

gi|17864088|ref|NP\_055947.1| 1 -----MLTEASLSIQGWGSGILVLELITFG----- 25 -----P---FVFFLYLTYHCFVGGGLVTLVLLFGKTN  
YML104C 1 -----MPKFPQRIIT--LVVFLYLSMI 20 -----Q-----SVITFSLSGFLNVCIFAYFV  
gi|164426626|ref|XP\_957576.2 1 MVL-----QGRDIALAAIAFTSISQYA-----VWVFFAI 29 -----R-----KANYFAGVLLVTVGLLALL  
gi|17506801|ref|NP\_492758.1| 1 ----- 0 ----- 0 ----- 0 -----  
Osa:LOC\_090550660 1 ----- 0 ----- 0 ----- 0 -----  
Bra:Br2026152 1 ----- 0 ----- 0 ----- 0 -----  
Bra:Br2026776 1 ----- 0 ----- 0 ----- 0 -----  
AT1G15240. 1 ----- 0 ----- 0 ----- 0 -----  
Cru:Carubv10008179m 1 ----- 41 ----- 0 ----- 0 -----  
Csa:Cucsa.359160.1 1 ----- 38 ----- 0 ----- 0 -----  
Mtr:Medtr4g012920 1 ----- 38 ----- 0 ----- 0 -----  
Gma:Glyma08g21950 1 ----- 38 ----- 0 ----- 0 -----  
Gma:Glyma07g00690 1 ----- 38 ----- 0 ----- 0 -----  
Egr:Eucgr.F03028 1 ----- 38 ----- 0 ----- 0 -----  
Vvi:GSVIT01017080001 1 ----- 38 ----- 0 ----- 0 -----  
Rco:30146.m003594|30146.m003594 1 ----- 37 ----- 0 ----- 0 -----  
Ptr:Potri.0030053200 1 ----- 39 ----- 0 ----- 0 -----  
Ptr:Potri.00183100synonym:POPTR\_0001s1 1 ----- 41 ----- 0 ----- 0 -----  
Ppa:Pp1s67\_32V6.1| 1 ----- 41 ----- 0 ----- 0 -----  
Ppa:Pp1s7\_51V6.1| 1 ----- 40 ----- 0 ----- 0 -----  
Ppa:Pp1s48\_155V6.1| 1 ----- 40 ----- 0 ----- 0 -----  
Ppa:Pp1s68\_34V6.1| 1 ----- 40 ----- 0 ----- 0 -----  
Smo:413327|413327 1 ----- 40 ----- 0 ----- 0 -----  
Zma:GRMZM2G026442\_T01 1 ----- 40 ----- 0 ----- 0 -----  
Osa:LOC\_0s11g06040 1 ----- 40 ----- 0 ----- 0 -----  
Egr:Eucgr.G01512 1 ----- 40 ----- 0 ----- 0 -----  
Gma:Glyma20g01140 1 ----- 37 ----- 0 ----- 0 -----  
Mtr:Medtr4g087210 1 ----- 37 ----- 0 ----- 0 -----  
Gma:Glyma02g15445 1 ----- 37 ----- 0 ----- 0 -----  
Gma:Glyma07g33040 1 ----- 37 ----- 0 ----- 0 -----  
Bra:Br2015246 1 ----- 37 ----- 0 ----- 0 -----  
Cru:Carubv10012892m 1 ----- 37 ----- 0 ----- 0 -----  
AT2G15900 1 ----- 37 ----- 0 ----- 0 -----  
Cru:Carubv10012885m 1 ----- 37 ----- 0 ----- 0 -----  
Csa:Cucsa.220190 1 ----- 37 ----- 0 ----- 0 -----  
Vvi:GSVIT01031845001 1 ----- 37 ----- 0 ----- 0 -----  
Rco:29851.m002502|29851.m002502 1 ----- 37 ----- 0 ----- 0 -----  
Ptr:Potri.0090108300 1 ----- 37 ----- 0 ----- 0 -----  
Ptr:Potri.004G146600 1 ----- 37 ----- 0 ----- 0 -----

gi|17864088|ref|NP\_055947.1| 55 SEKYLEQCE--- 63 -----HGFLEPSPGIVS3CLEEMRERARTIKIDRR-----LTGANIDEFP 103LQOVQFQSRDYV--OYVYVTLSDDES--FL  
YML104C 43 FPKSLP--- 48 -----DLPKPQRFVAVVSEBNT--VDVDEKELKSVGLIQDGAQEGKE 91ESLIVNLKIDFV--QWSTKIDKNDAEFELK  
gi|164426626|ref|XP\_957576.2 52 MLTSGRSHH--- 60 -----HMLRPPRPHGAFAVVGSGSKVAALRARQTSTKAPLYPESKUSVA 108LVDVYVIRDFI--QVWYSSSKNKPV--FT  
gi|17506801|ref|NP\_492758.1| 67 ----- 0 ----- 0 ----- 0 -----  
