```
Cre16.g660800|Cre16.g660800.t1.2              1 ------------------------------------------------------------ 0--------MA---------------------------------SQL
Vocar20010708m.g|Vocar20010708m               1 ------------------------------------------------------------ 0--------------------------------------------MN
Esi0086_0051                                  1 ------MLRLGRHGSTLKACS------------LRQPA----------------AA---- 22YARA----TRPSSIWRRDPIVPSGPHDNIVRGITTNTFTNTTTNTEQ
Phpat.004G075900|Phpat.004G075900.1           1 -------------------MA------------LRQLS----------------QR---- 9TGKALNGRGAAATILTRKLLLL-HGNGL------------PSTSSS
Phpat.012G024100|Phpat.012G024100.1           1 -------------------MT------------LQQVP----------------GR---- 9TAKALSVGGARATALTRRLLLLSREYGF-----------PIASPS
Bra036478|Bra036478                           1 ------------------------------------------------------------ 0--------MASRKLIRDLLITRQPLFL-------------RLAHQR
Bra036674|Bra036674                           1 ------------------------------------------------------------ 0--------MASRKLIRDLLITKQPLFL-------------QLARQR
Carubv10015970m.g|Carubv10015970m             1 ------------------------------------------------------------ 0--------MATRKLIRDLLITKQPFLR-------------QLLHQR
AT2G20510.1                                   1 ------------------------------------------------------------ 0--------MAIRKIIRDLLITKQPLLR-------------QLFHQR
Carubv10024977m.g|Carubv10024977m             1 ------------------------------------------------------------ 0--------MASRKLIRDLLITKQPIFQ-------------QLVHQR
AT2G36070                                     1 ------------------------------------------------------------ 0--------MASRKLVRDLLITKQPLLQ-------------QLVHQR
83588|83588                                   1 ------------------------------------------------------------ 0---------------------------------------------
Eucgr.B01552|Eucgr.B01552.1                   1 ------------------------------------------------------------ 0--------MAAKKLVRDLVLSGHPLRL-------------HLSSQA
Eucgr.G01944|Eucgr.G01944.1                   1 ------------------------------------------------------------ 0---------------------------------------------
Medtr4g029490|Medtr4g029490.1                 1 ------------------------------------------------------------ 0--------MTTRKLIRDFLLSHHHSLI-------------LPQQ--
Medtr2g083690|Medtr2g083690.1                 1 ------------------------------------------------------------ 0--------MASRKLLRDFLLSHRSLIL-------------PQQQ--
Glyma04g12120|Glyma04g12120.1                 1 ------------------------------------------------------------ 0--------MATRKLIRDLLLSKRSLLH-------------HQGW--
Glyma09g00505|Glyma09g00505.1                 1 ------------------------------------------------------------ 0---------------------------------------------
GRMZM2G095695|GRMZM2G095695_T02               1 ------------------------------------------------------------ 0--------MATTALLRALRRPSSEAAL-------------RLATK-
LOC_Os07g22700|LOC_Os07g22700.1               1 ------------------------------------------------------------ 0--------MATSALLRALRRPSSEAAL-------------RLAAS-
Cucsa.280740|Cucsa.280740.1                   1 ------------------------------------------------------------ 0---------------------------------------------
GSVIVG01028335001|GSVIVT01028335001           1 ------------------------------------------------------------ 0--------MGSRKLVRDLYLSKQPLLL-------------HLLSSQ
PGSC0003DMG400022489|PGSC0003DMT40005790      1 ------------------------------------------------------------ 0---------------------------------------------
30005.t000058|30005.m001292                   1 ------------------------------------------------------------ 0--------MAGKKLVRDLFLSRQPLFL-------------HLTSQQ
Potri.002G038300|Potri.002G038300.1           1 ------------------------------------------------------------ 0--------MASRKLVRDLFLSRQPLFL-------------RLTSKQ
Potri.005G224500|Potri.005G224500.1           1 ------------------------------------------------------------ 0--------MASRKLVRDLVLSRQPLFL-------------HFISKQ
CMJ253C|CMJ253CT                              1 ---------------------------MWRPITSRQLSVLCWRLGSTALTRTSAARVNAG 33RRRPNELRPLLRRPCTSETSTSAKPVSA-----------TART---
