

gi | 85092415 1 ----- 0 -----
gi | 85115828 1 ----- 0 -----
gi | 164424111 1 ----- 0 -----
gi | 11342664 1 ----- 0 -----
gi | 222136617 1 ----- 0 -----
Esi0024_0159 1 ----- 0 -----
Esi0021_0042 1 ----- 0 -----
Esi0103_0037 1 ----- 0 -----
gi | 193204309 1 ----- 0 -----
Esi0343_0016 1 ----- 0 -----
YOR211C 1 ----- 0 -----
gi | 71981891 1 ----- 0 -----
gi | 56549125|ref NP_001005362.1|dynamin-2 1 ----- 0 -----
gi | 59853099|ref NP_004399.2|dynamin-1 1 ----- 0 -----
PGSC0003DMG400010899 1 ----- 0 -----
Vocar20015232m.g|Vocar20015232m 1 ----- 0 -----
Cre17.g724150|Cre17.g724150.t1.1 1 ----- 0 -----
Vocar20001129m.g|Vocar20001129m 1 ----- 0 -----
gi | 85111713 1 ----- 0 -----
CME019C|CME019CT 1 ----- 0 -----
gi | 85099877 1 ----- 0 -----
gi | 71993833 1 ----- 0 -----
gi | 66816950|Dd 1 ----- 0 -----
Esi0029_0136 1 ----- 0 -----
101670|101670|Sm 1 ----- 0 -----
404911|404911|Sm 1 ----- 0 -----
Pphat.024G072600|Pphat.024G072600.1 1 MHETYDLLAHLRFGASSAKPGSKYLVIAGPPGAGKSTLANEVSGRVNKL-HQERNPGL 58VSE-TAIAVPMDFGH-LYKHQLDAMEDPEEAHARRGAPWTFNPSGLV
7242|437242|Sm 1 ----- 0 -----
Pphat.023G005400|Pphat.023G005400.1 1 ----- 0 -----
Pphat.020G019000|Pphat.020G019000.1 1 ----- 0 -----
Pphat.008G087300|Pphat.008G087300.1 1 ----- 0 -----
Pphat.023G066800|Pphat.023G066800.1 1 ----- 0 -----
gi | 66816205 1 ----- 0 -----
LOC_Os04g31190|LOC_Os04g31190.1 1 ----- 0 -----
AT2G14120 1 ----- 0 -----
Carubv10013019m.g|Carubv10013019m 1 ----- 0 -----
AT4G33650 1 ----- 0 -----
Carubv10004162m.g|Carubv10004162m 1 ----- 0 -----
Bra011458|Bra011458 1 ----- 0 -----
Bra036991|Bra036991 1 ----- 0 -----
Bra034579|Bra034579 1 ----- 0 -----
LOC_Os01g69130|LOC_Os01g69130.1 1 ----- 0 -----
GRMZM2G129155|GRMZM2G129155.T01 1 ----- 0 -----
GRMZM2G180335|GRMZM2G180335.T01 1 ----- 0 -----
Glyma20g06670|Glyma20g06670.1 1 ----- 0 -----
Medtr2g009690|Medtr2g009690.1 1 ----- 0 -----
Medtr4g093750|Medtr4g093750.1 1 ----- 0 -----
Glyma07g30150|Glyma07g30150.2 1 ----- 0 -----
Glyma08g07160|Glyma08g07160.1 1 ----- 0 -----
Glyma04g16340|Glyma04g16340.1 1 ----- 0 -----
Glyma13g32940|Glyma13g32940.1 1 ----- 0 -----
Glyma15g06380|Glyma15g06380.1 1 ----- 0 -----
Cucsa.331870|Cucsa.331870.1 1 ----- 0 -----
GSVIVG01012532001|GSVIVT01012532001 1 ----- 0 -----
Cucsa.218420|Cucsa.218420.1 1 ----- 0 -----
Potri.012G125300|Potri.012G125300.1 1 ----- 0 -----
Potri.007G118300|Potri.007G118300.1 1 ----- 0 -----
Potri.017G041800|Potri.017G041800.1 1 ----- 0 -----
29506.t000007|29506.m000169|Rc 1 ----- 0 -----
Eucgr.I02611|Eucgr.I02611.1 1 ----- 0 -----
29848.t000060|29848.m004504|Rc 1 ----- 0 -----
GSVIVG01036006001|GSVIVT01036006001 1 ----- 0 -----

gi | 85092415 1 ----- 0 -----
gi | 85115828 1 ----- 0 -----
gi | 164424111 1 ----- 0 -----
gi | 11342664 1 ----- 0 -----
gi | 222136617 1 ----- 0 -----
Esi0024_0159 1 ----- 0 -----
Esi0021_0042 1 ----- 0 -----
Esi0103_0037 1 ----- 0 -----
gi | 193204309 69 AFIGIAAASAARHL 81LKLRYFIATGVIGGSVAA-RTWYEEWKSNSLPLDSLPEWDFNSGNSWNEFSQMKMGKKGDPG 140ADGQNKWAEWMAKF-EQFKQKKE--DQNGN
Esi0343_0016 1 ----- 0 -----
YOR211C 62 HFPKII---SKI 70IRLPIY---VGGGMAA-AGSYIAYKMBE-ASS---FTKD-KLDRIKDLGSMKEKFN 118---KMFSG---DKS
gi | 71981891 1 ----- 0 -----
gi | 56549125|ref NP_001005362.1|dynamin-2 1 ----- 0 -----
gi | 59853099|ref NP_004399.2|dynamin-1 1 ----- 0 -----
PGSC0003DMG400010899 1 ----- 0 -----
Vocar20015232m.g|Vocar20015232m 1 ----- 0 -----
Cre17.g724150|Cre17.g724150.t1.1 1 ----- 0 -----
Vocar20001129m.g|Vocar20001129m 1 ----- 0 -----
gi | 85111713 1 ----- 0 -----
CME019C|CME019CT 1 ----- 0 -----
gi | 85099877 1 ----- 0 -----
gi | 71993833 1 ----- 0 -----
gi | 66816950|Dd 35 Y-----TIK 38-N-----KKYYSQYKYSIQFQNEF-----QKN-----LKI---YN 64NSNNNNNNN-----NNNKI
Esi0029_0136 1 ----- 0 -----
101670|101670|Sm 1 ----- 0 -----
404911|404911|Sm 104 DCLKAL---RSQ 112-Q-----WAYFFSFDHGVDG-P---VEQD-ILVSPKHVVLVREGNYL 148LLEDGEWKE-----LK
Pphat.024G072600|Pphat.024G072600.1 1 ----- 0 -----
437242|437242|Sm 1 ----- 0 -----
Pphat.023G005400|Pphat.023G005400.1 1 ----- 0 -----
Pphat.020G019000|Pphat.020G019000.1 1 ----- 0 -----
Pphat.008G087300|Pphat.008G087300.1 1 ----- 0 -----
Pphat.023G066800|Pphat.023G066800.1 1 ----- 0 -----
gi | 66816205 1 ----- 0 -----
LOC_Os04g31190|LOC_Os04g31190.1 1 ----- 0 -----
AT2G14120 1 ----- 0 -----
Carubv10013019m.g|Carubv10013019m 1 ----- 0 -----
AT4G33650 1 ----- 0 -----
Carubv10004162m.g|Carubv10004162m 1 ----- 0 -----
Bra011458|Bra011458 1 ----- 0 -----
Bra036991|Bra036991 1 ----- 0 -----
Bra034579|Bra034579 1 ----- 0 -----
LOC_Os01g69130|LOC_Os01g69130.1 1 ----- 0 -----
GRMZM2G129155|GRMZM2G129155.T01 1 ----- 0 -----
GRMZM2G180335|GRMZM2G180335.T01 1 ----- 0 -----
Glyma20g06670|Glyma20g06670.1 1 ----- 0 -----
Medtr2g009690|Medtr2g009690.1 1 ----- 0 -----
Medtr4g093750|Medtr4g093750.1 1 ----- 0 -----
Glyma07g30150|Glyma07g30150.2 1 ----- 0 -----
Glyma08g07160|Glyma08g07160.1 1 ----- 0 -----
Glyma04g16340|Glyma04g16340.1 1 ----- 0 -----
Glyma13g32940|Glyma13g32940.1 1 ----- 0 -----
Glyma15g06380|Glyma15g06380.1 1 ----- 0 -----
Cucsa.331870|Cucsa.331870.1 1 ----- 0 -----
GSVIVG01012532001|GSVIVT01012532001 13 CLERS---SSI 20-S-----RRFAAKFSGFFSNRKEDSPSH---FEAV-KLLLLKTKVLVI---FF 60CTVGTMYKG-----NKTFI
Cucsa.218420|Cucsa.218420.1 1 ----- 0 -----
Potri.012G125300|Potri.012G125300.1 1 ----- 0 -----
Potri.007G118300|Potri.007G118300.1 1 ----- 0 -----
Potri.017G041800|Potri.017G041800.1 1 ----- 0 -----
29506.t000007|29506.m000169|Rc 1 ----- 0 -----
Eucgr.I02611|Eucgr.I02611.1 1 ----- 0 -----
29848.t000060|29848.m004504|Rc 1 ----- 0 -----
GSVIVG01036006001|GSVIVT01036006001 1 ----- 0 -----

