3g107730.1-AtBOR7          ------------------------------------------MGAPFEGIIQDVKGRVKCYKQDWVCAICSGVSILAPTFYIFSASALPVIAFG 52
Medtr0459s0020.1-AtBOR4         ------------------------------------MLNCYWFYMKSFKTPFKGIVDDFTGRAVHYKDDWISGLTSGTGILAPTMYIFFASALPVIAFG 63
LOC_Os01g08020.1-AtBOR4         ----------------------------------------MDLLRTPFKGVVADIEGRVAWYKHDWVAGFRSGFRILAPTMYIFFASALPVIAFG 55
LOC_Os05g08430.1-AtBOR5         ----------------------------------------MTGTVKAPFEGVVNDFKGRLSCYKQDWIDGFRTGFRILAPTLYIFFASALPVVAFG 56
LOC_Os12g37840.1-AtBOR2         ----------------------------------------MEESFVPLRGIKNDLHGRLQCYKQDWTGGFRAGIRILAPTTYIFFASAIPVISFG 55
Phpat.001G035800.1.p-AtBOR2     MQDECSERKKLGDTDAERKGEDTSRKLRHTSDVSEQRLVHAGVFEVGLSGVPFNGVREDLRGRLACYKQDWTGGFNSTYRILAATAYIFFASALPVIAFG 100
ppa002139m-AtBOR2               ----------------------------------------MEETFVPFRGIRNDLQGRFMCYKQDWTGGLKAGFRILAPTTYIFFASAIPVISFG 55
ppa002104m-AtBOR2               ----------------------------------------MEETFVPLQGIKNDLRGRLMCYKQDWTGGFRAGFRILAPTTYIFFASAIPVISFG 55
ppa002100m-AtBOR2               ----------------------------------------MEETFVPFRGIKNDLKGRLLCYKQDWTGGLRAGIRILAPTTYIFFASAIPVISFG 55
Potri.002G191000.1-AtBOR2       ----------------------------------------MEETFVPFRGIKNDLRGRLMCYKQDWTGGFRAGFRILAPTTYIFFASAIPVISFG 55
Potri.006G249800.1-AtBOR4       ----------------------------------------MENMRRPFKGITNDVREPIGCYKDDWISGLCSGFRILAPTFYIFFASALPVIAFG 55
Potri.008G100300.1-AtBOR2       ----------------------------------------MEESFVPFRGIKNDLQGRLKCYKQDWTGGFKAGFRILAPTTYIFFASAIPVISFG 55
Potri.015G077600.1-AtBOR2       ----------------------------------------MEETFVPLRGIKNDLRGRLLCYKQDWKGGLRAGIRILAPTTYIFFASAIPVISFG 55
Potri.018G031700.1-AtBOR4       ----------------------------------------MESMKSPFRGIIKDVRGRTACYKDDWVSGLCSGLRILAPTFYIFFASALPVIAFG 55
Potri.012G081800.1-AtBOR2       ----------------------------------------MEETFVPLRGIKNDLRGRLSCYKQDWNGGFRAGIRILAPTTYIFFASAIPVISFG 55
Potri.001G174500.1-AtBOR4       ----------------------------------------MENMKTPFRGILNDVKGRIACYKQDWVAGILSGFGILAPTTYIFFASALPVIAFG 55
Potri.003G059700.1-AtBOR4       ----------------------------------------MEHIKTPFRGILNDVRGRAACYKQDWVAGILSGFGILAPTTYIFFASALPVIAFG 55
Potri.006G154700.1-AtBOR4       ----------------------------------------MKNLFNSPFKGIVEDFKSRKACYNQDWSNALCSGPRILAPTTYMFFASALPVIAFG 56
Phvul.001G053300.1-AtBOR6       ------------------------------------------MEPFGGIIQDFRGRVACYKHDWTSAFRSGIKILAPTFYIFFASALPVIAFG 51
Phvul.001G215700.1-AtBOR2       ----------------------------------------MEETFVPFEGIKNDLRGRLMCYKQDWTGGIKAGLRILAPTTYIFFASAIPVISFG 55
Phvul.005G174400.1-AtBOR4       ----------------------------------------MESLKAPFKGVKNDLRGRALHYKDDWTTGLYSGAGILAPTTYIFFASALPVIAFG 55
Phvul.009G178000.1-AtBOR2       ----------------------------------------MEETFVPFRGIKNDLKARITCYRQDWSSGFQAGVRILAPTTYIFFASAIPVISFG 55
Sobic.008G132300.1.p-AtBOR2     ----------------------------------------MEESFVPLRGIKDDLHGRLACYKQDWTGGFRAGIRILAPTTYIFFASAIPVISFG 55
Sobic.009G064200.1.p-AtBOR4     ------------------------------------MSGPNKAPFSGVAEDLKGRAACYKQDWNHGFRSGLRILAPTLYIFFASAVPVIAFG 56
Sobic.003G047900.1.p-AtBOR4     ----------------------------------------MDLLRHPFKGVVTDIKGRATWYKHDWVAGVHSGFRILAPTMYIFFASALPVIAFG 55
Solyc06g071500.2.1-AtBOR2       ----------------------------------------MEETFVPLRGIKNDLKGRLLCYKQDWTGGLRAGIRILAPTTYIFFASAIPVISFG 55
Solyc01g079150.2.1-AtBOR1       ----------------------------------------MEETFVPFRGIKNDLHGRLLCYKQDWTSGIKAGFRILAPTTYIFFASAIPVISFG 55
GSVIVT01007733001-AtBOR2        ----------------------------------------MEETFVPFRGIKNDLKGRILCYKQDWTGGLRAGIGILAPTTYIFFASAIPVISFG 55
GSVIVT01015478001-AtBOR4        ----------------------------------------MDNIKAPFKGIIKDFKGRKACYKQDWTSALRSGTSILAPTTYIFFASALPVIAFG 55
GSVIVT01035800001-AtBOR4        ----------------------------------------MGNIRVPFKGIINDYKGRAPCYKQDWTGAHGSGVRILAPTFYIFFASALPVIAFG 55
GSVIVT01017647001-AtBOR2        ----------------------------------------MEETFVPFRGIKNDLQGRLLCYKQDWTGGLRAGFRILAPTTYIFFASAIPVISFG 55
GSVIVT01028186001-AtBOR2        ----------------------------------------MEETFVPFRGIKNDLRGRLMCYKQDWAGGFRAGFRILAPTTYIFFASAIPVISFG 55
GSVIVT01017223001-AtBOR4        ----------------------------------------MEQIKTPFRGIAEDIRGRALCYRQDWTDGIRSRIRILAPTTYIFFASALPVIAFG 55
GRMZM2G082203_P01-AtBOR2        ----------------------------------------MEESFVPLRGIKNDLHGRLACYKQDWAGGFRAGIRILAPTTYIFFASAIPVISFG 55
GRMZM2G166159_P01-AtBOR2        ----------------------------------------MEESFVPLRGIKDDLHGRLACYKQDWTGGFRAGIRILAPTTYIFFASAIPVISFG 55
GRMZM2G051753_P01-AtBOR4        ----------------------------------------MDLLRHPFKGVVTDIKGRATWYKHDWVAGLHSGFRILAPTMYIFFASALPVIAFG 55
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                                   110       120       130       140       150       160       170       180       190       200
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AT3G06450.1-AtBOR3                 EQLERDTDGKITAVQTLVSTALCGVIHSIIGGQPLLILGVAEPTVIYTFMFNFAKSRTDLGSNLFLAWTGWVCLWTGLLLFLLAVLGACTFINRFTRLA 157
AT3G62270.1-AtBOR2                 EQLERSTDGVLTAVQTLASTAICGIIHSIIGGQPLLILGVAEPTVIYTFMFNFAKGRPELGRNLFLAWSGWVCVWTSLILFVLAICGACSFIINRFTRVA 155
AT4G32510.1-AtBOR7                 EQLSRETDRSLGIAESLASTAICGIIHSVFGGQPLLIVGVAEPTIIYTYLNSFSKSRPELGQKLYLAWAGWVCVWTAVLLMLLAMLNACNIISRFTRIA 155
AT2G47160.1-AtBOR1                 EQLERSTDGVLTAVQTLASTAICGVIHSIIGGQPLLILGVAEPTVIYTFMFNFAKARPELGRDLFLAWSGWVCVWTALMLFVLAICGACSIINRFTRVA 155
AT5G25430.1-AtBOR6                 EQLSKHTGGALSAVETLASTSICGIIHATIFGGQPLLIVGVAEPTIIYTYLYSFCISRPDIGRELYLAWVAWVCVWTSVLLILLSIFNAGTIITRFTRIA 157
AT1G15460.1-AtBOR4                 EQLSRDTEGALSTVETLASTAICGVIHSILGGQPLLILGVAEPTVLYVYLYNFAIGRPELGKQLYLAWAAWVCVWTALLLFVMAILNTADIINRFTRVA 160
AT1G74810.1-AtBOR5                 EQLSHDTERSLSTVETLASTAICGVIHSLLGGQPLLILGVAEPTVLYKYLYDFAKGRPELGKQLYLAWVAWVCVWTALLLFLMAIFNMAYIINRFTRIA 160
Bradi4g04420.1.p-AtBOR2            EQLERSTDGVLTAVQTLASTAICGIIHSIVGGQPLLILGVAEPTVIYTFMFSFAKDRPDLGPNLFLAWAGWVCVWTAILLFLLAVLGACSIINRFTRIA 155
Bradi2g34110.1.p-AtBOR4            EQLSKDTDGTLTTVETLASTAICGIIHSVMGGQPLLIVGVAEPTIIYTYIYNFAKNQPSLGERLFLAWAGWVCVWTAVMLFLMAMFNAAVALNRFTRFA 155
Bradi2g04690.1.p-AtBOR4            EQLSRETNGMLSTVETLASTAICGVIHSILGGQPLLIVGVAEPTIIYTYLYNFAKEEAGLGEQLYLAWAGWVCIWTAIMLFFLAMFNASNVISRFTRVA 155
Brara.D00064.1.p-AtBOR2            EQLERSTDGVLTAVQTLASTAICGIIHSIIGGQPLLILGVAEPTVIYTFMFNFAKGRPELGRNLFLAWSGWVCVWTSLILFVLAICGACSIINRFTRVA 155
Brara.A00544.1.p-AtBOR7            EQLSRETDRSLGIAESLASTAICGIIHSIFGGQPLLIVGVAEPTIIYTYLNSFSKGRPELGQKLYLAWAGWVCVWTAVLLILLATLNAANIISRFTRIA 155
Brara.C03154.1.p-AtBOR3            EQLERDTDGKITAVQTLVSTALCGVIHSIIGGQPLLILGVAEPTVIYTFMFNFAKNRQDLGSNLFLAWTGWVCLWTGLLLFLLAILGACSFIINRFTRLA 157
Brara.F01062.1.p-AtBOR4            EQLSRDTDGALSTVETLASTALCGVIHSILGGQPLLILGVAEPTVLYVYLYNFAKGRPELGKELYLAWVAWVCVWTAMLLFLMATLNAADIINRFTRVA 158
Brara.F02740.1.p-AtBOR6            EQLSKHTGGSLSAVETLASTSICGIIHATIFGGQPLLILGVAEPTIMYTYLYSFCISRPDLGRELYLAWVAWVCVWTAIFLILLSIFNACTIISRFTRIA 155
Brara.B02140.1.p-AtBOR4            EQLSRDTDGVLSPVETLTSTALCGVIHSILGGQPLLILGVAEPTVLYVYLYHFAKGRPELGKELFLAWAAWVCVWTALLLVVIAIFNVADIINRFTRIA 160
Cre10.g443900.t1.1-AtBOR1          LQLDSDTEGVLGVVQVLAATAITGVVQAVVGGQPLLIVGVAEPVVLIYGFMYDWAEGQQGLGRGRFLAWAAWVCVWTAVMVLLLAASGACRWVGAFTRFS 160
Cucsa.192570.1-AtBOR2              EQLERSTDGVLTAVQTLASTALCGIIHSIVGGQPLLILGVAEPTVIYTFMFNFAKERPELGRNLFLAWSGWVCVWTAALLFSMAILGACSIINRFTRLA 155
Cucsa.300580.1-AtBOR4              EQLSRDTDGRLSTVETLASTAICGILHSILGGQPLLVVGVAEPTIIYTYLYNFCKERKDIGGDLFLAWAGWVCVWTALLLFLLAIFNASRLINKFTRIA 155
Cucsa.098470.1-AtBOR2              EQLERNTYGTLTAVQTLASTALCGIIHSVFGGQPLLILGVAEPTVLYTFMFDFAKDRKELGQELFLAWTGWVCVWTALLLFLLAVLGACSLIINRFTRVA 155
Eucgr.C02816.1-AtBOR4              EQLSRDTNGSLSTVETLASTAICGIIHSIFGGQPLLILGVAEPTVIYTYLYNFAKGRSDLGAELYLAWAGWVCVWTAVLLFLLAIFNACTIITKFTRIA 155
Eucgr.J03035.1-AtBOR4              EQLSRETEGSLSTVETLASTAICGIIHSIFGGQPLLILGVAEPTVIYTYLYNFAKGRECLGSELYLAWAGWVCVWTALLLFLLAIFNAGNIINRFTRVA 155
Eucgr.H04094.1-AtBOR2              EQLERNTDGVLTAVQTLASTALCGIIHSVVGGQPLLILGVAEPTVIYTFLFNFAKDRPELGPKLFLAWTGWVCVWTAILLFLLAVLGACSIINRFTRLA 155
Eucgr.C04162.1-AtBOR4              EQLSRETDGSLSTVETLASTAICGIIHSILGGQPLLILGVAEPTVIYTYLYSFAKGQPDLGKELYLAWAGWVCIWTALLLFLLAIFNTCEIITKFTRIA 155
Eucgr.H00896.1-AtBOR1              EQLERSTEGVLTAVQTLASTAICGIIHSIIGGQPLLILGVAEPTVIYTFMFNFAKERSDLGRNLFLAWAAWVCVWTAALLFLMAILGACSIINRFTRVA 155
Eucgr.B00302.1-AtBOR2              EQLERNTDGTLTAVQTLSSTALCGVIHSLVGGQPLLILGVAEPTVLYTFMFDFVKDRKDLGQQLFLAWTGWVCVWTALLLFLLAVLGACSIINRFTRIA 155
Glyma.06G181900.1.p-AtBOR2         EQLERNTDGSLTAVQTLASTALCGVIHSIIGGQPLLILGVAEPTVLYTFMYNFAKDRKDLGHKLFLPWTGWVCVWTALLLFLLAVLGACSIINRFTRIA 155
Glyma.15G011200.1.p-AtBOR4         EQLSRDTDGSLSTVETLASTAICGIIHSILGGQPLLIVGVAEPTIIYTYLYNFAKNRDSLGRELFLAWAGWVCVWTALLLFLLAIFNAGNIINRFTRIA 155
Glyma.04G184000.1.p-AtBOR2         EQLERNTDGSLTAVQTLASTALCGIIHSIIGGQPLLILGVAEPTVLYTFMYNFAKDRQDLGHKLFLPWTGWVCVWTALLLFLLAVLGACSIINRFTRLA 155
Glyma.17G207700.1.p-AtBOR6         EQLNRDTGGSLSTLETLASTAICGIIHSIFGGQPLLILGVAEPTVIYTILYEFCTKTPELGAKMFLPWAGWVCVWTSFLLIILAIFNACTIITRFTRIA 159
Glyma.04G069500.1.p-AtBOR7         EQLNRDTDGTLSTVETLASTAICGVIHSILGGQPLLILGVAEPTVIYTYLYSFCQKTPELGGKLFLPWAGWVCVWTGVFLIILAIFNACTIITRFTRIA 152
Glyma.09G031400.1.p-AtBOR2         EQLERDTDGVLTAVQTLASTALCGIIHSIIGGQPLLILGVAEPTVIYTFMFNFAKSRPELGSKLFLAWTGWVCMWTAILLFLLAILGACSIINRFTRLA 155
Glyma.19G219500.1.p-AtBOR2         EQLERDTDGVLTAVQTLASTSICGIIHSILGGQPLLILGVAEPTVIYTFMFNFAKERPELGRDLFLAWTGWVCVWTALLLFLFAILGACSIINRFTRIA 155
Glyma.03G222300.1.p-AtBOR2         EQLERDTDGVLTAVQTLASTSICGIIHSILGGQPLLILGVAEPTVIYTFMFNFAKERPELGRDLFLAWTGWVCVWTALLLFLFAVLGACSIINRFTRIA 155
Gorai.005G135900.1-AtBOR2          EQLERNTDGSLTAVQTLASTALCGIIHSLVGGQPLLILGVAEPTVLYTFMFNFAKDRKDLGHKLFLAWTGWVCVWTALLLFTLAILGACSIINRFTRVA 155
Gorai.011G205300.1-AtBOR4          EQLSRDTDGALSTVETLASTAICGIIHSILGGQPLLIVGVAEPTIIYTYLYNFCKRRPELGQELFLAWAAWVCVWTAMLLIFLAIFNACTIINRFTRVA 155
Gorai.005G070200.1-AtBOR1          EQLERETDGILTAVQTLASTALCGIIHSIIGGQPLLILGVAEPTVIYTFMFNFAKNRLDLGSELFLAWTAWVCVWTAILLFLLAILGACSIINRFTRLA 155
Gorai.006G266200.1-AtBOR2          EQLERDTDGVLTAVQTLASTALCGIIHSIIGGQPLLILGVAEPTVIYRFMFDFAKNRPDLGSQLFLAWTGWVCVWTAILLFLLAILGACSIINRFTRLA 155
Gorai.008G137000.1-AtBOR1          EQLERNTDGVLTAVQTLASTAICGIIHSIIGGQPLLILGVAEPTVIYTFMFDFVKDRSDLGRDRFLAWTGWVCVWTAGLLFLLSILGACSIINRFTRVA 155
Gorai.004G146300.1-AtBOR2          EQLERNTDGVLTAVQTLASTALCGIIHSIIGGQPLLILGVAEPTVIYTFMFNFVKDVPDLGRDLFLAWSGWVCVWTAALLFLLSILGACSIINRFTRVA 155
Gorai.009G010600.1-AtBOR4          EQLSRDTDGALSPVETLASTALCGIIHSIVGGQPLLILGVAEPTIIYTYLYNFCKARAELGKQLFLAWAAWVCVWTALLLILLAIFNACTIITRFTRIA 154
Medtr2g032690.1-AtBOR1             EQLQRDTDGILTAVQTLASTALCGIIHSIIGGQPLLILGVAEPTVIYIFMFNFAKNRPDLGSKLFRAWTGWVCMWTSLLLFLLAIFNACSIVNRFTRVA 155
Medtr7g110000.1-AtBOR2             EQLERNTEGVLTAVQTLASTSICGIIHSIIGGQPLLILGVAEPTVIYTFMFNFAKERPELGRNLFLGWAGWVCVWTALILFLLAILGACSIINRFTRIA 155
Medtr3g077670.1-AtBOR2             EQLERNTDGTLTAVQTLASTALCGIIHSIIGGQPLLILGVAEPTVLYTFMYNFAKDREDLGHKLFLPWTGWVCVWTALLLFLLAILGACSIINRFTRLT 155
Medtr3g107730.1-AtBOR7             EQLSRDTDGSLSTVETLASTAICGIIHSIIGGQPLLILGVAEPTVIYTYLYTFCKNTPQLGTKLFLAWAGWVCVWTALMLILLAIFNACNIITRFTRIA 152
Medtr0459s0020.1-AtBOR4            AQLSRETYGSLSTVETLASTAICGIIHSIFGGQPLLILGVAEPTILYTYLYNYAKNKEGLGRELFLAWVGWVCVWTALLLFLLAIFNAAIIINRFTRIA 163
LOC_Os01g08020.1-AtBOR4            AQLSRETNGILTTVETLASTALCGIIHSILGGQPLLIVGVAEPTIIYTYLYNFAKNQQALGERLYLAWAGWVCIWTALMLFLLAMFNASNVISRFTRVA 155
LOC_Os05g08430.1-AtBOR5            EQLSNDTDGALTTVETLASTAICGIIHSILGGQPLLIVGVAEPTIIYTYIYNFAKNHPNLGERLFLPWAGWVCIWTAFMLFLMAMFNAAVVINRFTRFA 156
LOC_Os12g37840.1-AtBOR2            EQLERNTDGVLTAVQTLASTALCGIIHSFLGGQPLLILGVAEPTVLYTFMFNFAKDRPDLGRRLFLAWTGWVCVWTAILLFLLAILGACSIINRFTRIA 155
Phpat.001G035800.1.p-AtBOR2        EQLGRDTEGVITAVQTLSSTTICGIIQAIVGGQPLLIVGVSEPTSLYTFMYDFAKNRPEIGARFFLGWAAWVCVWSAFMLAALAILGACNFINRFTRVA 200
ppa002139m-AtBOR2                  EQLERDTDGVLTAVQTLASTALCGIIHSILGGQPLLILGVAEPTVIYTFMFNFAKNRPDLGSKLFLAWTGWVCVWTAILLFLLAILGACSIINRFTRLA 155
ppa002104m-AtBOR2                  EQLERNTDGVLTAVQTLVSTAVCGIIHSIIGGQPLLILGVAEPTVIYTFMFNFAKERADLGPKLFLAWSGWVCVWTAALLFLLAILGACSIINRFTRVA 155
ppa002100m-AtBOR2                  EQLERNTNGALTAVQTLASTSLCGVIHSIFGGQPLLILGVAEPTVLYTFMFNFAKDRKDLGQELFLAWTGWVCVWTALLLFLLAVLGACSIINRFTRIA 155
Potri.002G191000.1-AtBOR2          EQLERNTDGVLTAVQTLASTAVCGIIHSIIGGQPLLILGVAEPTVIYTFMFNFAKERADLGRNLFLAWTGWVCVWTSLLLFLLAVLGACSIINRFTRVA 155
Potri.006G249800.1-AtBOR4          EQLSRDTDGSLSTVETLASTAICGIIHSVFGGQPLLILGVAEPTVIYTYLYTFSKGREELGKKLYLAWAGWVCVWTALLLVLIAIFNAATIISKFTRIA 155
Potri.008G100300.1-AtBOR2          EQLDRDTDGVLTAVQTLASTALCGIIHSIIGGQPLLILGVAEPTVIYTFMFKFAKNIPDLGSKLFLAWSGWVCVWTAILLFLLSILGACSIISRFTRVA 155
Potri.015G077600.1-AtBOR2          EQLERDTDGTLTAVQTLVSTALCGIIHSIVGGQPLLILGVAEPTVLYTFMFDFAKDRKDLGPNLFLAWTGWVCVWTALLLFLLAVLGACSIINRFTRVA 155
Potri.018G031700.1-AtBOR4          EQLSRDTDGSLSTVETLASTAICGIIHSILGGQPLLILGVAEPTVIYTYLYNFSKGREELGQKLFLAWAGWVCVWTALLLVLLAIFNAATIIFKFTRIA 155
Potri.012G081800.1-AtBOR2          EQLERDTGGTLTAVQTLASTALCGIIHSIVGGQPLLILGVAEPTVLYTFMFDFAKDRKDLGPNLFLAWTGWVCVWTALLLFLLAVLGACSIINRFTRVT 155
Potri.001G174500.1-AtBOR4          EQLSRDTDGSLSTVETLVSTALCGIIHSILGGQPLLILGVAEPTVIYTYLYNFAKGREHLGQKLFLAWAGWVCVWTAVLLFLLAIFNACAIINRFTRLA 155
Potri.003G059700.1-AtBOR4          EQLRRDTDGSLSTVETLASTALCGIIHSILGGQPLLILGVAEPTVIYTYLYNFAKEREELGQKLFLAWAGWVCVWTALLLFLLAIFNACAIINRFTRVA 155
Potri.006G154700.1-AtBOR4          EQLSKETDGSLSTVHTLASTAICGIIHSLFGGQPLLILGVAEPTVIYSYLYSFAKGNNAIGKELYLAWVGWVCVWTALLLFLLAIFNACTIINRFTRVA 156
Phvul.001G053300.1-AtBOR6          EQLNRDTGGSLSTVETLTSTAICGIIHSIFGGQPLLILGVAEPTVIYTILYQFCTKSPDLGVELFLPWAGWVCVWTSLLLIMLAVFNACTIISRFTRLA 151
