

gi|112363098|ref|NP_032855.2| MTELQAKDPOVLHTSGAASPPPHIGSPLLARLDGPFQGSQHSDDVS-----SVVSPPIPIIS-LDGLLPPRSC-RGPELDPDGTGDOOSLSVVEGAFSGVREATHREGGRNSRAPEKDSRLLDSVLDSSLTPSGTEQSHASPPACEA 137
gi|12408292|ref|NP_074038.1| MTELQAKDPRTLHTSGAAPSPTHVGSPLLARLDPPDFQGSQHSDDAS-----SVVSPPIPIIS-LDRLLFSRSC-QAELPDEKTONQOSLSDVEGAFSGVEASRRRS-RNPRAPEKDSRLLDSVLDLTLAPSGPEQSTSPACEA 136
gi|110611914|ref|NP_000917.3| MTELKAKGPRAPHVAGGPPSP-EVGSPLLCRPAAGFPFGSQTSDTL-----PEVSAIPIIS-LDGLLPPRSC-CGQDPDDEKTONQOSLSDVEGAFSGRAEATRGAGGSSSSPPEKDSGLLSDLDTLLAPSGPGSQSPPPACEV 136
gi|50978746|ref|NP_001003074.1| MTERTGKDARAPHVAGGAPSPAPAAEPESRRRDGGRRLRASQTSADPRVAAAAAAAAAASAPSPDRLLFSRRG-----CGAD-PGGKAQDAQPRPVARADPRLRAASGADSPGPPRQDRGPLHGAPSTALRPAAGPQGRSSE-AWEY 146
gi|45383982|ref|NP_990593.1| MTEVKSKEITRAPSSAR-----DGAVLLQAPPSSRGE-----AEGIDVA-LDGLLPPRSDDEEEEEEENEEEEEEEPQQREEEEEEEDDCPSYRFGGSLSKDCLDVLDTFLAPAAH----- 109



gi|112363098|ref|NP_032855.2| ITSWCLFGPELPEPRSPVPAKGLLSPLMSRPEIKAGDSSGTGAGQKVLKPLGPPRQLLLPTSG-AHWPAGVVKPSQPPAAAGVEEDSGLETEGSAAPLLKSKPRALEGMCSSGGVTAAPGGVTLVPKEDSRFSAPRVS-LEQD 286
gi|12408292|ref|NP_074038.1| ITSWCLFGPELPEPRSPVPAKGLLSPLMSRPEIKAGDSSGTGAGQKVLKPAVPPRQLLLPTSG-AHWPAGVVKPSQPPAAVEVEEDSGLETEGSAAPLLKSKPRALEGMCSSGGVTAAPGGVTLVPKEDSRFSAPRVS-LEQD 285
gi|110611914|ref|NP_000917.3| ITSWCLFGPELPEPRSPVPAKGLLSPLMSRSPCKVGDSSGTAAGKVLPRGLSPARQLLLPASEPHWSPAGVVKPSQPPAAAVEVEEDSGSEEEAGPLLKSKPRALEGMAAGGAAAVPPGAAAGGVALVPKEDSRFSAPRVALVEQD 286
gi|50978746|ref|NP_001003074.1| RSPRCPSGPEPPEDPRGARSQGAACPLMSRPEKAGDCGTAAGKGPRLSPSROPPLPCGAHANPAGAGKAAQPAALGVVEDEGGFAAEGSPGPLLKGRPRPAGPAAAGAAPAGPTAPGGTAPVVKEDSRIPAKKGLABQD 296
gi|45383982|ref|NP_990593.1| AAPWSLFGPEVPEVP-----VAPMSRGPQKAVDAG-----PGAPPSR-----PRPGAPLWPGADSLNVAVKARPGPEDASENRAPGLPGAEEERGFPFERDAGPGEGGLAPAAAAAFAA----- 213