gi|17508985                                   1 ------------------------------------------------------------ 0----------------M---LSRICGN--------GIRLTRTR
gi|33636719                                   1 ------------------------------------------------------------ 0-----MAAAALRSGWCRC---PRRCLGS----------GIQFLSSH
YIL022W                                       1 ------------------------------------------------------------ 0--------MHRSTFIRTSGTSSRTLTA-----------RYRS----
gi|85117796                                   1 MNAYRHVLRT-SPGAPLRATAVPHTTHVRSPATSRLLSSRASRVNTTE------SRISPA 53TPISAQEIPLLRSPFTPN-AIQARSFHA-----------SFRALQQ

Cre16.g660800|Cre16.g660800.t1.2              6 G----------- 6----------RELVPLIASVQTQ-R-----AL----------LALAQPLGVA-LG----- 34--------------------------------
Vocar20010708m.g|Vocar20010708m               3 Q----------- 3----------SFLIPLASNGHTQ-R-----AL----------LGLVQPLAAFGTA----- 32--------------------------------
Esi0086_0051                                 66 QRS------VAL 71SRWIQADRRRGPHVGPAPAASVTQLQ-----QW----------RGLASGSSGKGKGGEEE 116GGMFDRLKKTFTEEIDKNPSLKESLSKLKD
Phpat.004G075900|Phpat.004G075900.1          43 L----------- 43---VSP----------G--VGR--------------------SL-TGQHV-IDR 60IRVLP---------------------------
Phpat.012G024100|Phpat.012G024100.1          44 M----------- 44---ASC----------S--VSR--------------------GL-MGGYS-IAR 61GRVLS---------------------------
Bra036478|Bra036478                          26 R----------- 26-------------------A--G---------------ERLGGFMPAIGCSINRR 45FSIFSDFSKKIRGEAESNPEFQKTVKELKEKA
Bra036674|Bra036674                          26 R----------- 26-------------------V--G---------------TRLG-FMPANGF-QRRQ 43FSVFSDLTKKIRGEAESNPEFQRTVKEIKEKA
Carubv10015970m.g|Carubv10015970m            26 L----------- 26-------------------VRAN---------------VR-SEFLPAIGYASHRQ 46FSILSDFSKNIE--ADSNSEFERRVKELKERA
AT2G20510.1                                  26 R----------- 26-------------------A--N---------------AR-SEFLPAIGYTSHRR 44FSVFTEFSKNIRGEAHSNPEFERTVKELKERT
Carubv10024977m.g|Carubv10024977m            26 R----------- 26-------------------V--G---------------AR-LGLLQGNGYASHRL 44FSVFSEFSKKIRGEADSNPEFQKTVKELKERA
AT2G36070                                    26 R----------- 26-------------------V--G---------------AR-LGLLQGNGFASHRR 44FSVFSEFSKKIRGEADSNPEFQKTVKEFKERA
83588|83588                                   1 ------------ 0--------------------------------------------------SPRN 4QSIFQEISKKLKGEIDSNPELQKSIKEFKEKADD
Eucgr.B01552|Eucgr.B01552.1                  26 QIFFLLELLLDF 37SLYISC----------NSQASSSR--------------LRLIT---AGGHSCNRR 65YSVFNEFSKKVKGEASGNPEFQKSVKQLKEKA
Eucgr.G01944|Eucgr.G01944.1                   1 ------------ 0---------------------------------------------------- 0---MSSLRKLKAKQAGMPIF---MKQLKEKAEE
Medtr4g029490|Medtr4g029490.1                24 ------------ 23------------------GVKTR--------------LFV-------NSVDRRG 38YSVFNEFSKKVKDETVKNPEFQKSVKELKEKA
Medtr2g083690|Medtr2g083690.1                24 ------------ 23------------------G------------------------------VKTIRR 30YGVFNEFSNKVKDETVKNPEFQKSVKELKEKA
Glyma04g12120|Glyma04g12120.1                24 ------------ 23------------------SRSRR--------------LPL-------VWEDRRR 38YSVFNEFSKNIKGQAVRNQEFQQSVKELKEKA
Glyma09g00505|Glyma09g00505.1                 1 ------------ 0---------------------------------------------------- 0-------------------------------
GRMZM2G095695|GRMZM2G095695_T02              25 ------------ 24--------------------AN--------------V---QTTNGYRHLNNRN 40LSVFNEFSKQLKGEAKSNPEFQKSMKEFS---
LOC_Os07g22700|LOC_Os07g22700.1              25 ------------ 24--------------------VR--------------V---QGVTGYRHLNNRN 40LSVFNEFSKQLKGEAKSNPEFQKSMKEFS---
Cucsa.280740|Cucsa.280740.1                   1 ------------ 0-----------------SSCTR--------------SQLLL---PSGYSINRR 19FSVFNEFSKKVKGEADKNTEFQQSVKELKEKAE
GSVIVG01028335001|GSVIVT01028335001          26 Q----------- 26------------------ASSAR--------------LRLISPN-G--CSGYRG 45FSVFNEFSNKIKGEVNRNSEFQQTVKELKEKA
PGSC0003DMG400022489|PGSC0003DMT40005790      1 ------------ 0---------------------------------------------------- 0-------------------------------
30005.t000058|30005.m001292                  26 G----------- 26-------------------SRTR--------------LRLPSTLPNGKNMGYRG 47FGVFSEFSKKVKGEVTRSQEFQQSVKELKDKA
