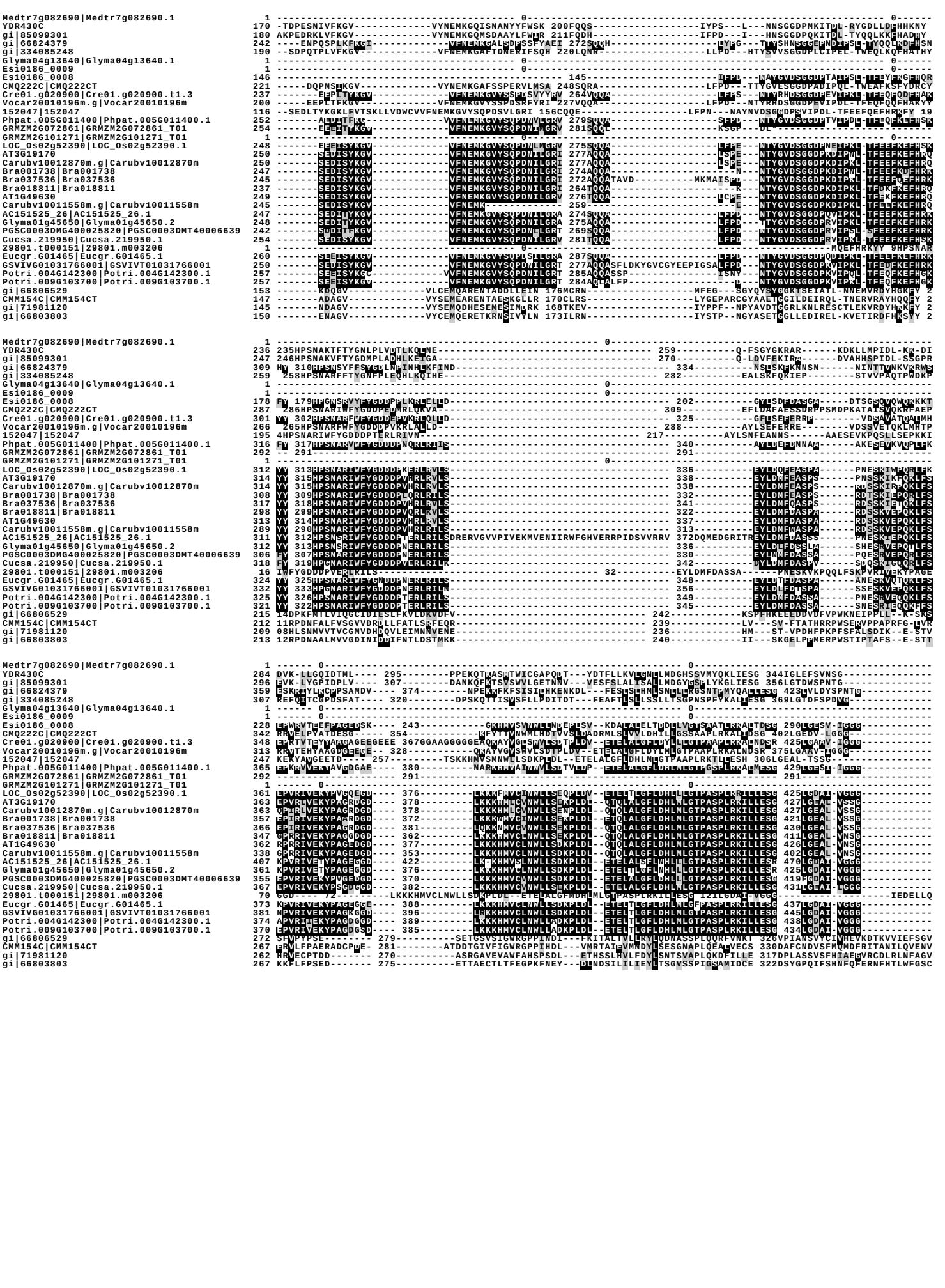
```
Medtr7g082690|Medtr7g082690.1                   1 ------------------------------------------------------------ 0-----------------------------------------------
YDR430C                                         1 ------------------------------------------------------------ 0-----------------------------------------------
gi|85099301                                     1 ------------------------------------------------------------ 0-----------------------------------------------
gi|66824379                                     1 -MIRLCKN-----------IKTIKPCVNSINNRVTSHGLK-----VSSSS--------- 33----------------SSSSSSLFNNNNNNNLDKRSFISS----PQT
gi|334085248                                    1 ------------------------------------------------------------ 0---------------------MWRCGGRQGLCVLRRLSG--------
Glyma04g13640|Glyma04g13640.1                   1 ------------------------------------------------------------ 0-----------------------------------------------
Esi0186_0009                                    1 ------------------------------------------------------------ 0-----------------------------------------------
Esi0186_0008                                    1 MSIGDILSQRFLTEMRRGTGLV-------------------------------LVA---T 26LGS----LREATSFTMLSGLRRTGARRGMMAF------LGSTGVPSS
CMQ222C|CMQ222CT                                1 --------------MQRHI-------------------------AFVC------------ 9-------------------APLYR-RAVQLQKK-GEHPHAVFRSSRC
Cre01.g020900|Cre01.g020900.t1.3                1 --------------MS--TVKRG----------------LASASAGV---GRSSVP---- 21-AVPLPGASRPMPLRLPASGASSFAAAGLMAPAL-RRMPG--AA---
Vocar20010196m.g|Vocar20010196m                 1 ------------------------------------------------------MI---- 2-APPHPTPHT-----------PTYTH-------------T--GG---
152047|152047                                   1 ------------------------------------------------------------ 0-----------------------------------------------
Phpat.005G011400|Phpat.005G011400.1             1 --------------MHAQAALRVTPLCVASNARGWMLRGVV--------RPRVSFAPVRR 38LGSSSFAGHRT-------INSKIFF-R-----GT-GLRAG-------
GRMZM2G072861|GRMZM2G072861_T01                 1 --------------MERVALLRT-SGRRLLH---------------RCRRGRPVVVPA-- 28-AAASSLARRASSFSLPARGYSALPRG-----GA-RFLVA--AAPLH
GRMZM2G101271|GRMZM2G101271_T01                 1 ------------------------------------------------------------ 0-----------------------------------------------
LOC_Os02g52390|LOC_Os02g52390.1                 1 --------------MERVALLRN-SGRRLLH---------------RCRRPRPVVQAA-- 28-GPSAPYRPSSSSH------SRAGLPG-----GA-RLLAA--AAPLH
AT3G19170                                       1 -------------------MLRT-VSCLASRSSSSLFFRFFRQFPRSYMSLTSSTAAL-- 38-RVPSRNLRRI--SSPSVAGRRLLLRR-----GL-RIPSA--A----
Carubv10012870m.g|Carubv10012870m               1 -------------------MLRT-VSCLASRSSASLFFRFFRQFPRSYMSLTSSTATL-- 38-RAPSRSLRRI--SSPSVAGRRLFLRR-----GL-RVPST--A----
Bra001738|Bra001738                             1 -------------------MLRT-ASCSASLTSASPFFRHF---PLSYSSLSSSTGAL-- 35-RAPGRNLRRV--ASPSSTGRRVFLRR-----GL-RVPST--A----
Bra037536|Bra037536                             1 -------------------MLRT-VSCSASLSSASPFFRFF---RHF---PRSSTAAL-- 32-RGPARNLRRI--SSPSAAGRRVLLRR-----GL-RVSSA--AA---
Bra018811|Bra018811                             1 ------------------MLLRS-LTRSSSNASTSLFFRLF---PRSYFSRSSP------ 32--ATGRNIRRL--SAA-GTGSELFLRR-----GL-RLLPA--AA---
AT1G49630                                       1 -------------------MLRS-LTCSSTITSTSLFFRSFRQLPRSYLSPSSSTTVV-- 38-GASGRNIRRL--STLEAAGRRLFLRR-----GL-KLLSA--AS---
Carubv10011558m.g|Carubv10011558m               1 -------------------MLRS-VNCTSSLGSTSLFFRFFHKYPRSCSSFSSSTT---- 36--AVSRNIRRL--STPEAAGRRLFTRR-----GF-NLRSA--AS---
AC151525_26|AC151525_26.1                       1 MEIGSCSSNS--TSMERAALVRS-LSTTRY----FSRTPSVL-SARF------------- 39-----------------SPPTLLLRR-----RS-LSTSS--TRLLS
Glyma01g45650|Glyma01g45650.2                   1 --------------MERAALVRC-LPCSSV----LCRRYLHS-HSHLCRPSSS-IS---- 35-----------------IIPSLSLPTI-----RP-LCLPR--RRSSS
PGSC0003DMG400025820|PGSC0003DMT40006639        1 --------------MERAVLLRS-LSSTSS---LAFSRIFSRSSHRF--------A---- 30-SYSAR-RHRL--LQ-NLHRRRSLVRS-----N--------------
Cucsa.219950|Cucsa.219950.1                     1 --------------MEKSVFLRS-LTCSSL----VCNRIFFRSAHRLCPSTLPPRS---- 37-SFVSRKLHRF--NP-SFSRRSLLP-R-----QL-KLLPA--YSQSR
29801.t000151|29801.m003206                     1 ------------------------------------------------------------ 0-----------------------------------------------
Eucgr.G01465|Eucgr.G01465.1                     1 --------------MERAALLRS-LSCSSL----ACTTRLFFSRSSSSSHPRRLLR---- 37-----PCGGRP--AN-GASRRP-LHLR-----RS-RLLPR--SSSSS
GSVIVG01031766001|GSVIVT01031766001             1 --------------MERAALLRS-ITCST----LACNRFFLR-SSHRLSLPSASFS---- 36-SSLSRSHHRS--FG-TLTRRSVLRR------HW-RLLPS--SSS--
Potri.004G142300|Potri.004G142300.1             1 --------------METAVLLRS-SNKLILNHRYYCPHKFFR-LLSSS-SSSP--S---- 37-SFTPRNSHRS--IN-PLTSRSLARRR-----RR-KLLPL--SAT--
Potri.009G103700|Potri.009G103700.1             1 --------------METAILLRS-SNKLLLFPRYYTPRNFFR-LFSSS-SKSPRSS---- 39-PFPPRNLHRP--IN-PLTSRSLLLRR-----RC-RLLPP--SAT--
gi|66806529                                     1 ------------------------------------------------------------ 0-----------------------------------------------
CMM154C|CMM154CT                                1 ------------------------------------------------------------ 0-----------------------------------------------
gi|71981120                                     1 ------------------------------------------------------------ 0-----------------------------------------------
gi|66803803                                     1 ------------------------------------------------------------ 0-----------------------------------------------

Medtr7g082690|Medtr7g082690.1                   1 -------------   0------------------------------------------------------------   0---------------------------------
YDR430C                                         1 -------------   0---MLRFQ-RFASSYAQA---------QA-VRKYP-VGGIFHGYEVRRILPVPELRLTAV  45DLVHSQTGAEHLHIDRDDKNNVFSIAFKTNPPD
gi|85099301                                     1 -------------   0---MLRNA-TKGAARRAV---------TE-LSQYPKPGEKLHGFTLLRSKHVPELELTAL  46HLQHDKTGAEHLHIARDDSNNVFSIGFKTNPPD
gi|66824379                                    61 NTTLKPNQTYVFD  73NQDIFKDI-KRGKDRN---------------KLNLKIGDEIHGFKVIKIREVPERQFKTY 117QFEHIETGAKYLHIDCEDTNNVFSVTFKTI
gi|334085248                                   19 -GHAHHRA-----  25----WRWN-SNRACER---------------ALQYKLGDKIHGFTVNQVTSVPELFLTAV  65KLTHDDTGARYLHLAREDTNNLFSVQFRTTPM
Glyma04g13640|Glyma04g13640.1                   1 -------------   0------------------------------------------------------------   0---------------------------------
Esi0186_0009                                    1 -------------   0------------------------------------------------------------   0---------------------------------
Esi0186_0008                                   64 SSTPKASSRW--V  74STA-------VMSASAQSVVS----DGPSLSVSKRKESVAHDAYDVVEEDFVAEYGATTT 123LYKHKKSGAEVLSVQIDDDNKT--------
CMQ222C|CMQ222CT                               36 KV-----------  37-GVQRQVRFTVPGLRATAVMPTPTQAPVRVQVPRRELGEKAFGFTLVRSEFVPEIQSYVR  96VYKHDRYGTELISVVNDDENKTFGVAFRTPPS
Cre01.g020900|Cre01.g020900.t1.3               62 -------------  61--SASRSALRCLASAAPAVA--------APPAP-AGVVSKAHGFTLTRQQYVKEYGSHVL 110MYTHDKTGAEVISVLNSDENKTFGVVFRTP
Vocar20010196m.g|Vocar20010196m                20 -------------  19--TLGRQPFRALATAAPAVASAA---ATAAAVP-VAIVEKAHGFTLQRQQYVKEYGSHVL  73LYKHDKTGAELISVLNSDLNKTFGVVLRTPVD
152047|152047                                   1 -------------   0------------------------------------------------------------   0-----------MSVVNEDENKVFGIVFRTPPKDS
Phpat.005G011400|Phpat.005G011400.1            65 ---SISAQRW--N  72PPSMTVRRELSLSPV--AVVA----PSPAKTGA-DSELVKELGFEEVQEQFVDEYKSTAT 125LYRHKKTGAEIMSVVNDDENKVFGIVFRTP
GRMZM2G072861|GRMZM2G072861_T01                67 CSG----RYW--P  73AA--APQLARRLSAS--AVSTSPSPV-PYDTDD-VHEYATKLGFEKVSEQTIDECKSIAV 127LYKHKKTGAEVMSVSNDDENKVFGIVFRTP
GRMZM2G101271|GRMZM2G101271_T01                 1 -------------   0------------------------------------------------------------   0---------------------------------
LOC_Os02g52390|LOC_Os02g52390.1                61 CAG----RYW--P  67HA--APRFVRRLSAP--AVSTSPSPV-PSDTDD-VHEYAAKLGFEKVSEQSIDECKSTAV 121LYKHKKTGAEVMSVSNDDENKVFGIVFRTP
AT3G19170                                      71 ------------V  71RS--VNGQFSRLSVR--AVATQPAPLY---PDV-GQDEAEKLGFEKVSEEFISECKSKAI 123LFKHKKTGCEVMSVSNEDENKVFGVVFRTP
Carubv10012870m.g|Carubv10012870m              71 ------------V  71RS--VNGQFSRLSVR--AVATQPAPLY---PDV-GRDEAEKLGFEKVSEEFISECKSKAI 123LFKHKKTGCEVMSVSNEDENKVFGVVFRTP
Bra001738|Bra001738                            68 ------------V  68RG--VNRQLSRLSVR--AVATQPAPSY---PDV-GQDEAEKLGFEKVSEEFISECKSKAT 120LFKHKKTGCEVMSVSNEDENKVFGIVLRTP
Bra037536|Bra037536                            66 ------------G  66RG--VNGQFSRLSVR--AVATQPAPSY---PDV-SQDEAEKLGFEKVSEEFISECKSKAT 118LFKHKKTGCEVMSVSNEDENKVFGIVLRTP
Bra018811|Bra018811                            64 ------------S  64GC--LSGQFSLAV-------STQTATS----YP-GQDEAEKLGFEKSREEFISECKSKAV 110LFRHKKTGCEVMSVSNDDENKVFGVVFRTP
AT1G49630                                      72 ------------R  72-G--LNGQFSRLSIR--AVATQSAPSS----YP-GQDEAEKLGFEKVSEEFISECKSKAV 122LFKHKKTGCEVMSVSNDDENKVFGIVFRTP
Carubv10011558m.g|Carubv10011558m              69 ------------R  69-S--LNGQFSRFSIR--AVATQPAP-S----YP-GQDEAEKLGFEKVSEEFISECKSKAV 118LFKHKKTGCEVISVSNDDENKVFGIVFRTP
AC151525_26|AC151525_26.1                      61 SSTSRPLFYF---  70-R--NRNHFST---R--ASLVSSPD-IGGGEVV-KDEVARELGFEKVSEEFIPECKSIAV 120LFKHVKTGAQVISVSNKDENKVFGIVFRTP
Glyma01g45650|Glyma01g45650.2                  58 SSRLLPLYFR--T  68TI--NRKHFSSLAPR--AVLSPSPS--SGFAEV-NDEVALKLGFEKVSEEFIPECKSKAV 121LFRHIKTGAQVMSVSNDDDNKVFGIVFRTP
PGSC0003DMG400025820|PGSC0003DMT40006639       54 ---VRGISS---S  60IN--LKRQFYPLSVR--AIATSSPQSSQEFLGA-DDEVAEKFGFEKVSEQFIDECKSKAV 115LYKHKKTGAEVMSVSNDDENKVFGVVFRTP
Cucsa.219950|Cucsa.219950.1                    72 S-----------S  73H---FRKQFSSLAPR--AVASPPAHSPPEFAEV-SDEVAEKLGFEKVSEEFIGECKSKAV 127LFRHKKTGAEVMSVSNDDENKVFGIVFRTP
29801.t000151|29801.m003206                     1 -------------   0------------------------------------------------------------   0---------------------------------
Eucgr.G01465|Eucgr.G01465.1                    68 SSSSSSSSSS--L  78RF--GRNFSSSLAPR--AIATPPTQPSPEVFGV-QDGVAEKYGFEKVSEEFIKECKSRAT 133LFRHKKTGAEVMSVSNDDENKVFGIVFRTP
