

CMB021C|CMB021CT 1 0 ---MVFMCMFVANGFV---GRFDASGQLQMGQKL
CMV086C|CMV086CT 1 0
gi|17555558|ref|NP\_497429.1| 1 0
gi|1542947 1 0
YLR259C 1 0
gi|164428039 1 0
gi|66806233 1 0
CMQ270C|CMQ270CT 1 0
405358|405358 1 0
Bsi0161\_0060 1 0
GRMZM2G0|GRMZM2G074790\_T01 1 0
LOC\_Os05g46290|LOC\_Os05g46290.1 1 0
Cucsa.360540|Cucsa.360540.1 1 0
Medtr8g017080|Medtr8g017080.1 1 0
Glyma07g01190|Glyma07g01190.1 1 0
Glyma08g20560|Glyma08g20560.1 1 0
Glyma08g20560|Glyma08g20560.2 1 0
Eucgr.F03134|Eucgr.F03134.1 1 0
MATNGPMGVLDLSNQHRISLLLVE---PYQNPCCRRGVAHVRRNPRELGELELALIP 57RRHLRNPVLYCCVYFLGKCGEGEMFR-IAAKLASSISHGY---SKKL
GSVIVG01016859001|GSVIVT01016859001 1 0
Bra001524|Bra001524 1 0
AT3G13860 1 0
Carubv10013333m.g|Carubv10013333m 1 0
PGSC0003DMG40002585|PGSC0003DMT4000664 1 0
Potri.003G037400|Potri.003G037400.1 1 0
28694.t000010|28694.m000667 1 0
Potri.003G039600|Potri.003G039600.1 1 0
74977|74977 1 0
Bra021836|Bra021836 1 0
Cre06.g309100|Cre06.g309100.t1.2 1 0
Vocar20007800m.g|Vocar20007800m 1 0
Bra005514|Bra005514 1 0
Bra022931|Bra022931 1 0
AT2G33210 1 0
Carubv10022887m.g|Carubv10022887m 1 0
Cucsa.078710|Cucsa.078710.1 1 0
LOC\_Os03g04970|LOC\_Os03g04970.1 1 0
GRMZM2G458208|GRMZM2G458208\_T01 1 0
GRMZM2G416120|GRMZM2G416120\_T01 1 0
LOC\_Os10g32550|LOC\_Os10g32550.1 1 0
Potri.002G252900|Potri.002G252900.1 1 0
PGSC0003DMG400011575|PGSC0003DMT40003026 1 0
Bra001934|Bra001934 1 0
AT3G23990 1 0
Carubv10013241m.g|Carubv10013241m 1 0
PGSC0003DMG401027165|PGSC0003DMT40006985 1 0
30204.t000086|30204.m001817 1 0
Potri.001G054400|Potri.001G054400.1 1 0
Potri.003G173900|Potri.003G173900.1 1 0
Glyma10g25630|Glyma10g25630.1 1 0
Glyma20g19980|Glyma20g19980.1 1 0
Glyma10g33680|Glyma10g33680.1 1 0
Glyma20g33910|Glyma20g33910.1 1 0
Medtr1g090140|Medtr1g090140.1 1 0
Medtr1g090140|Medtr1g090140.1 1 0
29904.t000134|29904.m003020 1 0
GSVIVG01029025001|GSVIVT01029025001 1 0
Cucsa.383180|Cucsa.383180.1 1 0
Eucgr.H02866|Eucgr.H02866.1 1 0
85251|85251 1 0
Pphat.02G069000|Pphat.02G069000.1 1 0
Pphat.013G023400|Pphat.013G023400.1 1 0
Pphat.004G086700|Pphat.004G086700.1 1 0
Pphat.026G009800|Pphat.026G009800.1 1 0
CMB021C|CMB021CT 30 SRRTPGRSSVL 41S---VSMARQOVHEEERRRLVRCINAVADAVRTHLQPKGRNVV
CMV086C|CMV086CT 1 0
gi|17555558|ref|NP\_497429.1| 2 LRLARKGLQTA 13VRSV---AKDVKFGADARALMVGVLADAVVMTGPKGRNVV
gi|1542947 11 MRPVSRLVAPL 22TRAV---AKDVKFGADARALMVGVLADAVVMTGPKGRNVV
YLR259C 8 R--SRATLRPL 17RRAV---SRHLLKFGVEARALMVGVLADAVVMTGPKGRNVV
gi|164428039 1 0
gi|66806233 5 ---IANKTKFG 13LRYN---STGDKIFGVEARALMVGVLADAVVMTGPKGRNVV
CMQ270C|CMQ270CT 18 SVGTL-CDAQAS 28SRRWLASQKDPGEGEARALMVGVLADAVVMTGPKGRNVV
405358|405358 1 0
Esi0161\_0060 1 0
GRMZM2G0|GRMZM2G074790\_T01 1 0
LOC\_Os05g46290|LOC\_Os05g46290.1 1 0
Cucsa.360540|Cucsa.360540.1 1 0
Medtr8g017080|Medtr8g017080.1 1 0
Glyma07g01190|Glyma07g01190.1 1 0
Glyma08g20560|Glyma08g20560.1 1 0
Glyma08g20560|Glyma08g20560.2 1 0
Eucgr.F03134|Eucgr.F03134.1 1 0
GSVIVG01016859001|GSVIVT01016859001 1 0
Bra001524|Bra001524 1 0
AT3G13860 1 0
Carubv10013333m.g|Carubv10013333m 1 0
PGSC0003DMG40002585|PGSC0003DMT4000664 1 0
Potri.003G037400|Potri.003G037400.1 1 0