Potri.002G038300|Potri.002G038300.1          26 V----------- 26-------------------SGRR--------------LQVLSNH-GCTYYGYRR 46FSVFNEFSNKVKGEADRNQEFKQSVKELKEKA
Potri.005G224500|Potri.005G224500.1          26 V----------- 26-------------------PSSR--------------LQVVSNY-GCPYSGYRR 46FSVFNEFSKKVKGEAQINLEFKQSVKELKEKA
CMJ253C|CMJ253CT                             66 SAA--------- 68-----P-EPRTTESA------STAEV----DQ-----HTSSSSVAEAAPEAVQAYRPGDR 107RPGWAGFFRGLFGGTQAAI--EDTLAAEAR
gi|17508985                                  17 LQ---------- 18-----F---------------QPSIV-----------------TFRD---YSNPAPK 35RGFLNNLIDNVRDEMQKNKELQEHQQQLKARM
gi|33636719                                  29 NL---------- 30-----P-HGSTYQM-----RRPGGEL-----------------PLSK---SYSSGNR 56KGFLSGLLDNVKQELAKNKEMKESIKKFRDEA
YIL022W                                      24 ------------ 23-------------------QYTGLLVARV--------------LFSTSTTRAQGGNP 47RSPLQIFRDTFKKEWEKSQELQENIKTLQDAS
gi|85117796                                  88 QEQ--------- 90-----P-KQQTPETEPKAQEEPTGKKESKSEEAKEEGEKSEGEPKKEKKEDAPPPPPHGD 144KTPWQVFMETMQTEFKQSQEWNESTKALAA

Cre16.g660800|Cre16.g660800.t1.2             35 --------------------------- 34---------SSRAIWTSR------------------------------------SA 45LSEPQKSEAST---SGA
Vocar20010708m.g|Vocar20010708m              33 --------------------------- 32---------HLRALSTSR------------------------------------CG 43LNEQQKAEGSQASTSGG
Esi0086_0051                                147 AEQKLRENPSVKENLAKLKEAEKKFRENPS 176VQENLSKLKDAEKKWREDAKSKQGEFAEQAEKAREKAQQGGGAFQEKFQELKQTLEEKL- 235-GKVG---GESG
Phpat.004G075900|Phpat.004G075900.1          66 --------------------------- 65---QF--YELVPSAS---------------------S-----------------SPM 79LDVLHF------SSRA
Phpat.012G024100|Phpat.012G024100.1          67 --------------------------- 66---QL--SEVVPSSS---------------------S-----------------SSA 80LSVCNF------SNRP
Bra036478|Bra036478                          78 EELK---GVKEDLKVK---TKE------ 93KTEQL--YKQVDGVWTEAESVAK--------------KVSSSVKDTFSAATEEVKESFK 136LGKEENAESASSSGT
Bra036674|Bra036674                          76 QELN---GVKEDLKVR---A-------- 89-------------------LAV--------------QVSSSVKDKFSAATEEVKESFK 114LGKEES------AGT
Carubv10015970m.g|Carubv10015970m            77 EELK---GVKEDLKVR---TKQ------ 92TTEQL--YNQVDGVWNEAEAAAQ--------------KVSSNVIDKLSAATEEVKESFK 135LGKEENAESVSSSGT
AT2G20510.1                                  77 EEFK---GVTEDLKVR---TKQ------ 92TTEKL--YKQADGVWTEAESAAK--------------KVSSSVKDKLSAASEEVKESFK 135LGKEENAESASSSGT
Carubv10024977m.g|Carubv10024977m            77 QELK---SVKEDLKVR---TKQ------ 92TTEQL--YKQVDGVWTEAESVAK--------------KVSSSVKDKLSAATEEVKESFK 135LGKEENAESASSSGT
AT2G36070                                    77 EELQ---GVKEDLKVR---TKQ------ 92TTEKL--YKQGQGVWTEAESVAK--------------KVSSSVKDKFSAATEEVKESFK 135LGKEESAESASSSGT
83588|83588                                  39 FK---SR----KCR---TKE------ 48TAEHL--YKHVDAAREEAETRAK---------------QVSSVIKEKISEASEQPRESPD 91AQEV---------PKED-
Eucgr.B01552|Eucgr.B01552.1                  98 EELK---GVKEELKVR---TKQ------ 113TTGQL--CKHVDGVWTEAEATAK--------------KVSANVREKISSATEEVKEQLG 156IGKQEESASASGSA
Eucgr.G01944|Eucgr.G01944.1                  28 LK---GVKEELKVR---TKQ------ 41TTGQL--YKHVDGVWTEAEATAK---------------KVSANVREKISSATEEVKEQLG 84IGKQEESASASGSAKHDA
Medtr4g029490|Medtr4g029490.1                71 EELK---GIKEGLKEK---TKQ------ 86TTEQL--YRQFDSVWKEAEAAAK--------------KVSHNVKEKISAAT-------- 121---------DFSTK
Medtr2g083690|Medtr2g083690.1                63 EELK---GVKEGLKEK---TKQ------ 78TTEQL--YKQFDGVWKEAEAAAK--------------KVSHNVKEKISAATEEVK--AG 119IGKQDSSGSTDSSTK
Glyma04g12120|Glyma04g12120.1                71 DELK---GVKEELKER---TKQ------ 86KTEKL--YKQVDEAWTEAEAAAR--------------KVSYNVKEKISAASEEVKETFG 129IGKQDSSGSTDSSTK
Glyma09g00505|Glyma09g00505.1                 1 --------------------------- 0---------------------------------------------------- 0--------------
GRMZM2G095695|GRMZM2G095695_T02              70 EKLD---VVKEDLKVR---TKK------ 85TTETI--YKRVDDVWSEAEETSK--------------KVTANIKEKMFAAKEEVKESFG 128VGKEESTSCRDGLPE
LOC_Os07g22700|LOC_Os07g22700.1              70 EKLS---GVKEDLKVR---TKQ------ 85TAETI--YKSVDDVLTEAEATSK--------------KVTANVKEKMSAATEEVKESFR 128LGKEDTSSCKDGSPE