GSVIVG01031766001|GSVIVT01031766001            69 ---IP--------  70----STRCFSSLSPK--AIATSPEQASSDAVGS-QDDLAEKYGFDKVSEQFIQECKSKAV 123LYKHKKTGAEVMSVSNDDENKVFGIVFRTP
Potri.004G142300|Potri.004G142300.1            71 ---SSSSSPS--F  78HF--NKHHFSTLSPH--AISTQ---YSPDVSNV-SDEVAAKYGFEKVSEEFIGECKSKAV 130LFKHKKTGAEVMSVSNDDENKVFGIVFRTP
Potri.009G103700|Potri.009G103700.1            73 ---P--CSSS--F  78HF--IKHHFSSSSPH--AIATR---CSPDVSTL-PDEVAAKYGFEKVSEDFIGECKSRAV 130LLKHKKTGAEVMSVSNDDENKVFGIVFRTP
gi|66806529                                     1 -------------   0---------------MSNK-YEELSKEFQFIDEF-DLPLAKDINVK  29RFVHKKSGLTLILNYCPGPKCNASIVVPTESIN
CMM154C|CMM154CT                                1 -------------   0---------------MTA---------WKQLAAVDVGTVRQKVTVE  22KHRSTTSGITVYLAQVPGPLVCGTLVFATEAHS
gi|71981120                                     1 -------------   0---------------MSA---SKL---WS-CT---ETVLNGGIKLF  21LYSSKNTKLRVAIGEVPGPMVHGAVSFVTEADS
gi|66803803                                     1 -------------   0---------------MTE--ISPLRDEYELLN---SFTVEKTILIE  26KYQHKKTKFTIYNVKVGGPLVNCLVIVPTETLS

Medtr7g082690|Medtr7g082690.1                   1 ------------------------------   0------------------------------------------------------------   0-----------------
YDR430C                                        79 STGVPHILEHTTLCGSVKYPVRDPFFK 105MLNKSLANFMNAMTGPDYTFFPFSTTNPQDFANLRGVYLDSTLNPLLKQE--DFDQEGWR 163LEHKNI---------
gi|85099301                                    80 DTGVPHILEHTTLCGSQKYPIRDPFFK 106MLPRTLSNFMNAFTASDHTFYPFATTNAQDFKNLMSVYLDATLHPLLKET--DFTQEGWR 164IGPENPQALVAAEGN
gi|66824379                                   148 PKDSTGVAHILEHTTLCGSKKYPVRDPFFN 177MLKRSLNTYMNAWTAPDHTSYPFGTQDPKDYYNLLSVYLDATFFPNLSEQ--DFRQEGHR 235LEFEQM------
gi|334085248                                   98 DSTGVPHILEHTVLCGSQKYPCRDPFFK 125MLNRSLSTFMNAFTASDYTLYPFSTQNPKDFQNLLSVYLDATFFPCLREL--DFWQEGWR 183LEHENP--------
Glyma04g13640|Glyma04g13640.1                   1 ------------------------------   0------------------------------------------------------------   0-----------------
Esi0186_0009                                    1 ------------------------------   0------------------------------------------------------------   0-----------------
Esi0186_0008                                  146 ------------------------------ 145------------------------------------------------------------ 145-----------------
CMQ222C|CMQ222CT                              129 DSTGVPHILEHSVLCGSRKYPVKEPFVE 156LLKTSMNTFLNAMTFPDKTCYPVASTNLRDFYNLVDVYLDAVFFPRLTPD--TLAQEGHH 214IELDAV--------
Cre01.g020900|Cre01.g020900.t1.3              141 VDDSTGIPHILEHSVLCGSRKYPIKEPFVE 170LMKSSLNTFLNAFTYPDRTCYPVASTNSQDFYNLVDVYLDAVFHPRCVSDRRVFEQEGWH 230YELDNK-------
Vocar20010196m.g|Vocar20010196m               106 DSTGIPHILEHSVLCGSRKYPIKEPFVE 133LMKSSLNTFLNAFTYPDRTCYPVASTNTQDFYNLVDVYLDAVFHPRCVSDRRVFEQEGWH 193FELDSK--------
152047|152047                                  24 KGIPHILEHSVLCGSRKYPLKEPFVE 49LLKGSLHTFLNAFTYPDRTCYPVASTNLKDFYNLVDVYLDAVFHPRCVSDPQIFQQEGWH 109YEVNDL----------
Phpat.005G011400|Phpat.005G011400.1           156 PTDSTGIPHILEHSVLCGSRKYPLKEPFVE 185LLKGSLQTFLNAFTYPDRTCYPVASTNLQDFYNLVDVYLDAVFYPRCVNDIHTFQQEGWH 245YELNDP------
GRMZM2G072861|GRMZM2G072861_T01               158 PKNSTGIPHILEHSVLCGSRKYPLKEPFVE 187LLKGSLHTFLNAFTYPDRTCYPVASTNTKDFYNLVDVYLDAVFFPKCVDDFQTFQQEGWH 247YELDNP------
GRMZM2G101271|GRMZM2G101271_T01                 1 ------------------------------   0------------------------------------------------------------   0-----------------
LOC_Os02g52390|LOC_Os02g52390.1               152 PKNSTGIPHILEHSVLCGSRKYPLKEPFVE 181LLKGSLHTFLNAFTYPDRTCYPVASTNAKDFYNLVDVYLDAVFFPRCVEDFQTFQQEGWH 241YELDNP------
AT3G19170                                     154 PKDSTGIPHILEHSVLCGSRKYPVKEPFVE 183LLKGSLHTFLNAFTYPDRTCYPVASTNTKDFYNLVDVYLDAVFFPKCVDDAHTFQQEGWH 243YELNDP------
Carubv10012870m.g|Carubv10012870m             154 PKDSTGIPHILEHSVLCGSRKYPLKEPFVE 183LLKGSLHTFLNAFTYPDRTCYPVASTNTKDFYNLVDVYLDAVFFPKCVDDVHTFQQEGWH 243YELNDP------
Bra001738|Bra001738                           151 PKDSTGIPHILEHSVLCGSRKYPLKEPFVE 180LLKGSLHTFLNAFTYPDRTCYPVASTNTKDFYNLVDVYLDAVFFPKCVDDVHTFQQEGWH 240YELNDP------
Bra037536|Bra037536                           149 PKDSTGIPHILEHSVLCGSRKYPVKEPFVE 178LLKGSLHTFLNAFTYPDRTCYPVASTNTKDFYNLVDVYLDAVFFPKCVEDVHTFQQEGWH 238YELNDP------
Bra018811|Bra018811                           141 PKDSTGIPHILEHSVLCGSRKYPLKEPFVE 170LLKGSLYTFLNAFTYPDRTCYPVASTNTKDFYNLVDVYLDAVFFPKCVDDVHTFQQEGWH 230YELNHP------
AT1G49630                                     153 PKDSTGIPHILEHSVLCGSRKYPMKEPFVE 182LLKGSLHTFLNAFTYPDRTCYPVASTNKKDFYNLVDVYLDAVFFPKCVDDVHTFQQEGWH 242YELNDP------
Carubv10011558m.g|Carubv10011558m             149 PKDSTGIPHILEHSVLCGSRKYPLKEPFVE 178LLKGSLHTFLNAFTYPDRTCYPVASTNTKDFYNLVDVYLDAVFFPKCVDDVHTFQQEGWH 238YELNDP------
AC151525_26|AC151525_26.1                     151 PNDSTGIPHILEHSVLCGSRKYPLKEPFVE 180LLKGSLHTFLNAFTYPDRTCYPVASTNTKDFYNLVDVYLDAVFFPKCVEDVQTFQQEGWH 240YELNHP------
Glyma01g45650|Glyma01g45650.2                 152 PKDSTGIPHILEHSVLCGSRKYPLKEPFVE 181LLKGSLHTFLNAFTYPDRTCYPVASTNAKDFYNLVDVYLDAVFFPRCVEDFQIFQQEGWH 241FELNDP------
PGSC0003DMG400025820|PGSC0003DMT40006639      146 PKDSTGIPHILEHSVLCGSRKYPLKEPFVE 175LLKGSLNTFLNAFTYPDRTCYPVASTNTKDFYNLVDVYLDAVFFPKCVEDFQTFQQEGWH 235YELNDP------
Cucsa.219950|Cucsa.219950.1                   158 PSDSTGIPHILEHSVLCGSRKYPVKEPFVE 187LLKGSLHTFLNAFTYPDRTCYPVASTNTKDFYNLVDVYLDAVFFPKCVEDFKTFQQEGWH 247YELNDP------
29801.t000151|29801.m003206                     1 ------------------------------   0------------------------------------------------------------   0-----------------
Eucgr.G01465|Eucgr.G01465.1                   164 PNNSTGIPHILEHSVLCGSRKYPLKEPFVE 193LLKGSLNTFLNAFTYPDRTCYPVASTNTKDFYNLVDVYLDAVFFPKCIDDIQTFQQEGWH 253YELNNP------
GSVIVG01031766001|GSVIVT01031766001           154 PKDSTGIPHILEHSVLCGSRKYPLKEPFVE 183LLKGSLHTFLNAFTYPDRTCYPVASTNTKDFYNLVDVYLDAVLFPKCVEDFQTFQQEGWH 243YELNNP------
Potri.004G142300|Potri.004G142300.1           161 PKDSTGIPHILEHSVLCGSRKYPLKEPFVE 190LLKGSLHTFLNAFTYPDRTCYPVASTNTKDFYNLVDVYLDAVFFPKCVEDYQTFQQEGWH 250FELNDP------
Potri.009G103700|Potri.009G103700.1           161 PKDSTGIPHILEHSVLCGSRKYPLKEPFVE 190LLKGSLHTFLNAFTYPDRTCYPVASTNTKDFYNLVDVYLDAVFFPKCVEDHHTFQQEGWH 250LELNNP------
gi|66806529                                   63 DKGLPHTLEHLIFTGCNDIPYREFLEV  89LSNRCLSAPCNAYTAEDHTCYSIDSIGPEAILTYLPIYLKYVLTPTLKEN--DFITEIYH 147IDSN-G----------
CMM154C|CMM154CT                               56 DAGEPHCLEHLVFMGSESYPYKGVLDL  82VANRSLAQGTNAWTETDHTAFTVETVGARAFLHVLPVYLDHLFFPLLRES--AFRTEVYH 140VVGETC----------
gi|71981120                                    55 DDGLPHTLEHLVFMGSKKYPFKGVLDV  81IANRCLADGTNAWTDTDHTAYTLSTVGSDGFLKVLPVYINHLLTPMLTAS--QFATEVHH 139ITGE-G----------
gi|66803803                                    60 NDGCPHTLEHLVFLGSENYPFKGYLDS  86VANLCFATGTNAFTDTDHTGYELETAGSDGFLQALPIYLDHIFYPTITEQ--AFTTEIHH 144INDK-G----------
```



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Medtr7g082690|Medtr7g082690.1                  1 ------------------- 0----------------------------------------------------MAKRE--- 5-------ELYINLLRSYAQDSNFLKG
YDR430C                                      355 ----VEPTTAVNLLTVGI---------------- 368--------------------------------------------QGVSD-IEIFK----- 378-------
gi|85099301                                  367 ----YDSSGKLGIFSIGL---------------- 380--------------------------------------------SGVQE-EDVPKVK--- 392-------
gi|66824379                                  434 -------FDDGLLESSFSVGG-------------- 447--------------------------------------------IGIKK-EDLEKVE--- 459----
gi|334085248                                 380 -----YNGYTREAYFSVGL---------------- 393------------------------------------------QGIAE-KDIETVR--- 405-----
Glyma04g13640|Glyma04g13640.1                  1 ------------------- 0------------------------------------------------------ 0---------------------------
Esi0186_0009                                   1 ------------------- 0------------------------------------------------------ 0---------------------------
Esi0186_0008                                 300 -------LSSELLQNTYSIGL-------------- 313--------------------------------------------KGVSK-EDVPKVE--- 325----
CMQ222C|CMQ222CT                             412 -----LESDLLQMTYSVGM---------------- 425------------------------------------------KGIAQEQDTERVA--- 438-----
Cre01.g020900|Cre01.g020900.t1.3             435 -------IDDDLKQPCFTLGL-------------- 448--------------------------------------------KGVDP-AEADKVD--- 460----
Vocar20010196m.g|Vocar20010196m              385 -----VDDDLKQPCFTLGL---------------- 398------------------------------------------KGVDP-ADADKVE--- 410-----
152047|152047                                316 --VEDDLLQPQFSIGM------------------- 329------------------------------------------KGVAE-SDIPAVE--- 341-------EL
Phpat.005G011400|Phpat.005G011400.1          439 -------IEDELRQPQFSIGL-------------- 452--------------------------------------------KGVAE-EDIPKVE--- 464----
GRMZM2G072861|GRMZM2G072861_T01              292 ---------------------------------- 291----------------------------------------------------------- 291----
GRMZM2G101271|GRMZM2G101271_T01                1 ------------------- 0------------------------------------------------------ 0---------------------------
LOC_Os02g52390|LOC_Os02g52390.1              435 -------VEDELLQPQFSIGL-------------- 448--------------------------------------------KGVSE-DNIKEVE--- 460----
AT3G19170                                    437 -------LSDELLQPQFGIGL-------------- 450--------------------------------------------KGVSE-ENVQKVE--- 462----
Carubv10012870m.g|Carubv10012870m            437 -------MSDELLQPQFSIGM-------------- 450--------------------------------------------KGVSE-DNVQKVE--- 462----
Bra001738|Bra001738                          431 -------MSDELLQPQFSVGM-------------- 444--------------------------------------------KGVSE-DNVQKVE--- 456----
Bra037536|Bra037536                          440 -------MSDELLQPQFSVGM-------------- 453--------------------------------------------KGVSQ-DNVQKVE--- 465----
Bra018811|Bra018811                          421 -------VEDELLQPQFSVGL-------------- 434--------------------------------------------KGVSD-DKVQKVE--- 446----
AT1G49630                                    436 -------MEDELLQPQFSIGL-------------- 449--------------------------------------------KGVSD-DNVQKVE--- 461----
Carubv10011558m.g|Carubv10011558m            412 -------MEDELLQPQFSIGL-------------- 425--------------------------------------------KGISD-ENVQKVE--- 437----