Phvul.001G215700.1-AtBOR2          EQLERDTDGVLTAVQTLASTSICGIIHSILGGQPLLILGVAEPTVIYTFMFNFAKERPELGRNLFLAWTGWVCVWTAVLLFLLAILGACSIINRFTRIA 155
Phvul.005G174400.1-AtBOR4          EQLSRDTDGSLSTVETLASTAICGIVHSILGGQPLLIVGVAEPTIIYTYLYNFAKDKDSLGRELFLAWAGWVCVWTALLLFLLAIFNAGNIINKFTRIA 155
Phvul.009G178000.1-AtBOR2          EQLERNTDGTLTAVQTLASTALCGIIHSVIGGQPLLILGVAEPTVLYTFMYDFAKDRQDLGHKLFLPWTGWVCVWTALLLFLLAILGACSIINRFTRVA 155
Sobic.008G132300.1.p-AtBOR2        EQLERNTDGVLTAVQTLASTAVCGIIHSIVGGQPLLILGVAEPTVLYTFMFNFAKDRPDLGRNLFLAWTGWVCVWTAILLFLLAILGACSIINRFTRIA 155
Sobic.009G064200.1.p-AtBOR4        EQLSKDTDGTLTTVETLASTAICGIIQSIIGGQPLLIVGVAEPTIIYTYIYNFAKNQPNLGEKMFLPWAAWVCIWTAVMLFLMAMFNVAAILNRFTRFS 156
Sobic.003G047900.1.p-AtBOR4        AQLSTATNGILTTVETLASTAICGIIHSILGGQPLLIVGVAEPTIIYTYLYNFAKNQQALGEKLYLAWAGWVCIWTAIMLFLLAMFNASNVISRFTRVA 155
Solyc06g071500.2.1-AtBOR2          EQLERSTDGSITAVQTLASTALCGVIHSILGGQPLLILGVAEPTVLYTFMFNFAKDRKDLGPNLFLAWTGWVCVWTAFLLFLLAVLGACSIINRFTRLA 155
Solyc01g079150.2.1-AtBOR1          EQLERNTDGILTAVQTLASTAICGITHSIIGGQPLLILGVAEPTVIYTFMFDFAKQRPDLGPGLFLPWTGWVCVWTAILLFLLAILGACSIINRFTRLA 155
GSVIVT01007733001-AtBOR2           EQLERYTNGTLTAVQTLASTALCGIIHSIVGGQPLLILGVAEPTVLYTFMFNFAKDRKDLGQELFLAWTGWVCVWTALLLFLLAILGACSIINRFTRIA 155
GSVIVT01015478001-AtBOR4           EQLSRETDGHLSTVETLTSTAICGIIHSIFGGQPLLILGVAEPTVIYTYLYNFAKGRADLGRELFLAWTGWVCFWTALFLFLLAIFNACTIITKFTRIA 155
GSVIVT01035800001-AtBOR4           EQLSRETDGHLSSVQTLASTAICGIIHSIFGGQPLLILGVAEPTVIYTYLYNFAKGKSDLGKDLYLAWAGWVCVWTALMLFLLAIFNACTIISRFTRVA 155
GSVIVT01017647001-AtBOR2           EQLEKNTDGVLTAVQTLASTALCGIIHSIIGGQPLLILGVAEPTVLYTFMFNFAKDRPDLGPKLFLAWTGWVCVWTSGLLFLLAILGASSIINRFTRIA 155
GSVIVT01028186001-AtBOR2           EQLERNTEGVLTAVQTLASTAICGIIHSIIGGQPLLILGVAEPTVIYTFMFNFAKERPDLGRKLFLAWTGWVCVWTAFLLFLLAILGACSIINRFTRVA 155
GSVIVT01017223001-AtBOR4           EQLSRDTDGSLSTVETLASTAICGIIHSILGGQPLLILGVAEPTVIYTYLYNFAKGRAELGQELFLAWAGWVCVWTALMLFLLAIFNACDIINRFTRIA 155
GRMZM2G082203_P01-AtBOR2           EQLERNTDGVLTAVQTLASTALCGVIHSIVGGQPLLILGVAEPTVLYTFMFSFAKDRPDLGRSLFLAWTGWVCVWTAILLFLLAILGACSIINRFTRVA 155
GRMZM2G166159_P01-AtBOR2           EQLERNTDGVLTAVQTLASTALCGIIHSIVGGQPLLILGVAEPTVLYTFMFNFAKERPDLGRNLFLAWTGWVCVWTAILLFLLAILGACSIINRFTRIA 155
GRMZM2G051753_P01-AtBOR4           AQLSTATNGILSTVETLASTAICGIIHSILGGQPLLIVGVAEPTIIYTYLYNFAKNHQALGEQLYLAWTGWVCIWTAIMLFLLATFNASNVISRFTRIA 155
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                                  210       220       230       240       250       260       270       280       290       300
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AT3G06450.1-AtBOR3        GELFGILIAMLFMQEAIRGIVDEFGVP--GRTNPR--SAEFQPAWVFANGMFGLVLSSGLLYTGLKSRKARSWRFGAEWLRGFIADYGVPVMVVVWTCIS 253
AT3G62270.1-AtBOR2        GELFGLLIAMLFMQQAIKGLVDEFRAP--AREDLK--LVEFLPSWRFANGMFALVLSFGLLITALRSRKARSWRYGTGWLRSLVADYGVPLMVLVWTGVS 251
AT4G32510.1-AtBOR7        GELFGMLITVLFIQEAVKGLIGEFLVPKSD--DPS--LEVYQFQWRYTNGLLAVIFSFGLLYTALKSRRARSWKYGFRWMRGFIGDYGTLLMLVLWSAFS 251
AT2G47160.1-AtBOR1        GELFGLLIAMLFMQQAIKGLVDEFRIP--ERENQK--LKEFLPSWRFANGMFALVLSFGLLLTGLRSRKARSWRYGTGWLRSLIADYGVPLMVLVWTGVS 251
AT5G25430.1-AtBOR6        GELFGMLIAVLFLQEAIKGLISEFHAPEIK--NQE--TGKSHFLLIYANGLLAVIFSLGLLITALKSRRAKSWKYGFGWLRSFIGDYGVPLMVLLWTALS 253
AT1G15460.1-AtBOR4        GELFGMLISVLFIQQAIKGMVSEFGMPKDE--DSK--LEKYKFEWLYTNGLLGLIFTFGLLYTALKSRKARSWRYGTGWYRSFIADYGVPLMVVVWTALS 256
AT1G74810.1-AtBOR5        GELFGMLIAVLFLQQTIKGMVSEFRIPKGE--DSK--LEKYQFEWLYTNGLLGLIFTVGLVYTALKSRKARSWPYGTGCCRSFVADYGVPLMVVVWTALS 256
Bradi4g04420.1.p-AtBOR2   GELFGLLIAMLFMQQAIKGLVDEFGIP--ERENIK--ARQFVPSWRFANGMFAIVLSFGLLLTALKSRKARSWRYGAGWLRGFIADYGVPLMVLVWTGIS 251
Bradi2g34110.1.p-AtBOR4   GELFGMLITILFMQEAVKGMLSEFSAPEGQ---DHN-LPIYQFHWVYINGLLGIIFSMGLLYTALRSRAARSSLYGTGWQRSLIADYGVPIMVILWTALS 251
Bradi2g04690.1.p-AtBOR4   GELFGMLITVLFLQQAIKGIVSEFSLPKAAEIVDRS-SLIYDFQWIYVNGLLGVIFSIGLLYTALKSRRARSWLYGIGCLRSFIADYGVPLMVIVWTALS 254
Brara.D00064.1.p-AtBOR2   GELFGLLIAMLFMQEAIKGLVDEFRSP--EREDLK--LLEFLPSWRFANGMFALVLSFGLLITALRSRKARSWRYGTGWLRSLIADYGVPLMVLVWTGVS 251
Brara.A00544.1.p-AtBOR7   GELFGMLITVLFFQEAVKGLLGEFLVPKSE--DPS--LEAYQSHWRYTNGLLAVIFSFGLLYTALKSRRARSWRYGFRWMRGFIGDYGTLLMLVLWSALS 251
Brara.C03154.1.p-AtBOR3   GELFGILIAMLFMQEAIRGVVDEFGVP--GRTNPS--SAQFQPAWVFANGMFGLVLSFGLLYTALKSRKARSWRFGAEWLRGFIADYGVPVMVVVWTCVS 253
Brara.F01062.1.p-AtBOR4   GELFGMLISVLFIQEAIKGMVGEFSMPKEG--DSK--LEKYKFEWLYTNGLLGLIFTFGLLYTALKSRKARSWRYGTGWYRSFIADYGVPLMVVVWTALS 254
Brara.F02740.1.p-AtBOR6   GELFGMLIAVLFLQEAIKGLVSEFQASKSE--HHDK-SGESDFLWLYTNGLLAVIFSLGLLITALKSRRAKSWKYGFGWLRSFIGDYGVPLMVLFWTALS 252
Brara.B02140.1.p-AtBOR4   GELFGMLIAVLFIQQTIKGMLSEFKMPDHE--DST--LEKYQFQWLYTNGLLGLIFTFGLLYTALKSRKARSWRYGTGWYRNFIADYGVPLMVVVWTALS 256
Cre10.g443900.t1.1-AtBOR1 GELFGGLIGVLFLQQAIKGLIAQFRLDPNASHSGEESAAADAYVWRLVNGLWSLLLAAGLLLGALAVVRARSWRFLSKPLRGLLADYGAPACVLVCTGVS 260
Cucsa.192570.1-AtBOR2     GELFGLLIAMLFMQQAVKGLVDEFQIP--ERENPK--LIEFIPSWRFANGMFALVLSFGLLFTALRSRKARSWRYGSGWLRSLIADYGVPLMVLVWTGIS 251
Cucsa.300580.1-AtBOR4     GELFGMLISVLFIQEAIKGVVSEFEVPETE--NTS--LENYQFHWIYTNGLLGIIFTFGLLYTALKSRKARSWLYGTGWLRSFIADYGVPLMVVVWTALS 251
Cucsa.098470.1-AtBOR2     GELFGLLIAMLFMQQAIRGVVEEFGIP--QRENPN--QVSLQAPWRFGNGMFALVLSFGLLLTALKSRKARSWRYGTGCLRGFIADYGVPLMVLIWTALS 251
Eucgr.C02816.1-AtBOR4     GELFGMLITVLFIQEAIKGLISEFNIPEAD--NPA--LEKYQFQWLYTNGLLASIFATGLLYTALKSRKARSWRYTTGWFRGFIADYGVPLMVLTWTALS 251
Eucgr.J03035.1-AtBOR4     GELFGMLITILFIQEAIKGAVSEFRIPKAE--DQN--LLKYQFQWLYTNGLLGIIFTFGLLYTALKSRKARSWLYGTGWLRNFTADYGVPLMVLLWTALS 251
Eucgr.H04094.1-AtBOR2     GELFGLLIAMLFMQQAIKGLVEEFRLP--ERENPS--LAEFQPPWRFANGMFALVLSFGLLLTALRSRKARSWKYGSGSLRGFIADYGVPLMVLVWTAIS 251
Eucgr.C04162.1-AtBOR4     GELFGMLIAVLFVQEAVKGVISEFHVPHAE--DSS--AERYHFQWRYVNGLLGIIFTFGLVSTALKSRRARSWPYGTGWFRSFIADYGVPLMVLIWSALA 251
Eucgr.H00896.1-AtBOR1     GELFGLLIAMLFMQQAIKGLVEEFRIP--KQENPK--LDEFLPSWRFANGMFALVLSFGLLLTALKSRKARSWRYGTGWLRSFIADYGVPLMVLVWTAVS 251
Eucgr.B00302.1-AtBOR2     GELFGLLIAMLFMQQAIRGVIEEFGIP--ERENPN--QAALLPSWRFGNGMFALVLSFGLLLTALRSRKARSWRYGTGWLRGFIADYGVPLMVLVWTAVS 251
Glyma.06G181900.1.p-AtBOR2 GELFGLLIAMLFMQQAIKGLVEEFGAPKNQREGTN--QVALQSSWLFGNGMFALVLSFGLLFTGLQSRKARSWRYGSGWLRGFIADYGVPLMVLVWTAVS 253
Glyma.15G011200.1.p-AtBOR4 GEIFGMLITVLFIQEAIKGMVSEFNVPEEG--DPT--MEKYQFHWLYANGLLGIIFTFGLLYTSLKSRRARSWLYGTGWFRSFIADYGVPEMVVVWTALS 251
Glyma.04G184000.1.p-AtBOR2 GELFGLLIAMLFMQQAIKGLVEEFGAPKNQREGTN--QIALQSSWLFGNGMFALVLSFGLLFTGLQSRKARSWRYGSGWLRGFIADYGVPLMVLIWTAVS 253
Glyma.17G207700.1.p-AtBOR6 EELFGMLITVLFFQEAIKGIIGEFNTPKDG--NLL--LEENQFHWRYANGLLAIILSFGLLITATMSRKARTWKYGSGWLRGFIADYGVPMMLVIWTGLS 255
Glyma.04G069500.1.p-AtBOR7 GELFGMLITVLFFQEAIKGLIGEFNMPKNE--NPS--SVEFQFQWLYTNGLLAIIFGFGLLVTALKSRRARTWRYGTGWLRGFIADYGVPMMVVLWTALS 248
Glyma.09G031400.1.p-AtBOR2 GELFGLLIAMLFMQEAVRGLIHEFHIP--ERANLT--SPEFQSSWRFGNGMFSLVLSFGLLHTALRSRKARSWRYGSGCLRGFIADYGVPLMVLLWTAVS 251
Glyma.19G219500.1.p-AtBOR2 GELFGMLIAMLFMQQAIKGLVDEFRIP--ERQNSK--SIEFIPSWRFANGMFALVLSFGLLLTALRSRKARSWRYGTGWLRSLIADYGVPLMVLVWTGVS 251
Glyma.03G222300.1.p-AtBOR2 GELFGMLIAMLFMQQAIKGLVDEFRIP--ERQNPK--SIEFISSWRFANGMFALVLSFGLLLTALRSRKARSWRYGTGWLRSLVADYGVPLMVLVWTGVS 251
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Gorai.011G205300.1-AtBOR4 GELFGMLITVLFLQEAVKGVISEFNVPKGE--NPK--LEKYQFPWLYTNGLLAVIFSFGVLFTSLKTRKARLWRYGTGWIRGFLADYGVPLMILGWTALS 251
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Gorai.006G266200.1-AtBOR2 GELFGLLIAMLFMQQAIKGLVDEFHIP--ERENPK--SVDFQLSWRFANGMFAMVLSFGLLFTALRSRKARSWRYACGSLRGFVADYGVPLMVLVWTAVS 251
Gorai.008G137000.1-AtBOR1 GELFGLLIAMLFMQQAIKGLVEEFRIP--HNENPN--LTQFIPSWRFANGMFALVLSFGLLFTALQSRKARSWRYGTGWLRSFIADYGVPLMVLIWTGVS 251
Gorai.004G146300.1-AtBOR2 GELFGLLIAMLFMQQAIKGIVEEFRIP--QHENPK--LTEFTPSWRFANGMFALVLSFGLLFSALRSRKARSWRYGTGWLRSFIADYGVPEMVLVWTAAS 251
Gorai.009G010600.1-AtBOR4 GELFGMLITVLFIQEAIKGVVSEFNIPKGE--NPN--LEKYQFHWLYTNGLLAVIFSFGLTITALKTRKARSWRYGTGWFRSFIAEYGVPLMVVGWTALS 250
Medtr2g032690.1-AtBOR1    GELFGLLIAMLFMQEAIKGLIHEFHIP--ERANPE--STEFQSSWRFGNGMFALVLSFGLLLTALRSRKARSWRYGSGCLRGFIADYGVALMVLLWTVVS 251
Medtr7g110000.1-AtBOR2    GELFGMLIAMLFMQQAIKGLVDEFRIP--KREDTK--AIEFLPSWRFANGMFALVLSFGLLLTALKSRKARSWRYGSGWLRSLIADYGVPLMVLVWTGVS 251
Medtr3g077670.1-AtBOR2    GELFGLLIAMLFMQQAIKGLVEEFGVPKTQTEGTN--QIALQSSWLFGNGMFALVLSFGLLFTGLGSRKARSWRYGTGWLRGFIADYGVPLMILVWTAVS 253
Medtr3g107730.1-AtBOR7    GELFGMLITVLFFQEAIKGLVGEFSTPKVE--NPS--SEELQFQWRYTNGLLAVIFSFGLIVTAVKSRKARTWRYGSRRLRGFIADYGVPVMVVLWTAVS 248
Medtr0459s0020.1-AtBOR4   GELFGMLITVLFIQEAIKGMVSEFEVPKEG--DPT--LDKYQFHWLYANGLLGIIFTFGLLYTSLKSRKARSWLYGTGWLRSFIADYGVPFLVVVWTALS 259
LOC_Os01g08020.1-AtBOR4   GELFGMLITVLFLQQAIKGIIEEFKVPRDA---DHS-SPIYQFQWLYVNGLLGVIFSIGLLYTALRSRRARSWVYGQGWLRGFIADYGVPLMVIVWTAFS 251
LOC_Os05g08430.1-AtBOR5   GELFGMLITILFMQEAVKGMLGEFSVPEGK---DHS-LPIYQFQWAYVNGLLGIIFSMGLLYTAIRSRSARSSLYGTGWQRSFIADYGVPLMVVVWTALS 252
LOC_Os12g37840.1-AtBOR2   GELFGLLIAMLFMQQAIKGLVDEFRIP--ERENRK--ALEFVSSWRFANGMFAIVLSFGLLLTALRSRKARSWRYGTGWLRGFIADYGVPLMVLVWTGVS 251
Phpat.001G035800.1.p-AtBOR2 GELFGLLIAVLFVQQAVKGAVNEFRIS--KFVNAT--EEQFQSSWRFGNGMFGILLTFGLLWTAIKSRNARSWNFGPGFFRRFIANYGVPILVIVWSAVS 296
ppa002139m-AtBOR2         GELFGLLIAMLFMQEAIKGLVHEFRIP--ERENPK--SVQFQPSWRFANGMFALVLSFGLLLTSLKSRKARSWRYGSGSLRGFVADYGVPLMVLIWSAVS 251
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ppa002100m-AtBOR2         GELFGLLIAMLFMQQAIRGLVEEFSVP--KRENPN--KIALQPAWRFGNGMFALVLSFGLLLTALRSRKARSWRYGAGWLRGFIADYGVPEMVVVWTAVS 251
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Potri.006G249800.1-AtBOR4 GELFGMLIAVLFIQEAVRGVISEFNIPKDE--NPK--LEKHQFQWLYANGLLSVIFSFGVLFTSLKSRRARTWRYGTGWLRGFIADYGVPLMVLLWTALS 251
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Phvul.001G053300.1-AtBOR6 EELFGMLITVLFFQEAILGIRNEFKTPKSE--NPS--TEEHQFHWRYINGLLSVIFSLGILLTALYSRRARTWKLGTGWQRALVADYGIPLMVVFWTGMS 247
Phvul.001G215700.1-AtBOR2 GELFGMLIAMLFMQQAIKGLVDEFRIP--ERQNPK--SIEFIPSWRFSNGMFALVLSFGLLLTALRSRKARSWRYGTGWLRSLIADYGVPLMVLVWTGVS 251
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GSVIVT01017647001-AtBOR2  GELFGLLIAMLFMQEAIKGLIDEFRIP--GRESPT--LTEFQPSWRFANGMFALVLSFGLFLTALRSRKARSWRYGSGCLRGFIADYGVPLMVLVWTAVS 251
GSVIVT01028186001-AtBOR2  GELFGLLIAMLFMQQAIKGIVDEFRIP--KQENAK--LTEFIPSWRFANGMFALVLSFGLLLTALRSRKARSWRYGTGWLRSLIADYGVPLMVLIWTAVS 251
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GRMZM2G051753_P01-AtBOR4  GELFGMLITVLFLQEAIKGMISEFSVPEDA---DSS-SPIYQFQWLYVNGLLGVIFSIGLLYTALRTRRARSWLYGTGWFRSFIADYGVPLMVIVWTGLS 251
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AT3G06450.1-AtBOR3        Y-IPWKS---VPQGIPRRLVSPNPW------SPGAYQNWTVIK---EMVDVPVLYILLAVVPASMIAVLYYFDHSVASQLAQQEDFNLRKPAYHYDLFL 340
AT3G62270.1-AtBOR2        Y-IPTGD---VPKGIPRRLFSPNPW------SPGAYENWTVVK---EMLQVPIVYIIGAFIPATMIAVLYYFDHSVASQLAQQKEFNLRKPSSYHYDLLL 338
AT4G32510.1-AtBOR7        Y-TVPRN---LPEGVPRRLELPLPW------ASESLYHWTVVK---DMAKVPPLYILAAFIPAIMIAGLYFFDHCVSAQMAQQKEFNLKNPTAYHYDIFI 338
AT2G47160.1-AtBOR1        Y-IPAGD---VPKGIPRRLFSPNPW------SPGAYGNWTVVK---EMLDVPIVYIIGAFIPASMIAVLYYFDHSVASQLAQQKEFNLRKPSSYHYDLLL 338
AT5G25430.1-AtBOR6        Y-TVPSE---VLPSVPRRLFCPLPW------EPASLYHWTVVK---DMGKVPIMYILAAFIPGVMIAGLYFFDHSVASQMAQQKEFNLKNPSAYHYDIFL 340
AT1G15460.1-AtBOR4        F-STPSK---LPSGVPRRLFSPLPW------DSPSLSHWTVIK---DMGKVSPGYIFAAFIPALMIAGLYFFDHSVASQLAQQKEFNLKKPSAYHYDILL 343
AT1G74810.1-AtBOR5        F-STPSK---LPSGVPRRLVSPLPW------DSVSLTHWTVIK---DMGKVSPGYIFAAFIPALMIAGLYFFDHSVVSQLAQQKEFNLKNPSAYHYDILL 343
Bradi4g04420.1.p-AtBOR2   Y-IPYDS---VPKGIPRRLFSPNPW------SPGAYDNWTVIK---DMPHVPLMYIIGAFIPATMIAVLYYFDHSVASQLAQQAEFNLRKPSFHYDLLL 338
Bradi2g34110.1.p-AtBOR4   Y-SLPSK---IPSGVPRRLFTPLPW------EPKSLQHWTVAK---DLFSVPPAYIFLAIVPAAMVAGLYFFDHSVASQMAQQKEFNLKNPSAYHYDILV 338
Bradi2g04690.1.p-AtBOR4   Y-TLPSK---VPSGVPRRLFSPLPW------ESSSLGHWTVAK---DLFSVPPAFIFAAIVPALMVAGLYFFDHSVASQLAQQKEFNLKKPSAYHYDILV 341
Brara.D00064.1.p-AtBOR2   Y-IPTGD---VPKGIPRRLFSPNPW------SPGAYENWTVVK---EMLQVPVVYIIGAFIPATMIAVLYYFDHSVASQLAQQKEFNLRKPSSYHYDLLL 338
Brara.A00544.1.p-AtBOR7   F-TVPRD---IPEGVPRRLELPLPW------DSESLYHWTVVK---DMGKVPPLYILAAFIPAIMIAGLYFFDHCVSAQMAQQKEFNLKNPSAYHYDIFI 338
Brara.C03154.1.p-AtBOR3   Y-IPWKS---VPQGIPRRLVSPNPW------SPGAYQNWTVVK---EMLDVPVVYIILALVPASMIAVLYYFDHSVASQLAQQEDFNLRKPSFHYDLLL 340
Brara.F01062.1.p-AtBOR4   F-TTPSK---LPTGVPRRLFSPLPW------DSASLEHWTVIK---DMGKVSPGYIFAAFIPALMIAGLYFFDHSVASKLAQQKEFNLKNPSAYHYDILL 341
Brara.F02740.1.p-AtBOR6   Y-TVPSK---VPENVPRRLFCPLPW------ETASLHHWTVVK---DMGKVPVMYIFAGIIPAVMIAGLYFFDHSVASQMAQQKEFNLRKPSAYHYDIFL 339
Brara.B02140.1.p-AtBOR4   F-STPST---LPSGVPRRLSSPLPW------DSASLGHWTVIK---DMGKVPPPYIFAGFIPALMIAGLYFFDHSVVAQLAQQKEFNLKNPSAYHYDVLL 343
Cre10.g443900.t1.1-AtBOR1 FAVSPQAHGAAPPGVPRRVSTGDVWSGSSIDGSSSSSGWRVAA---RMGEVPGTYIAAALLPAFVIAVLFYFDHSVSSLMAQQPEYRLARPPAFALDLAL 357
Cucsa.192570.1-AtBOR2     Y-IPSKS---VPEGIPRRLFSPNPW------SPGAYENWTVIK---DMLEVPVIYICGAFIPATMIAVLYYFDHSVASQLAQQKEFNLRKPSSYHYDLLL 338
Cucsa.300580.1-AtBOR4     F-SVPSK---VPVGVPRRLQSPLAW------QSTSLNHWTIVK---DMGKIPPAYIFAAFIPAVMIAGLYFFDHSVASQMAQQKEFNLKNPSAYHYDILL 338
Cucsa.098470.1-AtBOR2     Y-IPVNN---VPLGIPRRLFSPNPW------SQGAYSNWTVIK---EMLRVPPLYIVGAFIPATMIAVLYYFDHSVASQLAQQKEFNLKKPASYHYDLLL 338
Eucgr.C02816.1-AtBOR4     F-AVPKR---VPNGVPRRLFCPLPW------DTASLYHWTVIK---DMWKVPPTYIFAAFIPAMMIAGLYFFDHSVASQLAQQKEFNLKKPSAYHFDIFL 338
Eucgr.J03035.1-AtBOR4     F-SIPKK---LPSGVPRRLFSPLPW------ESASLHHWTVIK---DMGRVSPAYVFAAFIPAVMIAGLYFFDHSVASQLAQQKEFNLKNSSAYHYDIFL 338
Eucgr.H04094.1-AtBOR2     Y-APAGS---IPKGIPRRLFSPNPW------SPGAYENWGVIK---DMVKVPVLYIIGAFIPATMIAVLYYFDHSVASQLAQQKEFNLRKPSSFHYDLLL 338
Eucgr.C04162.1-AtBOR4     F-SVPKS---VPSGVPRRLYSPLPW------EPASLHHWSVIK---DMGRVPPAYIFAAFIPAVMVAGLYFFDHSVASQMAQQKEFNIKNPSAYHYDVLV 338
Eucgr.H00896.1-AtBOR1     Y-IPAKS---VPDGIPRRLVSPNPW------SPGASENWTVVK---DMLNVPFFYIIGAFIPATMIAVLYYFDHSVASQLAQQKEFNLRKPASYHYDLLL 338
