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                                                                                                .:  :                 *::::* * **** * :** ::::.*: *:*.  * ::** :****.  *     : :. :   :  * :
gi|17136226|ref|NP_476581.1|     ----------------------------------------MAAIKDS----------LLAQVAEV------LPSS-GHKVTIVGIGQVGMASAFSILAQNVSKEVCLIDVCADKLQGELMDLQHGSNFLKNPQITASTDFAASANSRL    91
gi|58385914|ref|XP_314306.2|     ----------------------------------------MSEVKAK----------LLTQIAEP------MTSS-GNKVTVVGIGQVGMACAFSILTQNVSSEVALIDVNADKLQGEMMDLQHGSAFMKNAHVSAGTDFSVSAGSRL    91
gi|17535107|ref|NP_496503.1|     ----------------------------------------MASTIKE----------VFAEIAAP------VENS-HGKVTVVGVGQVGMACAYSILQQNLANELCLVDVVADKLKGEMMDLQHGLAFTRHCTVKADTDYSITAGSKL    91
gi|5031857|ref|NP_005557.1|      ----------------------------------------MATLKDQ----------LIYNLLKE------EQTP-QNKITVVGVGAVGMACAISILMKDLADELALVDVIEDKLKGEMMDLQHGSLFLRTPKIVSGKDYNVTANSKL    91
gi|77539746|ref|NP_001029268.1|  ----------------------------------------MATLKDQ----------LIHNLLKE------EQTP-QNKITVVGVGAVGMACAISILMKDLADELALVDVIEDKLKGEMMDLQHGSLFLRTPKIVSGKDYNVTANSKL    91
gi|27806559|ref|NP_776524.1|     ----------------------------------------MATLKDQ----------LIQNLLKE------EHVP-QNKITIVGVGAVGMACAISILMKDLADEVALVDVMEDKLKGEMMDLQHGSLFLRTPKIVSGKDYNVTANSRL    91
gi|119920080|ref|XP_001251829.1| ----------------------------------------MATLKDQ----------LIQNLLKE------EHVP-QNKITIVGVGAVGMACAISILMKDLADEVALVDVMEDILKGEMMDLQHGSLFLRTPKIVSGKDYNVTANSRL    91
gi|73988675|ref|XP_865353.1|     ----------------------------------------MATLKDQ----------LIQNLLKE------DHTP-QNKITVVGVGAVGMACAISILMKDLADELALVDVMEDKLKGEMMDLQHGSLFLRTPKIVSGKDYNVTANSKL    91
gi|8393706|ref|NP_058721.1|      ----------------------------------------MAALKDQ----------LIVNLLKE------EQVP-QNKITVVGVGAVGMACAISILMKDLADELALVDVIEDKLKGEMMDLQHGSLFLKTPKIVSSKDYSVTANSKL    91
gi|62653460|ref|XP_576374.1|     ----------------------------------------MAALKEQ----------LIVNLLKE------EQVP-QNKITVVGVGAVGMACAISILMKDLADELALVDVIEDKLKGEMMDLQHGSLFLKTPKIVSSKDYSVTANSKL    91
gi|6754524|ref|NP_034829.1|      ----------------------------------------MATLKDQ----------LIVNLLKE------EQAP-QNKITVVGVGAVGMACAISILMKDLADELALVDVMEDKLKGEMMDLQHGSLFLKTPKIVSSKDYCVTANSKL    91