AC151525_26|AC151525_26.1                    480 -------LEDELLQPQFSIGM-------------- 493--------------------------------------------KGVSE-DDIPKVE--- 505----
Glyma01g45650|Glyma01g45650.2                435 -------VEDELLQPQFSIGM-------------- 448--------------------------------------------KGVSE-DDIHKVE--- 460----
PGSC0003DMG400025820|PGSC0003DMT40006639     429 -------IEDELLQPQFSIGL-------------- 442--------------------------------------------KGVSE-ENIQKVE--- 454----
Cucsa.219950|Cucsa.219950.1                  441 -------IEDELLQPQFSIGL-------------- 454--------------------------------------------KGVLD-DDIPKVE--- 466----
29801.t000151|29801.m003206                  138 PQFSIGL---------------- 144------------------------------------KNVAE-EDIEKVE--- 156-------ELIMSTLRK--
Eucgr.G01465|Eucgr.G01465.1                  447 -------IEDELLQPQFSIGL-------------- 460--------------------------------------------KGVSE-DDIPKVE--- 472----
GSVIVG01031766001|GSVIVT01031766001          455 -------MEDELLQPQFSIGL-------------- 468--------------------------------------------KGVSE-DDIHKVE--- 480----
Potri.004G142300|Potri.004G142300.1          448 -------IEDELLQPQFSIGL-------------- 461--------------------------------------------KGVFE-EDIQKVE--- 473----
Potri.009G103700|Potri.009G103700.1          444 -------VEDELLQPQFSIGL-------------- 457--------------------------------------------KGVSE-EDIEKVE--- 469----
gi|66806529                                  353 PIKYNKDKQQEEEKEVKQEEQQNGKSNEKVEEDK 386ENEEEGEEEEEEEEESKGSEEGSEEGSEEGSEEDDDLEEEKEKEKNCEDEDDIDEGDNNL 446FNERSIYD
CMM154C|CMM154CT                             357 PMHRLDDVFDRVMGILE---------------- 373---------------------------------------V------------ 374--------
gi|71981120                                  344 PVEKLDECAPKFFDKTV---------------- 360-------------------------------------REH------------ 363--------
gi|66803803                                  349 DSKRIDELKPKFLSI-I---------------- 364-------------------------------------KNL------------ 367--------

Medtr7g082690|Medtr7g082690.1                 25 -TAI----HAYF----------IKGHIPFTLFLQ 43NHLLNMYIK--------CKDLTSALQLFDEMPERNVVSWSSVMTGCVHNGGASDALSL-- 93----FSC---
YDR430C                                      379 DTVNNLFQNLLETEHPFDR-KRI----DAIIEQLELSKKDQKA---DFGLQLL 423YSILPGWTN--------KIDPFESLLFEDVL---------QRFRGDLETKG--
gi|85099301                                  393 AKVQEILRS--MRDKGFER-SKI----DGYLHQLELGLKHKTA---NFGMSLL 435HRLKPKWFV--------GVDPFDSLAWNDTI---------AAFETELAKGG--
gi|66824379                                  460 ---KVIIETLEK--SSRDGFAS-DVI----ESILHQYEFAQKDVSA---SFGLKLV 502GSLSSNWIH--------GGDPVDPLFLNEAI---------AKLRKELEKG
gi|334085248                                 406 -SLIDRTIDE--VVEKGFED-DRI----EALLHKIELQMKHQST---SFGLMLT 448SYIASCWNH--------DGDPVELLKLGNQL---------AKFRQCLQENP-
Glyma04g13640|Glyma04g13640.1                  1 ---------------------------FLDEFS-- 6--------I-------D-----------L---------QVFAQELLREHLVMKLRP-- 27------HLHVC
Esi0186_0009                                   1 ------------------------------------ 0--------------------------------------------------------- 0-----------
Esi0186_0008                                 326 ---ALVLETLQK--IAEDGFDQ-EAI----DASINSVEFNLREFNTGSFPRGLSFM 371LGAMSDWVY--------NRNPTESLHFEGPL---------KELKDDLASG
CMQ222C|CMQ222CT                             439 -DLIFETLRK--LSSEKLDD-NLV----LASLNTIEFRLRENNTGSFPRGLALM 484LRAMTTWLH--------DADPVLMLRFEEPL---------KKLRERIASGE-
Cre01.g020900|Cre01.g020900.t1.3             461 ---SLILTKLQE--LADSGFSA-SAV----EAAVNTIEFSLRENNTGSFPRGLSLM 506LRAVGAWIY--------DQDPFTQMQWEDAL---------ASFKSKLAAG
Vocar20010196m.g|Vocar20010196m              411 -ALITSKLEE--LAVSGFSA-SAI----EAAVNTIEFSLRENNTGSFPRGLSLM 456LRAVGAWIY--------DRDPFTQMQWEDAL---------SSFKSKLASGQ-
152047|152047                                344 IVSTLQK--LADEGFTS-EAV----EASMNTIEFALRENNTGSFPRGLSLM 387LRSMGNWLY--------GRDPFEPLRFAKPL---------EDLKAKIATEGAKAV
Phpat.005G011400|Phpat.005G011400.1          465 ---ELVFSTLKR--LSEEGFSA-DAV----EASMNTIEFSLRENNTGSFPRGLSLM 510LRSMGKWLY--------GLDPFEPLRFAKPL---------EHFKQRLQSE
GRMZM2G072861|GRMZM2G072861_T01              292 ---------------------------------------------------------- 291----------------------------------------------
GRMZM2G101271|GRMZM2G101271_T01                1 ------------------------------------ 0--------------------------------------------------------- 0-----------
LOC_Os02g52390|LOC_Os02g52390.1              461 ---ELVMQTLKN--LAEEGFAP-EAV----EASMNTIEFALRENNTGSFPRGLSLM 506LRSIGKWIY--------DMDPFEPLKYERPL---------QQLKARIAAE
AT3G19170                                    463 ---ELIMDTLKK--LAEEGFDN-DAV----EASMNTIEFSLRENNTGSFPRGLSLM 508LQSISKWIY--------DMDPFEPLKYTEPL---------KALKTRIAEE
Carubv10012870m.g|Carubv10012870m            463 ---ELIMATLKK--LAEEGFDN-DAV----EASMNTIEFSLRENNTGSFPRGLSLM 508LQSIAKWIY--------DMDPFEPLKYTEPL---------KALKTRIAKE
Bra001738|Bra001738                          457 ---ELIMSTLKK--LAEEGFES-DAV----EASMNTIEFSLRENNTGSFPRGLSLM 502LQSIAKWIY--------DMDPFEPLKYTEPL---------KALKARIAEE
Bra037536|Bra037536                          466 ---ELIMDTLKK--LAEEGFDS-DAV----EASMNTIEFSLRENNTGSFPRGLSLM 511LQSIAKWIY--------DMDPFEPLKYTEPL---------KALKARIAEE
Bra018811|Bra018811                          447 ---ELIMSTLRK--LADEGFDT-DAV----EASMNTIEFSMRENNTGSSPRGLSLM 492LQSIGKWIY--------DMDPFEPLKYEEPL---------KTLKARIAEE
AT1G49630                                    462 ---ELVMNTLRK--LADEGFDT-DAV----EASMNTIEFSLRENNTGSSPRGLSLM 507LQSIAKWIY--------DMDPFEPLKYEEPL---------KSLKARIAEK
Carubv10011558m.g|Carubv10011558m            438 ---ELIMNTLRK--LADEGFDT-DAV----EASMNTIEFSLRENNTGSFPRGLSLM 483LQSIAKWIY--------DMDPFTPLKYEEPL---------KSLKARIAEK
AC151525_26|AC151525_26.1                    506 ---ELIVNTLKK--LVEEGFDT-DAI----EASMNTIEFSLRENNTGSFPRGLSLM 551LQSIGKWIY--------DMNPLEPLKYEKPL---------QDLKSKIAKE
Glyma01g45650|Glyma01g45650.2                461 ---ELVTSTLKK--LAEEGFDT-DAI----EASMNTIEFSLRENNTGSFPRGLSLM 506LQSIGKWIY--------DMNPFEPLKYEKPL---------QDLKSRIAKE
PGSC0003DMG400025820|PGSC0003DMT40006639     455 ---ELIMSTLEG--LVEKGFDL-DAV----EASMNTIEFSLRENNTGSFPRGLALM 500LRSIGKWVY--------DMDPFEPLKYQKPL---------EALKARIAKE
Cucsa.219950|Cucsa.219950.1                  467 ---ELILNTFKK--LAEEGFDN-DAV----EASMNTIEFSLRENNTGSFPRGLSLM 512LRSIGKWIY--------DMNPFEPLKYEEPL---------KALKARIAAE
29801.t000151|29801.m003206                  166 LAEEGFET-DAV----EASMNTIEFSLRENNTGSFPRGLSLM 202LRSMGKWIY--------DRDPFEPLKYEKPL---------LDLKARIAKEGSKAVFSPLI 245
Eucgr.G01465|Eucgr.G01465.1                  473 ---ELIMSTLKK--LAEEGFDT-DAV----EASMNTIEFSLRENNTGSFPRGLSLM 518LRSMGKWIY--------DMDPFEPLKYEEPL---------MALKARIAKE
GSVIVG01031766001|GSVIVT01031766001          481 ---ELVMSTLKS--LAKEGFNS-EAV----EASMNTIEFSLRENNTGSFPRGLSLM 526LRSIGKWIY--------DMDPFEPLKYEKPL---------MALKARIAEE
Potri.004G142300|Potri.004G142300.1          474 ---ELVMSTLKK--LAEEGFET-EAV----EASMNTIEFSLRENNTGSFPRGLSLM 519LRSISKWIY--------DMNPFEPLKYEKPL---------MDLKARIAEE
Potri.009G103700|Potri.009G103700.1          470 ---ELVMSTLKK--LAEEGFET-DAV----EASMNTIEFSLRENNTGSFPRGLSLM 515LQSISKWIY--------DMDPFEPLKYEKPL---------MALKARIAEE
gi|66806529                                  455 RLIKVLKD--LKTNGFPEEDSIKKVIEKEMIKMLEVLEE-DPLSLVFGSL-- 501--LC-CIVFPSSSKTIKPNGDVEYSDIKSRF------FLKPVF-EELLEKP-SQ
CMM154C|CMM154CT                             375 ----------THEQGIDVNGRLRTIIERRRQFFAALED-GANDAILSLL-- 413--I-PEFLY-------NDQDDQ--GYFRQAL------DMPGVL-AHLAALD-ES
gi|71981120                                  364 ----------LEEANFDM-ERMGYLIDQTILNELVKLET-NAPKDIMSHI-- 401--I-GHQLF-------D-NEDE--ELFKKRT------NEIDFL-KKLKSEP-AS
gi|66803803                                  368 ----------VETKTIDI-ERIRDSIRQSKLNTKLTVES--DPKDVFSEI-- 404--IAGDFLY-------G-NNDF-----EKHV------DFENVF-EKLLKVD-KD

Medtr7g082690|Medtr7g082690.1                 97 ------------------------------------------------------ 96---------MHREGFVKPNE--FTFVSALQACSLSENVTQAYQIYSLV--------
YDR430C                                      458 DTLFQDL 464IRKYIVHKPCF--------TFSIQGSEEFSKSLDDEEQTRLREKITALDE-QDKK----- 510-NIF--KRGILLQEKQNEKED--LSCLPTLQIKDI
gi|85099301                                  470 --YLEGL 474IDKYLINDNTL--------SFTMAPSPTFSQELAQEEETRLSTKISEVVK-AAGSEEEAR 525AALEARELKLLAEQSKTNTED--LGCLPSVHVKDI
gi|66824379                                  536 G---FHETKL 542KEL-LNNPHRL--------YLTMENDENLQKEEQEKELQKLERIKSELTP-EQTK----- 587-EII--EVAKDLQFRQNQIQD--VSVLPKINI
gi|334085248                                 483 -KFLQEKV 489KQYFKNNQHKL--------TLSMRPDDKYHEKQAQVEATKLKQKVEALSP-GDRQ----- 535-QIY--EKGLELRSQQSKPQD--ASCLPALKVSD
Glyma04g13640|Glyma04g13640.1                 33 --------QFT-MPYPH--------GQKYFPHDPEKVAC-DEVAEL--- 60--PHATHGLRLKQETPDPPKA--LKIVPSLSLQKIPKEPIRVP-------------
Esi0186_0009                                   1 ------------------------------------------------ 0------------------------------------------------------
Esi0186_0008                                 405 K--KVFEGIV 412KNMLVNNGHRA--------TVESVPNTELEAAIDGKEKGKLDEVKKSMSE-QASSTP--- 460--TSG*-------------------
CMQ222C|CMQ222CT                             519 -PVFQKLI 525QEEFLTNTHRV--------QVVLRPDPDYAKRTEEAEQARLAALKQSLPA-AEIEKI--- 573--IQETQRLRAKQAAPDAPED--LAKVPSLHVSD
Cre01.g020900|Cre01.g020900.t1.3             540 G--DVFGPLI 547RKYLLDNKHRV--------AVRLLPDSAKAAAIEAAEKAELERARAAMKE-EDLEAV--- 595--VANTHALKELQETPDSPEA--LACIPALKL
Vocar20010196m.g|Vocar20010196m              491 -DVFGPLI 497RSFLLDNRHRV--------TVQLLPDPALAAATEAKERARLEAVRGTMQD-EQLEAV--- 545--VENTSALKELQETPDPPEA--LACIPALQLSD
152047|152047                                426 FSPLI 430QNFLLSNKHLV--------TVELQPDAEKSAEIEALEKERLAKVKASLAK-QELEEL--- 478--ARATEELKKRQETPDPPEA--LKAVPSLSLSDIPK
Phpat.005G011400|Phpat.005G011400.1          544 GVKGVFSPLI 553QNYIIDNPHRV--------TVELHPDAEKGKIDEMQEAERLAKVKASMTQ-EDLAEL--- 601--TRATEELRLKQETPDPPEA--LKAVPSLAL
GRMZM2G072861|GRMZM2G072861_T01              292 ---------- 291---------------------------------------------------------- 291---------------------------------
GRMZM2G101271|GRMZM2G101271_T01                1 -----------------------------------------MTQ-EDLAEL--- 9--ARSTWELKEKQETPDPPEA--LKAVPSLSLQDIPKKPIHVP-----
LOC_Os02g52390|LOC_Os02g52390.1              540 GSKAVFSPLL 549EKFLLNNAHRA--------TIEMQPDPEKASRDEAAEKEILKQVKASMTR-EDLAEL--- 597--ARATKELKDKQETPDPPEA--LKAVPSLSL
AT3G19170                                    542 GSKAVFSPLI 551EKLILNNSHRV--------TIEMQPDPEKATQEEVEEKNILEKVKAAMTE-EDLAEL--- 599--ARATEELKLKQETPDPPEA--LRCVPSLNL
Carubv10012870m.g|Carubv10012870m            542 GSKAVFSPLI 551EQFILNNSHRV--------TIEMQPDPEKATQEEVEEKNILEKVKASMTE-EDLAEL--- 599--ARATEELKLKQETPDPPEA--LRCVPSLNL
