

gi | 17536841 1 -----MAAVRDFDD-----IPDS  
gi | 10716801|dbj|BAB16408.1| 1 -----MAAAVAA 7AGAGEP-----QSPDELLPKGPKERPEELEEE-----DDDE  
gi | 85101402 1 -----NVQLTEV-----EDE-HFOOPQVG 0-----MFAL-----SEESK  
gi | 85081308 1 -----MRIIGL-----RYSALSMSKHEEELLPPQPTHGVVDGARCTAAAGT 43VGTGAAYPALRVSEVQVNNARLF-----EVPFDI-----RAKKRHN  
CMG115C 1 -----MVELTEIK-----DD-V-----VOLDEPQFS-----R----- 211--NQA-IV-----EKASAT--NNDVVDEDDSDSDFEDDFEN  
YNL131W 1 -----MAAK-----LTFNDE-----KRDNGP  
gi | 298709439 1 -----MAATAA-----DSGNEKK  
Phpat.003G070700 1 -----M-----MEDIQ  
9926|9926 1 -----M-----M-----NDDBA  
Cucsa.255780 1 -----MASI-----CNKRSLTS-----NSDPA  
30008.t000024 1 -----MASI-----CNKRSLTS-----NSDPA  
Cucsa.383300 1 -----MASR-----CNKRPSITN-----GDDNL  
GSVIVG01028415001 1 -----MASQ-----GRRVSDNR-----NPKNE  
Phpat.024G004500 1 -----M-----VAFSAIPKQKAG-----ASGKGG  
Medtrig045510 1 -----M-----M-----MA  
29398|29398 1 -----M-----M-----MSWD  
PGSC0003DMG400013457 1 -----M-----M-----M-----FAL-TG-----SSEB  
GRMZM2G318794 1 -----M-----M-----PTPSAKRGGDE-----G  
LOC\_Os02g03880 1 -----MASLSRGGGG-----GEG-  
LOC\_Os02g29400 1 -----MASLSRGGGG-----GEG-  
Carubv10028217 1 -----MAARVAG-----KSGGQ  
AT5G43970 1 -----MAARVAG-----KSGGQ  
Bra027518 1 -----MAARVAG-----KSGGQ  
Bra033708 1 -----MAARVAG-----KSGGQ  
Bra015286| 1 -----MAPRAG-----KSGGQ  
Carubv10012272 1 -----MAPRAG-----KSGGQ  
AT1G04070 1 -----MAPRAG-----KSGGQ  
Potri.008G171800 1 -----MAPRAG-----KSGGQ  
GSVIVG01027914001 1 -----M-----M-----MA-GGSSDSKNS  
29637.t000021 1 -----MASOSRGGVSLPARRSS-----KAQEP  
Potri.002G257200 1 -----MASOSRGGVSLPARRSS-----KAQEP  
Potri.014G192600 1 ERQLRERQDRTLHLILRLQDIRVWQDRAVAKAESGTHKTLNQPETLLPLGTT- 53--GAAYLS--STMASRGGVSLPARRS--G--SSQK  
Bucgr.K01430 1 -----MASTARKGVSLPDKRNR--GGAGAGAAQS  
Glymal1g23890 1 -----MASRGGVSLPARRS-----KSGGQ  
Glyma10g04590 1 -----MASRGGVSLPARRS-----KSGGQ  
Glyma13g18900|Glyma13g18900.1 1 -----MASRGGVSLPARRS-----KSGGQ  
Glyma02g18110 1 -----MASRGGVSLPARRS-----KSGGQ  
Glymal1g28430 1 -----MASRGGVSLPARRS-----KSGGQ

gi | 17536841 15 E-IHETIVEH- 24--EELGEMFPDALRSVHSTVDWSINGVWVFLKSTIIVVSTHSILAFLEYLEKERS 82DLEKTVQVQQRQ-----MLLGSAAIQ--Q  
gi | 10716801|dbj|BAB16408.1| 9 E-LDETLSEHL- 48--WGLTEMPFPERVSRAGHTFDLSLVAQNNYFSRRLMLGTTSEMLAVLVVVFTEKL 106QMMBQQQOQOQO-----LLGQNTGLS--Q  