gi|45384208|ref|NP_990615.1|     ----------------------------------------MSLKDH----------LIHNVHKE------EHAHAHNKISVVGVGAVGMACAISILMKDLADELTLVDVVEDKLKGEMLDLQHGSLFLKTPKIISGKDYSVTAHSKL    91
gi|18858959|ref|NP_571321.1|     ----------------------------------------MASTKEK----------LIAHVSKE------QPAGPTNKVTVVGVGMVGMAAAVSILLKDLTDELALVDVMEDKLKGEAMDLQHGSLFLKTHKIVADKDYSVTANSKV    92
gi|115465906|ref|NP_001056552.1| ------------------------------------MKKASSLSELGFDADGPS--FFRHLTLTDGDDGTLPRRRLIKISVIGAGNVGMAIAQTILTQDLADEIVLIDAVADKVRGEMLDLQHAAAFLPRVNIVSGTEVSLTRSSDL   109
gi|115443679|ref|NP_001045619.1| MSHKTTIDHFHFHFQERSTSPLAFHPVSEGGRSRSRSRDMKKASSLSELGFDAEGASSGFFRPVADG-GSTPTSHRRRLTKISVIGAGNVGMAIAQTILTRDMADEIALVDAVPDKLRGEMLDLQHAAAFLPRVRLVSDTDLAVTRGSDL   149
gi|15236012|ref|NP_193459.1|     ----------------------------------MEKNASTSSLKDLGPSGLDLTSAFFKPIHNS---DPSLPSNRRTKVSVVGVGNVGMAIAQTILTQDLADEIALVDAKPDKLRGEMLDLQHAAAFLPRTKITASVDYEVTAGSDL   111
                                 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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                                 ::*:*.**  **::*.*:***. ::: *:*     **.  :::******:***:**:**:*  **:*** ****:***.*:.::* : . . :.:::********.:**.:.: *: :                 :       ::: *
gi|17136226|ref|NP_476581.1|     CIVTAGVRQKEGESRLSLVQRNTDILKNIIPKLVEYSPDTILLMVSNPVDIMTYVAWKLSGLPKNRVIGSGTNLDSSRFRFLMSQRLGVAPTSCHGWIIGEHGDSSVPVWSGVNIAGVRLRELNPILGTG------EDPEKWN-ELHKQV   234
gi|58385914|ref|XP_314306.2|     IVITAGVRQKEGESRLDLVQRNTDILKGIIPKLVAQSPDCILLVVSNPVDILTYVAWKLSGLPKNRVIGSGTNLDSSRFRFLMSQKLGVAPTSCHGWIIGEHGDSSVPVWSGVNVAGVRLAEINPSIGTD------ADTEKWG-DLHHQV   234
gi|17535107|ref|NP_496503.1|     CVVTAGARQREGETRLSLVQRNVEIFKGIIPQLVKYSPDTCILVVSNPVDVLTYVTWKLSGLPRERVFGSGTNLDSARFRFLLSEKLNIAPSSCHGWIIGEHGDSSVAVWSGVNVAGVTLHEIKPDIGEK------TDNEHWEAEIHKKV   235
gi|5031857|ref|NP_005557.1|      VIITAGARQQEGESRLNLVQRNVNIFKFIIPNVVKYSPNCKLLIVSNPVDILTYVAWKISGFPKNRVIGSGCNLDSARFRYLMGERLGVHPLSCHGWVLGEHGDSSVPVWSGMNVAGVSLKTLHPDLGTD------KDKEQWK-EVHKQV   234
gi|77539746|ref|NP_001029268.1|  VIITAGARQQEGESRLNLVQRNVNIFKFIIPNVVKYSPNCKLLIVSNPVDILTYVAWKISGFPKNRVIGSGCNLDSARFRYLMGERLGVHPLSCHGWVLGEHGDSSVPVWSGMNVAGVSLKTLHPDLGTD------KDKEQWK-EVHKQV   234