gi | 85092415 99 ----- ATEKALSARFKMSTSFDF ----- HLPDIMEKA
gi | 85115828 98 ----- SSEQQLLFCRLINSSS ----- PFDLTMGA
gi | 164424111 97 ----- EAERKATLRYSRKLSSSTELR ----- DQFALKDEV
gi | 11342664 178 ----- 177 ----- LELQDPGQWEKE
gi | 222136617 131 ----- 130 ----- LELQDPGQWEKE
Esi024_0159 106 ----- 118 ----- RG ----- PDPHAA ----- GHVA ----- PSEVGVZ
Esi0021_0042 106 ----- 105 ----- QQQHGASSLWRKTSSTKTSADFFPCP ----- RSASTPELTKVIE
Esi0103_0037 317 ----- 116 ----- PKRS ----- HSASTPGQLTKLE
gi | 193204309 142 ----- 341 ----- HAVIGQ ----- DSSREF ----- DL ----- TKETDL
Esi0343_0016 87 ----- 86 ----- ADLSK ----- QHITGDEITSDIER -----
YOR211C 260 ----- 259 ----- NVTADF ----- PSVLR ----- YNDF
gi | 71981891 79 ----- 78 ----- RMEYAEF ----- LHKKG ----- HRFVDFDAEIRDF
gi | 56549125 | ref | NP_001005362.1 | | dynamin-2 0 ----- 76 ----- TBYAEF ----- LHCKG ----- KMTDFEVRLEIEA
gi | 59853099 | ref | NP_004399.2 | | dynamin-1 77 ----- 82 ----- GQDYAEF ----- GHLPR ----- TFFDFSLVQKEIQD
PGSC0003DMG400010899 83 ----- 81 ----- SAQDYGEF ----- SHAPG ----- RHIFSEDIRKEIED
Vocar20015232m.g | Vocar20015232m 82 ----- 85 ----- P ----- SGRSDFGEF ----- LHAFG ----- KMFDFDRREIHW
Cre17_g724130 | Cre17_g724150.t1.1 86 ----- 86 ----- 87SYR ----- NFNAAGRNWAEF ----- HHPFN ----- RRFDFDGVKREIEN
Vocar20001129m.g | Vocar20001129m 86 ----- 102 ----- RSIPPAENAYAEF ----- LKPKG ----- VRYFNDVDAIRHEA
CME019C | CME019C 90 ----- NE 98LDDNDAKNAIDWGEF ----- LHPFG ----- KRFFYDFNLRDEISR
gi | 85099877 97 ----- 81 ----- RSNGLTLLDWDWAF ----- EHTGS ----- KVDFDFDAIRKEID
gi | 71993833 82 ----- DN 22LYDNDNDNLEWGEF ----- GHGFT ----- WRFWQE
Esi0029_0136 | Dd 111 BSGVYTVGRQDSGSGLVGGRVAAPFGSSNGSVLPGGAPRTPSRTGRSGFAGGGLS 167PFPSPKPTPEREWEF ----- LHLPG ----- QKFFFAIRKEIIE
101670 | 101670 | Sm 105 ----- 104 ----- MDDR ----- EYSEWGEF ----- LHLPG ----- RRFDFDFAIRKEIQ
404911 | 404911 | Sm 245 ----- 244 ----- MDDR ----- EFSEWGEF ----- LHLPG ----- RRFDFDFAIRKEIQ
Pphat_024G072600 | Pphat_024G072600.1 108 ----- 107 ----- PEDRAM -----
437242 | 437242 | Sm 96 ----- 95 ----- GD ----- EVWGEF ----- LHLPG ----- RRFDFDFAIRKEIQ
Pphat_023G005400 | Pphat_023G005400.1 97 ----- 87 ----- SDESELVWGEF ----- LHLPG ----- RRFDFDFAIRKEIQ
Pphat_02G0190000 | Pphat_02G0190000.1 108 ----- 107 ----- PEDRA ----- ELWGEF ----- LHPFG ----- RRFDFDFAIRKEIQ
Pphat_008G087300 | Pphat_008G087300.1 108 ----- 107 ----- AEDQI ----- VEWGEF ----- LHPG ----- RRFDFDFAIRKEIQ
Pphat_023G066800 | Pphat_023G066800.1 102 ----- 101 ----- PEDRA ----- ELWGEF ----- LHPG ----- RRFDFDFAIRKEIQ
gi | 66816205 74 ----- 73 ----- DDGS ----- QTEWGEF ----- LHKFN ----- DMFDFSEIRREIR
LOC_0s04g31190 | LOC_0s04g31190.1 93 ----- 92 ----- FEWGEF ----- LHPG ----- RRFDFDFAIRKEIQ
AT2614120 92 ----- 91 ----- SGG ----- SEWGEF ----- LHPG ----- RRFDFDFAIRKEIQ
Carubv10013019m.g | Carubv10013019m 93 ----- 91 ----- SGG ----- SEWGEF ----- LHPG ----- RRFDFDFAIRKEIQ
AT4G33650 108 ----- 107 ----- ANGG ----- SDEWGEF ----- RHLPE ----- TRFDFSEIRREIE
Carubv10004162m.g | Carubv10004162m 105 ----- 104 ----- SGG ----- SDEWGEF ----- RHLPE ----- TRFDFSEIRREIE
Bra011458 | Bra011458 95 ----- 94 ----- ASGG ----- SDDWGEF ----- LHLPG ----- RRFDFDFAIRKEIQ
Bra036991 | Bra036991 96 ----- 95 ----- SGG ----- SDEWGEF ----- LHLPSNR ----- YDFSEIRREIEA
Bra034579 | Bra034579 19 ----- 105 ----- 3ANG ----- SDEWGEF ----- LHLPSNR ----- YDFSEIRREIEA
LOC_0s01g69130 | LOC_0s01g69130.1 99 ----- 98 ----- PADA ----- EADWGEF ----- LHLPG ----- RRFDFDFAIRKEIQ
GRMZM2G129155 | GRMZM2G129155.T01 99 ----- 98 ----- PADA ----- EADWGEF ----- LHLPG ----- RRFDFDFAIRKEIQ
GRMZM2G180335 | GRMZM2G180335.T01 102 ----- 101 ----- PADA ----- EADWGEF ----- LHLPG ----- RRFDFDFAIRKEIQ
Glyma20g06670 | Glyma20g06670.1 13 ----- 12 ----- PHCH ----- INHWQA -----
Medtr2g009690 | Medtr2g009690.1 93 ----- 92 ----- E ----- PADWGEF ----- LHLPG ----- RRFDFDFAIRKEIQ
Medtr4g093750 | Medtr4g093750.1 84 ----- 83 ----- R ----- SKP ----- SAEF ----- LHPG ----- RRFDFDFAIRKEIQ
Glyma07g30150 | Glyma07g30150.2 84 ----- 83 ----- P ----- SODWGEF ----- LHPG ----- RRFDFDFAIRKEIQ
Glyma08g07160 | Glyma08g07160.1 84 ----- 93 ----- P ----- EDLWGEF ----- LHPG ----- RRFDFDFAIRKEIQ
Glyma04g16340 | Glyma04g16340.1 94 ----- 92 ----- PNLD ----- NNDWGEF ----- LHLPG ----- RRFDFDFAIRKEIQ
Glymal3g32940 | Glymal3g32940.1 93 ----- 92 ----- PD ----- NDWGEF ----- LHLPG ----- RRFDFDFAIRKEIQ
Glymal5g06380 | Glymal5g06380.1 95 ----- 94 ----- 182 ----- 0 -----
Cucsa_31870 | Cucsa_31870.1 95 ----- 182 ----- 0 ----- PDGS ----- DEYGEF ----- LHLPG ----- RRFDFDFAIRKEIQ
GSVIVG01012532001 | GSVIVT01012532001 183 ----- 94 ----- BEYGEF ----- LHPG ----- RRFDFDFAIRKEIQ
Cucsa_218420 | Cucsa_218420.1 95 ----- 84 ----- GDGS ----- GELWGEF ----- LHPG ----- RRFDFDFAIRKEIQ
Potri_012G125300 | Potri_012G125300.1 91 ----- 90 ----- GDGS ----- GELWGEF ----- LHPG ----- RRFDFDFAIRKEIQ
Potri_007G118300 | Potri_007G118300.1 85 ----- 99 ----- GDGS ----- GEWGEF ----- LHPG ----- RRFDFDFAIRKEIQ
Potri_017G041800 | Potri_017G041800.1 100 ----- 97 ----- ADGS ----- EADWGEF ----- LHPG ----- RRFDFDFAIRKEIQ
29506.t000007 | 29506.m000169 | Rc 101 ----- 100 ----- PDGA ----- SEWGEF ----- LHPG ----- RRFDFDFAIRKEIQ
Eucgr_102611 | Eucgr_102611.1 101 ----- 92 ----- TDD ----- SIA ----- FGEF ----- RHLPG ----- RRFDFDFAIRKEIQ
29848.t000060 | 29848.m004504 | Rc 93 ----- 10 ----- GSD ----- DARWGEF ----- RHLPG ----- RRFDFDFAIRKEIQ
GSVIVG0103606001 | GSVIVT0103606001 43 -----

gi | 85092415 126 KNYMGIS --- 132 --- TQQCAFNHRRHAEVETGDRPHLHVDLDFGLHSHETKNTAAADYQLKQVVRSH 187MNSPSSKLAWVSNKNFANQVVMKARADDP
gi | 85115828 126 AELIAPK --- 132 --- VGFGRFAARDILVVEKKGDMPLLDLVDLDFGRVNRNKKKQGLEDIHICALSDRY 187MSRRTILAVFVNSHYVGAFLTKARHDDP
gi | 164424111 128 NVYMKKIKDKK 137N --- PFGRETFSRDIKIEKCCGTEDEYLVWDFPHRLSKGCTTESDRNLDVDDVW 194IKDKRTILAVFVNSHYVGAFLTKARHDDP
gi | 11342664 190 THK --- 197 --- AQNYM 197 --- AGNRGISHELELEITSPVFDLITLDFGITRVAVDNQRDGLKHALKIKY 252IQQRQNLNVVPCNVMDITLALSMAH
gi | 222136617 144 NK --- AQNAI 150 --- AGEQMGISHEHITLEISSRVPVPLDIDLPGRTRAVAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
Esi0024_0159 141 E --- LMNAV 146C --- EGGQNGFSSDFRAMEIKSPDCDDITLDFLPGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
Esi0021_0042 148 D --- LDGL 153T --- AGDQGFSTAESVQVQGLDITLDFLPGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
Esi0103_0037 135 R --- LDDG 140T --- STSMPSTENLVLSPPVDFVDFLPGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
gi | 193204309 356 QQLRNETV --- RMRN 368S --- VRDQTVSNVNSISLVKGNLRNLDVDFLPGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
Esi0343_0016 114 --- LTMG 117L --- AGDGTAVSAKPIYLKIFSPVLTMTLVDLDFGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
YOR211C 277 KEVKRMLM --- ELNN 288A --- VPTSEASEEPIQLHFKGSRVPLDITLDFLPGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
gi | 71981891 106 --- ETR 109V --- TGQNGKISPPHINLRFVSPVNLITLDFLPGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
gi | 56549125 | ref | NP_001005362.1 | | dynamin-2 104 --- ETR 107V --- TGNKNGISFPVNLIRVSPVNLITLDFLPGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
gi | 59853099 | ref | NP_004399.2 | | dynamin-1 111 --- ETR 141 --- TGKTRQISFVPHILSIVSPVNLITLDFLPGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
PGSC0003DMG400010899 104 --- ETR 113HLHKMGKQVSPFIYLVYVSNVNLITLDFLPGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
Vocar20015232m.g | Vocar20015232m 117 --- ETR 120L --- VGNKNVSDPKIRLKIIFSPVLTMTLVDLDFGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
Cre17_g724130 | Cre17_g724150.t1.1 117 --- ETR 120L --- VGNKNVSDPKIRLKIIFSPVLTMTLVDLDFGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
Vocar20001129m.g | Vocar20001129m 124 --- ETR 141V --- VGNKNVSDPKIRLKIIFSPVLTMTLVDLDFGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
gi | 85115828 138 --- ETR 141V --- VGNKNVSDPKIRLKIIFSPVLTMTLVDLDFGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
CME019C | CME019C 136 --- ETR 139K --- VGNKNVSDPKIRLKIIFSPVLTMTLVDLDFGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
gi | 85099877 116 --- ETR 119V --- VGNKNVSDPKIRLKIIFSPVLTMTLVDLDFGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
gi | 71993833 251 IKKEIR --- ETR 261T --- AGPNKDISSEPIVLRHYSKVPVPLDITLDFLPGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
gi | 66816205 | Dd 205 --- ETR 208L --- LGNKGISAKSINLRIYSPVNLITLDFLPGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
101670 | 101670 | Sm 136 A --- ETR 140E --- LGNKGISAKSINLRIYSPVNLITLDFLPGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
404911 | 404911 | Sm 267 PSHRIFLA --- ETR 280E --- AGDKGVSDKQIRLKIIFSPVLTMTLVDLDFGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
Pphat_024G072600 | Pphat_024G072600.1 115 --- ETR 114 --- KQRLKIFSPVNLITLDFLPGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
437242 | 437242 | Sm 126 --- ETR 129E --- LGNKGISAKSINLRIYSPVNLITLDFLPGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
Pphat_023G005400 | Pphat_023G005400.1 121 --- ETR 124D --- MGNKGISAKSINLRIYSPVNLITLDFLPGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
Pphat_02G0190000 | Pphat_02G0190000.1 140 A --- ETR 144E --- LGNKGISAKSINLRIYSPVNLITLDFLPGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
Pphat_008G087300 | Pphat_008G087300.1 140 A --- ETR 144E --- LGNKGISAKSINLRIYSPVNLITLDFLPGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
Pphat_023G066800 | Pphat_023G066800.1 134 A --- ETR 138E --- LGNKGISAKSINLRIYSPVNLITLDFLPGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
gi | 66816205 106 --- DTR 109M --- TGNKNGISAOINLKIYSPVNLITLDFLPGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
LOC_0s04g31190 | LOC_0s04g31190.1 120 --- EDK 123E --- AGNKGVSQKQIRLKIIFSPVLTMTLVDLDFGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
AT2614120 125 --- ENR 128V --- SGNKGVSDPKIRLKIIFSPVLTMTLVDLDFGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
Carubv10013019m.g | Carubv10013019m 125 --- ENR 128V --- SGNKGVSDPKIRLKIIFSPVLTMTLVDLDFGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
AT4G33650 137 A --- ETR 141L --- VGNKNVSDPKIRLKIIFSPVLTMTLVDLDFGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
Carubv10004162m.g | Carubv10004162m 127 --- ENR 130L --- VGNKGVSDPKIRLKIIFSPVLTMTLVDLDFGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
Bra011458 | Bra011458 129 --- ENR 132L --- AGNKGVSQKQIRLKIIFSPVLTMTLVDLDFGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
Bra036991 | Bra036991 138 A --- ETR 142L --- AGNKGVSQKQIRLKIIFSPVLTMTLVDLDFGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
Bra034579 | Bra034579 131 --- ETR 134E --- AGNKGVSQKQIRLKIIFSPVLTMTLVDLDFGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
LOC_0s01g69130 | LOC_0s01g69130.1 131 --- ETR 134E --- AGNKGVSQKQIRLKIIFSPVLTMTLVDLDFGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
GRMZM2G129155 | GRMZM2G129155.T01 133 A --- ETR 137E --- AGNKGVSQKQIRLKIIFSPVLTMTLVDLDFGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
GRMZM2G180335 | GRMZM2G180335.T01 36 --- KTR 39E --- VGNKGVSDPKIRLKIIFSPVLTMTLVDLDFGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
Glyma20g06670 | Glyma20g06670.1 122 --- ETR 125E --- AGNKGVSQKQIRLKIIFSPVLTMTLVDLDFGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
Medtr2g009690 | Medtr2g009690.1 113 --- ETR 116E --- AGNKGVSQKQIRLKIIFSPVLTMTLVDLDFGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
Medtr4g093750 | Medtr4g093750.1 113 --- ETR 116E --- AGNKGVSQKQIRLKIIFSPVLTMTLVDLDFGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
Glyma07g30150 | Glyma07g30150.2 113 --- ETR 116E --- AGNKGVSQKQIRLKIIFSPVLTMTLVDLDFGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
Glyma08g07160 | Glyma08g07160.1 123 --- ETR 128E --- AGNKGVSQKQIRLKIIFSPVLTMTLVDLDFGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
Glyma04g16340 | Glyma04g16340.1 125 --- ETR 128E --- AGNKGVSQKQIRLKIIFSPVLTMTLVDLDFGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
Glymal3g32940 | Glymal3g32940.1 122 --- ETR 125E --- VGNKGVSDPKIRLKIIFSPVLTMTLVDLDFGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
Glymal5g06380 | Glymal5g06380.1 122 --- ETR 125E --- VGNKGVSDPKIRLKIIFSPVLTMTLVDLDFGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
Cucsa_31870 | Cucsa_31870.1 208 HRIQA --- ETR 217E --- AGNKGVSQKQIRLKIIFSPVLTMTLVDLDFGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
GSVIVG01012532001 | GSVIVT01012532001 122 --- ETR 125E --- VGNKGVSDPKIRLKIIFSPVLTMTLVDLDFGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
Cucsa_218420 | Cucsa_218420.1 117 --- ETR 120E --- AGNKGVSQKQIRLKIIFSPVLTMTLVDLDFGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
Potri_012G125300 | Potri_012G125300.1 123 --- ETR 126E --- AGNKGVSQKQIRLKIIFSPVLTMTLVDLDFGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
Potri_007G118300 | Potri_007G118300.1 123 --- ETR 126E --- AGNKGVSQKQIRLKIIFSPVLTMTLVDLDFGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
Potri_017G041800 | Potri_017G041800.1 123 --- ETR 135E --- AGNKGVSQKQIRLKIIFSPVLTMTLVDLDFGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
29506.t000007 | 29506.m000169 | Rc 129 --- ETR 132E --- AGNKGVSQKQIRLKIIFSPVLTMTLVDLDFGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
Eucgr_102611 | Eucgr_102611.1 131 A --- ETR 135E --- AGNKGVSQKQIRLKIIFSPVLTMTLVDLDFGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
29848.t000060 | 29848.m004504 | Rc 125 --- ETR 128E --- AGNKGVSQKQIRLKIIFSPVLTMTLVDLDFGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH
GSVIVG0103606001 | GSVIVT0103606001 43 --- ETR 46G --- AGNKGVSQKQIRLKIIFSPVLTMTLVDLDFGITRVAAGNQPADIGYKILIKY 205IQQRQNTISLVVPSVNDITLALSMAH

