

CMAL28C 1 -----MASDQDDAGFPTLVQSMVICA 22LLCLAMGASIVYVNSHSEQNHLAQFQAKPGERPRRAFVFGQLRSRV
tr|D8RFR6|D8RFR6_SELML 1 -----MGVVSDLFETLTPAVLGSDDYR-----GVDLGGYDVTYKHLGGGLCGG 45LLGALYGLNLTTRWNYQM--STK--
GRMZM2G086935|GRMZM2G086935_T02 1 -----MGGSNLKGIVD-DEIVVTKGKRAAGIGL 26RFGSVYVGLHSMIFPG--RQV--
LOC_Os09g10740|LOC_Os09g10740.1 1 -----MELSNLNSGL-DEVMKTKGKRAAGIGL 26RFGSVYVGLHSMIFPG--RQV--
Pphat.005G082500|Pphat.005G082500.1 1 -----MESDKYAHMDEPDLRNLGGYDVAFAFASAGSSG 35LVGMLLGLATWATWHDV--PRV--
Pphat.006G036500|Pphat.006G036500.1 1 -----MEDDKYARMDPELENNLGGYDVAFAFASAGSSG 35LVGMLLGLATWATWHDV--PRV--
GRMZM2G038375|GRMZM2G038375_T01 1 -----MEDDDEPDKTKTKGKRAAGIGL 18RAGTWTGIVATWHDV--PRV--
LOC_Os02g48610|LOC_Os02g48610.1 1 -----MGLBEDPFWTKTVKRAATGL 20AAGTWTGIVATWHDV--PRV--
Eucgr.A02439|Eucgr.A02439.1 1 -----MPPFAERRYLEDDESLMKTIKGTATGL 28VAGTWTGIVATWHDV--PRV--
GSVIVG01033524001|GSVIVT01033524001 1 MFFFLTLTKIGFNSITFFAV--FSFHVFSQRRVMSLSTGKTSVIGKTSVIG 58VIGTWTGIVATWHDV--PRV--
Glyma03g29880|Glyma03g29880.3 1 -----MDPFAERRYLEDDESLMKTIKGTATGL 28VAGTWTGIVATWHDV--PRV--
Glyma19g32780|Glyma19g32780.1 1 -----MDPFAERRYLEDDESLMKTIKGTATGL 28VAGTWTGIVATWHDV--PRV--
Medtr7g092890.3 1 -----MPPFAERRYLEDDESLMKTIKGTATGL 28VAGTWTGIVATWHDV--PRV--
Bra004675|Bra004675 1 -----MDPFAERRYLEDDESLMKTIKGTATGL 27VAGTWTGIVATWHDV--PRV--
Bra016890|Bra016890 1 -----MDPFAERRYLEDDESLMKTIKGTATGL 27VAGTWTGIVATWHDV--PRV--
Carubv10024223m.g|Carubv10024223m 1 -----MDPFAERRYLEDDESLMKTIKGTATGL 27VAGTWTGIVATWHDV--PRV--
At2g42210 1 -----MDPFAERRYLEDDESLMKTIKGTATGL 27VAGTWTGIVATWHDV--PRV--
PGSC0003DMG400011432|PGSC0003DMT40002974 1 -----MDFAALRYLEEDDESLMKTIKGTATGL 28VAGTWTGIVATWHDV--PRV--
Cucsa.242840|Cucsa.242840.1 1 -----MDPFAERRYLEDDESLMKTIKGTATGL 27VAGTWTGIVATWHDV--PRV--
29269.t000008|29269.m000246 1 -----MDPFAERRYLEDDESLMKTIKGTATGL 27VAGTWTGIVATWHDV--PRV--
Potri.006G059300|Potri.006G059300.1 1 -----MDPFAERRYLEDDESLMKTIKGTATGL 27VAGTWTGIVATWHDV--PRV--