Osa:LOC\_090550660 67 ----- 0 ----- 0 ----- 0 -----  
Bra:Br2026152 67 ----- 0 ----- 0 ----- 0 -----  
Bra:Br2026776 67 ----- 0 ----- 0 ----- 0 -----  
AT1G15240. 67 ----- 0 ----- 0 ----- 0 -----  
Cru:Carubv10008179m 67 ----- 0 ----- 0 ----- 0 -----  
Csa:Cucsa.359160.1 67 ----- 0 ----- 0 ----- 0 -----  
Mtr:Medtr4g012920 67 ----- 0 ----- 0 ----- 0 -----  
Gma:Glyma08g21950 67 ----- 0 ----- 0 ----- 0 -----  
Gma:Glyma07g00690 67 ----- 0 ----- 0 ----- 0 -----  
Egr:Eucgr.F03028 67 ----- 0 ----- 0 ----- 0 -----  
Vvi:GSVIT01017080001 67 ----- 0 ----- 0 ----- 0 -----  
Rco:30146.m003594|30146.m003594 67 ----- 0 ----- 0 ----- 0 -----  
Ptr:Potri.0030053200 67 ----- 0 ----- 0 ----- 0 -----  
Ptr:Potri.00183100synonym:POPTR\_0001s1 67 ----- 0 ----- 0 ----- 0 -----  
Ppa:Pp1s67\_32V6.1| 58 EFRWFRPINCSEP 700Y-AAHQHRRK--KNDVDEPLGSLHVAATWRRR 01DSVWVEKA 112VDFRFRHLISEVWVLDWYSRIITPDK--EAP  
Ppa:Pp1s7\_51V6.1| 58 EFRWMLFSESEST 707SN--LHQLGHDPELSE-ASHAVVNWRRH 0QDSVVEAA 107VDDLRCGLIDEVWVLDWYSRIITPDK--EAP  
Ppa:Pp1s48\_155V6.1| 58 EFRWMLPPTQPS 70AEP--POHHRK--LGSCHNPLSE-AFHATVNNK 0DSASVEAA 106VNLRLSLVDEWVLDWYSRIITPDK--EAP  
Ppa:Pp1s68\_34V6.1| 58 EFRWLRPLPTQPS 70VOPHPHRRK--LGSCHNPLSE-ASHAANNRRH 0YNSVVEAA 112VDFRFRHLISEVWVLDWYSRIITPDK--EAP  
Smo:413327|413327 67 EFRWFRPINCSEP 700Y-AAHQHRRK--KNDVDEPLGSLHVAATWRRR 01DSVWVEKA 112VDFRFRHLISEVWVLDWYSRIITPDK--EAP  
Zma:GRMZM2G026442\_T01 67 EFRWFRPINCSEP 700Y-AAHQHRRK--KNDVDEPLGSLHVAATWRRR 01DSVWVEKA 112VDFRFRHLISEVWVLDWYSRIITPDK--EAP  
Osa:LOC\_0s11g06040 102 EFRWFRPINCSEP 700Y-AAHQHRRK--KNDVDEPLGSLHVAATWRRR 01DSVWVEKA 112VDFRFRHLISEVWVLDWYSRIITPDK--EAP  
Egr:Eucgr.G01512 1 ----- 0 ----- 0 ----- 0 -----  
Gma:Glyma20g01140 67 EFRWFRPINCSEP 700Y-AAHQHRRK--KNDVDEPLGSLHVAATWRRR 01DSVWVEKA 112VDFRFRHLISEVWVLDWYSRIITPDK--EAP  
Mtr:Medtr4g087210 67 EFRWFRPINCSEP 700Y-AAHQHRRK--KNDVDEPLGSLHVAATWRRR 01DSVWVEKA 112VDFRFRHLISEVWVLDWYSRIITPDK--EAP  
Gma:Glyma02g15445 67 EFRWFRPINCSEP 700Y-AAHQHRRK--KNDVDEPLGSLHVAATWRRR 01DSVWVEKA 112VDFRFRHLISEVWVLDWYSRIITPDK--EAP  
Gma:Glyma07g33040 67 EFRWFRPINCSEP 700Y-AAHQHRRK--KNDVDEPLGSLHVAATWRRR 01DSVWVEKA 112VDFRFRHLISEVWVLDWYSRIITPDK--EAP  
Bra:Br2015246 67 EFRWFRPINCSEP 700Y-AAHQHRRK--KNDVDEPLGSLHVAATWRRR 01DSVWVEKA 112VDFRFRHLISEVWVLDWYSRIITPDK--EAP  
Cru:Carubv10012892m 67 EFRWFRPINCSEP 700Y-AAHQHRRK--KNDVDEPLGSLHVAATWRRR 01DSVWVEKA 112VDFRFRHLISEVWVLDWYSRIITPDK--EAP  
AT2G15900 67 EFRWFRPINCSEP 700Y-AAHQHRRK--KNDVDEPLGSLHVAATWRRR 01DSVWVEKA 112VDFRFRHLISEVWVLDWYSRIITPDK--EAP  
Cru:Carubv10012885m 67 EFRWFRPINCSEP 700Y-AAHQHRRK--KNDVDEPLGSLHVAATWRRR 01DSVWVEKA 112VDFRFRHLISEVWVLDWYSRIITPDK--EAP  
Csa:Cucsa.220190 67 EFRWFRPINCSEP 700Y-AAHQHRRK--KNDVDEPLGSLHVAATWRRR 01DSVWVEKA 112VDFRFRHLISEVWVLDWYSRIITPDK--EAP  