gi | 85092415 220 PGRRT --- I-GVLTKPLDMDRGT 239SEKQYVDAKNN--QVEEFR LGVHVLNKKDSDKKAANN--VVVE 276
gi | 85115828 220 NGRRT --- I-GVLTKPLDMDRGT 238LEKQVVDVKNRNRHFR LGVYVLLNPGPRTTEGETWPSAEQ 280
gi | 164424111 227 UGRRT --- I-GVLTKPLDMDRGT 245AKAVCNVLTG--RKAANN LGVYLVNRRGGDDSDSDK--DSG 284
gi | 11342664 281 VDPEDGDRT --- I-GVLTKPLDMDRGT 303-EKSVNVRN--I-FYFLK-KGVYVNRKCGQOQIENRSL--LAE 341
gi | 222136617 235 VDPEDGDRT --- I-GVLTKPLDMDRGT 256-EKQVVDVKNR--I-FYFLK-KGVYVNRKCGQOQIENRSL--LAE 341
Esi0024_0159 233 PPSGKPLR --- I-GVLTKPLDMDRGT 253-EKQVVDVKNR--I-FYFLK-KGVYVNRKCGQOQIENRSL--LAE 341
Esi0021_0042 240 PPSGKPLR --- I-GVLTKPLDMDRGT 260-EDEAVLAKLN--VRKPK-KGVYVNRKCGQOQIENRSL--LAE 341
Esi0103_0037 246 PPSGKPLR --- I-GVLTKPLDMDRGT 246-EDEAVLAKLN--VRKPK-KGVYVNRKCGQOQIENRSL--LAE 341
gi | 193204309 447 VTLDSVSDPDSGKRT --- I-LVLTKVDMAEKLA 176NPDRIKKILEG--KLFPMKALGYFVGUVGRSSND--S-IDE 513
Esi0343_0016 206 GRRT --- I-GVLTKPLDMDRGT 223--PFAE--KARSELNN--KVPV--MGVGVITTT--E 229
YOR211C 366 ALASKAADPKGRT --- I-GVLTKPLDMDRGT 193--KARSELNN--KVPV--MGVGVITTT--E 229
gi | 71981891 193 GRRT --- I-GVLTKPLDMDRGT 216--KAREHEN--KPTLR-KGVYVNRKCGQOQIENRSL--LAE 276
gi | 56549125 ref | NP_001005362.1 | dynamin-2 197 GQRT --- I-GVLTKPLDMDRGT 214--KARDVLEN--KLLPLR-RGYI--VNRKCGQOQIENRSL--LAE 276
gi | 59853099 ref | NP_004399.2 | dynamin-1 204 GERL --- F-GVLTKPLDMDRGT 221--NALDVLGG--RAYRLQ-QPVI--VNRKCGQOQIENRSL--LAE 276
PGSC0003DMG400010899 206 GDRT --- I-GVLTKPLDMDRGT 223--KCRDVLGG--RTIKLK-HGWI--VNRKCGQOQIENRSL--LAE 276
Vocar20015232m.g | Vocar20015232m 210 GVRT --- I-GVLTKPLDMDRGT 227--KARSELNN--KVPV--MGVGVITTT--E 229
Cre17_g724150.t1.1 | Cre17_g724150.t1.1 217 GDRT --- I-GVLTKPLDMDRGT 234--NADDISG--RVYPLK-KGVY--VNRKCGQOQIENRSL--LAE 276
Vocar20001129m.g | Vocar20001129m 230 ECRRT --- I-GVLTKPLDMDRGT 248--DAMEVITG--KVIPLR-KGVY--VNRKCGQOQIENRSL--LAE 276
gi | 85099877 228 EGRRT --- I-GVLTKPLDMDRGT 246--DAMEVITG--KVIPLR-KGVY--VNRKCGQOQIENRSL--LAE 276
gi | 71993833 209 GQRT --- I-GVLTKPLDMDRGT 226--KARDVLEN--KLLPLR-RGYI--VNRKCGQOQIENRSL--LAE 276
Esi0616950 | Dd 342 KLAAQVDPDLGRT --- I-GVLTKPLDMDRGT 368--DAIDVLLG--NSVPLS-LGVYVNRKCGQOQIENRSL--LAE 276
Esi0029_0136 227 PPSGKPLR --- I-GVLTKPLDMDRGT 253-EKQVVDVKNR--I-FYFLK-KGVYVNRKCGQOQIENRSL--LAE 276
101670 | 101670 | Sm 227 PPSGKPLR --- I-GVLTKPLDMDRGT 247--DARSLLG--TVIPLR-LGYV--VNRKCGQOQIENRSL--LAE 276
404911 | 404911 | Sm 358 PSLQMAKLVDPDSGRT --- I-GVLTKPLDMDRGT 387--DARSLLG--TVIPLR-LGYV--VNRKCGQOQIENRSL--LAE 276
Phpat.024G072600 | Phpat.024G072600.1 191 PPSGKPLR --- I-GVLTKPLDMDRGT 212--DARNLLG--KVIPLR-KGVY--VNRKCGQOQIENRSL--LAE 276
437242 | 437242 | Sm 218 DGRRT --- I-GVLTKPLDMDRGT 236--DARNLLG--KVIPLR-KGVY--VNRKCGQOQIENRSL--LAE 276
Phpat.023G005400 | Phpat.023G005400.1 218 DGRRT --- I-GVLTKPLDMDRGT 236--DARNLLG--KVIPLR-KGVY--VNRKCGQOQIENRSL--LAE 276
Phpat.020G019000 | Phpat.020G019000.1 231 PPSGKPLR --- I-GVLTKPLDMDRGT 251--DARNLLG--KVIPLR-KGVY--VNRKCGQOQIENRSL--LAE 276
Phpat.008G087300 | Phpat.008G087300.1 231 PPSGKPLR --- I-GVLTKPLDMDRGT 251--DARNLLG--KVIPLR-KGVY--VNRKCGQOQIENRSL--LAE 276
Phpat.023G066800 | Phpat.023G066800.1 225 PPSGKPLR --- I-GVLTKPLDMDRGT 245--DARNLLG--KVIPLR-KGVY--VNRKCGQOQIENRSL--LAE 276
gi | 66816205 199 GQRT --- I-GVLTKPLDMDRGT 216--KAREHEN--KPTLR-KGVYVNRKCGQOQIENRSL--LAE 276
LOC_0s04g31190 | LOC_0s04g31190.1 212 DGRRT --- I-GVLTKPLDMDRGT 230--DARNLLG--KVIPLR-KGVY--VNRKCGQOQIENRSL--LAE 276
AT2G14120 217 DGRRT --- I-GVLTKPLDMDRGT 235--DARNLLG--KVIPLR-KGVY--VNRKCGQOQIENRSL--LAE 276
Carubv10013019m.g | Carubv10013019m 230 PPDGHRRT --- I-GVLTKPLDMDRGT 250--DARNLLG--KVIPLR-KGVY--VNRKCGQOQIENRSL--LAE 276
AT4G33650 228 PPDGHRRT --- I-GVLTKPLDMDRGT 248--DARNLLG--KVIPLR-KGVY--VNRKCGQOQIENRSL--LAE 276
Carubv10004162m.g | Carubv10004162m 219 DGRRT --- I-GVLTKPLDMDRGT 237--DARNLLG--KVIPLR-KGVY--VNRKCGQOQIENRSL--LAE 276
Bra011458 | Bra011458 221 DGRRT --- I-GVLTKPLDMDRGT 239--DARNLLG--KVIPLR-KGVY--VNRKCGQOQIENRSL--LAE 276
Bra036991 | Bra036991 229 PPDGHRRT --- I-GVLTKPLDMDRGT 249--DARNLLG--KVIPLR-KGVY--VNRKCGQOQIENRSL--LAE 276
Bra034579 | Bra034579 223 DGRRT --- I-GVLTKPLDMDRGT 241--DARNLLG--KVIPLR-KGVY--VNRKCGQOQIENRSL--LAE 276
LOC_0s01g69130 | LOC_0s01g69130.1 223 DGRRT --- I-GVLTKPLDMDRGT 241--DARNLLG--KVIPLR-KGVY--VNRKCGQOQIENRSL--LAE 276
GRMZ2G129155 | GRMZ2G129155.T01 224 PPSGKPLR --- I-GVLTKPLDMDRGT 244--DARNLLG--KVIPLR-KGVY--VNRKCGQOQIENRSL--LAE 276
GRMZ2G180335 | GRMZ2G180335.T01 132 T --- I-GVLTKPLDMDRGT 146--DARNLLG--KVIPLR-LGYV--VNRKCGQOQIENRSL--LAE 276
Glyma20g06670 | Glyma20g06670.1 214 EGNRT --- I-GVLTKPLDMDRGT 232--DARNLLG--KVIPLR-KGVY--VNRKCGQOQIENRSL--LAE 276
Medtr2g009690 | Medtr2g009690.1 206 GRT --- I-GVLTKPLDMDRGT 223--DARNLLG--KVIPLR-KGVY--VNRKCGQOQIENRSL--LAE 276
Medtr4g093750 | Medtr4g093750.1 206 GRT --- I-GVLTKPLDMDRGT 223--DARNLLG--KVIPLR-KGVY--VNRKCGQOQIENRSL--LAE 276
Glyma07g30150 | Glyma07g30150.2 215 UGNRT --- I-GVLTKPLDMDRGT 233--DARNLLG--KVIPLR-KGVY--VNRKCGQOQIENRSL--LAE 276
Glyma08g07160 | Glyma08g07160.1 217 DGNRT --- I-GVLTKPLDMDRGT 235--DARNLLG--KVIPLR-KGVY--VNRKCGQOQIENRSL--LAE 276
Glyma04g16340 | Glyma04g16340.1 214 DGNRT --- I-GVLTKPLDMDRGT 232--DARNLLG--KVIPLR-KGVY--VNRKCGQOQIENRSL--LAE 276
Glyma13g32940 | Glyma13g32940.1 229 KGNADDPDGYRT --- I-GVLTKPLDMDRGT 324--DARNLLG--KVIPLR-KGVY--VNRKCGQOQIENRSL--LAE 276
Glyma15g06380 | Glyma15g06380.1 214 DGNRT --- I-GVLTKPLDMDRGT 232--DARNLLG--KVIPLR-KGVY--VNRKCGQOQIENRSL--LAE 276
Cucsa_331870 | Cucsa_331870.1 209 DMSLLLRIFM --- I-GVLTKPLDMDRGT 234--DARNLLG--KVIPLR-KGVY--VNRKCGQOQIENRSL--LAE 276
GSVVG01012532001 | GSVIVT01012532001 215 DGNRT --- I-GVLTKPLDMDRGT 233--DARNLLG--KVIPLR-KGVY--VNRKCGQOQIENRSL--LAE 276
Cucsa_218420 | Cucsa_218420.1 224 DGRRT --- I-GVLTKPLDMDRGT 242--DARNLLG--KVIPLR-KGVY--VNRKCGQOQIENRSL--LAE 276
Potri_012G125300 | Potri_012G125300.1 221 PPSGKPLR --- I-GVLTKPLDMDRGT 242--DARNLLG--KVIPLR-KGVY--VNRKCGQOQIENRSL--LAE 276
Potri_007G118300 | Potri_007G118300.1 224 DGRRT --- I-GVLTKPLDMDRGT 242--DARNLLG--KVIPLR-KGVY--VNRKCGQOQIENRSL--LAE 276
Potri_017G041800 | Potri_017G041800.1 221 PPSGKPLR --- I-GVLTKPLDMDRGT 242--DARNLLG--KVIPLR-KGVY--VNRKCGQOQIENRSL--LAE 276
29506.t000007 | 29506.t000169 | Rc 227 PPSGKPLR --- I-GVLTKPLDMDRGT 242--DARNLLG--KVIPLR-KGVY--VNRKCGQOQIENRSL--LAE 276
Eucgr.i02611 | Eucgr.i02611.1 217 NGSRT --- I-GVLTKPLDMDRGT 235--DARNLLG--KVIPLR-KGVY--VNRKCGQOQIENRSL--LAE 276
29848.t000060 | 29848.t000540 | Rc 138 RT --- I-GVLTKPLDMDRGT 153--NACNLLG--NIVPLR-LGYV--VNRKCGQOQIENRSL--LAE 276
GSVVG0103606001 | GSVIVT0103606001 277 ---RDTMQLQ --- TOGATEL-P-LAHL-- 298 ---GIDKRRERSKVILKQASGEGVNWMEE 276
gi | 85115828 281 ---RRSTEDPE --- SKGKNSL-P-HSMG-- 302 ---GASAKQORSLQOQIENRSL--LAE 276
gi | 164424111 285 ---IRNRERDL --- QQSEWNL-P-EGVY-- 306 ---GVAALRERQDLGETTDKAVPGEA 276
gi | 11342664 342 ---ATKKTITFF --- QTHFYRVLLGEGSA 365 ---TVPFAERITELIMHXKSLPLENGQI 276
gi | 222136617 295 ---ALOREKIEF --- ENHPYRDLLEEGKA 318 ---TVPLCAEKLSTELTHICKSPLLENQI 276
Esi0024_0159 292 ---NDAEMDFE --- KSHAVFTVD-STCL-- 314 ---GVSLTKRVLNQLVHRTIHPDANKL 276
Esi0021_0042 298 ---SLSAEAEF --- QGFYKSLP-SFF-- 321 ---GVNLTARLNTLVOHRTIHPDANKL 276
Esi0103_0037 285 ---RREAEAEF --- RSEHFCDQK-PKFL-- 306 ---GVANLTKRNLVHRTIHPDANKL 276
Esi0103_0037 514 ---IRKYENFFS --- QLLRDKVQKPSMTTRM--SLAVSDCFWRM 555RDSIESQVDAFRAAKN--EAWKNHFLRIQNRDRELYDKARGSELDE 276
Esi0343_0016 230 ---VRAREROP --- QTNSMAGI-E---KEYW-- 252 ---GFTLVGRIVEIQAERVQFPIKPAQSKR--RTKLAQALRDMPKVFSNDLE 276
YOR211C 451 GEENTNGKQLVSHQEKAYF --- KENKXYFT--NC-- 481 ---QVSTKLRKELIKIIEIEMSNALPTSTLI 276
gi | 71981891 253 ---ALDREKFF --- ISHPSYRHM-ADRL-- 274 ---GTSYLOHTLNLQHTLTHIRDTPFVKNQI 276
gi | 56549125 ref | NP_001005362.1 | dynamin-2 251 ---ALANRERFF --- LSHPSYRHL-ADRM-- 272 ---GTYLQKVLNQLVHRTIHPDANKL 276
gi | 59853099 ref | NP_004399.2 | dynamin-1 258 ---ARAKERFFF --- ASHPYRDL-ASKM-- 279 ---GTYLQKVLNQLVHRTIHPDANKL 276
PGSC0003DMG400010899 260 ---ARAKERFFF --- ASHPYRDL-ASKM-- 279 ---GTYLQKVLNQLVHRTIHPDANKL 276
Vocar20015232m.g | Vocar20015232m 264 ---CRKRESEFF --- ASHPYRDL-ASKM-- 279 ---GTYLQKVLNQLVHRTIHPDANKL 276
Cre17_g724150.t1.1 | Cre17_g724150.t1.1 264 ---CRKRESEFF --- ASHPYRDL-ASKM-- 279 ---GTYLQKVLNQLVHRTIHPDANKL 276
Vocar20001129m.g | Vocar20001129m 271 ---AKKRESEFF --- ASHPYRDL-ASKM-- 279 ---GTYLQKVLNQLVHRTIHPDANKL 276
CME019C | CME019C 263 ---RREAEAEF --- RSEHFCDQK-PKFL-- 306 ---GVANLTKRNLVHRTIHPDANKL 276
gi | 85099877 283 ---RREAEAEF --- RSEHFCDQK-PKFL-- 306 ---GVANLTKRNLVHRTIHPDANKL 276
gi | 71993833 263 ---AVKDEGSM --- OKQYPL-ASRN-- 282 ---GTYLQKVLNQLVHRTIHPDANKL 276
Esi0616950 | Dd 405 ---MLADEWKWF --- DQHPVYHRI-TNQL-- 426 ---GTYLQKVLNQLVHRTIHPDANKL 276
Esi0029_0136 352 ---ALQKBAEYF --- RDHPYKGL-DKRV-- 373 ---GTTNLSRSLNQLVHRTIHPDANKL 276
101670 | 101670 | Sm 284 ---MLVAEAEF --- NSRVAYGL-ADRC-- 309 ---GTYLQKVLNQLVHRTIHPDANKL 276
404911 | 404911 | Sm 424 ---MLVAEAEF --- NSRVAYGL-ADRC-- 309 ---GTYLQKVLNQLVHRTIHPDANKL 276
Phpat.024G072600 | Phpat.024G072600.1 249 ---MLVAEAEF --- NSRVAYGL-ADRC-- 309 ---GTYLQKVLNQLVHRTIHPDANKL 276
437242 | 437242 | Sm 273 ---MLVAEAEF --- NSRVAYGL-ADRC-- 309 ---GTYLQKVLNQLVHRTIHPDANKL 276
Phpat.023G005400 | Phpat.023G005400.1 268 ---MLVAEAEF --- NSRVAYGL-ADRC-- 309 ---GTYLQKVLNQLVHRTIHPDANKL 276
Phpat.020G019000 | Phpat.020G019000.1 288 ---MLVAEAEF --- NSRVAYGL-ADRC-- 309 ---GTYLQKVLNQLVHRTIHPDANKL 276
Phpat.008G087300 | Phpat.008G087300.1 282 ---MLVAEAEF --- NSRVAYGL-ADRC-- 309 ---GTYLQKVLNQLVHRTIHPDANKL 276
Phpat.023G066800 | Phpat.023G066800.1 253 ---SLKSEIYV --- KNHFIYKSI-ANRS-- 274 ---GTYLQKVLNQLVHRTIHPDANKL 276
gi | 66816205 267 ---MLVAEAEF --- NSRVAYGL-ADRC-- 309 ---GTYLQKVLNQLVHRTIHPDANKL 276
AT2G14120 272 ---MLVAEAEF --- NSRVAYGL-ADRC-- 309 ---GTYLQKVLNQLVHRTIHPDANKL 276
Carubv10013019m.g | Carubv10013019m 272 ---MLVAEAEF --- NSRVAYGL-ADRC-- 309 ---GTYLQKVLNQLVHRTIHPDANKL 276
AT4G33650 285 ---MLVAEAEF --- NSRVAYGL-ADRC-- 309 ---GTYLQKVLNQLVHRTIHPDANKL 276
Carubv10004162m.g | Carubv10004162m 274 ---MLVAEAEF --- NSRVAYGL-ADRC-- 309 ---GTYLQKVLNQLVHRTIHPDANKL 276
Bra011458 | Bra011458 276 ---MLVAEAEF --- NSRVAYGL-ADRC-- 309 ---GTYLQKVLNQLVHRTIHPDANKL 276
Bra036991 | Bra036991 286 ---MLVAEAEF --- NSRVAYGL-ADRC-- 309 ---GTYLQKVLNQLVHRTIHPDANKL 276
Bra034579 | Bra034579 278 ---MLVAEAEF --- NSRVAYGL-ADRC-- 309 ---GTYLQKVLNQLVHRTIHPDANKL 276
LOC_0s01g69130 | LOC_0s01g69130.1 278 ---MLVAEAEF --- NSRVAYGL-ADRC-- 309 ---GTYLQKVLNQLVHRTIHPDANKL 276
GRMZ2G129155 | GRMZ2G129155.T01 281 ---MLVAEAEF --- NSRVAYGL-ADRC-- 309 ---GTYLQKVLNQLVHRTIHPDANKL 276
GRMZ2G180335 | GRMZ2G180335.T01 185 ---VAEENFF --- NHRIQV-F-SNSC-- 202 ---SVPLAKKLNQLVHRTIHPDANKL 276
Glyma20g06670 | Glyma20g06670.1 269 ---MLVAEAEF --- NSRVAYGL-ADRC-- 309 ---GTYLQKVLNQLVHRTIHPDANKL 276
Medtr2g009690 | Medtr2g009690.1 260 ---MLVAEAEF --- NSRVAYGL-ADRC-- 309 ---GTYLQKVLNQLVHRTIHPDANKL 276
Medtr4g093750 | Medtr4g093750.1 260 ---MLVAEAEF --- NSRVAYGL-ADRC-- 309 ---GTYLQKVLNQLVHRTIHPDANKL 276
Glyma07g30150 | Glyma07g30150.2 260 ---MLVAEAEF --- NSRVAYGL-ADRC-- 309 ---GTYLQKVLNQLVHRTIHPDANKL 276
Glyma08g07160 | Glyma08g07160.1 270 ---MLVAEAEF --- NSRVAYGL-ADRC-- 309 ---GTYLQKVLNQLVHRTIHPDANKL 276
Glyma04g16340 | Glyma04g16340.1 272 ---MLVAEAEF --- NSRVAYGL-ADRC-- 309 ---GTYLQKVLNQLVHRTIHPDANKL 276
Glyma13g32940 | Glyma13g32940.1 269 ---MLVAEAEF --- NSRVAYGL-ADRC-- 309 ---GTYLQKVLNQLVHRTIHPDANKL 276
Glyma15g06380 | Glyma15g06380.1 269 ---MLVAEAEF --- NSRVAYGL-ADRC-- 309 ---GTYLQKVLNQLVHRTIHPDANKL 276
Cucsa_331870 | Cucsa_331870.1 361 ---MLVAEAEF --- NSRVAYGL-ADRC-- 382 ---GTYLQKVLNQLVHRTIHPDANKL 276
GSVVG01012532001 | GSVIVT01012532001 269 ---MLVAEAEF --- NSRVAYGL-ADRC-- 309 ---GTYLQKVLNQLVHRTIHPDANKL 276
Cucsa_218420 | Cucsa_218420.1 270 ---MLVAEAEF --- NSRVAYGL-ADRC-- 309 ---GTYLQKVLNQLVHRTIHPDANKL 276
Potri_012G125300 | Potri_012G125300.1 279 ---MLVAEAEF --- NSRVAYGL-ADRC-- 300 ---GTYLQKVLNQLVHRTIHPDANKL 276
Potri_007G118300 | Potri_007G118300.1 276 ---MLVAEAEF --- NSRVAYGL-ADRC-- 297 ---GTYLQKVLNQLVHRTIHPDANKL 276
Potri_017G041800 | Potri_017G041800.1 279 ---MLVAEAEF --- NSRVAYGL-ADRC-- 300 ---GTYLQKVLNQLVHRTIHPDANKL 276
29506.t000007 | 29506.t000169 | Rc 272 ---MLVAEAEF --- NSRVAYGL-ADRC-- 293 ---GTYLQKVLNQLVHRTIHPDANKL 276
Eucgr.i02611 | Eucgr.i02611.1 191 LAYEDQFF --- HDHPYVHGL-SDCC-- 211 ---GVPLAKKLNQLVHRTIHPDANKL 276
GSVVG0103606001 | GSVIVT0103606001 277 ---RDTMQLQ --- TOGATEL-P-LAHL-- 298 ---GIDKRRERSKVILKQASGEGVNWMEE 276