Bra001738|Bra001738                          536 GSKAVFSPLI 545EQFILNNSHRV--------TIEMQPDPEKASQEEAEEKSILEKVKAGMTE-EDLAEL--- 593--ARATEELRLKQETPDPPEA--LRCVPSLNL
Bra037536|Bra037536                          545 GSKAVFSPLI 554EQFILNNSHRV--------TIEMQPDPEKASQEEAEEKSILEKVKAGMTE-EDLAEL--- 602--ARATEELRLKQETPDPPEA--LRCVPSLNL
Bra018811|Bra018811                          526 GSKAVFSPLI 535EKFILNNPHCV--------TIEMQPDLEKASQEEVEEKNILQKVKASMTD-EELAEL--- 583--ARATEELRLKQETPDSPEA--LKCVPSLNL
AT1G49630                                    541 GSKSVFSPLI 550EEYILNNPHCV--------TIEMQPDPEKASLEEAEEKSILEKVKASMTE-EDLTEL--- 598--ARATEELRLKQETPDPPDA--LKCVPSLNL
Carubv10011558m.g|Carubv10011558m            517 GSKAVFSPLI 526EKFILKNPHCV--------TIEMQPDPEKASQEEAEEKEILEKVKASMTE-EDLAEL--- 574--SRATEELTLKQETPDPPEA--LKCVPSLNL
AC151525_26|AC151525_26.1                    585 GSKSVFSPLI 594EKFILNNLHKV--------TVQMQPDPEKAAREEATEKQILQEVKASMTT-EDLAEL--- 642--TRATQELRLKQETPDPPEA--LKTVPSLSL
Glyma01g45650|Glyma01g45650.2                540 GSKSVFSPLI 549EKFILNNPHQV--------TVEMQPDPEKAARDEVAEKQILQKVKASMTT-EDLAEL--- 597--ARATHELRLKQETPDPPEA--LKTVPSLSL
PGSC0003DMG400025820|PGSC0003DMT40006639     534 GSKAVFAPLM 543DQYILRNPHRV--------TVEMQPDPEKASREEQIEKETLDKVKASMTQ-EDLAEL--- 591--ARATHELRLKQETPDPPEA--LKSVPSLSL
Cucsa.219950|Cucsa.219950.1                  546 GPKAVFSPLI 555EKFILNNPHRV--------TIEMQPDPEKASRDEATEKEILQKVKESMTE-EDLAEL--- 603--ARATQELRLKQETPDPPEA--LKCVPCLCL
29801.t000151|29801.m003206                  246 EKFILKNPHCV--------TVEMRPDPEKASRDEVAEREILEKVKGNMTE-EDLAEL--- 293--ARATQELRLKQETPDPPET--LKTVPSLSLNDIPKEPIRVP---
Eucgr.G01465|Eucgr.G01465.1                  552 GSKAVFSPLI 561EKFILNNPHLV--------TVEMQPDPEKDSRDEAAEKEVLDKVRRSMTE-EDLAEL--- 609--ARATQELRLKQETPDPPEA--LRTVPSLSL
GSVIVG01031766001|GSVIVT01031766001          560 GSKAVFSPLI 569EKYILNNPHCV--------TVEMQPDPEKASRDEAVEREILEKVKAGMTE-EDLAEL--- 617--ARATQELRLKQETPDPPEA--LKSVPSLSL
Potri.004G142300|Potri.004G142300.1          553 GYKAVFSPLI 562EKFILNNPHRV--------TVEMQPDPEKASHDEAAEREILEKVKASMTE-EDLAEL--- 610--ARATQELKLKQETPDPPEA--LRSVPSLFL
Potri.009G103700|Potri.009G103700.1          549 GSKAVFSPLI 558EKFILNNLHRV--------TIEMQPDPEKASRDEAAEREILEKVKASMTE-EDLAEL--- 606--ARATQELRLKQETPDPPEA--LRSVPSLSL
gi|66806529                                  545 FWFDLL 550DEFFI-DKPYV--------EILLKPDSKLSETIANETTQRMKDTIEKNGGEEGMKIIGEK 601LKCA-----IDS--SKSFPQELLTETMSKIE--SFD
CMM154C|CMM154CT                             448 FWREHI 453LRRWY-LPGDGDHGASLVSCIVCQPSKDEANRLRTEAALRIQERLERLSA-AERVALGQR 511LQES-----VAE-HQVSIPESLVPVCSGLLDPASIS
gi|71981120                                  435 YWVQLV 440NKYFT-AP-SA--------TVIGVPNEELVDKIAEEEEKRIAAQCEKLGK-KGLEEAGKS 489LEAA-----ILE-NTANHPSAELLDQLIVKDLEAFD
gi|66803803                                  436 YWIDLM 441DKVFL-KQACL--------EVQGVPSIQESKRISKEETDRLEKQVKELGQ-EKLKELGKI 491LEDA-----KAY-NDRPID-EKYFESIKIPSPNSIS
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Medtr7g082690|Medtr7g082690.1                  134 --- 133------------VRSGL-ECNV-FLLNAFLTALVRNGKLTEALQIFET-SPIRDTVTWNT 178MMGGYLEFSSEQIPVFWRYMNREGVKPDEFTFASALTGL
YDR430C                                        541 PRAGDKYS---------------- 548------------IEQKN-NTM----SRITDT---NG--ITYVRGKRLL-N---------- 575--DIIPFELFPYLPLFA
gi|85099301                                    559 PRQKDSVL---------------- 566------------LRHDN-TARVKTQWHEAPT---NG--LTYFRAINQL-E---------- 597---NLPDELRSLIPLFT
gi|66824379                                    615 CDIEKQQSKIDHID-TK---------- 630------------LSMTN-GDGVPLRILDLPT---NG--ISYFRSTIDI-S---------- 661---SMDPKLKPYVP
gi|334085248                                   565 IEPTIPVT---E-LD---------- 575------------V-VLT-AGDIPVQYCAQPT---NG--MVYFRAFSSL-N---------- 605---TLPEELRPYVPLF
Glyma04g13640|Glyma04g13640.1                  100 -- 99------------TEDLLSKSSGRCFTFCFHSSLVPNIREAWVEKVVET-P---------- 136---YMTPT---TSPLFFTPQFTTPISPYNQCGFNPLFETST
Esi0186_0009                                     1  0------------------------------------------ 0------------------MMETGTSEMDRVQLSRRIGSQTG----
Esi0186_0008                                   464 ------------------------------ 463--------------------------------------------------------------- 463---------------
CMQ222C|CMQ222CT                               604 LDRKVKTVP---------------- 612------------RHAENRAEGVTILSHPLAT---NG--IVYIDVGFDT-T---------- 644---QVPSELLPLLGIY
Cre01.g020900|Cre01.g020900.t1.3               624 SDIPKTITKVP---------------- 634------------TSSKALADGATLLGHDLFT---ND--VLYLEAAFDL-R---------- 666---SLPARLLPLVP
Vocar20010196m.g|Vocar20010196m                576 IPPTITKVP---------------- 584------------TSSKALADGATLLAHDLFT---NA--VLYLEAAFDL-R---------- 616---PVPSRLLPLVPLF
152047|152047                                  512 EPLHVP---------------- 517------------IAIGE-MHGATMLRHDIFT---ND--VLYAEVAFEL-R---------- 548---TVPSELLPLVPLFCQS
Phpat.005G011400|Phpat.005G011400.1            630 SDIPKKSATVP---------------- 640------------IEVGS-LKGSTVLRHDLFT---ND--VLYAEVAFDM-R---------- 671---AVRPDLLPLVP
GRMZM2G072861|GRMZM2G072861_T01                292 ------------------------------ 291--------------------------------------------------------------- 291---------------
GRMZM2G101271|GRMZM2G101271_T01                 49  48------------VEVGE-INGVKVLQHDLFT---ND--VIYSEVVFDM-G---------- 79---SMKKEHLQLLPLFCQSLLEMGTKDMDFVQLNQLIGRKTG--
LOC_Os02g52390|LOC_Os02g52390.1                626 QDIPKEPIHVP---------------- 636------------IEVGE-INGVKVLQHDLFT---ND--VVYSEIVFDM-S---------- 667---SLKKDHLQLLP
AT3G19170                                      628 GDIPKEPTYVP---------------- 638------------TEVGD-INGVKVLRHDLFT---ND--IIYTEVVFDI-G---------- 669---SLKHELLPLVP
Carubv10012870m.g|Carubv10012870m              628 GDIPKEPTYVP---------------- 638------------TEVGN-INGVKVLRHDLFT---ND--IIYAEVVFDM-G---------- 669---SLKHELLPLVP
Bra001738|Bra001738                            622 SDIPKEPSYVP---------------- 632------------TEVGD-INGVKVLRHDLFT---ND--IVYAEVVFDM-G---------- 663---SLKHELLPLVP
Bra037536|Bra037536                            631 SDIPKEPTYVP---------------- 641------------TEVGD-INGVKVLRHDLFT---ND--IVYAEVVFDM-G---------- 672---SLKHDLLPLVP
Bra018811|Bra018811                            612 RDIPKKPTYVP---------------- 622------------TEVGD-INGVKVLRHDLFT---ND--ILYTEVVFDM-G---------- 653---SLRHALLPLVP
AT1G49630                                      627 SDIPKEPIYVP---------------- 637------------TEVGD-INGVKVLRNDLFT---NN--ILYTEVVFDM-G---------- 668---SVKHELLQLIP
Carubv10011558m.g|Carubv10011558m              603 SDIPKEPIYVP---------------- 613------------SEVGD-INGVKVLRHDLFT---ND--ILYTEVVFDM-G---------- 644---SLKHELLPLIP
AC151525_26|AC151525_26.1                      671 QDIPKEPIHVP---------------- 681------------TEVGD-INGVKVLQHDLFT---ND--VLYTDIVFDM-S---------- 712---SLKQELLPLVP
Glyma01g45650|Glyma01g45650.2                  626 QDIPKEPIRVP---------------- 636------------TEVGD-INGVKVLQHDLFT---ND--VLYTEIVFNM-K---------- 667---SLKQELLPLVP
PGSC0003DMG400025820|PGSC0003DMT40006639       620 QDIPREPVLVP---------------- 630------------TEIGD-INGVKVLKHDLFT---ND--VLYAEVVFNL-S---------- 661---SLKQELLPLVP
Cucsa.219950|Cucsa.219950.1                    632 EDIPKEPTRVP---------------- 642------------TEIGN-VNGVTVLQHDLFT---ND--VLYSEVVFDM-S---------- 673---SLKQELLPLVP
29801.t000151|29801.m003206                    333 -------------- 332------------TEVGD-INGVKVLRHDLFT---ND--VLYAEVVFNM-R---------- 363---PLKQELLPLVPLFCQSLLEMGTKDL
Eucgr.G01465|Eucgr.G01465.1                    638 HDIPKEPIRVP---------------- 648------------TEVGD-INGVKVLRHDLFT---ND--VLYTEVVFNM-S---------- 679---SLKQELLQLVP
GSVIVG01031766001|GSVIVT01031766001            646 LDIPKEPIHVP---------------- 656------------IEIGV-INDVKVLRHDLFT---ND--VLYTEIVFDM-S---------- 687---SLKQDLLPLVP
Potri.004G142300|Potri.004G142300.1            639 CDIPKEPIHVP---------------- 649------------TEVGD-INGVKVLKHDLFT---ND--VLYAEIVFNM-R---------- 680---SLKQELLPLVP
Potri.009G103700|Potri.009G103700.1            635 LDIPKEPLHVP---------------- 645------------TEAGD-INGVKVLKHDLFT---ND--VLYAEIVFNM-R---------- 676---SLKQELLPLVP
gi|66806529                                    629 INKIPLIKIDTILN---------- 642---------RAYT--QNNPNPFTVQTLLVPSHF------IHSTIIFHVQQ---------- 675---SLPDHLRPWLTLFQI
CMM154C|CMM154CT                               542 RFRVETIRID-------------- 551---------------DVGSGVRLQIDDVDSEF------VRLTALLDT-R---------- 578---GLSGRQRLLLPLFLE
gi|71981120                                    520 RFPVQSL------TSNSPSLTPQ- 536---QSTFL---------AQFPFHANLHNCPTKF------VEIFFLLDS-S---------- 567---NLSIEDRSYLFLYTD
gi|66803803                                    521 CYSVYSVLNDKPLHSNSNSNSNEK 544KLIGEEKLAKYLIESNPNKIPFKIVFNQVDSLF------INIRVGFNT-N---------- 587---ELQDQLRDYLPLFLD

Medtr7g082690|Medtr7g082690.1                  218 ATISSLKM-----GM-----Q 228VHAQLVR-----SGYGD-DICVGNSLVDMYLKNQK--LEEGF--KAFDEIPHKDVCSWTQ 278MADGCLQWGEPRMALAVIAKM
YDR430C                                        591 ESLTNLGTTTESFSEIEDQIKLHTG----------GI-----S 618THVEVTSD----PNTT--EPR-----LIFGFDGWS--LN----------------SKTDH 64
gi|85099301                                    612 DSIMRLGTKDMTMEQLEDLIKLKTG----------GV-----S 639VGYHSASH----PTDFT-RAT-----EGLMFSGMA--LD----------------RHVPT 67
gi|66824379                                    673 IFCSLIDEMGAAEFDHKQLDTELNLHIG----------KF-----S 703VSPLITMG----HSDLD-YTQ-----ERIYIKGAA--LN----------------NNLLK
gi|334085248                                   619 CSVLTKLGCGLLDYREQAQQIELKTG----------GM-----S 647ASPHVLPD----DSHMDTYEQ-----VGVLFSSLC--LD----------------RNLPD 6
Glyma04g13640|Glyma04g13640.1                  172 D----------AE------ 174------------FNRLKSSPP-----PNIQDESKG--NG----------------D---- 195EVDGCFITIN----TNFKYDYMD
Esi0186_0009                                    24 ------GV-----Y 26ATFLADQPSAGGAVADPGALK-----QYLFLRGKA--VS----------------DKVSD 63MLSI-------------------------
Esi0186_0008                                   464 ---------------------------------------- 463-------------------------------------------------------------------
CMQ222C|CMQ222CT                               658 AESLFEVGTHREDFVALQRRIGRDTG----------GL-----R 686AAVLTTQQV---DERGDGAVI-----QRLFLRGKA--TA----------------NQVAS 7
Cre01.g020900|Cre01.g020900.t1.3               678 LFCRSLTQMGTATESFIELTERIGRKTG----------GV-----S 708VYPFTS------AVRGQEAPV-----SYVMIRGKA--MG----------------GKAAD
Vocar20010196m.g|Vocar20010196m                630 CRSLTQMGTSSESFVELTERIGRKTG----------GI-----S 658IYPFTS------AVRGKEQPV-----AYIMVRGKA--MS----------------GKFGD 6
152047|152047                                  565 LLEMGTKDMDFVSLNLLIGRKTG----------GI-----S 590VYPSTS------SVRGKKEPS-----SKMIIRGKA--MA----------------SQAQD 621L
