

sp|Q55C70 1 ----- 0 -----
77112|77112 1 ----- 0 -----
30026.t000051|30026.m001487 1 ----- 0 -----
Potri.004G062900 1 ----- 0 -----
Potri.011G072000 1 ----- 0 -----
gi|74966225 1 ----- 0 -----
gi|48526509 1 ----- 0 -----
gi|530417566 1 ----- 0 -----
Cre12.g505950|Cre12.g505950.t1.2 1 ----- 0 -----
Vocar20000934 1 ----- 0 -----
Esi0000_0471 1 MLLGRVGTLLPSCSRVATRRFLAKKAAGGGGGKGGSGTPKKGPAAIKARGAMPVSKAG 60KQGSRTGKTGGAAREAAATTTSTAKAAAAEAAASVKPPFVGGGGGF
gi|164427612 1 ----- 0 -----
CMN179C|CMN179CT 1 ----- 0 -----
Medtr5g095530|Medtr5g095530.1 1 ----- 0 -----
Glyma02g46900|Glyma02g46900.1 1 ----- 0 -----
Glyma14g01810|Glyma14g01810.1 1 ----- 0 -----
ATLG5900. 1 ----- 0 -----
Carubv10009325m.g|Carubv10009325m 1 ----- 0 -----
Bra030827|Bra030827 1 ----- 0 -----
Bra037095|Bra037095 1 ----- 0 -----
Cucsa.390900|Cucsa.390900.1 1 ----- 0 -----
Phpat.020G041400|Phpat.020G041400.1 1 ----- 0 -----
124475|124475 1 ----- 0 -----
Phpat.008G082000|Phpat.008G082000.1 1 ----- 0 -----
GRMZM5G896568|GRMZM5G896568.T01 1 ----- 0 -----
LOC_Os01g55700|LOC_Os01g55700.1 1 ----- 0 -----
LOC_Os05g43770|LOC_Os05g43770.1 1 ----- 0 -----
GRMZM2G035651|GRMZM2G035651.T01 1 ----- 0 -----
GRMZM2G441091|GRMZM2G441091.T01 1 ----- 0 -----
Eucgr.F02057|Eucgr.F02057.1 1 ----- 0 -----
GSVIVG01030074001|GSVIVT01030074001 1 ----- 0 -----
GSVIVG01014657001|GSVIVT01014657001 1 ----- 0 -----
PGSC0003DMG400022178|PGSC0003DMT40005708 1 ----- 0 -----
PGSC0003DMG400022178|PGSC0003DMT40005708 1 ----- 0 -----
PGSC0003DMG400022178|PGSC0003DMT40005708 1 ----- 0 -----
29629.t000047|29629.m001396 1 ----- 0 -----
Potri.001G364500|Potri.001G364500.1 1 ----- 0 -----
Potri.001G366300|Potri.001G366300.1 1 ----- 0 -----
Potri.011G093000 1 ----- 0 -----

sp|Q55C70 1 ----- 0 -----
77112|77112 1 ----- 0 -----
30026.t000051|30026.m001487 1 ----- 0 -----
Potri.004G062900 1 ----- 0 -----
Potri.011G072000 1 ----- 0 -----
gi|74966225 1 ----- 0 -----
gi|48526509 1 ----- 0 -----
gi|530417566 1 ----- 0 -----
Cre12.g505950|Cre12.g505950.t1.2 1 ----- 0 -----
Vocar20000934 1 ----- 0 -----
Esi0000_0471 1 TKSEMLAARKARK 120ASVTARTAAAAATAKAAAPAAGAGAGRTGGAGAAASAAAGAGGAKGGQKGGWGTSLVAGTSS 180VGLAALGIAWQLKPFDEMRLKLLDSSPIDHF
gi|164427612 1 ----- 0 -----
CMN179C|CMN179CT 1 ----- 0 -----
Medtr5g095530|Medtr5g095530.1 1 ----- 0 -----
Glyma02g46900|Glyma02g46900.1 1 ----- 0 -----
Glyma14g01810|Glyma14g01810.1 1 ----- 0 -----
ATLG5900. 1 ----- 0 -----
Carubv10009325m.g|Carubv10009325m 1 ----- 0 -----
Bra030827|Bra030827 1 ----- 0 -----
Bra037095|Bra037095 1 ----- 0 -----
Cucsa.390900|Cucsa.390900.1 1 ----- 0 -----
Phpat.020G041400|Phpat.020G041400.1 1 ----- 0 -----
124475|124475 1 ----- 0 -----
Phpat.008G082000|Phpat.008G082000.1 1 ----- 0 -----
GRMZM5G896568|GRMZM5G896568.T01 1 ----- 0 -----
LOC_Os01g55700|LOC_Os01g55700.1 1 ----- 0 -----
LOC_Os05g43770|LOC_Os05g43770.1 1 ----- 0 -----
GRMZM2G035651|GRMZM2G035651.T01 1 ----- 0 -----
