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gi|55769533|ref|NP_002574.2|      * *                               * * * *                               *
MATGG-----YRTS-----SGLGGSTTDFLE-----EWAKEKREKMRAK-----GNPPGPAPPGGGSSDAAGKP---PAGALGTPAAAAANELN 150
gi|114646044|ref|XP_509236.2|    MATGG-----YRTS-----SGLGGSTTDFLE-----EWAKEKREKMRAK-----GNPPGPAPPGGGSSDAAGKP---PAGALGTPAAAAANELN 150
gi|87196490|ref|NP_473397.1|     MATGG-----YRS-----GGSTTDFLE-----EWAKEKREKMRAK-----GNPAGPGSSGG---DPAAKS---PAGSLTPTAVAGTSELNHG 150
gi|15741228|ref|NP_277020.1|     MATGG-----YRS-----SGS-TDFLE-----EWAKEKREKMRAK-----GNVVGPGSSGG---DPAAKS---PAGPLAQTTAAGTSELNHG 150
gi|194666688|ref|XP_001788067.1| MPVGEVWVLPSPFLSVGIWGLEQRLKAPVLTCHHSFPEIERRLRGELPGWNAACRRNDSARPLAVLSDTSRPEWSNERPNDRPRIIILDWWRIGSSQVLAVRPNLKEAVSPDSGRGLEVHKSLSLHRRRGGPFQFFYSACXXXXXXX 150
gi|118082445|ref|XP_416112.2|    MERGE-----GGRGEPRAPE-----LRSFRAVGG-----RCRSPGGAGAGDRPCR 150
gi|54400532|ref|NP_001006015.1|  MATGG-----FKSN-----SANDFLE-----EWAKEKREKMRAK-----MLGDIAAATG-----RTTELNNNGSSSVN 150

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gi|55769533|ref|NP_002574.2|    ---LPGGAPAAPVPGPGVNCVAVGSAMLTRAAPGRRSEDE-PPAASAS-AAAPPQRDEEEDGVPKGGKSSGSPARKGKGQIEKRKLEKRRSTGVVNIIPAAECLDEYEDDEAGQKERKREDAITQONTIONEAVNLLDPGSSYLLOE 300
gi|114646044|ref|XP_509236.2|    ---LPGGAPAAPVPGPGVNCVAVGSAMLTRAAPGRRSEDE-PPAASAS-AAAPPQRDEEEDGVPKGGKSSGSPARKGKGQIEKRKLEKRRSTGVVNIIPAAECLDEYEDDEAGQKERKREDAITQONTIONEAVNLLDPGSSYLLOE 300
gi|87196490|ref|NP_473397.1|     ---PAG--AAAPAAPGALNCAHGSSTLPRAPGSRRAEDECPAAGAA--GAPASRGDEEEDPAEKGRSSGSPARKGKGQIEKRKLEKRRSTGVVNIIPAAECLDEYEDDEAGQKERKREDAITQONTIONEAAALPDGTSYLPQD 300
gi|15741228|ref|NP_277020.1|     ---PAG--AAAPAAPGALNCAHGSSTLPRAPGSRRAEDECPAAGAA--GAPASRGDEEEDPAEKGRSSGSPARKGKGQIEKRKLEKRRSTGVVNIIPAAECLDEYEDDEAGQKERKREDAITQONTIONEAAALPDGTSYLPQD 300
gi|194666688|ref|XP_001788067.1| XXXXXXXXXXXAAPAGPGVNCVAVGPAQLSRAAPGRRPEDESPPAAAAATSGAAPARGGEEERDCAPEKSKSSGSPARKGKGQIEKRKLEKRRSTGVVNIIPAAECLDEYEDDEAGQKERKREDAITQONTIONEAVSLLDPGSSYLLOE 300
gi|118082445|ref|XP_416112.2|    ---DRAGREPPPG-----PAAGREPAKQPPAAAAA--APGPTGEEKP---AGKGGKSSGSPARKGKGQIEKRKLEKRRSTGVVNIIPAAESLDEYEDDEAGQKERKREDAITQONTIONEASSADSTG--SYLIQD 300
gi|54400532|ref|NP_001006015.1|  S--SAPSPVARSSSSSALKDEPKTPEPPGNLKKTPKVSAPVQADSPAPAGVDDSDKESPTHEKSKKSSGSPARKGKGQIEKRKLEKRRSTGVVSIIPNESLDELDDDDGEEKERKMEENLQHTVONEALTS--EHAHVSQD 300

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gi|55769533|ref|NP_002574.2|    PPRIVSGRYKSTISVSEEDVSSRYSDTRSGFPRYNRDANVSGTLVSSS--TLEKKIEDLEKEVVRERQENLRRLVRLMDKEEMIGLKEEIDLLNRDLDDIEDENEOLKQENKTLKVVVGQLTR 424
gi|114646044|ref|XP_509236.2|    PPRIVSGRYKSTISVSEEDVSSRYSDTRSGFPRYNRDANVSGTLVSSS--TLEKKIEDLEKEVVRERQENLRRLVRLMDKEEMIGLKEEIDLLNRDLDDIEDENEOLKQENKTLKVVVGQLTR 424
gi|87196490|ref|NP_473397.1|     PPRIVSGRYKSTISVSEEDVSSRYSDTRSGFPRYNRDANVSGTLVSSS--TLEKKIEDLEKEVVRERQENLRRLVRLMDKEEMIGLKEEIDLLNRDLDDIEDENEOLKQENKTLKVVVGQLTR 424
gi|15741228|ref|NP_277020.1|     PPRIVSGRYKSTISVSEEDVSSRYSDTRSGFPRYNRDANVSGTLVSSS--TLEKKIEDLEKEVVRERQENLRRLVRLMDKEEMIGLKEEIDLLNRDLDDIEDENEOLKQENKTLKVVVGQLTR 424
gi|194666688|ref|XP_001788067.1| PPRIVSGRYKSTISVSEEDVSSRYSDTRSGFPRYNRDANVSGTLVSSS--TLEKKIEDLEKEVVRERQENLRRLVRLMDKEEMIGLKEEIDLLNRDLDDIEDENEOLKQENKTLKVVVGQLTR 424
gi|118082445|ref|XP_416112.2|    SRRMVSSRYKSTGNAPGDDALNRYSLTERTTTSRYSRDANSSGSSVPSN-ALEKRIEELERELAKERQENVRMLKMTODKEEVIGLKEEIDLLNRDLDDIEDENEOLKQENKTLKVVVGQLTR 424
gi|54400532|ref|NP_001006015.1|  NRRRS--HKS-----DEGSRHR-----HRHGRDSSDGAPT-----ALERRVEELERELALEREENERLLKAYQEQDELIMKLKEEIDLLNRDLDDIEDENEOLKQENKTLKVVVGQLTR 424

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