Vvi:GSVIT01031845001 67 EFRWFRPINCSEP 700Y-AAHQHRRK--KNDVDEPLGSLHVAATWRRR 01DSVWVEKA 112VDFRFRHLISEVWVLDWYSRIITPDK--EAP  
Rco:29851.m002502|29851.m002502 67 EFRWFRPINCSEP 700Y-AAHQHRRK--KNDVDEPLGSLHVAATWRRR 01DSVWVEKA 112VDFRFRHLISEVWVLDWYSRIITPDK--EAP  
Ptr:Potri.0090108300 67 EFRWFRPINCSEP 700Y-AAHQHRRK--KNDVDEPLGSLHVAATWRRR 01DSVWVEKA 112VDFRFRHLISEVWVLDWYSRIITPDK--EAP  
Ptr:Potri.004G146600 67 EFRWFRPINCSEP 700Y-AAHQHRRK--KNDVDEPLGSLHVAATWRRR 01DSVWVEKA 112VDFRFRHLISEVWVLDWYSRIITPDK--EAP

gi|17864088|ref|NP\_055947.1| 131 LSHRQTLQNAHQFATRQKEDNDQWYFH-- 158 -----TRVVDGFLHRLVREKAKQKTEKDDQVKGTAEDLVTF 198EVFVEMKRGVCR  
YML104C 132 YKWRLLQTLVVKDKLKNDSASLIV-- 148 -----LKLPIFNKHHSFDAREVSDI-LTERRKSNADLQI 187AVFBNKMYKHLH  
gi|164426626|ref|XP\_957576.2 136 DEVDKALGALLTVRDLAQLDIDATLL-- 163 -----TRVPLTHTAFRFDVYEAERSVGRKKNRSVTDLGLAI 203AKYRD--GKHS  
gi|17506801|ref|NP\_492758.1| 1 ----- 0 ----- 0 ----- 0 -----  
Osa:LOC\_090550660 1 ----- 0 ----- 0 ----- 0 -----  
Bra:Br2026152 1 ----- 0 ----- 0 ----- 0 -----  
Bra:Br2026776 1 ----- 0 ----- 0 ----- 0 -----  
AT1G15240. 1 ----- 0 ----- 0 ----- 0 -----  
Cru:Carubv10008179m 1 ----- 0 ----- 0 ----- 0 -----  
Csa:Cucsa.359160.1 1 ----- 0 ----- 0 ----- 0 -----  
Mtr:Medtr4g012920 1 ----- 0 ----- 0 ----- 0 -----  
Gma:Glyma08g21950 1 ----- 0 ----- 0 ----- 0 -----  
Gma:Glyma07g00690 1 ----- 0 ----- 0 ----- 0 -----  
Egr:Eucgr.F03028 1 ----- 0 ----- 0 ----- 0 -----  
Vvi:GSVIT01017080001 1 ----- 0 ----- 0 ----- 0 -----  
Rco:30146.m003594|30146.m003594 1 ----- 0 ----- 0 ----- 0 -----  
Ptr:Potri.0030053200 1 ----- 0 ----- 0 ----- 0 -----  
Ptr:Potri.00183100synonym:POPTR\_0001s1 1 ----- 0 ----- 0 ----- 0 -----  
Ppa:Pp1s67\_32V6.1| 136 EELINLVNGLVGEISRRFRNNVLDLTL 167 -----RDLINLCCHLFRRAAIAKREKQHTDS--TSESDEDEI 206KIVLAABEDKLP  
Ppa:Pp1s7\_51V6.1| 141 EELVFIINDVLDGEISRRFRNNVLDLTL 168 -----RDLINLCCHLFRRAAIAKREKQHTDS--TSESDEDEI 207KIVLAABEDKLP  
Ppa:Pp1s48\_155V6.1| 141 EELVFIINDVLDGEISRRFRNNVLDLTL 167 -----RDLINLCCHLFRRAAIAKREKQHTDS--TSESDEDEI 206KIVLAABEDKLP  
Ppa:Pp1s68\_34V6.1| 141 EELVFIINDVLDGEISRRFRNNVLDLTL 167 -----RDLINLCCHLFRRAAIAKREKQHTDS--TSESDEDEI 206KIVLAABEDKLP  
Smo:413327|413327 141 EELVFIINDVLDGEISRRFRNNVLDLTL 167 -----RDLINLCCHLFRRAAIAKREKQHTDS--TSESDEDEI 206KIVLAABEDKLP  
Zma:GRMZM2G026442\_T01 141 EELVFIINDVLDGEISRRFRNNVLDLTL 167 -----RDLINLCCHLFRRAAIAKREKQHTDS--TSESDEDEI 206KIVLAABEDKLP  
Osa:LOC\_0s11g06040 141 EELVFIINDVLDGEISRRFRNNVLDLTL 167 -----RDLINLCCHLFRRAAIAKREKQHTDS--TSESDEDEI 206KIVLAABEDKLP  
Egr:Eucgr.G01512 141 EELVFIINDVLDGEISRRFRNNVLDLTL 167 -----RDLINLCCHLFRRAAIAKREKQHTDS--TSESDEDEI 206KIVLAABEDKLP  