28694.t000010|28694.m000667 1 0
Potri.003G039600|Potri.003G039600.1 1 0
74977|74977 1 0
Bra021836|Bra021836 1 0
Cre06.g309100|Cre06.g309100.t1.2 1 0
Vocar20007800m.g|Vocar20007800m 1 0
Bra005514|Bra005514 1 0
Bra022931|Bra022931 1 0
AT2G33210 1 0
Carubv10022887m.g|Carubv10022887m 1 0
Cucsa.078710|Cucsa.078710.1 1 0
LOC\_Os03g04970|LOC\_Os03g04970.1 1 0
GRMZM2G458208|GRMZM2G458208\_T01 1 0
GRMZM2G416120|GRMZM2G416120\_T01 1 0
LOC\_Os10g32550|LOC\_Os10g32550.1 1 0
Potri.002G252900|Potri.002G252900.1 1 0
PGSC0003DMG400011575|PGSC0003DMT40003026 1 0
Bra001934|Bra001934 1 0
AT3G23990 1 0
Carubv10013241m.g|Carubv10013241m 1 0
PGSC0003DMG401027165|PGSC0003DMT40006985 1 0
30204.t000086|30204.m001817 1 0
Potri.001G054400|Potri.001G054400.1 1 0
Potri.003G173900|Potri.003G173900.1 1 0
Glyma10g25630|Glyma10g25630.1 1 0
Glyma20g19980|Glyma20g19980.1 1 0
Glyma10g33680|Glyma10g33680.1 1 0
Glyma20g33910|Glyma20g33910.1 1 0
Medtr1g090140|Medtr1g090140.1 1 0
Medtr1g090140|Medtr1g090140.1 1 0
29904.t000134|29904.m003020 1 0
GSVIVG01029025001|GSVIVT01029025001 1 0
Cucsa.383180|Cucsa.383180.1 1 0
Eucgr.H02866|Eucgr.H02866.1 1 0
85251|85251 1 0
Pphat.02G069000|Pphat.02G069000.1 1 0
Pphat.013G023400|Pphat.013G023400.1 1 0
Pphat.004G086700|Pphat.004G086700.1 1 0
Pphat.026G009800|Pphat.026G009800.1 1 0





CMB021C|CMB021CT 519 --KPFYGYMNAAGCEYCDMTEAGIDDPKVRTALD 552NPIISVAGVLLTTEAVVTEPEKDDKKA----DDC---MDDIPGHSY 594  
CMV086C|CMV086CT 469 -NPNLGYDAANRRFVNIIEAGIDDPKVRTALD 502NARSIAAMVLLTECHIVPKPSGK\*----- 526  
gi|17555558|ref|NP\_497429.1| 489 --SNTSYGYDALNGKGVDMVEEAGIDDPKVRTALD 522DASGVASLLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 568  
gi|31542947| 497 --SSSEYGYDAMAGDFVDMVEKGIIDDPKVRTALD 530DAAGVALLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 573  
YLR259C 495 VQDFFAKGVDAAGSSEYDAMAGDFVDMVEKGIIDDPKVRTALD 530DAAGVALLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 572  
gi|164428039| 418 ENKQFSSAKAKYVDMTEAGIDDPKVRTALD 499DASGVASLLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 490  
gi|66806233| 489 -RDFEYEMNNAOKGVDMVEEAGIDDPKVRTALD 522DASGVASLLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 556  
CMQ270C|CMQ270CT 507 --SDKNLGFDAAGKGVDMVEEAGIDDPKVRTALD 540RASSVAGVLLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 586  
405358|405358 451 ENDSFGFTAGGVEYDMVEKAGIIDDPKVRTALD 484DAVSVSLLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 507  
Esi0161\_0060 497 --EDDQWGHNAAGCEYCDMTEAGIDDPKVRTALD 530DASGVASLLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 578  
GRMZM2G0|GRMZM2G074790.T01 509 --EDLGFDAAGKGVDMVEEAGIDDPKVRTALD 542DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 580  
LOC\_0805g46290|LOC\_0805g46290.1 510 --DNLNMGYDAAKGEYDMVKAGIIDDPKVRTALD 543DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 581  
Cucsa.360540|Cucsa.360540.1 499 --DPRNFGEADAAGEYDMVKAGIIDDPKVRTALD 532DASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 570  
Medtr8g017080|Medtr8g017080.1 505 --DDNLFGEADAAGEYDMVKAGIIDDPKVRTALD 538DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 576  