Cucsa.280740|Cucsa.280740.1                  53 ELK---GVKEDLKVR---TKQ------ 67TTEQI--YKQVDGVWSEAEATAR---------------KVSADVKEKLSAATEEVKEAFG 110FSPKNSSGSTCSSTDH
GSVIVG01028335001|GSVIVT01028335001          78 EELK---GVKEELKVR---TKQ------ 93TTEQL--YKHVDGVWTEAEATAK--------------KVSANVKEKISAATEDVKETFG 136KGKQEFSESAGTSAK
PGSC0003DMG400022489|PGSC0003DMT40005790      1 --------------------------- 0---------------------------------------------------- 0--------------
30005.t000058|30005.m001292                  80 EELK---GVKEDLRIR---TKE------ 95TTEQL--YKHVDGAWTEAEATAK--------------KVSANVKEKISAAKEEVKETLN 138IGKQESSGSTKSSDK
Potri.002G038300|Potri.002G038300.1          79 EELK---GAKEELKVR---TKQ------ 94TTEQL--YKHVDGVWTEAEATAK--------------KVSANVKEKISAATEEVKETFG 137IGKE-SSESAGTSAK
Potri.005G224500|Potri.005G224500.1          79 EELK---GVKEELKVR---TKQ------ 94TTEKL--YKHVDCVWTEAEATAK--------------KVSANVKEKVSAATEEVKETFG 137IGKEESSESAGTSAK
CMJ253C|CMJ253CT                            136 RRGQLNDAEPVRASVQRAHRSR-------- 157------------------------------------------SAATSH------ 163----------
gi|17508985                                  68 QELNESDALKDARKKFEIVE-------- 87------------------------------KETLKSSEVVKQKIEELSDHMKKMVH 113--EIQKTEAGKKMTE
gi|33636719                                  89 RRLEESDVLQEARRKYKTIE-------- 108-------------------------------SETVRTSEVLRKKLGELTGTVKESLH 134--EVSKSDLGRKIK
YIL022W                                      80 GKLGESEAYKKAREAYLKAQ-------- 99------------------------------RG-STIVGKTLKKTGETMEH---IAT 121--KAWESELGKNTR-
gi|85117796                                 175 SANQIAESEAIRRARQAYEATS-------- 196-----------------------------GTVSSTAGKVVKTTATAVGK---GAQ 219--WTWETPVMKG

Cre16.g660800|Cre16.g660800.t1.2             60 GQQQ---SQQQ---QEQASSSASSSEQQAQNFYNNFKAGFEDL 96KNKAGAAAGAAAGAAGGAGAGAGGEPAAQRLIQTLAQDLRETLLPAQDITSATRAYTGPV 156
Vocar20010708m.g|Vocar20010708m              61 EQHE---Q--Q---Q---RQDSTSSSDHAQNFYNTFKAGYEHV 92KSKAA----------GAAGGGSGQEPAAKRLLQTLAQDLREVLLPAQDITSATRVYTGPV 142
Esi0086_0051                                244 DGKDGGEGKD-GAENEFVRASKEKFSGAQKALDENSLFSKLRVKTQAF 290REAVAGASSELFPSE-----GQKAESAVVKKLKQPKKEKKKKKK-----K-KDGKEKA
Phpat.004G075900|Phpat.004G075900.1          90 GE-SEK--QPSQSS-NETSSSSSSS-IPTSRVLLKKVSDSVRNA 128ASSAGNV---VHKMK-----EAKLVDSVRTGYNFLKEEMTSTTP-----R-RKPNTSASE 1
Phpat.012G024100|Phpat.012G024100.1          91 GE-SEE--SQSKFS-QNPSSSFPAS-VPSPQVVIKKVSDAFRNA 129ASSTGDV---MHRMR-----EAKLVDSVRTGYTFLKEEMNRTSP-----Q-RKPKYSAPD 1
Bra036478|Bra036478                         152 GNSKEEN---------HQQQQQSGTT-EGGQHTLFEKIKSSIS-- 184S---------------------PLDIARKGIDIVKDELRGGTP-----K-KKHLEYTPP
Bra036674|Bra036674                         124 GTSTEED---------HQQQQQTGTT-EGVQNTLFEKFKSSMS-- 156S---------------------PLDLARKGLDIVKDELRGGSS-----R-KKHLEYTPP
Carubv10015970m.g|Carubv10015970m           151 GTSEAEQ---------QQ-LQQSGST-E-ELPTFFEKLKSSIS-- 181SPKVSEA---FYKLK-----EAKALDFVKKGLDIVKNELCGNPS-----R-RKFLQCTPP
AT2G20510.1                                 151 RASQGEK---------Q----QSGST-E-ELHTFFAKFKSSLS-- 178SPKVSEV---FYRLK-----EAKPFDIVKQALDIVKDELRGNPS-----R-KKFLEHTPP
Carubv10024977m.g|Carubv10024977m           151 GTTEGEK---------QQ---QSGTT-E-EQHTFFGKFKSSIS-- 179SPMLSEA---LHKLK-----EAKPLDFAKKGLDIVKDELHGNPS-----K-RKHLEYTPP
AT2G36070                                   151 GTTEGEK---------QQ--QQSGST-E-EQDTFFGKFKSSIS-- 180SPKLSEA---FH----------KPLDFAKKGLDIVKDELRGNPS-----K-RKHLEYTPP
83588|83588                                 100 --KEHGG-TDSS-QQKAQQSA---P-GGGAFAGKVKSVL--- 130-----------DSMR-----IGSVASVAKDGYNLIVEELTSTRK-----V-KKSK----- 163
Eucgr.B01552|Eucgr.B01552.1                 171 IHDAHAKG-GNEGKST-EEKCKQAGSG-D-NTESFFGKYRTSFFSS 212SPKVSST---FQKLK-----GVKVVDLAKQGYDIVKDELSGSPS-----K-RKHMEHAPT
Eucgr.G01944|Eucgr.G01944.1                 103 HAKG-GNEGKST-EEKCKQAGSG-D-NTESFFGKYRTSFFSS 140SPKVSST---FQKLK-----GVKVVDLAKQGYDIVKDELSGSPS-----K-RKHMEHAPT 186
Medtr4g029490|Medtr4g029490.1               127 QNADAKQ-GSQKSPE-EEKNEESPSG-N-ASESLFGKFKSTF--S 165SPMVSTS---FQKLK-----DE------------ELSSNSP-----K-RQRIRF---
Medtr2g083690|Medtr2g083690.1               135 QDADAKQ-GRQTSPE-EEKNQESASG-N-ASESLFGKFKSTF--S 173SPKVSTS---FQKLK-----DAKIVDMTKKGYDILKEELSGNTP-----K-RQPVHSTP-