gi | 85092415 327 326 ----DFKFAACNAIQKGLD--FRANJE--DEGRLYMVTLS----- 358 ----QSFQSLVKAA-----VDGTYNH--
gi | 85115828 331 330 ----EAKDCCDDMFKSLGT--AKGFP--EMRLELLELF----- 362 ----YFNSLVVPA-----VHGFPYKPP
gi | 16442411 335 334 ----RKKLAAREQODALGP--PRTE--REQQYLAQA----- 366 ----AKFQIVVRA-----LEFNYSSTH
gi | 11342664 394 ----RESHQKATEELRCGA-DIPSQE--IDRMFPIEIKI----- 426 ----KMNQNDIEKL-----VGE-
gi | 222136617 347 346 ----KEHQRTSLELQKGV-DIPE--AKMFFMDKV----- 379 ----NLEQDITL-----MGG-
Esi0024_0159 339 342 ----QSGEVEVBLVLAQ-HAFQFK--GDECHTQVLI----- 375 ----GVPCRLRSL-----LQGYRD
Esi0021_0042 350 349 ----OTQVKAABELKPKMLK-GVPHTT--AGHTTQMKIV----- 382 ----SDVCRLLQOS-----ARGYRD
Esi0103_0037 336 335 ----ETALVSRVTEELKLSYGNATP--GDRQMVTVT----- 369 ----QEVSRHLSV-----VQGYRD
604 IVNLSLIGVE 613EWEKLLQDKNSGISSHVFDQ-ILMPAYAS-SSSGSF--NTTVDIKLKHFAADQLAQK 668ITGTGWDLKEVFFRQINQDARTKDDHDPVFA
304 303LWEKFRKV--VSTREELKDLITFGS-NRAITG--QDESDMIDH--PH 343VTAMYKAVATGIRDVV--PNFFTDEYHQV--C
512 511 ----HEARERLRLTQVQELDDT--VPLFVFNDR--HTPKSYLLNNT--DV 543LKLGGKFKFQKPHRNL--WSTLRA
303 302 ----QKMFAMKEDVAYKVN-YQNPND--GRKFKVGMV----- 335 ----TQFNADIERG-----LEGS
gi | 71981891 1 0 ----GQQLLSIEKEVEYKVN-FRPDDP--ARKTKALQOMV----- 333 ----QQFADFVEKR-----LEGG-
gi | 56549125 ref|NP_001005362.1|dynamin-2 301 300 ----NQSDIESEMDHLGR-FHSVDA--GNOLYITTEPC----- 340 ----RAPDKFKHE-----LDGGR
gi | 59853099 ref|NP_004399.2|dynamin-1 309 308 ----DDTIARPKELQALQG-DVSHSR--GMLHMTDQC----- 341 ----QKLERAFERRI-----VDGGR
PGSC0003DMG400010899 314 313 ----HEALVDELELRALGD-PDVEQS--KAKGAVLQD----- 347 ----VAYARVYAM-----LDGR
Vocar20015232m.g|Vocar20015232m 321 320 ----NTLNGTQOELASVGD-MHFSG--KEBRSYDQDM----- 353 ----TRASSFLAS-----IDGTS
Cre17_g724150|Cre17_g724150.t1.1 335 334 ----SQQAERWKLQTLGP-AFEGSA--DDLIGGALNVI----- 366 ----NRMSEEAQS-----LEGS
Vocar20001129m.g|Vocar20001129m 303 302 ----SSQYKQYTLSESLGP-SILGNS--ANLVNHT----- 362 ----TEFTNEVRT-----LDGKS
gi | 85099877 311 310 ----SINNAQQSDLVAFGE-PVDEK--NRTMIOI----- 339 ----TRFATYDST-----LEGT
gi | 71993833 455 454 ----RQMKKKKEDDKYGE-DPLFR--AKSRLLLDL----- 349 ----NFSRKYRAD-----LEGT
Esi0029_0136|Dd 402 401 ----NVMMSQSVQELALGE-FHDCVS--GSLRTRHETL----- 435 ----497--NFSRKYRAD-----LEGT
101670|101670.Sm 334 333 ----NTOMVALLKELTSLYGE-ATDSK--SGQGAMLLNAL----- 365 ----TKYFHFVSSV-----LDGKN
404911|404911.Sm 499 498 ----NTQMVALKELTSLYGE-ATDSK--SGQGAMLLNAL----- 530 ----TKYFHFVSSV-----LDGKN
Phpat_024G072600|Phpat_024G072600.1 270 269 ----NVLVYVSV-HIFWG--SGQGAMLLNIL----- 293 ----SKYSH-----LDGKN
437242|437242.Sm 323 322 ----NTOMVALLKELTSLYGE-ITDSK--NGGQALLNIL----- 354 ----TKYFHFVSSV-----LDGKN
Phpat_023G005400|Phpat_023G005400.1 332 321 ----NMAFVAKHESYGE-ITDSK--AGGALLNIL----- 349 ----SKYDADFSSM-----VEGKN
Phpat_02G0190000|Phpat_02G019000.1 338 337 ----STOMTLQKELASVGE-ITDSK--SGQALNNIL----- 366 ----TKYSHGFQSV-----LDGGR
Phpat_008G087300|Phpat_008G087300.1 338 337 ----STOMTLQKELASVGE-ITDSK--SGQALNNIL----- 369 ----TKYSHGFQSV-----LDGGR
Phpat_023G066800|Phpat_023G066800.1 332 331 ----STOMTLQKELASVGE-ITDSK--SGQALNNIL----- 363 ----TKYSHGFQSV-----LDGGR
gi | 66816205 303 302 ----SKMLSDVQEGELSYGD-PLYDT--KNSQAGLLNIL----- 335 ----TIFSSNFKDA-----IDGKL
LOC_Os04g31190|LOC_Os04g31190.1 317 316 ----NQSLVAVAKHESYGE-ITDSK--AGGQALLNIL----- 348 ----SKYCEAFSSM-----VEGKN
AT2G14120 322 321 ----NMAFVAKHESYGE-ITDSK--AGGQALLNIL----- 353 ----TKYDADFSSM-----VEGKN
Carubv10013019m.g|Carubv10013019m 337 336 ----SNALVAVAKHESYGE-ITDSK--AGGQALLNIL----- 368 ----SKYCEAFSSM-----LEGS
AT4G33650 335 334 ----SNALVAVAKHESYGE-ITDSK--AGGQALLNIL----- 366 ----SKYCEAFSSM-----LEGS
Carubv10004162m.g|Carubv10004162m 324 323 ----SNALVAVAKHESYGE-ITDSK--AGGQALLNIL----- 355 ----SKYCEAFSSM-----LEGS
Bra011458|Bra011458 326 325 ----SNALVAVAKHESYGE-ITDSK--AGGQALLNIL----- 357 ----SKYCEAFSSM-----LEGS
Bra036991|Bra036991 336 335 ----SNALVAVAKHESYGE-ITDSK--AGGQALLNIL----- 367 ----SKYCEAFSSM-----LEGK
LOC_Os01g69130|LOC_Os01g69130.1 328 327 ----SQSLVAVAKHESYGE-ITDSK--AGGQALLNIL----- 359 ----AKYCEAFSSM-----VEGKN
GRMZM2G129155|GRMZM2G129155.T01 328 327 ----SQSLVAVAKHESYGE-ITDSK--AGGQALLNIL----- 359 ----AKYCEAFSSM-----VEGKN
GRMZM2G180335|GRMZM2G180335.T01 331 330 ----SQSLVAVAKHESYGE-ITDSK--AGGQALLNIL----- 362 ----AKYCEAFSSM-----VEGKN
Glyma20g06670|Glyma20g06670.1 231 230 ----STSLVAVAKHESYGE-ITDSK--ADGGALLNIL----- 264 ----SKYCEVNNK-----N
Medtr2g009690|Medtr2g009690.1 319 318 ----SNLAVVAKHESYGE-ITDSK--AGGQALLNIL----- 350 ----SKYCEAFSSM-----VEGKN
Medtr4g093750|Medtr4g093750.1 310 309 ----SASLVVAKHESYGE-ITDSK--AGGQALLNIL----- 341 ----SKYDADFSSM-----VEGKN
Glyma07g30150|Glyma07g30150.2 310 309 ----SASLVVAKHESYGE-ITDSK--AGGQALLNIL----- 341 ----SKYDADFSSM-----VEGKN
Glyma08g07160|Glyma08g07160.1 320 319 ----SASLVVAKHESYGE-ITDSK--AGGQALLNIL----- 351 ----SKYCEAFSSM-----VEGKN
Glyma04g16340|Glyma04g16340.1 322 321 ----SASLVVAKHESYGE-ITDSK--AGGQALLNIL----- 353 ----SKYCEAFSSM-----VEGKN
Glyma13g32940|Glyma13g32940.1 319 318 ----SASLVVAKHESYGE-ITDSK--AGGQALLNIL----- 350 ----SKYCEAFSSM-----LEGKN
Glyma15g06380|Glyma15g06380.1 319 318 ----SASLVVAKHESYGE-ITDSK--AGGQALLNIL----- 350 ----SKYCEAFSSM-----LEGKN
Cucsa_331870|Cucsa_331870.1 411 410 ----NSALVAVAKHESYGE-ITDSK--AGGQALLNIL----- 417 ----SKYAEAFSSR-----VE
GSVIVG01012532001|GSVIVT01012532001 319 318 ----SASLVVAKHESYGE-ITDSK--AGGQALLNIL----- 350 ----SKYCEAFSSM-----VEGKN
Cucsa_218420|Cucsa_218420.1 264 263 ----SASLVVAKHESYGE-ITDSK--AGGQALLNIL----- 263 ----SKYCEAFSSM-----VEGKN
Potri_017G041800|Potri_017G041800.1 320 319 ----SASLVVAKHESYGE-ITDSK--AGGQALLNIL----- 354 ----SKYCEAFSSM-----LEGKN
Potri_017G041800|Potri_017G041800.1 329 328 ----SASLVVAKHESYGE-ITDSK--AGGQALLNIL----- 360 ----SKYDADFSSM-----VEGKN
Eucgr_102611|Eucgr_102611.1 322 321 ----NLRMTVFNALTYGE-VMESK--NDGQVLLNIL----- 353 ----KRYCAEAFSSM-----VDGK
29848.t0000600|29848.m004504|rc 322 321 ----NLRMTVFNALTYGE-VMESK--NDGQVLLNIL----- 353 ----KRYCAEAFSSM-----VDGK
GSVIVG0103606001|GSVIVT0103606001 240 9 ----NCHMTAVKLEQTSGE-VVESK--VEQGAVLLSIL----- 271 ----KKYCEAFSSM-----VDGKS