Eucgr.B00302.1-AtBOR2     Y-IPVRD---VPRGIPRRLFSPNPW------SPGAYSNWTVVK---EMLNVPPLYIVGAFIPATMIAVLYYFDHSVASQLAQQKEFNLKKPSSYHYDLLL 338
Glyma.06G181900.1.p-AtBOR2 Y-IPVNE---VPKGIPRRLFSPNPW------SPGAYSNWTVVK---EMLNVPPLYIVGAFIPATMIAVLYYFDHSVASQLAQQKEFNLRKPSSYHYDLLL 340
Glyma.15G011200.1.p-AtBOR4 F-IVPSK---VPSGVPRRLTSPLAW------ESTSLHHWTVIK---DMGEVSLAYIFAAFIPALMIAGLYFFDHSVASQMAQQKEFNLRKPSAYHYDILL 338
Glyma.04G184000.1.p-AtBOR2 Y-IPVNE---VPRGIPRRLFSPNPW------SPGAYSNWTVVK---EMLNVPPLYIVGAFIPATMIAVLYYFDHSVASQLAQQKEFNLRKPSSYHYDLLL 340
Glyma.17G207700.1.p-AtBOR6 Y-TLPGK---IPSAVPRRLVCPLPW------ES--TYHWTVVK---DMGKVPLGYIFGAFIPAVMIAGLYFFDHSVASKMAQQKEFNLQKPSAYHYDILV 340
Glyma.04G069500.1.p-AtBOR7 Y-TVPGK---VPDGVPRRLISPLPW------DAASLYHWTVVK---DMGKVPVVYIFGAIIPALMIAGLYFFDHSVASQMAQQKEFNLQKPSAYHYDVLL 335
Glyma.09G031400.1.p-AtBOR2 Y-IPAGS---IPKGIPRRLFSPNPW------SSGAFENWTVIK---DMLNVPVLYIIGAFIPATMIAVLYYFDHSVASQLAQQKEFNLRKPSFHYDLLL 338
Glyma.19G219500.1.p-AtBOR2 Y-IPAGS---VPHGIPRRLFSPNPW------SPGAYENWTVIK---DMVHVPVVYIIGAFIPATMIAVLYYFDHSVASQLAQQKEFNLRKPSSYHYDLLL 338
Glyma.03G222300.1.p-AtBOR2 Y-MPAGS---VPHGIPRRLFSPNPW------SPGAYENWTVIK---DMVHVPVVYIIGAFIPATMIAVLYYFDHSVASQLAQQKEFNLRKPSSYHYDLLL 338
Gorai.005G135900.1-AtBOR2 Y-IPVND---VPRGIPRRLFSPNPW------SPGAYSNWTVIK---EMVNVPPLYIVGAFIPATMIAVLYYFDHSVASQLAQQKEFNLKKPSYHYDLLL 338
Gorai.011G205300.1-AtBOR4 Y-MIPGQ---VSSGVPRRLFCPLLW------ESESLHHWTVIK---DMGKVPIMYIFAAFIPAVMIAGLYFFDHSVASQLAQQKEFNLKNPSAYHYDILL 338
Gorai.005G070200.1-AtBOR1 Y-IPAGS---TPKGIPRRLFSPNPW------SPGAYENWTVMK---DMLKVPVLYIIGAFIPATMLAVLYYFDHSVASQLAQQKEFNLRKPSFHYDLLL 338
Gorai.006G266200.1-AtBOR2 Y-IPAGT---IPKGIPRRLFSPNPW------SPGAYENWTVVK---DMLKVPVLYIIGASVPATMIAVLYYFDHSVASQLAQQKEFNLRKPSFHYDLLL 338
Gorai.008G137000.1-AtBOR1 Y-IPAGD---VPKGIPRRLFSPNPW------SPGAYENWTVIK---DMLDVPLVYIIGAFIPATMIAVLYYFDHSVASQLAQQKEFNLRKPSCYHYDLLL 338
Gorai.004G146300.1-AtBOR2 Y-IPSAS---VPKGVPRRLFSPNPW------SPGAYENWTVIK---DMLNVPVVYIIGAFIPATMIAVLYYFDHSVASQLAQQKEFNLRKPSCYHYDLLL 338
Gorai.009G010600.1-AtBOR4 Y-TVPRK---VNSGIPRRLFCPLLW------EPESLPHWTVIK---DMGNVPIEYIFAAIIPALMIAGLYFFDHSVASQLAQQKEFNLKYPSTYHYDVLL 337
Medtr2g032690.1-AtBOR1    Y-IPAGN---TPKGIPRRLFSPNPW------SHGEYENWTVIK---DMQNVPVLYIIGAFIPATMIAVLYYFDHSIASQLSQQKEFNLRKPSFHYDLLL 338
Medtr7g110000.1-AtBOR2    Y-MPTAS---VPNGIPRRLFSPNPW------SPGAYDNWTVVK---DMVQVPVVFIIGAFIPATMIAVLYYFDHSVASQLSQQKEFNLRKPSSYHYDLLL 338
Medtr3g077670.1-AtBOR2    Y-IPVNE---VPRGVPRRLFSPNPW------SPGAYSNWTVVK---EMLNVPLLYIIGAFIPATMIAVLYYFDHSVASQLAQQKEFNIRKPSSYHYDLLL 340
Medtr3g107730.1-AtBOR7    Y-IMPDD---IPNGVPRRLFCPLPW------EPASLYHWTVVK---DMWKVPVVYIFGAIIPALMIAGLYFFDHSVASQMAQQKEFNLQKPSAYHYDVFL 335
Medtr0459s0020.1-AtBOR4   FTVVASK---VPSGVPRRLVAPLAW------ESASLHHWTVIK---DMGKVSLEHIFAAFVPALMIAGLYFFDHSVASQLAQQKEFNLKKSSAYHYDILL 347
LOC_Os01g08020.1-AtBOR4   Y-TLPKD---VPSGVPRRLFSPLPW------ESSSLQHWTVAK---DLFSVPPAYIFAAILPALMVAGLYFFDHSVASQLAQQKEFNLKKPSAYHYDILV 338
LOC_Os05g08430.1-AtBOR5   Y-SLPSK---IPSGVPRRLFTPLPW------EPKSLQHWTVAK---DLFSVPPPYIFLAIVPAVMVAGLYFFDHSVASQLAQQKEFNLKNPSAYHYDILV 339
LOC_Os12g37840.1-AtBOR2   Y-IPYGS---VPKGIPRRLFSPNPW------SPGAYDNWTVIR---DMPNVPLLYIIGAFIPATMIAVLYYFDHSVASQLAQQKEFNLRKPSFHYDLLL 338
Phpat.001G035800.1.p-AtBOR2 Y-ARVGS---VPAGIPRRLTSPNPWK-----SPIATTHWDVVA---DMNDIPGVYIAAAIVPALMIVLYYFDHCVSAQLAQQPEFNLRKPFSYHYDLLL 384
ppa002139m-AtBOR2         Y-IPAGN---VPKGIPRRLFSPNPW------SPGAYENWT------DMLSVPVIYIIGAFIPATMIAVLYYFDHSVASQLAQQKEFNLRKPSFHYDLLL 335
ppa002104m-AtBOR2         Y-IPTST---VPHGIPRRLFSPNPW------SPGAYDNWTVIK---DMLNVPVLYIIGAFIPATMIAVLYYFDHSVASQLSQQKEFNLRKPSSYHYDLLL 338
ppa002100m-AtBOR2         Y-IPVND---VPRGIPRRLFSPNPW------SPGAYSNWTVVK---EMMNVPPLYIVGAFIPATMIAVLYYFDHSVASQLAQQKEFNLNKPASYHYDLLL 338
Potri.002G191000.1-AtBOR2 Y-IPTGN---VPKGIPRRLFSPNPW------SPGAYENWTVVKASSEMLDVPISYIIGAFIPATMIAVLYYFDHSVASQLAQQKEFNLRKPSSYHYDLLL 341
Potri.006G249800.1-AtBOR4 Y-AGPGK---VPSGVPRRVHVPLLW------DSESLEHWTVIN---DMLKVPLTYIFAALIPAVMIAGLYFFDHSVASQMAQQKEFNLKNPSAYHYDVFL 338
Potri.008G100300.1-AtBOR2 Y-IPSGS---VPKGIPRRLFSPNPW------SPGAFENWT------DMLKVPVLYIIGAFIPATMIAVLYYFDHSVASQLAQQREFNLRKPSFHYDLLL 335
Potri.015G077600.1-AtBOR2 Y-IPVNN---VPRGIPRRLFSPNPW------SAGAYSNWTVIK---EMVNVPPLYIVGAFIPATMIAVLYYFDHSVASQLAQQKEFNLKKPSSYHYDLLL 338
Potri.018G031700.1-AtBOR4 Y-VRPSE---VPSGVPRRVHVPLLS------DAESVHHWTVIK---DMGKVPLTYIFAALIPAVMIAGLYFFDHSVASQMAQQKEFNLKNPSAYHYDVLL 338
Potri.012G081800.1-AtBOR2 Y-IPVND---VPRGIPRRLFSPNPW------SVGAHSNWTVIK---EMVNVPPLYIVGSFIPATMIAVLYYFDHSVASQLAQQKEFNLKKPSSYHYDLLL 338
Potri.001G174500.1-AtBOR4 F-SIPSK---VPSGVPRRLFSPLPR------DSASLHHWTVIK---DMGNVPPAYIFAAFIPAVMIAGLYFFDHSVASQMAQQKEFNLKNPSAYHYDILL 338
Potri.003G059700.1-AtBOR4 F-SIPSK---VPSGVPRKLFSPLPW------ESASLHHWTVIK---DMGNVPPAYIFAAFVPAVMIAGLYFFDHSVASQMAQQKEFNLKNPSAYHYDILL 338
Potri.006G154700.1-AtBOR4 F-GVPGK---LPSGVPRRLESPLPW------NTASLKHWTVIK---DMAKVPPAYLFAAFIPAVMVAGLYFFDHSVASQMAQQKNFNLRKPSAYHYDILV 339
Phvul.001G053300.1-AtBOR6 Y-TVPSK---VPSTIPRRLVCPLPW------ESESLYHWTVIM---DMGKVPVLYIFAAFIPAVMVAGLYFFDHSVASKMAQQKEYNLQKPSSFHYDMFL 334
Phvul.001G215700.1-AtBOR2 Y-LPAGS---VPHGIPRRLFSPNPW------SPGAYENWTVIK---DMVHVPVVYIIGAFIPATMIAVLYYFDHSVASQLSQQSEFNLRKPSSYHYDLLL 338
Phvul.005G174400.1-AtBOR4 F-IVPSK---VPSGVPRRLTSPLVW------DSTSLHHWTVIN---DMGKVSPSYIFAAFIPALMIAGLYFFDHSVASQLAQQKEFNLKKPSAYHYDILL 338
Phvul.009G178000.1-AtBOR2 Y-IPVNK---VPRGVPRRLFSPNPW------SPGAYSNWTVVK---EMLNVPILYIIGAFIPATMIAVLYYFDHSVASQLAQQKEFNLRKPSSYHYDLLL 340
Sobic.008G132300.1.p-AtBOR2 Y-IPYGN---VPKGIPRRLFSPNPW------SPGAYDNWTVIK---DMTQVPLLYILGAFIPATMIAVLYYFDHSVASQLAQQKEFNLRKPSFHYDLLL 338
Sobic.009G064200.1.p-AtBOR4 Y-SLPSK---IPSGVPRRLFTPLPW------EPKSLQHWTVAK---DLFSVPPAHIFLAIVPAAMVAGLYFFDHSVASQMAQQKEFNLKNPSAYHYDILV 339
Sobic.003G047900.1.p-AtBOR4 Y-TLPGK---LPSGVPRRLFSPLPW------ESSSQGHWTIAR---DLFSVPPAYIFAAILPALMVAGLYFFDHSVASQLAQQKEYNLKKPSAYHYDILV 338
Solyc06g071500.2.1-AtBOR2 Y-IPARD---VPQGIPRRLFSPNPW------SPGAYSNWTVIK---EMMHVPPLYIVGAFIPATMIAVLYYFDHSVASQLSQQKEFNLKKPSSYHYDLLL 338
Solyc01g079150.2.1-AtBOR1 Y-IPSES---VPERIPRRLLSPNPW------SPGAYENWTVIK---DMLNVPVIYILGAFVPATMIAVLYYFDHSVASQLAQQKEFNLRKPSSFHYDLLL 338
GSVIVT01007733001-AtBOR2  Y-IPVND---VPKGIPRRLFSPNPW------SPGAYSNWTVIK---EMLDVPPLYIVGAFIPATMIAVLYYFDHSVASQLAQQKEFNLKKPASYHYDLLL 338
GSVIVT01015478001-AtBOR4  F-SVPSK---VPSGVPRRLFSPLPW------ESASLQHWTVIK---DMGKIPPAYILAAIIPAVMIAGLYFFDHSVASQMSQQKEFNLKNPSAYHYDILL 338
GSVIVT01035800001-AtBOR4  Y-SIPKK---VPSGVPRRLFCRAPW------DSDSNYQWAVVQ---DMGKVPLGYIFAALIPAVMIAGLYFFDHSVASQMAQQKEFNLKNPSAYHYDLFL 338
GSVIVT01017647001-AtBOR2  Y-IPAGS---IPKGIPRRLFSPNPW------SPGSYENWTIIK---DMLNVPVLYIIGAFIPATMIAVLYYFDHSVASQLAQQKEFNLRKPSFHYDLLL 338
GSVIVT01028186001-AtBOR2  Y-IPAGS---VPKGIPRRLVSPNPW------SPGAYENWTVIK---DMLDVPVLYIVGAFIPATMIAVLYYFDHSVASQLAQQKEFNLRKPSFHYDLLL 338
GSVIVT01017223001-AtBOR4  F-SVPSK---VPSGVPRRLNSPLPW------DSESVYHWTVIK---DMGNVPPAYIFAAIIPALMIAGLYFFDHSVASQMAQQKEFNLKKPSAYHHDILL 338
GRMZM2G082203_P01-AtBOR2  Y-IPYGN---VPKAIPRRLFSPNPW------SPGAYDNWTVIK---DMTQVPLLYIIGAFIPATMIAVLYYFDHSVASQLAQQKEFNLRKPSFHYDLLL 338
GRMZM2G166159_P01-AtBOR2  Y-IPYGN---VPKGIPRRLFSPNPW------SPGAYDNWTVVK---DMTQVPLLYILGAFIPATMIAVLYYFDHSVASQLAQQKEFNLRKPSFHYDLLL 338
GRMZM2G051753_P01-AtBOR4  Y-LHPGK---VPSGVPRRLSSPLPW------ESSSLGHWTTAR---DLFSVPPAYIFGAILPAFMVAGLYFFDHSVASQLAQQKEYNLKKPSAYHYDILV 338
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                                   410       420       430       440       450       460       470       480       490       500
                          ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
AT3G06450.1-AtBOR3        LGFLTILCGLIGIPPSNGVIPQSPMHTKSLATLNHQ-------------------LLRNKLVAAARKCIRNNATIGEVYGSMEEAYQQMQSPLIHQEPS 420
AT3G62270.1-AtBOR2        LGFLTLMCGLLGIPPSNGVIPQSPMHTKSLATLKYQ-------------------LLRNRLVATARKSIKQNASLGQLYGNMQDVYNQMQTPLVYQQP- 417
AT4G32510.1-AtBOR7        LGIMTLICGLLGLPPSNGVIPQSPMHTKSLAVLKKQ-------------------QMRKKMVQKAKECMREKASNSEIYGRMQDVFIEMETSP----KA 414
AT2G47160.1-AtBOR1        LGFLTLMCGLLGVPPSNGVIPQSPMHTKSLATLKYQ-------------------LLRNRLVATARRSIKTNASLGQLYDNMQEAYHHMQTPLVYQQP- 417
AT5G25430.1-AtBOR6        LGIITLICGLLGLPPSNGVLPQAPMHTKSLAVLNRQ-------------------LIRKKMVKKAKECMKMKASKSEIYGRMQSVFIEMETSPP---QD 417
AT1G15460.1-AtBOR4        LGFMTLICGLLGLPPSNGVLPQSPMHTKSLAVLKRQ-------------------LIRKKMVKTAKESIRKRETSSQVYENMQEVFIEMDKSPLAQT-D 422
AT1G74810.1-AtBOR5        LGFMVLICGMLGLPPSNGVLPQSPMHTKSLAVFKRQ-------------------LMRKKMVMTAKESIRQKATSSQVYEDMEQVFIEMDKSPLAET-H 422
Bradi4g04420.1.p-AtBOR2   LGFLTLLCGLIGIPPSNGVLPQSPMHTKSLATLKHQ-------------------ILRNRLVATARQSMRQNASLSQLYGSMQDAYQQIQTPLIYQQQS 418
Bradi2g34110.1.p-AtBOR4   LSFSVLICGLLGIPPSNGVLPQSPMHTRSLAVLRRQ-------------------ALRKKMIQTAKEGMMNNANCSEVYGKMQEVFIEMDDKSNE---- 414
Bradi2g04690.1.p-AtBOR4   LGFMVLLCGLIGIPPSNGVLPQSPMHTRSLAVLKGQ-------------------LMRNKMLQTAKEGMTNRASSLEIYGKMQEVFIQMDREKNT---- 417
Brara.D00064.1.p-AtBOR2   LGFLTLICGLLGIPPSNGVIPQSPMHTKSLATLKYQ-------------------LLRNRLVATARRSIKQNASLGQLYGNMQEAYNQMQTPLVYQQP- 417
Brara.A00544.1.p-AtBOR7   LGIMTLICGLLGLPPSNGVIPQSPMHTKSLAVLKRQ-------------------QMRKKMVQKAKECMKAKASNSEIYGKMQDVFIEMETSPKIPVQA 418
Brara.C03154.1.p-AtBOR3   LGFLTILCGLLGIPPSNGVIPQSPMHTKSLATLKHQ-------------------LLRNKLVAAARKCIRNKATLGEVYGSMEEAYQQMQSPLIHQGAS 420
Brara.F01062.1.p-AtBOR4   LGFMTLICGLLGLPPSNGVLPQSPMHTKSLAVLKRQ-------------------LIRKKMVKTAKESIRKRATSSEVYENMQEVFIEMDKSPIAQT-N 420
Brara.F02740.1.p-AtBOR6   LGIMTLICGLLGLPPSNGVIPQAPMHTKSLAILNRQ-------------------LTRKKMVKSAKEGMKMKASKSEIYGRMQTVFIEMETSSP---QV 416
Brara.B02140.1.p-AtBOR4   LGFMVLVCGLLGLPPSNGVLPQSPMHTKSLAVLKRQ-------------------LIRKKMVMTAKESMRKRASSSQVYENMQEVFIEMDKSPLVQT-N 422
Cre10.g443900.t1.1-AtBOR1 LAAMTLGCGLMGLPPVNGVLPQAPMHTRSLATLGTRGVKGAAGRQPGPAADEDEVERRHSSGVEPAAPTANGNSNSAVNGVVNGAITAAMHFPTAAVEL 457
Cucsa.192570.1-AtBOR2     LGFLTLICGLLGIPPSNGVIPQSPMHTKSLATLKHQ-------------------LLRNKLVETARSSMRKNASLGQLYGSMQQAYQQMQTPLIYQQPS 418
Cucsa.300580.1-AtBOR4     LGFMTLLCGLIGLPPSNGVLPQSPMHTKQLATLRRR-------------------LMRRKMVKSAKESIERKASDSEIYGQMQAVFLEMESNPIQTT-- 416
Cucsa.098470.1-AtBOR2     LGFLVILCGLIGIPPANGVIPQSPMHTKSLATLKHQ-------------------LLRSKLVAAARQSFRKNSNLSQFYQNMQEAYNGMQTPLIYQNPP 418
Eucgr.C02816.1-AtBOR4     LGLLTLLCGLLGLPPSNGVLPQSPMHTKSLAVLNKQ-------------------IIRKRMVQSAKECMKQQATNSEIYGKMQEVFIEMDRTPT----F 414
Eucgr.J03035.1-AtBOR4     LGFLTLLCGLIGLPPSNGVLPQSPMHTKSLAVLKRQ-------------------HIRRKMIESAKESIRRKASNSEIYGKMQDAFFKTESSPVTS--- 415
Eucgr.H04094.1-AtBOR2     LGFLTILCGLLGIPPSNGVIPQSPMHTKSLATLKHQ-------------------LLRNRLVSTARKCMGKNASMGQVYGSMQEAYQQMQTPLFYQAPS 418
Eucgr.C04162.1-AtBOR4     LGLMTLLCGLIGLPPSNGVLPQSPMHTKSLAVLKRQ-------------------LIRKKMVESAKECMKQKASKSEIYGKMQQVFVEMDSTP-----T 413
Eucgr.H00896.1-AtBOR1     LGFLTLMCGLIGVPPANGVIPQSPMHTKSLATLKHQ-------------------LLRNRLVTTARRSIQNNASLGQLYGNMQEAYRQMQTPLVYQGAS 418
Eucgr.B00302.1-AtBOR2     LGFLTILCGLIGIPPSNGVIPQSPMHTKSLATLKHQ-------------------LLRNKLTSTARNSMRRNSNLVQLYRNMQEAYNEMQTPLAYQMPP 418
Glyma.06G181900.1.p-AtBOR2 LGFLTILCGLIGIPPSNGVIPQSPMHTKSLATLKHQ-------------------LLRNKLVSTARKSMRRNVNLSQLYQSMKEAYDEIQTPLVPQMPL 420
Glyma.15G011200.1.p-AtBOR4 LGLTTLLCGLIGLPPSNGVLPQSPMHTKSLAVLKKQ-------------------LIRRKMVKSAKESIRQKASKSEIYGKMQQAYFIEMDSCPDNH--- 415
Glyma.04G184000.1.p-AtBOR2 LGFLTILCGLIGIPPSNGVIPQSPMHTKSLATLKHQ-------------------LLRNKLVSTARKSMRRNVNLSQLYQNMKEAYDEIQTPLVPQMPT 420
Glyma.17G207700.1.p-AtBOR6 LGIMTLICGILGLPPSNGVLPQSPMHTKSLIVLRKQ-------------------LIRKKVVKS----VKQQGSNSELYGKMQVVFVEMDTTPT----- 411
Glyma.04G069500.1.p-AtBOR7 LGIMTLICGILGLPPSNGVLPQSPMHTKSLAVLRRR-------------------MIRKKVVKSAKECIKQRRTNSELYGKMQEVIVEMDTDPT----- 410
Glyma.09G031400.1.p-AtBOR2 LGFMVIICGLIGIPPSNGVIPQSPMHTKSLATLKHQ-------------------LLRNRLVATARSSMKKLESLGQVYGGMQDAYWKMQTPLVHQEPS 418
Glyma.19G219500.1.p-AtBOR2 LGFLTLMCGLIGIPPANGVIPQSPMHTKSLATLKHQ-------------------LLRNKLVVTARKSMGKNASLGQLYGNMLEAYNQMQTPLVYQDPS 418
Glyma.03G222300.1.p-AtBOR2 LGFLTLMCGLIGIPPANGVIPQSPMHTKSLATLKHQ-------------------LLRNKLVVAARKSMGKNASLGQLYGNMQEAYNQMQTPLVYQDSS 418
Gorai.005G135900.1-AtBOR2 LGFLVILCGLIGIPPSNGVIPQSPMHTKSLATLKHQ-------------------LLHNKLVSTARKSISRNSSLSQLYQSMQEAYNEMQTPLVYQLPS 418
Gorai.011G205300.1-AtBOR4 LGIMTLICGLLGLPPSNGVLPQSPMHTKSLAVLKRQ-------------------LIRKKMVQSAKEGISQLASNSEIYGRMQAVFIEMDESPA----P 414
Gorai.005G070200.1-AtBOR1 LGFLTILCGLIGVPPANGVIPQSPMHTKSLATLKHQ-------------------LLRNRIVETARKCMHNNASLGQVYDSMQEAYQQMQSPLVYQEPS 418
Gorai.006G266200.1-AtBOR2 LGFLTILCGLIGIPPANGVIPQSPMHTKSLATLKHQ-------------------LLRNGLVTTARQFIHKNASLGQVYERMQEAYQQMQTPLVYQEPS 418
Gorai.008G137000.1-AtBOR1 LGFLTLLCGLIGVPPANGVIPQSPMHTKSLATLKHQ-------------------LLRNRLVTTARKSISKNASLGQLYGNMQEAYQQMQTPLVYQEPS 418
Gorai.004G146300.1-AtBOR2 LGFLTLLCGLIGIPPANGVIPQSPMHTKSLATLKHQ-------------------LLRNRLVATARKCIRKNASLGQLYGNMQEAYQQMQTPLVYQEPS 418
Gorai.009G010600.1-AtBOR4 LGVMTLICGLLGLPPSNGVLPQSPMHTKSLSVLKKQ-------------------LIRKKMVKSAKEGKLQHASNSEIYGRMQAVFIKMDQSPA----- 412
Medtr2g032690.1-AtBOR1    LGFMVLLCGLLGIPPSNGVIPQSPMHTKSLATLKHQ-------------------LLRNRLIATARNCMRKQQPLGQVYGSMQNAYRQMQTALTHQEPY 418
Medtr7g110000.1-AtBOR2    LGFLTLLCGLIGIPPANGVIPQSPMHTKSLATLKHQ-------------------LLRNRLVITARNSISKNASLGQLYGNMQEVYHQMQTPLIYQDPS 418
Medtr3g077670.1-AtBOR2    LGFLTLLCGLIGIPPSNGVIPQSPMHTKSLATLKHQ-------------------LLRHKLVSTARTSMEKNMNLSQLYESMKEAYDVMQTPLVPQIPP 420
Medtr3g107730.1-AtBOR7    LGIMTLICGLLGLPPSNGVLPQSPMHTKSLAVLRRQ-------------------LIRKRVVKSAKECMEQQSTSSELYGKMQAVFIEMDTAPT----- 410
Medtr0459s0020.1-AtBOR4   LGFMTLLCGLIGLPPSNGVLPQSPMHTKSLAVLKKQ-------------------LIRKKMVKSAKESIGKKASNSEIYGMMQAVFIEMDNDPNNH--- 424
LOC_Os01g08020.1-AtBOR4   LGFMVLLCGLIGIPPSNGVLPQSPMHTRSLAVLKGQ-------------------LLRKKMVQTANEGLMNRASSLEIYGKIQGVFIEMDCEKNT---- 414
LOC_Os05g08430.1-AtBOR5   LSFMVLICGLIGIPPSNGVLPQSPMHTRSLAVLKGQ-------------------LLRKKMVQTAKEGMMNNASSSEVYGKMQEVFIKMDDKSNA---- 415