Glyma07g01190|Glyma07g01190.1 503 --DDNLFGEADAAGEYDMVKAGIIDDPKVRTALD 536DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 574  
Glyma08g20560|Glyma08g20560.1 503 --DDNLFGEADAAGEYDMVKAGIIDDPKVRTALD 536DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 574  
Glyma08g20560|Glyma08g20560.2 363 NLGFDAAGKGVDMVEEAGIDDPKVRTALD 399DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 431  
Eucgr.F03134|Eucgr.F03134.1 580 LEQ--DNLNMGYDAAKGEYDMVKAGIIDDPKVRTALD 616DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 653  
GSVIVG01016859001|GSVIVT01016859001 494 --DNLNMGYDAAKGEYDMVKAGIIDDPKVRTALD 527DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 565  
Bra001524|Bra001524 503 --DDCNFGEADAAGEYDMVKAGIIDDPKVRTALD 536DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 572  
AT3J13860 503 --DDCNFGEADAAGEYDMVKAGIIDDPKVRTALD 536DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 572  
Carubv10013333m.g|Carubv10013333m 503 --DDCNFGEADAAGEYDMVKAGIIDDPKVRTALD 536DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 572  
PGSC0003DMG40002585|PGSC0003DMT4000664 458 DDN--DNLNMGYDAAKGEYDMVKAGIIDDPKVRTALD 491DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 511  
Potri.003G037400|Potri.003G037400.1 318 GYDAAGKGVDMVEEAGIDDPKVRTALD 346DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 383  
28694.t000010|28694.m000667 503 --DDNLFGEADAAGEYDMVKAGIIDDPKVRTALD 536DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 572  
Potri.003G039600|Potri.003G039600.1 437 DYNLGYDAK-- 447----- 447  
74977|74977 471 --SSEYGYDAMAGDFVDMVEEAGIDDPKVRTALD 504DASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 548  
Bra021836|Bra021836 398 --NPDIGYDAAKGEYDMVKAGIIDDPKVRTALD 431DASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 447  
Cre06.g309100|Cre06.g309100.t1.2 502 --ARFQMEYDAAKGEYDMVKAGIIDDPKVRTALD 535DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 571  
Vocar20007800m.g|Vocar20007800m 502 --EDPAMGVNNAAGCEYCDMTEAGIDDPKVRTALD 535DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 571  
Bra005514|Bra005514 477 --DNDPLGYDAAKGEYDMVKAGIIDDPKVRTALD 510DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 559  
Bra022931|Bra022931 477 --DNDPLGYDAAKGEYDMVKAGIIDDPKVRTALD 510DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 557  
AT2G33210 504 --DNDPLGYDAAKGEYDMVKAGIIDDPKVRTALD 537DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 585  
Carubv10022887m.g|Carubv10022887m 504 --DNDPLGYDAAKGEYDMVKAGIIDDPKVRTALD 537DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 583  
Cucsa.078710|Cucsa.078710.1 504 --DNLNMGYDAAKGEYDMVKAGIIDDPKVRTALD 537DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 572  
LOC\_0803g04970|LOC\_0803g04970.1 504 --DNDPLGYDAAKGEYDMVKAGIIDDPKVRTALD 537DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 572  
GRMZM2G458208|GRMZM2G458208.T01 383 -- 382----- 382  
GRMZM2G4616120|GRMZM2G4616120.T01 506 --GNTPDLGYDAAKGEYDMVKAGIIDDPKVRTALD 539DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 576  
LOC\_0801g32550|LOC\_0801g32550.1 562 EQ--DNDPLGYDAAKGEYDMVKAGIIDDPKVRTALD 597DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 634  