GRMZM2G441091|GRMZM2G441091.T01 1 ----- 0 -----
Eucgr.F02057|Eucgr.F02057.1 1 ----- 0 -----
GSVIVG01030074001|GSVIVT01030074001 1 ----- 0 -----
GSVIVG01014657001|GSVIVT01014657001 1 ----- 0 -----
PGSC0003DMG400022178|PGSC0003DMT40005708 1 ----- 0 -----
PGSC0003DMG400022178|PGSC0003DMT40005708 1 ----- 0 -----
PGSC0003DMG400022178|PGSC0003DMT40005708 1 ----- 0 -----
29629.t000047|29629.m001396 1 ----- 0 -----
Potri.001G364500|Potri.001G364500.1 1 ----- 0 -----
Potri.001G366300|Potri.001G366300.1 1 ----- 0 -----
Potri.011G093000 1 ----- 0 -----

sp|Q55C70 1 ----- 0 -----
77112|77112 1 ----- 0 -----
30026.t000051|30026.m001487 1 ----- 0 -----
Potri.004G062900 1 ----- 0 -----
Potri.011G072000 1 ----- 0 -----
gi|74966225 1 ----- 0 -----
gi|48526509 1 ----- 0 -----
gi|530417566 1 ----- 0 -----
Cre12.g505950|Cre12.g505950.t1.2 1 ----- 0 -----
Vocar20000934 1 ----- 0 -----
Esi0000_0471 1 F1WFMGKALYSSPVKDKLLDCLPLPGALP 240PPTLVLDLEGTLGTYTRKKGWRVAKRPLDGLFLKEMSQLYEIVVFTDSMGLADEWIT 300QMPDQGTISQR
gi|164427612 1 ----- 0 -----
CMN179C|CMN179CT 1 ----- 0 -----
Medtr5g095530|Medtr5g095530.1 1 ----- 0 -----
Glyma02g46900|Glyma02g46900.1 1 ----- 0 -----
Glyma14g01810|Glyma14g01810.1 1 ----- 0 -----
ATLG5900. 1 ----- 0 -----
Carubv10009325m.g|Carubv10009325m 1 ----- 0 -----
Bra030827|Bra030827 1 ----- 0 -----
Bra037095|Bra037095 1 ----- 0 -----
Cucsa.390900|Cucsa.390900.1 1 ----- 0 -----
Phpat.020G041400|Phpat.020G041400.1 1 ----- 0 -----
124475|124475 1 ----- 0 -----
Phpat.008G082000|Phpat.008G082000.1 1 ----- 0 -----
GRMZM5G896568|GRMZM5G896568.T01 1 ----- 0 -----
LOC_Os01g55700|LOC_Os01g55700.1 1 ----- 0 -----
LOC_Os05g43770|LOC_Os05g43770.1 1 ----- 0 -----
GRMZM2G035651|GRMZM2G035651.T01 1 ----- 0 -----
GRMZM2G441091|GRMZM2G441091.T01 1 ----- 0 -----
Eucgr.F02057|Eucgr.F02057.1 1 ----- 0 -----
GSVIVG01030074001|GSVIVT01030074001 1 ----- 0 -----
GSVIVG01014657001|GSVIVT01014657001 1 ----- 0 -----
PGSC0003DMG400022178|PGSC0003DMT40005708 1 ----- 0 -----
PGSC0003DMG400022178|PGSC0003DMT40005708 1 ----- 0 -----
PGSC0003DMG400022178|PGSC0003DMT40005708 1 ----- 0 -----
29629.t000047|29629.m001396 1 ----- 0 -----
Potri.001G364500|Potri.001G364500.1 1 ----- 0 -----
Potri.001G366300|Potri.001G366300.1 1 ----- 0 -----
Potri.011G093000 1 ----- 0 -----

sp|Q55C70 1 ----- 0----- 0-----
77112|77112 1 ----- 0----- 0-----
30026.t000051|30026.m001487 1 ----- 0----- 0-----
Potri.004G062900 1 ----- 0----- 0-----
Potri.011G072000 1 ----- 0----- 0-----
gi|74966225 1 ----- 0----- 0-----
gi|48526509 1 ----- MSL 3SKLTQT ----- CF ----- S ----- 12-----
gi|530417566 1 ----- MASA 4LSLGNK ----- CDPFLRCVLCRG ----- 22-----
Cre12.g505950|Cre12.g505950.t1.2 1 ----- 0----- 0-----
Vocar20000934 1 ----- 0----- 0-----
Esi0000_0471 312 VYRDGTRGYIDGKVKYKDLNALNRPLEQTLIIDDNADCISMQPFNAIKVKA 360FSLSDGSDPTADTALYDLAFLRALATGGVADFRDVLRLPHVGEDSNVAVDPRFSKVN
gi|164427612 1 ----- 0----- 0-----