Phpat.005G011400|Phpat.005G011400.1            683 LFCQSLLEMGTADLDFVQLSQLIGRKTG----------GI-----S 713VYPSTS------AVRGRTEPS-----SHIFIKGKA--MA----------------GQTAD
GRMZM2G072861|GRMZM2G072861_T01                292 ---------------------------------------- 291-------------------------------------------------------------------
GRMZM2G101271|GRMZM2G101271_T01                119 --------GI-----S 121VYPFTS------SVRGKEDPL-----TRIIVRGKA--MA----------------PRVED 152LFNL--------------------
LOC_Os02g52390|LOC_Os02g52390.1                679 LFCQSLLEMGTKDMDFVQLNQLIGRKTG----------GI-----S 709VYPFTS------SIRGKDDPL-----TRIVVRGKS--MA----------------TRVED
AT3G19170                                      681 LFCQSLLEMGTKDLTFVQLNQLIGRKTG----------GI-----S 711VYPLTS------SVRGKDEPC-----SKIIVRGKS--MA----------------GRADD
Carubv10012870m.g|Carubv10012870m              681 LFCQSLLEMGTKDLTFVQLNQLIGRKTG----------GI-----S 711VYPLTS------SVRGKDEPC-----SKIIVRGKS--MA----------------GRAED
Bra001738|Bra001738                            675 LFCQSLLEMGTKDLSFVQLNQLIGRKTG----------GI-----S 705VYPLTS------SVRGKDEPC-----SKIIVRGKS--MA----------------GRADD
Bra037536|Bra037536                            684 LFCQSLMEMGTKDLSFVQLNQLIGRKTG----------GL-----S 714VYPLTS------SVRGKAEPC-----SKFVVRGKS--MA----------------GRAED
Bra018811|Bra018811                            665 LFCQSLLEMGTQDMSFVQLNQLIGRKTG----------GI-----T 695VYPFTS------SVWGSDVPC-----SKIIVRGKS--MV----------------GRAED
AT1G49630                                      680 LFCQSLLEMGTQDLTFVQLNQLIGRKTG----------GI-----S 710VYPLTS------SVYGRDDPC-----SKIIVRGKS--MV----------------GRAED
Carubv10011558m.g|Carubv10011558m              656 LFCQSLLEMGTKDLTFVQLNQLIGRKTG----------GI-----S 686VYPLTS------SVWGRDDPC-----SKIIVRGKS--MV----------------GRAED
AC151525_26|AC151525_26.1                      724 LFCQSLLEMGTKDLTFVQLNQLIGRKTG----------GI-----S 754VYPFTS------SVQGKEDPC-----SHMIVRGKA--MA----------------GRAED
Glyma01g45650|Glyma01g45650.2                  679 LFCQSLLEMGTKDLTFVQLNQLIGRKTG----------GI-----S 709VYPFTS------SVRGKEDPC-----SHMVIRGKA--MA----------------GHIED
PGSC0003DMG400025820|PGSC0003DMT40006639       673 LFCQSLLEMGTKDLDFVQLNQLIGRKTG----------GL-----S 703VYPFTS------SVHGKVEPC-----SKIIVRGKA--MS----------------QRTED
Cucsa.219950|Cucsa.219950.1                    685 LFCQSLLEMGTKDLTFVQLNQLIGRKTG----------GI-----S 715VYPFTS------SIRGNDKAC-----THMVVRGKA--MS----------------GCAED
29801.t000151|29801.m003206                    389 TFVQLNQLIGRRTG----------GI-----S 405VYPFTS------SVRGLAEPC-----SHIIVRGKA--MA----------------GRAED 436LFDL------
Eucgr.G01465|Eucgr.G01465.1                    691 LFCQSLLEMGTKDLSFVQLNQLIGRKTG----------GI-----S 721VYPFTS------SVRGKEDPC-----SHIIVRGKA--MA----------------GRTED
GSVIVG01031766001|GSVIVT01031766001            699 LFCQSLMEMGTKDMDFVQLNQLIGRKTG----------GI-----S 729VYPFTS------SVRGKEYPC-----SHIIVRGKA--MA----------------GCAED
Potri.004G142300|Potri.004G142300.1            692 LFCQSLLEMGTKDLTFVQLNQLIGRKTG----------GI-----S 722LYPFTS------SVRGREDPC-----SHIVARGKA--MA----------------GRVED
Potri.009G103700|Potri.009G103700.1            688 LFCQSLLEMGTKDLTFVQLNQLIGRKTG----------GI-----S 718VYPFTS------SIQGREDPC-----SHIIAQGKA--MA----------------GRVED
gi|66806529                                    691 ILFETDLLVDSDQVVVADNDERNKSTTTKKEKSKLLIPYKK 732VCKSMAEQ----V--LSFEAV-------LGFSNST------F-TCSSSELFRITASCQVE 772
CMM154C|CMM154CT                               594 TLFNTRVGERDHR----------------------------A 607VRDALLAD----T--VDYGCA-------IGLSKEGGDAGAGFAIGAFSQLISVTIKSERA 654
gi|71981120                                    583 LLFESPA-MIDGVLTSAD-----------------------D 600VAKHFTKD----L--IDHSIQ-------VGVSG-------L-----YDRFVNLRIKVGAD 635
gi|66803803                                    603 LLLMSSIKKEDGTIINHD-----------------------Q 621VDSLVLKY----A--IKLTTS-------IGYSS-------NYEGGDFAQYCFLACDLKQD 661

Medtr7g082690|Medtr7g082690.1                  300 K-KMGVKPNKFTLATALNACACLASMEEGKQFHGLRIKL 337GSDVDVCVDNALLDMYAKCGC--MDSAWTVFRST-NSRSVVSWTTMIMACAQNGQPGE-- 392---
YDR430C                                        650 9IFEF------------------------------------------------------------ 653------------------WSKILLETDFHKNSDKL--KVLIR---
gi|85099301                                    672 1MFDL------------------------------------------------------------ 675------------------LRKLVVETDFDSPQAAQQIRQLLQ---
gi|66824379                                    736  735MFSL-------------------------------------------------------------- 739------------------LQKILLENKWNNPD---LLKNLLN
gi|334085248                                   681 80MMQL----------------------------------------------------------- 684------------------WSEIFNNPCFEEEE---HFKVLVK--
Glyma04g13640|Glyma04g13640.1                  215 KQHMLETYQAWQ------ATYIN------------- 231-LVGHVCSPRIFFTA--------------------------LS---PRRSALA*------ 254-----
Esi0186_0009                                    68 --------------------------------- 67------------------MFDVMTDAHLDSQQ---RVVEMLK---ESKARLASSIQGSGH 103SFANTRLEARYTV
Esi0186_0008                                   464  463-------------------------------------------------------------- 463-------------------------------------------------
CMQ222C|CMQ222CT                               721 20LFDI------------------------------------------------------------ 724------------------LTDVLHEIKFDDRE---RIRQLVV--
Cre01.g020900|Cre01.g020900.t1.3               740  739LLDL-------------------------------------------------------------- 743------------------MRDVLLTARLDDKA---RFGQMVA
Vocar20010196m.g|Vocar20010196m                690 89MLDL------------------------------------------------------------ 693------------------MRDILLTARLDDRQ---RFTQMVA--
152047|152047                                  623 FSL------------------------------------------------------------ 625------------------MRTILQDVQFTDKE---RFKQFVS---QS
Phpat.005G011400|Phpat.005G011400.1            745  744LFDL-------------------------------------------------------------- 748------------------MRKVLQDVRFNDQG---RFKQFVL
GRMZM2G072861|GRMZM2G072861_T01                292  291-------------------------------------------------------------- 291-------------------------------------------------
GRMZM2G101271|GRMZM2G101271_T01                157 ---------------------------------- 156------------------MYIILQDVQFTEQQ---RFKQFVS---QSKARMENRLRGSGH 192GIAAARMD
LOC_Os02g52390|LOC_Os02g52390.1                741  740LFNL-------------------------------------------------------------- 744------------------IYCILQDVQFTEQQ---RFKQFVS
AT3G19170                                      743  742LFNL-------------------------------------------------------------- 746------------------MNCLLQEVQFTDQQ---RFKQFVS
Carubv10012870m.g|Carubv10012870m              743  742LFNL-------------------------------------------------------------- 746------------------MNCLLQEVQFTDQQ---RFKQFVS
Bra001738|Bra001738                            737  736LFNL-------------------------------------------------------------- 740------------------MNCLLQEVQFTDQQ---RFKQFVS
Bra037536|Bra037536                            746  745LFNLCLLWDAPNVFSCLHYEYL---IMVDNHFDWK------TCFVC-------------- 782-WDIIQCNLDTETDSINRMNCLLQEVQFTDQQ---RFKQFVS
Bra018811|Bra018811                            727  726LFNL-------------------------------------------------------------- 730------------------MNCVLQEVRFTDKQ---RFKQFIS
AT1G49630                                      742  741LFNL-------------------------------------------------------------- 745------------------MNCVLQEVRFTDQQ---RFKQFVS
Carubv10011558m.g|Carubv10011558m              718  717LFNL-------------------------------------------------------------- 721------------------MNCVLQEVRFTDQQ---RFKQFVS
AC151525_26|AC151525_26.1                      786  785LYDL-------------------------------------------------------------- 789------------------VNSVLQDVQFTDQQ---RFKQFVS
Glyma01g45650|Glyma01g45650.2                  741  740LYDL-------------------------------------------------------------- 744------------------VNSVLQDVQFTDQQ---RFKQFVS
PGSC0003DMG400025820|PGSC0003DMT40006639       735  734LFYL-------------------------------------------------------------- 738------------------INRVLQDVQLDDQK---RFKQFVS
Cucsa.219950|Cucsa.219950.1                    747  746LFNL-------------------------------------------------------------- 750------------------MNCILQEVQFTDQQ---RFKQFVS
29801.t000151|29801.m003206                    441 ---------------------------------------------------- 440------------------VNRVLQEVQFTDQQ---RFKQFVS---QSKARMENRLR
Eucgr.G01465|Eucgr.G01465.1                    753  752LFNL-------------------------------------------------------------- 756------------------VNCILQEVQFTDQQ---RFKQFVS
GSVIVG01031766001|GSVIVT01031766001            761  760LFNL-------------------------------------------------------------- 764------------------VNCILQEVQFTDQQ---RFKQFVS
Potri.004G142300|Potri.004G142300.1            754  753LFNL-------------------------------------------------------------- 757------------------VNCVLQEVQFTDQQ---RFKQFVS
Potri.009G103700|Potri.009G103700.1            750  749LFNL-------------------------------------------------------------- 753------------------VNCVLQEVQFTDQQ---RFKQFVS
gi|66806529                                    773 KFDHLIYWIFNGLFNF-------------------------------------------- 788--------------------------SLNLK----RLSTLLT---N
CMM154C|CMM154CT                               655 LYETCVHWLYDILYRS-------------------------------------------- 670--------------------------QLETN----RVRIAAQ---K
gi|71981120                                    636 KYPLLAKWAQIFTQGV-------------------------------------------- 651--------------------------VFDPS----RIHQCAQ---K
gi|66803803                                    662 YYNQLIELLKDILVNI-------------------------------------------- 677--------------------------IIEPE----RIKIVAK---K
```

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Medtr7g082690|Medtr7g082690.1                  393 ------ALQIFDEM--KETSVEPNYITFICVLYACSQGGF----------------- 424---------------------------------------------VDEG
YDR430C                                        676 LLASSNTSSVADAGH 690AFARGYSAAHYRSSGAI--NETLNGIEQLQFINRLHSL---LD----------------- 728------------------
gi|85099301                                    700 ASADGVVNDIASSGH 714AYARRAAESGLTWDSFL--KEQVSGLSQVKLVTSLASR---PE----------------- 752------------------
gi|66824379                                    761 ---QKQASVIEGIPSSGL 775SYAKILSSSKFSRAAQL--SEQWSGLSQVRLINEIVSS---ND----------------- 813----------------