gi|27806559|ref|NP_776524.1|     VIITAGARQQEGESRLNLVQRNVNIFKFIIPNIVKYSPNCKLLVVSNPVDILTYVAWKISGFPKNRVIGSGCNLDSARFRYLMGERLGVHPLSCHGWILGEHGDSSVPVWSGVNVAGVSLKNLHPELGTD------ADKEQWK-AVHKQV   234
gi|119920080|ref|XP_001251829.1| VIITAGARQQEGESRLNLVQRNVNIFKFIIPNIVKYSPNCKLLVVSNPVDILTYVAWKISGFPKNRVIGSGCNLDSARFRYLMGERLGVHPLSCHGWILGEHGDSSVPVWSGVNVAGVSLKNLHPELGTD------ADKEQWK-AVHKQV   234
gi|73988675|ref|XP_865353.1|     VIITAGARQQEGESRLNLVQRNVNIFKFIIPNIVKYSPNCKLLVVSNPVDILTYVAWKISGFPKNRVIGSGCNLDSARFRYLMGERLGVHPLSCHGWVLGEHGDSSVPVWSGVNVAGVSLKNLHPDLGTD------ADKEQWK-QVHKQV   234
gi|8393706|ref|NP_058721.1|      VIITAGARQQEGESRLNLVQRNVNIFKFIIPNVVKYSPQCKLLIVSNPVDILTYVAWKISGFPKNRVIGSGCNLDSARFRYLMGERLGVHPLSCHGWVLGEHGDSSVPVWSGVNVAGVSLKSLNPQLGTD------ADKEQWK-DVHKQV   234
gi|62653460|ref|XP_576374.1|     VIITSGARQQEGESQLNLVQRNVNIFKFIIPNVVKYSPQCKLLIVSNPVDILTYVAWKISGFPKNRVIGSGCNLDSARFRYLMGERLGVHPLSCHGWVLGEHGDSSVPVWSGVNVTGVSLKSLNPQLGTD------ADKEQWK-DVHKQV   234
gi|6754524|ref|NP_034829.1|      VIITAGARQQEGESRLNLVQRNVNIFKFIIPNIVKYSPHCKLLIVSNPVDILTYVAWKISGFPKNRVIGSGCNLDSARFRYLMGERLGVHALSCHGWVLGEHGDSSVPVWSGVNVAGVSLKSLNPELGTD------ADKEQWK-EVHKQV   234
gi|45384208|ref|NP_990615.1|     VIVTAGARQQEGESRLNLVQRNVNIFKFIIPNVVKYSPDCKLLIVSNPVDILTYVAWKISGFPKHRVIGSGCNLDSARFRHLMGERLGIHPLSCHGWIVGEHGDSSVPVWSGVNVAGVSLKALHPDMGTD------ADKEHWK-EVHKQV   234
gi|18858959|ref|NP_571321.1|     VVVTAGARQQEGESRLNLVQRNVNIFKFIIPNIIKYSPNCILLVVSNPVDILTYVAWKLSGLPRNRVIGSGTNLDSARFRYLMGEKLGIHPSSCHGWVVGEHGDSSVPVWSGVNVAGVSLQALNPDLGTD------KDKEDWK-SVHKMV   235
gi|115465906|ref|NP_001056552.1| VIVTAGARQIPGETRLNLLQRNVSLFRKIVPAAAEASPESVLVIVSNPVDVLTYVAWKLSGFPASRVIGSGTNLDSSRFRFLLAEHLEVSAQDVQAYMVGEHGDSSVALWSSISVGGMPVLAHLQKNHRSAATAKKFDEAALE-GIRRAV   258
gi|115443679|ref|NP_001045619.1| AIVTAGARQIPGESRLNLLQRNVALFRKIVPALAEHSPEALLLIVSNPVDVLTYVAWKLSGFPASRVIGSGTNLDSSRFRFLLAEHLQVNAQDVQAYMVGEHGDSSVAIWSSMSVAGMPVLKSLRESHQS------FDEEALE-GIRRAV   292
gi|15236012|ref|NP_193459.1|     CIVTAGARQNPGESRLNLLQRNVALFRHIIPPLAKASPDSILIIVSNPVDVLTYVAWKLSGFPVNRVLGSGTNLDSSRFRFLIADHLDVNAQDVQAFIVGEHGDSSVALWSSISVGGIPVLSFLEKNQIA------YEKQTLE-DIHQAV   254
                                 .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
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gi|17136226|ref|NP_476581.1|     VDSAYEVIKLKGYTSWAIGLSTASLASAILRNTSSVAAVSTSVLG-EHGIDKD--VFLSLPCVLNANGVTSVV-KQILTPTEVEQLQKSANIMSDVQAGLKF   332