CMN179C|CMN179CT 1 ----- 0----- 0-----
Medtr5g095530|Medtr5g095530.1 1 ----- 0----- 0-----
Glyma02g46900|Glyma02g46900.1 1 ----- 0----- 0-----
Glyma14g01810|Glyma14g01810.1 1 ----- 0----- 0-----
ATLGS5900 1 ----- 0----- 0-----
Carubv10009325m.g|Carubv10009325m 1 ----- 0----- 0-----
Bra030827|Bra030827 1 ----- 0----- 0-----
Bra037095|Bra037095 1 ----- 0----- 0-----
Cucsa.390900|Cucsa.390900.1 1 ----- 0----- 0-----
Phpat.020G041400|Phpat.020G041400.1 1 ----- 0----- 0-----
124475|124475 1 ----- 0----- 0-----
Phpat.008G082000|Phpat.008G082000.1 1 ----- 0----- 0-----
GRMZM5G896568|GRMZM5G896568.T01 1 ----- 0----- 0-----
LOC_Os01g55700|LOC_Os01g55700.1 1 ----- 0----- 0-----
LOC_Os05g43770|LOC_Os05g43770.1 1 ----- 0----- 0-----
GRMZM2G035651|GRMZM2G035651.T01 1 ----- 0----- 0-----
GRMZM2G441091|GRMZM2G441091.T01 1 ----- 0----- 0-----
Eucgr.F02057|Eucgr.F02057.1 1 ----- 0----- 0-----
GSVIVG01030074001|GSVIVT01030074001 1 ----- 0----- 0-----
GSVIVG01014657001|GSVIVT01014657001 1 ----- 0----- 0-----
PGSC0003DMG400022178|PGSC0003DMT40005708 1 ----- 0----- 0-----
PGSC0003DMG400022178|PGSC0003DMT40005708 1 ----- 0----- 0-----
PGSC0003DMG400022178|PGSC0003DMT40005708 1 ----- 0----- 0-----
29629.t000047|29629.m001396 1 ----- 0----- 0-----
Potri.001G364500|Potri.001G364500.1 1 ----- 0----- 0-----
Potri.001G366300|Potri.001G366300.1 1 ----- 0----- 0-----
Potri.011G093000 1 ----- 0----- 0-----

sp|Q55C70 1 ----- 0----- 0-----
77112|77112 1 ----- 0----- 0-----
30026.t000051|30026.m001487 1 ----- 0----- 0-----
Potri.004G062900 1 ----- 0----- 0-----
Potri.011G072000 1 ----- 0----- 0-----
gi|74966225 1 ----- 0----- 0-----
gi|48526509 23 ----- 0----- 0-----
gi|530417566 1 ----- 0----- 0-----
Cre12.g505950|Cre12.g505950.t1.2 1 ----- 0----- 0-----
Vocar20000934 1 ----- 0----- 0-----
Esi0000_0471 418 AVR 420QKEDAEEKSKGLGLVLRQIAPVVGAGGPAAGMGLTSKDIVGDAPETLSPGMAAAAAATA 480GGKGGGGGGGSKPLAEKQKGLWKSLEQEGNKEREDDFM
gi|164427612 1 ----- 0----- 0-----
CMN179C|CMN179CT 1 ----- 0----- 0-----
Medtr5g095530|Medtr5g095530.1 1 ----- 0----- 0-----
Glyma02g46900|Glyma02g46900.1 1 ----- 0----- 0-----
Glyma14g01810|Glyma14g01810.1 1 ----- 0----- 0-----
ATLGS5900 1 ----- 0----- 0-----
Carubv10009325m.g|Carubv10009325m 1 ----- 0----- 0-----
Bra030827|Bra030827 1 ----- 0----- 0-----
Bra037095|Bra037095 1 ----- 0----- 0-----
Cucsa.390900|Cucsa.390900.1 1 ----- 0----- 0-----
Phpat.020G041400|Phpat.020G041400.1 1 ----- 0----- 0-----
124475|124475 1 ----- 0----- 0-----
Phpat.008G082000|Phpat.008G082000.1 1 ----- 0----- 0-----
GRMZM5G896568|GRMZM5G896568.T01 1 ----- 0----- 0-----
LOC_Os01g55700|LOC_Os01g55700.1 1 ----- 0----- 0-----
LOC_Os05g43770|LOC_Os05g43770.1 1 ----- 0----- 0-----
GRMZM2G035651|GRMZM2G035651.T01 1 ----- 0----- 0-----
GRMZM2G441091|GRMZM2G441091.T01 1 ----- 0----- 0-----
Eucgr.F02057|Eucgr.F02057.1 1 ----- 0----- 0-----
GSVIVG01030074001|GSVIVT01030074001 1 ----- 0----- 0-----
