

gi|85089859 1 ----- 0 -----
YGR029W 1 ----- 0 -----
Esi0202_0015 1 ----- 0 -----
gi|17507677 1 ----- 0 -----
gi|85093549 ref|XP_959716.1 1 ----- 0 -----
Cre03.g173200|Cre03.g173200.t1.2 1 QQLPFS----NGSSSGKQWASARPLSHVY-----QGGAAWVAVPGLRHPSL 59HVSHPHAAVDRD 59HVSHPHAAVDRD
Vocar20008072m.g|Vocar20008072m 1 GAAPV----TRGSDARNWAARKSTTSSVGVSGLTGRGSDTDPGSRQGGIPAAATANPCP 64LLSVP-PCWGAIKPRN-----QHQLKT-----
CMT484C|CMT484C 1 ----- 0 -----
gi|66823895 1 ----- 0 -----
Cre14.g633000|Cre14.g633000.t1.2 1 SEQPVVNAVAALGASV----SQAPAGPVDGTAVALGAGTH----- 96-----MPNAAA-----VSEAA-----AT-----FAARK
gi|54112432 ref|NP_005253.3 1 ----- 0 -----
Potri.001G296000|Potri.001G296000.1 1 ----- 0 -----
Medtr8g045480|Medtr8g045480.1 1 ----- 0 -----
Glymal3g26970|Glymal3g26970.1 1 ----- 0 -----
Glymal5g38020|Glymal5g38020.3 1 ----- 0 -----
Phpat.019G062000|Phpat.019G062000.1 1 ----- 0 -----
GRMZM2G114234|GRMZM2G114234.T01 1 ----- 0 -----
LOC_0e03g10850|LOC_0e03g10850.1 1 ----- 0 -----
Cucsa.097440|Cucsa.097440.1 1 ----- 0 -----
Bra014223|Bra014223 1 ----- 0 -----
AT1G49880 1 ----- 0 -----
Carubv10010320m.g|Carubv10010320m 1 ----- 0 -----
28152.t000030|28152.m000901 1 ----- 0 -----
Potri.009G090200|Potri.009G090200.1 1 ----- 0 -----
Eucgr.G01264|Eucgr.G01264.1 1 ----- 0 -----
GSVIVG01037859001|GSVIVT01037859001 1 ----- 0 -----
PGSC0003DMG400002983|PGSC0003DMT40000772 1 ----- 0 -----
105740|105740 1 ----- 0 -----
Phpat.002G149100|Phpat.002G149100.1 1 ----- 26---VDKIRWVWPNPKRGG-----LQKIMSHEPI---AGML---NAVGN

gi|85089859 1 ---MARRPHITM 10LVVGVV----LFFVITTYLSSSG-----SS-GVVQHSE-T-L- 40---DLGGSS-----GSDGHSKS---GDGSK-S
YGR029W 28 KPC--RSCNTHL 37-DQVYVWG-----KISNGLN-N----- 52---L-----SSNGKLAG-----TGAL
12 ABCDPAADRA 43-DTAKGR-----MAARKIKKASST 43---T-----ADGKAG-----SQAQ
gi|17507677 1 ----- 0 -----
gi|85093549 ref|XP_959716.1 43 KPC--RSTSTSP 52-AMASQAK-----HTLKTSH-DMSST 71---A-----
Cre03.g173200|Cre03.g173200.t1.2 57 ----- 0 -----
Vocar20008072m.g|Vocar20008072m 57 ----- 0 -----
CMT484C|CMT484C 57 ----- 0 -----
gi|66823895 1 ----- 0 -----
Cre14.g633000|Cre14.g633000.t1.2 54 ----- 0 -----
gi|54112432 ref|NP_005253.3 12 ----- 0 -----
Potri.001G296000|Potri.001G296000.1 12 ----- 0 -----
Medtr8g045480|Medtr8g045480.1 5 ----- 0 -----
Glymal3g26970|Glymal3g26970.1 5 ----- 0 -----
Glymal5g38020|Glymal5g38020.3 5 ----- 0 -----
Phpat.019G062000|Phpat.019G062000.1 1 MGAGCENMLL 12KIKVMSAGVH-----LSRIQARFSS-----D-----VSENEE---SGDEE---D---DDSETQ
