

gi | 110665742 | ref | NP_613059.2 | -----METEN---DKTM-EESTKRKE--KKKRSRVKQVLADIAKQVDFWFGDANLHKDRFLREQIEKSRDGYVDISLLVFNKMKKLTLDGKLIARALKSSSVVELDLEGTRIRRKKPLG 110
gi | 109458788 | ref | XP_001077220.1 | -----METESGNOEKVMEESSTEKKKEVEKKKRSRVKQVLADIAKQVDFWFGDANLHKDRFLREQIEKSRDGYVDISLLVFNKMKKLTLDGKLIARALKSSAVVELDLEGTRIRRKKPLG 116
gi | 109809739 | ref | NP_056269.1 | -----METESGNOEKLMEEESTTEKKKEVEKKKRSRVKQVLADIAKQVDFWFGDANLHKDRFLREQIEKSRDGYVDISLLVFNKMKKLTLDGKLIARALKSSAVVELDLEGTRIRRKKPLG 150
gi | 114595713 | ref | XP_001144338.1 | MTGHRVVEDLKRIIWP CVLKGKIKETKAMTPNIEGMEETESGNOEKLMEEESTTEKKKEVEKKKRSRVKQVLADIAKQVDFWFGDANLHKDRFLREQIEKSRDGYVDISLLVFNKMKKLTLDGKLIARALKSSAVVELDLEGTRIRRKKPLG 115
gi | 74002382 | ref | XP_535698.2 | -----METESGNOEKAM-EECTEKKKEVEKKKRSRVKQVLADIAKQVDFWFGDANLHKDRFLREQIEKSRDGYVDISLLVFNKMKKLTLDGKLIARALKSSAVVELDLEGTRIRRKKPLG 114
gi | 194667594 | ref | XP_001787730.1 | -----MEAESGNKEKAM-EEIEKKKE-EKKKRSRVKQVLADIVKQVDFWFGDANLHKDRFLREQIEKSRDGYVDISLLVFNKMKKLTLDGKLIARALKSSAVVELDLEGTRIRRKKPLG 118
gi | 118090340 | ref | XP_420643.2 | -----MTGMEEAAR-DKAMEEESTTEKKKEVEKKKRSRVKQVLADIAKQVDFWFGDANLHKDRFLREQIEKSRDGYVDISLLVFNKMKKLTLDGKLIARALKSSAVVELDLEGTRIRRKKPLG 124
gi | 41053963 | ref | NP_956224.1 | -----MKVCQRKTIETKMSVSGDLCADLSEKKNDEKKKRSRVKQVLLSDVKKQVEFWFGDANLHKDRFLREQIEKSRDGYVDIAVLTTFNRMKNLTADVLIARALKSSAVVELDLEGTRIRRKKPLG 139
gi | 24640787 | ref | NP_524795.2 | -----MAAKSIEKKEGEGEPALSAEKPDPAAPTEPAEENSKPEAPEDASPKDKGGRKRRHLFNSIRGOMEFYFGDANLSKDRFLRRYVE--DPVVPLEIFLFNKIKTLQDVFQIAKALSNQLLELDETELKVRRTKLP 112
gi | 158296988 | ref | XP_317298.4 | -----SME-----SQEKF-----NAGDKADKDKAVTKAKG-RHRSKHKFNIRKQIEFYFSDANLHKDRYMGQLLRN-GPFTPLEEFLFKIKALTINVDIETANALKSNLLELSDDRRAKVRRTKLP 1
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi | 110665742 | ref | NP_613059.2 | ERPKDEBERTVYVELLPKNVTHSWIERVFGKCGNVVYISIPHYKSTGDPKGFVAFVETKEQAAKAEFLNPPPEAPRKPPIFPTVKNKPIPALSIR-----VAEKKKKK-----KKKGRIRKKEEVCQA-----KESAVDSSESGVCKATKR 248
gi | 109458788 | ref | XP_001077220.1 | ERPKDEBERTVYVELLPKNVTHSWIERVFGKCGNVVYISIPHYKSTGDPKGFVAFVETKEQAAKAEFLNPPPEAPRKPPIFPTVKNKPIPALSIR-----VVEKKKKK-----KKKGRMKKEDNICA-----KEENMDTNTSISKM-KR 253
