

A

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AT4G24230_L_At ---EKFAFAAAVNLLEESGKAE---E-IGAEAKMELYGLHKIATEGSCRE-AQPMAMLSARAKWNAWQKLGNMSEAEAMEQYIALVSKETIP
BnaA01g13710D_L_Bn ---EIAFAAASNLLEESGKGE---D-IGAEAKMELYGLHKIATEGSCRE-AQPMAMLSARAKWNAWQKLGNMSEAEAMEQYIALVSKETIP
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BnaA03g48810D_L_Bn DEAFSAATLFFVTTAAADRSLR---K-VPGVQKQLYGLHKIATEGPGTA-PQPSALKLTARAKWQAWRKLGMPTTEAEAMEKYIEIVVQLYP
XP_013644236_L_Bn ---EKFAFAATSSLLLEVSQKAE---E-IGDEVKMEYLYGLHKIATEGSCRE-TQPMAMLSARAKWNAWQKLGNMSEAEAMEQYIALVSKETIP
XP_013644237_L_Bn ---EKFAFAATSSLLLEVSQKAE---E-IGDEVKMEYLYGLHKIATEGSCRE-TQPMAMLSARAKWNAWQKLGNMSEAEAMEQYIALVSKETIP
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XP_013671521_L_Bn ---FSAAASNLLEESGKGE---E-ITAEAKMELYGLHKIATEGSCRE-AQPMAMLSARAKWNAWQKLGNMSEAEAMEQYIALVSKETIP
XP_013671522_L_Bn ---FSAAASNLLEESGKGE---E-ITAEAKMELYGLHKIATEGSCRE-AQPMAMLSARAKWNAWQKLGNMSEAEAMEQYIALVSKETIP
XP_013671523_L_Bn ---FSAAASNLLEESGKGE---E-ITAEAKMELYGLHKIATEGSCRE-AQPMAMLSARAKWNAWQKLGNMSEAEAMEQYIALVSKETIP
XP_013738023_L_Bn ---EKFAFAATSSLLLEVSQKAE---E-VGDEVKMEYLYGLHKIATEGSCRE-TQPMAMLSARAKWNAWQKLGNMSEAEAMEQYIALVSKETIP
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XP_013739038_L_Bn ---EIAFAAASNLLEESGKGE---D-IGAEAKMELYGLHKIATEGSCRE-AQPMAMLSARAKWNAWQKLGNMSEAEAMEQYIALVSKETIP
XP_013739042_L_Bn ---EIAFAAASNLLEESGKGE---D-IGAEAKMELYGLHKIATEGSCRE-AQPMAMLSARAKWNAWQKLGNMSEAEAMEQYIALVSKETIP
XP_013741591_L_Bn DEAFSAATLFFVTTAAADRSLR---K-VPGVQKQLYGLHKIATEGPGTA-PQPSALKLTARAKWQAWRKLGMPTTEAEAMEKYIEIVVQLYP
XP_013598135_L_Bn ---EIAFAAASNLLEESGKGE---D-IGAEAKMELYGLHKIATEGSCRE-AQPMAMLSARAKWNAWQKLGNMSEAEAMEQYIALVSKETIP
XP_013598633_L_Bo ---EKAFATASNLLEVSQKAE---E-IGDEVKMEYLYGLHKIATEGSCRE-TQPMAMLSARAKWNAWQKLGNMSEAEAMEQYIALVSKETIP
XP_013598634_L_Bo ---EKAFATASNLLEVSQKAE---E-IGDEVKMEYLYGLHKIATEGSCRE-TQPMAMLSARAKWNAWQKLGNMSEAEAMEQYIALVSKETIP
XP_013601844_L_Bo ---FSAAASNLLEESGKGE---E-ITAEAKMELYGLHKIATEGSCRE-AQPMAMLSARAKWNAWQKLGNMSEAEAMEQYIALVSKETIP
XP_013601898_L_Bo ---FSAAASNLLEESGKGE---E-ITAEAKMELYGLHKIATEGSCRE-AQPMAMLSARAKWNAWQKLGNMSEAEAMEQYIALVSKETIP
XP_013601960_L_Bo ---FSAAASNLLEESGKGE---E-ITAEAKMELYGLHKIATEGSCRE-AQPMAMLSARAKWNAWQKLGNMSEAEAMEQYIALVSKETIP
XP_013620900_L_Bo -----MTARAKWQAWRKLGMPTTEAEAMEKYIEIVVQLYP
XP_009137429_L_Br ---EKFAFAATSSLLLEVSQKAE---E-VGDEVKMEYLYGLHKIATEGSCRE-TQPMAMLSARAKWNAWQKLGNMSEAEAMEQYIALVSKETIP
XP_009137430_L_Br ---EKFAFAATSSLLLEVSQKAE---E-VGDEVKMEYLYGLHKIATEGSCRE-TQPMAMLSARAKWNAWQKLGNMSEAEAMEQYIALVSKETIP
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XP_009137819_L_Br ---EIAFAAASNLLEESGKGE---D-IGAEAKMELYGLHKIATEGSCRE-AQPMAMLSARAKWNAWQKLGNMSEAEAMEQYIALVSKETIP
XP_009137826_L_Br ---EIAFAAASNLLEESGKGE---D-IGAEAKMELYGLHKIATEGSCRE-AQPMAMLSARAKWNAWQKLGNMSEAEAMEQYIALVSKETIP