GRMZM2G114234|GRMZM2G114234.T01 4 TGW--NFAEVL 130VAAFSRELLIA-P-----DA-----GLDDHRLRPLIA 41-LSLSPFPF-----
LOC_0e03g10850|LOC_0e03g10850.1 6 WGWGNSPEFV 17HVAAFSRELLIA-P-----DA-----MPDEARLRPLLS 45-LSLSPFPF-----
Cucsa.097440|Cucsa.097440.1 5 ----- 0 -----
Bra014223|Bra014223 5 ----- 0 -----
AT1G49880 5 ----- 0 -----
Carubv10010320m.g|Carubv10010320m 17 ----- 0 -----
28152.t000030|28152.m000901 5 ----- 0 -----
Potri.009G090200|Potri.009G090200.1 5 ----- 0 -----
Eucgr.G01264|Eucgr.G01264.1 5 ----- 0 -----
GSVIVG01037859001|GSVIVT01037859001 1 ----- 0 -----
PGSC0003DMG400002983|PGSC0003DMT40000772 1 ----- 0 -----
105740|105740 1 ----- 0 -----
Phpat.002G149100|Phpat.002G149100.1 61 AVQCGHRAMEGLV 73QQGIRSNLCKIE-LPNFLRGRKQOAS-----QVRELVEEQEPPARA---114-A-VSPANVLMQAQGANNAAYTGVNGSO

gi|85089859 63 AFG-IS-DNIPKGGSTAPLENATAK 86AELGRASQRLPHTMMARFPTTAEESLAKRTY-----TOLFARL 126VPCGDCQASHQKLLK
YGR029W 66 TGE-NS-EMRGSSTIRKVPFPH 87VCGRSGSRLPHTMMARFPTTAEESLAKRTY-----LNGHPTL 127VPCGDCQASHQKLLK
Esi0202_0015 57 TSSGSA-ETDEHASSSDGCPDK 81BELGRATWFLHLLAAQYPPDPTRQOKDVKEL-----VQGLGL 121VPCGDCQASHQKLLK
gi|17507677 39 B-----STSTGAKLHGCVK 54BELGRATWFLHLLAAQYPPDPTRQOKDVKEL-----LNSLQGT 94VPCGDCQASHQKLLK
gi|85093549 ref|XP_959716.1 73 B-----S-TAASATLSTRRTDCAVD 93BELGRATWFLHLLAAQYPPDPTRQOKDVKEL-----MSLQGT 133VPCGDCQASHQKLLK
Cre03.g173200|Cre03.g173200.t1.2 115 PLA-----AG--AASMAAORAAATAK 150AEVGRATWFLHLLAAQYPPDPTRQOKDVKEL-----VDCLTR 190VPCGDCQASHQKLLK
Vocar20008072m.g|Vocar20008072m 163 PVE-----APTSGVASAAAAGLAAA 194AEVGRATWFLHLLAAQYPPDPTRQOKDVKEL-----VDCLTR 234VPCGDCQASHQKLLK
CMT484C|CMT484C 91 W-----LFTMLTKAPGKPFQDKPWR 115AELGRAGTWFLHLLAAQYPPDPTRQOKDVKEL-----IASFAAL 155VPCGDCQASHQKLLK
gi|66823895 94 WGNMNDNMKNMNSDYKWRPFPPT 191BELGRATWFLHLLAAQYPPDPTRQOKDVKEL-----LQSPKV 159VPCGDCQASHQKLLK
Cre14.g633000|Cre14.g633000.t1.2 134 ACAAEAGGAAGTAGGAGGASGAPPLCPDPT 232WELGRATWFLHLLAAQYPPDPTRQOKDVKEL-----VGLAEP 263VPCGDCQASHQKLLK
gi|54112432 ref|NP_005253.3 75 VDFK--M--MRTQKRDFTFRDCCPDR 99BELGRATWFLHLLAAQYPPDPTRQOKDVKEL-----IMFSEK 139VPCGDCQASHQKLLK
Potri.001G296000|Potri.001G296000.1 65 -----SK--TYPANIDTPTGSAABAATK 85BELGRATWFLHLLAAQYPPDPTRQOKDVKEL-----VQGLGL 121VPCGDCQASHQKLLK
Medtr8g045480|Medtr8g045480.1 47 LK--AT--SVCPRPDPVLRKASHTVTK 69BELGRATWFLHLLAAQYPPDPTRQOKDVKEL-----VQGLGL 121VPCGDCQASHQKLLK
Glymal3g26970|Glymal3g26970.1 51 SRT--T--SGLPATAVLRKASHTVTK 74BELGRATWFLHLLAAQYPPDPTRQOKDVKEL-----VQGLGL 121VPCGDCQASHQKLLK
Glymal5g38020|Glymal5g38020.3 54 AKT--S--SGLPATAVLRKASHTVTK 77BELGRATWFLHLLAAQYPPDPTRQOKDVKEL-----VQGLGL 121VPCGDCQASHQKLLK