gi | 85101402 10 -----ERMG 13K-----LDDLSVIVHYGYLP-----MLLYLQYFRVSPRPSILRMSPLS 53-----  
gi | 85081308 39 YE-SQETFLDR- 49--YALRDMVSPTRGRVYFHKYSTTTNFVKEITLGFAGRAAWVVSGLLGVFFAIAFAMD 107QNYAAMECEARMRELGSDDVLTAGGEGQA--  
CMG115C 82 WNRVTVDLEDNK 94DSVTEKWKVQVVERVASSGY-----TFVRAFGLGGRVAVISAHSALVIVVPLVYIDRE 149QDANAASSSAAAAGGS--GVGSSSTAGR--  
YNL131W 56 ET-----LLDR- 62--VALKDVVFGKRCQIISNFFGFTSSVNRNAPFSGNLAWTLTALMLVPLSLILAE 120QGLHMKKFLQSDANMLLAQEKDAA--A  
gi | 298709439 17 G-----VQ 19--OPLVYVGRSLVAGF-----GWQWAKKRRGRTGQVW-----VAVVVFETHE 69AQTPEBKTHIN-----MLLHSGTQETAQ  
Phpat.003G070700 14 W-----GRAVST 20NLSSGLGYEERKRVKNTIV-----QVQNNMWSRKAAMVAGTLLVAVLAPFFHIDQE 75AQTVEEGETS-----HGEVSPATP-RSS  
9926|9926 5 -----VLSRVS 11-----SGAASRVAASSTC-----VFGRRVLRSTGKAAMVAGTFFLLVPLVLEMDRE 60QOLDELESQAA-----LGGAAVHAA-KAA  
Cucsa.255780 20 G-----VLSRVS 26RSDBSSEIVYRSKRAASNTA-----LVNKLRLSTGKAAMVAGTFFLLVPLVLEMDRE 81QOLNELELQAA-----LGGAAVHAA-KAA  
30008.t000024 16 G-----VAKFT 22RTVDSATVYAKGANDAG-----MVAKRILKSTGKAAMVAGTFFLLVPLVLEMDRE 77QOFHELELQOQS-----LGGAPTTVH-K--  
Cucsa.383300 16 G-----LISRVS 25RSVDSGSRKXKLSGDA-----VSKKLLRSTGKAAMVAGTFFLLVPLVLEMDRE 80QOLNELELQOQS-----LGGAPTTVH-K--  
GSVIVG01028415001 19 G-----LISRVS 25RSVDSGSRKXKLSGDA-----VSKKLLRSTGKAAMVAGTFFLLVPLVLEMDRE 80QOLNELELQOQS-----LGGAPTTVH-K--  
Phpat.024G004500 21 W-----GRGNF 27GCVNHPELDFDKRKAASNDV-----RFSKLLRSTGKAAMVAGTFFLLVPLVLEMDRE 82QOLVDESQOAG-----LGGAPLEGS-PPA  
Medtrig045510 3 K-----KQSSAI 9ARVCNHPELDFDKRKAASNDV-----VIAKRLRSTGKAAMVAGTFFLLVPLVLEMDRE 64QOLNELESQAA-----LGGAPLEGS-PPA  
29398|29398 11 S-----LWAVVS 17NRVVOSSLVYHKSRAASLSSNS-----YASRKLMSSTGKAAMVAGTFFLLVPLVLEMDRE 72QOLNELELQOQS-----LGGAPTTVH-K--  
PGSC0003DMG400013457 18 S-----KNDGV 24ARVDSSEIVYRSKRAASNTA-----MVSKKILKSTGKAAMVAGTFFLLVPLVLEMDRE 79QOLNELELQOQS-----LGGAPTTVH-K--  
GRMZM2G318794 16 G-----DCFL 19AKISNSLIVSQRRAAGDAV-----EVSCKLLRSTGKAAMVAGTFFLLVPLVLEMDRE 70QOLNELELQOQS-----LGGAPTTVH-K--  
LOC\_Os02g03880 15 -----EGIL 18AFSFRSVAAGRBA-----TMAKKILRSTGKAAMVAGTFFLLVPLVLEMDRE 69QOLNELELQOQS-----LGGAPTTVH-K--  
LOC\_Os02g29400 15 -----EGIL 18AFSFRSVAAGRBA-----TMAKKILRSTGKAAMVAGTFFLLVPLVLEMDRE 69QOLNELELQOQS-----LGGAPTTVH-K--  