Gma:Glyma20g01140 141 EELVFIINDVLDGEISRRFRNNVLDLTL 167 -----RDLINLCCHLFRRAAIAKREKQHTDS--TSESDEDEI 206KIVLAABEDKLP  
Mtr:Medtr4g087210 141 EELVFIINDVLDGEISRRFRNNVLDLTL 167 -----RDLINLCCHLFRRAAIAKREKQHTDS--TSESDEDEI 206KIVLAABEDKLP  
Gma:Glyma02g15445 141 EELVFIINDVLDGEISRRFRNNVLDLTL 167 -----RDLINLCCHLFRRAAIAKREKQHTDS--TSESDEDEI 206KIVLAABEDKLP  
Gma:Glyma07g33040 141 EELVFIINDVLDGEISRRFRNNVLDLTL 167 -----RDLINLCCHLFRRAAIAKREKQHTDS--TSESDEDEI 206KIVLAABEDKLP  
Bra:Br2015246 141 EELVFIINDVLDGEISRRFRNNVLDLTL 167 -----RDLINLCCHLFRRAAIAKREKQHTDS--TSESDEDEI 206KIVLAABEDKLP  
Cru:Carubv10012892m 141 EELVFIINDVLDGEISRRFRNNVLDLTL 167 -----RDLINLCCHLFRRAAIAKREKQHTDS--TSESDEDEI 206KIVLAABEDKLP  
AT2G15900 141 EELVFIINDVLDGEISRRFRNNVLDLTL 167 -----RDLINLCCHLFRRAAIAKREKQHTDS--TSESDEDEI 206KIVLAABEDKLP  
Cru:Carubv10012885m 141 EELVFIINDVLDGEISRRFRNNVLDLTL 167 -----RDLINLCCHLFRRAAIAKREKQHTDS--TSESDEDEI 206KIVLAABEDKLP  
Csa:Cucsa.220190 141 EELVFIINDVLDGEISRRFRNNVLDLTL 167 -----RDLINLCCHLFRRAAIAKREKQHTDS--TSESDEDEI 206KIVLAABEDKLP  
Vvi:GSVIT01031845001 141 EELVFIINDVLDGEISRRFRNNVLDLTL 167 -----RDLINLCCHLFRRAAIAKREKQHTDS--TSESDEDEI 206KIVLAABEDKLP  
Rco:29851.m002502|29851.m002502 141 EELVFIINDVLDGEISRRFRNNVLDLTL 167 -----RDLINLCCHLFRRAAIAKREKQHTDS--TSESDEDEI 206KIVLAABEDKLP  
Ptr:Potri.0090108300 141 EELVFIINDVLDGEISRRFRNNVLDLTL 167 -----RDLINLCCHLFRRAAIAKREKQHTDS--TSESDEDEI 206KIVLAABEDKLP  
Ptr:Potri.004G146600 141 EELVFIINDVLDGEISRRFRNNVLDLTL 167 -----RDLINLCCHLFRRAAIAKREKQHTDS--TSESDEDEI 206KIVLAABEDKLP

gi|17864088|ref|NP\_055947.1| 211 DM--VCSFKP-----DEEGFRDCEVLYLPPGQFNKIMSYFVRSIARGILLPLINQISPPDY-- 218  
YML104C 201 LSLKFNALQK-----EIEKSRKTIGLPHLEPDELDLSDLLVSLMTVPLTGLISPLFKFDDSDS 210  
gi|164426626|ref|XP\_957576.2 215 MATLSFSSTK----- 225 TQDQVPRKVVVRLPKKIKPKSMLASGAVSALVREITACAVVFFIMRMLEPPDT--  
Osa:LOC\_0s05g50660 1 0  
Bra:Bra026152 225  
Bra:Bra026776 227  
AT1G15240. 218  
Cru:Carubv10008179m 219  
Csa:Cucsa.359160.1 217  
Mtr:Medtr4g012920 219  
Gma:Glyma08g21950 220  
Gma:Glyma07g00690 220  
Egr:Eucgr.F03028 216  
Vvi:GSVIT01017080001 218  
Rco:30146.m003594|30146.m003594 217  
Ptr:Potri.003g053200 219  
Ptr:Potri.001g183100synonym:POPTR\_0001s1 219  
Ppa:Pp1s67\_32V6.1| 219  
Ppa:Pp1s7\_51V6.1| 214  
Ppa:Pp1s48\_155V6.1 213  
Ppa:Pp1s68\_34V6.1 219  
Smo:413327|413327 219  
Zma:GRMZM2G026442.T01 219  
Osa:LOC\_0s11g06040 258  
Egr:Eucgr.G01512 1  
Gma:Glyma20g01140 224  
Mtr:Medtr4g087210 220  
Gma:Glyma02g15445 215  
Gma:Glyma07g33040 218  
Bra:Bra015246 212  
Cru:Carubv10012892m 218  
AT2G15900 218  
Cru:Carubv10012885m 218  
Csa:Cucsa.220190 218  
Vvi:GSVIT01031845001 219  
Rco:29851.m002502|29851.m002502 219  
Ptr:Potri.009g108300 219  
Ptr:Potri.004g146600 219