gi | 85092415 376 ----DFFKDKDPT--GYRO 389RI--RNVVQTLNEKFADEIASRGHHYAIETHSRVVDK----- 426 ----M-----
gi | 85115828 382 KTIFFRVVADPK-GMFAQ 398NL--RRAAEENDRFARIRADGRKFKLSASDPSADK----- 435 ----Q-----
gi | 16442411 386 AF----DEHQ 392RL--TSQVVTVIDIFNRMQRKGTYSFGKIDTGWGSSDNNKADDSEEE 440NASEHGTEQNIATNAKERRAFPE
gi | 11342664 441 ----EVV--RNET 448RL--YNKIREDFKNVWGLAT--NTQVKVNI----- 476 ----
gi | 222136617 394 ----ETV--GEDI 401RL--FTRLRHFPHKWTIEN--NFQGHKIL----- 429 ----
Esi0024_0159 393 PALN----THPE 401RV--WSVADRAFRLDQSGVASL--NPGFPHDP----- 430 ----
Esi0021_0042 400 DVLS----AKT 408RL--HAASQAFKQLHNTAAT--VPGFNDVF----- 437 ----
Esi0103_0037 387 RVIV----VHPQ 387LG--SASLVVAKHESYGE-ITDSK--AGGQALLNIL----- 359 ----AKYCEAFSSM-----VEGKN
gi | 193204309 701 LKEAVIEPAMLTGHWDDKANDYLRLVQL 728NAMEADRAVDKRSWDAACNLFHKAASERLAAV--KKQLTDDRGGPWGSKWMLWTKPTADN 786H-YSCVIQDDELYSI
Esi0343_0016 374 AAF----KRVGMAFLPNL 387LG--GRVFSALFCE--IFSEELGVSRSE--410
YOR211C 567 ELDKQVLVDLATRYKDDNQLDSSSKL 594ES--GARINRILFHE--DTDMLYWHKK--LELASSG 613
gi | 71981891 351 0 ----A-KLVSTNEL 359SG--GARINRILFHE--RPFPEIV----- 378 ----
gi | 56549125 ref|NP_001005362.1|dynamin-2 349 348 ----D-Q-IDYVEL 356SG--GARINRILFHE--RPFPEIV----- 375 ----
gi | 59853099 ref|NP_004399.2|dynamin-1 356 355 ----P-Q-IDYVEL 356SG--GARINRILFHE--RPFPEIV----- 375 ----
PGSC0003DMG400010899 357 356 ----D-Q-IDYVEL 356SG--GARINRILFHE--RPFPEIV----- 375 ----
Vocar20015232m.g|Vocar20015232m 353 352 ----L-DLHMAAQL 371SG--GARVREVTFE--HFLPQLH----- 390 ----
Cre17_g724150|Cre17_g724150.t1.1 363 362 ----L-DLHMAAQL 371SG--GARVREVTFE--HFLPQLH----- 389 ----
Vocar20001129m.g|Vocar20001129m 362 361 ----T-RISKREL 376CC--GARVREVTFE--HFLPQLH----- 395 ----
CME019C|CME019C 378 377 ----Q-TYKTEL 370YQ--GARVREVTFE--HFLPQLH----- 409 ----
gi | 85099877 378 377 ----T-BLEGOEL 385SG--GARVREVTFE--HFLPQLH----- 404 ----
gi | 71993833 355 354 ----R-NLEWEL 362CC--GARVREVTFE--HFLPQLH----- 381 ----
gi | 66816950|Dd 499 DGTN----E--ELLINEF 510NG--GARIRYIFSK--AFQSTTAAAT 534S
Esi0029_0136 451 ----SSPDGIEMNLE 461YG--GARIRYIFSK--AFQSTTAAAT 534S
101670|101670.Sm 384 383 ----Q-EMSTREL 373TG--GARIRYIFSK--AFQSTTAAAT 534S
404911|404911.Sm 541 IDGKN----Q-EMSTREL 533SG--GARIRYIFSK--AFQSTTAAAT 534S
Phpat_024G072600|Phpat_024G072600.1 299 298 ----E-EMSTREL 373TG--GARIRYIFSK--AFQSTTAAAT 534S
437242|437242.Sm 365 364 ----E-EMSTREL 372SG--GARIRYIFSK--AFQSTTAAAT 534S
Phpat_023G005400|Phpat_023G005400.1 382 381 ----E-EMSTREL 389SG--GARIRYIFSK--AFQSTTAAAT 534S
Phpat_02G0190000|Phpat_02G019000.1 389 388 ----E-EMSTREL 386SG--GARIRYIFSK--AFQSTTAAAT 534S
Phpat_008G087300|Phpat_008G087300.1 351 350 ----T-DLSNNE 358YG--GARISYIFNE--IYSHCVN----- 377 ----
gi | 66816205 364 363 ----K-MSDDEL 370SG--GARIRYIFSK--AFQSTTAAAT 534S
LOC_Os04g31190|LOC_Os04g31190.1 369 368 ----K-EMSTREL 376SG--GARIRYIFSK--AFQSTTAAAT 534S
AT2G14120 369 368 ----K-EMSTREL 376SG--GARIRYIFSK--AFQSTTAAAT 534S
Carubv10013019m.g|Carubv10013019m 382 381 ----E-EMSTREL 389SG--GARIRYIFSK--AFQSTTAAAT 534S
AT4G33650 371 370 ----E-EMSTREL 380SG--GARIRYIFSK--AFQSTTAAAT 534S
Carubv10004162m.g|Carubv10004162m 373 372 ----E-EMSTREL 390SG--GARIRYIFSK--AFQSTTAAAT 534S
Bra011458|Bra011458 375 374 ----E-EMSTREL 382CC--GARIRYIFSK--AFQSTTAAAT 534S
Bra036991|Bra036991 378 377 ----E-EMSTREL 385SG--GARIRYIFSK--AFQSTTAAAT 534S
Bra034579|Bra034579 276 275 ----I-FMRHENY 283--GARIRYIFSK--AFQSTTAAAT 534S
LOC_Os01g69130|LOC_Os01g69130.1 366 365 ----E-EMSTREL 373TG--GARIRYIFSK--AFQSTTAAAT 534S
GRMZM2G129155|GRMZM2G129155.T01 366 365 ----E-EMSTREL 373TG--GARIRYIFSK--AFQSTTAAAT 534S
GRMZM2G180335|GRMZM2G180335.T01 276 275 ----I-FMRHENY 283--GARIRYIFSK--AFQSTTAAAT 534S
Glyma20g06670|Glyma20g06670.1 366 365 ----E-EMSTREL 373TG--GARIRYIFSK--AFQSTTAAAT 534S
Medtr2g009690|Medtr2g009690.1 357 356 ----E-AMSTREL 3648G--GARIRYIFSK--AFQSTTAAAT 534S
Medtr4g093750|Medtr4g093750.1 357 356 ----E-EMSTREL 3648G--GARIRYIFSK--AFQSTTAAAT 534S
Glyma07g30150|Glyma07g30150.2 367 366 ----E-EMSTREL 374FG--GARIRYIFSK--AFQSTTAAAT 534S
Glyma08g07160|Glyma08g07160.1 369 368 ----E-EMSTREL 375FG--GARIRYIFSK--AFQSTTAAAT 534S
Glyma04g16340|Glyma04g16340.1 366 365 ----E-EMSTREL 372SG--GARIRYIFSK--AFQSTTAAAT 534S
Glyma13g32940|Glyma13g32940.1 366 365 ----E-K-SNNKL 372JG--GARIRYIFSK--AFQSTTAAAT 534S
Glyma15g06380|Glyma15g06380.1 459 GKN----E-EMSTREL 4698G--GARIRYIFSK--AFQSTTAAAT 534S
Cucsa_331870|Cucsa_331870.1 366 365 ----E-EMSTREL 373TG--GARIRYIFSK--AFQSTTAAAT 534S
GSVIVG01012532001|GSVIVT01012532001 376 375 ----E-EMSTREL 377AG--GARIRYIFSK--AFQSTTAAAT 534S
Cucsa_218420|Cucsa_218420.1 370 369 ----E-EMSTREL 383SG--GARIRYIFSK--AFQSTTAAAT 534S
Potri_012G125300|Potri_012G125300.1 376 375 ----E-EMSTREL 380SG--GARIRYIFSK--AFQSTTAAAT 534S
Potri_007G18300|Potri_007G18300.1 376 375 ----E-EMSTREL 383SG--GARIRYIFSK--AFQSTTAAAT 534S
Potri_017G041800|Potri_017G041800.1 376 375 ----E-EMSTREL 383SG--GARIRYIFSK--AFQSTTAAAT 534S
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Eucgr_102611|Eucgr_102611.1 369 368 ----Q-EMSTREL 376CC--GARIRYIFSK--AFQSTTAAAT 534S
29848.t0000600|29848.m004504|rc 287 286 ----Q-EMSTREL 294SG--GARIRYIFSK--AFQSTTAAAT 534S
GSVIVG0103606001|GSVIVT0103606001 313 312 ----Q-EMSTREL 294SG--GARIRYIFSK--AFQSTTAAAT 534S