LOC_Os12g37840.1-AtBOR2   LGFLTLLCGLIGIPPANGVIPQSPMHTKSLATLKHQ-------------------LLRNRLVATARQSMSQNASLSQLYGSMQEAYQQMQTPLIYQQPS 418
Phpat.001G035800.1.p-AtBOR2 LGFTVLLCGLLGLPPSIGVLPQSPMHTRALASLKKE-------------------LVRSKLIKRAKISLAHNPSGEKLQDDLHDGYRQTETPLSS---- 460
ppa002139m-AtBOR2         LGFMVIICGLIGIPPSNGVIPQSPMHTKSLATLKHQ-------------------LLRNRLVATARRCMKNNASLGQVYGSMQQAYQQMQTPLTYQEPS 415
ppa002104m-AtBOR2         LGFLTLMCGLLGIPPSNGVIPQSPMHTKSLATLKHQ-------------------LLRNRLVATARKSMRKNASLGQLYGNMQEAYRQMQTPLIYQEAS 418
ppa002100m-AtBOR2         LGFLVILCGLLGIPPSNGVIPQSPMHTKSLATLKHQ-------------------LLRNKLALTARNSIRKNSSLSQLYQSMQEAYNQMQTPLVYQRPP 418
Potri.002G191000.1-AtBOR2 LGFLTLMCGLIGIPPSNGVIPQSPMHTKSLATLKYQVIY---------PEISQKIKLLRNRLVATARTSLRKNASLGQLYGNMQEAYHQIQTPLMYQQPS 432
Potri.006G249800.1-AtBOR4 LGLMTLICGLLGLPPSNGVLPQSPMHTKSLAVLRRQ-------------------LIRKKMVKRAKECIGRKASNLEIYGSMQAVFLEMDASSP----D 414
Potri.008G100300.1-AtBOR2 LGFMVILCGLIGIPPSNGVIPQSPMHTKSLATLKHQ-------------------ILRNRLVATARKCMGKDASLGQVYDSMQEAYQHMQTPLIYQEPS 415
Potri.015G077600.1-AtBOR2 LGFLVILCGLIGIPPSNGVIPQSPMHTKSLATLKHQ-------------------LLRNKLVSTARKSMGKNSNLGQLYQSMQEAYNEIQTPLVYQLPS 418
Potri.018G031700.1-AtBOR4 LGFMTLICGLLGLPPSNGVLPQSPMHTKSLAVLKRQ-------------------LIRKKMVKSAKECIGQKASNSEIYGRMHAVFLEMDAPSP----D 414
Potri.012G081800.1-AtBOR2 LGFLVILCGLIGIPPSNGVIPQSPMHTKSLATLKHQ-------------------LLRNKLVSTARKSMGKNSNLCQLYRSMQEAYNEMQTPLAYQQPP 418
Potri.001G174500.1-AtBOR4 LGFMTLLCGLIGLPPSNGVLPQSPMHTKSLAVLKRQ-------------------LIRKKMVASAKESIKQKVSNSEIYGNMQAVFIEMDSIPIN---- 414
Potri.003G059700.1-AtBOR4 LSFMTLLCGLIGLPPSNGVLPQSPMHTKSLAVLKRQ-------------------LIRKKMVESAKESIKQKASNSEIYGKMQDVFIEMDSSPIT---- 414
Potri.006G154700.1-AtBOR4 LGVLTLFCGLIGLPPSNGVLPQSPMHTKSLAVLSKQ-------------------LIRKKMVKGAKECMKQNASNSEIYGKMQAVFIEINRTP-----L 414
Phvul.001G053300.1-AtBOR6 LGIMTLICGLLGLPPSNGVLPQSPMHTKSLAVLRTQ-------------------LIRKKVVKSAKDCIKQQGNTTELYGKMQAVLIEMDSEPS----- 409
Phvul.001G215700.1-AtBOR2 LGFLTLMCGLLGIPPANGVIPQSPMHTKSLATLKHQ-------------------LLRNKLVVTARKSMGKNASLGQLYGNMVEAYHQMQTPLIYQDPS 418
Phvul.005G174400.1-AtBOR4 LGLTTLLCGLIGLPPSNGVLPQSPMHTKSLAVLKKQ-------------------LIRRKMVKSAKESINQKASNSEIYGKMQAVFIEMDNCPDNH--- 415
Phvul.009G178000.1-AtBOR2 LGFLTILCGLLGIPPSNGVIPQSPMHTKSLATLKHQ-------------------LLRNKLVSTARKSMRRNVNLSQLYQNMKEAYDEMQTPLVPQMPP 420
Sobic.008G132300.1.p-AtBOR2 LGFLTLMCGLIGIPPSNGVIPQSPMHTKSLATLKHQ-------------------LLRNRLVATARKSMSQNASLSQLYGSMQDAYQQMQTPLVYQQQS 418
Sobic.009G064200.1.p-AtBOR4 LSLTTLLCGLLGIPPSNGVLPQSPMHTRSLAVLKRQ-------------------LLRKKMVQTAKEGMMNNATSSEVYGKMQDVFIKMDHGGDT---- 415
Sobic.003G047900.1.p-AtBOR4 LGIMVLLCGLLGIPPSNGVLPQSPMHTKSLAVLKRQ-------------------LLSKKMVDTAKDSIGRSATTLEIYGKMEEIFIEMDSEQNT---- 414
Solyc06g071500.2.1-AtBOR2 LGFLVIICGLIGIPPSNGVIPQSPMHTKSLATLKHQ-------------------LLRNKLASTAKKNIDKNANLGQLYRSMQEAYNEMQTPLVYQTPS 418
Solyc01g079150.2.1-AtBOR1 LGFLTLMCGLVGIPPSNGVIPQSPMHTKSLATLKHQ-------------------LLRNRLVDTARKSMQKNSSLGQLYGNMQEAYQQMQTPLIYQESS 418
GSVIVT01007733001-AtBOR2  LGFLVILCGLIGIPPSNGVIPQSPMHTKSLATLKHQ-------------------LLRNKLVSTVRKSMRKNANLGQLYSSMQEAYNEMQTPLVYQTPP 418
GSVIVT01015478001-AtBOR4  LGVMTLLCGFLGLPPSNGVLPQSPMHTKSLAVLKRR-------------------LIRRKMVQSAKECIKQQASNTEIYRKMQAVFIEMDMAP-----S 413
GSVIVT01035800001-AtBOR4  LGVMTLLCGLLGFPPSNGVLPQSPMHTKSLAVLKKL-------------------LIRKKMVKSAKECIKEQASNSEMYGRMQAVFIEMDTAPN----D 414
GSVIVT01017647001-AtBOR2  LGFMVILCGLIGIPPANGVIPQSPMHTKSLATLKHQ-------------------LLRNRLVETARKCIRENSSLGQMYESMQEAYQHMQTPLVYQEPS 418
GSVIVT01028186001-AtBOR2  LGFLTIMCGLIGIPPSNGVIPQSPMHTKSLATLKHQ-------------------LLRNRLVATARISMRKNSSLSQLYGNMQEAYQQMQTPLIYQEPS 418
GSVIVT01017223001-AtBOR4  LGFMTLLCGLLGLPPSNGVLPQSPMHTKSLATLKRQ-------------------LIRKKMVKSAKESIKQKAANPEIYSNMQAVFIKMDNTQPTK--- 415
GRMZM2G082203_P01-AtBOR2  LGFLTLMCGLIGIPPSNGVIPQSPMHTKSLATLKHQ-------------------LLRNRLVATARKSMSQNASLSQLYGSMQDAYQQMQTPLVYQQQS 418
GRMZM2G166159_P01-AtBOR2  LGFLTLMCGLIGIPPSNGVIPQSPMHTKSLATLKHQ-------------------ILRNRLVATARKGMSQNASLSQLYGSMQDAYQQMQTPLVYQQQS 418
GRMZM2G051753_P01-AtBOR4  LGFVVLLCGLLGIPPSNGVLPQSPMHTKSLAVLKRQ-------------------LLSKKMVDTAKESIGGSATSLEIYGKMEEVFIKMDSEQNT---- 414
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                                            ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
AT3G06450.1-AtBOR3                R-----IQGLKQSHIQK----AS------------------------------------------------------------------------ 434
AT3G62270.1-AtBOR2                ----QGLKELRESTIQATTFTG------------------------------------------------------------------------- 435
AT4G32510.1-AtBOR7                TSVVKELENLKEAVMKADDGGG------------------------------------------------------------------------- 436
AT2G47160.1-AtBOR1                ----QGLKELKESTIQATTFTG------------------------------------------------------------------------- 435
AT5G25430.1-AtBOR6                NSVATDLKELKEVVMRPDEGGD------------------------------------------------------------------------- 439
AT1G15460.1-AtBOR4                PSVIIELQDLKEAVMKSNDEE-------------------------------------------------------------------------- 443
AT1G74810.1-AtBOR5                TTLINELQDLKEAVMKKSDDD-------------------------------------------------------------------------- 443
Bradi4g04420.1.p-AtBOR2           VK---GLNELKDSTVQLASSMG------------------------------------------------------------------------ 437
Bradi2g34110.1.p-AtBOR4           VSVHKELRDLKDAVIPEGNGAG------------------------------------------------------------------------ 436
Bradi2g04690.1.p-AtBOR4           DSVDKELKSLKDAVLREGDEEG------------------------------------------------------------------------ 439
Brara.D00064.1.p-AtBOR2           ----QGLKELRESTIQATTFTG------------------------------------------------------------------------- 435
Brara.A00544.1.p-AtBOR7           TSVVKELENLKEAVMKADGGGG------------------------------------------------------------------------ 440
Brara.C03154.1.p-AtBOR3           R-----IQGLKQSQMQKG-LGSV----------------------------------------------------------------------- 437
Brara.F01062.1.p-AtBOR4           RTVILELQDLKEAVMKSNEDE------------------------------------------------------------------------- 441
Brara.F02740.1.p-AtBOR6           CSVANDLKDLKEVVMRPDEGGD------------------------------------------------------------------------ 438
Brara.B02140.1.p-AtBOR4           STHIMELQDLKDAVMKKTDEE------------------------------------------------------------------------- 443
Cre10.g443900.t1.1-AtBOR1         AAASARLRPRRHPPAAAPAAVAASGGGGGGVGSVGGVITDVAAGGVRQPSTRVDGPHLGPPPGAALPAALASRPPSHLAQQPSPPAASAAAALRPQRLGS 557
Cucsa.192570.1-AtBOR2             VR---GLNELKETTIQAASSMG------------------------------------------------------------------------ 437
Cucsa.300580.1-AtBOR4             -TVVKELEDLKEAVMKGES--------------------------------------------------------------------------- 434
Cucsa.098470.1-AtBOR2             VAG---LKELKDSTIQLASRTG------------------------------------------------------------------------ 437
Eucgr.C02816.1-AtBOR4             TSTVKELQELKDAVLKADDGGD------------------------------------------------------------------------ 436
Eucgr.J03035.1-AtBOR4             -SVVKELEDLKEAVIQSSK--------------------------------------------------------------------------- 433
Eucgr.H04094.1-AtBOR2             TL---GLKDLKDSTIQMASSMG------------------------------------------------------------------------ 437
Eucgr.C04162.1-AtBOR4             LSVAKELKQLKDAVMGSEDEDN------------------------------------------------------------------------ 435
Eucgr.H00896.1-AtBOR1             SR---GLNELKETTIQAASSMG------------------------------------------------------------------------ 437
Eucgr.B00302.1-AtBOR2             MLG---LKELKDSTIQLASSTG------------------------------------------------------------------------ 437
Glyma.06G181900.1.p-AtBOR2        TLQG--LKELKESTIELASSQG------------------------------------------------------------------------ 440
Glyma.15G011200.1.p-AtBOR4        -LVVKELEDLKEVVLNGED--------------------------------------------------------------------------- 433
Glyma.04G184000.1.p-AtBOR2        TLG---LKELKESTIELASSQG------------------------------------------------------------------------ 439
Glyma.17G207700.1.p-AtBOR6        ---TKELENLKEAVMKSNEKNA------------------------------------------------------------------------ 430
Glyma.04G069500.1.p-AtBOR7        ---VKELENLKEAVMQSDSKDG------------------------------------------------------------------------ 429
Glyma.09G031400.1.p-AtBOR2        SQ---GLKELKESTIQLASSMG------------------------------------------------------------------------ 437
Glyma.19G219500.1.p-AtBOR2        ARA-QGLRELKESTIQAATSMG------------------------------------------------------------------------ 439
Glyma.03G222300.1.p-AtBOR2        ARA-QGLRDLKESTIQAATSMG------------------------------------------------------------------------ 439
Gorai.005G135900.1-AtBOR2         TLG---LKELKESTVQLASSTG------------------------------------------------------------------------ 437
Gorai.011G205300.1-AtBOR4         TSVDKELKNLKEAVMKR-DGRE------------------------------------------------------------------------ 435
Gorai.005G070200.1-AtBOR1         AR---GLKELKESTIQMASTMG------------------------------------------------------------------------ 437
Gorai.006G266200.1-AtBOR2         AR---GLKELKESTIEMASNME------------------------------------------------------------------------ 437
Gorai.008G137000.1-AtBOR1         T---RGLNELKESTVQAATCSG------------------------------------------------------------------------ 437
Gorai.004G146300.1-AtBOR2         A---RGLHELKESTVQAATCTG------------------------------------------------------------------------ 437
Gorai.009G010600.1-AtBOR4         LAVDNELKNLKEAVMRGGDGDD------------------------------------------------------------------------ 434
Medtr2g032690.1-AtBOR1            AP---GLKELKESTIQLASSTG------------------------------------------------------------------------ 437
Medtr7g110000.1-AtBOR2            ARA-QGLKELKETTIQAATSMG------------------------------------------------------------------------ 439
Medtr3g077670.1-AtBOR2            TLG---LKELKESTVALASSHG------------------------------------------------------------------------ 439
Medtr3g107730.1-AtBOR7            ---VKELETLKEAVMKSDTKGC------------------------------------------------------------------------ 429
Medtr0459s0020.1-AtBOR4           -SVVKELEDLKDFVLNGED--------------------------------------------------------------------------- 442
LOC_Os01g08020.1-AtBOR4           DSVDKELKSLKDAMLQEGDKEG------------------------------------------------------------------------ 436
LOC_Os05g08430.1-AtBOR5           KSVRKELKELKDAVIPEGNGAG------------------------------------------------------------------------ 437
LOC_Os12g37840.1-AtBOR2           VK---GLNELKDSTVQMASSMG------------------------------------------------------------------------ 437
Phpat.001G035800.1.p-AtBOR2       ------------PCAPRVN--------------------------------------------------------------------------- 467
ppa002139m-AtBOR2                 AR---GLKELKDSTFQMASSMG------------------------------------------------------------------------ 434
ppa002104m-AtBOR2                 AR---GLNELKESTIQAASSMGN----------------------------------------------------------------------- 438
ppa002100m-AtBOR2                 ALG---LKELKESTVQLASSAG------------------------------------------------------------------------ 437
Potri.002G191000.1-AtBOR2         ----QGLKEFKESTIQAATCTG------------------------------------------------------------------------ 450
Potri.006G249800.1-AtBOR4         VSVHKELEDFKQAVMKAAEGWD------------------------------------------------------------------------ 436
Potri.008G100300.1-AtBOR2         AR---GLKELKESTIQMAASMG------------------------------------------------------------------------ 434
Potri.015G077600.1-AtBOR2         ALG---LKELKESTIQLSSSTG------------------------------------------------------------------------ 437
Potri.018G031700.1-AtBOR4         VSVHKELENLKQAVMKSDDEED------------------------------------------------------------------------ 436
Potri.012G081800.1-AtBOR2         SLG---LKELKESTIQLASSTG------------------------------------------------------------------------ 437
Potri.001G174500.1-AtBOR4         -AVIKELEDLKEAVMKGED--------------------------------------------------------------------------- 432
Potri.003G059700.1-AtBOR4         -TVVRELEDLKEAVMKGEN--------------------------------------------------------------------------- 432
Potri.006G154700.1-AtBOR4         PSAANELKDLKDTAMKDDDGGI------------------------------------------------------------------------ 436
Phvul.001G053300.1-AtBOR6         ---TKTMTNLKEAVMKSSENNG------------------------------------------------------------------------ 428
Phvul.001G215700.1-AtBOR2         ARA-QGLKELKESTIQAATSMG------------------------------------------------------------------------ 439
Phvul.005G174400.1-AtBOR4         -SVVKELEDLKEVVLNGED--------------------------------------------------------------------------- 433
Phvul.009G178000.1-AtBOR2         TLG---LKELKESTIELASSQG------------------------------------------------------------------------ 439
Sobic.008G132300.1.p-AtBOR2       VRR--GLNELKDSTVQLASSMG------------------------------------------------------------------------ 438
Sobic.009G064200.1.p-AtBOR4       VSAHKELKDLKDAIIPEGNGAG------------------------------------------------------------------------ 437
Sobic.003G047900.1.p-AtBOR4       GSVDKELKNFKDAVLQEGNEEG------------------------------------------------------------------------ 436
Solyc06g071500.2.1-AtBOR2         GLG---LKELKETTVQRASSTG------------------------------------------------------------------------ 437
