

gi|85104848 1 -----MPSQA--V-----TYTTAA-VAAMAHG-FLAYAVYEDYKRRNDPEFR 38RQLRRSARRQ-----AHOEKEYAELLSQQAQRORI
YGR181W 1 MGLSSIEGGGAPSSQOKEAATTAKTTPNPIAKKKNQACELAVANATBLV-NKISENCFE 59KCLTSPSYA--TRNDAGTDQCLAKVMRSWNVLVSKAVI
gi|17506427 1 -----MDQLLDVETL-----KKLSPSEQQEQVVISGVKQQAALANAQNLV-TDISEKCFN 47KCTAPGSSSIASGKOCLOKCMDFMESWNLVSGTHQ
gi|85109802 1 -----M-----SDSTSETVKKALIKQVLESSANARTLM-EKIGENCF 39SCKVFKPGSSISNKGKQVQCTEKYMAWNVVNTTYL
CMB148C 1 -----MDKIDOLTPS-----QRAPMEDVRNEMLEKROAFODLV-ORVTEKCFE 41KCVTKPSATLTSGEORCLAKCVDRYESMGVVSKAMI
Vocar20012438m 1 -----MDFSGGA--GY-----CAPGGKVDSDTMMBOVKSOIQMOMVOEYF-OLVVRDKCFK 46VCLSNPGSSISNDORCLNRCMDRYODANVTKVVL
g15745.t1 1 -----MDFSGGL--P-----CAPGGKMDHAILMDOVKSOIQMOMVOEYF-OLVVRDKCFK 45ACLSNPGSSISNDORCLNRCMDRYODANVTKVVL
gi|11024700 1 -----MEGFGGSD--FG-----GSSGSKLDGLLMMOVKVOIAVANAQELF-QRMTDKCFR 48KCTKPGSSISNKGKQVQCTEKYMAWNVVNTTYL
Phpat.025G038900 1 -----MDFSPS--SPPP-----SSGLGVSNVMMGQVQOLAQAYAEEFL-ETVVRDKCFR 47KCVTKPSATLTSGEORCLAKCVDRYESMGVVSKAMI
Bra015863|Bra015863 1 -----MDFSSSPPM-----GGGSPSEALMBQVQOLAQAYAEEFL-ETVVRDKCFD 45KCVTKPSATLTSGEORCLAKCVDRYESMGVVSKAMI
Bra003766 1 -----MDFSSSPPM-----GASPSPEALMBQVQOLAQAYAEEFL-ETVVRDKCFD 46KCTKPGSSISNKGKQVQCTEKYMAWNVVNTTYL
Carubv10021223 1 -----MDFSSSPPM-----GGA--SPSEALMBQVQOLAQAYAEEFL-ETVVRDKCFD 45KCTKPGSSISNKGKQVQCTEKYMAWNVVNTTYL
AT1G61570 1 -----MDFSSSPPM-----GSSGSKLSDVPMBSVKTOLAQAYAEEFL-ETVVRDKCFD 47KCVTKPSATLTSGEORCLAKCVDRYESMGVVSKAMI
228905|228905 1 -----MD--FS-----SP--SSSDVMMDDOLKNOAQAAYAEEFL-ETVVRDKCFD 40KCVTKPSATLTSGEORCLAKCVDRYESMGVVSKAMI
GRMZM2G058432 1 -----MDFSSSPP--SS-----SG--FGANEDVMMBOVKSOIQMOMVOEYF-OLVVRDKCFE 46KCVTKPSATLTSGEORCLAKCVDRYESMGVVSKAMI
LOC_Os02g45820 1 -----MDFSSS--SS-----SG--SPPNTEALMDOLKNOAQAAYAEEFL-ETVVRDKCFD 43KCVTKPSATLTSGEORCLAKCVDRYESMGVVSKAMI
Cucsa.193350 1 -----MDFSSSPPS-----GSSPOFSANBFRDOLKNOAQAAYAEEFL-ETVVRDKCFD 46KCTKPGSSISNKGKQVQCTEKYMAWNVVNTTYL
PGSC0003DMG400012109 1 -----MDFSSSPPF-----GASSOFTSDMDOLKNOAQAAYAEEFL-ETVVRDKCFD 46KCTKPGSSISNKGKQVQCTEKYMAWNVVNTTYL
30068.t000104 1 -----MDFSSSPPS-----GGSPOFSANBFRDOLKNOAQAAYAEEFL-ETVVRDKCFD 47KCTKPGSSISNKGKQVQCTEKYMAWNVVNTTYL
Potri.001G452100 1 -----MDFSSSPPS-----GSSGPOISAEDFKDOLKNOAQAAYAEEFL-ETVVRDKCFD 48KCTKPGSSISNKGKQVQCTEKYMAWNVVNTTYL
Potri.011G149800 1 -----MDFSSSPPS-----GSSGPOISAEDFKDOLKNOAQAAYAEEFL-ETVVRDKCFE 48KCTKPGSSISNKGKQVQCTEKYMAWNVVNTTYL
Eucgr.L00349 1 -----MDFSSSPPS-----GSSSOFSTEDFDOLKNOAQAAYAEEFL-ETVVRDKCFE 47KCTKPGSSISNKGKQVQCTEKYMAWNVVNTTYL
GSVIVG01019698001 1 -----MDFSSSPPS-----GSSSOFSTEDFDOLKNOAQAAYAEEFL-ETVVRDKCFE 48KCTKPGSSISNKGKQVQCTEKYMAWNVVNTTYL
Medtr3g080670 1 -----MDFSSSPPF-----RPSOLSPODMDOLKNOAQAAYAEEFL-ETVVRDKCFD 46KCTKPGSSISNKGKQVQCTEKYMAWNVVNTTYL
Glyma08g48290 1 -----MDFSSNOS--R-----GSSOLSPODMDOLKNOAQAAYAEEFL-ETVVRDKCFE 46KCVTKPSATLTSGEORCLAKCVDRYESMGVVSKAMI
Glyma13g10250 1 -----MDFSSNFS--S-----GSSHOLSADHDKKNOAQAAYAEEFL-ETVVRDKCFE 46KCVTKPSATLTSGEORCLAKCVDRYESMGVVSKAMI