Phpat.019G062000|Phpat.019G062000.1 62 LTV--LA--GDLSELPVLRKASHTVTK 85BELGRATWFLHLLAAQYPPDPTRQOKDVKEL-----VQGLGL 121VPCGDCQASHQKLLK
GRMZM2G114234|GRMZM2G114234.T01 50 -----MP--PQPEVRKKEKDAKAPTK 70EEVGRATWFLHLLAAQYPPDPTRQOKDVKEL-----MHTLSRL 110VPCGDCQASHQKLLK
LOC_0e03g10850|LOC_0e03g10850.1 54 HP--SP--PPPPPEVLRKASHTVTK 76EEVGRATWFLHLLAAQYPPDPTRQOKDVKEL-----MHTLSRL 110VPCGDCQASHQKLLK
Cucsa.097440|Cucsa.097440.1 56 HD--TT--SS--MOSIDVHTPAAPVTK 76EEVGRATWFLHLLAAQYPPDPTRQOKDVKEL-----MHTLSRL 110VPCGDCQASHQKLLK
Bra014223|Bra014223 52 IA--TN--SS--OKLPLKSGPVTK 74BELGRATWFLHLLAAQYPPDPTRQOKDVKEL-----MHTLSRL 110VPCGDCQASHQKLLK
AT1G49880 66 IA--TN--SS--OKLPLKSGPVTK 78BELGRATWFLHLLAAQYPPDPTRQOKDVKEL-----MHTLSRL 110VPCGDCQASHQKLLK
Carubv10010320m.g|Carubv10010320m 66 IA--TN--SS--OKLPLKSGPVTK 78BELGRATWFLHLLAAQYPPDPTRQOKDVKEL-----MHTLSRL 110VPCGDCQASHQKLLK
28152.t000030|28152.m000901 59 RD--TS--SPVCPKDVLRKASHTVTK 81BELGRATWFLHLLAAQYPPDPTRQOKDVKEL-----MHTLSRL 110VPCGDCQASHQKLLK
Potri.009G090200|Potri.009G090200.1 56 AN--FQ--APGPEVLRKASHTVTK 78BELGRATWFLHLLAAQYPPDPTRQOKDVKEL-----MHTLSRL 110VPCGDCQASHQKLLK
Eucgr.G01264|Eucgr.G01264.1 52 IA--TN--SS--OKLPLKSGPVTK 74BELGRATWFLHLLAAQYPPDPTRQOKDVKEL-----MHTLSRL 110VPCGDCQASHQKLLK
GSVIVG01037859001|GSVIVT01037859001 1 -----M--LQHSSEPKKESGPKVTK 79BELGRATWFLHLLAAQYPPDPTRQOKDVKEL-----MHTLSRL 110VPCGDCQASHQKLLK
PGSC0003DMG400002983|PGSC0003DMT40000772 1 -----M--LQHSSEPKKESGPKVTK 79BELGRATWFLHLLAAQYPPDPTRQOKDVKEL-----MHTLSRL 110VPCGDCQASHQKLLK
105740|105740 1 -----M--LQHSSEPKKESGPKVTK 79BELGRATWFLHLLAAQYPPDPTRQOKDVKEL-----MHTLSRL 110VPCGDCQASHQKLLK
Phpat.002G149100|Phpat.002G149100.1 142 QEEQT--ES--FFPEFRVPEISSGAVTK 167EDLGRATWFLHLLAAQYPPDPTRQOKDVKEL-----MHTLSRL 207VPCGDCQASHQKLLK

gi|85089859 142 KYFPWTSGRNAAAGQACVANNENRKRKIQEQQDNK-----IGDFVD 183C-G--GDEGAKKAGEAGAEVKTETKEDLKM----- 216
YGR029W 143 EAPVQVRESEPLGRNMCVHNNRKRKIQEQQDNK-----WEHRK 184DG--WDE----- 189
Esi0202_0015 137 KLEPVDVSRVALHMACOQHNLNKKKCKTGCPL-PALDERK 180GKFKSVEGG-----MEGV*----- 194
gi|17507677 111 SPKVRESREPAALWCCGHHNNEKTKPFPCRD--VMWRW 151DG-----WKDG-----SCDY*----- 161
gi|85093549 ref|XP_959716.1 149 KEFKTGRSDRDFEQLCABHNENRKRKIQEQQDNK-----WQERWR 190TG-----WKDG-----SCD*----- 199
Cre03.g173200|Cre03.g173200.t1.2 187 TVRRDPPAVGSGREFRWLCCVHNVNRSRIGLTPVNDL-----VEARWA 247PLG--CSAEAAA-AGEPAAAGKCGCGLLWGAAGKR*----- 281
Vocar20008072m.g|Vocar20008072m 237 LVRRDPPVSSGPAFRWLCVHNVNRSRIGLTPVNDL-----VESRWA 291PLG--CSAEAAA-AGEPAAAGKCGCGLLWGAAGKR* 331