GSVIVG01014657001|GSVIVT01014657001 1 ----- 0----- 0-----
PGSC0003DMG400022178|PGSC0003DMT40005708 1 ----- 0----- 0-----
PGSC0003DMG400022178|PGSC0003DMT40005708 1 ----- 0----- 0-----
PGSC0003DMG400022178|PGSC0003DMT40005708 1 ----- 0----- 0-----
29629.t000047|29629.m001396 1 ----- 0----- 0-----
Potri.001G364500|Potri.001G364500.1 1 ----- 0----- 0-----
Potri.001G366300|Potri.001G366300.1 1 ----- 0----- 0-----
Potri.011G093000 1 ----- 0----- 0-----

sp|Q55C70 1 ----- 0----- 0-----
77112|77112 1 ----- 0----- 0-----
30026.t000051|30026.m001487 1 ----- 0----- 0-----
Potri.004G062900 1 ----- 0----- 0-----
Potri.011G072000 1 ----- 0----- 0-----
gi|74966225 1 ----- 0----- 0-----
gi|48526509 1 ----- 0----- 0-----
gi|530417566 1 ----- 0----- 0-----
Cre12.g505950|Cre12.g505950.t1.2 1 ----- 0----- 0-----
Vocar20000934 1 ----- 0----- 0-----
Esi0000_0471 520 RRNEAFQVRVMEKRM 533--AREKAKRDEQAQQQ YPFWHGLSLRNSVRLNSRALRVVPSAAN ---TLTSVQAS 583
gi|164427612 11 10----- 0----- 0-----
CMN179C|CMN179CT 3 2--VDRIAGL ----- 0----- 0-----
Medtr5g095530|Medtr5g095530.1 1 0----- 0----- 0-----
Glyma02g46900|Glyma02g46900.1 1 0----- 0----- 0-----
Glyma14g01810|Glyma14g01810.1 1 0----- 0----- 0-----
ATLGS5900 1 0----- 0----- 0-----
Carubv10009325m.g|Carubv10009325m 21 20--LEKTPKS ----- E-MAS ---TALRSRL--PFLAKLRSRHLR--LFGAEAA 59SSNSA ---RVQGIS
Bra030827|Bra030827 1 0----- 0----- 0-----
Bra037095|Bra037095 1 0----- 0----- 0-----
Cucsa.390900|Cucsa.390900.1 1 0----- 0----- 0-----
Phpat.020G041400|Phpat.020G041400.1 7 6--LRRSSTA ----- VAL ----- RGEVQLP--PSSGLIARR ----- FSSSPSS 40-----
124475|124475 1 0----- 0----- 0-----
Phpat.008G082000|Phpat.008G082000.1 7 6--LRRSAGA ----- VQEVL ----- QGQPRAM--A--AFLPQG ----- FST--AS 38-----
GRMZM5G896568|GRMZM5G896568.T01 1 0----- 0----- 0-----
LOC_Os01g55700|LOC_Os01g55700.1 1 0----- 0----- 0-----
LOC_Os05g43770|LOC_Os05g43770.1 1 0----- 0----- 0-----
GRMZM2G035651|GRMZM2G035651.T01 1 0----- 0----- 0-----
GRMZM2G441091|GRMZM2G441091.T01 1 0----- 0----- 0-----
Eucgr.F02057|Eucgr.F02057.1 1 0----- 0----- 0-----
GSVIVG01030074001|GSVIVT01030074001 1 0----- 0----- 0-----
GSVIVG01014657001|GSVIVT01014657001 1 0----- 0----- 0-----
PGSC0003DMG400022178|PGSC0003DMT40005708 1 0----- 0----- 0-----
PGSC0003DMG400022178|PGSC0003DMT40005708 1 0----- 0----- 0-----
PGSC0003DMG400022178|PGSC0003DMT40005708 1 0----- 0----- 0-----
29629.t000047|29629.m001396 1 0----- 0----- 0-----
Potri.001G364500|Potri.001G364500.1 1 0----- 0----- 0-----
Potri.001G366300|Potri.001G366300.1 1 0----- 0----- 0-----
Potri.011G093000 1 0----- 0----- 0-----

ep|Q55C70
77112|77112
30026.t000051|30026.m001487
Potri.004G062900
Potri.011G072000
g1|74966225
g1|48526509
g1|530417566
Crel2.g505950|Crel2.g505950.t1.2
Vocar20000934
Esi0000.0471
g1|164427612
CMN179C|CMN179C
Medtr5g095530|Medtr5g095530.1
Glyma02g46900|Glyma02g46900.1
Glyma14g01810|Glyma14g01810.1
AT1G55900.