gi|58385914|ref|XP_314306.2|     VNSAYEVIRLKGYTSWAIGLSVASLASAILRNTYNVHAVSTLVKG-EHGIDDE--VYLSLPCVLGRNGVSHVV-KQILTPEETKKLQASATLMAQVQSGIKF   332
gi|17535107|ref|NP_496503.1|     VDSAYEIIKLKGYTSWAIGLSVAKIAQGIFSNSRNVFALSTNVKG-FHGINDD--VYLSLPVVLGSAGLTHVV-KQQLTEAEVQKLHNSAKALLEVQNGIVM   333
gi|5031857|ref|NP_005557.1|      VESAYEVIKLKGYTSWAIGLSVADLAESIMKNLRRVHPVSTMIKG-LYGIKDD--VFLSVPCILGQNGISDLV-KVTLTSEEEARLKKSADTLWGIQKELQF   332
gi|77539746|ref|NP_001029268.1|  VESAYEVIKLKGYTSWAIGLSVADLAESIMKNLRRVHPVSTMIKG-LYGIKDD--VFLSVPCILGQNGISDLV-KVTLTSEEEARLKKSADTLWGIQKELQF   332
gi|27806559|ref|NP_776524.1|     VDSAYEVIKLKGYTSWAIGLSVADLAESIMKNLRRVHPISTMIKG-LYGIKED--VFLSVPCILGQNGISDVV-KVTLTHEEEACLKKSADTLWGIQKELQF   332
gi|119920080|ref|XP_001251829.1| VDSAYEVIKLKGYTSWAIGLSVADLAESIMKNLRRVHPISTMIKG-LYGIKED--VFLSVPCILGQNGISDVV-KVTLTHEEEACLKKSADTLWGIQKELQF   332
gi|73988675|ref|XP_865353.1|     VDSAYEVIKLKGYTSWAIGLSVADLAESIMKNLRRVHPISTMIKG-LYGIKDD--VFLSVPCILGQNGISDVV-KVTLTPEEEARLKKSADTLWGIQKELQF   332
gi|8393706|ref|NP_058721.1|      VDSAYEVIKLKGYTSWAIGLSVADLAESIMKNLRRVHPISTMIKG-LYGIKED--VFLSVPCILGQNGISDVV-KVTLTPDEEARLKKSADTLWGIQKELQF   332
gi|62653460|ref|XP_576374.1|     VDSAYEVIKLKGYTSWAIGLSVADLAESIMKNLRRVHPISTMIKS-LYGIKED--VFLSVPCILGQNGISDVV-KVTLTPDEEARLKKSADTLWGIQKELQF   332
gi|6754524|ref|NP_034829.1|      VDSAYEVIKLKGYTSWAIGLSVADLAESIMKNLRRVHPISTMIKG-LYGINED--VFLSVPCILGQNGISDVV-KVTLTPEEEARLKKSADTLWGIQKELQF   332
gi|45384208|ref|NP_990615.1|     VDSAYEVIKLKGYTSWAIGLSVADLAETIMKNLRRVHPISTAVKG-MHGIKDD--VFLSVPCVLGSSGITDVV-KMILKPDEEEKIKKSADTLWGIQKELQF   332
gi|18858959|ref|NP_571321.1|     VDSAYEVIKLKGYTSWAIGMSVADLCESILKNMHKCHPVSTLVKG-MHGVNEE--VFLSVPCILGNNGLTDVV-HMTLKPEEEKQLVKSAETLWGVQKELTL   333
gi|115465906|ref|NP_001056552.1| VGSAYEVIKLKGYTSWAIGYSVASIAWSLLRDQRRIHPVSVLAKGLVRGVPADRELFLSLPARLGRAGVLGVAAELVLTDEEERRLRISAETLWGYCHALGL   360
gi|115443679|ref|NP_001045619.1| VDSAYEVISLKGYTSWAIGYSVASLAASLLRDQHRIHPVSVLASG-FHGIPQDHEVFLSLPARLGRAGVLGVA-EMELTEEEARRLRRSAKTLWENCQLLDL   392
gi|15236012|ref|NP_193459.1|     VGSAYEVIGLKGYTSWAIGYSVANLARTILRDQRKIHPVTVLARG-FYGVDGG-DVFLSLPALLGRNGVVAVT-NVHMTDEEAEKLQKSAKTILEMQSQLGL   353
                                 .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400..
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