Potri.002G252900|Potri.002G252900.1 505 --DNDPLGYDAAKGEYDMVKAGIIDDPKVRTALD 538DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 575  
PGSC0003DMG400011575|PGSC0003DMT40003026 504 --DNDPLGYDAAKGEYDMVKAGIIDDPKVRTALD 537DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 575  
Bra001934|Bra001934 503 --DNDPLGYDAAKGEYDMVKAGIIDDPKVRTALD 536DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 577  
AT3G23990 503 --DNDPLGYDAAKGEYDMVKAGIIDDPKVRTALD 536DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 577  
Carubv10013241m.g|Carubv10013241m 541 EQ--ENTDPLGYDAAKGEYDMVKAGIIDDPKVRTALD 576DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 617  
PGSC0003DMG401027165|PGSC0003DMT40006985 504 --DNDPLGYDAAKGEYDMVKAGIIDDPKVRTALD 537DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 573  
30204.t000086|30204.m001817 504 --DNDPLGYDAAKGEYDMVKAGIIDDPKVRTALD 537DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 575  
Potri.001G054400|Potri.001G054400.1 504 --DNDPLGYDAAKGEYDMVKAGIIDDPKVRTALD 537DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 574  
Potri.003G173900|Potri.003G173900.1 504 --DNDPLGYDAAKGEYDMVKAGIIDDPKVRTALD 537DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 574  
Glyma10g25630|Glyma10g25630.1 504 --BNHPLGYDAAKGEYDMVKAGIIDDPKVRTALD 537DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 575  
Glyma20g19980|Glyma20g19980.1 504 --BNHPLGYDAAKGEYDMVKAGIIDDPKVRTALD 537DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 575  
Glyma10g33680|Glyma10g33680.1 504 --DNDPLGYDAAKGEYDMVKAGIIDDPKVRTALD 537DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 577  
Glyma20g33910|Glyma20g33910.1 504 --DNDPLGYDAAKGEYDMVKAGIIDDPKVRTALD 537DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 575  
Medtr1g090130|Medtr1g090130.1 504 --DNDPLGYDAAKGEYDMVKAGIIDDPKVRTALD 537DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 576  
Medtr1g090140|Medtr1g090140.1 504 --DNDPLGYDAAKGEYDMVKAGIIDDPKVRTALD 537DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 574  
29904.t000134|29904.m003020 505 --DNDPLGYDAAKGEYDMVKAGIIDDPKVRTALD 538DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 575  
GSVIVG01029025001|GSVIVT01029025001 504 --DNDPLGYDAAKGEYDMVKAGIIDDPKVRTALD 537DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 575  
Cucsa.383180|Cucsa.383180.1 504 --DNDPLGYDAAKGEYDMVKAGIIDDPKVRTALD 537DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 575  
85251|85251 504 --DNDPLGYDAAKGEYDMVKAGIIDDPKVRTALD 537DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 575  
Pphat.02G069000|Pphat.02G069000.1 486 --DNLNMGYDAAKGEYDMVKAGIIDDPKVRTALD 519DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 557  
Pphat.013G023400|Pphat.013G023400.1 502 --NMSIYDAAKGEYDMVKAGIIDDPKVRTALD 535DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 577  
Pphat.004G086700|Pphat.004G086700.1 503 --ANLNIYDAAKGEYDMVKAGIIDDPKVRTALD 536DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 578  
Pphat.02G0690800|Pphat.02G0690800.1 503 --NMSIYDAAKGEYDMVKAGIIDDPKVRTALD 536DAASVSLTTEAVVTEPEKBAVGGP---AGMGCMGCGMGGMGGG-F 580