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                                   :*:. * :  :.    ::::* *  . :       : :*:   ::*:   : . : :..:*  :.                                                  * *:****: *.*
gi|21358365|ref|NP_649352.1|      ---MAG--VLFEDIFNVKDMDPEGKKFDRVSRLHCES--ESFKMDLILDINSWLYPMELGDKFRLVLATTLREDGC---------PDSGEYNPMEHEGTRADSFEYVMYGKIYRIEGD-EAHNEAS-RLSAYVSFGGLLMRLQGDANNLH   132
gi|58393552|ref|XP_320161.2|      ---MSG--ILFEDIFNVKDMDPEGKKFDRVSRLHCES--ESFKMDLILDINSWLYPLELGDKFRLVLATTLHEDGT---------AASMEYNAAEIEGSRADSFEYVMFGKVYRIEGD-DSQTESSNRLSAYVSFGGLLMRLQGDANNLH   133
gi|62955177|ref|NP_001017600.1|   ---MAG--ILFEDIFDVKDIDPDGKKFDRVSRLHCES--ESFKMDLILDVNIQIYPVDLGDKFRLVIASTLYEDGT---------PDDGEYNPQDDRPSRADQFDYVMYGKVYRIEGD-ETSTEAATRLSAYVSYGGLLMRLQGDANNLH   133
gi|125851151|ref|XP_001331089.1|  ---MAG--ILFEDIFDVKDIDPDGKKFDRVSRLHCES--ESFKMDLILDVNIQIYPVDLGDKFRLVIASTLYEDGT---------PDDGEYNPQDDRPSRADQFDYVMYGKVYRIEGD-ETSTEAATRLSAYVSYGGLLMRLQGDANNLH   133
gi|14589953|ref|NP_006223.2|      ---MAG--ILFEDIFDVKDIDPEGKKFDRVSRLHCES--ESFKMDLILDVNIQIYPVDLGDKFRLVIASTLYEDGT---------LDDGEYNPTDDRPSRADQFEYVMYGKVYRIEGD-ETSTEAATRLSAYVSYGGLLMRLQGDANNLH   133
gi|50752375|ref|XP_422761.1|      ---MAG--ILFEDIFDVKDIDPEGKKFDRVSRLHCES--ESFKMDLILDVNIQIYPVDLGDKFRLVIASTLYEDGT---------LDDGEYNPTDDRPSRADQFEYVMYGKVYRIEGD-ETSTEAATRLSAYVSYGGLLMRLQGDANNLH   133
gi|62658151|ref|XP_573313.1|      ---MAG--ILFEDIFDVKDIDPEGKKFDRVSRLHCES--ESFKMDLILDVNIQIYPVDLGDKFRLVIASTLYEDGT---------LDDGEYNPTDDRPSRADQFEYVMYGKVYRIEGD-ETSTEAATRLSAYVSYGGLLMRLQGDANNLH   133
gi|109489487|ref|XP_213574.3|     ---MAG--ILFEDIFDVKDIDPEGKKFDRVSRLHCES--ESFKMDLILDVNIQIYPVDLGDKFRLVIASTLYEDGT---------LDDGEYNPTDDRPSRADQFEYVMYGKVYRIEGD-ETSTEAATRLSAYVSYGGLLMRLQGDANNLH   133
gi|21704118|ref|NP_663607.1|      ---MAG--ILFEDIFDVKDIDPEGKKFDRVSRLHCES--ESFKMDLILDVNIQIYPVDLGDKFRLVIASTLYEDGT---------LDDGEYNPTDDRPSRADQFEYVMYGKVYRIEGD-ETSTEAATRLSAYVSYGGLLMRLQGDANNLH   133
gi|61887551|ref|XP_581913.1|      ---MAG--ILFEDIFDVKDIDPEGKKFDRVSRLHCES--ESFKMDLILDVNIQIYPVDLGDKFRLVIASTLYEDGT---------LDDGEYNPTDDRPSRADQFEYVMYGKVYRIEGD-ETSTEAATRLSAYVSYGGLLMRLQGDANNLH   133
gi|57109920|ref|XP_535826.1|      ---MAG--ILFEDIFDVKDIDPEGKKFDRVSRLHCES--ESFKMDLILDVNIQIYPVDLGDKFRLVIASTLYEDGT---------LDDGEYNPTDDRPSRADQFEYVMYGKVYRIEGD-ETSTEAATRLSAYVSYGGLLMRLQGDANNLH   133
gi|114590780|ref|XP_526411.2|     ---MAG--ILFEDIFDVKDIDPEGKKFDRVSRLHCES--ESFKMDLILDVNIQIYPVDLGDKFRLVIASTLYEDGT---------LDDGEYNPTDDRPS-----------------------------SSAYVSYGGLLMRLQGDANNLH   105
gi|17553210|ref|NP_498036.1|      ---MAG--IIFDDMFKVKSVDPDGKKFDRVSRYFCDA--ESFKMELIIDINSQIYPLKQNDKVRLVLATTLREDGL---------ADEGEYDP-KAEYPRIKQYEYVMYGKVYRLEDD-DTGTDGG-KLAAYASFGGLLMRLKGEAINLH   131
gi|15221759|ref|NP_175827.1|      ---MASNIILFEDIFVVDQLDPDGKKFDKVTRVQATS--HNLEMFMHLDVNTEVYPLAVGDKFTLALAPTLNLDGT---------PDTGYFTP-GAKKTLADKYEYIMHGKLYKISE----RDGKTPKAELYVSFGGLLMLLKGDPAHIS   131