gi|17864088|ref|NP\_055947.1| 272 -- 271-----INQYIWMIRDEN----- 284  
YML104C 264 - 263-----WNLRIVLSLQNYFEKHKVH-KIRRLMSK 291LELDHRKVMNDVA-----NKGVGEPSSEKLELNAEYI  
gi|164426626|ref|XP\_957576.2 279 -- 278-----WNQLMENYGRSLQDRSTVR-KLRAALDQ 306HASPAPRVNKPVA-----FFR----MIPGD  
gi|17506801|ref|NP\_492758.1| 1 0  
Osa:LOC\_0s05g50660 283 -- 282----- 282  
Bra:Bra026152 276 -- 275----- 275  
Bra:Bra026776 277 -- 276----- 276  
AT1G15240. 276 -- 275----- 275  
Cru:Carubv10008179m 275 -- 274----- 274  
Csa:Cucsa.359160.1 321 -- 320----- 320  
Mtr:Medtr4g012920 278 -- 277----- 277  
Gma:Glyma08g21950 278 -- 277----- 277  
Gma:Glyma07g00690 274 -- 273----- 273  
Egr:Eucgr.F03028 276 -- 275----- 275  
Vvi:GSVIT01017080001 275 -- 274----- 274  
Rco:30146.m003594|30146.m003594 281 -- 280----- 280  
Ptr:Potri.003g053200 277 -- 276----- 276  
Ptr:Potri.001g183100synonym:POPTR\_0001s1 272 -- 271----- 271  
Ppa:Pp1s67\_32V6.1| 271 -- 270----- 270  
Ppa:Pp1s7\_51V6.1| 272 -- 271----- 271  
Ppa:Pp1s48\_155V6.1 271 -- 270----- 270  
Ppa:Pp1s68\_34V6.1 277 -- 276----- 276  
Smo:413327|413327 273 -- 272----- 272  
Zma:GRMZM2G026442.T01 277 -- 276----- 276  
Osa:LOC\_0s11g06040 317 -- 316----- 316  
Egr:Eucgr.G01512 44 ----- 43----- INEV  
Gma:Glyma20g01140 282 -- 281----- 281  
Mtr:Medtr4g087210 282 YK 283RGLNGNDIHRHYGAERVSGVGDRLYGWVPLVWSEETISMPGDNFQKHQAGILQVVLHL 343ESS-CSFTSPDVCKTMSIFCLANSFVGKEE-KELETN--  
Gma:Glyma02g15445 273 -- 272----- 272  
Gma:Glyma07g33040 273 -- 272----- 272  
Bra:Bra015246 276 -- 275----- 275  
Cru:Carubv10012892m 270 -- 269----- 269  
AT2G15900 276 -- 275----- 275  
Cru:Carubv10012885m 276 -- 275----- 275  
Csa:Cucsa.220190 276 -- 275----- 275  
Vvi:GSVIT01031845001 277 -- 276----- 276  
Rco:29851.m002502|29851.m002502 277 -- 276----- 276  
Ptr:Potri.009g108300 277 -- 276----- 276  
Ptr:Potri.004g146600 277 -- 276----- 276

gi|17864088|ref|NP\_055947.1| 285 --CNYBAFNNIKLSDNIGE 302LEAVR--DKDQVLEQVLRSLDTAGDDI-NTIKNQINSLFVVKKVCDSRIQRLOSQKIBINT 359-----VHMAA  
YML104C 324 GKQPEHYLNDGLLEDDG 342HQVVA--YSLNKKTYLQK--ENEHLTKENLYKRRLLSLNLSLSEKLFSPSIDTAG 396KLLAREANYPDENMNGNIVLKRH  
gi|164426626|ref|XP\_957576.2 328 NERKFKFKHRAIKRNNNSD 347ARRFR--SEVSIQIKRDS---QQE--NVDQVYLRRLLEMGKRLLDQKVHHLAAG---- 393-----GDRRALPQTALTALP  
gi|17506801|ref|NP\_492758.1| 1 0  
Osa:LOC\_0s05g50660 283 -----INERIEIAVLSH 294ANKAENGVAESLE-----HMT 310MVKQREPP-MPTVPELAALIDP  
Bra:Bra026152 276 -----INERIEAAVNSR 287IKTDD-GSSAAKS-----TS 301QSE--DLS-EVSHFFARVLDLP  
Bra:Bra026776 276 -----INERIEAAVNSR 287TKTNG-GSSAAKS-----TS 301QSE--DLS-EVSHFFARVLDLP  
Cru:Carubv10008179m 276 -----INERIEAAVNSR 288IKTIL-RSSAAKE-----AS 301PEE--DLS-NVSPDHFSSRLDP  
Csa:Cucsa.359160.1 275 -----INERIEIAVNSR 286KK-PK-TVESNHE-----NL 299GSKTDGSP-SLTPSDHSSQLDLP  