Carubv10009325m.g|Carubv10009325m
Bra030827|Bra030827
Bra037095|Bra037095
Cucsa.390900|Cucsa.390900.1
Phpat.020G041400|Phpat.020G041400.1
124475|124475
Phpat.008G082000|Phpat.008G082000.1
GRMZM5G896568|GRMZM5G896568.T01
LOC_Os01g55700|LOC_Os01g55700.1
LOC_Os05g43770|LOC_Os05g43770.1
GRMZM2G035651|GRMZM2G035651.T01
GRMZM2G041091|GRMZM2G041091.T01
Bucgr.F02057|Bucgr.F02057.1
GSVIVG01030074001|GSVIVT01030074001
GSVIVG01014657001|GSVIVT01014657001
PGSC0003DMG400022178|PGSC0003DMT40005708
PGSC0003DMG400022178|PGSC0003DMT40005708
PGSC0003DMG400022178|PGSC0003DMT40005708
29629.t000047|29629.m001396
Potri.001G364500|Potri.001G364500.1
Potri.001G366300|Potri.001G366300.1
Potri.011G093000

258 TNEKYFTGL 266VYPTGKIKERNQFSKKEEMDIDDSKV--EFDAN--SPYDHPVNVINCKEKSNS----317DKKALTELELVVSSFSKNDLVEPESIQQNI
148 HR 150LVNRESCRYGGGLVYKLSLGLDQSHV--IVDNPSPHVALPQNAVPTSFIDN---204RDRELELIPYGV--SEFDNVTAALNSCRYE--MLK--
LISHR 204LVYRDSQVDEGDKFVKDLSEMRGDKKRV-VIVDDNPNCYTFQPDNAIKKFFDDL----258DGLGKRAKFFNGCC--DQVEDMNRVAKQFVCGEGDN
194 VISHR 198LVYRDSQVDEGDKFVKDLSEMRGDKKRV-VIVDDNPNCYTFQPDNAIKKFFDDL----252DGLGKRAKFFNGCC--DQVEDMNRVAKQFVCGEGDN
193 LISHR 197LVYRDSQVDEGDKFVKDLSEMRGDKKRV-VIVDDNPNCYTFQPDNAIKKFFDDL----252DGLGKRAKFFNGCC--DQVEDMNRVAKQFVCGEGDN
314 WYDFDPKQ-RIMYK 318LRFKATKMGKNGKHYRDLSKLNRRDPKVI-LVSGHAFENSLOPENCVCKPKWKEE---372DTSLDLALFKLHLSDAKVEPFR
307 LIDSVDPHG-FISYR 320LRFKATKMGKNGKHYRDLSKLNRRDPKVI-LVSGHAFENSLOPENCVCKPKWKEE---374DORVLDLALFKLHLSDAKVEPFR
103 YR 104LPHDARYMDGHHVYKLSCLNLRDPKRV-VVVDCKKEAPRLQPYNGVALRVPWGDNS----158DDRVLLLSAFKLTALNGVEVDVLEHYALDEDDPLA--
255 PQRVAVMHR 263VYPTGKIKERNQFSKKEEMDIDDSKV--EFDAN--SPYDHPVNVINCKEKSNS----317DKKALTELELVVSSFSKNDLVEPESIQQNI
226 PHRV-PRR 233VYPTGKIKERNQFSKKEEMDIDDSKV--EFDAN--SPYDHPVNVINCKEKSNS----317DKKALTELELVVSSFSKNDLVEPESIQQNI
287 LFSNVY-MYSSKALADLHIVSYR 281LRFKATKMGKNGKHYRDLSKLNRRDPKVI-LVSGHAFENSLOPENCVCKPKWKEE---372DTSLDLALFKLHLSDAKVEPFR
272 MDVFR-FIMM 281LRFKATKMGKNGKHYRDLSKLNRRDPKVI-LVSGHAFENSLOPENCVCKPKWKEE---372DTSLDLALFKLHLSDAKVEPFR
210 NG-VYTHR 216VYPTGKIKERNQFSKKEEMDIDDSKV--EFDAN--SPYDHPVNVINCKEKSNS----317DKKALTELELVVSSFSKNDLVEPESIQQNI
254 PKH-CHRYR 263VYPTGKIKERNQFSKKEEMDIDDSKV--EFDAN--SPYDHPVNVINCKEKSNS----317DKKALTELELVVSSFSKNDLVEPESIQQNI
