

gi|112363098|ref|NP\_032855.2| MTELQAKDPOVLHTSGAASPPPHIGSPLLARLDGPFQGSQHSDDVS-----SVVSPPIPIIS-LDGLLPPRSC-RGPELDPDGTGDOOSLSVVEGAFSGVRAATHREGGRNSRAPEKDSRLLDVLDLTPSGTEQSHASPPACEA 137  
gi|12408292|ref|NP\_074038.1| MTELQAKDPRTLHTSGAAPSPTHVGSPLLARLDPPDFQGSQHSDDAS-----SVVSPPIPIIS-LDRLLFSRSC-QAELPDEKTONQOOSLSDVEGAFSGVEASRRRS-RNPRAPEKDSRLLDVLDLTPSGTEQSHASPPACEA 136  
gi|110611914|ref|NP\_000917.3| MTELKAKGPRAPHVAGGPPSP-EVGSPLLCRPAAGFPFGSQTSDTL-----PEVSAIPIIS-LDGLLPPRSC-CGQDPDDEKTONQOOSLSDVEGAFSGVRAATHREGAGSSSSPPPEKDSRLLDVLDLTPSGTEQSHASPPACEV 136  
gi|50978746|ref|NP\_001003074.1| MTERTGKDARAPHVAGGAPSPAPAAEPESRRRDGGRRLRASQTSADPRVAAAAAAAAAASAPSPAPSDRLLFSRRG-----CGAD-PGGKAQDAQPRPVARADPRLRAASGADSPGPPRQDRGPLHGAPSTALRPAAGPQGRSSE-AWEY 146  
gi|45383982|ref|NP\_990593.1| MTEVKSKEKTRAPSSAR-----DGAVLLQAPPSSRGE-----AEGIDVA-LDGLLPPRSDDEEEEEEENEEEEEEEPQQREEEEEEEDDCPSYRFGGGSLSKDCLDVLDLTPFLAPAAH----- 109



gi|112363098|ref|NP\_032855.2| ITSWCLFGPELPEPDRSPVPAKGLLSPLMSRPEIKAGDSSGTGACQKVLKPLGPPRQLLLPTSG-AHWPAGVVKPSPPAAAGVEEDSGLEEGSAAPLLKSKPRALEGSGGGVAANAASAPGGVTLVPKEDSRFSAPRVS-LEQD 286  
gi|12408292|ref|NP\_074038.1| ITSWCLFGPELPEPDRSPVPAKGLLSPLMSRPEIKAGDSSGTGACQKVLKPLKAVPPRQLLLPTSG-AHWPAGVVKPSPPAAATVEVEDDGLTEGSAAGLLKSKPRALEGSMCSGGGVANAPGAAPGGVTLVPKEDSRFSAPRVS-LEQD 285  
gi|110611914|ref|NP\_000917.3| ITSWCLFGPELPEPDRSPVPAKGLLSPLMSRSPCKVGDSSGTAAAHKVLPRGLSPARQLLLPASEPHWSPAGVVKPSPPAAAVVEEEDGSEEEAGLLKSKPRALGAAAGGGAAAVPPGAAAGGVALVPKEDSRFSAPRVALVEQD 286  
gi|50978746|ref|NP\_001003074.1| RSPRCPSGPEPDRPGARSQGAACPLMSRPEKAGDCGTAHAKGPPRGLSPSROPPLPCGAHANPAGAGKAAQPAALGVVEDEGGFAEESPPGLLKGKPRPAGPAAAGAAPAGPTAPGGTAPVPKEDSRFPAPKGLSLABQD 296  
gi|45383982|ref|NP\_990593.1| AAPWSLFGPEVPEVP-----VAPMSRGPQKAVDAG-----PGAPPSR-----PRPGAPLWPGADSLNVAVKARPGPEDASENRAPGLPGAEEERGFPFERDAGPGEGGLAPAAAAAFAA----- 213