Mtr:Medtr4g012920 321 -----INERIEAVVNSK 332TKANK-EVDAAOE-----VS 346HKAD-EL-QTSSDHFSSQLDLP  
Gma:Glyma08g21950 278 -----VNERIESVNVNK 289TKVNK-GVPAAOE-----AS 303HKPD-EI-QTSSDHFSSQLDLP  
Gma:Glyma07g00690 278 -----INERIESVNVNK 289TKVNK-GVPAAOE-----AS 303HKAD-EI-QTSSDHFSSQLDLP  
Egr:Eucgr.F03028 274 -----INERIESVNVSK 285TKANK-GTAAHAE-----AS 299PEE--WT-RHSDHSSQLDLP  
Vvi:GSVIT01017080001 276 -----INERIESVNSA 287AKANK-GGTAAOE-----AS 301QPKNGSS-RHSDHSSQLDLP  
Rco:30146.m003594|30146.m003594 275 -----INERIEIAVNSK 286--ANK-GVPAAOE-----AS 298QKSKNGSS-KHSDHSSQLDLP  
Ptr:Potri.003g053200 281 -----INERIEIAVNSK 292--ANK-GVPAAOE-----TS 304HKPKNGSS-RHSDHSSQLDLP  
Ptr:Potri.001g183100synonym:POPTR\_0001s1 277 -----INERIEIAVNSK 288--ANK-GVPAAOE-----AS 300HKPKNGSS-RHSDHSSQLDLP  
Ppa:Pp1s67\_32V6.1| 272 -----INERIEIAVNSK 288TEKERQ-SEKASL-----TS 301FAVQVSD-FT-LSQAK  
Ppa:Pp1s7\_51V6.1| 272 -----INERIEIAVNSK 283HKARAAEAEAE-----NR 299AKORLDD-R-----VQKRF  
Ppa:Pp1s48\_155V6.1 271 -----INERIEIAVNSK 282TERARAAEAEAE-----NR 295AKORLDD-R-----ILQRF  
Ppa:Pp1s68\_34V6.1 277 -----INERIEIAVNSK 288MERARAAEAEAE-----NR 301AKORLDD-R-----ILQRF  
Smo:413327|413327 273 -----INERIEIAVNSK 284RSRLSKGKKAFAE-----IR 300ADSSQFDD-S-----GLMPTD  
Zma:GRMZM2G026442.T01 277 -----INERIEIAVNSK 288DTGS--AGTNN----- 298--NT-G--TVT--  
Osa:LOC\_0s11g06040 317 -----INERIEIAVNSK 328NTNS--GGNLD----- 338--NT-G--SVTV--  
Egr:Eucgr.G01512 48 IELVILAL 55KEDGKVFGA-TQ----- 67--ATN-V-----ANKHFFSGTAAQAK  
Gma:Glyma20g01140 282 -----INERIEIAVNSK 293NDEICINWTTGGGDH----- 306--STN-T-----  
Mtr:Medtr4g087210 379 KGVLLKEP INERIEIAVNSK 398NNDNSKKWGGDQ----- 411--STN-V-----  
Gma:Glyma02g15445 273 -----INERIEIAVNSK 284ND-DGTGGMGSDQ----- 296--STN-V-----  
Gma:Glyma07g33040 273 -----INERIEIAVNSK 284ND-DGTGGMGSDQ----- 296--STN-V-----  
Bra:Bra015246 276 -----INERIEIAVNSK 287REGNFEQTSREQ----- 300--SVY-S-----  
Cru:Carubv10012892m 270 -----INERIEIAVNSK 287REGNFEQTSREQ----- 300--NVN-S-----  
AT2G15900 276 -----INERIEIAVNSK 287REGNFEQTSREQ----- 300--NVN-S-----  
Cru:Carubv10012885m 276 -----INERIEIAVNSK 287REGNFEQTSREQ----- 300--NVN-S-----  
Csa:Cucsa.220190 276 -----INERIEIAVNSK 287RANSDVGGGQDQ----- 300--TYS-S-----  
Vvi:GSVIT01031845001 276 -----INERIEIAVNSK 287RANSDVGGGQDQ----- 300--FST-V-----  
Rco:29851.m002502|29851.m002502 277 -----INERIEIAVNSK 288DGLMBUSGDF----- 301--AGD-A-----  
Ptr:Potri.009g108300 277 -----INERIEIAVNSK 288DGLMBUSGDF----- 301--AGD-A-----  
Ptr:Potri.004g146600 277 -----INERIEIAVNSK 288DGLMBUSGDF----- 301--AGD-A-----





gi|17864088|ref|NP\_055947.1|
YML104C
gi|164426626|ref|XP\_957576.2
gi|17506801|ref|NP\_492758.1
Osa:LOC\_0s05950660
Bra:Bra026152
Bra:Bra026776
AT1G15240.