XP_018513251_L_Br ---EKFAFAATSSLLLEVSQKAE---E-VGDEVKMEYLYGLHKIATEGSCRE-TQPMAMLSARAKWNAWQKLGNMSEAEAMEQYIALVSKETIP
XP_018513258_L_Br DEAFSAATLFFVTTAAADRSLR---K-VPGVQKQLYGLHKIATEGPGTA-PQPSALKLTARAKWQAWRKLGMPTTEAEAMEKYIEIVVQLYP
XP_016681245_L_Gh ---EKDFGAAVCFLESRRNADQILK-LGNNLKMQLYALQKVATEGPGCHE-THPMAFKLSARAKWSAWKRLGNMSEAEAMEQYITILLRSRSTIP
XP_016681248_L_Gh ---EKDFGAAVCFLESRRNADQILK-LGNNLKMQLYALQKVATEGPGCHE-THPMAFKLSARAKWSAWKRLGNMSEAEAMEQYITILLRSRSTIP
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XP_016705060_L_Gh ---EKDFGAAVSFLVQKSNADQVLK-LGNDLKMQLYGLHKIATQGPCHC-PQPMFFKLSARAKW-----
XP_016717761_L_Gh ---EIVFGSASKFTEQEGDLG----IGNDVQCMELYGLHKVATEGPGCHE-POPFAFMVASRSKKNWNAWQKLGNMSEAEAMEQYIVALVSDKWIP
XP_016717762_L_Gh ---EIVFGSASKFTEQEGDLG----IGNDVQCMELYGLHKVATEGPGCHE-POPFAFMVASRSK-----
XP_016717763_L_Gh ---EIVFGSASKFTEQEGDLG----IGNDVQCMELYGLHKVATEGPGCHE-POPFAFMVASRSK-----
XP_016717764_L_Gh ---EIVFGSASKFTEQEGDLG----IGNDVQCMELYGLHKVATEGPGCHE-POPFAFMVASRSK-----
XP_016730278_L_Gh ---EKDFGAAVSFSVQKSNADQDLK-LGNDLKMQLYGLHKIATQGPCHC-PQPMFFKLSARAKW-----
XP_016732243_L_Gh ---EIVFGSASKFTEQEGDLG----IGNDVQCMELYGLHKVATEGPGCHE-SQPFAFMVASRSKKNWNAWQKLGNMSEAEAMEQYIVALVSDKWIP
XP_003517332_L_Gm ---ERRFGAAVVFVGSKSNAN----LSNDVKMELHGYHRIATQGPCHC-POPMAFKLSARAKWIARQLGIMSEAEAMEQYITILLSENIP
XP_003550311_L_Gm ---EKFFMAATEFVSGEENLGLG---G-VGSNLMELYGLKIVATEGLCRE-POPMAFKLSARAKWNAWQKLGNMSEAEAMEQYITILLSDKFI
XP_021983463_L_Ha ---EKVFRAMAIDYGLKNDGLQSG---LGSIVQCMELYGLHKVATEGPGCRE-AQPMALKVSARAKWNSWQKLGNMSEAEAMEQYITALLSEVAF
XP_021998495_L_Ha ---KXTFGAAVAFVHDSKSSLR-VNLDNEVKVELYGLHKVATEGSCFE-POPMAFKVSARAKWNSWKRFEENLGREAMEQYITILLQCHIF
XP_022011286_L_Ha ---ERRFGAAVAFVHDAKVNNSG-VNLDNEVKVELYGLHRAVATEGSCFE-POPMAFKVSARAKWNSWKRFEENLGREAMEQYITALLSRHIF
XP_012068250_L_Jc ---NHVFAKAVNLVESADDDGGSRS-IGSDVQCMELYGLHKVATEGPGCRE-QPPFAFKLSARAKWNAWQKLGNMSEAEAMEQYIVALVSDKWIP
XP_012079368_L_Jc ---EKLFGAAVAFVGSINNAKILLNNSDKLKLHGLQVVAIEGPGCHV-PQPRPFKVSARAKWNAWQKLGNMSEAEAMEQYINLVSRSTIP
XP_022844505_L_Oe -----K-VSNELCQQLYGLHKIATEGPGSA-PQPSALKLTARAKWQAWRKLGMPTTEAEAMEKYIEIVVQLYP
Os03g14000_L_Os ---EKRFVVAFAFASDDGMAALSK-LDSVQCMELYGLKVAIDGPGCYB-STQPIHTRPSSRAKWSAWQKLGNMSEAEAMEQYINLVSRSTIP
AFZ62129_L_Vf ---EQIFAKAAKFFVESGDDEGLTS-VGSDVQCMELYGLHKVATEGPGCRE-QPPMAFKVSARAKWNAWQKLGNMSEAEAMEQYIVALVSDKWIP
AQK69810_L_Zm -----TALSQ-INSDEHVQQLQGLLKVAIIDDPQYB-STQPIHTRPSSRAKWSAWQKLGSMHPEETALEKYINLVSRSTIP
ONL95884_L_Zm -----SK-LDSVQCMELYGLKVAIDGPGCYB-STQPIHTRPSSRAKWSAWQKLGNMSEAEAMEQYINLVSRSTIP
ONL95885_L_Zm -----SK-LDSVQCMELYGLKVAIDGPGCYB-STQPIHTRPSSRAKWSAWQKLGNMSEAEAMEQYINLVSRSTIP

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Consensus EK FFAAS LLE SGKAE IG EVKMEYLYGLHKIATEGSCRE QPMAMLSARAKWNAWQKLGNMSEAEAMEQYIALVSKETIP