gi | 85092415 561 ----- 560 ----- 560 -----
gi | 85115828 562 ----- 561 ----- 561 -----
gi | 164424111 610 ----- 609 ----- 609 -----
gi | 11342664 599 ----- 598 ----- 598 -----
Esi022136617 552 ----- 551 ----- 551 -----
Esi0024_0159 556 ----- 555 ----- 555 -----
Esi0021_0042 562 ----- 561 ----- 561 -----
Esi0103_0037 549 ----- 548 ----- 548 -----
gi | 193204309 908 ----- 907 ----- 907 -----
Esi0343_0016 503 ----- 502 ----- 502 -----
YOR211C 728 ----- 728 ----- 728 -----
gi | 71981891 519 ----- 518-QVIR-IGW- LSLG- NVSFVR-GSDNWFVMSD-SLSWYK- 554 ----- DEEKEKKYM- SNLQKETL-
gi | 56549125 ref NP_001005362.1|dynamin-2 312 ----- LTIN- NISLMMKSGSEYWFVLTAE-SLSWYK- 61 ----- EEKEKKYM- LPIDLNLK- IRDVEKGF 86S
gi | 59853099 ref NP_004399.2|dynamin-1 57 EI- 518-LVIR-IGW- NIGMKGSGSEYWFVLTAE-SLSWYK- 555 ----- DEEKEKKYM- LSVLDL-
PGSC0003DMG400010899 499 ----- 498 ----- 498 -----
Vocar20015232m.g|Vocar20015232m 502 ----- 501 ----- 501 -----
Cre17_g724150|Cre17_g724150.t1.1 524 ----- 523 ----- 523 -----
Vocar20001129m.g|Vocar20001129m 540 ----- 539 ----- 539 -----
gi | 85111713 524 ----- 523 ----- 523 -----
CME019C|CME019C 551 ----- 550 ----- 550 -----
gi | 85099877 547 ----- 546 ----- 546 -----
gi | 71993833 523 ----- 522 ----- 522 -----
gi | 66816950|Dd 673 ----- 672 ----- 672 -----
Esi0029_0136 622 ----- 621 ----- 621 -----
101670|101670 Sm 551 ----- 550 ----- 550 -----
404911|404911 Sm 707 ----- 706 ----- 706 -----
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437242|437242 Sm 538 ----- 537 ----- 537 -----
Phpat.023G005400|Phpat.023G005400.1 535 ----- 534 ----- 534 -----
Phpat.020G019000|Phpat.020G019000.1 533 ----- 532 ----- 532 -----
Phpat.008G087300|Phpat.008G087300.1 551 ----- 550 ----- 550 -----
Phpat.023G066800|Phpat.023G066800.1 547 ----- 546 ----- 546 -----
gi | 66816205 524 ----- 523 ----- 523 -----
LOC_0s04g31190|LOC_0s04g31190.1 531 ----- 530 ----- 530 -----
AT2G14120 566 ----- 565 ----- 565 -----
Carubv10013019m.g|Carubv10013019m 537 ----- 536 ----- 536 -----
AT4G33650 552 ----- 551 ----- 551 -----
Carubv10004162m.g|Carubv10004162m 550 ----- 549 ----- 549 -----
Bra011458|Bra011458 539 ----- 538 ----- 538 -----
Bra036991|Bra036991 541 ----- 540 ----- 540 -----
Bra034579|Bra034579 543 ----- 542 ----- 542 -----
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GRMZM2G180335|GRMZM2G180335.T01 546 ----- 545 ----- 545 -----
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Medtr2g009690|Medtr2g009690.1 562 ----- 561 ----- 561 -----
Medtr4g093750|Medtr4g093750.1 525 ----- 524 ----- 524 -----
Glyma07g30150|Glyma07g30150.2 525 ----- 524 ----- 524 -----
Glyma08g07160|Glyma08g07160.1 535 ----- 534 ----- 534 -----
Glyma04g16340|Glyma04g16340.1 536 ----- 535 ----- 535 -----
Glyma13g32940|Glyma13g32940.1 533 ----- 532 ----- 532 -----
Glyma15g06380|Glyma15g06380.1 527 ----- 526 ----- 526 -----
Cucsa.331870|Cucsa.331870.1 527 ----- 526 ----- 526 -----
GSVIVG01012532001|GSVIVG01012532001 634 ----- 633 ----- 633 -----
Cucsa.218420|Cucsa.218420.1 524 ----- 523 ----- 523 -----
Potri.012G125300|Potri.012G125300.1 264 ----- 263 ----- 263 -----
Potri.007G118300|Potri.007G118300.1 538 ----- 537 ----- 537 -----
Potri.017G041800|Potri.017G041800.1 544 ----- 543 ----- 543 -----
29506.t000007|29506.m000169|Rc 544 ----- 543 ----- 543 -----
Eucgr.i02611|Eucgr.i02611.1 544 ----- 543 ----- 543 -----
29848.t000006|29848.m004504|Rc 532 ----- 531 ----- 531 -----
GSVIVG0103606001|GSVIVG0103606001 455 ----- 454 ----- 454 -----

