

Vocar20009060m 1 -----MLRG----- 4--MEMEKYVEYQNSILSKKTFYGFIPLVLFKGRW-SMKNPNIAE
gi|66811268 1 0--NDLAKKLEQAVDVIIVYGGPHVHWGIPAVLHVGMLTRRBRPTTG
Cre10.g437500.t1.2 1 10--PRKKSAPLLEKVLAVAKPIRNGIPFVLLMGK-SEPPFLLE
gi|298707615 1 9--DGHAVAAQATIKKESQAMMWRKAVITHYGFIPLVIIIGMN-SEPKPFLS
Rucgr.H00014 1 19DGHAVAAQATIKKESQAMMWRKAVITHYGFIPLVIIIGMN-SEPKPFLS
PGSC0003DMG402013687 1 26AVAVTTFVKKWSTWAKKAKVITHYGFIPLVIIIGMN-SEPKPFLS
PGSC0003DMG400021021 1 25AVAVVGGKFKWSTWAKKAKVITHYGFIPLVIIIGMN-SEPKPFLS
Medtr3g061970 1 20--RSMIDSVKWKTWGLKHKRVTHYGFIPLVIIIGMN-SDQKPOLY
30115.t000065 1 25--KSTIQCKEWSFWLKKRKYVITHYGFIPLVIIIGMN-SEPKPOLY
Potri.0060077500 1 24--KSAQYFKWSTWAKKAKVITHYGFIPLVIIIGMN-SEPKPOLY
Potri.018G145400 1 24--KSAQYFKWSTWAKKAKVITHYGFIPLVIIIGMN-SEPKPOLY
Potri.T161400 1 24--KSAQYFKWSTWAKKAKVITHYGFIPLVIIIGMN-SEPKPOLY
Potri.018G146500 1 24--KSAQYFKWSTWAKKAKVITHYGFIPLVIIIGMN-SEPKPOLY
Medtr3g055500 1 20--RSMIDSVKWKTWGLKHKRVTHYGFIPLVIIIGMN-SDQKPOLY
Cucsa.073030 1 23--KSAQAFKEWTTAVKAKVITHYGFIPLVIIIGMN-SEPKPOLY
Glyma05g36420 1 22--RSCCHKEWTTAVKAKVITHYGFIPLVIIIGMN-SEPKPOLY
Glyma08g03150 1 22--RSCCHKEWTTAVKAKVITHYGFIPLVIIIGMN-SEPKPOLY
LOC.Oe05g50654 1 33AAAARRSVKRWSTWAKKAKVITHYGFIPLVIIIGMN-SEPKPOLY
59958|59958 1 8ASDAARKVLEKWFVAMKRLKTAHYGFIPLVIIIGMN-SEPKPOLY
Phpat.014G076800 1 MHRRLLEETLNGRHSVAIHRVCLLLFLALEKSCA--VERSK--Q-TDMAKV 48EPVGGKLLIKWFWLILKAKTIVTHYGFIPLVIIIGMN-SEPKPOLY
Phpat.017G070000 1 48EPVGGKLLIKWFWLILKAKTIVTHYGFIPLVIIIGMN-SEPKPOLY
GRMZM2G339503 1 27AAAATVRLKAWTWTLSKAVVAHYGFIPLVIIIGMN-SEPKPOLY
Carubv10021245 1 25SAPKFDVLPKFWNSLKKAKVITHYGFIPLVIIIGMN-SEPKPOLY
AT1G64220 1 25SAPKFDVLPKFWNSLKKAKVITHYGFIPLVIIIGMN-SEPKPOLY
Bra027687 1 19SSSKYVFKWSTWAKKAKVITHYGFIPLVIIIGMN-SEPKPOLY
Bra027750 1 20SSSKYVFKWSTWAKKAKVITHYGFIPLVIIIGMN-SEPKPOLY
Bra025479 1 13--ALBLKRWNSLKKAKVITHYGFIPLVIIIGMN-SEPKPOLY
Bra041087 1 13--ALBLKRWNSLKKAKVITHYGFIPLVIIIGMN-SEPKPOLY
Carubv10006750 1 22DKKRFVVKWNSLKKAKVITHYGFIPLVIIIGMN-SEPKPOLY
AT5G41685 1 23DDKRFVVKWNSLKKAKVITHYGFIPLVIIIGMN-SEPKPOLY
YNL070W 1 4PFIILSDSKERIKLITLTHVAHYGFIPLVIIIGMN-SEPKPOLY
gi|85101402 1 0-MFALSDSKERIKLIDISRVVHYGYLPLIILYGYTRSVPFPIIR
gi|17557031 1 0-MFALSDSKERIKLIDISRVVHYGYLPLIILYGYTRSVPFPIIR
gi|9506859 1 0-MVLSFAKQRLQQLFKGSGFAIRWGFVFPVVLGFKKGADEGMP--