Solyc01g079150.2.1-AtBOR1         AR---GLKELKESTIQLASSMG------------------------------------------------------------------------ 437
GSVIVT01007733001-AtBOR2          ALG---LKELKESTIQLASSTG------------------------------------------------------------------------ 437
GSVIVT01015478001-AtBOR4          LLVTEELKDLKEAIMKGEDGKN------------------------------------------------------------------------ 435
GSVIVT01035800001-AtBOR4          VSVDKELKDLKEAVMNSEDGGD------------------------------------------------------------------------ 436
GSVIVT01017647001-AtBOR2          AL---GLKELKDSTIQLASSMG------------------------------------------------------------------------ 437
GSVIVT01028186001-AtBOR2          AR---GLKELKESTIQLASSMG------------------------------------------------------------------------ 437
GSVIVT01017223001-AtBOR4          -SVVKELEDLKEAVMKGENKQA------------------------------------------------------------------------ 436
GRMZM2G082203_P01-AtBOR2          VRR--GLNELKDSTVQLASSMG------------------------------------------------------------------------ 438
GRMZM2G166159_P01-AtBOR2          VRR--GLNELKDSTVQLASSMG------------------------------------------------------------------------ 438
GRMZM2G051753_P01-AtBOR4          DSVDRELKNFKDAVLQEGDEEG------------------------------------------------------------------------ 436
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                                   610       620       630       640       650       660       670       680       690       700
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AT3G06450.1-AtBOR3        ------------------------------------------------------NADALVDETVFDIETEVE------------------------ 452
AT3G62270.1-AtBOR2        ------------------------------------------------------NLDAPVDETLFDIEKEID------------------------ 453
AT4G32510.1-AtBOR7        -------------------------------------------------------ETKGKKFDFEVHIE------------------------ 450
AT2G47160.1-AtBOR1        ------------------------------------------------------NLNAPVDETLFDIEKEID------------------------ 453
AT5G25430.1-AtBOR6        ---------------------------------------------------------TKG-KFDFDVHIE------------------------ 451
AT1G15460.1-AtBOR4        ------------------------------------------------------RE-GDEESGFDFEKHLD------------------------ 459
AT1G74810.1-AtBOR5        ------------------------------------------------------GD-TGEESGFDFEKHVD------------------------ 459
Bradi4g04420.1.p-AtBOR2   ------------------------------------------------------NIDAPVDETIFDIEKEID------------------------ 455
Bradi2g34110.1.p-AtBOR4   -------------------------------------------------------NVPEVFDFEKHLE------------------------ 449
Bradi2g04690.1.p-AtBOR4   ----------------------------------------------------------KLAGEFDFRKHIE------------------------ 452
Brara.D00064.1.p-AtBOR2   ------------------------------------------------------NLDAPVDETLFDIEKEID------------------------ 453
Brara.A00544.1.p-AtBOR7   -------------------------------------------------------GDTKGKKFDFEVLIE------------------------ 455
Brara.C03154.1.p-AtBOR3   ------------------------------------------------------NADTLVDEAVFDVETEVE------------------------ 455
Brara.F01062.1.p-AtBOR4   ------------------------------------------------------GE-RDEESGFDFEKHLD------------------------ 457
Brara.F02740.1.p-AtBOR6   ---------------------------------------------------------TKG-KFDFDVHIE------------------------ 450
Brara.B02140.1.p-AtBOR4   ------------------------------------------------------GD-SSEEGGFDFEKHLE------------------------ 459
Cre10.g443900.t1.1-AtBOR1 SGSGQGGQGAACAGQAGCRLGWQGAAGEGAEGGDGGAGDAGQPAAAAARRLLNGRTSTEDAAAEQEAYRGEAAVGRGNPAAEMPHGTEGICRGSTSAPP 657
Cucsa.192570.1-AtBOR2     ------------------------------------------------------SFDAPVDETMFDIEKEID------------------------ 455
Cucsa.300580.1-AtBOR4     ------------------------------------------------------KD-ENANVTFDFEKHID------------------------ 450
Cucsa.098470.1-AtBOR2     ------------------------------------------------------YIDAPVDETVFDVDKDID------------------------ 455
Eucgr.C02816.1-AtBOR4     ---------------------------------------------------------G-NTKFDFEKYVD------------------------ 448
Eucgr.J03035.1-AtBOR4     ------------------------------------------------------GD-EE-KASFDFEKQID------------------------ 448
Eucgr.H04094.1-AtBOR2     ------------------------------------------------------RMDAPVDETVFDVEKEID------------------------ 455
Eucgr.C04162.1-AtBOR4     ---------------------------------------------------------V-DGQFEAKHID------------------------ 445
Eucgr.H00896.1-AtBOR1     ------------------------------------------------------NLNAPVDETVFDVDKEID------------------------ 455
Eucgr.B00302.1-AtBOR2     ------------------------------------------------------YIDAPIDETIFDVDKDID------------------------ 455
Glyma.06G181900.1.p-AtBOR2 ------------------------------------------------------YLDAPVDELVFDVNKDVD------------------------ 458
Glyma.15G011200.1.p-AtBOR4 ------------------------------------------------------KG-LNNKSTFDFEKHID------------------------ 449
Glyma.04G184000.1.p-AtBOR2 ------------------------------------------------------YIDAPVDEVVFDVNKDVD------------------------ 457
Glyma.17G207700.1.p-AtBOR6 ---------------------------------------------------------AKENFDFDKHID------------------------ 442
Glyma.04G069500.1.p-AtBOR7 ---------------------------------------------------------AKEKFDFEKHID------------------------ 441
Glyma.09G031400.1.p-AtBOR2 ------------------------------------------------------SINAPVDESVFDIEKEID------------------------ 455
Glyma.19G219500.1.p-AtBOR2 ------------------------------------------------------NVDAPVDETIFDVEKEID------------------------ 457
Glyma.03G222300.1.p-AtBOR2 ------------------------------------------------------NVDAPVDETIFDVEKEID------------------------ 457
Gorai.005G135900.1-AtBOR2 ------------------------------------------------------NIDAPVDETIFDVAKEID------------------------ 455
Gorai.011G205300.1-AtBOR4 ---------------------------------------------------------NGKENFDFEKHID------------------------ 448
Gorai.005G070200.1-AtBOR1 ------------------------------------------------------IIDAPVDETVFDVEKEID------------------------ 455
Gorai.006G266200.1-AtBOR2 ------------------------------------------------------NINAPVDESVFDIEKEIN------------------------ 455
Gorai.008G137000.1-AtBOR1 ------------------------------------------------------NIDAPLDETLFDIEKEID------------------------ 455
Gorai.004G146300.1-AtBOR2 ------------------------------------------------------NIDAPIDETLFDIEKEID------------------------ 455
Gorai.009G010600.1-AtBOR4 ---------------------------------------------------------DAKENFDFEKDID------------------------ 447
Medtr2g032690.1-AtBOR1    ------------------------------------------------------SLNNAVDESIFDIEKEID------------------------ 455
Medtr7g110000.1-AtBOR2    ------------------------------------------------------NVDAPVDETIFDVEKEID------------------------ 457
Medtr3g077670.1-AtBOR2    ------------------------------------------------------YIDAPVDEVVFDVNKDVD------------------------ 457
Medtr3g107730.1-AtBOR7    ---------------------------------------------------------AMEPFDFEKYID------------------------ 441
Medtr0459s0020.1-AtBOR4   ------------------------------------------------------KG-DNNKSTFDLEKHID------------------------ 458
LOC_Os01g08020.1-AtBOR4   ---------------------------------------------------------TLAEEFDFIKHIE------------------------ 449
LOC_Os05g08430.1-AtBOR5   ---------------------------------------------------------RVSEVFDFEKHIE------------------------ 450
LOC_Os12g37840.1-AtBOR2   ------------------------------------------------------NIDAPVDETVFDIEKEID------------------------ 455
Phpat.001G035800.1.p-AtBOR2 ----------------------------------------------------------------FDFEKDVD------------------------ 475
ppa002139m-AtBOR2         ------------------------------------------------------NINAPVDETVFDVEKEID------------------------ 452
ppa002104m-AtBOR2         ------------------------------------------------------YIDAPVDETVFDVEKEID------------------------ 456
ppa002100m-AtBOR2         ------------------------------------------------------YIDAPVDETVFDVDKDID------------------------ 455
Potri.002G191000.1-AtBOR2 ------------------------------------------------------HIDAPVDETVFDIEKEID------------------------ 468
Potri.006G249800.1-AtBOR4 ---------------------------------------------------------D-KNKFDFEKHID------------------------ 448
Potri.008G100300.1-AtBOR2 ------------------------------------------------------NIDAPVDETVFDIEKEID------------------------ 452
Potri.015G077600.1-AtBOR2 ------------------------------------------------------YIDAPVDETVFDVDKDID------------------------ 455
Potri.018G031700.1-AtBOR4 ---------------------------------------------------------A-KKKFDFEKHID------------------------ 448
Potri.012G081800.1-AtBOR2 ------------------------------------------------------YIDAPVDETTFDVHKDID------------------------ 455
Potri.001G174500.1-AtBOR4 ------------------------------------------------------PK-D----TFDFEKHID------------------------ 444
Potri.003G059700.1-AtBOR4 ------------------------------------------------------PK-D----TFDFEKHID------------------------ 444
Potri.006G154700.1-AtBOR4 ---------------------------------------------------------A-YGNFDFEKHID------------------------ 448
Phvul.001G053300.1-AtBOR6 ---------------------------------------------------------ENPKFDFEKHID------------------------ 440
Phvul.001G215700.1-AtBOR2 ------------------------------------------------------NMDAPIDETLFDVEKEID------------------------ 457
Phvul.005G174400.1-AtBOR4 ------------------------------------------------------KG-VDNKSNFDFEKHID------------------------ 449
Phvul.009G178000.1-AtBOR2 ------------------------------------------------------YIDAPVDEVVFDVNKDVD------------------------ 457
Sobic.008G132300.1.p-AtBOR2 ------------------------------------------------------NIDAPVDETVFDIEKEID------------------------ 456
Sobic.009G064200.1.p-AtBOR4 ---------------------------------------------------------TVPEVFDFEKHVD------------------------ 450
Sobic.003G047900.1.p-AtBOR4 ---------------------------------------------------------KLAREFDFRKHIE------------------------ 449
Solyc06g071500.2.1-AtBOR2 ------------------------------------------------------YIDAPVDETVFDVDKDID------------------------ 455
Solyc01g079150.2.1-AtBOR1 ------------------------------------------------------HINAPVDETIFDVEKEID------------------------ 455
GSVIVT01007733001-AtBOR2  ------------------------------------------------------FIDAPVDETVFDVDKDVD------------------------ 455
GSVIVT01015478001-AtBOR4  ---------------------------------------------------------A-DDKFDFEKHID------------------------ 447
GSVIVT01035800001-AtBOR4  ---------------------------------------------------------T-KGKFDFEKHID------------------------ 448
GSVIVT01017647001-AtBOR2  ------------------------------------------------------NMEAPIDETLFDIENEID------------------------ 455
GSVIVT01028186001-AtBOR2  ------------------------------------------------------AIDAPVDETVFDVEKEID------------------------ 455
GSVIVT01017223001-AtBOR4  ------------------------------------------------------NKE-ENATGTFDFEQHID------------------------ 453
GRMZM2G082203_P01-AtBOR2  ------------------------------------------------------NIDAPVDETVFDIEKEID------------------------ 456
GRMZM2G166159_P01-AtBOR2  ------------------------------------------------------NIDAPVDETVFDIEKEID------------------------ 456
GRMZM2G051753_P01-AtBOR4  ---------------------------------------------------------RLAREFDFRKHIE------------------------ 449
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                                   710       720       730       740       750       760       770       780       790       800
                          ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
AT3G06450.1-AtBOR3        ------------------------NILPVEVKEQRVSNFLQAMMVAGCVAAMPLIKKRIPSSVLWGYFAYMAIESLPGNQFWERIVLLFTAPSRR-FKVLE 527
AT3G62270.1-AtBOR2        ------------------------DLLPIEVKEQRVSNLLQAVMVGGCVAAMPLLKMIPTSVLWGYFAFMAIESLPGNQFWERILLLFTAPSRR-FKVLE 528
AT4G32510.1-AtBOR7        ------------------------DHLPVRVNEQRVSNLLQSVLVGLLILAVPVLRMIPTSVLWGYFTYMAVDSLPGNQFWERLQLLFITPGRR-FKVLE 525
AT2G47160.1-AtBOR1        ------------------------DLLPVEVKEQRVSNLLQSTMVGGCVAAMPILKMIPTSVLWGYFAFMAIESLPGNQFWERILLLFTAPSRR-FKVLE 528
AT5G25430.1-AtBOR6        ------------------------ANLPVRVNEQRVSNLLQSVLVGLTLLAVTVIKMIPSSVLWGYFAYMAIDSLPGNQFWERLLLFIPPSRL-FKVLE 526
AT1G15460.1-AtBOR4        ------------------------AYLPVRVNEQRVSNLLQSLLVAGAVLAMPAIKLIPTSILWGYFAYMAIDSLPGNQFFERLTLLFVPTSRR-FKVLE 534
AT1G74810.1-AtBOR5        ------------------------AYLPVRVNEQRVSNLLQSLLVIGAVFALPVIKLIPTSLLWGYFAYMAIDSLPDNQFFERTVLLFVPPTRR-FKVLE 534
Bradi4g04420.1.p-AtBOR2   ------------------------DLLPMEVKEQRLSNLLQAAMVGGCVAAMPLLKKIPTAVLWGYFAFMAIESLPGNQFWERILLLFTAPSRR-YKVLE 530
Bradi2g34110.1.p-AtBOR4   ------------------------AYLPVRVNEQRVSNLLQSLLVAGCVGVMPIIQKIPTSVLWGYFAYMSIDSLPGNQFWERFQLLFVAPQRR-YKVLE 524
Bradi2g04690.1.p-AtBOR4   ------------------------AHLPVRVNEQRLSNLLQSLLVGGCVGAMPVIKMIPTSVLWGYFAYMAIDSLPGNQFWERIKLLFIGSTRR-YKVLE 527
Brara.D00064.1.p-AtBOR2   ------------------------DLLPIEVKEQRVSNLLQALMVGGCVAAMPILKMIPTSVLWGYFAFMAIESLPGNQFWERILLLFTAPSRR-FKVLE 528
Brara.A00544.1.p-AtBOR7   ------------------------DHLPVRVNEQRVSNLLQSILVGLLIFVVPLLRMIPTSVLWGYFTYMAVDSLPGNQFWERLLLLFITPGRR-FKVLE 530
Brara.C03154.1.p-AtBOR3   ------------------------NVLPVEVKEQRLSNFLQAMLVAGCVAAMPLIKRIPSSVLWGYFAYMAIESLPGNQFWERIVLLFTAPSRR-FKVLE 530