gi | 85092415 561 ----- 560 ----- 560 -----
gi | 85115828 562 ----- 561 ----- 561 -----
gi | 164424111 610 ----- 609 ----- 609 -----
gi | 11342664 599 ----- 598 ----- 598 -----
Esi022136617 552 ----- 551 ----- 551 -----
Esi0024_0159 556 ----- 555 ----- 555 -----
Esi0021_0042 562 ----- 561 ----- 561 -----
Esi0103_0037 549 ----- 548 ----- 548 -----
gi | 193204309 908 ----- 907 ----- 907 -----
Esi0343_0016 503 ----- 502 ----- 502 -----
YOR211C 728 ----- 728 ----- 728 -----
gi | 71981891 519 ----- 518-QVIR-IGW- LSLG- NVSFVR-GSDNWFVMSD-SLSWYK- 554 ----- DEEKEKKYM- SNLQKETL-
gi | 56549125 ref NP_001005362.1|dynamin-2 312 ----- LTIN- NISLMMKSGSEYWFVLTAE-SLSWYK- 61 ----- EEKEKKYM- LPIDLNLK- IRDVEKGF 86S
gi | 59853099 ref NP_004399.2|dynamin-1 57 EI- 518-LVIR-IGW- NIGMKGSGSEYWFVLTAE-SLSWYK- 555 ----- DEEKEKKYM- LSVLDL-
PGSC0003DMG400010899 499 ----- 498 ----- 498 -----
Vocar20015232m.g|Vocar20015232m 502 ----- 501 ----- 501 -----
Cre17_g724150|Cre17_g724150.t1.1 524 ----- 523 ----- 523 -----
Vocar20001129m.g|Vocar20001129m 540 ----- 539 ----- 539 -----
gi | 85111713 524 ----- 523 ----- 523 -----
CME019C|CME019C 551 ----- 550 ----- 550 -----
gi | 85099877 547 ----- 546 ----- 546 -----
gi | 71993833 523 ----- 522 ----- 522 -----
gi | 66816950|Dd 673 ----- 672 ----- 672 -----
Esi0029_0136 622 ----- 621 ----- 621 -----
101670|101670 Sm 551 ----- 550 ----- 550 -----
404911|404911 Sm 707 ----- 706 ----- 706 -----
Phpat.024G072600|Phpat.024G072600.1 421 ----- 420 ----- 420 -----
437242|437242 Sm 538 ----- 537 ----- 537 -----
Phpat.023G005400|Phpat.023G005400.1 535 ----- 534 ----- 534 -----
Phpat.020G019000|Phpat.020G019000.1 533 ----- 532 ----- 532 -----
Phpat.008G087300|Phpat.008G087300.1 551 ----- 550 ----- 550 -----
Phpat.023G066800|Phpat.023G066800.1 547 ----- 546 ----- 546 -----
gi | 66816205 524 ----- 523 ----- 523 -----
LOC_0s04g31190|LOC_0s04g31190.1 531 ----- 530 ----- 530 -----
AT2G14120 566 ----- 565 ----- 565 -----
Carubv10013019m.g|Carubv10013019m 537 ----- 536 ----- 536 -----
AT4G33650 552 ----- 551 ----- 551 -----
Carubv10004162m.g|Carubv10004162m 550 ----- 549 ----- 549 -----
Bra011458|Bra011458 539 ----- 538 ----- 538 -----
Bra036991|Bra036991 541 ----- 540 ----- 540 -----
Bra034579|Bra034579 543 ----- 542 ----- 542 -----
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GRMZM2G180335|GRMZM2G180335.T01 546 ----- 545 ----- 545 -----
Glyma20g06670 284 ----- 283 ----- 283 -----
Medtr2g009690|Medtr2g009690.1 562 ----- 561 ----- 561 -----
Medtr4g093750|Medtr4g093750.1 525 ----- 524 ----- 524 -----
Glyma07g30150|Glyma07g30150.2 525 ----- 524 ----- 524 -----
Glyma08g07160|Glyma08g07160.1 535 ----- 534 ----- 534 -----
Glyma04g16340|Glyma04g16340.1 536 ----- 535 ----- 535 -----
Glyma13g32940|Glyma13g32940.1 533 ----- 532 ----- 532 -----
Glyma15g06380|Glyma15g06380.1 527 ----- 526 ----- 526 -----
Cucsa.331870|Cucsa.331870.1 527 ----- 526 ----- 526 -----
GSVIVG01012532001|GSVIVG01012532001 634 ----- 633 ----- 633 -----
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Potri.012G125300|Potri.012G125300.1 264 ----- 263 ----- 263 -----
Potri.007G118300|Potri.007G118300.1 538 ----- 537 ----- 537 -----
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29506.t000007|29506.m000169|Rc 544 ----- 543 ----- 543 -----
Eucgr.i02611|Eucgr.i02611.1 544 ----- 543 ----- 543 -----
29848.t000006|29848.m004504|Rc 532 ----- 531 ----- 531 -----
GSVIVG0103606001|GSVIVG0103606001 455 ----- 454 ----- 454 -----

gi | 85092415 561 ----- 560 ----- 560 -----
gi | 85115828 562 ----- 561 ----- 561 -----
gi | 164424111 610 ----- 609 ----- 609 -----
gi | 11342664 599 ----- 598 ----- 598 -----
Esi022136617 552 ----- 551 ----- 551 -----
Esi0024_0159 556 ----- 555 ----- 555 -----
Esi0021_0042 562 ----- 561 ----- 561 -----
Esi0103_0037 549 ----- 548 ----- 548 -----
gi | 193204309 908 ----- 907 ----- 907 -----
Esi0343_0016 503 ----- 502 ----- 502 -----
YOR211C 728 ----- 728 ----- 728 -----
gi | 71981891 519 ----- 518-QVIR-IGW- LSLG- NVSFVR-GSDNWFVMSD-SLSWYK- 554 ----- DEEKEKKYM- SNLQKETL-
gi | 56549125 ref NP_001005362.1|dynamin-2 312 ----- LTIN- NISLMMKSGSEYWFVLTAE-SLSWYK- 61 ----- EEKEKKYM- LPIDLNLK- IRDVEKGF 86S
gi | 59853099 ref NP_004399.2|dynamin-1 57 EI- 518-LVIR-IGW- NIGMKGSGSEYWFVLTAE-SLSWYK- 555 ----- DEEKEKKYM- LSVLDL-
PGSC0003DMG400010899 499 ----- 498 ----- 498 -----
Vocar20015232m.g|Vocar20015232m 502 ----- 501 ----- 501 -----
Cre17_g724150|Cre17_g724150.t1.1 524 ----- 523 ----- 523 -----
Vocar20001129m.g|Vocar20001129m 540 ----- 539 ----- 539 -----
gi | 85111713 524 ----- 523 ----- 523 -----
CME019C|CME019C 551 ----- 550 ----- 550 -----
gi | 85099877 547 ----- 546 ----- 546 -----
gi | 71993833 523 ----- 522 ----- 522 -----
gi | 66816950|Dd 673 ----- 672 ----- 672 -----
Esi0029_0136 622 ----- 621 ----- 621 -----
101670|101670 Sm 551 ----- 550 ----- 550 -----
404911|404911 Sm 707 ----- 706 ----- 706 -----
Phpat.024G072600|Phpat.024G072600.1 421 ----- 420 ----- 420 -----
437242|437242 Sm 538 ----- 537 ----- 537 -----
Phpat.023G005400|Phpat.023G005400.1 535 ----- 534 ----- 534 -----
Phpat.020G019000|Phpat.020G019000.1 533 ----- 532 ----- 532 -----
Phpat.008G087300|Phpat.008G087300.1 551 ----- 550 ----- 550 -----
Phpat.023G066800|Phpat.023G066800.1 547 ----- 546 ----- 546 -----
gi | 66816205 524 ----- 523 ----- 523 -----
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747 --- --P-SR-ATMSAS 755D--- --AGLPSR-LG---G--- --VPAQP--- 771 --- --GKWFHLG---HNQIGLHGGTR
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773 ES--- --A-SR-PASSF- 782D--- --ATGLPPATK---G--- -- 775 --- --
762 --- -- 761 --- -- 761 --- --
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846 --- -- 846 --- -- 846 --- --
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797 R--- --RKSSEH--- --SGLQSPHYLA--- --DS-NGS--- 817 --- --G-RTYMPGLYPTVD--- --F*--- 831
801 R--- --RKSSEH--- --SGLQSPHYLA--- --DS-NGS--- 823 --- --S-RPYMPGLYPTVD--- --L*--- 837
799 FKS--RKSSEH--- --SGLQSPFYANADS--- --NGS--- 823 --- --G-RPFMSGFYPTLD--- --M*--- 837
778 KIPRLYY--- --SGLQSPHYLA--- --S-NGL--- 797 --- -- 797 --- --
698 --- -- 697 --- -- 697 --- --

gi | 85092415
gi | 85115828
gi | 164424111
gi | 11342664
gi | 222136617
Esi0024_0159
Esi0021_0042
Esi0103_0037
gi | 193204309
Esi0343_0016
YOR211C
gi | 71981891
gi | 56549125 | ref | NP_001005362.1 | dynamin-2
gi | 59853099 | ref | NP_004399.2 | dynamin-1
PGSC0003DMG400010899
Vocar20015232m.g | Vocar20015232m
Cre17_g724150 | Cre17_g724150.t1.1
Vocar20001129m.g | Vocar20001129m
gi | 85111713
CME019C | CME019C
gi | 85099877
gi | 71993833
gi | 66816950 | Dd
Esi0029_0136
101670 | 101670 | Sm
404911 | 404911 | Sm
Pphat.024G072600 | Pphat.024G072600.1
437242 | 437242 | Sm
Pphat.023G005400 | Pphat.023G005400.1
Pphat.020G019000 | Pphat.020G019000.1
Pphat.008G087300 | Pphat.008G087300.1
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gi | 66816205
LOC_Os04g31190 | LOC_Os04g31190.1
AT2G14120
Carubv10013019m.g | Carubv10013019m
AT4G33650
Carubv10004162m.g | Carubv10004162m
Bra011458 | Bra011458
Bra036991 | Bra036991
Bra034579 | Bra034579
LOC_Os01g69130 | LOC_Os01g69130.1
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GRMZM2G180335 | GRMZM2G180335.T01
Glyma20g06670 | Glyma20g06670.1
Medtr2g009690 | Medtr2g009690.1
Medtr4g093750 | Medtr4g093750.1
Glyma07g30150 | Glyma07g30150.2
Glyma08g07160 | Glyma08g07160.1
Glyma04g16340 | Glyma04g16340.1
Glyma13g32940 | Glyma13g32940.1
Glyma15g06380 | Glyma15g06380.1
Cucsa.331870 | Cucsa.331870.1
GSVIVG01012532001 | GSVIVT01012532001
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Potri.007G118300 | Potri.007G118300.1
Potri.017G041800 | Potri.017G041800.1
29506.t000007 | 29506.m000169 | Rc
Eucgr.I02611 | Eucgr.I02611.1
29848.t000060 | 29848.m004504 | Rc
GSVIVG0103606001 | GSVIVT0103606001

764 --- -- 763 --- -- 763 --- --
750 --- --ECGQLDA-LYD-S--- -- 760 --- --ERKLTQNK-TDPDKNGVSP--- --PSVPDHPMKR 789
734 --- -- 733 --- -- 733 --- --
716 --- -- 715 --- -- 715 --- --
663 --- -- 662 --- -- 662 --- --
764 FAGSK--PERRATEARDGSLAHFVYT-KDGDNGGLI 796YWLGRHRRHRRKFFENPHDAGLVFVSTSGFKDGGPST--- --LVSRRRVPCSTTDE 846DGSWYC
743 LAQ--- --AWGR--- --STST 753DWSSTAMS-RFAANAAAASGT--- --STSYGAGGLGG--- --RQSSGGS--- 791
753 LKQ--- --RRT--- --VILT 763--- --LL-RQA*--- -- 769 --- --
965 --- -- 964 --- -- 964 --- --
633 --- -- 632 --- -- 632 --- --
802 --- -- 801 --- -- 801 --- --
311 --- -- 330 --- -- 330 --- --
613 --- --PGA--- --SPDP--- -- 612 --- -- 612 --- --
629 --- -- 628 --- -- 628 --- --
860 AAAVAAA--RNASGAG-YHQHL--GGSGPG 880--- --AT--PPSAMLPLPTVPFPNGTAS--- --ASS*--- 904
842 AAAVAAA--ASTHSEG-MPGYL-LGNGVGV 866--- --M--- --GTGHGSLPPVPTGGFGS--- --PGYGG-DGIDRSQSMVA--- 901
802 --- -- 801 --- -- 801 --- --
707 --- -- 706 --- -- 706 --- --
713 --- -- 712 --- -- 712 --- --
921 --- -- 920 --- -- 920 --- --
848 --- -- 847 --- -- 847 --- --
929 --- -- 928 --- -- 928 --- --
645 --- --S--- --YSN--GSMAGYYAPT VKS--- --VSS*--- 644
712 RVADTGTFSPFPVAKQRVRLVVAATDDCGAK 825--- --ST--KSDE-NSSPFA