gi|334085248                                   706 -MTAQELANGIPDSGH 720LYASIRAGRTLTPAGDL--QETFSGMDQVRLMKRIAEM---TD----------------- 758-----------------
Glyma04g13640|Glyma04g13640.1                  255 ------------------------------------------------------ 254----------------------------------------
Esi0186_0009                                   117 DGYL--GELQGGVTYVNTVKDMLDE---AE----------------- 141------------------------------------NDW---------
Esi0186_0008                                   464 ---------------- 463------------------------------------------------------------ 463-------------------
CMQ222C|CMQ222CT                               746 -EERAGLETRLVPSGH 760VMTASRLKAQYRRSDWV--NEQLNGISYLRYLRALQKR---VE----------------- 798------------------
Cre01.g020900|Cre01.g020900.t1.3               765 ---ETKAGMESGIISGGH 779SYAAKRLGAQRSLAGAV--GEAMGGLSYLEYVRQLAKR---VE----------------- 817----------------
Vocar20010196m.g|Vocar20010196m                715 -ETKASMESGIISGGH 729SYAGKRLAAQRGLAGVL--SETMGGLSYLEFIRGLAKK---IE----------------- 767------------------
152047|152047                                  649 KSGMESRLRGAGH 661RIVASRLDAMLNIPGAV--GEKMGGLSYLDYLRELEKQ---VD----------------- 699--------------------
Phpat.005G011400|Phpat.005G011400.1            770 ---QSKSRMEGRVSGGGH 784SVAAARLDGKLNTAGWI--SEQMGGLSYLEYLRDLEKR---VD----------------- 822----------------
GRMZM2G072861|GRMZM2G072861_T01                292 ------------------ 291------------------------------------------------ 291------------------
GRMZM2G101271|GRMZM2G101271_T01                201 AKLNAAGWI--SEQMGGVSYLEYLRDLETK---ID----------------- 230-------------------------------------QDW----
LOC_Os02g52390|LOC_Os02g52390.1                766 ---QSKARMENRLRGSGH 780GIAAARMDAKLNAAGWI--AEQMGGISYLEYLRDLETK---ID----------------- 818----------------
AT3G19170                                      768 ---QSRARMENRLRGSGH 782GIAAARMDAMLNIAGWM--SEQMGGLSYLEFLHTLEKK---VD----------------- 820----------------
Carubv10012870m.g|Carubv10012870m              768 ---QSRARMENRLRGSGH 782GIAAARMDAMLNIAGWM--SEQMGGLSYLEYLHTLEKK---VD----------------- 820----------------
Bra001738|Bra001738                            762 ---QSIARMENRLRGSGH 776GVAAARMDAMLNIAGWM--SEQMGGLSYLEFLRTLEKK---VD----------------- 814----------------
Bra037536|Bra037536                            821 ---QSIARMENRLRGSGH 835GIAAARMDAMLNVAGLM--SEQMGGLSYLEFLHTLAKK---VD----------------- 873----------------
Bra018811|Bra018811                            752 ---QSRAGMENRLRGSGQ 766GIAAARMDAMLNAAGWM--SEQMNGLSYIEFLHTLEQK---VD----------------- 804----------------
AT1G49630                                      767 ---QSRARMENRLRGSGQ 781GIAAARMDAMLNVAGWM--SEQMGGLSYLEFLHTLEQK---VD----------------- 819----------------
Carubv10011558m.g|Carubv10011558m              743 ---QSRAGMENQLRGSGQ 757AIAAARMEAMLNVAGWM--SEQMGGLSYLEYLHTLEQK---VD----------------- 795----------------
AC151525_26|AC151525_26.1                      811 ---QSRARMENRLRGSGH 825GIAAARMDAKLNAAGWM--SEKMGGLSYLEFLQTLEKR---ID----------------- 863----------------
Glyma01g45650|Glyma01g45650.2                  766 ---QSRARMENRLRGSGH 780GIAAARMDAKLNAAGWM--SEKMGGLSYLEFLRTLEER---VD----------------- 818----------------
PGSC0003DMG400025820|PGSC0003DMT40006639       760 ---QSRSRMENRLRGSGH 774SIAAARMGAKLNVAGWI--SEQMGGVSYLEFLKVLEDQ---VE----------------- 812----------------
Cucsa.219950|Cucsa.219950.1                    772 ---QSKSRMENRLRGSGH 786GIAAARMDAKLNSAGWI--SEQMGGLSYMEFLQTLEEK---VD----------------- 824----------------
29801.t000151|29801.m003206                    473 GSGH 476GIAAARMDAKLNVAGWI--SEQMGGVSYLEFLQGLEEK---VD----------------- 514-------------------------------
Eucgr.G01465|Eucgr.G01465.1                    778 ---QSKARMENRLRGSGH 792GIAAARMDAKLNVAGWI--SEQMGGVSYLEFLRDLEER---VD----------------- 830----------------
GSVIVG01031766001|GSVIVT01031766001            786 ---QSKARMENRLRGSGH 800GIAAARMDAKLNTAGWI--AEQMGGVSYLEFLQALEEK---VD----------------- 838----------------
Potri.004G142300|Potri.004G142300.1            779 ---QSKARMENRLRGSGH 793GIAAARMDAKLNVAGWI--SEQMGGVSYLEFLKALEKR---VD----------------- 831----------------
Potri.009G103700|Potri.009G103700.1            775 ---QSKAGMENRLRGSGH 789RIAATRMDAKLNVTGWI--SEQMGGVSYLEFLQALEER---VD----------------- 827----------------
gi|66806529                                   802 IYSSLQDVENDS-T 814TMCGLYSLNKLFPNPKISNEANISIFKQKEFLKSIISIIKSKNQIEIDYI------FNMI 868TQVRDCIIS------------------
CMM154C|CMM154CT                               684 LLNDVAQHRRDG-S 696ALVAWLSNEVLYGANDEANIPAMAPFRQRHLLRQVLKLLGENRNDRDEDEHDDDDEHDGD 756MKYDDCGEAHSFDAPERVIPSTLHHRAD
gi|71981120                                    665 LAGEARDRKRDG-C 677TVASTAVASMVYGK------------------------------------------ 691--NTNCILFDEL-VLEKL-----HEKIS
gi|66803803                                    691 LLDAIPERKESS-D 703KMVKSVIQHNQFNHDK-SNSSHLNYLKQYKFLKNIINILGGDD---EDDEHEDDEEQEGN 759GCGHGCKHNHNNEEKEDD-----HEDDD

Medtr7g082690|Medtr7g082690.1                  429 W---------- 429--KYLS-SMDKDYGIIPGEDHYICMVSILGRAGLIKEA-----KELILRMPF-HP----- 475-GVRVWQ-----------------------
YDR430C                                        729 ------------------NEETFQ--------- 734--REVVDKLTELQKYIVDTN--NMNFFITSDSDVQAKTVESQISKFMERLPH-GSCL--P 787NGPKTS---
gi|85099301                                    753 ------------------SD--PL--------- 756--EDVIAKLKQIQQFALAGN--L-RTAITCDSGSVSDN-AKALLNFVNSLPS-EAVT--F 807PS-------
gi|66824379                                    814 --------------------I------------ 814--NSLINKLLALNEFILDRS--LMKCLITTEKENISNL-ENNLSNFLKPFSN-KNT---P 865IIVNSL
gi|334085248                                   759 ------------------I------------- 759--KPILRKLPRIKKHLLNGD--NMRCSVNATPQQMPQT-EKAVEDFLRSIGR-SKKERRP 813VRPHTVE-
Glyma04g13640|Glyma04g13640.1                  255 --------- 254-------------------------------------------------------------------- 254------------------
Esi0186_0009                                   145 - 144--PKMLKRLQRVRATLLSKK--QFLSVL-------DGS-SEAVSEFLSRLPE-ETEGAAT 191NT-APLA------------EQ-----------------
Esi0186_0008                                   464 --------------------------------- 463--------------------------------------------------- 463------
CMQ222C|CMQ222CT                               799 -------------------QDW---------- 801--DQVKADLERLHQCVISRQ--GVIVNVTYPQ--IDEV-MSHVDAFLEALPA-RALSAAA 853DTNAAPA-
Cre01.g020900|Cre01.g020900.t1.3               818 -------------------SEEGW---------- 822--QAVRADLEAIRAALLQRK--GAIVNLTADNATLAAA-ESAVADFLSALPA-TAAATAT 876AGANDW
Vocar20010196m.g|Vocar20010196m                768 -----------------TDDGW---------- 772--QEIKSDLEAIRSALLQRN--GAIVNMTADSATLAAA-EGPVSDFLSALPA-SSAALSS 826----QSL-
152047|152047                                  700 -----------------TDW---------- 702--PAVQQNLERIRTSFLSRK--GAIVNLTADEKNLTKA-DSFVSSLLEALPE-TEPV--- 753--VCTW-----
Phpat.005G011400|Phpat.005G011400.1            823 ---------------------EDW---------- 825--PSVAESLNEIRNELLSRK--GTIVNLTADERTLTNA-ESHVAAFLDAMPE-TGGN--- 876--IVNW
GRMZM2G072861|GRMZM2G072861_T01                292 --------------------------------- 291--------------------------------------------------- 291------
GRMZM2G101271|GRMZM2G101271_T01                234 ------ 233--DSISSSLEEMRKSLFSKN--GCLINLTSDGKNLEKS-RQHIAKFLDSLPS-SPSI--- 284-GSDPW-------------------------
LOC_Os02g52390|LOC_Os02g52390.1                819 ---------------------QDW---------- 821--DKISSSLEEMRQSLFRKD--GCLVNITSDWKNLEKS-NKHIAKFLDSLPS-TTSL--- 872-GSDPW
AT3G19170                                      821 ---------------------EDW---------- 823--EGISSSLEEIRRSLLARN--GCIVNMTADGKSLTNV-EKSVAKFLDLLPE-NPSG--- 874-GLVTW
Carubv10012870m.g|Carubv10012870m              821 ---------------------EDW---------- 823--EGISSSLEEIRRSLLARN--GCIVNMTADGKSLTNV-EKSVAKFLDLLPE-NPSG--- 874-GLVTW
Bra001738|Bra001738                            815 ---------------------EDW---------- 817--EGISSSLEEIRRSLLAKN--GCIVNMTADGKSLTNI-EKSLEKFLDLLPE-NPSG--- 868-GLVTW
Bra037536|Bra037536                            874 ---------------------EDW---------- 876--EGISSSLEEIRRSLLARN--GCLVNMTADGKSLTNI-EKSVEKFLNLLPE-TPSG--- 927-GLVTW
Bra018811|Bra018811                            805 ---------------------QDW---------- 807--EGISSSLEEIRTSLLSKN--GCIVNMTADGKSLTST-EKFVGKFLDSLPE-KPSS--- 858-GQVTW
AT1G49630                                      820 ---------------------QDW---------- 822--EGISSSLEEIRRSFLSRN--GCIVNMTADGKSLTNT-EKYVGKFLDLLPE-NPSG--- 873-ELVTW
Carubv10011558m.g|Carubv10011558m              796 ---------------------QDW---------- 798--EGISSSLEEIRRSFLSRN--GCIVNMTADGKSLTNT-EKFVGKFLDSLPE-NTSG--- 849-GLVTW
AC151525_26|AC151525_26.1                      864 ---------------------QDW---------- 866--ADISSSLEEIRKTVFSKQ--GCLINITADGKNLANT-DKFVSKFVDMLPT-SSPIA-- 918-TPNIW
Glyma01g45650|Glyma01g45650.2                  819 ---------------------QDW---------- 821--ADISSSLEEIRKSIFSKQ--GCLINVTADRKNLAKT-EKVLSKFVDLLPT-SSPIA-- 873-T-TTW
PGSC0003DMG400025820|PGSC0003DMT40006639       813 ---------------------KDW---------- 815--PQISSSLEEIRKSLLSKN--GCLINLTADGKNLNNA-EKHISEFLDLLPS-TSLV--- 866-ESAAW
Cucsa.219950|Cucsa.219950.1                    825 ---------------------QNW---------- 827--TEISSSLEEIRQSLLSRK--NCLVNITADGKNLIKS-EKFIGKFLDLLPN-QPII--- 878-KNSTW
29801.t000151|29801.m003206                    515 ---------QDW---------- 517--PLVSSSLEEIRSSLLSRN--SCLINLTADGKNLTNS-EKLVGKFLDLLPS-NSFA--- 568-DNAAW-------------
Eucgr.G01465|Eucgr.G01465.1                    831 ---------------------QNW---------- 833--DGISSSLEEIRKSLLSRD--GCLINMTADGRNMENS-EKFVSKFLDMLPS-NSNV--- 884-GANTW
GSVIVG01031766001|GSVIVT01031766001            839 ---------------------QDW---------- 841--IGISSSLEEIRKSLLSRK--GCLINMTSEGKNLMNS-EKYVSKFLDLLPG-SSSV--- 892-EKTTW
Potri.004G142300|Potri.004G142300.1            832 ---------------------QDW---------- 834--AGVSSSLEEIRMSLFSKN--GCLINMTADGKNLTNS-EKYVSKFLDLLPS-KSSV--- 885-EAAAW
Potri.009G103700|Potri.009G103700.1            828 ---------------------QDW---------- 830--AGVSSSLEEIRTSLLSKN--GCLINMTADGKNLTNS-EKYVSKFLDLLPS-KSSV--- 881-EAAAW
gi|66806529                                    878 ----------------------------NPE 880AMFIQISHSPLVSNQSFTQR--------------------FIDKWNEYLENSNIKLNKK 919RKPQQDQQHD
CMM154C|CMM154CT                               785 EMPSRVWTANALATDASASPDWSRTTGTSQRY 816SMTALLDELEALRRSLTSPG--------------------KVFLHAVLHCDERLDAL 853LE--PW----
gi|71981120                                    712 KDV----------------------MKNPE 719AVL---EKLEQVRSALFSNG--------------------VNAHFVADVD-SIDPKMLS 754SDLWTW----
gi|66803803                                    783 DDEK---D-N----DEK-EEEEKELKPIKITD 805DVLILIDQLKKIQ-NYFTTK--------------------TENVFVGVGG-NIMQLKSP 842KDP--W----

