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                                  ..**  :   :*:* *.:*::***:*** :** .*  ::*****                :* :::****:**:*:***:.*.**::**** ** *:******::* **...*::**::.* **:*. *.* *   : *  .. .
gi|117676374|ref|NP_035156.2|     ---MAGCCSVLRAFLFEYDTPRIVLIRSRKVGLMNRVVQLLILAYVIG----------------WVFVWEKGYQETDSVVSSVTTKAKGVAVTNTSQLGFRIWDVADYVVPAQEENSLFIMTNMIVTVNQTQGTCPEIPDKTSICDSDAN   131
gi|13928806|ref|NP_113782.1|      ---MAGCCSVLGSFLFEYDTPRIVLIRSRKVGLMNRAVQLLILAYVIG----------------WVFVWEKGYQETDSVVSSVTTKAKGVAVTNTSQLGFRIWDVADYVIPAQEENSLFIMTNMIVTVNQTQSTCPEIPDKTSICNSDAD   131
gi|28416927|ref|NP_002551.2|      ---MAGCCAALAAFLFEYDTPRIVLIRSRKVGLMNRAVQLLILAYVIG----------------WVFVWEKGYQETDSVVSSVTTKVKGVAVTNTSKLGFRIWDVADYVIPAQEENSLFVMTNVILTMNQTQGLCPEIPDATTVCKSDAS   131
gi|114647406|ref|XP_001164210.1|  ---MAGCCAALAAFLFEYDTPRIVLIRSRKVGLMNRAVQLLILAYVIGCYYPHLAEVEIESPRRWVFVWEKGYQETDSVVSSVTTKVKGVAVTNTSKLGFRIWDVADYVIPAQEENSLFVMTNVILTMNQTQGLCPEIPDATTVCKSDAS   147
gi|57105832|ref|XP_543389.1|      ---MAGCCAALAPFLFEYDTPRIVLIRSRKVGLMNRAVQLLILAYVIG----------------WVFVWEKGYQETDSVVSSVTTKAKGVTVTNTSILGFRVWDVADYVVPVQEENSLFIMTNMIITLNQTQGLCPELPDKTTVCKSDAN   131
gi|77404277|ref|NP_001029221.1|   ---MTGCCTVLGAFLFEYDTPRIVLIRSRKVGLMNRTVQLLILAYVIG----------------WVFVWEKGYQETDSVVSSVTVKAKGVTMTNTSKLGFRIWDVADYVIPAQEENSVFIMTNMVITMNQTQGLCPEIPGKTTVCETDAN   131
gi|45383558|ref|NP_989622.1|      ---MAACCGAVRGFLFEYDTPRIVLIRSRKVGLINRAVQLAILAYVIG----------------WVFLWEKGYQETDSVVSSVTTKVKGVTMTNTSTLGSRIWDVADYVIPPQEKNAVFVMTNMIFTLNQSQSHCPELPDDNTECNNNSS   131
gi|24119259|ref|NP_705939.1|      MSESVGCCDSVSQCFFDYYTSKILIIRSKKVGTLNRFTQALVIAYVIG----------------YVCVYNKGYQDTDTVLSSVSTKVKGIALTNTSELGERIWDVADYIIPPQEDGSFFVLTNMIITTNQTQSKCAENPTPASTCTSHRD   134
                                  1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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                                  *  *  .::..*: ** *: :. ::***** :***:*.    * *.:*  *****:*:**** ******.******.:.::**. *::.  *** ******* **  * ..** :*:.**:**:*:.*:*:** . * *:*:*:*****.