Carubv10028217 16 -----PNIL 19AKISNSLIVSQRRAAGDAV-----EVSCKLLRSTGKAAMVAGTFFLLVPLVLEMDRE 74QOLNELELQOQS-----LGGAPTTVH-K--  
AT5G43970 16 -----PNIL 19AKISNSLIVSQRRAAGDAV-----EVSCKLLRSTGKAAMVAGTFFLLVPLVLEMDRE 74QOLNELELQOQS-----LGGAPTTVH-K--  
Bra027518 16 -----SNIL 19GRISSIVYRKNKBAADAA-----FVAKKILRSTGKAAMVAGTFFLLVPLVLEMDRE 77QOLNELELQOQS-----LGGAPTTVH-K--  
Bra033708 17 -----SNIL 20AKISNSLIVSQRRAAGDAV-----EVSCKLLRSTGKAAMVAGTFFLLVPLVLEMDRE 75QOLNELELQOQS-----LGGAPTTVH-K--  
Bra015286| 16 -----SNIL 19AKISNSLIVSQRRAAGDAV-----EVSCKLLRSTGKAAMVAGTFFLLVPLVLEMDRE 74QOLNELELQOQS-----LGGAPTTVH-K--  
Carubv10012272 13 -----SNIL 16AKISNSLIVSQRRAAGDAV-----EVSCKLLRSTGKAAMVAGTFFLLVPLVLEMDRE 71QOLNELELQOQS-----LGGAPTTVH-K--  
AT1G04070 13 -----SNIL 16AKISNSLIVSQRRAAGDAV-----EVSCKLLRSTGKAAMVAGTFFLLVPLVLEMDRE 71QOLNELELQOQS-----LGGAPTTVH-K--  
Potri.008G171800 1 0----- 0-----FMARPKRSTGKAAMVAGTFFLLVPLVLEMDRE 42YQNLNLDLPEKS-----LGGAPTTVH-K--  
GSVIVG01027914001 13 G-----LVSRHS 19NSLIGSQQHMFHQKRAASDAA-----MVSKKILRSTGKAAMVAGTFFLLVPLVLEMDRE 74QOLNELELQOQS-----LGGAPTTVH-K--  
29637.t000021 25 T----- 27AKISNSLIVSQRRAAGDAV-----EVSCKLLRSTGKAAMVAGTFFLLVPLVLEMDRE 82QOLNELELQOQS-----LGGAPTTVH-K--  
Potri.002G257200 26 H----- 28AKISNSLIVSQRRAAGDAV-----EVSCKLLRSTGKAAMVAGTFFLLVPLVLEMDRE 83QOLNELELQOQS-----LGGAPTTVH-K--  
Potri.014G192600 84 PN----- 87AKLNNOVAVKGGQAAADL-----FVAKKILRSTGKAAMVAGTFFLLVPLVLEMDRE 142QOLNELELQOQS-----LGGAPTTVH-K--  
Bucgr.K01430 30 G----- 32SRVDSSEIVYRSKRAASLSSNS-----LVNKLRLSTGKAAMVAGTFFLLVPLVLEMDRE 87QOLNELELQOQS-----LGGAPTTVH-K--  
Glymal1g23890 20 S----- 22AKISNSLIVSQRRAAGDAV-----EVSCKLLRSTGKAAMVAGTFFLLVPLVLEMDRE 77QOLNELELQOQS-----LGGAPTTVH-K--  
Glyma10g04590 20 S----- 22AKISNSLIVSQRRAAGDAV-----EVSCKLLRSTGKAAMVAGTFFLLVPLVLEMDRE 77QOLNELELQOQS-----LGGAPTTVH-K--  
Glyma13g18900|Glyma13g18900.1 20 S----- 22AKISNSLIVSQRRAAGDAV-----EVSCKLLRSTGKAAMVAGTFFLLVPLVLEMDRE 77QOLNELELQOQS-----LGGAPTTVH-K--  
Glyma02g18110 20 S----- 22AKISNSLIVSQRRAAGDAV-----EVSCKLLRSTGKAAMVAGTFFLLVPLVLEMDRE 77QOLNELELQOQS-----LGGAPTTVH-K--  
Glymal1g28430 20 S----- 22AKISNSLIVSQRRAAGDAV-----EVSCKLLRSTGKAAMVAGTFFLLVPLVLEMDRE 77QOLNELELQOQS-----LGGAPTTVH-K--

gi | 17536841 106 AKTA----- 109-----  
