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                                                                                                                .: .       **    .  :: .        * :   ::   ::  .: *          * ::    :
gi|21356375|ref|NP_647847.1|     -----MEFLHESVALG--VDLLILGLCAREYVHYKRTAKVLKAAPQYNIDGDLKSVVERQRDKKIPYAVIRGTVTPIGVPLRSSLVPSVSGVLQIVKLHEHRVTR-GFAGFWTEQHKLLHESANEMPFELRNQSH----GVEIVDALSAA   138
gi|31215281|ref|XP_315995.1|     -----MEYLQEAVLLG--IDLLVLVVCSNQYYKLRKNCRALKDAPQLQIDDQLADRLRKEPDQKLKYAVIRGSVTPIGTALRSAMSPSVTGVLQTMTLTEHRVAR-AMFGFWQEEKQIIHVSANETPFRLVNGKQ----GVEIVSGLSAE   138
gi|171542821|ref|NP_078820.2|    MESGGRPSLCQFILLG--TTSVVTAALYSVYRQKARVSQELKGAKKVHLGEDLKSILSEAPGKCVPYAVIEGAVRSVKETLNSQFVENCKGVIQRLTLQEHKMVWNRTTHLWNDCSKIIHQRTNTVPFDLVPHEDGVDVAVRVLKPLDSV   148
gi|114554453|ref|XP_001161118.1| MESGGRPSLCQFILLG--TTSVVTAALYSVYRQKARVSQELKGAKKVHLGEDLKSILSEAPGKCVPYAVIEGAVRSVKETLNSQFVENCKGVIQRLTLQEHKMVWNRTTHLWNDCSKIIHQRTNTVPFDLVPHEDGVDVAVRVLKPLDSV   148
gi|73950663|ref|XP_544520.2|     MESGGRPSLGQFILLG--TSSVVTAVLYSVYRQKAQVAQELKGAKRIHLGEDLKSILSEAPGKCVPYAVIEGAVRSVKETLNSQFVENCKGVIQRLTLQEHKMVWNRTTHLWNDYSKIIHQRTNTVPFDLVPHEDGVGVAVRVLKPLDSQ   148
gi|31541787|ref|NP_080965.2|     MESGSRPSLGQVILLG--TSSMVTAVLYSIYRQKAQVAQELKGAKKIHLGEDLKGILSEAPGKCVPYAVIEGAVRSVKETLNSQFVENCKGVIQRLSLQEHKMVWNRTTHLWNDYSKIIHQRTNTVPFDLVPHEDGVAVSVRVLKPLDSV   148
gi|27716275|ref|XP_233584.1|     MESGSRPSLGQVILLG--TSSMVTAVLYSIYRQKAQVAQELKGAKKIHLGEDLKAILSEAPGKCVPYAVIEGAVRSVKETLNSQFVENCKGVIQRLTLQEHKMVWNRTTHLWNDYSKIIHQRTNTVPFDLVPHEDGVAMAVRVLKPLDSV   148
gi|61846229|ref|XP_585175.1|     MESGGRPSLGQFILLG--TSSVVTAFLYSVYRQKAQVAQELKGAKRIHLGEDLKSILSEAPGKCVPYAVIEGAVRSVKETLNSQFVENCKGVIQRLTLQEHKMVWNRTTHLWNDCSKIIHQRTNTVPFDLVPHEDGAGVAVRVLKPLDAV   148
gi|118108991|ref|XP_424579.2|    ------------------------------------------------------------------------VVRSVRDTLSSQFVENCKGVGQRLTLQEHKMGWNRTTHLWNDYEKIIHQRTNTTAFDLAPLEDGTGVAVRVMKPLEAA    78
gi|148922854|ref|NP_001092230.1| MEASGKPSTAQIVLLA--TSSALTAVLYTIYKRKSSHVARLREAKKMSLNPELKTILSEAPGKCVPYAVIEGVVRSVKETLNSQFVDNCKGVIQRLTLNEKKMVWNRTTNLWNDCEKVIHQRTNTVPFDLAPHDDTVPTTVRVLRPLDAA   148