gi|15231714|ref|NP_191519.1|      ---MASNIIMFEDIFVVDKLDPDGKKFDKVTRVEARS--HNLEMFMHLDVNTEVYPLAVGDKFTLAMAPTLNLDGT---------PDTGYFTP-GAKKTLADKYEYIMHGKLYKISE----RDGKTPKAELYVSFGGLLMLLQGDPAHIS   131
gi|115456559|ref|NP_001051880.1| ---MAE--FLFEDIFTVTRLDPDGKKFDRVSRIEARS--DQFDMYMQLDVATDVYPMHPGDRFTMVLVPTLNLDGT---------PDSAFFTQ-AGRKTLADKYEYVMHGKLYKISEDKDTSDQNAKKVEMYASFGGLLVMLKGDPSSAA   133
gi|50306807|ref|XP_453379.1|      -----MSSALFDDVFTVQEVDTG--RYNKVSRIEAQS-TSQESCKLTLDINSELFPIKTQDQLAVMITTSLQLDGS---EEPQGTSWRAPP-AGT--RSLADDYDYVMYGTAYKFEEV----KGNKDLLAVYYSFGGLLMRLEGNYRLLN   132
gi|45185797|ref|NP_983513.1|      -----MSSTLFDDIFTIQEVDQG--RYNKVSRIEAIS-TSQDTCKLTLDVNTELFPLQPQQQLTVMLATTLNLDGT---EDSHG-SWRPPA-PGA--RSLADDFDYVTYGTAYKFEEA----NGNKDMLAVYYSFGGLLMRLEGNYRLLS   131
gi|6324798|ref|NP_014867.1|       -----MSNTLFDDIFQVSEVDPG--RYNKVCRIEAAS-TTQDQCKLTLDINVELFPVAAQDSLTVTIASSLNLEDTPANDSSATRSWRPPQ-AGD--RSLADDYDYVMYGTAYKFEEV----S--KDLIAVYYSFGGLLMRLEGNYRNLN   133
gi|39971529|ref|XP_367155.1|      MAVATSDAQLFEGVFKVTEVNQQ--KYDRVARIWARSDASTDLMDMTLDINTELFPMSEGEVFRVVLATSLSLDGS---KDDDKAGWRDATKLGG-PATLADSFDYVCHGKIYKFEDS----E-DGDNIKAYISFGGLLMCLNGPYKKLT   139
gi|85109003|ref|XP_962700.1|      MSALTSDAQLFEDEFKVERISDP--KYDRVDRLYCTS--VDGQTSMQLDVNKELFPVKVGEYLRIALATSLSLDGS---KDDER-GWRDAAKLGSVEQTLADSYEYVCHGKVYKFEDG----K-DGQTIKAYMSYGGLLMALDGPYKKLT   137
                                  1.......10........20........30........40........50........60........70........80........90........100.......110.......120.......130.......140.......150
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                                   :. :   :** .
gi|21358365|ref|NP_649352.1|      GFEVDQHMYLLMKRLAF   149
gi|58393552|ref|XP_320161.2|      GFEIDQHMFLLMKKLAF   150
gi|62955177|ref|NP_001017600.1|   GFEVDSRVYLLMKKLAF   150
gi|125851151|ref|XP_001331089.1|  GFEVDSRVYLLMKKLAF   150
gi|14589953|ref|NP_006223.2|      GFEVDSRVYLLMKKLAF   150
gi|50752375|ref|XP_422761.1|      GFEVDSRVYLLMKKLAF   150
gi|62658151|ref|XP_573313.1|      GFEVDSRVYLLMKKLAF   150
gi|109489487|ref|XP_213574.3|     GFEVDSRVYLLMKKLAF   150
gi|21704118|ref|NP_663607.1|      GFEVDSRVYLLMKKLAF   150
gi|61887551|ref|XP_581913.1|      GFEVDSRVYLLMKKLAF   150
gi|57109920|ref|XP_535826.1|      GFEVDSRVYLLMKKLAF   150
gi|114590780|ref|XP_526411.2|     GFEVDSRVYLLMKKLAF   122
gi|17553210|ref|NP_498036.1|      GFEVDMNLYLLMKKTDF   148
gi|15221759|ref|NP_175827.1|      HFELDQRLFLLMRKL--   146
gi|15231714|ref|NP_191519.1|      HFELDQRLFLLMRKL--   146
gi|115456559|ref|NP_001051880.1| NFELDQRLFLLMRKV--   148
gi|50306807|ref|XP_453379.1|      NLKQEN-AYLLCRK---   145
gi|45185797|ref|NP_983513.1|      NFKQEN-VYLLCRR---   144
gi|6324798|ref|NP_014867.1|       NLKQEN-AYLLIRR---   146
gi|39971529|ref|XP_367155.1|      PLRVDY-IYLLIKGNKD   155
gi|85109003|ref|XP_962700.1|      PLRVDY-VYLLANRNA-   152
                                  .......160.......
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