Glyma04g12120|Glyma04g12120.1               145 QGADANG-GNQTSRE-EEKNQQSGSS-K-DADSLFGKFKSTL--S 183SPNVSAA---FQKLK-----DAKLVDITKKGYDIVKEELSSTPT-----K-RKRVPFAS-
Glyma09g00505|Glyma09g00505.1                 1 ------------------------------------------ 0------------------------------------------------------- 0------
GRMZM2G095695|GRMZM2G095695_T02             144 GS-----KHEKTEAS-SHSDGTTEDA-T-DSHTLFTKLKSTISSA 180SPVVSGA---FAKLK-----DTKVSTLAKQGYEIVKDELSSNSS-----R-KKHQARHA
LOC_Os07g22700|LOC_Os07g22700.1             144 TS-----KHEYSETS-SHSDDKSQAG-T-SGYTLFNKLRSTLSSA 180SPVLSGA---FAKLR-----DTRVSTYAKQGYEIFKDELSSSSS-----R-KKRNHARHA
Cucsa.280740|Cucsa.280740.1                 127 GADAKKHGSEASSE-NAKDQHPGSS-G-SSETFFGKFKSSIP-- 165SPGISSA---FERLK-----STKLIDLAKRGCEIVKDELSGKPH-----K-KKHLEYEAS 2
GSVIVG01028335001|GSVIVT01028335001         152 SEADVNK-GS-SSSG-EEKHHKSGPS-D-TAETLFGKFKSSVSTV 191SPKVSLA---FEKLK-----EAKVLDLAKKGYGIVKDELSSNPS-----K-RKQMQRAAS
PGSC0003DMG400022489|PGSC0003DMT40005790      1 ------------------------------------------ 0------------------------------------------------------- 0------
30005.t000058|30005.m001292                 154 DGADVKD-DKKSSSG-EETDEQTGSS-D-NAESFFGKFKSSTP-- 192SSKLSSA---FQKLK-----EAKVTDFVKKGYDVVKDELYGNPS-----K-RKHLEYTPP
Potri.002G038300|Potri.002G038300.1         152 DGAGAEE-GTKASTG-EEADKQTGTG-D-TAESFFGKFKSRIP-- 190SSNVSSA---YQKLK-----EARVSEMMKKGYDVVKDELYGNTN-----K-RKHLEHTPP
Potri.005G224500|Potri.005G224500.1         153 DGVGAEE-CRKAFPG-EEADKQTGTS-D-TTETLFGKFKSSIP-- 191SSKVSSA---FQKLK-----EARVSEMMKKGYDVVKDELYGNTN-----T-RKHLEYTPP
CMJ253C|CMJ253CT                            164 -------ATS-TA----------SAA------------------- 171NREAGTA---LVPQG-----RV----------RSHDDDAQGDA-----STTTGYAS
gi|17508985                                 127 AGAEALK-QA----------RKA---------------------- 138AEHVEKV---AEKVG-----DTEVYKHVSTSMKTVKDEIDNI-------ADVRMYSRPE
gi|33636719                                 147 EGVEEAAK-TA----------KQS--------------------- 159AESVSKG---GEKLG-----RTAAFRALSQGVESVKKEIDDSVL------GQTGPYRRPQ
YIL022W                                     134 ------K-AA----------AAT---------------------- 139AKKLDES---EEPVR-----QTKIYKEV-------SEVIDDGES------SRYGGFITKE
gi|85117796                                 230 VR-------K-GA----------NIT------------------- 237GEVLDKA---TKPIR-----ETEAYKNV-------KDVIDDGSS------SRYGGWAE
```

```
Cre16.g660800|Cre16.g660800.t1.2             157 A--------------------AATYDGPTALVLAKQQATGWQKVWNSVSEKLGTIPGVA 195NLLNLKVTDTSAYKKGQE----------LVEDLKDKYETSDHPVVH
Vocar20010708m.g|Vocar20010708m              143 A--------------------SATYDGPTALVLARQQATGWQKAWDTVQEKLSGIPVVS 181KLLNLKVTDTAAYKKGQE----------LVEDLKDKYETSDHPVVH
Esi0086_0051                                 338 PV 339E----------GEDDEEEEEE-EEEKGGMGSLMIVKT----AGEAWERLQERLKESPIIQ 384DLLGAS-RVVASGSLGQGAKSAKDTVKDKVEDVQEAWETS
Phpat.004G075900|Phpat.004G075900.1          175 74D----------ARV----REA-PPENTTVNAIVPVVKKTTGWEKRWETLKEKARSHPAFK 219RIKTVTDHPVVTKG--QE----------LAEDIRERWETSDSPV
Phpat.012G024100|Phpat.012G024100.1          176 75D----------SAV----RDI-PPVNTTVNSIVPVVKKTTGWEKRWEDLKKKAKSHPAFK 220RFKTVTGHPVVTKG--QE----------LAEDIRERWETSDSPV
Bra036478|Bra036478                          217 216P----------PF---------TGVKSTRTDLVVTPTKQSKWQKKWESLREKMQAHPAFK 257RLSGIS-EPVVNKS--QE----------IAEDVVERWETSDNP
Bra036674|Bra036674                          189 188P----------PF---------TGVRSTRTDLVVTPTKQSKLQQKWESLREKMQAHPAFK 229RLSGMS-EPVVNKS--QE----------IAEDVVERWETSDNP
Carubv10015970m.g|Carubv10015970m            228 227P----------PF---------TGERSTRTEMVATALKQS----KWESFKEKMQSYPIYK 264CISRMS-EPVVNKS--QE----------IAEDVMEIWETSDNP
AT2G20510.1                                  225 224P----------PF---------TGERSMRTEMVVTQTKQSKLQQKWESFREKMQGSPVFK 265RLSGMS-EPVVNKS--QE----------IAEDVREIWETSDNP
Carubv10024977m.g|Carubv10024977m            226 225A----------PF---------TGERSTRTEMVITSTKQSKWQKKWESLRQKMQGYPVFK 266RLSGMS-EPVVNKS--QE----------IAEDVMERWETSDNP
AT2G36070                                    222 221P----------PF---------TGERSTRTEMVIMPTKQSKWQKKWESLREKMQGYPVFK 262RLSGMS-EPVVNKS--QE----------IAEDVREKWETSDNP
83588|83588                                  164 -----------P---------GFSRSSATDIVPVAKKTTGWRKHLDDLKEKATSHPLYR 202RFKNVKDHPVVQKT--NE----------IADEMRDRWETSDSPVVH