gi|112363098|ref|NP\_032855.2| SPIAPGRSPLATTVDFIHVPIILPLNHALLAARTQLLEGDH-YDGGATAQGFAPPRGSPSAPSPPVPCGDFPDPCTVPLEGDPKEDVFPFLYGFDFTPGLKIKKEEEEGADAAVRSPRPYLSAGASSTFPDPF--LAPAP--QRAPSSR 430  
gi|12408292|ref|NP\_074038.1| APVAPGRSPLATTVDFIHVPIILPLNHALLAARTQLLEGDH-YDGGAAAQVPFAPPRGSPSAPSPPVPCGDFPDPCTVPPEGDPKEDGFPVYGFDFPGLKIKKEEEEGTEAASRSPRPYLLAGASAAATPDPF--LPPRP--PRAPPSR 429  
gi|110611914|ref|NP\_000917.3| APMAPGRSPLATTVDFIHVPIILPLNHALLAARTQLLEDEH-YDGGAGAASAFAPPRSPSCASSTPVAVGDFPDCAYPDAEPKDDAYPLYSDFPFPALKIKKEEEEGEAASRSPRSLVAGANPAAFDPF--LGPPPLPPRATPSR 433  
gi|50978746|ref|NP\_001003074.1| AP-APGCSPLATTMDFIHVPIILPLSFAFLAARTQLLEAEH-YDAGA----FAPPRGSPSAPCAPLAAGDFPDCAYPDAEPKDDAFPLYGFDFPALKIKKEEEEGEAASRSPRSLVAGPHSCVAFADAPPALPALPPLPRAPSSR 439  
gi|45383982|ref|NP\_990593.1| --VEPGAG--QDYLHVPIILPLNSAFILASRTRQLLEDAAYDGSAFG-----PRSPVVP-----AADLAEYGVPP-PDGKEGFP-AYGEFQS-ALKIKKEGVLPAA--PPFFLGAKAAPADFAQPF-----R 322



gi|112363098|ref|NP\_032855.2| PGE-AAVAGGPPSSAAVSPASSSGSALCECILYKAEAGAPPQGSFAPLPCKPPAAGSCLLPRDSLPL---AAPATAAAPAIYQPLGLNLGLP-LGYQAAVLKDSLQVYPPYLNLYLRPDSSEASQSPQYGFDSLQKIKLICGDEASGCHYGV 574  
gi|12408292|ref|NP\_074038.1| PGE-AAVAAP--AAVSPVSSSSGSALECILYKAEAGAPPQGSFAPLPCKPPAASCLLPRDSLPL---AAPSSAAPAIYPPGLNLGLP-LGYQAAVLKDSLQVYPPYLNLYLRPDSSEASQSPQYGFDSLQKIKLICGDEASGCHYGV 571  
gi|110611914|ref|NP\_000917.3| PGE-AAVTAAAPASAVSSSSGSALECILYKAEAGAPPQGFPAAPPCKAPGASCLLPRDGLPSTASAAAAGAAPALYALGLNLGLP-LGYQAAVLKDSLQVYPPYLNLYLRPDSSEASQSPQYGFDSLQKIKLICGDEASGCHYGV 581  
gi|50978746|ref|NP\_001003074.1| PGGGAPAAAAAGCASSASSPGLCEVLKYKAEAGAPPQGFPAAPCRVPGAGACLLPRDGLPAA--AASAGAAAGSALYQPLGLNLGLP-LGYQAAVLKDSLQVYPPYLNLYLRPDSSEASQSPQYGFDSLQKIKLICGDEASGCHYGV 587  
gi|45383982|ref|NP\_990593.1| AGQ-----EPSLECVLYKAE--PP-----LLPGAYPEPAAP-----DSLPL-----SLSAAPPGLYSPLGLNGHQAALGFPAAVLKDSLQVYPPYLNLYLRPDSSEASQSPQYGFDSLQKIKLICGDEASGCHYGV 435