gi|117676374|ref|NP_035156.2|     CTLGSSDTHSSGIGTGRCVPFNASVKTCEVAAWCPVENDAGVPTPAFLKAAENFTLLVKNNIWYPKFNFSKRNILPNITTSYLKSCIYNARTDPFCPIFRLGQIVADAGHSFQEMAVEGGIMGIQIKWDCNLDRAASHCLPRYSFRRLDT   281
gi|13928806|ref|NP_113782.1|      CTPGSVDTHSSGVATGRCVPFNESVKTCEVAAWCPVENDVGVPTPAFLKAAENFTLLVKNNIWYPKFNFSKRNILPNITTSYLKSCIYNAQTDPFCPIFRLGTIVGDAGHSFQEMAVEGGIMGIQIKWDCNLDRAASLCLPRYSFRRLDT   281
gi|28416927|ref|NP_002551.2|      CTAGSAGTHSNGVSTGRCVAFNGSVKTCEVAAWCPVEDDTHVPQPAFLKAAENFTLLVKNNIWYPKFNFSKRNILPNITTTYLKSCIYDAKTDPFCPIFRLGKIVENAGHSFQDMAVEGGIMGIQVNWDCNLDRAASLCLPRYSFRRLDT   281
gi|114647406|ref|XP_001164210.1|  CTAGSAGTHSNGVSTGRCVAFNGSVKTCEVAAWCPVEDDTHVPQPAFLKAAENFTLLVKNNIWYPKFNFSKRNILPNITTTYLKSCIYDAKTDPFCPIFRLGKIVENAGHSFQDMAVEGGIMGIQVNWDCNLDRAASLCLPRYSFRRLDT   297
gi|57105832|ref|XP_543389.1|      CVAGSSGTHSNGIATGKCVLFNGTVKTCEVAAWCPVEDDTHVPEPAFLKAAENFTLLVKNNIWYPKFNFSKRNILPNITTTYLKSCIYDAVTDPFCPIFRLGKIVESAGHSFQDMAIEGGIMGIQINWNCNLDRTSSLCLPRYSFRRLDT   281
gi|77404277|ref|NP_001029221.1|   CTAGSAGTHSSGVATGRCVSFNGTLKTCEVAAWCPVEDDTEVPKPAFLKAAENFTLLVKNNIWYPKFNFSKRNILPNITTAYLKTCIYDAKTDPFCPIFRLGKIVESAGHSFQDIAIEGGIMGIQIKWNCNLDRAASFCLPRYSFRRLDT   281
gi|45383558|ref|NP_989622.1|      CVPGYVSTHSNGIQTGACIPYNSSIKTCEVFAWCPVEDDYHIPNPAFLQGAENFTILVKNNIWYPKFNFSKRNILPTFSSSYLKNCIYDAQTDPFCPIFRLGKIVEAAGQNFQEMAVEGGVMGLQINWDCNLDRAASHCVPKYSFRRLDN   281
gi|24119259|ref|NP_705939.1|      CKRGFNDARGDGVRTGRCVSYSASVKTCEVLSWCPLEKIVDPPNPPLLADAENFTVLIKNNIRYPKFNFNKRNILPNINSSYLTHCVFSRKTDPDCPIFRLGDIVGEAEEDFQIMAVHGGVMGVQIRWDCDLDMPQSWCVPRYTFRRLDN   284
                                  .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
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gi|117676374|ref|NP_035156.2|     RDLEHNVSPGYNFRFAKYYRDLAGNEQRTLTKAYGIRFDIIVFGKAGKFDIIPTMINVGSGLALLGVATVLCDVIVLYCMKKRYYYRDKKYKYVEDYEQGLSGETDQ   388
gi|13928806|ref|NP_113782.1|      RDLEHNVSPGYNFRFAKYYRDLAGKEQRTLTKAYGIRFDIIVFGKAGKFDIIPTMINVGSGLALLGVATVLCDVIVLYCMKKKYYYRDKKYKYVEDYEQGLSGEMNQ   388
gi|28416927|ref|NP_002551.2|      RDVEHNVSPGYNFRFAKYYRDLAGNEQRTLIKAYGIRFDIIVFGKAGKFDIIPTMINIGSGLALLGMATVLCDIIVLYCMKKRLYYREKKYKYVEDYEQGLASELDQ   388
gi|114647406|ref|XP_001164210.1|  RDVEHNVSPGYNFRFAKYYRDLAGNEQRTLIKAYGIRFDIIVFGKAGKFDIIPTMINIGSGLALLGMATVLCDIIVLYCMKKRLYYREKKYKYVEDYEQGLASELDQ   404
gi|57105832|ref|XP_543389.1|      RDVDHNVSPGYNFRFAKYYSDLTGAERRTLIKAYGIRFDIIVFGKAGKFDIIPTMINIGSGLALLGVATVLCDIIVLYCMKKRYYYREKKYKYVEDYEQGLGGEMDQ   388
gi|77404277|ref|NP_001029221.1|   RDLAHNVSPGYNFRFAKYYSDLKGAEHRTLIKAYGIRFDIIVFGKAGKFDIIPTMINIGSGLALLGVATVLCDVIVLYCMKKRYYYREKKYKYVEDYEQGLGNQMEQ   388
gi|45383558|ref|NP_989622.1|      KDSANTISPGYNFRFAKYYKDSSGIETRTLIKAYGIRLDIIVFGKAGKFDVIPTMINIGSGLALFGVATVLCDIVVLYCMKKRYFYREKKYKYVEDYELGTSET---   385
gi|24119259|ref|NP_705939.1|      KDPDNNVAPGYNFRFAKYYKNSDGTETRTLIKGYGIRFDVMVFGQAGKFNIIPTLLNIGAGLALLGLVNVICDWIVLTFMKRKQHYKEQKYTYVDDFGLLHNEDK--   389
                                  .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......
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