Brara.F01062.1.p-AtBOR4   ------------------------AYLPVRVNEQRVSNLLQSLLVAGAVLAMPAIKLMPTSVLWGYFAYMAIDSLPGNQFFERMMLLFVLPSRR-FKVLE 532
Brara.F02740.1.p-AtBOR6   ------------------------ANLPVRVNEQRVSNLLQSVLVGLTLLAVPVIKMIPSSVLWGYFAYMAIDSLPGNQFWERLLLLFIPQSRL-FKVLE 525
Brara.B02140.1.p-AtBOR4   ------------------------AFLPVRVNEQRVSNLLQSLLVAGAVLAIPAIKLIPTSLLWGYFAYMAIDSLPGNQFFERTVLLFVPPSRR-FKVLE 534
Cre10.g443900.t1.1-AtBOR1 SLLPRLQQQQQQQQQPPGVPPARGTALPLCVLEQRLSGLLQSLGVAACLFATPAIRQIPQAALWGYFAFMAVESFQGSQLVDRVLLLLTDPARRPALAAA 757
Cucsa.192570.1-AtBOR2     ------------------------DLLPVEVKEQRVSNLLQAAMVGGCVAAMPVLKMIPTSVLWGYFAFMAIESLPGNQFWERILLLFTAPSRR-YKVLE 530
Cucsa.300580.1-AtBOR4     ------------------------AYLPVRVNEQRLSNLLQSLLVAASVFALPAIKKIPTSVLWGYFAYMAIDSLPGNQFWERILLLFVMPSRR-YKVLE 525
Cucsa.098470.1-AtBOR2     ------------------------DLLPVEVKEQRLSNLLQAVMVGGCVAAMPLLKKIPTSVLWGYFAFMAIESLPGNQFWERILLLFTAPNRR-YKVLE 530
Eucgr.C02816.1-AtBOR4     ------------------------AHLPVRVNEQRMSNLLQSCLVGISVGAIPVIKLIPTSVLWGYFAYMAIDSLPGNQFWERILILFITPGRR-YKVLE 523
Eucgr.J03035.1-AtBOR4     ------------------------AYLPVRVNEQRLSNLLQSVLVAASVGAMPIIKLIPTSVLWGYFAYMAIDSLPGNQFWERMLFLFITPSRR-YRVLE 523
Eucgr.H04094.1-AtBOR2     ------------------------DLLPVEVKEQRISNLLQATMVGGCVAAMPLLKKIPTSVLWGYFAFMAIENLPGNQFWERILLLFTAPSRR-YKVLE 530
Eucgr.C04162.1-AtBOR4     ------------------------AHLPVRVNEQRVSNLLQSLLLGAAILAMPVIKQIPTSVLWGYFAYMAIDSLPGNQFWERILLLFVTPRRR-YKILE 520
Eucgr.H00896.1-AtBOR1     ------------------------DLLPVEVKEQRVSNLLQSMMVGGCVAAMPILKMIPTSVLWGYFAFMAIESLPGNQFWERILLLFTAPSRR-YKVLE 530
Eucgr.B00302.1-AtBOR2     ------------------------DLLPVEVKEQRLSNLLQALMVGGCVAAMPLLKKIPSSVLWGYFAFMAIESLPGNQFWERILLLFTAPSRR-YKVLE 530
Glyma.06G181900.1.p-AtBOR2 ------------------------DLLPVEVKEQRLSNLLQALMVAACVAAMPVLKKIPTSVLWGYFAFMAIESLPGNQFWERILYLFTAPSRR-YKILE 533
Glyma.15G011200.1.p-AtBOR4 ------------------------AYLPVRVKEQRVSNLLQSLLVGASVFAMPAIKKIPTSVLWGYFAYMAIDSLPGNQFWERILLLFVTPSRW-YKILE 524
Glyma.04G184000.1.p-AtBOR2 ------------------------DLLPVEVKEQRLSNLLQALMVAACVAAMPVLKKIPTSVLWGYFAFMAIESLPGNQFWERILYLFTAPSRR-YILLE 532
Glyma.17G207700.1.p-AtBOR6 ------------------------AYLPVRVNEQRMSNLLQSLLIGLSIFSVNIIKMIPTSVLWGYFAYMAIDSLPGNQFWERISLLFIPPSRR-YKILE 517
Glyma.04G069500.1.p-AtBOR7 ------------------------EYLPVRVNEQRMTNLLQSLLVAVSILAMSVIKRIPTSVLWGYFAYMAIDSLPGNQFWERILLLFVTSSRR-YKILE 516
Glyma.09G031400.1.p-AtBOR2 ------------------------DLLPVEVKEQRVSNLLQSLMVGGCVAAMPFLKKIPTSVLWGYFAFMAIENLPGNQFWERILLIFTAPSRR-YKVLE 530
Glyma.19G219500.1.p-AtBOR2 ------------------------DLLPVEVKEQRLSNLLQSTMVGGCVAAMPLLKKIPTSVLWGYFAFMAIESLPGNQFWERILLLFTAPSRR-YKVLE 532
Glyma.03G222300.1.p-AtBOR2 ------------------------DLLPVEVKEQRLSNFLQSIMVGGCVAAMPLLKKIPTSVLWGYFAFMAIESLPGNQFWERILLLFTAPSRR-YKVLE 532
Gorai.005G135900.1-AtBOR2 ------------------------ELLPVEVKEQRFSNLLQALMVGGCVAAMPLLKKIPTSVLWGYFAFMAIESLPGNQFWERILLLFTAPGRR-YKVLE 530
Gorai.011G205300.1-AtBOR4 ------------------------AHLPVRVNEQRMSNLLQSFLVGLSLGALPVVKMIPTSVLWGYFAYMAIDSLPGNQFWERMLLLFITPSRR-YKVLE 523
Gorai.005G070200.1-AtBOR1 ------------------------DLLPIEVKEQRLSNLLQATMVGGCLAAMPFIKKIPTSVLWGYFAFMAIESLPGNQFWERILLLFTAPSRR-YKVLE 530
Gorai.006G266200.1-AtBOR2 ------------------------DLLPIEVKEQRLSNLLQATMVGGCVAAMPLIKKIPTSVLWGYFAFMAIESLPGNQFWERMLLLFTAPSRR-YKVLE 530
Gorai.008G137000.1-AtBOR1 ------------------------DLLPVEVKEQRLSNLLQATMVGGCVAAMPILKMIPTSVLWGYFAFMAIESLPGNQFWERILLLFTAPSRR-YKVLK 530
Gorai.004G146300.1-AtBOR2 ------------------------DLLPVEVKEQRLSNLLQATMVGGCVAAMPILKMIPTSVLWGYFAFMAIESLPGNQFWERILLLFTAPGRR-YKVLE 530
Gorai.009G010600.1-AtBOR4 ------------------------AYLPVRVNEQRVSNLLQSLLVGLSLGALPVIKMIPTSVLWGYFAYMAIDSLPGNQFWERLLLLFITPSRR-YKVFE 522
Medtr2g032690.1-AtBOR1    ------------------------DLLPVEVEEQRVSNLLQSLMVGGCVAAMSVLKMIPTSVLWGYFAFMAIENLPGNQFWERILFIFTATSKR-YKVLE 530
Medtr7g110000.1-AtBOR2    ------------------------DLLPVEVKEQRVSNLLQSVLVGGCVAAMPILKKIPTSVLWGYFAFMAIESLPGNQFWERILLLFTAPSRR-YKVLE 532
Medtr3g077670.1-AtBOR2    ------------------------DLLPVEVKEQRLSNLLQALMVAVCVAAMPVLKKIPTSVLWGYFAFMAIESLPGNQFWERILYLFTAPSRR-YKILE 532
Medtr3g107730.1-AtBOR7    ------------------------TYLPVRVNEQRMTNLLQSLLIGLSIIGISVIKRIPTSVLWGYFAYMAIDSLPGNQFWERILLLFVTPSRR-FKILQ 516
Medtr0459s0020.1-AtBOR4   ------------------------TYLPVRVKEQRVSNLLQSLFVGVAVFAMPAIKMIPTSVLWGYFAYMAIDSLPGNQFWERILLLFVRPSRW-YKLLE 533
LOC_Os01g08020.1-AtBOR4   ------------------------AHLPVRVNEQRLSNLLQSLLVGACVGAMPVIKMIPTSVLWGYFAYMAIDSLPGNQFWERIRLIFIPSSRR-YKVLE 524
LOC_Os05g08430.1-AtBOR5   ------------------------AYLPVRVNEQRVSNLLQSLLIAGCVGVMPIIQKIPTSVLWGYFAYMSIDSVPGNQFWERTQLLFISPQRR-YKLLE 525
LOC_Os12g37840.1-AtBOR2   ------------------------DLLPIEVKEQRLSNLLQATMVGGCVAAMPLLKKIPTSVLWGYFAFMAIESLPGNQFWERILLLFTAPSRR-YKVLE 530
Phpat.001G035800.1.p-AtBOR2 ------------------------PLLPVEVKEQRLSNLLQSLLVAACIGAMPALKKIPSSVLWGYFAYMAIESLPGNQFWGRICLLFSSSAKR-YKALE 550
ppa002139m-AtBOR2         ------------------------DLLPVEVKEQRLSNLLQATFVGGCVAAMPFLKMIPTSVLWGYFAFMAVESLPGNQCWERILLLFTAPSRR-YKVLE 527
ppa002104m-AtBOR2         ------------------------DLLPVEVKEQRLSNLLQAILVGGCVAAMPILKKIPTSVLWGYFAFMAIESLPGNQFWERILLLFTAPSRR-YKVLE 531
ppa002100m-AtBOR2         ------------------------DLLPIEVKEQRLSNLLQALMVGGCVAAMPVLKKIPTSVLWGYFAFMAIESLPGNQFWERILFLFTAPSRR-YKVLE 530
Potri.002G191000.1-AtBOR2 ------------------------DLLPVEVKEQRVSNLLQATMVGGCVAAMPFLKMIPTSVLWGYFAFMAIESLPGNQFWERILLLFTAPSRR-YKVLE 543
Potri.006G249800.1-AtBOR4 ------------------------AYLPVRVNEQRISNLLQSTLVGASMGALPLIKRIPTSVLWGYFAYMAIDSLPGNQFWERMLLLFVTPSRR-YKVLE 523
Potri.008G100300.1-AtBOR2 ------------------------DLLPVEVKEQRLSNLLQAIMVGGCVAAMPFIKKIPTSVLWGYFAFMAIESLPGNQFWERILLLFTAPSRR-YKLLE 527
Potri.015G077600.1-AtBOR2 ------------------------DLLPVEVKEQRLSNLLQALMVGGCVAAMPVLKKIPSSVLWGYFAFMAIESLPGNQFWERILLLFTAPSRR-YKVLE 530
Potri.018G031700.1-AtBOR4 ------------------------AYLPVRVNEQRMSNLIQSILVGVSMGALPLIKRIPTSVLWGYFAYMAIDSLPGNQFWERMLLLFITPSRR-YKVLE 523
Potri.012G081800.1-AtBOR2 ------------------------DLLPVEVKEQRLSNLLQSLMVGGCVAAMPILKKIPTSVLWGYFAFMAIESLPGNQFWERILLLFTAPSRR-YKVLE 530
Potri.001G174500.1-AtBOR4 ------------------------AYLPVRVNEQRVSNFLQSLLVAASVGAMPAIKLIPTSVLWGYFAYMAIDSLPGNQFWERMLLLFIAPGRR-YKVLE 519
Potri.003G059700.1-AtBOR4 ------------------------AYLPVRVNEQRVSNFLQSLLVAASVSAVPAIKLIPTSVLWGYFAYMAIDSLPGNQFWERMLLLFVTPGRR-YKVLE 519
Potri.006G154700.1-AtBOR4 ------------------------AHLPVQVNEQRFSNLLQSLLVGVSLLAMPIIKKIPTSVLWGYFAYMAIDSLPGNQFWERILLLFVTPSRC-HKILE 523
Phvul.001G053300.1-AtBOR6 ------------------------AYIPVRVNEQRVSNLLQSLLIGLSIFSISVIKTIPTSVLWGYFAYMAIDSLPGNQFYERILLLFVSQSRR-KKILE 515
Phvul.001G215700.1-AtBOR2 ------------------------DLLPVEVKEQRLSNFLQAIMVGGCVAAMPVLKKIPTSVLWGYFAFMAIESLPGNQFWERILLLFTAPSRR-YKVLE 532
Phvul.005G174400.1-AtBOR4 ------------------------AYLPVRVKEQRVSNLLQSILIGASIFGMPVIKQIPTSVLWGYFAYMAIDSLPGNQFWERILLLFVRPSRW-YKLLE 524
Phvul.009G178000.1-AtBOR2 ------------------------DLLPVEVKEQRLSNLLQALMVAACVAAMPLLKKIPTSVLWGYFAFMAIESLPGNQFWERILYLFTAPSRR-YKVLE 532
Sobic.008G132300.1.p-AtBOR2 ------------------------DLLPIEVKEQRLSNLLQASMVGGCVAAMPLLKKIPTSVLWGYFAFMAIESLPGNQFWERIKLLFTAPSRR-YKVLE 531
Sobic.009G064200.1.p-AtBOR4 ------------------------AYLPVRVNEQRVSNLLQSLLIAGCIGITPLIQRIPTSVLWGYFAYMSIDSLPGNQFWERIKLLFITPQRR-YKVLE 525
Sobic.003G047900.1.p-AtBOR4 ------------------------AHLPVRVNEQRLSNLLQSILVGGCVGAMPVIRMIPTSVLWGYFAYMAIDSLPGNQFWERIQLLFVAESRL-YKVLE 524
Solyc06g071500.2.1-AtBOR2 ------------------------ELLPVEVKEQRLSNLLQALMVGACVAAMPILKRIPSSVLWGYFAFMAIESLPGNQFWERILLLFTAPSRR-YKVLE 530
Solyc01g079150.2.1-AtBOR1 ------------------------DLLPVEVKEQRVSNLLQATMVGGCVAAMPVLRMIPTSVLWGYFAYMAIESLPGNQFWERILLLFTAPSRR-YKVLE 530
GSVIVT01007733001-AtBOR2  ------------------------DLLPVEVKEQRLSNLLQAMMVGACVAAMPVLKKIPTSVLWGYFAFMAIESLPGNQFWERILLLFTAPSRR-YKVLE 530
GSVIVT01015478001-AtBOR4  ------------------------DYLPVRVNEQRVSNLLQSILVGASVFSMPIIRRIPTSVLWGYFAYMAIDSLPGNQFWERMLLLFITPARR-YKVLE 522
GSVIVT01035800001-AtBOR4  ------------------------PYLPVRVNEQRVTNLLQSLLVGISVGAIPVIKAIPTSVLWGYFAYMAVDSLPGNQFWERILLLFITPGRR-YKVLE 523
GSVIVT01017647001-AtBOR2  ------------------------DLLPVEVKEQRLSNLLQAIMVGGCVAAMPFLKKIPTSVLWGYFAFMAVESLPGNQFWERILLLFTAPSRR-YKVLE 530
GSVIVT01028186001-AtBOR2  ------------------------DLLPVEVKEQRLSNLLQAAAVGGCVAAMPILKMIPTSVLWGYFAFMAIESLPGNQFWERILLLFTAPSRR-YKVLE 530
GSVIVT01017223001-AtBOR4  ------------------------PYLPVRVNEQRVSNLLQSLLVAAAVFAMPLIKKIPTSVLAGYFAYMAIDSLPGNQFWERFLLVFITPQRL-YKVKE 528
GRMZM2G082203_P01-AtBOR2  ------------------------DLLPIEVKEQRLSNLLQASMVGGCVAAMPLLKKIPTSVLWGYFAFMAIESLPGNQFWERILLLFTAPSRR-YKVLE 531
GRMZM2G166159_P01-AtBOR2  ------------------------DLLPIEVKEQRLSNLLQASMVVGCVAAMPLLKKIPTSVLWGYFAFMAIESLPGNQFWERILLLFTAPSRR-YKVLE 531
GRMZM2G051753_P01-AtBOR4  ------------------------AHLPVRVNEQRLSNLLQSILVGGCVGAMPVIRMIPTSVLWGYFAYMAIDSLPGNQFWERIQLLFITESRR-YKVLE 524
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                                   810       820       830       840       850       860       870       880       890       900
                          ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
AT3G06450.1-AtBOR3        DNHAVFIETVPFKTMAMFTLFQTAYLLVCFG-ITWVPVAGVLFPLMIMFLVPVRQYVLPNLFKQAHLQDLDAAEYEEAPAI------------------ 607
AT3G62270.1-AtBOR2        DNHATFVETVPFKTMAMFTIFQTTYLLTCFG-LTWIPIAGVMFPLLIMFLIPVRQYILPRLFKSAHLQDLDAAEYEEAPA------------------- 607
AT4G32510.1-AtBOR7        GLHASFVEIVPYKSIVMFTLFQLLYFLICYG-VTWIPVGGILFPLPFFILIALRQYILQRLFDRSHLQVLDSSEYEEMVGAPQ---------------- 607
AT2G47160.1-AtBOR1        DYHATFVETVPFKTMAMFTLFQTTYLLICFG-LTWIPIAGVMFPLMIMFLIPVRQYLLPRLFKQAHLQDLDAAEYEEAPA------------------- 607
AT5G25430.1-AtBOR6        GVHASFVELVPYRVIVTFTLFQLVYFLLCYG-MTWIPVAGIFFPALFFLISIREHLLPKLFDNQHLQVLDASDYEEIVAAPI---------------- 608
AT1G15460.1-AtBOR4        GAHASFVEKVPYKSMAAFTLLQIFYFGLCYG-VTWIPVAGIMFPVPFFLLIAIRQYILPKLFNRAHLRELDAAEYEEIPGTPR---------------- 616
AT1G74810.1-AtBOR5        GAHASFVEKVPHKSIAAFTLFQILYFGLCYG-VTWIPVAGIMFPVLFFLLVAIRQYLLPKLFKRAYLRELDAAEYEEIPGTPR---------------- 616
Bradi4g04420.1.p-AtBOR2   EYHTTFVETVPFKTMAMFTLFQTTYLLVCFG-ITWIPIAGVLFPLMIMLVPVRQYILPKLFKQAHLNDLDAAEYEESPA------------------- 609
Bradi2g34110.1.p-AtBOR4   GAHASFLESVPFNKIFAFTLFQLFYLLIVWG-MTWIPVAGILFPLLFFFVLIRQHFLPKLFDSRHLWELDASEYEECEGVRRD---------------- 607
Bradi2g04690.1.p-AtBOR4   GPHASFVESVPSKTISVFTIFQLVYLLICFG-TTWIPIAGILFPVPFFLMILIRQHLLPKLFDRNHLRELDAAEYEELEGVQNE---------------- 610
Brara.D00064.1.p-AtBOR2   DNHATFVETVPFKTMAMFTIFQTTYLLICFG-LTWIPIAGVMFPLMIMFIIPVRQYILPRLFKQAHLQDLDAAEYEEAPA------------------- 607
Brara.A00544.1.p-AtBOR7   GLHASFMEIVPYKSIVMFTLFQLLYFLICYG-VTWIPVGGILFPLPFFFIALRQYILPKLFDRSHLQVLDSSEYEEMVGAT------------------ 611
Brara.C03154.1.p-AtBOR3   DNHAVFETVPFKTMAMFTLFQTGYLLVCFG-ITWVPVAGVLFPLMIMFLVPVRQYVLPNLFKQAHLQDLDAAEYEEAPAL------------------ 610
Brara.F01062.1.p-AtBOR4   GAHASFVEKVPYKSMAAFTILQIVYFGLCYG-VTWIPVAGIMFPVPFFLLIAIRQYILPKLFNRSHLRELDAAEYEEIPGTPR---------------- 614
Brara.F02740.1.p-AtBOR6   GVHASFVELVPYKVIVMFTLFQLVYFLLCYG-MTWVPVAGIFFPALFFLISIREHLLPKLFDRQHLQVLDAADYEEIVAAPI---------------- 607
Brara.B02140.1.p-AtBOR4   GAHASFVEKVPYKSMAAFTMLQIFYFGLCYG-VTWIPVAGIMFPVPFFLLIAIRQYLLPKLFKRAHLRELDASEYEEIPGTPR---------------- 616
Cre10.g443900.t1.1-AtBOR1 GPHAPYLETVPFAVTAAFTGLQVLLLAGVWALVTWAGVAGVAFPLPIMALVPLRAFVLPRLFRREHLRELDAAEYEQVPPAPPPPALPPPALLGSLSPPL 857
Cucsa.192570.1-AtBOR2     DYHATFVETVPFTSIVLFTIFQTVYLFICFG-LTWVPIAGVMFPLMIMLLVPVRQYLLPKLFKQAHLQDLDAAEYEEAPA------------------- 609
Cucsa.300580.1-AtBOR4     GFHASFVESVPFKYIAAFTLFQFVYLLLCFG-VTWIPIAGVLFPLPFFLIGIRHRVLPKLLQRHYLQELDAVEYEEVTGTSV---------------- 607
Cucsa.098470.1-AtBOR2     EYHATFLETVPFKTIATFTLFQTVYLLVCFG-LTWIPIAGVLFPLLIMLLVPVRQYLLPKLFKQAHLQDLDAAEYEEAPA------------------- 609
Eucgr.C02816.1-AtBOR4     GVHASFVESVPFKSIAMFTLFQFVYLLICFG-VTWVPIAGILFPLPFFLIISIRQHILPKLFKRDHLQELDAAEYEEIAATPY---------------- 605
Eucgr.J03035.1-AtBOR4     GVHTSYVESVPSKYIAAFTIFQFVYLLLCFG-VTKIPIAGVLFPLPFFLIISIRQHVLPKLINRHHLRELDAAEYEEVTRTPR---------------- 605
Eucgr.H04094.1-AtBOR2     EYHATFVETVPFKTIVVFTLFQTSYLLVCFG-ITWVPLAGVLFPLMIMALVPVRQYILPKLFKYAHLQDLDAAEYVEAPA------------------ 609
Eucgr.C04162.1-AtBOR4     GAHASFVESVPFKWMAAFTLFQVVYLLVCFG-VTWIPVAGILFPLPFFLIISIREHILPKLFHRHYLHELDAAGYEEIPGNPH---------------- 602
Eucgr.H00896.1-AtBOR1     EYHATFVETVPFKAIVTFTLFQTIYLLICFG-LTWVPIAGVMFPLMIMLLVPVRQYALPKLFKQVHLQDLDAAEFEEAPA------------------ 609
Eucgr.B00302.1-AtBOR2     KYHATFIETVPFKTIAFFTLFQTTYLLICFG-ITWIPIAGVLFPLLIMLLVPVRQYFLPKLFKQAHLQDLDAAEYEEAPA------------------ 609
Glyma.06G181900.1.p-AtBOR2 EYHATFVETVPFKTIAMFTVFQTLYLLLCFG-ITWIPIAGVLFPLLIMLLVPVRQYFLPKLFKQAHLQELDAAAYEEAPA------------------ 612
Glyma.15G011200.1.p-AtBOR4 GDHASFVESVPYKYIVFFTLFQCVYFLVCFG-VTWIPIAGILFPLPFFLITLRQHILPKLFKRHHLRELDAAEYEEIVGAPA---------------- 606
Glyma.04G184000.1.p-AtBOR2 EYHATFVETVPFKTIAMFTVFQTVYLLLCFG-ITWIPIAGVLFPLLIMLLVPVRQYFLPKLFKQAHLQELDAAAYEEAPA------------------ 611
Glyma.17G207700.1.p-AtBOR6 GYHASFVESVPFKTIAVFTILQFVYFLICFG-VTWIPVGGILFPLPFFLITIREHLLPKLFKRNHLQELDASGYEEIVGAPH---------------- 599
Glyma.04G069500.1.p-AtBOR7 GSHASFVETVPFKTIAAFTALQLVYFALCFG-VTWIPIGGILFPVPFFLLIIIREHLLPKLFKRNHLQELDASGYEEIIGAPH---------------- 598
Glyma.09G031400.1.p-AtBOR2 ECHATYVETVPFKTIAVFTAFQTAYLLVCFG-ITWVPIAGVLFPLMIMLLVPVRQYILPKLFKQAHLQDLDAAEYEEVPA------------------ 609
Glyma.19G219500.1.p-AtBOR2 DYHATFVETVPFKTIATFTIFQTIYLLICFG-LTWVPIAGVMFPMMIMLLVPVRQYFLPKLFKQVHLQDLDAAAYEEQTA------------------ 611
Glyma.03G222300.1.p-AtBOR2 DYHATFVETVPFKTIVTFTIFQTIYLLICFG-LTWVPIAGVMFPMMIMLLVPVRQYFLPKLFKQIHLQDLDAAAYEEQTA------------------ 611
Gorai.005G135900.1-AtBOR2 DSHATFVEIVPFKTIATFTLFQTVYLLVCFG-ITWIPIAGVLFPLLIMLLVPVRQYLLPKLFKQAHLQDLDAAEYEEAPA------------------ 609
Gorai.011G205300.1-AtBOR4 GVHASFVESVPFKSILMFTLFQLVYFLLCFG-VTWIPIAGILFPLPFFLIISIRQHILPKLFARFHLRELDAAEYEEILGTPR---------------- 605