gi|112363098|ref|NP\_032855.2| LITGSKVFFKRAMEGQHNYLCAGRNDICIVDKIRRNKCPACRLRKCQAGMVLGGRKFKKFNKVRVVRMLDVALPQSVGLPNESQALGORITFSPNQEIQLVPPILNLLMSIEPDVVIYAGHDNTPKPTSSSLLTSLNQLGERQLLSVVK 724  
gi|12408292|ref|NP\_074038.1| LITGSKVFFKRAMEGQHNYLCAGRNDICIVDKIRRNKCPACRLRKCQAGMVLGGRKFKKFNKVRVVRMLDVALPQSVAFPNESQALGORITFSPNQEIQLVPPILNLLMSIEPDVVIYAGHDNTPKPTSSSLLTSLNQLGERQLLSVVK 721  
gi|110611914|ref|NP\_000917.3| LITGSKVFFKRAMEGQHNYLCAGRNDICIVDKIRRNKCPACRLRKCQAGMVLGGRKFKKFNKVRVVRMLDVAVALPQVGVIPNESQALSQRFITFSPGDIQLVPPILNLLMSIEPDVVIYAGHDNTPKPTSSSLLTSLNQLGERQLLSVVK 731  
gi|50978746|ref|NP\_001003074.1| LITGSKVFFKRAMEGQHNYLCAGRNDICIVDKIRRNKCPACRLRKCQAGMVLGGRKFKKFNKVRVVRMLDVAVALPQVGVIPNESQALSQRFITFSPGDIQLVPPILNLLMSIEPDVVIYAGHDNTPKPTSSSLLTSLNQLGERQLLSVVK 737  
gi|45383982|ref|NP\_990593.1| LITGSKVFFKRAMEGQHNYLCAGRNDICIVDKIRRNKCPACRLRKCQAGMVLGGRKFKKFNKVRVVRMLD-VALQPAVLQDEQSLTORLESFSPNQEIQLVPPMISVLRGIEFVVIYAGHDNTPKPTSSSLLTSLNHLGERQLLSVVK 584



gi|112363098|ref|NP\_032855.2| WSKSLPGFRNLHIDDQIILIQYSWMSLMVFGLGWRYSYKHVSGQMLYFAPDLILNEQRMKELSFYSICLIMWQIPQEFVKLVQVHEEFLCMKVLVLLNLTIPLEGLRSQSFEMRSSYIRELIKAIGLRQKGVVPSQRFYQLTKLLDLSLH 874  
gi|12408292|ref|NP\_074038.1| WSKSLPGFRNLHIDDQIILIQYSWMSLMVFGLGWRYSYKHVSGQMLYFAPDLILNEQRMKELSFYSICLIMWQIPQEFVKLVQVHEEFLCMKVLVLLNLTIPLEGLRSQSFEMRSSYIRELIKAIGLRQKGVVPSQRFYQLTKLLDLSLH 871  
gi|110611914|ref|NP\_000917.3| WSKSLPGFRNLHIDDQIILIQYSWMSLMVFGLGWRYSYKHVSGQMLYFAPDLILNEQRMKESFYSICLIMWQIPQEFVKLVQVHEEFLCMKVLVLLNLTIPLEGLRSQSFEMRSSYIRELIKAIGLRQKGVVPSQRFYQLTKLLDNLH 881  
gi|50978746|ref|NP\_001003074.1| WSKSLPGFRNLHIDDQIILIQYSWMSLMVFGLGWRYSYKHVSGQMLYFAPDLILNEQRMKESFYSICLIMWQIPQEFVKLVQVHEEFLCMKVLVLLNLTIPLEGLRSQSFEMRSSYIRELIKAIGLRQKGVVPSQRFYQLTKLLDNLH 887  
gi|45383982|ref|NP\_990593.1| WSKLLPGFRNLHIDDQIILIQYSWMSLMVFAMGWRYSYKHVSGQMLYFAPDLILNEQRMKESFYSICLIMWQIPQEFVRLQVQVEEFLCMKVALVLLNLTIPLEGLRSQSFEMRSTYIRELVAIGLRQKGVVANSQRFYQLTKLMSMH 734



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*****.*.....*.*:*****
gi |112363098|ref|NP_032855.2| DLVKQLHLYCLNTFIQSRRLAVFEPFEMMSEVIAAQLPKILAGMVKPLLFHKK 926
gi |12408292|ref|NP_074038.1| DLVKQLHLYCLNTFIQSRRLAVFEPFEMMSEVIAAQLPKILAGMVKPLLFHKK 923
gi |110611914|ref|NP_000917.3| DLVKQLHLYCLNTFIQSRRLAVFEPFEMMSEVIAAQLPKILAGMVKPLLFHKK 933
gi |50978746|ref|NP_001003074.1| DLVKQLHLYCLNTFIQSRRLAVFEPFEMMSEVIAAQLPKILAGMVKPLLFHKK 939
gi |45383982|ref|NP_990593.1| DLVKQLHLYCLNTFIQSRRLAVFEPFEMMSEVIAAQLPKILAGMVKPLLFHKK 786
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