gi|112363098|ref|NP_032855.2| SPIAPGRSPLATTVDFIHVPIILPLNHALLAARTRQLLEGDH-YDGGATAQGFAPPRGSPSAPSPPVPCGDFPDPCTVPLEGDPKEDVFPPLYGDFQTPGLKIKKEEEEGADAAVRSRPRYLSAGASSTFPDPF--LAPAP--QRAPSSR 430
gi|12408292|ref|NP_074038.1| APVAPGRSPLATTVDFIHVPIILPLNHALLAARTRQLLEGDH-YDGGAAAQVPFAPPRGSPSAPSPPVPCGDFPDPCTVPPEGDPKEDGFPVYGEFQPPGLKIKKEEEEGTEAASRSRPRYLLAGASAAATPDPF--LPPRP--PRAPPSR 429
gi|110611914|ref|NP_000917.3| APMAPGRSPLATTVDFIHVPIILPLNHALLAARTRQLLEDEH-YDGGAGAASAFAPPRSPSCASSTPVAVGDFPDCAYPDAEPKDDAYPLYSDFPQALKIKKEEEEGEAASARSRPRSYLVAGANPAAFDPF--LGPPPLPRATPSR 433
gi|50978746|ref|NP_001003074.1| AP-APGCSPLATTMDFIHVPIILPLGSAFLAARTRQLLEAEH-YDAGA----FAPPRGSPSAPCAPLAAGDFPDCAYPDAEPKDDAFPLYGDFQPPALKIKKEEEEGEAASARSRPRYLAAGPHSCVFADAPPALPALPPLPRAPSSR 439
gi|45383982|ref|NP_990593.1| --VEPGAG--QDYLHVPIILPLNSAFLASRTRQLLEDAAYDGSAFG-----PRSPVVP-----AADLAEYGVPP-PDGKEGFP-AYGEFQS-ALKIKKEGVLPAA--PPFFLGAKAAPADFAQPF-----R 322



gi|112363098|ref|NP_032855.2| PGE-AAVAGGPPSSAAVSPASSSGSALCECILYKAEAGAPPQGSFAPLPCKPPAAGSCLLPRDSLPL---AAPATAAAPAIYQPLGLNLGLP-LGYQAAVLKDSLPQVYPPYLNLYLRPDSASQSPQYGFDSLQKIKLICGDEASGCHYGV 574
gi|12408292|ref|NP_074038.1| PGE-AAVAAP--AAVSPVSSSSGSALECILYKAEAGAPPQGSFAPLPCKPPAASCLLPRDSLPL---AAPSSAAPAIYPPGLNLGLP-LGYQAAVLKDSLPQVYPPYLNLYLRPDSASQSPQYGFDSLQKIKLICGDEASGCHYGV 571
gi|110611914|ref|NP_000917.3| PGE-AAVTAAAPASAVSSSSGSALECILYKAEAGAPPQGFPAAPPCKAPGASCLLPRDGLPSTASAAAAAGAAPALYALGLNLGLP-LGYQAAVLKDSLPQVYPPYLNLYLRPDSASQSPQYGFDSLQKIKLICGDEASGCHYGV 581
gi|50978746|ref|NP_001003074.1| PGGGAPAAAAAGCASSASSPGLCELVLYKAEAGAPPQGFPAAPCRVPGAGACLLPRDGLPAA-AAAAGAAAGSALYQPLGLNLGLP-LGYQAAVLKDSLPQVYPPYLNLYLRPDSASQSPQYGFDSLQKIKLICGDEASGCHYGV 587
gi|45383982|ref|NP_990593.1| AGQ-----EPSLECVLYKAE-PP-----LLPGAYPEPAAP-----DSLPL-----SLSAAPPGLYSPLGLNGHQAALGFPAAVLKEGLPQLCPYVLYGVYRPTIETSQSSQYGFDSLQKIKLICGDEASGCHYGV 435