Gorai.005G070200.1-AtBOR1 EYHATFVETVPFKTIAVFTIFQTAYLLVCFG-MTWIPLAGVLFPLMIMLLVPVRQYILPKLFKQVHLQDLDAAEYEESPA------------------ 609
Gorai.006G266200.1-AtBOR2 EYHATFVETVPFKTIAMFTIFQTIYLFVCFG-ITWVPVAGVLFPLMIMLLVPVRQYVLPKLFKQAHLQDLDAAEYEESPD------------------ 609
Gorai.008G137000.1-AtBOR1 QKHATFVETVPFKTIAIFTVFQTIYLLICFG-LTWVPIAGVMFPLMIMLLVPVRQYLLPKLFKQAHLYDLDAAEYEEAPA------------------ 609
Gorai.004G146300.1-AtBOR2 QQHATFVETVPFKTIAMFTIFQTAYLLVCFG-LTWIPIAGVMFPLMIMLLVPVRQYVLPKLFKQAHLYDLDAAEYEEAPA------------------ 609
Gorai.009G010600.1-AtBOR4 GAHASFVESVPFKPILMFTLFQFVYLVICFG-VTWIPIAGILFPLPFFLITIREHIFPKLFHYEHLRELDAAEYEEKSGTPR---------------- 604
Medtr2g032690.1-AtBOR1    ECHASYMETIPFKIVAVFTLFQTVYLLVCFG-ITWVPIAGVLFPLMIMLLVPVRQYILPKLFKRAHLQQLDAAEYEEVLT------------------ 609
Medtr7g110000.1-AtBOR2    DYHATFVETVPFKTIALFTIFQTIYLFICFG-LTWVPIAGVMFPLMIMLLVPLRQYFLPKLFKQAHLQDLDAAEYEEQTA------------------ 611
Medtr3g077670.1-AtBOR2    EHHATFVETVPLKAIALFTLFQTAYLLLCFG-ITWIPIAGVLFPLLIMLLVPVRQYFLPTLFKQAHLQELDAAAYEEAPA------------------ 611
Medtr3g107730.1-AtBOR7    DTHASFVETVPFKTIAGFTALQLAYFLFCFG-VTWIPIGGILFPLPFFLIILRERLLPKLFKRNHLQELDASEYEEIIGAPC---------------- 598
Medtr0459s0020.1-AtBOR4   GDHASFVESVPFKHIVLFTLFQCVYFLVCFG-VTWIPIAGMLFPLPFFLITLRQYILPKLFSRNHLMELDAAEYEEIPGAPR---------------- 615
LOC_Os01g08020.1-AtBOR4   GPHASFMESVPSKTITVFTIFQLVYLLICFG-ITWIPIAGILFPLPFFLMILIRQHVLPKLFERNDLRELDAAEYEELEGVHHD---------------- 607
LOC_Os05g08430.1-AtBOR5   GAHASFMESVPIKKISAFTIFQLVYLLIVWG-MTWIPVAGILFPLLFFFIVIRQYILPKLFDRRHLWELDAAEYEELEGVRRD---------------- 608
LOC_Os12g37840.1-AtBOR2   EYHTTFVETVPFKTIAMFTLFQTMYLLVCFG-ITWIPIAGVLFPLMIMLLVPVRQYILPKLFKQAHLTDLDAAEYEESPA------------------ 609
Phpat.001G035800.1.p-AtBOR2 TTHPMFMHTVPFKVTATFTIFQLVYMICCYG-ITWIPIGGVLFPVLIMLIPVRQFVLPRLFKREYLQQLDSAEYEEVAP------------------ 629
ppa002139m-AtBOR2         EYHATFVETVPFKTIAAFTIFQTAYLFVCFG-ITWIPIAGVLFPLMIMFLVPVRQYVLPKLFKQAHLQDLDAAEYEEAPA------------------ 606
ppa002104m-AtBOR2         EYHATFVETVPFKSIGLFTVFQTLYLLVCFG-LTWVPIAGVMFPLMIMLLVPVRQYVLPKLFKQAHLQDLDAAEYEEAPA------------------ 610
ppa002100m-AtBOR2         KYHGTFLETVPFKTIATFTLFQTAYLLVCFG-LTWIPIAGVLFPLLIMLLVPVRQYLLPKLFKRAHLQDLDAAEYEEAPT------------------ 609
Potri.002G191000.1-AtBOR2 DFHATFVETVPFKSIAMFTIFQTAYLLICFG-LTWIPIAGLMFPLMIMLLVPVRQYCLPKLFKQAHLQDLDAAEYEEAPA------------------ 622
Potri.006G249800.1-AtBOR4 GLHASFVELVPFKQIAIFTIFQLVYFLICFG-VTWIPIAGILFPLPFFIIGIRQRILPKLFDRDHLQELDADEYEEMTG--A----------------- 603
Potri.008G100300.1-AtBOR2 EYHTSFVESVPFKTIAIFTIFQTAYLLVCFG-ITWIPIAGVLFPLMIMLLVPVRQYILPKLFKAAHLQDLDAAEYEEIPA------------------ 606
Potri.015G077600.1-AtBOR2 DYHATFIETVPFKTIATFTLFQTSYLLLCFG-LTWIPIAGVLFPLLIMLLVPVRQYVLPKLFKQAHLQDLDAAEYEEAPA------------------ 609
Potri.018G031700.1-AtBOR4 GVHASFVEVVPFKQIAIFTIFQFVYFFICFG-VTWIPIAGILFPLPFFLIGIRQRILPKLFQRNHLQELDADEYEEIAGAPA---------------- 605
Potri.012G081800.1-AtBOR2 EYHATFIETVPFKTIATFTLFQTAYLLLCFG-LTWIPIAGVLFPLLIMLLVPVRQYVLPKLFKQAHRQDLDAAEYEEAPA------------------ 609
Potri.001G174500.1-AtBOR4 GIHASFVESIPFKYIAIFTIFQFVYFLVCFG-VTWIPIAGILFPLPFFIISIRQHVLPKLFRRNHLRELDAAEYEEITGAPR---------------- 601
Potri.003G059700.1-AtBOR4 GVHASFVESVPFKYIAIFTIFQFVYFLFCYG-VTWIPIAGILFPLLFFVLISIRQHILPKLFCRNHLRELDAAEYEEITGTPR---------------- 601
Potri.006G154700.1-AtBOR4 APHASFVENVPFRHISMFTLFQLAYLLICFG-VTWIPVAGILFPLPFFLISIRQHVLPKLFHRFYLHELDAAEYEEIEGAPR---------------- 605
Phvul.001G053300.1-AtBOR6 GPHASFVESVPFKTIAIFTILQCAYFLVCYG-VQLIPIGGILFPLPFFLIFIREHVLPLLFNRADLHELDAAEYEEILGVPN---------------- 597
Phvul.001G215700.1-AtBOR2 DYHATFVETVPFKTIATFTIFQTIYLLVCFG-LTWVPIAGVMFPMMIMLLVPVRQYFLPKLFKQAHLQDLDAAAYEEQTA------------------ 611
Phvul.005G174400.1-AtBOR4 GDHASFVESVPHKYIVAFTIFQFVYFLVCFG-VTWIPIAGILFPLPFFFITLRQHILPKLFKRHHLRELDAAEYEEIVAAPG---------------- 606
Phvul.009G178000.1-AtBOR2 EYHATFVETVPFKTVAMFTVFQTVYLLLCFG-LTWIPIAGVLFPLLIMLLVPVRQYCLPKLFKQVHLQELDAAAYEEAPA------------------ 611
Sobic.008G132300.1.p-AtBOR2 EYHTTFVETVPFKTIAMFTLFQTMYLLVCFG-ITWIPIAGVLFPLMIMLLVPVRQYILPKLFKQAHLTDLDAAEYEESPA------------------ 610
Sobic.009G064200.1.p-AtBOR4 GAHASFMESVPFNTICAFTAFQLIYLLIVFG-MTWIPVAGILFPLLFFFLIVIRQHLIPKLFDRSHLRELDAAEYEELEGFTPD---------------- 608
Sobic.003G047900.1.p-AtBOR4 GPHASFVESVVPKTITIFTIFQLVYLLICFG-ITWIPIAGILFPVPFFLMILIRQYLLPKLFDRIVLRELDAAEYEELDGIALE---------------- 607
Solyc06g071500.2.1-AtBOR2 DNHATFVETVPFKTIAWFTLFQTFYLLLCFG-ITWIPIAGVLFPLLIMLLVPVRQYLLPKLFKQAHLQDLDAAEYEEAPA------------------ 609
Solyc01g079150.2.1-AtBOR1 DYHATFVETVPFKSIVAFTIFQTLYLLACFG-ITWVPIAGVLFPLLIMLLVPVRQYILPRLFKQAHLQDLDAADYEESPA------------------ 609
GSVIVT01007733001-AtBOR2  ECHATFVETVPFKAIATFTLFQTVYLLVCFG-ITWIPIAGVLFPMMIMLLVPVRQYLLPKLFKQVHLQELDAAEYEEAPA------------------ 609
GSVIVT01015478001-AtBOR4  GVHASFVESVPFKYIFMFTLFQFVYLLLVCFG-VTWIPIAGILFPLPFFLIIIRQHVLPKLFHRHDLQELDAAEYEEIAGVWS---------------- 604
GSVIVT01035800001-AtBOR4  GVHASFVETVPFKYIATFTLFQLVYLMICFG-ITWIPIAGILFPVPFFLISIRQYILPKLFQTQHLRELDAAEYEEIAGAPQ---------------- 605
GSVIVT01017647001-AtBOR2  DYHATFVETVPFKTIAMFTIFQTAYLLVCFG-ITWVPIAGVLFPLMIMLLVPVRQYILPKLFKQAHLQDLDAAEYEEVPA------------------ 609
GSVIVT01028186001-AtBOR2  EYHATFVETVPFKSIATFTIFQTAYLLICFG-ITWVPIAGLLFPLMIMLLVPVRQYFLPKLFKQAHLQDLDAAEYEEAPA------------------ 609
GSVIVT01017223001-AtBOR4  GVHASFVDMVPFKSITMFTLFQLAYFMLCFG-VTWIPIAGILFPLPFFIIGIRQYILPKLFDSHLRELDAAEYEEVAVALTG---------------- 611
GRMZM2G082203_P01-AtBOR2  EYHTTFVETVPFKTIAMFTMFQTAYLLVCFG-ITWIPIAGVLFPLMIMLLVPVRQYILPKLFKQAHLTDLDAAEYEESPA------------------ 610
GRMZM2G166159_P01-AtBOR2  EYHTTFVETVPFKTIAMFTVFQTAYLLVCFG-ITWIPIAGVLFPLMIMLLVPVRQYILPKLFKQAHLTDLDAAEYEESPA------------------ 610
GRMZM2G051753_P01-AtBOR4  GPHASFVESVVPKTVTIFTIFQLVYLLICFG-ITWIPIAGILFPVPFFLMIVIRQYLLPKLFDRVVLRELDAAEYEELDGVPLE---------------- 607
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                                          910       920       930       940       950       960       970       980       990      1000
                                  ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
AT3G06450.1-AtBOR3                ------------------------------------------LSFNLKP-EGEV----------SRATSFADSGEVMDGMFTRSRGEIRKVS-SLKL 650
AT3G62270.1-AtBOR2                ------------------------------------------LPFHLAVPEAEM----------GSTASYPCDSEILDEFITRSRGEFRHTC-SPKV 651
AT4G32510.1-AtBOR7                ------------------------------------------RNSSFGFNGELREAHNIPLSVVENSEDEFYDAEILDEITT-SRGELKHRTLSVK- 660
AT2G47160.1-AtBOR1                ------------------------------------------LPFNLAA-ETEI----------GSTTSYPGDLEILDEVMTRSRGEFRHTS-SPKV 650
AT5G25430.1-AtBOR6                ------------------------------------------QHSSFAYRKLG---SSHHLSEGE---DEFYDAEILDEMTT-SRGEIRIRTISFK- 655
AT1G15460.1-AtBOR4                ------------------------------------------NPLELSFRSNDSK-----------RGVQEGDAEILDELTT-SRGELKVRTLNLN- 658
AT1G74810.1-AtBOR5                ------------------------------------------NPLELSFRSNNSA-----------RGVQECDAEILDELTT-SRGELKVRTLGHN- 658
Bradi4g04420.1.p-AtBOR2           ------------------------------------------IPFNLATQDIDV----------ALGRTQ--SAEILDMVTRSRGEIKRLN-SPKI 651
Bradi2g34110.1.p-AtBOR4           ------------------------------------------PSISEADNESI---------AHGGEAPPEYAHDILEEFTT-HRGELKHRAPSFR- 651
Bradi2g04690.1.p-AtBOR4           ------------------------------------------H--TLEEDGSI---------SGSCDSRND--AEILDELTT-NRGELKHRSVSHR- 650
Brara.D00064.1.p-AtBOR2           ------------------------------------------LPFNLAVAEDEM----------GSTASYPCDSEILDEVMTRSRGEFRHTC-SPKV 651
Brara.A00544.1.p-AtBOR7           ------------------------------------------HSSFGINGEP---HNLPMSSVEISEDDFYDAEILDEITT-SRGELKHRTLSAR- 660
Brara.C03154.1.p-AtBOR3           ------------------------------------------LSFNLKP-EGEV----------SRATSFADSGEVMDGMFTRSRGEIRRVN-SIKL 653
Brara.F01062.1.p-AtBOR4           ------------------------------------------DPLELSFRATDTT-----------KGVPENDAEIFDELTT-RRGELKVRTLSLN- 656
Brara.F02740.1.p-AtBOR6           ------------------------------------------QHSSFAYRKLG---SSRHLSEGEE-EDEFHDAEILDEMTT-SRGEIRIRTISLK- 656
Brara.B02140.1.p-AtBOR4           ------------------------------------------NPLELSFRSTGSM-----------KDVLECDAEILDELTT-SRGELRVRPASLS- 658
Cre10.g443900.t1.1-AtBOR1         SPLGSTASAPGRPGAAAELGQPTDEVPGLGGLLAGGGGAPLSPTGGAAAMVAAGTQPAVEVEAGEGAGAGAGAGGGLEPLVAVVVSGSGSGRGRQLQPHT 957
Cucsa.192570.1-AtBOR2             ------------------------------------------LPFNLAT-EAEL----------GAGASFGGDGEILDEVITRSRGEFRRIS-SPKI 652
Cucsa.300580.1-AtBOR4             ------------------------------------------LSLSLSLKEKNS-----THIVDSEDEVKICDAEILDELTT-HRGELKVRTKSFN- 655
Cucsa.098470.1-AtBOR2             ------------------------------------------IAFNPSFEDR-----------MGRTPNIDDGEILDEMITRSRGEIRRTP-SSKV 651
Eucgr.C02816.1-AtBOR4             ------------------------------------------RSRSLSFKDIR----PSDSGDEE-SEEDFNDAEILDEMTT-SRGELKLRTVSFK- 653
Eucgr.J03035.1-AtBOR4             ------------------------------------------LSHSLSLQEREIP-----HFVSVEDEDERTDAEIFDELTT-NRGELKVRTVSFT- 653
Eucgr.H04094.1-AtBOR2             ------------------------------------------VSFHLSP-ERRL----------SRATSFADDGEVLDSMITRSRGEIRRTG-SSKA 652
Eucgr.C04162.1-AtBOR4             ------------------------------------------GRHGVSLTQGV----DREYSVEENEEMDISDSEVLDEITT-SRGELKLRSVSF-- 650
Eucgr.H00896.1-AtBOR1             ------------------------------------------LPFNLAT-ETEI----------GAGASYGGGGEILDEVITRSRGEVRHLS-SPKI 652
Eucgr.B00302.1-AtBOR2             ------------------------------------------IPFNMPLEDQEI----------PTRSTDINSGEILDEMITRSRGEVRRTH-SPKI 653
Glyma.06G181900.1.p-AtBOR2        ------------------------------------------IAFNMSFEGPSN----------QAPTVNISGGEILDEVITRSRGEFRHTQ-SPKT 656
Glyma.15G011200.1.p-AtBOR4        ------------------------------------------LSFNKSFREVESP---------LVGSKEIGNAEILDELTT-NRGELKVRTVSFG- 650
Glyma.04G184000.1.p-AtBOR2        ------------------------------------------IAFNMSFEGPSS----------QAPTINISGGEILDEVITRSRGEFRRTQ-SPKT 655
Glyma.17G207700.1.p-AtBOR6        ------------------------------------------ITHNIPPREKE----SNDPDSDDMSSEDYYDAEILDKMTT-NRGELKLRTVS--- 646
Glyma.04G069500.1.p-AtBOR7        ------------------------------------------G----SLRDKE----P-DTDTDG-SSEDFYDAEILDEMTT-NRGELKLRTVS--- 639
Glyma.09G031400.1.p-AtBOR2        ------------------------------------------LPFNLVT-EGDL----------SRTASFADDGEVLDGIITRSRGEVRRVC-SPKV 652
Glyma.19G219500.1.p-AtBOR2        ------------------------------------------LPFNLAT-HSEF----------GAGASQVGEGEILDEVITRSRGEFRHTS-SPKI 654
Glyma.03G222300.1.p-AtBOR2        ------------------------------------------LPFNLAT-HSEF----------GAGASQVGEGEILDEVITRSRGEFRHTS-SPKI 654
Gorai.005G135900.1-AtBOR2         ------------------------------------------IAYNMTFEDQER----------QATATNSDGLEILDEIMTRSRGEIRRTQ-SPKV 653
Gorai.011G205300.1-AtBOR4         ------------------------------------------RNLSLSFKGRE----SFVSHNEG-SEDNFSDAEILDEMTT-HRGELKLRTVSFK- 653
Gorai.005G070200.1-AtBOR1         ------------------------------------------VPFSLVT-EGEL----------IRTASFADDGEILDGMFTRSKGEIRRIS-SLKV 652
Gorai.006G266200.1-AtBOR2         ------------------------------------------VPFNLIT-EGEL----------VRTASFADDGEILDGMITRSRGEIRHMC-SPKV 652
Gorai.008G137000.1-AtBOR1         ------------------------------------------LPFNLAT-ETEL----------GHGASYEGEGEIFDEVITRSRGEFRHSS-SPKI 652
Gorai.004G146300.1-AtBOR2         ------------------------------------------LPYNLAT-ETEL----------GQGAAYAGDSEILDEVITRSRGEFRHTC-SPKI 652
Gorai.009G010600.1-AtBOR4         ------------------------------------------RNFDL-IREEQ----STDSRSEG-SEDDFYDAEILDEITT-NRGELKLRSRSTK- 651
Medtr2g032690.1-AtBOR1            ------------------------------------------LQLNLSA-EGEL----------SRTTSFVDDGEILNGIITRSQGEVRQTC-IPKS 652
Medtr7g110000.1-AtBOR2            ------------------------------------------LPFNLAS-QSEF----------GAGASHIGEGEIFDEVITRSRGEFRHTTNSPKI 655
Medtr3g077670.1-AtBOR2            ------------------------------------------IAFNISFDDLSN----------HGTTMNINGGEILDEIITRSRGEIRHTH-SPKA 655
Medtr3g107730.1-AtBOR7            ------------------------------------------AVRSMSLRDRE----PRDSDNDG-SSEDYYDAEILDEMTT-NRGELKLRTVSFND 647
Medtr0459s0020.1-AtBOR4           ------------------------------------------LSFNISYKEVESP---------KVGSKEIGNAEILDELTT-NRGELKVRTIYEL- 659
LOC_Os01g08020.1-AtBOR4           ------------------------------------------H--TLEDGASD---------SESCGSRDD--AEILDELTT-NRGELKHRTFNHR- 647
LOC_Os05g08430.1-AtBOR5           ------------------------------------------P--STDEDASV---------SRCSDASPEYASEILDEFTT-NRGELKHRTKSFR- 650
LOC_Os12g37840.1-AtBOR2           ------------------------------------------IPF-IAAQDIDV----------ALARTQ--SAEILDDIVTRSRGEIKRLN-SPKI 650
Phpat.001G035800.1.p-AtBOR2       ------------------------------------------LPQSLALKEAEAQG--------LSVGSDTSDDASLDHFATAARGEIKHPLPLPLH 676
ppa002139m-AtBOR2                 ------------------------------------------LPFNLAT-EREM----------SRQASFADDVEILDGIVTRSRGEIRHIC-SPRM 649
ppa002104m-AtBOR2                 ------------------------------------------LPFNLAT-EAEL----------GAGASYAGDAEILDEVMTRSRGEFRHVS-SPRI 653
ppa002100m-AtBOR2                 ------------------------------------------IAFNMSFEDQDL----------QSRITNIDGGEILDEIITRSRGEIRHTQ-SPKA 653
Potri.002G191000.1-AtBOR2         ------------------------------------------LPFNLAT-EAEL----------GGGAAYGGDGEILDEVITRSRGEFRHTS-SPKI 665
Potri.006G249800.1-AtBOR4         ------------------------------------------KPRSLSLRERE----PPDVGSDG-GADDFYDAEILDEMTT-NRGELKLRTSSLK- 651
Potri.008G100300.1-AtBOR2         ------------------------------------------LSFSLAT-EAEM----------SRAASFADDGEILDGIITRSRGEIKRMC-SPRV 649
Potri.015G077600.1-AtBOR2         ------------------------------------------VSYNMTFEDQDP----------QARTTNIDDGEILDEIITRSRGEIRRTQ-SPKV 653