Vocar20009060m 5 FIFGPGIMEQ- 4-----KW--KKLNACFADFLVTVAVYVLP- KSGRTDRSPFTAGSPA 44SKAAHNPLLNRLDQLPHTQLPHTSNAQSIQ
gi|66811268 45 QMM-WLG* 55----- 55-----
Cre10.g437500.t1.2 56 QMM-WLG* 61----- 61-----
gi|298707615 53 QMM-WLG* 57----- 57-----
Rucgr.H00014 66 QLL-SP*QPHDAS 77PSFLPQPHFLFELQ-ELCPTCYFDLHLNLTNYSLIVSFKHRRGRRHT--AASLPA 1338GCSNNSVSSPGLKRTVWGE----ENT-
PGSC0003DMG402013687 73 QLL-SP* 78----- 78-----
PGSC0003DMG400021021 72 QLL-SP* 77----- 77-----
Medtr3g061970 65 QLL-SPVRRRCL 76FDGV--LWNQSGFVVCFWDF* 96-----
30115.t000065 70 QLL-SP* 75----- 75-----
Potri.0060077500 69 QLL-SP* 74----- 74-----
Potri.018G145400 69 QLL-SP* 74----- 74-----
Potri.T161400 69 QLL-SP* 74----- 74-----
Potri.018G146500 69 QLL-SP* 74----- 74-----
Medtr3g055500 65 QLL-SP*TTISNMV 76SELV--ELKG-RL--NLFTNQVRV--LVV 99RGCIKKNPSPITLDK-Q-DSGE----EPIKR
Cucsa.073030 68 QLL-SP* 73----- 73-----
Glyma05g36420 67 QLL-SP* 72----- 72-----
Glyma08g03150 66 QLL-SP* 72----- 72-----
LOC.Oe05g50654 80 QLL-SPH* 85----- 85-----
59958|59958 56 LF-SPV* 60----- 60-----
Phpat.014G076800 95 QLL-SPV* 100----- 100-----
Phpat.017G070000 52 LF-SPV* 56----- 56-----
GRMZM2G339503 74 QLL-SPV* 79----- 79-----
Carubv10021245 72 QLL-SPV* 77----- 77-----
AT1G64220 72 QLL-SPV* 77----- 77-----
Bra027687 66 QLL-SPV* 71----- 71-----
Bra027750 67 QLL-SPV* 72----- 72-----
Bra025479 56 QLL-SPV* 61----- 61-----
Bra041087 56 QLL-SPV* 61----- 61-----
Carubv10006750 69 QLL-SPV* 74----- 74-----
AT5G41685 70 QLL-SPV* 75----- 75-----
YNL070W 53 LF-SPLSV* 60----- 60-----
gi|85101402 48 LF-SPLS 53----- 53-----
gi|17557031 47 LF-SPLS 53----- 53-----
gi|9506859 46 LF-SPLS 53----- 53-----

Vocar20009060m 78 VQVQVQVRLHNTAPRTPAYPTRLM 104LSYSSDGFNATSTGRRCSCTPFISSVIGRSPNSIQISKQSIQAV* 151
gi|66811268 56 ----- 55----- 55-----
Cre10.g437500.t1.2 62 ----- 61----- 61-----
gi|298707615 58 ----- 57----- 57-----
Rucgr.H00014 158 T----- 78----- 78----- 164
PGSC0003DMG402013687 79 ----- 77----- 77-----
PGSC0003DMG400021021 78 ----- 77----- 77-----
Medtr3g061970 97 ----- 96----- 96-----
30115.t000065 76 ----- 75----- 75-----
Potri.0060077500 74 ----- 74----- 74-----
Potri.018G145400 75 ----- 74----- 74-----
Potri.T161400 75 ----- 74----- 74-----
Potri.018G146500 74 ----- 74----- 74-----
Medtr3g055500 124 RQS 126LAYK----- PVS-----*-- 133
Cucsa.073030 74 ----- 73----- 73-----
Glyma05g36420 73 ----- 72----- 72-----
Glyma08g03150 73 ----- 72----- 72-----
LOC.Oe05g50654 86 ----- 85----- 85-----
59958|59958 61 ----- 60----- 60-----
Phpat.014G076800 101 ----- 100----- 100-----
Phpat.017G070000 57 ----- 56----- 56-----
GRMZM2G339503 80 ----- 79----- 79-----
Carubv10021245 78 ----- 77----- 77-----
AT1G64220 78 ----- 77----- 77-----
Bra027687 72 ----- 71----- 71-----
Bra027750 73 ----- 72----- 72-----
Bra025479 62 ----- 61----- 61-----
Bra041087 62 ----- 61----- 61-----
Carubv10006750 75 ----- 74----- 74-----
AT5G41685 76 ----- 75----- 75-----
YNL070W 61 ----- 60----- 60-----
gi|85101402 54 ----- 53----- 53-----
gi|17557031 59 ----- 58----- 58-----
gi|9506859 56 ----- 55----- 55-----