213 KH-CHRYR 219VYPTGKIKERNQFSKKEEMDIDDSKV--EFDAN--SPYDHPVNVINCKEKSNS----317DKKALTELELVVSSFSKNDLVEPESIQQNI
211 KH-CHRYR 217VYPTGKIKERNQFSKKEEMDIDDSKV--EFDAN--SPYDHPVNVINCKEKSNS----317DKKALTELELVVSSFSKNDLVEPESIQQNI
253 QNC-CHRYR 263VYPTGKIKERNQFSKKEEMDIDDSKV--EFDAN--SPYDHPVNVINCKEKSNS----317DKKALTELELVVSSFSKNDLVEPESIQQNI
279 DPNL-CHRYK 281LRFKATKMGKNGKHYRDLSKLNRRDPKVI-LVSGHAFENSLOPENCVCKPKWKEE---372DTSLDLALFKLHLSDAKVEPFR
250 PNC-VLYRK 257VYPTGKIKERNQFSKKEEMDIDDSKV--EFDAN--SPYDHPVNVINCKEKSNS----317DKKALTELELVVSSFSKNDLVEPESIQQNI
234 NY-VLYRK 240VYPTGKIKERNQFSKKEEMDIDDSKV--EFDAN--SPYDHPVNVINCKEKSNS----317DKKALTELELVVSSFSKNDLVEPESIQQNI
192 H-CIRYR 197LRFKATKMGKNGKHYRDLSKLNRRDPKVI-LVSGHAFENSLOPENCVCKPKWKEE---372DTSLDLALFKLHLSDAKVEPFR
252 QKC-CHRYR 259VYPTGKIKERNQFSKKEEMDIDDSKV--EFDAN--SPYDHPVNVINCKEKSNS----317DKKALTELELVVSSFSKNDLVEPESIQQNI
93 R-VLADKATYKMGKNGKHYRDLSKLNRRDPKVI-LVSGHAFENSLOPENCVCKPKWKEE---372DTSLDLALFKLHLSDAKVEPFR
251 QKC-CHRYR 259VYPTGKIKERNQFSKKEEMDIDDSKV--EFDAN--SPYDHPVNVINCKEKSNS----317DKKALTELELVVSSFSKNDLVEPESIQQNI
237 KC-NURHR 243VYPTGKIKERNQFSKKEEMDIDDSKV--EFDAN--SPYDHPVNVINCKEKSNS----317DKKALTELELVVSSFSKNDLVEPESIQQNI
238 PKC-CVORR 243VYPTGKIKERNQFSKKEEMDIDDSKV--EFDAN--SPYDHPVNVINCKEKSNS----317DKKALTELELVVSSFSKNDLVEPESIQQNI
243 TKG-FHTGR 250VYPTGKIKERNQFSKKEEMDIDDSKV--EFDAN--SPYDHPVNVINCKEKSNS----317DKKALTELELVVSSFSKNDLVEPESIQQNI
250 SRG-TSHRR 257VYPTGKIKERNQFSKKEEMDIDDSKV--EFDAN--SPYDHPVNVINCKEKSNS----317DKKALTELELVVSSFSKNDLVEPESIQQNI
70 YD-EPATKYKMGKNGKHYRDLSKLNRRDPKVI-LVSGHAFENSLOPENCVCKPKWKEE---372DTSLDLALFKLHLSDAKVEPFR
242 QKC-CHRYR 242VYPTGKIKERNQFSKKEEMDIDDSKV--EFDAN--SPYDHPVNVINCKEKSNS----317DKKALTELELVVSSFSKNDLVEPESIQQNI
248 KKU-CHRYR 255VYPTGKIKERNQFSKKEEMDIDDSKV--EFDAN--SPYDHPVNVINCKEKSNS----317DKKALTELELVVSSFSKNDLVEPESIQQNI
189 -----188-----188-----

ep|Q55C70
77112|77112
30026.t000051|30026.m001487
Potri.004G062900
Potri.011G072000
g1|74966225
g1|48526509
g1|530417566
Crel2.g505950|Crel2.g505950.t1.2
Vocar20000934
Esi0000.0471
g1|164427612
CMN179C|CMN179C
Medtr5g095530|Medtr5g095530.1
Glyma02g46900|Glyma02g46900.1
Glyma14g01810|Glyma14g01810.1
AT1G55900.
