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                        *****:** **:********* :.***: * *.* **   ** * *. **.*******:**.*     :****.***. **  ***:*:****:******.:********************************** * ***:.******
gi|6680241|ref|NP_032288.1|     MNAQLTMEAIGELHGVSHEPVPAPADLLGG-SPHARSSVGHRGSHLPPAHPRSMGMASLLDGGSGGSDYHHHHRAPEHS-LAGPLHPTMTMACETPPGMSMPTTYTTLTPLQPLPPISTVSDKFPHHHHHHHHHHPHHHQRLAGNVSGS   150
gi|12083605|ref|NP_073162.1|     MNAQLTMEAIGELHGVSHEPVPAPADLLGG-SPHARSSVGHRGSHLPPAHPRSMGMASLLDGGSGGSDYHHHHRAPEHS-LAGPLHPTMTMACETPPGMSMPTTYTTLTPLQPLPPISTVSDKFPHHHHHHHHHHPHHHQRLAGNVSGS   150
gi|114657130|ref|XP_001170549.1| MNAQLTMEAIGELHGVSHEPVPAPADLLGG-SPHARSSVAHRGSHLPPAHPRSMGMASLLDGGSGGSDYHHHHRAPEHS-LAGPLHPTMTMACETPPGMSMPTTYTTLTPLQPLPPISTVSDKFPHHHHHHHHHHPHHHQRLAGNVSGS   150
gi|24307887|ref|NP_004489.1|     MNAQLTMEAIGELHGVSHEPVPAPADLLGG-SPHARSSVAHRGSHLPPAHPRSMGMASLLDGGSGGGDYHHHHRAPEHS-LAGPLHPTMTMACETPPGMSMPTTYTTLTPLQPLPPISTVSDKFPHHHHHHHHHHPHHHQRLAGNVSGS   150
gi|74000187|ref|XP_851227.1|     MNAQLTMEAIGELHGVSHEPVPAPADLLGG-SPHARSSVAHRGSHLPPAHPRSMGMASLLDGGGGGGDYHHHHRAPEHS-LAGPLHPTMTMACETPPGMSMPTTYTTLTPLQPLPPISTVSDKFPHHHHHHHHHHPHHHQRLAGNVSGS   150
gi|119902640|ref|XP_001251107.1| MNAQLTMEAIGELHGVSHEPVPAPADLLGG-SPHARSSVAHRGSHLPPAHPRSMGMASLLDGGGGSGDYHHHHRAPEHS-LAGPLHPTMTMACETPPGMSMPTTYTTLTPLQPLPPISTVSDKFPHHHHHHHHHHPHHHQRLAGNVSGS   150
gi|41055714|ref|NP_956867.1|    MNAQLSMENIGDLHGVSHEPVHSAADLMTGDSAHHRS---HR-SSLS-AHARSMGMASILDSGD-----YHHHRPPEHPGLATHLHPAMSMACEAPPGMSMSSTYTTLTPLQPLPPISTVSDKFPHHHHHHHHHH-HPHQRIPGNVSGS   150
                        1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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                        ******:****.*****:*******.*********.***..********* *****::**::******.*********.******::.:**.***** :  **************:**::** * * *.*:*:.***.******:*****
gi|6680241|ref|NP_032288.1|     FTLMRDERGLASMNNLYTPYHKDVAGMGQSLSPLSGSGLGSIHNSQQGLPHYAHPGAAMPTDKMLTPNGFEAHHPAMLGRHGEQHLTPTSAGMVPINGLPPHHPHAHLNAQGHGQLLGTAREPNPS-VTGAQVSNGSNSGQMEEINTKEV   300
gi|12083605|ref|NP_073162.1|     FTLMRDERGLASMNNLYTPYHKDVAGMGQSLSPLSGSGLGSIHNSQQGLPHYAHPGAAMPTDKMLTPNDFEAHHPAMLGRHGEQHLTPTSAGMVPINGLPPHHPHAHLNAQGHGQLLGTAREPNPS-VTGAQVSNGSNSGQMEEINTKEV   300
gi|114657130|ref|XP_001170549.1| FTLMRDERGLASMNNLYTPYHKDVAGMGQSLSPLSSSGLGSIHNSQQGLPHYAHPGTTMPTDKMLTPNGFEAHHPAMLGRHGEQHLTPTSAGMVPINGLPPHHPHAHLNAQGHGQLLGTAREPNPS-VTGAQVSNGSNSGQMEEINTKEV   300
gi|24307887|ref|NP_004489.1|     FTLMRDERGLASMNNLYTPYHKDVAGMGQSLSPLSSSGLGSIHNSQQGLPHYAHPGAAMPTDKMLTPNGFEAHHPAMLGRHGEQHLTPTSAGMVPINGLPPHHPHAHLNAQGHGQLLGTAREPNPS-VTGAQVSNGSNSGQMEEINTKEV   300
gi|74000187|ref|XP_851227.1|     FTLMRDERGLASMNNLYTPYHKDVAGMGQSLSPLSSSGLSGIHNSQQGLPHYAHPGAAMPTDKMLTPNGFEAHHPAMLGRHGEQHLTPTSAGMVPINGLPPHHPHAHLNAQGHGQLLGTAREPNPS-VTGAQVSNGSNSGQMEEINTKEV   300
