

gi | 73964977 | ref | XP\_540460.2 | MAOPLTFVLSVPEPTPEHGC --PEPSPYDESEVHDSFYQLIQEQSQWVAEEGLELQORER --GPPETPGSGHQTLLGPEPLVHSTATLRILASMPERTIGRSRGAIISQYVNRVLRRLRRVSRPELQVGRSARPSLRLYDLELDPAVALE 146  
gi | 115498002 | ref | NP\_001068676.1 | MSQSPAFVNLVLETPEDPEGSOEPSPYDESEVHDSFHQLIQEQSRRWVAEEGLELQORERPETGALGASGSDHETMLGPEGAPVYSMATLRILASMPERTIGRSRGAIISQYVNRVLRRLRRRAGRPQLRDMGRSARPSLRLYDLELDPAVALE 150  
gi | 187608791 | ref | NP\_001120670.1 | MAOPLAFILDVPETPGDCG --QGPSPYDESEVHDSFQQLIQEQSQCQAQEGLELQORER --EVTGSSQQLTWRPEG --IQSTATLRILASMPERTIGRSRGAIISQYVNRVLRRLRRRAGRPQLRDMGRSARPSLRLYDLELDPAVALE 141  
gi | 32441274 | ref | NP\_663414.2 | MACSLALALDVPETGDEG --LEPSPYEESVHDSFHQLIQEQSRLRVAEEGLELPLGL --GRGDQTLPGLEGAPALSSATLRILASMPERTIGRSRGAIISQYVNRVLRRLRRRAGRPQLRDMGRSARPSLRLYDLELDPAVALE 140  
gi | 118099867 | ref | XP\_420092.2 | -----MFFFGEIQVVAR ----- 13  
gi | 50540484 | ref | NP\_001002705.1 | MACRVSFSGDLDHTD -----VESPADEGDVHDSFCQLIEEGCYGRHDDGEMETPLDP -----DVEDESRDDVV --VLGDGARNWSESLSDAPQHFPHARPSLRGYSVEIDGAGFQ 103  
gi | 118780900 | ref | XP\_310494.3 | -----LSIDGDLIT -----SASVDVHITMELGQRELMEDNVPVAQLRIETIKS -----IAHKIKTKRQIRQLARIVHRRATRAKS ----- 73  
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi | 73964977 | ref | XP\_540460.2 | EEC-DRGLKAKALRWEAGAI ---QVNGVSRSGAATSAPREEIRLTLTKRRRGRRRRGLLPCCGRLRDCAVLALHSLGLLGLSLHALMPWRVALKRIGGQFGSSVLSYFLFLKLLAFNALLLLPLLAFLVGVQAAFPPASPGAVPAF 292  
gi | 115498002 | ref | NP\_001068676.1 | EEE-KRGLLVKELGGLIAAQRDMLRGMPLSLAEKRRLRESRPPRGKHRACWHR-GLLSCDDLRDSCVLASNLGLALLSGLQALMPWHVALKRIGGRFGSSVLSYFLFLKLLAFNALLLLPLLAFLVGVQAAFPP-AFTGFPVPAF 297  
gi | 187608791 | ref | NP\_001120670.1 | EEE-KQSLLVKELGSLVAQRDMLRGMPLSLAEKRRLRESRPPRGKWRGQPGSGVCSGGLRLYACMLALHSLGLALLSALQALMPWRVALKRIGGQFGSSVLSYFLFLKLLAFNALLLLPLLAFLVGVQAAFPP-ALPGPAPVCT 289  
gi | 32441274 | ref | NP\_663414.2 | EDE-KRSLLVKELGSLAAQRDMLRGMPLSLGKRCRLRESRPPGKRRLHQLGSGAFSCCSRLRYTCMLALHSLGLALLSGLYAARPWRVALKRIGGQFGSSVLSYFLFLKLLAFNALLLLPLLAFLVGVQAAFPP-DPAGPVPFIS 288  
gi | 118099867 | ref | XP\_420092.2 | -----LGRVLLAVRSPQ -----VLLCISIP 33  
gi | 50540484 | ref | NP\_001002705.1 | EENKRRRLVNNLQNLVSDRVRMLRAMPPLSLAEKELRMLVNLKGEHSLSE ---NQTPCCSOLKYIINAVRHGWYSWLSLVSSLQLWQALKCVSGRFGTGVLSYFVFLRLLFFNIFLFLFHALFLAVPQAVLPPAQDTHNNTSR 249  
gi | 118780900 | ref | XP\_310494.3 | -----TGLLRRYRYGAKRYVARAARLQCFVTNFEFFYGSMMQIEGHFGSRIISAFKFLRLLVNLVLAFLVGSFVIFPOLLAGPEPPDARQAFQL 165  
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....300