gi|85104848 68 ROMVDEAKEE-GFPTTSDEKEY 89FLE-----QVQAGEILGQDPTKAIIDASLAFYKALK----- 119-----
YGR181W 94 SRITONASASGEI* 105----- 105-----
gi|17506427 85 KRLOEEMASSGGMGGGGQGPS- 106FS----- 108-----
gi|85109802 77 RRKQEQEMGNQ- 86----- 86-----
CMB148C 79 EQQRS- 84----- 84-----
Vocar20012438m 84 NO* 85----- 85-----
g15745.t1 83 NO* 84----- 84-----
gi|11024700 86 SFLQERANM- 95----- 95-----
Phpat.025G038900 85 SSNPR* 89----- 89-----
Bra015863|Bra015863 83 SVLTKMFRKRTTSQAEQENNEA 105LREAKIKEVKTLLIGELSGRSSLYCSDPCLKRYLEARNWNVGKAKKMLEETLKRSTFFKE 165EIRWDEVSG
Bra003766 82 -----FSQORH* 86----- 88-----
Carubv10021223 84 -----FTQR- 87----- 86-----
AT1G61570 77 -----FNATK* 81----- 87-----
228905|228905 83 -----FISQR* 87----- 81-----
GRMZM2G058432 80 -----FSSST* 84----- 87-----
LOC_Os02g45820 83 -----FKTPH* 87----- 84-----
Cucsa.193350 83 -----FSQR* 86----- 87-----
PGSC0003DMG400012109 84 -----FNAPH- 88----- 86-----
30068.t000104 85 -----FNAPH* 89----- 88-----
Potri.001G452100 85 -----FSAPF* 89----- 89-----
Potri.011G149800 84 -----FSAPF* 88----- 89-----
Eucgr.L00349 85 -----FSAPF* 89----- 88-----
GSVIVG01019698001 83 -----FSSQO* 87----- 89-----
Medtr3g080670 83 -----FSSQO* 86----- 87-----
Glyma08g48290 61 ----- 60----- 86-----
Glyma13g10250 61 ----- 60----- 60-----