gi | 109809739 | ref | NP_056269.1 | ERPKDEBERTVYVELLPKNVTHSWIERVFGKCGNVVYISIPHYKSTGDPKGFVAFVETKEQAAKAEFLNPPPEAPRKPPIFPTVKNKPIPALSIR-----VVEKKKKK-----KKKGRMKKEDNICA-----KEENMDTNTSISKM-KR 287
gi | 114595713 | ref | XP_001144338.1 | ERPKDEBERTVYVELLPKNVTHSWIERVFGKCGNVVYISIPHYKSTGDPKGFVAFVETKEQAAKAEFLNPPPEAPRKPPIFPTVKNKPIPALSIR-----VSEKKKKK-----KKKGRMKKEDNICT-----KELNTDIDKESVAKM-KR 252
gi | 74002382 | ref | XP_535698.2 | ERPKDEBERTVYVELLPKNVTHSWIERVFGKCGNVVYISIPHYKSTGDPKGFVAFVETKEQAAKAEFLNPPPEAPRKPPIFPTVKNKPIPALSIR-----VTEKKKKK-----KKKGRMKKEDNICT-----KESNMDAKESGCK-KR 250
gi | 194667594 | ref | XP_001787730.1 | ERPKDVDSRTVYVELLPKNVTHSWIERVFGKCGNVVYISIPHYKSTGDPKGFVAFVETKEQAAKAEFLNPPPEAPRKPPIFPTVKNKPIPALSIRNSVNSVVEKKKK-----KKKSKIKKEGVCQAAVEAKESVNTTTEQAPKS-KR 264
gi | 118090340 | ref | XP_420643.2 | ERPKDVDSRTVYVELLPKTVTHIWLERVFSKCGHVYISIPRYKSTRHSKGFVAFVETKEQAAKAVEMLNPPPEAPRKPPIFPTVKNKPIPALSIRNSVNSVVEKKKK-----VTDNDEDG-----KKKTELKNTSEET-----GSNMDDQDQ 254
gi | 41053963 | ref | NP_956224.1 | DR-RDVNDKLYEALPANATHDWLKEVFSRYGVAIVSLPHYPTKIKIEFAFIEFEKSSLEKAVKAFQIQGLVSVET-DPSDLASVRSFQQQQIIOKKAEPHSEARQVELPKRNLKREAADKD-----REEIHEVKKRVLEEGQPS 283
gi | 24640787 | ref | NP_524795.2 | VK-ANSEETIYVESLPPKADHDWVRNVFSSYGTVAIVSLPKFPNSKIKIEFGFVEEASVQKALKAFTQFGVLAYETTPAKMASIKTVEPEAKFTQGHVGDNKRREDGDEPPAKRHKIDPISDE-----DDTQDDQSDRDANGOK 257
VK.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi | 110665742 | ref | NP_613059.2 | PRTAIEGSEAEPTPEAKOPAKK-KKKRDRVEASSLP-EARAGKRERCSAEDDEDCLPPRPKAKKRAQKDGVCQAASEVSKESRDLEFCSTBEKETDRKGDLSLKRKRKHKKHKRHKMGEEVPLRVLKTEWMD-LKKEYLALQKAE 394
gi | 109458788 | ref | XP_001077220.1 | SRPTSEGSDIESTEPKQCSKK-KKKRDRVEASSLP-EVRIGKRKRSSSEDAESLAPRSKVKKIIQKDP-IIKEASEASKENRDIESTEBEEDTDGLKDSLLKTKRKHKKKHKRHKMGEEVPLRVLKSEWMD-LKKEYLALQKAE 398
gi | 109809739 | ref | NP_056269.1 | SRPTSEGSDIESTEPKQCSKK-KKKRDRVEASSLP-EVRIGKRKRSSSEDAESLAPRSKVKKIIQKDP-IIKEASEASKENRDIESTEBEEDTDGLKDSLLKTKRKHKKKHKRHKMGEEVPLRVLKSEWMD-LKKEYLALQKAE 432