Potri.018G031700.1-AtBOR4         ------------------------------------------RSRSLSLMERE----PPDVDSEK-SEDDFYDAEILDEMTT-NRGELKLRTLSFK- 653
Potri.012G081800.1-AtBOR2         ------------------------------------------VSYNMTFEDQDP----------QARNTNIDGVEILDEMITRSRGEIRHTQ-SPKI 653
Potri.001G174500.1-AtBOR4         ------------------------------------------LSLSFSFKAYYSPD--LSCYLLILCKVEMCDAEILDELTT-SRGELKVRTVSFR- 652
Potri.003G059700.1-AtBOR4         ------------------------------------------LSLSLSFKAYYSPD--LSRYLLILWEVEMCDAEIFDELTT-SRGELKVRTVSFS- 652
Potri.006G154700.1-AtBOR4         ------------------------------------------RGGAVSFKE-------RNGSVDG-IDLSLCDSEILDELST-RRGELKLISKSFG- 650
Phvul.001G053300.1-AtBOR6         ------------------------------------------THK--------------NPEDDD---DDDYNAELLDEMTT-HRGELKLRTVT--- 631
Phvul.001G215700.1-AtBOR2         ------------------------------------------LPFNLAT-QSEF----------GGGASHVGEGEILDEVITRSRGEFRHTS-SPKI 654
Phvul.005G174400.1-AtBOR4         ------------------------------------------LTFNRSFREMESP---------GVGSVEIVNAEILDELTT-NRGELKVRTVSFT- 650
Phvul.009G178000.1-AtBOR2         ------------------------------------------IAFNMSFEGPGS----------QAPAVNMSGGEILDEVITRSRGEIRRTQ-SPKT 655
Sobic.008G132300.1.p-AtBOR2       ------------------------------------------IPFSLAAQDIDV----------ALGRTQ--SAEILDDMVTRSRGEIKRLN-SPKI 652
Sobic.009G064200.1.p-AtBOR4       ------------------------------------------P--SVCEDESV---------RSR-DAQPGYASEILEEFTT-HRGELKRRNSSFR- 649
Sobic.003G047900.1.p-AtBOR4       ------------------------------------------H--NLEDEVSE---------VASCPSRPD--AEILDELTT-NRGEVKHRTSSLR- 647
Solyc06g071500.2.1-AtBOR2         ------------------------------------------IAYNMSYGDQDP----------QGRPACIDSGEVLDDMITRSRGEIRRSC-SPRV 653
Solyc01g079150.2.1-AtBOR1         ------------------------------------------VPFNLPM-EGEF----------GSRPSHAENGEILDEMITRSRGEVKRIN-SPKI 652
GSVIVT01007733001-AtBOR2          ------------------------------------------MTFNMSCEDQDP----------QARTTHIDSGEILDEMITRSRGEIRNTQ-SPKV 653
GSVIVT01015478001-AtBOR4          ------------------------------------------HSRTFKFKDLE----PTHSGHKE-GEVEICDAEILDELTT-SRGELKLRSLSCP- 652
GSVIVT01035800001-AtBOR4          ------------------------------------------RSRSISIRERE----EAVPGSQG-TDEDFFDAEILDEMTT-NRGELKLRTVSFN- 653
GSVIVT01017647001-AtBOR2          ------------------------------------------LSFNLTS-EREL----------SRRSSFADHGEVLDGIITRGRGEIRRTC-SLKM 652
GSVIVT01028186001-AtBOR2          ------------------------------------------LPFNLAM-EGEM----------GAGASLAEGGEILDEIITRSRGEIRHMC-SPKI 652
GSVIVT01017223001-AtBOR4          ------------------------------------------HPLGLSSKEVEST-----HSGKAEDGMDLSDGEILDELTT-SRGEVKRRTLSFG- 659
GRMZM2G082203_P01-AtBOR2          ------------------------------------------IPFSLAAQDIDV----------AFGNTQ--SAEILDNMVTRSRGEIKRIN-SPKI 652
GRMZM2G166159_P01-AtBOR2          ------------------------------------------IPFSLAAQDIDV----------ALGRSQ--SAEILDDMVTRSRGEIKRLN-SPKI 652
GRMZM2G051753_P01-AtBOR4          ------------------------------------------H--KLEDEASE---------VGSCPSRPD--AEILDELTT-NRGELKHRSSSLR- 647
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                                        1010      1020      1030      1040      1050      1060      1070      1080
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AT3G06450.1-AtBOR3              GG-GGSGSTVGSPAGGGVELMRRVVSFQNPRVSEKVYIRSLSDFRGGGEISPRSS-AGRAPFSPRSATGGG--GGEQRLSNLGKSV--- 732
AT3G62270.1-AtBOR2              TSST-------------STPVYNRN-------LSQVFSPRVIDLRG--EMSPRLS--GKGQNSPKPS-----PLNPSSSSK-------- 703
AT4G32510.1-AtBOR7              -------------------------------EDRSQ-----MVKIYN--HS------------------------------------ 673
AT2G47160.1-AtBOR1              TSSS-------------STPVNNRS-------LSQVFSPRVSGIRLG-QMSPRVV--G---NSPKPASCGRSPLNQSSSN--------- 704
AT5G25430.1-AtBOR6              -------------------------------EVHPE-----PEEKHVTFEPH----------------------------------- 671
AT1G15460.1-AtBOR4              -------------------------------EDK-----GNQIYPKEKVKAGDGDMSTTRE--------------------------- 683
AT1G74810.1-AtBOR5              -------------------------------EDK-----GHQIYPKEIVEVGDGDMSSSRE--------------------------- 683
Bradi4g04420.1.p-AtBOR2         TSSG-------------GTPVAELKGIRSPCISEKAYSPRVTELRH-----ERSP--LGERDSPRTGETRASKLGEGSAPK-------- 712
Bradi2g34110.1.p-AtBOR4         -------------------------------DERLIRLNSVQMTRQFSRIAS-----LAPERP------------------------- 678
Bradi2g04690.1.p-AtBOR4         -------------------------------EERHLQV-------HSNAVQPSV---------------------------------- 666
Brara.D00064.1.p-AtBOR2         TSST-------------STPVYHRN-------LSQVFSPRVNELRGGGMMSPSLA--GKGHNSPKPS-----PLNPSSSSPSK------ 707
Brara.A00544.1.p-AtBOR7         -------------------------------EGTSH-----MVYPENSGHS------------------------------------ 675
Brara.C03154.1.p-AtBOR3         AGSVGGGSTGGSPAGG-VELMRRVVSFQNPRVSEKVYIRSLSDYRGGGESSPRSP-AGRAPLSPRFAAAGGGAGGEQRLSNLGKSV--- 737
Brara.F01062.1.p-AtBOR4         -------------------------------EDK-----GNQIYPKEKVQAED-ETRVLRDSQ-------------------------- 682
Brara.F02740.1.p-AtBOR6         -------------------------------EPRLE-----SEERRVTFEPH----------------------------------- 672
Brara.B02140.1.p-AtBOR4         -------------------------------PDK-----GHQIYPNEIVEAGDGDISTPRE-------------------------- 683
Cre10.g443900.t1.1-AtBOR1       DVLATAG----------SGDAAGGGATAAAGALDWEAERGLIESEHVGVQPVHHLTRSQLRQRMAAGAPAGVEAGVGATGQHAGG---- 1032
Cucsa.192570.1-AtBOR2           TSST-------------ATPISDRKSID---SPHRSFSPRLSELKG--EHSPRAG--GRGTPGQRSAEAKPSSLGKSPLNNTASK---- 717
Cucsa.300580.1-AtBOR4           -------------------------------EDR----------HNQ-------------------------------------- 661
Cucsa.098470.1-AtBOR2           TSSS-------------PTTLEGIKSIYSPQIPQKLYSPRINELRR--ERSSLSP--GKGLDFKLNGSPSPSEEPGPGPSFRN------ 717
Eucgr.C02816.1-AtBOR4           -------------------------------EEMLI-----RVRSEDASRK------------------------------------ 668
Eucgr.J03035.1-AtBOR4           -------------------------------EDR-----HGHVHPEDTISLE---------------------------------- 669
Eucgr.H04094.1-AtBOR2           TSSC-AT----------PSRELK--GIQ----SPRIYSPRISELR--GDQSPQLS--GRSPSSPRT---RPSNLGKTG----------- 706
Eucgr.C04162.1-AtBOR4           -------------------------------DEKFV-----QVFPEDEEQPRDS----------------------------------- 668
Eucgr.H00896.1-AtBOR1           TSST-------------TTPAHDSKSTLQ--SPRPSFSPRVSELRG--ERSP-YG--GRGPYSPRTGEKQPSHLGKSPSNPASG----- 716
Eucgr.B00302.1-AtBOR2           TSST-------------PSSTDDIKPALSPRMSQRAFSP-------------NFT--GKAVVEKQTHSPGPSSLGKNTYGSSSN----- 709
Glyma.06G181900.1.p-AtBOR2      TSST-------------PTSMGDIRPANSPQLTRRISSPPVTELRG--ESSLRPT--RKEIKLMQTPSPRSPGLGKVTKDSPST----- 723
Glyma.15G011200.1.p-AtBOR4      -------------------------------EER-----NCQVYPDENGSPLTDF-------------------------------- 669
Glyma.04G184000.1.p-AtBOR2      TSST-------------PTSTGDIRPANSPQLARRIPSPRVTELRG--ESSLRPT--GKEIKLMQTPSPRSPGLGKVTKDLP------- 720
Glyma.17G207700.1.p-AtBOR6      -------------------------------RNNSK-----SFSYSSSEDMQH---------------------------------- 663
Glyma.04G069500.1.p-AtBOR7      ---------------------------SFNDRNHS-------FSEDRHTQVYPGNAV------------------------------ 662
Glyma.09G031400.1.p-AtBOR2      MKST-------------PNLSQELTS--PRLTDKVYSPRISHLR--GNQSPRG----VGRGSFSPAEVRPSNLRKGG----------- 708
Glyma.19G219500.1.p-AtBOR2      TSST-------------PTPRTDPKSHL---SPRLSFSARVGEFKT--EQSPRSG--ARGPLSPKAGEVRLSNLGRSPLNPDSKQQDQN 723
Glyma.03G222300.1.p-AtBOR2      TSST-------------PTPRTDTNSHL---SPRLSFSSRMGEFKT--EQSPRSG--ARGPLSPKAGEVRLSHLGRSPLNPDSKQHDHN 723
Gorai.005G135900.1-AtBOR2       SSTT-------------PSSVGDIKPSYSPGVLQNAYSPRISQLR-------GKT--EKVLELKQTPSPGPSTLGQSSRASSSI----- 715
Gorai.011G205300.1-AtBOR4       -------------------------------EERLH-----QVHP----------------------------------------- 662
Gorai.005G070200.1-AtBOR1       TSAT-AT----------PSKEFKGTEIESPCFSEQGYSPRVNELRA-GRRSPRN--VGRGPFSPRTSEVRPSNLGKSG----------- 716
Gorai.006G266200.1-AtBOR2       TSSTGTT----------PSKEFK--SIQSPRFSEKVYSPRISQLR--GELSPGN--AGRGPFSPRANEK-PSNLGKG----------- 712
Gorai.008G137000.1-AtBOR1       TSST-------------STPANYPRSHLSP-CLSS--SPHLGELRG--ERSPRAR--GNEPHSPMT------AIGRSPLNPSPS----- 710
Gorai.004G146300.1-AtBOR2       TSST-------------ATPANGPRSHQSP-RLSCN-SPRLNELKG--ERSPRAS--GNGSHSPRTGELKPSNLGKSPLNRGSN----- 717
Gorai.009G010600.1-AtBOR4       -------------------------------EERLY-----QVHPEEKAELNSSSNRF------------------------------ 673
Medtr2g032690.1-AtBOR1          SKIQ--------------GYQIKYTTFRIPRLPDQVQNPHVNQLR--GNPNIVT----LEVEVLGEDPLGREDKVH------------ 708
Medtr7g110000.1-AtBOR2          SSST-------------PTPRNDPKSRL---SPHLSFNSRVGEFAT--EQSPRSG--VRGTNSPMTKEMRLSGRGISPLNPDSKHQDKK 724
Medtr3g077670.1-AtBOR2          SSST-------------ATPISGIRSANS--LQGTIPSPRVAALRG--ENSLGSN--GKELKSKQTP---------------------- 703
Medtr3g107730.1-AtBOR7          RNRS-----------------------NSFNDRNHSN-----SFNDRNHSNSFNEDRHN----------------------------- 678
Medtr0459s0020.1-AtBOR4         ------------------------------------------------------------------------------------------ 659
LOC_Os01g08020.1-AtBOR4         -------------------------------EERHPQA-------HTKAVQPRCGDTENWSEC------------------------- 672
LOC_Os05g08430.1-AtBOR5         -------------------------------DERLIQLNSVKMTRELSRIPT-----FTPPRS------------------------- 677
LOC_Os12g37840.1-AtBOR2         TSSG-------------GTPVAELKGIRSPCISERAYSPCITELRH-----DRSP--LGGRGSPRTGETRSSKLGEGSTPK-------- 711
Phpat.001G035800.1.p-AtBOR2     -------------------------------NHFGIPTSSTEFNSHSTNTHEDQL------------------------------- 700
ppa002139m-AtBOR2               ASSA-TT----------PSKEFK--SIQSPLFSDKIYSPRLSELR--GEPSPQNGGNGQ--FSPRTGEARSSNLAKSG----------- 710
ppa002104m-AtBOR2               TSST-------------STPGNAPKILG---SPHSSFSPRVNELRG--ERSPRSG--GRGPNSPRTPGS-SSILGKSPSDNTTS----- 716
ppa002100m-AtBOR2               SSLT-------------PTSLEGIKPAHSPRTSQRVYSPHLSELRG--ERSPR-----QGLERTQTPSPGSSILGQTTPGSSS------ 716
Potri.002G191000.1-AtBOR2       SSST-------------TTPANNPKSLQSP-RLSYTYSPRISELRG--QKSPKSS--GRGLNSPRTGDQKLSKLGKSPSSSEQN----- 731
Potri.006G249800.1-AtBOR4       -------------------------------EERLH-----QARNTHLLCP------------------------------------- 666
Potri.008G100300.1-AtBOR2       PSSD-AT----------ASKEFR--SIQSPRFSDKVYSPRVSEVR--GDYSPRLGGTGRGPFSPRIGESRLSNLGKSG----------- 712
Potri.015G077600.1-AtBOR2       TSST-------------PGSVENMKSSYSPRLSQRAYSPRVSEPRV--DRNPRFT--GKGAELKQTPSPGFSNLGQSNPGSSSC----- 720
Potri.018G031700.1-AtBOR4       -------------------------------EDRLH-----QVYPHEQG------------------------------------- 666
Potri.012G081800.1-AtBOR2       TSST-------------PGSVEDIKSSYNPCLSQRAYSPRVGELRV--DQSPRFS--GKGVELKQNPSPVPSNLGQSSHASSSC----- 720
Potri.001G174500.1-AtBOR4       -------------------------------EEN-----ATQVCSNGAVQPE----------------------------------- 668
Potri.003G059700.1-AtBOR4       -------------------------------EEKNTLRFIPRVLSNQNETINHLGQD------------------------------ 678
Potri.006G154700.1-AtBOR4       -------------------------------DDKIF-----QVHPGEDSEGGL---------------------------------- 667
Phvul.001G053300.1-AtBOR6       -------------------------------LKKRT-----PVEDPMQQINIYE--------------------------------- 649
Phvul.001G215700.1-AtBOR2       TSST-------------TTPRTDPKSHL---SPRVSFSSRVGELKT--EQSPRSG--ARGSLSPNAGEVRLSNLGRSPLNPDSKQQDHN 723
Phvul.005G174400.1-AtBOR4       -------------------------------EER-----NHQIHPDENGSQAQIVSDGR----------------------------- 673
Phvul.009G178000.1-AtBOR2       TSST-------------PTSTGDIRPANSPRIGKSIPSPRVSELRG--ESSLRPT--GKEIKLIQTPSPHSPALGKVTKGSPSS----- 722
Sobic.008G132300.1.p-AtBOR2     TSSG-------------GTPVAELKGIRSPSISEKAYSPRLTELRH-----ERSP--LGGRNSPRTPS----KLGEGSTPK-------- 709
Sobic.009G064200.1.p-AtBOR4     -------------------------------DGRLLQLNSVRMTRELSRAPSRIELSRAPSRVPRVMEQ------------------- 687
Sobic.003G047900.1.p-AtBOR4     -------------------------------EERPIQV-------ATNAVQPSL--------------------------------- 663
Solyc06g071500.2.1-AtBOR2       TSST-------------PTSLDEIKSTHSPQLSQRAYSPRINVLRG--ERSPRFN--GKGLEIKQTPSPQPSKLGQNDRGPSSI----- 720
Solyc01g079150.2.1-AtBOR1       TSST-------------ATPIRDTKLLQSPRISEKAYSPQINKLRG--QQSPLSG--GRGTFSPRTGEPKPSNLGTSPRTSTPND---- 720
GSVIVT01007733001-AtBOR2        TSSS-------------PASLGDMKPAYSPRLSQRAYSPRLSELRA--EQSPRFT--GKGVELKETPSPRPSILGKSPHGSSSS----- 720
GSVIVT01015478001-AtBOR4        -------------------------------ADWIS-----QVHPKKDEEHNDRDTNEA--------------------------- 675
GSVIVT01035800001-AtBOR4        -------------------------------EDRFF-----QVHP----EDTSRTQ------------------------------- 669
GSVIVT01017647001-AtBOR2        TSST-AM----------PSKDFK--STKS--FSDRVCSPRITELR--GIRSPRFG--GRGPFSPRTGEARQSNLGKSGQNSDIN----- 717
GSVIVT01028186001-AtBOR2        TSST-------------ATPTKDPRNFQSPRLSEKAYSPRVSELRG--EHSPQSS--GRGKYSPKTGEVKPSNLGKSPHSSN------- 717
GSVIVT01017223001-AtBOR4        -------------------------------EEK---------HAQERY------------------------------------- 668
GRMZM2G082203_P01-AtBOR2        TSSG-------------GTPVAELKGIRSPSISEKAYSPRVIELWH-----ERS----------PRTPS----MLGEGSTPK-------- 702
GRMZM2G166159_P01-AtBOR2        TSSG-------------GTPVAELKGIRSPSISEKAYSPRLTELQH-----ERSP--LGGRSRPRTPS----KLGEGSAPK-------- 709
GRMZM2G051753_P01-AtBOR4        -------------------------------EERPIQVTVSTHMVASSAVQPSL--------------------------------- 670
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Figure S1 Sequence alignment of BOR1 homologs in 18 plant species. Tyrosine-based motifs were specified with red frame. Acidic di-leucine motif was specified with green frame. Lysine residue was specified with blue frame.