Eucgr.B01552|Eucgr.B01552.1                  259  258T----------S---------TVERSTRTDIVVLPSKQSPWSKKWEAFKAKVKGHPMFK 298RIGNI-----------------------AEDMRERWETSDS
Eucgr.G01944|Eucgr.G01944.1                  187 T----------S----------TVERSTRTDIVVLPSKQSPWSKKWEAFKEKVKGHPMFK 226RIGNVS-EPVVTKG--QE----------IAEDMRERWETSDSPVVH
Medtr4g029490|Medtr4g029490.1                194 193-------------------TGEISTKTDLVVMPSNQSWWSKKVDEFRDKVRRHPVSK 231NFVKYI-DPVKTTS--RD----VRSTPVIVDDVRDIIDRIDNP
Medtr2g083690|Medtr2g083690.1                219 218-------------------SGETSTKTDLVVMPSNQSWWSKKFDEIRDKVKSHPASK 256RFFKYT-DPVKTKS--QE----------MVDDLRDRIETSDNP
Glyma04g12120|Glyma04g12120.1                229 228-------------------SGETSTRTDLVVMPSKQSWWSKKFDEFREKVKGHPVSK 266RFLKYS-DPVKTKG--QE----------IVEDLRERYETSDSP
Glyma09g00505|Glyma09g00505.1                  1 ----------------------------------------------0----------------------------------------------
GRMZM2G095695|GRMZM2G095695_T02              227 226S----------A----------KVEKSTRTDLVLTPTKKTVLGEKWEEFKNKIRGHPVYR 266RVDEYT-KPVVTKG--QE----------VAEDVRERWETSDNP
LOC_Os07g22700|LOC_Os07g22700.1              227 226S----------AG---------TVEKSTRTELVIVPTKKSVLGEKWEAFKNKMRGHPAYK 267RVNEYT-KPVVNIG--QE----------VAEDVRERWETSDNP
Cucsa.280740|Cucsa.280740.1                  212 11A----------SP---------KVERSTRTDVVVLPSKQSRWSKKWEAFREKMQGHPVYK 252RVTGYS-EPVISRS--QE----------PKVLF----------I
GSVIVG01028335001|GSVIVT01028335001          238 237S----------AS---------PGERSTKTDIVIVPSKQSRWSKKWEALKD-KASHPVFK 277RISGLS-EPVVTKG--QE----------LAEDVRERWETSDNP
PGSC0003DMG400022489|PGSC0003DMT40005790       1 ---------------------------------------MQGHPVFK 8RFTGMS-EPVVTKS--QE---------IAEDIRERWETSDHPVVHK-------
30005.t000058|30005.m001292                  239 238P----------SF---------KGETSTRTDIVVLPSKQSRWNKKWEAFREKMQGHPLFK 279RFAGIS-EPVVTKS--QE----------IAEDMRERWETSDNP
Potri.002G038300|Potri.002G038300.1          237 236P----------AF---------SGEISTKTDVVVLPSKQSRWSKKWEAFREKMQGHPLFK 277RFSGLS-EPVVTKG--QE----------IAEDMRERWETSDSP
Potri.005G224500|Potri.005G224500.1          238 237P----------SF---------SGEISTKTDIAVLPSKQSRWSKKWEAIREKMQGHPLFK 278HFAGLS-EPVVTKG--HE----------IAEDMRDRWETSDSP
CMJ253C|CMJ253CT                             205 V- 205------------------------------------LNRIFSRFAG----SPFMR 220SVLEA--------------------------KERVSERLDES
gi|17508985                                  183 182ALTKRT--D--GFDLEKERVVEANDS-ATDV---TLHKDSKWYSGWKNFSES---NTYYH 231KLLDW--------------------------KIKYDESDNM
gi|33636719                                  206  205RLRKRT--EFAGDKFKEEKVFEPNEE-ALGV---VLHKDSKWYQQWKDFKEN---NVVFN 256RFFEM---------------------------KMKYDESDN
YIL022W                                      179 178QRRLKRERDLASG--KRHRAVKSNEDAGTAVVATNIESKESFGKKVEDFKEK---TVVGR 233SIQSL--------------------------KNKLWDESENP
gi|85117796                                  275 KE 276ERRKRREKWLKESAGKGPQILEEDPNAGTNVT---LHKDAAWKEAWRDFRDS---NKFVQ 330NVFGL-----------------------------KTVYEES

Cre16.g660800|Cre16.g660800.t1.2             232 K-------VEELKS 238SMFTGSEASRAMREIRVRDQAFDMNRFVQSVKLDA-PVVVKAFLKHDLDTLSQHCGPELM 297ERFAGIFKHFNEQGL-FEDPSILFIGDV
Vocar20010708m.g|Vocar20010708m              218 K-------VEDLKA 224RMFTGSEASRAMREIRVRDPAFDMNRFVQSVKLDA-PTVVRAFLKHDLEALSQHCGPELL 283ERFAGIFKHFNEQGV-FEDPSILFIGDV
Esi0086_0051                                 424 QHPLVYK-------LSSAWD 436SLTAESDEGIGVRELRRLDPSFSVEDWKRDIQELFLPEFMSAFLRGDVKLLKQWTGEACY 496NKLASEAKQRKADGM-VLDPHV
Phpat.004G075900|Phpat.004G075900.1          252 VHR-------IQDLNE 260SIFGETATAVAMREIRRHDPSFTFSDFLAEVQEEIRP-TLRAYLKGDFATLRKKCSREVV 319ERCQAERRALESQGI-FLDNEILHIS
Phpat.012G024100|Phpat.012G024100.1          253 VHR-------IQDMNE 261SLFGETATAVAMREIRRHDPSFTFSDFLAEMQEEIRP-TLRAYLKGDVPTLKKKCCREVL 320ERCQAERSALESQGI-FLSNEILHIS
Bra036478|Bra036478                          288 IVHK-------IQDLNE 297AVFNETDSGSTYKEIRRRDPSFSLTDFAAEVHEAIKP-VLSAYSKGDAETLKKYCSPEVI 356ERCTAELAALKGHDL-FFDHKILHI
Bra036674|Bra036674                          260 IVHK-------IQDLNE 269AVFNETDSGSTYKEIRRRDPSFSLPDFAAEVHEAIRP-VLSAYSKGDAEALNKYCSTEVI 328ERCTAERAALKSHGL-FFDHKILHI