gi | 10716801|dbj|BAB16408.1| 129 GGMGALPSLPKGI----- 142-----  
gi | 85101402 54 ----- 53-----  
gi | 85081308 136 -GTAEKTLAAIGGEGARPAL----- 154-----  
CMG115C 176 PAATR----- 180-----  
YNL131W 150 TAN\*----- 152-----  
gi | 298709439 96 MGLYS-ALDPNVMGPEAS----- 112-----  
Phpat.003G070700 101 PIK\*----- 103-----  
9926|9926 86 AAK\*----- 89-----  
Cucsa.255780 105 ----- 104-----  
30008.t000024 101 ----- 100-----  
Cucsa.383300 104 ----- 103-----  
GSVIVG01028415001 101 ----- 100-----  
Phpat.024G004500 108 VK\*----- 109-----  
Medtrig045510 91 WFFYTHIHYHHNNMATAAGMASLFPSSI 117NTVKCLRKNKSLDTSNRMFVSLISQSVPELSIGTTVSHKLWFRPISVAVAQEAAVVA 177VEDEKVVVEEERKE  
29398|29398 91 ----- 90-----  
PGSC0003DMG400013457 103 ----- 102-----  
GRMZM2G318794 95 ----- 94-----  
LOC\_Os02g03880 86 ----- 85-----  
LOC\_Os02g29400 100 ----- 93-----  
Carubv10028217 100 ----- 99-----  
AT5G43970 100 ----- 99-----  
Bra027518 100 ----- 99-----  
Bra033708 98 ----- 97-----  
Bra015286| 97 ----- 96-----  
Carubv10012272 95 ----- 94-----  
AT1G04070 63 ----- 62-----  
Potri.008G171800 98 ----- 97-----  
GSVIVG01027914001 104 ----- 103-----  
29637.t000021 109 ----- 108-----  
Potri.002G257200 166 FK\*----- 167-----  
Bucgr.K01430 110 ----- 109-----  
Glymal1g23890 98 ----- 97-----  
Glyma10g04590 98 ----- 97-----  
Glyma13g18900|Glyma13g18900.1 61 ----- 60-----  
Glyma02g18110 87 ----- 86-----  
Glymal1g28430 98 ----- 97-----

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gi |17536841 110 ----- 109-----
gi |10716801|dbj|BAB16408.1| 143 - 142-----
gi |85101402 54 ----- 53----- 53
gi |85081308 155 -- 154-----
CMG115C 181 -- 180----- 180
YNL131W 153 -- 152----- 152
gi |298709439 113 ----- 112-----
Pphat.003G070700 104 ----- 103-----
99926|99926 90 ----- 89----- 89
Cucsa.255780 105 ----- 104-----
30008.t000024 101 ----- 100-----
Cucsa.383300 104 ----- 103-----
GSVIVG01028415001 101 ----- 100-----
Pphat.024G004500 110 ----- 109-----
Medtrig045510 193 EEEVVEEKENIGGETVAEVDTRTKLYFGNLPYSVDSALLAGLIEE 237YGS AELIEVLVYDRDTGKSRGFVAFVTMSCVEDCNAVIQNLGKEFMGRTLRLVNFSDKPKPK 90
29398|29398 91 ----- 90----- 90
PGSC0003DMG400013457 103 ----- 102-----
GRMZM2G318794 95 ----- 94----- 94
LOC_Os02g03880 86 ----- 85----- 85
LOC_Os02g29400 94 ----- 93----- 93