Carubv10009325m.g|Carubv10009325m
Bra030827|Bra030827
Bra037095|Bra037095
Cucsa.390900|Cucsa.390900.1
Phpat.020G041400|Phpat.020G041400.1
124475|124475
Phpat.008G082000|Phpat.008G082000.1
GRMZM5G896568|GRMZM5G896568.T01
LOC_Os01g55700|LOC_Os01g55700.1
LOC_Os05g43770|LOC_Os05g43770.1
GRMZM2G035651|GRMZM2G035651.T01
GRMZM2G041091|GRMZM2G041091.T01
Bucgr.F02057|Bucgr.F02057.1
GSVIVG01030074001|GSVIVT01030074001
GSVIVG01014657001|GSVIVT01014657001
PGSC0003DMG400022178|PGSC0003DMT40005708
PGSC0003DMG400022178|PGSC0003DMT40005708
PGSC0003DMG400022178|PGSC0003DMT40005708
29629.t000047|29629.m001396
Potri.001G364500|Potri.001G364500.1
Potri.001G366300|Potri.001G366300.1
Potri.011G093000

351 SKQSLTKMLDYLSTHNNRSRQK---374-----374-----
239 RY*-----240-----240-----
294 K-KVNVQV-----300-----300-----
288 E-VLLITN-----F-----DL 298CFSNYALPCYDFAFIPQLLEK-----320-----KSDLQLSKPC
287 E-EQVYV*-----292-----292-----
400 QYVQYDPAK-EFRSRAVLSQEQKQNP 430DDSCM-LKYS-GRFSGRHH-----VNA-----452-----
402 EHVYLDDEPLA-EFKGQSRSLGQQRILAE 432SKNK-QNPLGSLTSRLWPRSKQ-----P-----456-----
197 AFKQQRSLQEQOORLAE 216SKNK-QNPLGSLTSRLWPRSKQ-----P-----240-----
351 DMVPA-AFKARLQQAASHQKQVRR-374-----PSELA-----PH*-----382-----
321 QDHPA-AFKARLQQAASHQKQVRR-343-----GFLM-----PFR*-----350-----
880 YLATQTKDVPFLNSFDK-NLA-BEFDHRVKKLDFK-YGDHK-922-----GGNWAMTALGLG-----NSLGS-----TKF-----
367 GG-HIT 281LRFKATKMGKNGKHYRDLSKLNRRDPKVI-LVSGHAFENSLOPENCVCKPKWKEE---372DTSLDLALFKLHLSDAKVEPFR
350 DIPS-EFIRRSKEHORR-OBQK-329-----RGRFWK-----*-----335-----
306 DIPS-EFIRRSKEHORR-OBQK-327-----RGRFWK-----*-----333-----
348 DITAK-EFLERSKDYORR-OBQK-369-----QGRWR-----R*-----376-----
345 DVAK-EFLERSKDYORR-OBQK-356-----QGRWR-----R*-----403-----
328 DVAK-EFLERSKDYORR-OBQK-348-----QGRWR-----R*-----355-----
286 IPT-EFIRRSKEHORR-OBQK-306-----QGRWR-----R*-----313-----
347 DVPT-EFIRRSKEHORR-OBQK-368-----TGRWR-----GSSV*-----378-----
187 BERNKQORF-----197-----SWI-----SI*-----202-----
346 IPT-EFIRRSKEHORR-OBQK-367-----TGRWR-----GRQ*-----376-----
333 DVAK-EFIRRSKEHORR-OBQK-352-----QGRWR-----R*-----359-----
333 DMVA-EFIRRSKEHORR-OBQK-354-----QGRWR-----R*-----361-----
338 DVAA-EFIRRSKEHORR-OBQK-359-----QGRWR-----R*-----366-----
346 DVAA-EFIRRSKEHORR-OBQK-367-----QGRWR-----R*-----374-----
165 TERSKEHORR-OBQK-180-----LGRLWR-----R*-----187-----
330 NLAG-EFLERSKDYORR-OBQK-351-----TGRWR-----R-----352-----
334 DVPT-EFIRRSKEHORR-OBQK-355-----QGRWR-----R*-----362-----
343 DITAK-EFIRRSKEHORR-OBQK-364-----QGRWR-----R*-----371-----
189 -----188-----188-----
213 IAK-EFIRRSKEHORR-OBQK-338-----TGRWR-----R*-----345-----
313 EFIRRSKEHORR-OBQK-230-----TGRWR-----R*-----237-----
367 DVAK-EFLERSKDYORR-OBQK-353-----QGRWR-----R-----360-----
332 DVGK-EFLERSKDYORR-OBQK-353-----QGRWR-----R*-----360-----
333 DLGK-EFLERSKDYORR-OBQK-354-----QGRWR-----R*-----361-----

ep|Q55C70
77112|77112
30026.t000051|30026.m001487
Potri.004G062900
Potri.011G072000
g1|74966225
g1|48526509
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Crel2.g505950|Crel2.g505950.t1.2
Vocar20000934
Esi0000.0471
g1|164427612
CMN179C|CMN179C
Medtr5g095530|Medtr5g095530.1
Glyma02g46900|Glyma02g46900.1
Glyma14g01810|Glyma14g01810.1
AT1G55900.