Carubv10015970m.g|Carubv10015970m            295 IVHK-------IQDMNE 304IFLEETDSASAYEEIYGRDPSFSLQDFAAEVEEAIRL-VLDAYSKGDVETLKKYCSKEVI 363ERCPGELTYYQSHGI-FFDNKLLHV
AT2G20510.1                                  296 IVHK-------IQDMNE 305KFLKETDSASTYKEIRSRDPSFSLPDFAAEIEEVIKP-VLNAYSEGDVETLKKYCSKEVI 364ERCTAERTAYQTHGV-LFDNKLLHI
Carubv10024977m.g|Carubv10024977m            297 IVHK-------IQDINE 306KIFEETGSAATYKEIRRRDPSFSLPDFAAEVQEAIRP-VLHAYSKGDTETLKKYCSNELI 365ERCTAEHRAFQSHGY-FFDHKLLHI
AT2G36070                                    293 IVHK-------IQDMNE 302RIFEETGSASTYKEIRRRDPSFSLPDFVSEIQEAIRP-VLNAYSKGDAKTLKKYCSKELI 361ERCTAEHRAFTSQGY-FFDHKLLHV
83588|83588                                  237 K-------IQDLNE 243SFFGETATAAAFKEIRSRDPTFSFPDFVLEVQEDIRP-ILTAYLKGDYDTLRKKVCKEVV 302ERCRAEHRALQSQGL-YVDTKILYISEL
Eucgr.B01552|Eucgr.B01552.1                  317 PVVHK-------IQDLNE 327TIFQETDAAASMKEIRRRDPSFSLPEFVAEVQEVVKP-VLNAYIK-------------- 371--------------------ILH
Eucgr.G01944|Eucgr.G01944.1                  260 K-------IQDLNE 266TIFQETDAAASMKEIRRRDPSFSLPEFVAEVQEVVKP-VLNAYIKGDVETLKKYCSSEII 325ERCKAEHGAYQSHGI-FFDNRILHVSDV
Medtr4g029490|Medtr4g029490.1                268 IIDK-------IQRCTY 277SLYIREDE----------DVHGPLDDFVGEVQEAIKP-VLNAYIKGDFETLKKYCAPQLI 326ERCKAEHGAYKDRGI-FYDNKILHI
Medtr2g083690|Medtr2g083690.1                287 IINK-------IQDIND 296TIFQETDAALAHKEIHRRDPKFSLPEFVAEVQEAIKP-VLNAYIKGDVETLKKYCSPQLI 355ERCKAEHGAYKSHGI-FFDNKILHV
Glyma04g12120|Glyma04g12120.1                297 IIHK-------IQDIND 306SMFQETDAAISYKEIRQRDPYFSLPEFVGEVQEAIKP-VLNAYIKGDVETLKKYCSPELI 365ERCKAEHNAYQSHGI-FFDNKILHV
Glyma09g00505|Glyma09g00505.1                  1 ------ 0------------------------------------------------- 0------------------------------M--MGS
GRMZM2G095695|GRMZM2G095695_T02              297 VVQK-------IQDLNE 306SLLEETSAAVTFREIRQRDPSFSLSDFVADVQEMIKP-VLTAYSKGDAETLKNYCTKEVI 365ERCKGEREAYASQGI-FFDHKILHI
LOC_Os07g22700|LOC_Os07g22700.1              298 VVQK-------IQDLNE 307SIFEETATAVSFREIRQRDPSFSLPDFAGDVQEMIKP-VLTAYSKGDVKTLKKYCTKEVI 366ERCKGERDAYASQGI-FFDHKILHI
Cucsa.280740|Cucsa.280740.1                  274 DLI-------FHSINE 282TVFQESDAATSFKEIRRRDPSFSLPDFVAEVQEVIKP-VLTSYIKGDSETLKKHCSTEVI 341ERCKAEHRAYQSQGI-FFDNKILHIS
GSVIVG01028335001|GSVIVT01028335001          308 VVHK-------IQDLNE 317SVFGETAAAMSFKEIRRRDPSFSLPDFVSEVQEVIRP-VLNAYIKGDAETLKKYCSPEVI 376ERCKAEHGAYQTMGI-IFDNKILHI
PGSC0003DMG400022489|PGSC0003DMT40005790      43 IQDINE 48TVFGESTAALSFKEIRRRDPSFSLPEFVAEVQEVIRP-VLGAFFKGDSEVLKKYCSKEVI 107ERCKAEHQAFESQGI-IFDNKILHISDVEVRETKM--
30005.t000058|30005.m001292                  310 IVHK-------IQDVSD 319TIFQETDAAASFKEIRRRDPSFSLMDFVAEVQEAVRP-VLNAYIKGDLETLKKYCTSEVI 378TRCEAEHKAFQSHGI-FFDNKILHI
Potri.002G038300|Potri.002G038300.1          308 IVIK-------IQDVSD 317SIFQESDAAASFKEIRRKDPSFSLMDFVAEVQEAVRP-VLNAYIKGDIDTLKKYCTPEVI 376NRCEAEHKAFQAHGI-FFDNKILHI
Potri.005G224500|Potri.005G224500.1          309 IVHK-------IQDVSD 318SIFQESDAAASIKEIRRRDLSFSLMDFVAEVQEAIRP-VLNAYMKGDIETLKKYCTSEVI 377NRREAEHKAFEAHGI-FFDNKILHI
CMJ253C|CMJ253CT                             237 DHPVVNVFRTIHD------- 249RFFAENEMAQVIGAIRTLDPKFTISRFLVDIESRLIPTVLGAYLAGDLETLQEHCTEEAF 309AMMAASIHERRLSGI-VMDTRI
gi|17508985                                  247 AVRMMRGVTEKIGSVFS 263G---QNEVSEVLTEIHKIDANFDKQEWLRFCETKIIPNILEAFIRFDLEVLQSWCHERAY 320TQLSTVVKEYQKMHFSTKDSRIIDI
gi|33636719                                  271 AFIRASRALTDKVTDLLG 288GLFSKTEMSEVLTEILRVDPAFDKDRFLKQCENDIIPNVLEAMISGELDILKDWCYEATY 348SQLAHPIQQAKALGL-QFHSRILD
YIL022W                                      250 LIVVMRKITNKVG---- 262GFFAETESSRVVSQFKLMDPTFSNESFTRHLREYIVPEILEAYVKGDVKVLKKWFSEAPF 322NVYAAQQKIFKEQDV-YADGRILDI
gi|85117796                                  343 ENPLISTARSITDKIG---- 358SFFAENETAQVLKKLRELDPGFNMENFLMELREYILPEVLEAYVKGDVETLKLWLSEAQY 418SVYEALTKQYLQAGL-KSDGRI

Cre16.g660800|Cre16.g660800.t1.2             325 EIVEVRL--MDDDPFIIAQFHCQQLKCTRDKF 354-GNVVDGDA---NTIQRVYYFWGLQQERSPVVTAEGKVLPPRWVIKDMMWQSMLALV*- 407
Vocar20010708m.g|Vocar20010708m              311 EIVEVRL--MDDDPFIIAQFHCQQLKCTRDKF 340-GNVIDGSA---NQIQRVYYFWGLQQERSPVVTAEGKVLPPRWVIKDMMWQSMLALV*- 393
Esi0086_0051                                 518 LDIRQGEVLAIKADAGKANPTIALQFMCQQINCVRNKK 555-GEILEGAE---DDIRATYYILAFQREFND------DEAELRWRVVDMMVVGAFPWY*- 602