gi|85104848 120 ----- 119----- VYPTPGDLIS
YGR181W 106 ----- 105-----
gi|17506427 109 ----- 108-----
gi|85109802 87 ----- 86-----
CMB148C 85 ----- 84-----
Vocar20012438m 86 ----- 85-----
g15745.t1 85 ----- 84-----
gi|11024700 96 ----- 95-----
Phpat.025G038900 90 ----- 89-----
Bra015863|Bra015863 175 EGETGKVYKAGPHDRSGRTVLILRPLGLQNTKSLNQMHLVYLIENAIMNL 225PEDQEQMSWLIDFTDWSLSTSVPIKSARETINILQNHYPRLAVA
Bra003766 89 ----- 88-----
Carubv10021223 87 ----- 86-----
AT1G61570 88 ----- 87-----
228905|228905 82 ----- 81-----
GRMZM2G058432 88 ----- 87-----
LOC_Os02g45820 85 ----- 84-----
Cucsa.193350 88 ----- 87-----
PGSC0003DMG400012109 87 ----- 86-----
30068.t000104 89 ----- 88-----
Potri.001G452100 90 ----- 89-----
Potri.011G149800 90 ----- 89-----
Eucgr.L00349 89 ----- 88-----
GSVIVG01019698001 90 ----- 89-----
Medtr3g080670 88 ----- 87-----
Glyma08g48290 87 ----- 86-----
Glyma13g10250 61 ----- 60-----

gi|85104848 130 IYDKT-VAKPILDI 142LAEMIAYDPSLKIGTNYTGGVDVAELMREMASAPGVGLD----- 181-----
YGR181W 106 ----- 105----- 105-----
gi|17506427 109 ----- 108----- 108-----
gi|85109802 87 ----- 86----- 86-----
CMB148C 85 ----- 84----- 84-----
Vocar20012438m 86 ----- 85----- 85-----
g15745.t1 85 ----- 84----- 84-----
gi|11024700 96 ----- 95----- 95-----
Phpat.025G038900 90 ----- 89----- 89-----
Bra015863|Bra015863 271 FLYNPPRLFEAFWKI 285VKYFIDAKTFIKVKFVYKPNPESVELMSSFFDEENLPTFEGGKALLQYNHEEFSKQMNQD 345DVKTADFVGLVHSNNH
Bra003766 89 ----- 88----- 88-----
Carubv10021223 87 ----- 86----- 86-----
AT1G61570 88 ----- 87----- 87-----
228905|228905 82 ----- 81----- 81-----
GRMZM2G058432 88 ----- 87----- 87-----
LOC_Os02g45820 85 ----- 84----- 84-----
Cucsa.193350 88 ----- 87----- 87-----
PGSC0003DMG400012109 87 ----- 86----- 86-----
30068.t000104 89 ----- 88----- 88-----
Potri.001G452100 90 ----- 89----- 89-----
Potri.011G149800 90 ----- 89----- 89-----
Eucgr.L00349 89 ----- 88----- 88-----
GSVIVG01019698001 90 ----- 89----- 89-----
Medtr3g080670 88 ----- 87----- 87-----
Glyma08g48290 87 ----- 86----- 86-----
Glyma13g10250 61 ----- 60----- 60-----

gi 85104848	182	-----	181
YGR181W	106	-----	105
gi 17506427	109	-----	108
gi 85109802	87	-----	86
CMB148C	85	-----	84
Vocar20012438m	86	-----	85
g15745.t1	85	-----	84
gi 11024700	96	-----	95
Phpat.025G038900	90	-----	89
Bra015863 Bra015863	363	QQSSSGFSGAEIPEPIQTNT*	384
Bra003766	89	-----	88
Carubv10021223	87	-----	86
AT1G61570	88	-----	87
228905 228905	82	-----	81
GRMZM2G058432	88	-----	87
LOC_Os02g45820	85	-----	84
Cucsa.193350	88	-----	87
PGSC0003DMG400012109	87	-----	86
30068.t000104	89	-----	88
Potri.001G452100	90	-----	89
Potri.011G149800	90	-----	89
Eucgr.L00349	89	-----	88
GSVIVG01019698001	90	-----	89
Medtr3g080670	88	-----	87
Glyma08g48290	87	-----	86
Glyma13g10250	61	-----	60