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                                 ******:************: ** ************. *  .*:*      :**  ** ** * ::***. * *::.   **:********:.: :*:***:.*::: ** *  ***. ..: .: :*: ::::: : ::** ***.*
gi|27894330|ref|NP_000566.3|     MAKVPDMFEDLKNCYSENEEDSSSIDHLSLNQKSFYHVSYGPLHEGCMDQSVSLSISETSKTSKLTFKESMVVVATN---GKVLKKRRLSLSQSITDDDLEAIANDSEEEIIKPRSAPFSFLSNVKYNFMRIIKYEFILNDALNQSIIRA   147
gi|55600522|ref|XP_525866.1|     MAKVPDMFEDLKNCYSENEEDSSSIDHLSLNQKSFYHVSYGPLHEGCMDQSVSLSISETSKTSKLTFKESMVVVATN---GKVLKKRRLSLSQSITDDDLEAIANDSEEEIIKPRSAPFSFLSNVKYNFMRIIKYEFILNDALNQSIIRA   147
gi|50978882|ref|NP_001003157.1|  MAKVPDLFEDLKNCYSENEEYSSEIDHLSLNQKSFYDMSCDPLHED----CMSLSTSEISKTSQLTFKENVVVVAAN---GKILKKRRLSLSQFITDDDLEGIANDTEEVIMKPRSVAYNFHNNEKYNYIRIIKSQFILNDNLNQSIVRQ   143
gi|27806577|ref|NP_776517.1|     MAKVPDLFEDLKNCYSENEDYSSEIDHLSLNQKSFYDASYEPLREDQMNKFMSLDTSETSKTSKLSFKENVVMVAAS---GKILKKRRLSLNQFITDDDLEAIANNTEEEIIKPRSAHYSFQSNVKYNFMRVIHQECILNDALNQSIIRD   147
gi|47059075|ref|NP_034684.2|     MAKVPDLFEDLKNCYSENEDYSSAIDHLSLNQKSFYDASYGSLHETCTDQFVSLRTSETSKMSNFTFKESRVTVSATSSNGKILKKRRLSFSETFTEDDLQSITHDLEETIQ-PRSAPYTYQSDLRYKLMKLVRQKFVMNDSLNQTIYQD   149
gi|8393593|ref|NP_058715.1|      MAKVPDLFEDLKNCYSENEEYSSAIDHLSLNQKSFYDASYGSLHENCTDKFVSLRTSETSKMSTFTFKESRVVVSATSNKGKILKKRRLSFNQPFTEDDLEAIAHDLEETIQ-PRSAPHSFQNNLRYKLIRIVKQEFIMNDSLNQNIYVD   149
                                 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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                                    :* :: *::*:  ***** **   .  *:: .* *::*.::*:*:**.**:******:** ** *  .**:*:***:  .: .**.*.* *:*:***::   * :* * **: **::
gi|27894330|ref|NP_000566.3|     N-DQYLTAAALHNLDEAVKFDMGAYKSSKDDAKITVILRISKTQLYVTAQDEDQPVLLKEMPEIPKTITGSETNLLFFWETHGTKNYFTSVAHPNLFIATKQDYWVCLAGGPPSITDFQILENQA   271
gi|55600522|ref|XP_525866.1|     N-DQYLTAAALHNLDEAVKFDMGAYKSSKDDAKITVILRISKTQLYVTAQDEDQPVLLKEMPEIPKTITGSETNLLFFWETHGTKNYFTSVAHPNLFIATKQDYWVCLAGGPPSITDFQILENQA   271
gi|50978882|ref|NP_001003157.1|  TGGNYLMTAALQNLDDAVKFDMGAY-TSE-DSKLPVTLRISKTRLFVSAQNEDEPVLLKEMPETPKTIR-DETNLLFFWERHGSKHYFKSVAQPKLFIATQERKLVHMARGQPSITDFRLLETQP   265
gi|27806577|ref|NP_776517.1|     MSGPYLTATTLNNLEEAVKFDMVAY-VSEEDSQLPVTLRISKTQLFVSAQNEDEPVLLKEMPETPKIIK-DETNLLFFWEKHGSMDYFKSVAHPKLFIATKQEKLVHMASGPPSITDFQILEK--   268
gi|47059075|ref|NP_034684.2|     VDKHYLSTTWLNDLQQEVKFDMYAYSSGGDDSKYPVTLKISDSQLFVSAQGEDQPVLLKELPETPKLITGSETDLIFFWKSINSKNYFTSAAYPELFIATKEQSRVHLARGLPSMTDFQIS----   270
gi|8393593|ref|NP_058715.1|      MDRIHLKAASLNDLQLEVKFDMYAYSSGGDDSKYPVTLKVSNTQLFVSAQGEDKPVLLKEIPETPKLITGSETDLIFFWEKINSKNYFTSAAFPELLIATKEQSQVHLARGLPSMIDFQIS----   270
                                 .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.....
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