Phpat.004G075900|Phpat.004G075900.1          345 DVEIKETKL--LGNAPIIIINFQTQQIHCARNKD 376-GNIIEGAR---DDIHTVFYAWAMQQESPEETNR--GEFHTRWKLREMQQAGMQALI*- 427
Phpat.012G024100|Phpat.012G024100.1          346 DIEIKETKL--LGNSPIIIINFQTQQIHCARDKA 377-GNIIEGAR---DDIHTVFYAWAMQQESPEETSH--GEFQTRWKLREMQQAGIQALI*- 428
Bra036478|Bra036478                          381 SEVEVEETKM--MGTIPTIIIVRFQTQEIFCVRDKK 413-GNIKEGGQ---DTIHSVYYKWAMQQVEA---GE--ESMYPIWRLRDICKLGAAQALI* 462
Bra036674|Bra036674                          353 SEVEVEETKM--MGTTPIIIVR------------- 372-----------DTIHSVYYKWAMQQVEA---GE--ESMYPIWRLRDVHKLGAAQALI* 413
Carubv10015970m.g|Carubv10015970m            388 SEVSIQESKM--MGTSPVILVWFQTQEIYCVRDKN 420-GEIQDGGQ---DTIHTVYHEWAMQQVEAAELDE--DALYPIWRLREMLRDDVQALI*-- 471
AT2G20510.1                                  389 SEVSVSVTKM--MGDSPIIIAKFQTQEIYCVRDEN 421-GEIQEGGQ---DTIHTVYHEWAMQQVETTELGE--DAIYPIWRLREMCRNGVQALI*-- 472
Carubv10024977m.g|Carubv10024977m            390 SEVEIQETKM--MGTYPVILVRFQTQEIYCVRDKN 422-GKIKEGGQ---DTIHMVFYDWAMKQVEASELGE--EAIYPIWRLSEMRRAGIQALI*-- 473
AT2G36070                                    386 SEVDIQETKM--MGTTPVIIVRFQTQEIFCVRDQD 418-GKIKEGGQ---DTIHTVYYDWAMQQVDAAELGE--DAIYPIWRLREMLRAGVQALI*-- 469
83588|83588                                  330 EVRESKL--IGNEPVIILSFQTQQNYCVRDEF 359-GHIREGSKASIDDIRTILYAWAMQQVSLDEMDP--DEFTPRWRLREMQQTGFPALI*- 413
Eucgr.B01552|Eucgr.B01552.1                  375 VSDVDVRETKM--MGTSPIIIVGFQTQQIYCVRDKN 408-GAITEGGK---DTIHTVYYAWAMQQVDPEELGE--GAIFPIWRLREMQQIGVQALI*- 459
Eucgr.G01944|Eucgr.G01944.1                  353 DVRETKM--MGTSPIIIVGFQTQQIYCVRDKN 382-GAITEGGK---DTIHTVYYAWAMQQVDPEELGE--GAIFPIWRLREMQQIGVQALI*- 433
Medtr4g029490|Medtr4g029490.1                351 SDADVREVKI--LESSPFIIVVFQTQQIHCVRDRN 383-GEITEGGK---DTIHSVYYLWALQ-MDSEDHAE--DGIYLNWRLREMQQQGIQALI*- 433
Medtr2g083690|Medtr2g083690.1                380 SDADVREAKM--LESSPVIIVVFQTQQIYCVRDRN 412-GEITEGGK---DTIHTVFYLWALQQMEDGDHGE--DAIYYTWKLREMQQQGIQALI*- 463
Glyma04g12120|Glyma04g12120.1                390 SDLEIRETKM--MGSSPVIIVMFQTQQIYCVRDRN 422-GAITEGGK---DTIHTVFYFWALQQMDQEDRGE--DGIYLMWRLREMQQQGIQALI*- 473
Glyma09g00505|Glyma09g00505.1                  5 SPVIIVMFQTQQIYCVRDRN 24-GAITEGGK---DTIHTVFYFWALQQMDQEDRGE--DGIYLMWRLREMQQQGIQALI*- 75
GRMZM2G095695|GRMZM2G095695_T02              390 SEADVLETKM--FGSSPIIILRFQTQQIYCVRDRE 422-GQVTEGGQ---DTIQTVFYSWAMQLMDSDEVPEE-ESYYPVWRLREMQQAGIKALI*- 474
LOC_Os07g22700|LOC_Os07g22700.1              391 SDADVRETKM--MGSTPIIIVGFQTQQIYCVRDRE 423-GQVTEGGQ---DTIQTVFYAWAMQLMDSDEVPEE-ESYYPVWRLREIQQVGIKALI*- 475
Cucsa.280740|Cucsa.280740.1                  367 DVEVRETKM--MGSTPIIIVAFQTQQVYCVRDAN 398-GSIREGGK---DTIHTVYYAWAMQMLDPEEVGE--GALHAIWRIREMQQFGVQALI*- 449
GSVIVG01028335001|GSVIVT01028335001          401 SDVEVRETKM--MGTSPIIIVAFQTQQVYCVRSAD 433-GSIKEGGK---DTIHTVYYAWAMQQVDAEELGE--GAIYPIWRLREMQQLGVQALI*- 484
PGSC0003DMG400022489|PGSC0003DMT40005790     142 MGDSPIIILAFQTQQVYCIRDKL 164-GSIKEGGQ---DTIHTVYYAWAMQLVEAEELGE--GAIHPIWRLKEMQQLGVAALI*- 215
30005.t000058|30005.m001292                  403 SEVEVRETKM--MGTSPIIIVAFQTQQVHCVRDRD 435-GAITEGGQ---DTIHTVYYAWAMQQVEPEELGG--GAIYPIWKLREMQQLGIQALI-- 486
Potri.002G038300|Potri.002G038300.1          401 TDVEVRETKM--MGTSPIIIVVFQTQQVHCVRDRH 433-GAITEGGQ---DTIHTVYYAWAMRQVDAEELGG--GAIYPIWKLMEMQQLGVQTLI*- 484
Potri.005G224500|Potri.005G224500.1          402 SDVEVREIKM--MGTSPLIIVAFQTQQVHCIRDQN 434-GAITEGGQ---DTIHTVYYAWAMRQVDPEELGG--GAIYPIWKLMEMQQLGVQSLI*- 485
CMJ253C|CMJ253CT                             331 LDLDHVELVTG----------------------- 341------------------------------------------------- 341
gi|17508985                                  346 NKVEMATGKMMEQG--PVLIISFQVYMINVTKNAD 378-GKVVEGDP---DNPKRINHIWVLCRDVEEYNP------ALAWKLLEVHMQETPLAL-- 425
gi|33636719                                  372 IDNVDLAMGKMMEQG--PVLIITFQAQLVMVVRNPK 405-GEVVEGDP---DKVLRMLYVWALCRDQDELNP------YAAWRLLDISASSTEQIL-- 452
YIL022W                                      347 RGVEIVSAKLLAPQDIPVLVVGCRAQEINLYRKKK 381TGEIAAGDE---ANILMSSYAMVFTRDPEQIDD----DETEGWKILEFVRGGSRQFT*- 431
gi|85117796                                  440 LDIRGVDVLKARMLEPGDLPVFVITCRTQEVHVYKNAK 477TGKLAAGME---DKVQLVTYAIGITRIPEDVNN----PETRGWRLIEMQKSGRDYI--- 526
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