Medtr7g082690|Medtr7g082690.1                  482 -------------------------TLLS 485ACQI-HGDVETGKLAA---EHAIKHDKNDPSSYVLLSNMLAE--TSNWDCVVSLRELMET 539RNVKKVPGSRIAA
YDR430C                                        794 ---------------------------------DYPLIGSKCKHT- 805LIKF-PFQVHYTSQAL---LGV-PYTHKDGSALQVMSNMLTF--KHLHREVREK-
gi|85099301                                    810 ---------------------------------RGPPNFTRDIKT- 821FYPL-PYQVYYGALAL---PTA-SYTASVNAPLQILSQLLTH--KHLHHEIREK-
gi|66824379                                    872 D--------------NANEEI------------------------TNSSRLN- 885FFPI-PATVNYISKTY---QAV-PYTHVDSAPIQILTKVL-S--EFLHKEIR
gi|334085248                                   821 -----KPVP--SSSGGDAHVPHGSQVIRK-------L-VMEPTFKPWQMKT- 856HFLM-PFPVNYVGECI---RTV-PYTDPDHASLKILARLMTA--KFLHTEIREK
Glyma04g13640|Glyma04g13640.1                  255 ----------------------------- 254------------------------------------------------- 254---------------
Esi0186_0009                                   200 ---------VKLLQEKDE- 208GFVV-PTQVNYVVKGG---PLY-KPGEVVPGQASVX------------------------ 239-------------------
Esi0186_0008                                   464 ------------------------------------------------------- 463----------------------------------------
CMQ222C|CMQ222CT                               861 ------------LD-------------------------GVSLRPMNE- 871GLVI-PARVNYVGKAA---NLF-DAGFRVHGALLLAARYLSN--TYLWEEVRVR
Cre01.g020900|Cre01.g020900.t1.3               883 A------------SS-------------------------GLLLPRNSE- 894ALTV-PTQVNYVAKAA---NLYADGGYELQGSAYVVEKYLGN--TWLWDRVR
Vocar20010196m.g|Vocar20010196m                830 ------------TS---------------------------SLLLPRTNE- 840ALCV-PTQVNYVAKGA---NLFLDAGYELNGSAYVVEKYLGN--TWLWDRVRVV
152047|152047                                  758 ---------------------------------------NGILQPCNE- 766GIIV-PTQVNYVGKAA--NLY-DTGYELDGSAYVISKYIGN--TWLWDRVRVS---
Phpat.005G011400|Phpat.005G011400.1            881 ------------------------------------------DRRLPLVNE- 889GLVI-PTQVNYVGKAG---NIY-DAGYKLDGSAYVIQKVIGT--TWLWDRVR
GRMZM2G072861|GRMZM2G072861_T01                292 ------------------------------------------------------ 291-------------------------------------------
GRMZM2G101271|GRMZM2G101271_T01                290 --------------LSRLPSVNE- 298AIVV-PTQVNYVGKAG---NLY-QSGYQLNGSAYVISKHISN--TWLWDRVRVS------ 345-------GGAYGGFCD--
LOC_Os02g52390|LOC_Os02g52390.1                878 ------------------------------------------LSRLPSVNE- 886AIVV-PTQVNYVGKAG---NLY-QSGYQLNGSAYVISKHISN--TWLWDRVR
AT3G19170                                      880 ------------------------------------------DGRLPLRNE- 888AIVI-PTQVNYVGKAG---NIY-STGYELDGSAYVISKHISN--TWLWDRVR
Carubv10012870m.g|Carubv10012870m              880 ------------------------------------------DGRLPLRNE- 888AIVI-PTQVNYVGKAG---NIY-STGYELDGSAYVISKHISN--TWLWDRVR
Bra001738|Bra001738                            874 ------------------------------------------DGRLPLRNE- 882AIVI-PTQVNYVGKAG---NIY-STGYELDGSAYVISKHISN--TWLWDRVR
Bra037536|Bra037536                            933 ------------------------------------------DGRLPLRNE- 941AIVI-PTQVNYVGKAG---NIY-STGYELDGSAYVISKHISN--TWLWDRVR
Bra018811|Bra018811                            864 ------------------------------------------DARLPLRNE- 872AIVI-PTQVNYVGKAG---NIY-SSGYKLDGSSYVISKHIGN--TWLWDRVR
AT1G49630                                      879 ------------------------------------------DARLPLRNE- 887AIVI-PTQVNYVGKAG---NIY-SSGYKLDGSSYVISKHISN--TWLWDRVR
Carubv10011558m.g|Carubv10011558m              855 ------------------------------------------DARLPLRNE- 863AIVI-PTQVNYVGKAG---NIY-SSGYELDGSSYVISKHIGN--TWLWDRVR
AC151525_26|AC151525_26.1                      924 ------------------------------------------NVRLPLTNE- 932AIVI-PTQVNYVGKAT---NVY-DAGYKLNGSAYVISKYISN--TWLWDRVR
Glyma01g45650|Glyma01g45650.2                  878 ------------------------------------------NVRLPLTNE- 886AIVI-PTQVNYIGKAA---NIY-DTGYRLNGSAYVISKYISN--TWLWDRVR
PGSC0003DMG400025820|PGSC0003DMT40006639       872 ------------------------------------------NAQLSRSNE- 880AFVV-PTQVNYVGKAA---NLY-EAGYELKGSAYVISNYISN--TWLWDRVR
Cucsa.219950|Cucsa.219950.1                    884 ------------------------------------------NARLSSDNE- 892AIVI-PTQVNYVGKAA---NIY-ETGYQLDGSAYVISKFISN--TWLWDRVR
29801.t000151|29801.m003206                    574 ------------------------------NARLSPGNE- 582AIVI-PTQVNYVGKAA---NLY-DTGYQLNGSAYVISKYISN--TWLWDRVRVS------ 629--
Eucgr.G01465|Eucgr.G01465.1                    890 ------------------------------------------RACLSRENE- 898AIVI-PTQVNYVGKAA---NVY-ETGYQLDGSAYVISKYISN--TWLWDRVR
GSVIVG01031766001|GSVIVT01031766001            898 ------------------------------------------NGRLSSENE- 906AIVI-PTQVNYVGKAT---NIY-DTGYQLKGSAYVISKYISN--TWLWDRVR
Potri.004G142300|Potri.004G142300.1            891 ------------------------------------------NARLSPGNE- 899AIVI-PTQVNYVGKAA---NIY-DTGYQLNGSAYVISKYISN--TWLWDRVR
Potri.009G103700|Potri.009G103700.1            887 ------------------------------------------NARLSPGNE- 895AIVI-PTQVNYVGKAA---NIY-DTGYQLNGSAYVISKYISN--TWLWDRVR
gi|66806529                                    930 QQQQQQHQHHNNNHNNEIENQQQNIPF----FQPLERLKTKIPTPFSEQL 975IIK--GSESNSLLQYV---TLPISSTHEDYPAVSLLCNIFNGKEG----EIRKK--
CMM154C|CMM154CT                               858 --KQTFGVISG-----MLPNGNGPLPAHPQLVQFSHEVRPSASVP-RRCI 899VAGVDGVDSCYAKLIS---DGPKSFLDPDYPLYLVLFELLDALEGPLWRDIRGA--
gi|71981120                                    761 --VQADPRF--GPGH-----------------QFSAEAGENVSLELGKEL 789LIGVGGSESSFIYQTSFLDA---NWNSEELIPAMIFGQYLSQCEGPLWRAIRGD--
gi|66803803                                    847 --LNEFSFINGGGGKNVIDNSNQEIKSNPSSFQYQLINKENMISLRGKQL 894AITTAGSSSSTVQRVILNNITYDDVISKEYVALYVSMNYLEQLEGPFWKLLRGA--
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Medtr7g082690|Medtr7g082690.1                553 YALQECENLKKEALGSNLGCLMKKVYMYRLSR-----YGYMVKMIWL 594SITR-----NIYDDTPTKVIIETIGDVDAYQLNDAKPKRYTANYACFSFRLRYAAVGIT
YDR430C                                      853 ----- 852-------GGAYGGGAS---------YSALAGI--FSFYSYRDPQPLKSLETFKNSGRYI 893LNDA-----KWGVTDLDEAKLTIFQQVDAPKSPKGEG
gi|85099301                                  869 ----- 868-------GGAYGGGSY----------ARPLDGI--FGFYSYRDPNPVNTLKIMRNAGQWA 909V-DK-----EWTDRDLEDAKISVFQGVDAPKAVNEEG
gi|66824379                                  930 EK------ 931-------GGAYGGGSS------------V--DSGV--ISFYSYRDPNLIKTLDAFDQSIQWS 970L-NN-----KITLENIENAQLSIFSDFDSPESPS
gi|334085248                                 904 ------ 903-------GGAYGGGAK----------LS-HNGI--FTLYSYRDPNTIETLQSFGKAVDWA 943K-SG-----KFTQQDIDEAKLSVFSTVDAPVAPSDK
Glyma04g13640|Glyma04g13640.1                255 ---------------------------------------------- 254----------------------------------------------------------------
Esi0186_0009                                 240 -------------------------------------- 239-------------------------------------------------------------------- 239-----
Esi0186_0008                                 464 -------- 463------------------------------------------------------------------ 463------------------------------------
CMQ222C|CMQ222CT                             919 ------ 918-------GGAYGGFCR----------LDPRTGT--FLFLSYRDPNVEKTVDIYDGACDFL 959R-RI-----QLSRDEIDKSIIGTIGDMDAYELPDAK
Cre01.g020900|Cre01.g020900.t1.3             941 VV------ 942-------GGAYGGFCS----------FDSHSGM--FTYMSYRDPNLLDTIESYDGSAAYL 983R-GL-----ELSSEELTKAIIGTMGDIDAYQLPD
Vocar20010196m.g|Vocar20010196m              889 ------ 888-------GGAYGGFCS----------FDSHSGM--FTYMSYRDPNLLDTLEAYDGSADYL 929R-SL-----QLTKDELTKAIIGTMGDIDAYQLPDAK
152047|152047                                814 --- 813-------GGAYGGFCD----------FDSHSGV--FTYLSYRDPNLAKTIDNYDLTVQFL 854R-EL-----ELDDDALTKAIIGTIGDVDSYQLPDAKGYS
Phpat.005G011400|Phpat.005G011400.1          935 VV------ 936-------GGAYGGFCD----------FDSHSGV--FTYLSYRDPNLVKTLDNYDATVQFL 977R-QL-----EVHNDALTKAIIGTIGDVDSYQLPD
GRMZM2G072861|GRMZM2G072861_T01              292 -------- 291---------------------------------------------------------------- 291------------------------------------
GRMZM2G101271|GRMZM2G101271_T01              355 --------FDTHSGV--FSYLSYRDPNLLKTLEVYDETARFL 386R-EL-----ELDDDALTKAIIGTIGDVDAYQLPDAKGYSSL----------MRYLLGITD 430
LOC_Os02g52390|LOC_Os02g52390.1              932 VS------ 933-------GGAYGGFCD----------FDTHSGV--FSYLSYRDPNLLKTLEVYDETAKFL 974R-EL-----EMDDDCLTKAIIGTIGDVDSYQLPD
AT3G19170                                    934 VS------ 935-------GGAYGGFCD----------FDSHSGV--FSYLSYRDPNLLKTLDIYDGTGDFL 976R-GL-----DVDQETLTKAIIGTIGDVDSYQLPD
Carubv10012870m.g|Carubv10012870m            934 VS------ 935-------GGAYGGFCD----------FDSHSGV--FSYLSYRDPNLLKTLDIYDGTGDFL 976R-GL-----DVDQETLTKAIIGTIGDVDSYQLPD
Bra001738|Bra001738                          928 VS------ 929-------GGAYGGFCD----------FDSHSGV--FSFLSYRDPNLLKTLDIYDGTGDFL 970R-GL-----DVDQETLTKAIIGTIGDVDSYQLPD
Bra037536|Bra037536                          987 VS------ 988-------GGAYGGFCD----------FDSHSGV--FSFLSYRDPNLLKTLDIYDGTGDFL 1029R-GL-----DVDQETLTKAIIGTIGDVDSYQLP
Bra018811|Bra018811                          918 VS------ 919-------GGAYGGFCD----------FDSHSGV--FSFLSYRDPNLLKTLDIYDGTGDFL 960R-CL-----DVDEDTLTKAVIGTIGDVDSYQLPD
AT1G49630                                    933 VS------ 934-------GGAYGGSCD----------FDSHSGV--FSFLSYRDPNLLKTLDIYDGTGDFL 975R-GL-----DVDEDTLTKAIIGTIGDVDSYQLPD
Carubv10011558m.g|Carubv10011558m            909 VS------ 910-------GGAYGGFCD----------FDSHSGT--FSFLSYRDPNLLKTLDIYDGTGDFL 951R-GL-----DVDEDTLTKAIIGTIGDVDSYQLPD
AC151525_26|AC151525_26.1                    978 VS------ 979-------GGAYGGFCD----------FDTHSGV--FSFLSYRDPNLLKTLEVYDGTGDFL 1020R-EL-----EIDDDTLTKAIIGTIGDVDSYQLP
Glyma01g45650|Glyma01g45650.2                932 VS------ 933-------GGAYGGFCD----------FDTHSGV--FSFLSYRDPNLLKTLDVYDGTGDFL 974R-EL-----QIDDDTLTKAIIGTIGDVDAYQLPD
PGSC0003DMG400025820|PGSC0003DMT40006639     926 VS------ 927-------GGAYGGFCS----------FDSHSGV--FSFLSYRDPNLLKTLDVYDGTSSFL 968K-EL-----EMDDDALTKAIIGTIGDVDSYQLPD
Cucsa.219950|Cucsa.219950.1                  938 VS------ 939-------GGAYGGFCD----------FDSHSGV--FSFLSYRDPNLLKTLDVYDGTVDFL 980R-EL-----ELDDDTLAKAIIGTIGDVDSYQLPD
29801.t000151|29801.m003206                  630 -----GGAYGGFCD----------FDTHSGV--FSFLSYRDPNLLKTLDVYDGTGDFL 670R-DI-----EMDDDTLTKAIIGTIGDVDAYQLPDAKGYSSL-------
Eucgr.G01465|Eucgr.G01465.1                  944 VS------ 945-------GGAYGGFCD----------FDTHSGV--FSFLSYRDPNLLKTLDIYDATGAFL 986R-EL-----EMDDDALTKAIIGTIGDVDSYQLPD