gi|30696917|ref|NP_176574.2|     -----------MIPWGGVTCCLSAAALYLLGRSSGRDAEVLETVTRVNQLKELAQLLELDS-KILPFIVAVSGRVGSETPIKCEHSG-IRGVIVEETAEQH-FLKHNETGSWVQDSALMLSMSKEVPWFLDDGTS----RVHVMGARGAT   132
gi|115473747|ref|NP_001060472.1| ----------MLIPWGGVGCCLSAAALYLLGRSSGRDAEVLRSVARAGSTKDLAAILDTAS-KVLPLVVAVSGRVGSDTPLICQQSG-MRGVIVEETAEQH-FLKHNDAGSWIQDSAVMLSVSKEVPWYLDDGTG----RVFVVGARGAA   133
                                 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150

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gi|21356375|ref|NP_647847.1|     VLDVDVVYDNYEPSNLSLFDHVFGFFSGVRQRGLQTTEEVLREGSFLTAIGELELDGD-TLRMQP-S-NEGPLFLTTATKSTLIKRFEDAKTTTILKLVVCSTISAILVAFIAKKLYRKRKQEREEAKIRERLDTERRERRA--------   277
gi|31215281|ref|XP_315995.1|     LLDMDTVYENYEPSSLTVFDHLFGLFSGVRQKGLQTTEEMLRDGSFITAVGELELDDT-GVRLHPPS-NGWPMFLTTATKSTLLKRLEEAKSSTLLKVILSGTISAVLIVLITRKLYKRKKQEWEEDKLRKQLEQSRATRRA--------   278
gi|171542821|ref|NP_078820.2|    DLGLETVYEKFHPSIQSFTDVIGHYISGERPKGIQETEEMLKVGATLTGVGELVLDNN-SVRLQPPK-QGMQYYLSSQDFDSLLQRQESSVRLWKVLALVFGFATCATLFFILRKQYLQRQERLRLKQMQEEFQEHEAQLLS--------   288
gi|114554453|ref|XP_001161118.1| DLGLETVYEKFHPSIQSFTDVIGHYISGERPKGIQETEEMLKVGATLTGVGELVLDNN-SVRLQPPK-QGMQYYLNSQDFDSLLQRQESSVRLWKVLALVFGFATCATLFFILRKQYLQRQERLRLKQMQEEFQEHEAQLLS--------   288
gi|73950663|ref|XP_544520.2|     DLGLETVYEKFHPSIQSFTDVIGHYISGERPKGIQETEEMLKVGATLTGVGELVLDNN-SVRLQPPK-QGMQYYLSSQDFDSLLQRQESSVRLWKVLTLVFGFATCAALFFILRKHYLQRQERQRLRQMEKEFQEHEAQLLS--------   288
gi|31541787|ref|NP_080965.2|     DLGLETVYEKFHPSVQSFTDAIGHYISGERPKGIQETEEMLKVGATLTGIGELVLDNN-AVRLQPPK-QGMQYYLSSQDFDSLLHRQESSVRLWKILVLVFGFATCATLFFILRKQYLHRQERLRQQQLQEEFLEHEAQLLS--------   288
gi|27716275|ref|XP_233584.1|     DLGLETVYEKFHPSVQSFTDAIGHYISGERPKGVQETEEMLKVGATLTGIGELVLDNN-SVRLQPPK-QGMQYYLSSQDFDSLLHRQESSVRLWKVLVLVFGFATCATLFFILRKQYLQRQERLRQQQLQDEFLEHEAHLLS--------   288
gi|61846229|ref|XP_585175.1|     DLGLETVYERFHPSTPSFTDVVGHYLSGERPKGVQETEEMLKVGAPLTGVGELVLDHS-CVRLQPPKGPGMQYYLSSQDFDSLLQRQESSVRLWKVLALVFGFAACASLFFLLRKQYLRR--RRERQRPEEEFRERACPEED--------   287
gi|118108991|ref|XP_424579.2|    ELSLETVHEKFHPSVQSFPDVIGHYISGERPKGIQETEQMLKVGAALTGVGELVLDNN-TIKLQPPK-QGLRYYLTSSDFDALLRKQESSAKLWKMLTILFGFATCAALFFLLRKQYRHHRERQHLKQMQEEFRQAQERLMR--------   218