Cru:Carubv10008179m
Csa:Cucsa.359160.1
Mtr:Medtr4g012920
Gma:Glyma08g21950
Gma:Glyma07g00690
Egr:Eucgr.F03028
Vvi:GSVIT0101708001
Rco:30146.m003594|30146.m003594
Ptr:Potri.003053200
Ptr:Potri.00183100synonym:POPTR\_0001s1
Ppa:Pp1s7\_51v6.1
Ppa:Pp1s8\_34v6.1
Ppa:Pp1s8\_155v6.1
Ppa:Pp1s8\_34v6.1
Smo:413327|413327
Zma:GRMZM20026442.T01
Osa:LOC\_0s11906040
Egr:Eucgr.001512
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Cru:Carubv10012892m
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Csa:Cucsa.220190
Vvi:GSVIT01031845001
Rco:29851.m002502|29851.m002502
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598 TYRYSYSDHEDHHRMLTISQ 615PESLSSLL-LDQCK...
822 ARRYNEFELNLTLYKN 838FRDLMLQLDQLFPEK...
930 VTRRYSEFELHHRHQLKRSQ 947YSVRRNL...
224 --QIPQKPPF--K--LSBQQDLSRRRGLQYLE...
727 KRRRSHPEELHRRLLKLV 743PFSYNYLH...
646 KRRRSHPEELHRRLLKLV 662PFSYNYLH...
647 KRRRSHPEELHRRLLKLV 663PFSYNYLH...
649 KRRRSHPEELHRRLLKLV 665PFSYNYLH...
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719 KRRRSHPEELHRRLLKLV 735PFSYNYLH...
715 KRRRSHPEELHRRLLKLV 731PFSYNYLH...
727 KRRRSHPEELHRRLLKLV 743PFSYNYLH...
692 WRRYRNFEOLHRRLLKLV 708PFSYNYLH...
702 WRRYRNFEOLHRRLLKLV 718PFSYNYLH...
698 WRRYRNFEOLHRRLLKLV 714PFSYNYLH...
575 WRRYRNFEOLHRRLLKLV 591PFSYNYLH...
589 WRRYRNFEOLHRRLLKLV 605PFSYNYLH...
631 WRRYRNFEOLHRRLLKLV 648PFSYNYLH...
310 KE\_3111PNYTLH --LPPKRFSSS--TDAFVHRCIO...
537 WRRYRNFEOLHRRLLKLV 553PFSYNYLH...
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gi|17506801|ref|NP\_492758.1
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Bra:Bra026776
AT1G15240.
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Csa:Cucsa.359160.1
Mtr:Medtr4g012920
Gma:Glyma08g21950
Gma:Glyma07g00690
Egr:Eucgr.F03028
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Ppa:Pp1s7\_51v6.1
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Smo:413327|413327
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Osa:LOC\_0s11906040
Egr:Eucgr.001512
Gma:Glyma20g01140
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Bra:Bra015246
Cru:Carubv10012892m
AT2G15900
Cru:Carubv10012885m
Csa:Cucsa.220190
Vvi:GSVIT01031845001
Rco:29851.m002502|29851.m002502
Ptr:Potri.0090108300
Ptr:Potri.004G146600

680 KGGQD-FARKMDTFNPNFRNSMRNYSNAVKS...
906 LNRK-YMHD-D--ILEE...
1007 PTTAT-HQQL-S--SDESK--KMMRLYDSM...
293 T-RRSI 297TSSL-PFT...
805 LDTLGVLOLDS-V-NLDE--RSKKNKTSN-S...
744 KRSR-RNFERLHRRLLKLV 719PFSYNYLH...
724 KRSR-RNFERLHRRLLKLV 724PFSYNYLH...
725 KRSR-RNFERLHRRLLKLV 725PFSYNYLH...
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653 KRSR-RNFERLHRRLLKLV 653PFSYNYLH...
667 KRSR-RNFERLHRRLLKLV 667PFSYNYLH...
386 NVDD--AVDDIVRC-FKGV 401SNGMRRK...
615 FKGSSSVVRTIA-V-NVDD--AVDDIVRC-FKGV...
781 FKGSSSVVRTIA-V-NVDD--AVDDIVRC-FKGV...
657 FKGSSSVVRTIA-V-NVDD--AVDDIVRC-FKGV...
657 FKGSSSVVRTIA-V-NVDD--AVDDIVRC-FKGV...
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gi|17506801|ref|NP\_492758.1
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Bra:Bra026776
AT1G15240.