gi|112363098|ref|NP_032855.2| LITGSKVFFKRAMEGQHNYLCAGRNDICIVDKIRRNKCPACRLRKCQAGMVLGGRKFKKFNKVRVVRILDGVALPQSVGLPNESQALGORITFSPNQEIQLVPPILNLLMSIEPDVVIYAGHDNTKPDTSSSLTSLNQLGERQLLSVVK 724
gi|12408292|ref|NP_074038.1| LITGSKVFFKRAMEGQHNYLCAGRNDICIVDKIRRNKCPACRLRKCQAGMVLGGRKFKKFNKVRVVRALDVALPQSVAFPNESQALGORITFSPNQEIQLVPPILNLLMSIEPDVVIYAGHDNTKPDTSSSLTSLNQLGERQLLSVVK 721
gi|110611914|ref|NP_000917.3| LITGSKVFFKRAMEGQHNYLCAGRNDICIVDKIRRNKCPACRLRKCQAGMVLGGRKFKKFNKVRVVRALDVALPQSVGIPNESQALSQRITFSPGDIQLPPLINLLMSIEPDVVIYAGHDNTKPDTSSSLTSLNQLGERQLLSVVK 731
gi|50978746|ref|NP_001003074.1| LITGSKVFFKRAMEGQHNYLCAGRNDICIVDKIRRNKCPACRLRKCQAGMVLGGRKFKKFNKVRVVRILDVALPQVGVIPNESQALSQRITFSPGDIQLPPLINLLMSIEPDVVIYAGHDNTKPDTSSSLTSLNQLGERQLLSVVK 737
gi|45383982|ref|NP_990593.1| LITGSKVFFKRAMEGQHNYLCAGRNDICIVDKIRRNKCPACRLRKCQAGMVLGGRKFKKFNKVRVVRILD-VALQPAVLQDEQSLTORLESFSPNQEIPVFPVPMISVLRGIEFVVIYAGHDNTKPEFSSLLTSLNHLGERQLLSVVK 584



gi|112363098|ref|NP_032855.2| WSKSLPGFRNLHIDDQIILIQYSWMSLMVFGLGWRYSYKHVSGQMLYFAPDLILNEQRMKELSFYSICLIMWQIPQEFVKLVQVHEEFLCMKVLVLLNTIPELGRSQSQFEMRSSYIRELIKAIGLRQKGVVPSQRFYQLTKLLDSLH 874
gi|12408292|ref|NP_074038.1| WSKSLPGFRNLHIDDQIILIQYSWMSLMVFGLGWRYSYKHVSGQMLYFAPDLILNEQRMKELSFYSICLIMWQIPQEFVKLVQVHEEFLCMKVLVLLNTIPELGRSQSQFEMRSSYIRELIKAIGLRQKGVVPSQRFYQLTKLLDSLH 871
gi|110611914|ref|NP_000917.3| WSKSLPGFRNLHIDDQIILIQYSWMSLMVFGLGWRYSYKHVSGQMLYFAPDLILNEQRMKESFYSICLIMWQIPQEFVKLVQVHEEFLCMKVLVLLNTIPELGRSQSQFEMRSSYIRELIKAIGLRQKGVVPSQRFYQLTKLLDNLH 881
gi|50978746|ref|NP_001003074.1| WSKSLPGFRNLHIDDQIILIQYSWMSLMVFGLGWRYSYKHVSGQMLYFAPDLILNEQRMKESFYSICLIMWQIPQEFVKLVQVHEEFLCMKVLVLLNTIPELGRSQSQFEMRSSYIRELIKAIGLRQKGVVPSQRFYQLTKLLDNLH 887
gi|45383982|ref|NP_990593.1| WSKLLPGFRNLHIDDQIILIQYSWMSLMVFAMGWRYSYKHVSGQMLYFAPDLILNEQRMKESFYSICLIMWQIPQEFVRLVQVHEEFLCMKVLVLLNTIPELGRSQSQFEMRSTSYIRELVAIGLRQKGVVPSQRFYQLTKLLDSMH 734



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gi |112363098|ref|NP_032855.2| DLVKQLHLYCLNTFIQSRRLAVFPEMSEVIAAQLPKILAGMVKPLLFHKK 926
gi |12408292|ref|NP_074038.1| DLVKQLHLYCLNTFIQSRALAVFPEMSEVIAAQLPKILAGMVKPLLFHKK 923
gi |110611914|ref|NP_000917.3| DLVKQLHLYCLNTFIQSRALAVFPEMSEVIAAQLPKILAGMVKPLLFHKK 933
gi |50978746|ref|NP_001003074.1| DLVKQLHLYCLNTFIQSRALAVFPEMSEVIAAQLPKILAGMVKPLLFHKK 939
gi |45383982|ref|NP_990593.1| DLVKQLHLYCLNTFIQSRALAVFPEMSEVIAAQLPKILAGMVKPLLFHKK 786
.....910.....920.....930.....940.....950..

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