CMT484C|CMT484C 170 RHPPLLESQPVKWRANNAWLRIGFPTCDLQDLDRWR 215DCH--CDEE-----PQNMIRARLIERFPNAG 243
gi|66823895 173 MKETPEILDSQDFANLCAHANNVNLGKPTDFCDL-----INKRW 216INN--NNEFH-----PQNMIRARLIERFPNAG 243
Cre14.g633000|Cre14.g633000.t1.2 216 BQVAARFPQVGSARENMLWLCGHNNEVNLGKPLDFCAR-----VGERWR 320EPG--AD-G-----SCD*----- 329
gi|54112432 ref|NP_005253.3 154 CRNHPTDTRACTQWLCVHNVNRSRIGLTPVNDL-----VDERWR 196DGW--KD-G-----SCD----- 205
Potri.001G296000|Potri.001G296000.1 122 ---C-TWVHTTFFSOWLCHVNVNRSRIGLTPVNDL-----VDARWG 160KLD--CE-N-----ACDLSR*----- 165
Medtr8g045480|Medtr8g045480.1 125 EWPVQAGSABFSSOWLCHVNVNRSRIGLTPVNDL-----VDARWG 160KLD--CE-N-----ACDLSR*----- 165
Glymal3g26970|Glymal3g26970.1 130 ANPVAQGSABFSSOWLCHVNVNRSRIGLTPVNDL-----VDARWG 173KLD--CE-N-----ACDLSR*----- 197
Glymal5g38020|Glymal5g38020.3 131 ANPVAQGSABFSSOWLCHVNVNRSRIGLTPVNDL-----VDARWG 174KLD--CE-N-----ACDLSR*----- 200
Phpat.019G062000|Phpat.019G062000.1 143 ANPVAQGSABFSSOWLCHVNVNRSRIGLTPVNDL-----VDARWG 182TFN--CE-G-----ACDLSR*----- 196
GRMZM2G114234|GRMZM2G114234.T01 126 ANPVAQGSABFSSOWLCHVNVNRSRIGLTPVNDL-----VDARWG 167KLD--CE-N-----ACDLSR*----- 188
LOC_0e03g10850|LOC_0e03g10850.1 132 ANPVAQGSABFSSOWLCHVNVNRSRIGLTPVNDL-----VDARWG 173KLD--CE-N-----ACDLSR*----- 194
Cucsa.097440|Cucsa.097440.1 132 ANPVAQGSABFSSOWLCHVNVNRSRIGLTPVNDL-----VDARWG 173KLD--CE-N-----ACDLSR*----- 194
Bra014223|Bra014223 130 ANPVAQGSABFSSOWLCHVNVNRSRIGLTPVNDL-----VDARWG 173KLD--CE-N-----ACDLSR*----- 189
AT1G49880 132 ANPVAQGSABFSSOWLCHVNVNRSRIGLTPVNDL-----VDARWG 173KLD--CE-N-----ACDLSR*----- 191
Carubv10010320m.g|Carubv10010320m 144 ANPVAQGSABFSSOWLCHVNVNRSRIGLTPVNDL-----VDARWG 185KLD--CE-N-----ACDLSR*----- 203
28152.t000030|28152.m000901 135 VNPVQAGSHAFSSOWLCHVNVNRSRIGLTPVNDL-----VDARWG 176KLD--CE-N-----ACDLSR*----- 196
Potri.009G090200|Potri.009G090200.1 157 VNPVQAGSHAFSSOWLCHVNVNRSRIGLTPVNDL-----VDARWG 198KLD--CE-N-----ACDLSR*----- 218
Eucgr.G01264|Eucgr.G01264.1 136 ANPVAQGSABFSSOWLCHVNVNRSRIGLTPVNDL-----VDARWG 175KLD--CE-N-----ACDLSR*----- 195
GSVIVG01037859001|GSVIVT01037859001 135 ANPVAQGSABFSSOWLCHVNVNRSRIGLTPVNDL-----VDARWG 175KLD--CE-N-----ACDLSR*----- 198
PGSC0003DMG400002983|PGSC0003DMT40000772 79 VQAGSABFSSOWLCHVNVNRSRIGLTPVNDL-----VDARWG 177KLD--CE-N-----ACDLSR*----- 196
105740|105740 64 RANSVDLSQWMCVHNVNRSRIGLTPVNDL-----VDARWG 101ALH--CD-G-----ACDLSR*----- 120
Phpat.002G149100|Phpat.002G149100.1 220 ILKAYPVKADSGAELAQWCVHNVNRSRIGLTPVNDL-----VDARWG 264ALH--CDEAG-----ACDLSR*----- 283