gi | 73964977 | ref | XP\_540460.2 | ---GLELLGAGRFTHTVMYGYYSNTLNLQPCVPLDGGCCSREADGLPYNMLLAYLFTVGVAFFITCITLVYSMSHSFSGESYRV--GSTAGVHAVIVFCSWDHKVTKQKRASRVQHDNIRIHLKELLAEWQLRQVPRSLCGRRLQVAV 436  
gi | 115498002 | ref | NP\_001068676.1 | ---GLELLGGGYFTHSVMYGYYSNANLNQPCASPLDGSQCPEAGSLPYSMPLAYLFTLGAFFITCITLVYSMSRSFSGESYRV--GSTSGVHAITVFCSDWKVTKQRAWATRLQHDNIRIHLKELLAEWQSRQHRRSACGLRRVAV 441  
gi | 187608791 | ref | NP\_001120670.1 | ---GLELLGAGCFHTVMYGYYSNANLNQPCGSPLDGSCCPRVGGGLPYNMLLAYLFTVGVSAFFITCITLVYSMAHSFSGESYRV--GSTSGIHAITVFCSDWKVTKQKRASRLQHDNIRIHLKELLAEWQSRVSVCCGRRLQVAV 433  
gi | 32441274 | ref | NP\_663414.2 | ---GLELLGGGRFTHTVMYGYYSNSNLSLPSDAPREGGCCSPLRGLSLPYNMLLAYLFTMGATFFITCITLVYSMSHSFSGESYRV--GSTKGIHAITVFCSDWKVTKQKRASRVQDSICHLKELLAEWHLRKRPRVCCGLRQVAV 432  
gi | 118099867 | ref | XP\_420092.2 | ---QGSFTHSLLYGYYSNTLNLDPSSAETPSGNTSPPRATQPLPYNMLLAYLFTIGASFFATCITLVYSIYHFGKSYRV--GSSIGVLAIKVFCWDFKVVORRQVVKLQSENICHLKELLAEWQLRSCPLSLPQRLRHIV 170  
gi | 50540484 | ref | NP\_001002705.1 | RBSWGLVLTGAGYFSDVLYGYYSNQRLQSGRRCSQSSNGTSCDAT-PSYNMPLVYFFITGAAFFI----- 316  
gi | 118780900 | ref | XP\_310494.3 | R-----DLLTCEGLSDSVMYGYYSNRRFTLVV-----GTAEYSLPHAYFLITITLLATFVVFVSMGHAYRISFIESATVQNILLTKIVCSWDYGIANGKAARLKHATILSELRDVLAQRNRTPAVPRGRWRLRTEIL 297  
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi | 73964977 | ref | XP\_540460.2 | LGLVWLLCLGTLGCTVAVYAFSELMIKSPVSTIEGALLALPITVVCVNLGTPYLRCCLAALERHDSVPLEVYVAICRNLLKLMVILGILCYHWLGRRVGVLKEOCWENFVGOELVRLMVDLDFVLLDILFGLVWRLISEKKLKRRE- 585  
gi | 115498002 | ref | NP\_001068676.1 | LGLVWLLCLGTLGCTLAVYTFSELMIKSPVSAEREAVALLLPLLVVCLNLGGPVLFRILAALERHDSVPLEVYVAICRNLLKLMVILGILCYHWLGRRVGVLKDCWENFVGOELVRLMVDLDFVLLDILFGLVWRLISEKQLKRRG 591  
gi | 187608791 | ref | NP\_001120670.1 | LGLVWLLCLGTLGCAVAVVTFSEFMIOQPEAAGQEAVALLVPLVGLNLGAPVLCRVLAALPHDSVPLEVYVAICRNLLKLAIGLTCYHWLGRRVGVLGQCWEDFVGOELVRLVMDLDFVLLDILFGLVWRLISEKKLKRRE 583  
gi | 32441274 | ref | NP\_663414.2 | LGLWLLCLGSLTMGCTVAVLTFSEVMIQRPAGGGQVEALALPLVVSVLNLGASVYFRGLALRERHDSVPLEVYVAICRNLLKMAVGLVLCYHWLGRRVVLLGQCWEDFVGOELVRFVMDLDFVLLDILFGLVWRLISEKKLKRRE 582  
gi | 118099867 | ref | XP\_420092.2 | LLLAWLLALGTVLGCVVAVYTFSEHMH-----VNNKQ 202  
gi | 50540484 | ref | NP\_001002705.1 | -----FMILLDFFG-----EFLWRLFSQALKKRKR 341  
gi | 118780900 | ref | XP\_310494.3 | NAVAHAVLALIAVAACLWAVLDRFGPADHFAAWSALYVSLASNGTMAALG--YVCOGLGRLERYRHGAQLNINLLRHFLQLLIVAVLFAHWLTPRPPG--CWETAIGQELVRLVDFVIFISVLLSARVGRVYLLHARYGPARG 442  
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