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gi |85092415 764 ----- 763-----
gi |85115828 791 ----- 799-----
gi |164424111 734 ----- 733-----
gi |11342664 716 ----- 715-----
gi |222136617 663 ----- 662-----
Esi0024_0159 901 ----- 900-----
Esi0021_0042 898 ----- 897-----
Esi0103_0037 792 ----- 791-----
Esi0343_0016 965 64----- 964-----
YOR211C 633 ----- 632-----
gi |71981891 882 81----- 881-----
gi |56549125|ref|NP_001005362.1|dynamin-2 369 ----- 376-----
gi |59853099|ref|NP_004399.2|dynamin-1 860 ----- 859-----
PGSC0003DMG400010899 613 ----- 612-----
Vocar20015232m.g|Vocar20015232m 629 ----- 628-----
Cre17.g724150|Cre17.g724150.t1.1 905 ----- 904-----
Vocar20001129m.g|Vocar20001129m 902 ----- 901-----
gi |85111713 802 ----- 801-----
CME019C|CME019C 769 ----- 768-----
gi |85099877 707 ----- 706-----
gi |71993833 713 ----- 712-----
gi |66816950|Dd 921 ----- 920-----
Esi0029_0136 848 ----- 847-----
101670|101670|Sm 801 ----- 800-----
404911|404911|Sm 986 985----- 985-----
Pphat.024G072600|Pphat.024G072600.1 645 ----- 644-----
437242|437242|Sm 863 ----- 862-----
Pphat.023G005400|Pphat.023G005400.1 712 ----- 711-----
Pphat.020G019000|Pphat.020G019000.1 776 ----- 775-----
Pphat.008G087300|Pphat.008G087300.1 847 ----- 846-----
Pphat.023G066800|Pphat.023G066800.1 762 ----- 761-----
gi |66816205 854 ----- 853-----
LOC_Os04g31190|LOC_Os04g31190.1 798 ----- 797-----
AT2G14120 810 ----- 809-----
Carubv10013019m.g|Carubv10013019m 782 ----- 781-----
AT4G33650 807 ----- 806-----
Carubv10004162m.g|Carubv10004162m 808 ----- 807-----
Bra011458|Bra011458 808 ----- 807-----
Bra036991|Bra036991 808 ----- 807-----
Bra034579|Bra034579 808 ----- 807-----
LOC_Os01g69130|LOC_Os01g69130.1 819 ----- 818-----
GRMZM2G129155|GRMZM2G129155.T01 818 ----- 817-----
GRMZM2G180335|GRMZM2G180335.T01 822 ----- 821-----
Glyma20g06670|Glyma20g06670.1 284 ----- 283-----
Medtr2g009690|Medtr2g009690.1 853 ----- 852-----
Medtr4g093750|Medtr4g093750.1 760 ----- 759-----
Glyma07g30150|Glyma07g30150.2 813 ----- 812-----
Glyma08g07160|Glyma08g07160.1 815 ----- 814-----
Glyma04g16340|Glyma04g16340.1 818 ----- 817-----
Glyma13g32940|Glyma13g32940.1 827 ----- 826-----
Glyma15g06380|Glyma15g06380.1 824 ----- 823-----
Cucsa.331870|Cucsa.331870.1 823 ----- 822-----
GSVIVG01012532001|GSVIVT01012532001 924 ----- 923-----
Cucsa.218420|Cucsa.218420.1 814 ----- 813-----
Potri.012G125300|Potri.012G125300.1 264 ----- 263-----
Potri.007G118300|Potri.007G118300.1 836 ----- 835-----
Potri.017G041800|Potri.017G041800.1 832 ----- 831-----
29506.t000007|29506.m000169|Rc 838 ----- 837-----
Eucgr.I02611|Eucgr.I02611.1 838 ----- 837-----
29848.t000060|29848.m004504|Rc 798 ----- 797-----
GSVIVG01036006001|GSVIVT01036006001 698 ----- 697-----

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gi |85092415 764 ----- 763-----
gi |85115828 800 ----- 799-----
gi |164424111 734 ----- 733-----
gi |11342664 716 ----- 715-----
gi |222136617 663 ----- 662-----
Esi0024_0159 901 ----- 900-----
Esi0021_0042 898 ----- 897-----
Esi0103_0037 792 ----- 791-----
Esi0343_0016 965 64----- 964-----
YOR211C 633 ----- 632-----
gi |71981891 839 ----- 838-----
gi |56549125|ref|NP_001005362.1|dynamin-2 377 ----- 376-----
gi |59853099|ref|NP_004399.2|dynamin-1 865 ----- 864-----
PGSC0003DMG400010899 613 ----- 612-----
Vocar20015232m.g|Vocar20015232m 629 ----- 628-----
Cre17.g724150|Cre17.g724150.t1.1 905 ----- 904-----
Vocar20001129m.g|Vocar20001129m 925 ----- 924-----
gi |85111713 802 ----- 801-----
CME019C|CME019C 769 ----- 768-----
gi |85099877 707 ----- 706-----
gi |71993833 713 ----- 712-----
gi |66816950|Dd 921 ----- 920-----
Esi0029_0136 848 ----- 847-----
101670|101670|Sm 801 ----- 800-----
404911|404911|Sm 986 985----- 985-----
Pphat.024G072600|Pphat.024G072600.1 645 ----- 644-----
437242|437242|Sm 918 ----- 917-----
Pphat.023G005400|Pphat.023G005400.1 713 ----- 712-----
Pphat.020G019000|Pphat.020G019000.1 776 ----- 775-----
Pphat.008G087300|Pphat.008G087300.1 847 ----- 846-----
Pphat.023G066800|Pphat.023G066800.1 762 ----- 761-----
gi |66816205 854 ----- 853-----
LOC_Os04g31190|LOC_Os04g31190.1 798 ----- 797-----
AT2G14120 810 ----- 809-----
Carubv10013019m.g|Carubv10013019m 782 ----- 781-----
AT4G33650 807 ----- 806-----
Carubv10004162m.g|Carubv10004162m 808 ----- 807-----
Bra011458|Bra011458 808 ----- 807-----
Bra036991|Bra036991 808 ----- 807-----
Bra034579|Bra034579 808 ----- 807-----
LOC_Os01g69130|LOC_Os01g69130.1 819 ----- 818-----
GRMZM2G129155|GRMZM2G129155.T01 818 ----- 817-----
GRMZM2G180335|GRMZM2G180335.T01 822 ----- 821-----
Glyma20g06670|Glyma20g06670.1 284 ----- 283-----
Medtr2g009690|Medtr2g009690.1 853 ----- 852-----
Medtr4g093750|Medtr4g093750.1 760 ----- 759-----
Glyma07g30150|Glyma07g30150.2 813 ----- 812-----
Glyma08g07160|Glyma08g07160.1 815 ----- 814-----
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Glyma13g32940|Glyma13g32940.1 827 ----- 826-----
Glyma15g06380|Glyma15g06380.1 824 ----- 823-----
Cucsa.331870|Cucsa.331870.1 823 ----- 822-----
GSVIVG01012532001|GSVIVT01012532001 924 ----- 923-----
Cucsa.218420|Cucsa.218420.1 814 ----- 813-----
Potri.012G125300|Potri.012G125300.1 264 ----- 263-----
Potri.007G118300|Potri.007G118300.1 836 ----- 835-----
Potri.017G041800|Potri.017G041800.1 832 ----- 831-----
29506.t000007|29506.m000169|Rc 838 ----- 837-----
Eucgr.I02611|Eucgr.I02611.1 838 ----- 837-----
29848.t000060|29848.m004504|Rc 798 ----- 797-----
GSVIVG01036006001|GSVIVT01036006001 698 ----- 697-----

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gi 85092415	764	-----	763	-----	763	-----	763
gi 85115828	800	-----	799	-----	799	-----	799
gi 164424111	734	-----	733	-----	733	-----	733
gi 11342664	716	-----	715	-----	715	-----	715
gi 222136617	663	-----	662	-----	662	-----	662
Esi0024_0159	951	-----	950	-----	950	-----	960
Esi0021_0042	1000	LADPLGSPAAGSSVGGGGARVGE	1025EADRYGLFPASTGGAAGGSRVAQSRSRDALFGEETKSNASTRRSDGTRRRRTDTS	1085LFGEDGTR*	1093		
Esi0103_0037	770	-----	769	-----	769	-----	769
gi 193204309	965	-----	964	-----	964	-----	964
Esi0343_0016	633	-----	632	-----	632	-----	632
YOR211C	882	-----	881	-----	881	-----	881
gi 71981891	839	-----	838	-----	838	-----	838
gi 56549125 ref NP_001005362.1 dynamin-2	377	-----	376	-----	376	-----	376
gi 59853099 ref NP_004399.2 dynamin-1	865	-----	864	-----	864	-----	864
PGSC0003DMG400010899	613	-----	612	-----	612	-----	612
Vocar20015232m.g Vocar20015232m	629	-----	628	-----	628	-----	628
Cre17.g724150 Cre17.g724150.t1.1	905	-----	904	-----	904	-----	904
Vocar20001129m.g Vocar20001129m	925	-----	924	-----	924	-----	924
gi 85111713	802	-----	801	-----	801	-----	801
CME019C CME019C	769	-----	768	-----	768	-----	768
gi 85099877	707	-----	706	-----	706	-----	706
gi 71993833	713	-----	712	-----	712	-----	712
gi 66816950 bd	921	-----	920	-----	920	-----	920
Esi0029_0136	848	-----	847	-----	847	-----	847
101670 101670 Sm	801	-----	800	-----	800	-----	800
404911 404911 Sm	986	-----	985	-----	985	-----	985
Phpat.024G072600 Phpat.024G072600.1	645	-----	644	-----	644	-----	644
437242 437242 Sm	930	-----	929	-----	929	-----	929
Phpat.023G005400 Phpat.023G005400.1	713	-----	712	-----	712	-----	712
Phpat.02G019000 Phpat.02G019000.1	776	-----	775	-----	775	-----	775
Phpat.008G087300 Phpat.008G087300.1	847	-----	846	-----	846	-----	846
Phpat.023G066800 Phpat.023G066800.1	762	-----	761	-----	761	-----	761
gi 66816205	854	-----	853	-----	853	-----	853
LOC_Os04g31190 LOC_Os04g31190.1	798	-----	797	-----	797	-----	797
AT2G14120	810	-----	809	-----	809	-----	809
Carubv10013019m.g Carubv10013019m	782	-----	781	-----	781	-----	781
AT4G33650	810	-----	809	-----	809	-----	809
Carubv10004162m.g Carubv10004162m	807	-----	806	-----	806	-----	806
Bra011458 Bra011458	808	-----	807	-----	807	-----	807
Bra036991 Bra036991	808	-----	807	-----	807	-----	807
Bra034579 Bra034579	808	-----	807	-----	807	-----	807
LOC_Os01g69130 LOC_Os01g69130.1	819	-----	818	-----	818	-----	818
GRMZM2G129155 GRMZM2G129155.T01	818	-----	817	-----	817	-----	817
GRMZM2G180335 GRMZM2G180335.T01	822	-----	821	-----	821	-----	821
Glyma20g06670 Glyma20g06670.1	284	-----	283	-----	283	-----	283
Medtr2g009690 Medtr2g009690.1	853	-----	852	-----	852	-----	852
Medtr4g093750 Medtr4g093750.1	760	-----	759	-----	759	-----	759
Glyma07g30150 Glyma07g30150.2	813	-----	812	-----	812	-----	812
Glyma08g07160 Glyma08g07160.1	815	-----	814	-----	814	-----	814
Glyma04g16340 Glyma04g16340.1	818	-----	817	-----	817	-----	817
Glyma13g32940 Glyma13g32940.1	827	-----	826	-----	826	-----	826
Glyma15g06380 Glyma15g06380.1	824	-----	823	-----	823	-----	823
Cucsa.331870 Cucsa.331870.1	823	-----	822	-----	822	-----	822
GSVIVG01012532001 GSVIVT01012532001	924	-----	923	-----	923	-----	923
Cucsa.218420 Cucsa.218420.1	814	-----	813	-----	813	-----	813
Potri.012G125300 Potri.012G125300.1	264	-----	263	-----	263	-----	263
Potri.007G118300 Potri.007G118300.1	836	-----	835	-----	835	-----	835
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29506.t000007 29506.m000169 Rc	838	-----	837	-----	837	-----	837
Eucgr.I02611 Eucgr.I02611.1	838	-----	837	-----	837	-----	837
29848.t000060 29848.m004504 Rc	798	-----	797	-----	797	-----	797
GSVIVG0103606001 GSVIVT0103606001	698	-----	697	-----	697	-----	697

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gi 164424111							
gi 11342664							
gi 222136617							
Esi0024_0159							
Esi0021_0042	1094						
Esi0103_0037							
gi 193204309	965	-	964				
Esi0343_0016							
YOR211C	882	-	881				
gi 71981891							
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Vocar20015232m.g Vocar20015232m							
Cre17.g724150 Cre17.g724150.t1.1							
Vocar20001129m.g Vocar20001129m							
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CME019C CME019C							
gi 85099877							
gi 71993833							
gi 66816950 bd	921		920				
Esi0029_0136							
101670 101670 Sm							
404911 404911 Sm	986	--	985				
Phpat.024G072600 Phpat.024G072600.1							
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LOC_Os04g31190 LOC_Os04g31190.1							
AT2G14120							
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