Carubv10028217 100 ----- 99----- 99
AT5G43970 100 ----- 99----- 99
Bra027518 100 ----- 99----- 99
Bra033708 98 ----- 97----- 97
Bra015286| 97 ----- 96----- 96
Carubv10012272 95 ----- 94----- 94
AT1G04070 95 ----- 94----- 94
Potri.008G171800 63 ----- 62----- 62
GSVIVG01027914001 98 ----- 97----- 97
29637.t000021 104 ----- 103----- 103
Potri.002G257200 109 ----- 108----- 108
Potri.014G192600 168 ----- 167----- 167
Eucgr.K01430 110 ----- 109-----
Glyma11g23890 98 ----- 97----- 97
Glyma10g04590 98 ----- 97----- 97
Glyma13g18900|Glyma13g18900.1 61 ----- 60----- 60
Glyma02g18110 87 ----- 86----- 86
Glyma11g28430 98 ----- 97----- 97

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gi |17536841 110 109----- 109----- 109
gi |10716801|dbj|BAB16408.1| 143 - 142----- 142
gi |85101402 54 ----- 53----- 53
gi |85081308 155 -- 154----- 154
CMG115C 181 -- 180----- 180
YNL131W 153 -- 152----- 152
gi |298709439 113 112----- 112----- 112
Pphat.003G070700 104 103----- 103----- 103
99926|99926 90 ----- 89----- 89
Cucsa.255780 105 104----- 104----- 104
30008.t000024 101 100----- 100----- 100
Cucsa.383300 104 103----- 103----- 103
GSVIVG01028415001 101 100----- 100----- 100
Pphat.024G004500 110 109----- 109----- 109
Medtrig045510 298 297EPLYPETEKLVFNGLAWVTSESLTQAFQEHGTVVGARVLFDPGETGKSRGVGFVSYATK 357SEMDTALAIMDNVELEGRTLRVSLAQGKRS* 387
29398|29398 91 ----- 90----- 90
PGSC0003DMG400013457 103 102----- 102----- 102
GRMZM2G318794 95 ----- 94----- 94
LOC_Os02g03880 86 ----- 85----- 85
LOC_Os02g29400 94 ----- 93----- 93
Carubv10028217 100 ----- 99----- 99
AT5G43970 100 ----- 99----- 99
Bra027518 100 ----- 99----- 99
Bra033708 98 ----- 97----- 97
Bra015286| 97 ----- 96----- 96
Carubv10012272 95 ----- 94----- 94
AT1G04070 95 ----- 94----- 94
Potri.008G171800 63 ----- 62----- 62
GSVIVG01027914001 98 ----- 97----- 97
29637.t000021 104 103----- 103----- 103
Potri.002G257200 109 ----- 108----- 108
Potri.014G192600 168 -- 167----- 167----- 167
Eucgr.K01430 110 109----- 109----- 109
Glyma11g23890 98 ----- 97----- 97
Glyma10g04590 98 ----- 97----- 97
Glyma13g18900|Glyma13g18900.1 61 ----- 60----- 60
Glyma02g18110 87 ----- 86----- 86
Glyma11g28430 98 ----- 97----- 97

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