gi | 114595713 | ref | XP_001144338.1 | SRPTSEGSEVEIITPEKPPSKK-KKKRERQEVSSLP-IVRIGKRKRISSEASPLTPRSKVKKGGTKDP-IKKEDLEVSCKENKDLVSTEBEEDTDGVDKGSLLKAKRKHKKKHKRHKMGEEVPLRVLKSLKGANWIEKRVFSIAKGO 399
gi | 74002382 | ref | XP_535698.2 | SRPTSEGSEVEIITPEKPPSKK-KKKRERQEVSSLP-IVRIGKRKRISSEASPLTPRSKVKKGGTKDP-IKKEDLEVSCKENKDLVSTEBEEDTDGVDKGSLLKAKRKHKKKHKRHKMGEEVPLRVLKSEWMD-LKKEYLALQKAE 395
gi | 194667594 | ref | XP_001787730.1 | HRTSSECEMGGTEVHHRQLSKREKRKWRDRESSEVPVSRPGKRKRSSSGDGE--TSVAKVKKTQKDEVHPVKEETTEAPKDSNEVPLEDDDKDGDKDTLSLSKSRKHKKHKRHKMGEEVPLRVLKTEWMD-LKQEVYLLQKRC 410
gi | 118090340 | ref | XP_420643.2 | MLESIVTSEPNLATTSTVSKAKKRLRSQFEAS--SGEDQFEMS--SKMRKVEBEK-----SELKDLSSENKD-----BELNSLKKKDDVLRKAKRKRKHKRHKMGEEVPLRVLKSEWMD-LKQEVYLLQKRC 380
gi | 41053963 | ref | NP_956224.1 | ETSVAGEVASETDAEGTAEASEQEDKTEATDGD-----EAAKRRRKRKKAIVDKP-NIEPSALELKVLPKTSWSMRNKYLN-----LORRIVSEAKSLWRENHPQNOHPHHQOTSHPNHPKPPQLP-----EAVKEEETGG 413
gi | 158296988 | ref | XP_317298.4 | QIEPASEEFPQSDIEEPVSGDNKDETDQAKDDQDVKQDQKCKKCRQRKCSIIKELQLDDKVIYELKIMTKKEWRLRNKLYLN-----LQREAKKLLK-RLPHQTDKPHHHHHHQRGGHKKITASHPSGG-----IAKSKSSP 394
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi | 110665742 | ref | NP_613059.2 | MASLKKTIISQIKLE--SEMETDCKAPT-----AGSGQECSSQEKVSAQGFQFVIGVIVKISGEPLPGRKQVKDILATIIEVVYIDLLEGGTECHARFKTPEDAQAVINAQTEIRKKHSWNLEVLSDHEQRYWQKILVDROAKLNQ 534
gi | 109458788 | ref | XP_001077220.1 | MASLKKTIISQIKSE--SEMETDSGVPTNGMKNEKTANREBECRQEKVNATGPOFVSGVIVKIIITEPLPGRKQVRDTLAAISEVLVVDLLEGGTECHARFKTPEDAQAVINAYTEINKKHCKWLEILSDHEQRYWQKILVDROAKLNQ 40
gi | 109809739 | ref | NP_056269.1 | MASLKKTIISQIKSE--SEMETDSGVPTNGMKNEKTANREBECRQEKVNATGPOFVSGVIVKIIITEPLPGRKQVRDTLAAISEVLVVDLLEGGTECHARFKTPEDAQAVINAYTEINKKHCKWLEILSDHEQRYWQKILVDROAKLNQ 546
gi | 114595713 | ref | XP_001144338.1 | MASLKKTIISQIKSE--SEMETDSGVPTNGMKNEKTANREBECRQEKVNATGPOFVSGVIVKIIITEPLPGRKQVRDTLAAISEVLVVDLLEGGTECHARFKTPEDAQAVINAYTEINKKHCKWLEILSDHEQRYWQKILVDROAKLNQ 580
gi | 74002382 | ref | XP_535698.2 | HASLKKTIISQMKSE--SKMETN-GVPTTSEIKTEKINS-BECCQEKVNAAGPOFVSGVIVKIIITEPLPGRKQVRDTLAAISEVVYVDLLEGGTECHARFKTPEDAQAVINACTEIKKKYCWLEILSDHEQRYWQKILVDROAKLNQ 545