CMAL28C 70 RPVDFTSATSAG 82GAPVHEPAIQSPWRTVAAHAGFLSILGLFVVGVEYSARALRGDHPDPPNSIAGGCLAGS-A 141FGVR-----NGSLCIVGVGICIV
66 -----G 66SEIVR-AV--NRYQMTIEYGALIGAGAMALTAICERYR--GRADYWNSTYAGWAAGAM 121LGLR-----NGSVRGLTAAAS
46 -----G 46NIVYIPOLIRLIRTKVGHYRAASLAVFGATFVGVCEALARYR--MRKDIINGAVAGGFAAGA-S 104LGS-----NGSFRAFFSGSA
46 -----G 46SNVYIPDLRIRTKVGHYRAASLAVFGATFVGVCEALARYR--MRKDIINGAVAGGFAAGA-S 104LGS-----NGSFRAFFSGSA
Pphat.005G082500|Pphat.005G082500.1 55 -----E 55RNVALPGLIRTKKMMGNVGLTFAAIGGVYIGVEQLVQNYR--MKRDFNNGAVGGFVAGASV 106LGYR-----ARSIFTAIAAGAT
Pphat.006G036500|Pphat.006G036500.1 55 -----E 55RNVALPGLIRTKKMMGNVGLTFAAIGGVYIGVEQLVQNYR--MKRDFNNGAVGGFVAGASV 106LGYR-----ARSIFTAIAAGAT
GRMZM2G038375|GRMZM2G038375_T01 38 -----E 38RNVALPGLIRTKKMMGNVGLTFAAIGGVYIGVEQLVQNYR--MKRDFNNGAVGGFVAGASV 106LGYR-----ARSIFTAIAAGAT
LOC_Os02g48610|LOC_Os02g48610.1 40 -----E 40RNVALPGLIRTKKMMGNVGLTFAAIGGVYIGVEQLVQNYR--MKRDFNNGAVGGFVAGASV 106LGYR-----ARSIFTAIAAGAT
Eucgr.A02439|Eucgr.A02439.1 1 -----E 0-----MGNVGMFFAAIGGVYIGVEQLVQNYR--MKRDFNNGAVGGFVAGASV 46LGYR-----GIFPKV-----
GSVIVG01033524001|GSVIVT01033524001 78 -----E 78RNVALPGLIRTKKMMGNVGLTFAAIGGVYIGVEQLVQNYR--MKRDFNNGAVGGFVAGASV 106LGYR-----ARSIFTAIAAGAT
Glyma03g29880|Glyma03g29880.3 48 -----E 48RNVALPGLIRTKKMMGNVGLTFAAIGGVYIGVEQLVQNYR--MKRDFNNGAVGGFVAGASV 106LGYR-----ARSIFTAIAAGAT
Glyma19g32780|Glyma19g32780.1 48 -----E 48RNVALPGLIRTKKMMGNVGLTFAAIGGVYIGVEQLVQNYR--MKRDFNNGAVGGFVAGASV 106LGYR-----ARSIFTAIAAGAT
Medtr7g092890.3 1 -----E 0-----MGNVGMFFAAIGGVYIGVEQLVQNYR--MKRDFNNGAVGGFVAGASV 46LGYR-----GIFPKV-----
Bra004675|Bra004675 47 -----E 47RNVALPGLIRTKKMMGNVGLTFAAIGGVYIGVEQLVQNYR--MKRDFNNGAVGGFVAGASV 106LGYR-----ARSIFTAIAAGAT
Bra016890|Bra016890 47 -----E 47RNVALPGLIRTKKMMGNVGLTFAAIGGVYIGVEQLVQNYR--MKRDFNNGAVGGFVAGASV 106LGYR-----ARSIFTAIAAGAT
Carubv10024223m.g|Carubv10024223m 47 -----E 47RNVALPGLIRTKKMMGNVGLTFAAIGGVYIGVEQLVQNYR--MKRDFNNGAVGGFVAGASV 106LGYR-----ARSIFTAIAAGAT
At2g42210 47 -----E 47RNVALPGLIRTKKMMGNVGLTFAAIGGVYIGVEQLVQNYR--MKRDFNNGAVGGFVAGASV 106LGYR-----ARSIFTAIAAGAT
PGSC0003DMG400011432|PGSC0003DMT40002974 48 -----E 48RNVALPGLIRTKKMMGNVGLTFAAIGGVYIGVEQLVQNYR--MKRDFNNGAVGGFVAGASV 106LGYR-----ARSIFTAIAAGAT
Cucsa.242840|Cucsa.242840.1 47 -----E 47RNVALPGLIRTKKMMGNVGLTFAAIGGVYIGVEQLVQNYR--MKRDFNNGAVGGFVAGASV 106LGYR-----ARSIFTAIAAGAT
29269.t000008|29269.m000246 47 -----E 47RNVALPGLIRTKKMMGNVGLTFAAIGGVYIGVEQLVQNYR--MKRDFNNGAVGGFVAGASV 106LGYR-----ARSIFTAIAAGAT
Potri.006G059300|Potri.006G059300.1 47 -----E 47RNVALPGLIRTKKMMGNVGLTFAAIGGVYIGVEQLVQNYR--MKRDFNNGAVGGFVAGASV 106LGYR-----ARSIFTAIAAGAT

CMAL28C 159 LGAPGCHFLDWSFKSSEPALN---PQPGV 185R-HCVMLAEQADEAARSAR 203
139 LBAVTVVDLTLAQNHLKKNKNEPEPED 168R----- 169
122 VALDSVLLDVTGCK--TDEEEKQH* 145----- 145
122 LAPTSLVLLDVTGCK--TDEEAKTGKAH* 148----- 148
131 LAACAVIADAGGCT-VPTPTGKRYEYLPRT 159NPD*----- 163
131 LAACAVIADAGGCT-VPTPTGKRYEYLPRT 159NPD*----- 163
116 AFTSALDVGQNT-TRVDNKEYYPYVE 143KRA*----- 148
118 AFTSALDVGQNT-TRVDNKEYYPYVE 145NPAH*----- 150
80 TSALLDVGQNT-TRVDNKEYYPYTT 105KKTAVDS*----- 112
155 LAHSAFIDSGGQNT-TRVDNKEYYPYTT 183NKTTH*----- 189
125 LAPTSLDVGQNT-LKHDGKEYAAYTT 153KRPSTA*----- 160
125 LAPTSLDVGQNT-LKHDGKEYAAYTT 153KRPSTA*----- 160
57 ----- 56
124 LAVTSALIDSGGQNT-TRVDNKEYYPYTT 152EKRAQES*----- 160
124 LAVTSALIDSGGQNT-TRVDNKEYYPYTT 152EKTAQADA*----- 161
124 LAVTSALIDSGGQNT-TRVDNKEYYPYTT 152KRA-EADS*----- 159
124 LAVTSALIDSGGQNT-TRVDNKEYYPYTT 152KRA-EADS*----- 159
125 LAVTSALIDSGGQNT-TRVDNKEYYPYTT 153KRVVA*----- 159
124 LAVTSALIDSGGQNT-TRVDNKEYYPYTT 152KRSHE*----- 158
124 LAVTSALIDSGGQNT-TRVDNKEYYPYTT 152KRSVEG*----- 159
124 LAVTSALIDSGGQNT-TRVDNKEYYPYTT 152KRSVEG*----- 159