GSVIVG01031766001|GSVIVT01031766001          952 VS------ 953-------GGAYGGFCD----------FDTHSGV--FSFLSYRDPNLLKTLDVYDGTGDFL 994R-QL-----EMDDDTLTKAIIGTIGDVDAYQLPD
Potri.004G142300|Potri.004G142300.1          945 VS------ 946-------GGAYGGFCD----------FDTHSGV--FSFLSYRDPNLLKTLDVYDGSGAFL 987R-EL-----EMDDDTLAKAIIGTIGDVDSYQLAD
Potri.009G103700|Potri.009G103700.1          941 VS------ 942-------GGAYGGFCD----------LDTHSGV--FSFLSYRDPNLLKTLDVYDGTGAFL 983R-QL-----EMDDDTLSKAIIGTIGDVDSYQLPD
gi|66806529                                 1021 ---- 1020-------GYSYGHSLL----------TDTTKGT--LIFGLTESSSPIKALAEFHK---WL 1058KNVRDRPTEIITQQSIETAICSEIYDFYSTRS----
CMM154C|CMM154CT                             951 ---- 950-------GLAYGYNLG----------CTPESGT--VSLSLYRSTAFEGALSAALG---VL 988ERFHQQPQELIDENTVASACSGVLCTLLNQES-----T
gi|71981120                                  841 ---- 840-------GLAYGANVF----------VKPDRKQ--ITLSLYRCAQPAVAYERTRD---II 878RKIVES--GEISKAEFEGAKRSTVFEMMKREG-----T
gi|66803803                                  949 ---- 948-------GYCYGYRIS----------ANPESGL--MTFKISRSTNPEMALQVGKQ---II 986QDSLEK---PFNKKWFEGARSSSTFEIANKEK-----N

Medtr7g082690|Medtr7g082690.1                649 E 649E-ERQMRCEERLSTCLKDFKQFIDAMEA-VKD-KRVVVAVAS-HVHIDVANKELSSFYHV 705KKSL*----------------------------------
YDR430C                                      926 VT-------------YFMSGVTD 935D-MKQARREQLLDVSLLDVHRVAEKYLL-NK--EGVSTVIGP-GIEGKTVS----PNWEV 986KEL*---------------
gi|85099301                                  941 MA-------------QFLYGITD 950E-MKQKRREELLDVTKDQVREVAQEYVV-KALNNGSERVVFL-GEKRDWVD----KSWAV 1003KEMDINGST---------
gi|66824379                                  999 NKGVG-------------EWMRDITN 1011E-MKQTRRNNLLSITKPKLEEIATKYLF-NNQNNYT-TVLGS-KDNQELNK----FTWNN 1063INV-----------
gi|334085248                                 974 GMD-------------HFLYGLSD 984E-MKQAHREQLFAVSHDKLLAVSDRYLG-TGKSTHGLAILGP-ENPKIAKD----PSWII 1037Q----------------
Glyma04g13640|Glyma04g13640.1                255 254--------------------------------------------------------------- 254----------------------------------------
Esi0186_0009                                 240 ------------------------------------------------------- 239----------------------------------------------------
Esi0186_0008                                 464 ------------------------ 463--------------------------------------------------------------- 463----------------
CMQ222C|CMQ222CT                             990 GFNSA----------LRYLTGETD 1003E-LRQKRRDEIFSARIEDFRRLADALAQ-VREH-GSVVVLGA-SESIRRAESCL-KLERV 1058EPALPGTDV-------
Cre01.g020900|Cre01.g020900.t1.3            1012 AKGYSAL----------VRHLLGVSD 1027E-ERQQRRDQILATSNKDFKNFADAIEC-VRGSAGRVVAVTS-PEKAGKVLEEKPGFWEL 1084KKVL*---------
Vocar20010196m.g|Vocar20010196m              960 GYSAL----------VRHMLGVTD 973E-ERQIRRDEILSTSNKDFKAFAEAIEC-VRGAAGRVVAVTS-PEKAKAVLEERPDFWDV 1030KKVL*-----------
152047|152047                                888 SM----------LRYILGITE 898E-ERKLRREQILSTSLRDFKAFADVLEH-VKE-KGIVAAVAS-AEDVESANKERPGLLQP 954KKVSL*-------------
Phpat.005G011400|Phpat.005G011400.1         1006 AKGYSSM----------MRYIMGITD 1021E-ERQQRREEILSTSVKDFHAFADALES-VKE-KGVIVAVAS-ADDIAAANKERPGLLEV 1077RKVL*---------
GRMZM2G072861|GRMZM2G072861_T01              292 ------------------------- 291-------------------------------------------------------------- 291----------------
GRMZM2G101271|GRMZM2G101271_T01              431 E-ERQQRREEILATSPKDFKEFADAVET-IKD-NGVVVAVAS-IDDVEAANKENPLFPEV 486KKCL*-------------------------------------------
LOC_Os02g52390|LOC_Os02g52390.1             1003 AKGYSSL----------MRYLLGITV 1018E-ERQQRREEILSTSLKDFKEFADAVET-IND-NGVVVAVAS-PEDVEAANKENPLFSDV 1074KKCL*---------
AT3G19170                                   1005 AKGYSSL----------LRHLLGVTD 1020E-ERQRKREEILTTSLKDFKDFAQAIDV-VRD-KGVAVAVAS-AEDIDAANNERSNFFEV 1076KKAL----------
Carubv10012870m.g|Carubv10012870m           1005 AKGYSSL----------LRHLLGVTD 1020E-ERQRKREEILTTSLKDFKNFAEAIDA-VRD-NGVAVAVAS-AEDIDAANNARSNFFEV 1076KKAL*---------
Bra001738|Bra001738                          999 AKGYSSL----------MRHLLGVTD 1014E-ERLRKREEILTTSLKDFKDFAEAIDV-VRD-NGVAVAVAS-AEDIDAANNARSNFFEV 1070KKAL*---------
Bra037536|Bra037536                         1057 DAKGYSSL---------MRHLLGVTD 1073E-ERQRKREEILTTSLKDFKEFAEAIDV-VRE-KGVAVAVAS-AEDIDAANQARSNFFEV 1129KKAL*--------
Bra018811|Bra018811                          989 AKGYSSL----------LRHLLNVTD 1004E-ERQIRREEILSTSLKDFKEFAEAVDS-VRD-KGVAVAVAS-QEDIDAANKERSDFFEV 1060KKAL*---------
AT1G49630                                   1004 AKGYTSL----------LRHLLNVTD 1019E-ERQIRREEILSTSLKDFKEFAEAIDS-VSD-KGVAVAVAS-QEDIDAANRERSNFFEV 1075KKAAL---------
Carubv10011558m.g|Carubv10011558m            980 AKGYTSL----------LRHLLNVTD 995E-ERQIRREEILSTSLKDFKEFAEAIDS-VRD-KGVTVAVAS-QEDIDAANKERPNFFEV 1051KKVLFIFYVRISQYK
AC151525_26|AC151525_26.1                   1048 DAKGYSSM---------LRYILGITE 1064E-ERQKRRGEILSTSLKDFKQFIDAMEA-VKD-KGVVVAVAS-PDDVDAANKELSNFFQI 1120KRAL*--------
Glyma01g45650|Glyma01g45650.2               1003 AKGYSSM----------LRYLLGITE 1018E-ERQRRREEILSTSLKDFKIFMDAMEA-VKD-KGVVVAVAS-PEDVDTANKDRPDFFQV 1074KKAL*---------
PGSC0003DMG400025820|PGSC0003DMT40006639     997 AKGYSSL----------LRYLLGVTD 1012E-ERQRRREEILSTSLEDFRKFGDVMEA-VKD-KGVVVAVAS-PDDVEAANKERSNFLEV 1068KKAL*---------
Cucsa.219950|Cucsa.219950.1                 1009 AKGYSSL----------LRYLLGITE 1024E-ERQRRREEILSTSLKDFKNFADALEA-VRN-KGVVVSVAS-PEDVETAHGERPGFFQV 1080KKAL*---------
29801.t000151|29801.m003206                  706 ---LRYLLGVTE 714D-ERQRRREEILSTSLKDFKEFADAIDA-VKS-KGVVVAVAS-PEDVDVANKEFPNYFQV 770KKALELNDPSEEISYKGVVF---NEMKGVY
Eucgr.G01465|Eucgr.G01465.1                 1015 AKGYSSL----------LRYLLGITE 1030E-ERQRRREEILSTSLKDFRNFADVIES-VKG-KGVVASVAS-PDDVEAANKERPNFFQV 1086KNVL*---------
GSVIVG01031766001|GSVIVT01031766001         1023 AKGYSSL----------LRYLLGVTE 1038E-ERQKRREEILSTSLKDFKEFADAIEA-AKH-KGVVVAVAS-PDDVDAANKEHPNFFQV 1094KKAL*---------
Potri.004G142300|Potri.004G142300.1         1016 AKGYSSL----------LRYLLGITE 1031E-ERQKRREEILSTSLKDFKEFGEVIEA-VKD-KGVSVVVAS-PEDVHAANKERSNYFDV 1087KKAL*---------
Potri.009G103700|Potri.009G103700.1         1012 AKGYSSL----------LRYLLGITE 1027E-ERQKRREEILSTSLKDFKEFGEVIEA-VKD-KWVSVAVAS-PDDVDDANKERSNYFDV 1083KKAL*---------
gi|66806529                                 1091 -APQELVIESYI----NIFKGHND 1109FQQSIDFLNRFKVVTYDQIINVFNKYFIQFLDPNHLFLSLTVNPSSAKPLETELKETFDI 1169SIT---------SKYP
CMM154C|CMM154CT                            1022 VEAAAFQRLC----NSCRGFEG 1039D-YTGELLAKVINVTPAKLTEFATRVLAAFRLEHCLVTVVTN-PAKAPAAMEVLQSRGAL 1097RTT---------C------
gi|71981120                                  910 VSGAAKISIL----NNFRQTPH 927P-FNIDLCRRIWNLTSEEMVKIGGPPLARLFDEKCFVRSIAVHPSKLNEMKKAFPG---- 982-SS---------K-------
gi|66803803                                 1017 YDSVLENCYF----DLIRGWVD 1034K-SYRDFYKLIFEVTEEDCKLAIKKFISPLFDDSTSLIVISSESARLESFKKTYPD---- 1089-LQ---------I-----

Medtr7g082690|Medtr7g082690.1                710 ------------------- 709---- 709
YDR430C                                      990 ----------------------------------------- 989---- 989
gi|85099301                                 1013 ------------------------------------------ 1012---- 1012
gi|66824379                                 1067 ---------------------------------------------- 1066---- 1066
gi|334085248                                1039 ------------------------------------------- 1038---- 1038
Glyma04g13640|Glyma04g13640.1                255 ----------------- 254---- 254
Esi0186_0009                                 240 --------- 239---- 239
Esi0186_0008                                 464 ------------------------------------------- 463---- 463
CMQ222C|CMQ222CT                            1068 ------------------------------------------- 1067---- 1067
Cre01.g020900|Cre01.g020900.t1.3            1089 --------------------------------------------- 1088---- 1088
Vocar20010196m.g|Vocar20010196m             1035 ------------------------------------------ 1034---- 1034
152047|152047                                960 -------------------------------------- 959---- 959
Phpat.005G011400|Phpat.005G011400.1         1082 --------------------------------------------- 1081---- 1081
GRMZM2G072861|GRMZM2G072861_T01              292 ------------------------------------------- 291---- 291
GRMZM2G101271|GRMZM2G101271_T01              491 -------------- 490---- 490
LOC_Os02g52390|LOC_Os02g52390.1             1079 --------------------------------------------- 1078---- 1078
AT3G19170                                   1081 --------------------------------------------- 1080---- 1080
Carubv10012870m.g|Carubv10012870m           1081 --------------------------------------------- 1080---- 1080
Bra001738|Bra001738                         1075 --------------------------------------------- 1074---- 1074
Bra037536|Bra037536                         1134 ---------------------------------------------- 1133---- 1133
Bra018811|Bra018811                         1065 --------------------------------------------- 1064---- 1064
AT1G49630                                   1081 --------------------------------------------- 1080---- 1080
Carubv10011558m.g|Carubv10011558m           1067 FSRIF---VYLLGFKTS---LV*-------------------- 1082---- 1082
AC151525_26|AC151525_26.1                   1125 ---------------------------------------------- 1124---- 1124
Glyma01g45650|Glyma01g45650.2               1079 --------------------------------------------- 1078---- 1078
PGSC0003DMG400025820|PGSC0003DMT40006639    1073 --------------------------------------------- 1072---- 1072
Cucsa.219950|Cucsa.219950.1                 1085 --------------------------------------------- 1084---- 1084
29801.t000151|29801.m003206                  798 SQPDNILGRTAQQAISLFFDHPPPSEGCLG 827SLMI 831
Eucgr.G01465|Eucgr.G01465.1                 1091 --------------------------------------------- 1090---- 1090
GSVIVG01031766001|GSVIVT01031766001         1099 --------------------------------------------- 1098---- 1098
Potri.004G142300|Potri.004G142300.1         1092 --------------------------------------------- 1091---- 1091
Potri.009G103700|Potri.009G103700.1         1088 --------------------------------------------- 1087---- 1087
gi|66806529                                 1177 SQLYIPFNYEEYKLSCKK------------------------- 1194---- 1194
CMM154C|CMM154CT                            1102 ----VDSLDDFFALEKTV--------------------- 1115---- 1115
gi|71981120                                  986 --IKISDLQFAC------------------------- 995---- 995
gi|66803803                                 1093 ----VDPETYFV--------------------------- 1100---- 1100
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