gi|119902640|ref|XP_001251107.1| FTLMRDERGLASMNNLYTPYHKDVAGMGQSLSPLSGSGLGGIHNSQQGLPHYAHPGAAMPTDKMLTPNGFEAHHPAMLGRHGEQHLTPTSAGMVPINGLPPHHPHAHLNAQGHGQLLGTAREPNPS-VTGAQVSNGSNSGQMEEINTKEV   300
gi|41055714|ref|NP_956867.1|    FTLMRDDRGLAPMNNLYSPYHKDVASMGQSLSPLSGSGLSGIHNSQQGLPPYAHPGATMPAEKMLTPNGFEAHHPAMLARHGEQHMSASSASMVPIN-VIHHHPHAHLNAQGHGQVLGSTREQNHSSVPGSQLNNGSSSGQMEEVNTKEV   300
                        .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
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gi|6680241|ref|NP_032288.1|     AQRITTELKRYSIPQAIFAQRVLCRSQGTLSDLLRNPKPWSKLKSGRETFRRMWKWLQEPEFQRMSALRLA--------------------------ACKRKEQEHGK-DRGNTPKKPRLVFTDVQRRTLHAIFKENKRPSKELQITIS   450
gi|12083605|ref|NP_073162.1|     AQRITTELKRYSIPQAIFAQRVLCRSQGTLSDLLRNPKPWSKLKSGRETFRRMWKWLQEPEFQRMSALRLA--------------------------ACKRKEQEHGK-DRGNTPKKPRLVFTDVQRRTLHAIFKENKRPSKELQITIS   450
gi|114657130|ref|XP_001170549.1| AQRITTELKRYSIPQAIFAQRVLCRSQGTLSDLLRNPKPWSKLKSGRETFRRMWKWLQEPEFQRMSALRLA--------------------------ACKRKEQEHGK-DRGNTPKKPRLVFTDVQRRTLHAIFKENKRPSKELQITIS   450
gi|24307887|ref|NP_004489.1|     AQRITTELKRYSIPQAIFAQRVLCRSQGTLSDLLRNPKPWSKLKSGRETFRRMWKWLQEPEFQRMSALRLA--------------------------ACKRKEQEHGK-DRGNTPKKPRLVFTDVQRRTLHAIFKENKRPSKELQITIS   450
gi|74000187|ref|XP_851227.1|     AQRITTELKRYSIPQAIFAQRVLCRSQGTLSDLLRNPKPWSKLKSGRETFRRMWKWLQEPEFQRMSALRLAEGGSGGRDPRVEIEEGGPQSLSVPHLTACKRKEQEHGK-DRGNTPKKPRLVFTDVQRRTLHAIFKENKRPSKELQITIS   450
gi|119902640|ref|XP_001251107.1| AQRITTELKRYSIPQAIFAQRVLCRSQGTLSDLLRNPKPWSKLKSGRETFRRMWKWLQEPEFQRMSALRLA--------------------------ACKRKEQEHGK-DRGNTPKKPRLVFTDVQRRTLHAIFKENKRPSKELQITIS   450
gi|41055714|ref|NP_956867.1|    AQRITTELKRYSIPQAIFAQRVLCRSQGTLSDLLRNPKPWSKLKSGRETFRRMWKWLQEPEFQRMSALRLAG---------------------ERTIACKRKEQEHGKGERGNISKKPRLVFTDVQRRTLHAIFKENKRPSKELQITIS   450
                        .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450
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                        *******:***************** *:*.***..***** *****
gi|6680241|ref|NP_032288.1|     QQLGLELSTVSNFFMNARRRSLDKWQDEGGSNSGSSSSSSSTCTKA   496
gi|12083605|ref|NP_073162.1|     QQLGLELSTVSNFFMNARRRSLDKWQDEGSSNSGNSSSSSSTCTKA   496
gi|114657130|ref|XP_001170549.1| QQLGLELSTVSNFFMNARRRSLDKWQDEGSSNSGNSSSSSSTCTKA   496
gi|24307887|ref|NP_004489.1|     QQLGLELSTVSNFFMNARRRSLDKWQDEGSSNSGNSSSSSSTCTKA   496
gi|74000187|ref|XP_851227.1|     QQLGLELSTVSNFFMNARRRSLDKWQDEGSSNSGNSSSSSSTCTKA   496
gi|119902640|ref|XP_001251107.1| QQLGLELSTVSNFFMNARRRSLDKWQDEGGSNSGNSSSSSSTCTKA   496
gi|41055714|ref|NP_956867.1|    QQLGLELATVSNFFMNARRRSLDKWLDDGSSNSANSSSSS-TCTKA   496
                        .......460.......470.......480.......490......
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