

```

Cucsa.113270.1_CUCSA      1  MADDSSSVKVKVNLFSGTANSVETVKSFFNSOVYDEEKWALNMLG----RLRGELDVM 55HLGWFSIEFHSEKSMFOLKPRLFMSMVCVMIKITKLIC
gi|158282668              1  -----MA-ENDLTSAQKWLREBYTNEAKFGANRLLRGIAIFGCAGVEV- 43-----FRNFGEALFGA-----
Phpat.003G139800          1  -----MAQSTLQKLNKRWAAETRDDEKLAHLRLLRVAVGMPAGSVMT- 42-----MRNFGDLMAV*-----
Phpat.012G084700          1  -----MAISMLQKLNKRWAAETRDDEKLAHLRLLRVAVGMPAGSVMT- 42-----MRNFGDLMAV*-----
GRMZM2G058057            1  -----MAASSAVEKIKVLDVSOVNDDEQWALNYKLLRAAGLPAAGSTFL- 43-----MRNFGDLMAT*-----
LOC_Os12g38650           1  -----MAAAAAVEKIKVLDVSOVNDDEQWALNYKLLRAAGLPAAGSTFL- 44-----MRNFGDLMAT*-----
Bra005963                 1  -----MAKSVTSMDDQKALWHSEVHDERKWAANMKLVRALGVFAGGIFFL- 44-----MRNFGDLMAV*-----
Bra028674                 1  -----MVKSVTSMDDQKALWHSEVHDERKWAANMKLVRALGVFAGGIFFL- 44-----MRGFGDLMAV*-----
Carubv10002362           1  -----MANNVTSIDDKLKAFWHSEVHDERKWAANMKLVRALGVFAGGIFFL- 44-----MRSVGDLMAV*-----
AT5G08040                 1  -----MVNNVTSIDDKLKAFWHSEVHDERKWAANMKLVRALGVFAGGIFFL- 44-----MRSVGDLMGV*-----
PGSC0003DMG400024536    1  -----MVDVTSIDDKLKAFWHSEVHDERKWAANMKLVRALGVFAGGIFFL- 44-----MRQVGDLMAT*-----
GSVIVG01008105001       1  -----MADVTSIDDNLKAFWNSQIHDEEKWALNMKLLRAAGLPAAGSTFL- 44-----MRNFGDLMAT*-----
Glyma05g00341            1  -----MADSVTSHOYLKDFVNSQIYDDEKWAANAKLLRAAGLPAAGSTFL- 44-----MRNFGDLMAT*-----
Glyma17g08701            1  -----MADSVTSHOYLKDFVNSQIYDDEKWAANAKLLRAAGLPAAGSTFL- 44-----MRNFGDLMAT*-----
30138.t000139            1  -----MADSMISVEKIKAFVNSQIHDEEKWALNMKLLRAAGLPAAGSTFL- 44-----MRNFGDLMAT*-----
Potri.015G058500         1  -----MADSVTSHOYLKAFVNSQIHDEEKWALNMKLLRAAGLPAAGSTFL- 44-----MRNFGDLMAT*-----
sp|Q8N4H5                  1  -----MADSVTSHOYLKAFVNSQIHDEEKWALNMKLLRAAGLPAAGSTFL- 44-----MRNFGDLMAT*-----
gi|197333732              1  -----MADSVTSHOYLKAFVNSQIHDEEKWALNMKLLRAAGLPAAGSTFL- 44-----MRNFGDLMAT*-----
YPR133W-A                 1  -----MADSVTSHOYLKAFVNSQIHDEEKWALNMKLLRAAGLPAAGSTFL- 44-----MRNFGDLMAT*-----
gi|301014722              1  -----MADSVTSHOYLKAFVNSQIHDEEKWALNMKLLRAAGLPAAGSTFL- 44-----MRNFGDLMAT*-----
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0-----MFRTEGLAPKLDPEEMK-----RKMREDVIS
0-----MFG--L-PQEVSEBEK-----RAHQEQTEK
0-----MFG--GFQPPFLSRBEL-----QAABEATF

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Phpat.012G084700          53  ----- 52----- 52
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LOC_Os12g38650           55  ----- 54----- 54
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Bra028674                 55  ----- 54----- 54
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AT5G08040                 55  ----- 54----- 54
PGSC0003DMG400024536    55  ----- 54----- 54
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Glyma05g00341            55  ----- 54----- 54
Glyma17g08701            55  ----- 54----- 54
30138.t000139            55  ----- 54----- 54
Potri.015G058500         55  ----- 54----- 54
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gi|197333732              27  SIRNFLIYVALRVSECLPGCD 48CETSGELTDGHPLTLRGHRGLRTELNAFFILKKLDSI-- 85
YPR133W-A                 24  TLQAAAYVAAFVWVSPMIW--- 42-----HLVKKQWK 50
gi|301014722              25  TIQRAVFTAVAVLSFFVI--- 43-----DAVSKVL- 50

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