gi|148922854|ref|NP_001092230.1| ELDLETTYENFHPSQQSLTNVIGHFISGERPQGIQETEEMLRLGASMTGVGELVLDNN-LVRLQPPK-KGLRYFLSRLDYDTLLSKQEGHLRIWRVLTVLLGLTACATFFYLLWRQYVLRKERRKEQSVLDEYRKWQSKRFQ--------   288
gi|30696917|ref|NP_176574.2|     GFALTVGSEVFEESGRSLVRGTLDYLQGLKMLGVKRIERVLPTGIPLTIVGEAVKDDIGEFRIQKPD--RGPFYVSSKSLDQLISNLGKWSRLYKYASMGFTVLGVFLITKHVIDSVLERRRRRQLQKRVLDAAAKRAELESEGSNGTRE   280
gi|115473747|ref|NP_001060472.1| GLVLTVASEVFEESGRTLVRGTLDYLQGLKMLGVKRTERVLPTGTSLTVVGEAIKDDVGTIRIQRPH--KGPFYVSPKSIDQLIMNLGKWAKLYQLASMGFAAFGVFLLAKRALQHFLERKRRHELQKR---------------------   260
                                 .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300

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gi|21356375|ref|NP_647847.1|     --RSRPHTLSQ-DQLCVVCSTNPKEIILLPCGHVCLCEDCAQKIS--VTCPVCRGSIVSKAAAFIA   338
gi|31215281|ref|XP_315995.1|     --RMRTTGLAE-EQLCVVCIVNPKEVICLPCGHVCLCENCAQKIS--LHCPVCRTVIETKAAAFIS   339
gi|171542821|ref|NP_078820.2|    --RAKPEDRESLKSACVVCLSSFKSCVFLECGHVCSCTECYRALPEPKKCPICRQAITRVIPLYNS   352
gi|114554453|ref|XP_001161118.1| --RAKPEDRESLKSACVVCLSSFKSCVFLECGHVCSCTECYRALPEPKKCPICRQAITRVIPLYNS   352
gi|73950663|ref|XP_544520.2|     --RAKPEDRESLKSACVVCLNSFKSCVFLECGHVCSCAECYRALPEPKRCPICRQEITRVIPLYNS   352
gi|31541787|ref|NP_080965.2|     --QASPEDRESLKSACVVCLSNFKSCVFLECGHVCSCRQCYLALPEPKRCPICRREITRVIPLYNS   352
gi|27716275|ref|XP_233584.1|     --QASPEDRESLKSACVVCLSNFKSCVFLECGHVCSCRQCYLALPEPKRCPICRRGITRVIPLYNS   352
gi|61846229|ref|XP_585175.1|     --RPE-EDREGPKGACVVCLNNFRSCVFLECGHLCACTECYRALPEPRRCPICRQEISRVVRLYNS   350
gi|118108991|ref|XP_424579.2|    --EVNAEGGETLKNACVICLSSAKSCVFLECGHVCSCTECYRALPEPKRCPICRQAITRVVPLYNS   282
gi|148922854|ref|NP_001092230.1| --ELHLAKEDVSPTACTICLNHERSCVFLECGHVCACEGCYRALPEPKKCPICRATIDRIVSLYNS   352
gi|30696917|ref|NP_176574.2|     SISDSTKKEDAVPDLCVICLEQEYNAVFVPCGHMCCCTACSSHLT---SCPLCRRRIDLAVKTYRH   343
gi|115473747|ref|NP_001060472.1| ---------------CVLT-----NHLFG------FRRTCYSHLH---SSVVCS----LC------   287
                                 .......310.......320.......330.......340.......350.......360......
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