Carubv10009325m.g|Carubv10009325m
Bra030827|Bra030827
Bra037095|Bra037095
Cucsa.390900|Cucsa.390900.1
Phpat.020G041400|Phpat.020G041400.1
124475|124475
Phpat.008G082000|Phpat.008G082000.1
GRMZM5G896568|GRMZM5G896568.T01
LOC_Os01g55700|LOC_Os01g55700.1
LOC_Os05g43770|LOC_Os05g43770.1
GRMZM2G035651|GRMZM2G035651.T01
GRMZM2G041091|GRMZM2G041091.T01
Bucgr.F02057|Bucgr.F02057.1
GSVIVG01030074001|GSVIVT01030074001
GSVIVG01014657001|GSVIVT01014657001
PGSC0003DMG400022178|PGSC0003DMT40005708
PGSC0003DMG400022178|PGSC0003DMT40005708
PGSC0003DMG400022178|PGSC0003DMT40005708
29629.t000047|29629.m001396
Potri.001G364500|Potri.001G364500.1
Potri.001G366300|Potri.001G366300.1
Potri.011G093000

375 -----374-----374-----
241 -----240-----240-----
301 -----300-----300-----
331 KTFKMNVSPTVQSGWMTICEVCK-----356-----356-----
293 -----292-----292-----
453 -----452-----452-----
457 -----456-----456-----
383 -----240-----240-----
382 -----382-----382-----
351 -----350-----350-----
945 -944-PLLDLHEEGQKNYLM-FMKMIEEKEKIRIQEQMGQTFT 984LKDYVGNLPSPEEQMKIQLEKQKEDALFEEKKKKKIAE
437 ARERGMNRYLAMBEETKKNNGEMWLMKQEAQKA-QKEMMNQSS 481VFGVFGG-APSGEQSGES EKKA-----503-----
381 -SASSPAAQVDPDQSIWTLR-----374-----374-----
336 -----335-----335-----
334 -----333-----333-----
377 -----376-----376-----
404 -----403-----403-----
373 -----372-----372-----
314 -----313-----313-----
309 -----308-----308-----
273 -----202-----202-----
379 -----376-----376-----
367 -----361-----361-----
372 -----366-----366-----
375 -----374-----374-----
188 -----187-----187-----
359 -----358-----358-----
363 -----362-----362-----
372 -----371-----371-----
189 -----188-----188-----
236 -----237-----237-----
348 -----345-----345-----
396 -----395-----395-----
361 -----360-----360-----
362 -----361-----361-----

sp|Q55C70
77112|77112
30026.t000051|30026.m001487
Potri.004G062900
Potri.011G072000
gi|74966225
gi|48526509
gi|530417566
Cre12.g505950|Cre12.g505950.t1.2
Vocar20000934
Esi000.0471
gi|164427612
CMN179C|CMN179CT
Medtr5g095530|Medtr5g095530.1
Glyma02g46900|Glyma02g46900.1
Glyma14g01810|Glyma14g01810.1
At1G5900
Carubv10009325m.g|Carubv10009325m
Bra030827|Bra030827
Bra037095|Bra037095
Cucsa.390900|Cucsa.390900.1
Phpat.020G041400|Phpat.020G041400.1
124475|124475
Phpat.008G082000|Phpat.008G082000.1
GRMZM5G896568|GRMZM5G896568.T01
LOC_Os01g55700|LOC_Os01g55700.1
LOC_Os05g43770|LOC_Os05g43770.1
GRMZM2G035651|GRMZM2G035651.T01
GRMZM2G441091|GRMZM2G441091.T01
Eucgr.F02057|Eucgr.F02057.1
GSVIVG01030074001|GSVIVT01030074001
GSVIVG01014657001|GSVIVT01014657001
PGSC0003DMG400022178|PGSC0003DMT40005708
PGSC0003DMG400022178|PGSC0003DMT40005708
PGSC0003DMG400022178|PGSC0003DMT40005708
29629.t000047|29629.m001396
Potri.001G364500|Potri.001G364500.1
Potri.001G366300|Potri.001G366300.1
Potri.011G093000

1026 SK* 1027