Cru:Carubv10008179m
Csa:Cucsa.359160.1
Mtr:Medtr4g012920
Gma:Glyma08g21950
Gma:Glyma07g00690
Egr:Eucgr.F03028
Vvi:GSVIT0101708001
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Ppa:Pp1s7\_51v6.1
Ppa:Pp1s8\_34v6.1
Ppa:Pp1s8\_155v6.1
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Smo:413327|413327
Zma:GRMZM20026442.T01
Osa:LOC\_0s11906040
Egr:Eucgr.001512
Gma:Glyma20g01140
Mtr:Medtr4g087210
Gma:Glyma02g15445
Gma:Glyma07g33040
Bra:Bra015246
Cru:Carubv10012892m
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Csa:Cucsa.220190
Vvi:GSVIT01031845001
Rco:29851.m002502|29851.m002502
Ptr:Potri.0090108300
Ptr:Potri.004G146600

731 RLCQDIH--GQFFK...
931 --S-NSSVDV...
1050 LSLAGNLAAANTQOLAA...
348 Y--SSASCLLLR--359KFI...
867 VDLKSRKRNKQNLGI...
800 VDLKSRKRNKQNLGI...
783 VDLKSRKRNKQNLGI...
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786 VDLKSRKRNKQNLGI...
849 PNCDELNSKDATTEKS...
881 ANGLGPKNSNPLRPFPA...
862 ANGLGPKNSNPLRPFPA...
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845 WRRYRNFEOLHRRLLKLV...
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YML104C	1124	-	1123---ICND*-----	1127
gi 164426626 ref XP_957576.2	1245	-DI---	1246----LFGBIQGRKQPPG-----	1260
gi 17506801 ref NP_492758.1	579	-----	578	
Osa:LOC_0805g50660	1117	E	1117M--DITVKKWHDWQOLYALE*	1136
Bra:Bra026152	1015	E	114M--EQSPKQLQEBEHLFGQYTPPT*	1036
Bra:Bra026776	997	E	96M--EKAFKQLHEEHLFGQYTSN*	1017
AT1G15240.	999	E	98M--EQAFKQLHYEHLFGQYTPPN*	1020
Cru:Carubv10008179m	1000	E	99M--EQAFKQLHYEHLFGQYTPPN*	1021
Csa:Cucsa.359160.1	1100	E	1099L--DSVFKQLHERKEKFGKLDHV*	1121
Mtr:Medtr4g012920	1205	E	1205M--DITVKKWHDWQOLYALE*	1225
Gma:Glyma08g21950	1120	E	1120M--DITVKKWHDWQOLYALE*	1141
Gma:Glyma07g00690	1117	E	1117L--DITVKKWHDWQOLYALE*	1138
Egr:Eucgr.F03028	1070	E	1069L--DSVFKQLYDEKHLFGQYTSN*	1090
Vvi:GSVIVT01017080001	1067	E	1066L--DDVFKQLFEERKFGFEKAN*	1087
Rco:30146.m003594 30146.m003594	1063	E	1062L--DYVFRQLHEEKKRFGELKTT*	1083
Ptr:Potri.0036053200	1120	E	1120M--DITVKKWHDWQOLYALE*	1141
Ptr:Potri.001G183100synonym:POPTR_0001s1	1123	E	1123M--DITVKKWHDWQOLYALE*	1144
Ppa:Ppls67_32V6.1	1175	FE	1176M--HDLILNVRSSVT*	1189
Ppa:Ppls7_51V6.1	1152	E	1152L--HDLILNVRSSVT*	1165
Ppa:Ppls48_155V6.1	1148	E	1148L--HDLILNVRSSVT*	1164
Ppa:Ppls68_34V6.1	1146	FE	1147M--HDLILNVRSSVT*	1160
Smo:413327 413327	950	49E	--EDLLEHGATA*-----	962
Zma:GRMZM2G026442.T01	1011	010L	--RDLLEHGATA*-----	1033
Osa:LOC_0s11g06040	1055	1054L	--RDLLEHGATA*-----	1077
Egr:Eucgr.G01512	755	MRVEQPA*	-----	761
Gma:Glyma20g01140	963	62L	--RNVVLSVHENMNVHQPV*	980
Mtr:Medtr4g087210	1128	E	1128M--RNVVLSVHENMNVHQPV*	1146
Gma:Glyma02g15445	1011	010L	--RNVVLSVHENMNVHQPV*	1022
Gma:Glyma07g33040	1012	011L	--RNVVLSVHENMNVHQPV*	1023
Bra:Bra015246	982	81L	--KDLIRIETRENSHGRSE*	998
Cru:Carubv10012892m	976	75L	--QDLIRIETRENSHGRSE*	992
AT2G15900	978	77L	--QDLIRIETRENSHGRSE*	994
Cru:Carubv10012885m	996	95L	--QDLIRIETRENSHGRSE*	1012
Csa:Cucsa.220190	1026	025L	--RDLLEHGATA*-----	1043
Vvi:GSVIVT01031845001	978	77L	--RDLLEHGATA*-----	989
Rco:29851.m002502 29851.m002502	1016	015L	--QDLIRIETRENSHGRSE*	1032
Ptr:Potri.009G108300	1035	034L	--RDLLEHGATA*-----	1051
Ptr:Potri.004G146600	1034	033L	--RDLLEHGATA*-----	1050