gi | 73964977 | ref | XP\_540460.2 | -----KPEFDIAGNVLELIYQTLTTLWLVLFSPLLPAIQIILKLLCFYIKKSLMANCQAPRRPWLASHMSTVVFVLLCFPSFLGAAVFLCYAVWQVRRPSSCGPFRRLDITMYEAGKVVWRRLLEQAGPSVSWPWIHRVLENVF 725  
gi | 115498002 | ref | NP\_001068676.1 | -----KPEFDIAGNVLELIYQTLTTLWLVLFSPLLPAMQIILKLLLFYIKKASLMANCQAPRRPWLASHMSTVVFVLLCFPSFLGAAVFLCYAVWQVRRPSSCGPFRRLDITMYEAGKVVWRRLLEKAGPRVSWPWIHRVLENVF 731  
gi | 187608791 | ref | NP\_001120670.1 | -----KPEFDIARNVLELIYQTLTTLWLVLFSPLLPAVQIILKLLVVFYIKKSLMANCQAPRRPWLASHMSTVVFVLLCFPAFLGAAVFLCYAVWQVRRPSSCGPFRRLDITMYEAGRVVWRRLLEAAGPRVSWPWIHRVLENVF 723  
gi | 32441274 | ref | NP\_663414.2 | -----KPEFDIARNVLDLIYQTLTTLWLVLFSPLLPAVQIILRLLFLPHIKKASLMANCQAPRRPWLASHMSTVVFVLLCFPSFLGAAVFLCYAVWQVRRPSSCGPFRRLDITMYEAGTVVWRRLLEHAGSGASWLPWIHRVLENVF 722  
gi | 118099867 | ref | XP\_420092.2 | -----KPEFDIARNVPLIYQTLTTLWLVLFAPLLPAVQVLLKLLLFYIKKSLMNCQSPKQPWASHMSTVVFVLLCFPSFLGAAVFVSYIWSVQPSSETGPFQGLQIYQILKVVVLELLESNPNLAWFSWIPQVLENVF 342  
gi | 50540484 | ref | NP\_001002705.1 | -----KPVFDIARNVLELIYQTLTTLWLVLFSPLLPVVQIILKLLVVFYIKKSLMNCQVSGKPRWASQMTLIFLILCFPSFLGAAVCVTYIWMVTKPSSCGGPFGRKIMFQAGLWVRDLALNPSLWVLESAHTVLENVF 481  
gi | 118780900 | ref | XP\_310494.3 | RAGPLAPVLLPPPCIEHSLGLVYVNLWLVFGLFAPLLVLLVALLKLLVFNKCELMYLCQPPARLWRSQTOQLIFLIVLVVFLGVLTLTGYLIMQVVPVSEGGPFGRQTYMYLQFMQGLKILREHFLWFRVWITKPAITGGV 591  
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750



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gi | 73964977 | ref | XP_540460.2 |          : : * * : ** : *
gi | 115498002 | ref | NP_001068676.1 | PIVLVSALLLAVIYLNIQVVKGQRRVMCLLKEQISNEGEDKIFLINKLHIVYERKER----- 783
gi | 187608791 | ref | NP_001120670.1 | FVFLVSALLLAVIYLNIQVVRGQRKVICLLKEQISNEGEDKIFLINKLHIVYERKERERSRVGTTEHAAAPPALLTDEQDA----- 769
gi | 32441274 | ref | NP_663414.2 | FLFLASALLLAVIYFNIQVVKGQRKVICLLKEQIRNEGEDKIFLINKLHIVYEEGRSRPGRTDAPPAWHEGGDQKPCNPRSP----- 805
gi | 118099867 | ref | XP_420092.2 | FLFFLTGVVLAIIYLNTHVLRGQHRIRLLEQIANEGEDKRFILIRKIRSIYEHKEHCA----- 810
gi | 50540484 | ref | NP_001002705.1 | FLFLSAAVFLIIVFHSQVLDGQRKIIELLQEQIENEGEDKKFLIMRLQDIHERRRVSRRRGQRDTEGSSFS----- 401
gi | 118780900 | ref | XP_310494.3 | LLTMG----VATYYLRAKERAQIAKVLLKELLCLEAKDKFLLANLSKVARGKDCTEQLDRIELVGGRLNGPADRYYLDPCAWRVYEEPRKPDVAGGTASAGLITNSTSSSSGYC 554
          .....760.....770.....780.....790.....800.....810.....820.....830.....840.....850.....860..... 705

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