gi | 194667594 | ref | XP_001787730.1 | MASLKKTIISQIKS--SEMETN-GVPTNSGMKNEKSGG--LVFLGSLVGLLAYGILAPRVEVEVPP--LEVRDTLAAISEVVYVDLLEGGTECHARFKTPEDAQAVINACTEIKKKYCWLEILSDHEQRYWQKILVDROAKLNQ 536
gi | 118090340 | ref | XP_420643.2 | MASLKKTIISQIKPEVPGEMETNSCAPKNLQCKNGESTS-EDGAPPVKANTMGPOFVSGVIVKIIITEPLPGRKQIKDALAMLADVAVYDMLLEGGTECHVRFNTPEDAQAVINAYTEINKKHCKWLEILSDHEQRYWQKILVDROAKLNQ 559
gi | 41053963 | ref | NP_956224.1 | MAHLKOSVFCINQK-----PTNYHIVKLLK-----EDDTNAFYKDTPKKELTSGPEFLSGVIVKISYNOPLPSKRCIKDMLSELSPPVAVYVDLLEGGTEGHVRFKSSSEDAQKVIKARFEFQKYNWNLLELSDHERRVYQKILVDROAKLNT 521
gi | 24640787 | ref | NP_524795.2 | EVPDGGEGEVAEAPVPAKRRKAVHKMNMNFYAGGVVESTKSEEPSERTPLPKYVEPLIVCSLLKPCNTNVKFEKAEKMQVDPDIKVVYDLEGGDQVALLRGLTPAAAEELLRQVNCSE-----QLKVLSSGQETLYWRKIEQDREAKLSK 559
gi | 158296988 | ref | XP_317298.4 | RVNFCAMPVEEDHEEGDQGTGSHLLQP-----EAAEEAATAKPLFSFEPGLIVSIFKREPCVDVDFRAELKQVYVYKVIDLLEGGDFEAFVYVDTTPASAVLVKVEYCSAEH-----SAGILSSEGEQYDQKMMRDREPKLK 531
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



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      : : ** * :
gi | 110665742 | ref | NP_613059.2 | --PREKKRGTEKLIITKAEKIRLAKTQQAASQHIRFSEYD 570
gi | 109458788 | ref | XP_001077220.1 | --PLEKKRGTEKLVITKAEKIRLAKTQQAASQHIRFSEYD 76
gi | 109809739 | ref | NP_056269.1 | --PREKKRGTEKLIITKAEKIRLAKTQQAASKHIRFSEYD 582
gi | 114595713 | ref | XP_001144338.1 | --PREKKRGTEKLIITKAEKIRLAKTQQAASKHIRFSEYD 616
gi | 74002382 | ref | XP_535698.2 | --PREKKRGTEKLIITKAEKIRLAKTQQAASKHIRFSEYD 581
gi | 194667594 | ref | XP_001787730.1 | --PREKKRGTEKLIITKAEKIRLEKTQQAASQHIRFSEYD 572
gi | 118090340 | ref | XP_420643.2 | --PREKKRGTEKLIITKAERMRLEKTQQAASKHIRFSEYD 595
gi | 41053963 | ref | NP_956224.1 | --PREKKRGTEKLIITKAEKIITAKAKEASNHIRFDD-- 555
gi | 24640787 | ref | NP_524795.2 | KVRVQKRGREKVGKMLGKHIKFDDEDEVQAAMD-- 595
gi | 158296988 | ref | XP_317298.4 | RVKTEIRIGRTKLIRKINSHIKFDDE----- 559
      .....610.....620.....630.....

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