```
                                 *:** :   :*.* :*.  :*:  .*  :* **:*****:.* ****::**** .* *:::**.**********:*::********* *************:** .* .    .: ::::.*:   *.** :*****  . **.:*:* .*
gi|31981819|ref|NP_034115.2|     MTLTAHLSYFLVLLLAG--QGLSDSLLTKDAGPRPLELKEVFKLFQIRFNRSYWNPAEYTRRLSIFAHNLAQAQRLQQEDLGTAEFGETPFSDLTEEEFGQLYGQERSPERTPNMTKKVESNTWGESVPRTCDWRKAKNIISSVKNQGSC   148
gi|66730453|ref|NP_001019413.1|  MTLTAHLFYFLALLLAG--QGLSDSLLTKDAGPRPLELKEVFKLFQIQFNRSYSNPAEYTRRLGIFAHNLAQAQRLQEEDLGTAEFGQTPFSDLTEEEFGQLYGHQRAPERILNMAKKVKSERWGESVPPTCDWRKVKNIISSIKNQGNC   148
gi|23110964|ref|NP_001326.2|     MALTAHPSCLLALLVAGLAQGIRGPLRAQDLGPQPLELKEAFKLFQIQFNRSYLSPEEHAHRLDIFAHNLAQAQRLQEEDLGTAEFGVTPFSDLTEEEFGQLYGYRRAAGGVPSMGREIRSEEPEESVPFSCDWRKVAGAISPIKDQKNC   150
gi|114638622|ref|XP_001170363.1| MALTAHPSCLLALLVAGLAQGIRGPLRAQDLGPQPLELKEAFKLFQIQFNRSYLSPEEHAHRLDIFAHNLAQAQRLQEEDLGTAEFGVTPFSDLTEEEFGQLYGYRRAAGGVPSMGREIRSEEPEESVPFSCDWRKVAGAISPIKDQKNC   150
gi|73983670|ref|XP_540846.2|     MALTIYLSCLLALSVASLAHGIKRSLKNQDPGPQPLELKQVFALFQIQYNRSYSNPEEYARRLDIFAHNLAQAQQLEDEDLGTAEFGVTPFSDLTEEEFGQFYGHQRMAGEAPSVGRKVESEEWGEPVPPTCDWRKLPGIISPIKQQGNC   150
                                 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
```

```
                                 .****:***.**:** *   : *:********* ***:**:***.***::********** :**** *. :.*** ..**:******** **..**: ** ***  ********** *: *:****:** ::***: *:*********.
gi|31981819|ref|NP_034115.2|     KCCWAMAAADNIQALWRIKHQQFVDVSVQELLDCERCGNGCNGGFVWDAYLTVLNNSGLASEKDYPFQGDRKPHRCLAKKYKKVAWIQDFTMLSNNEQAIAHYLAVHGPITVTINMKLLQHYQKGVIKATPSSCDPRQVDHSVLLVGFGK   298
gi|66730453|ref|NP_001019413.1|  RCCWAIAAADNIQTLWRIKTQQFVDVSVQELLDCDRCGNGCNGGFVWDAYITVLNNSGLASEEDYPFQGHQKPHRCLADKYRKVAWIQDFTMLSSNEQVIAGYLAIHGPITVTINMKLLQYYQKGVIKATPSTCDPHLVNHSVLLVGFGK   298
gi|23110964|ref|NP_001326.2|     NCCWAMAAAGNIETLWRISFWDFVDVSVQELLDCGRCGDGCHGGFVWDAFITVLNNSGLASEKDYPFQGKVRAHRCHPKKYQKVAWIQDFIMLQNNEHRIAQYLATYGPITVTINMKPLQLYRKGVIKATPTTCDPQLVDHSVLLVGFGS   300
gi|114638622|ref|XP_001170363.1| NCCWAMAAAGNIETLWRISFWDFVDVSVQELLDCSRCGDGCQGGFVWDAFITVLNNSGLASEKDYPFQGKVRAHRCHPKKYQKVAWIQDFIMLQNNEHRIAQYLATYGPITVTINMKPLRLYRKGVIKATPTTCDPQLVDHSVLLVGFGS   300
gi|73983670|ref|XP_540846.2|     RCCWAMAAAGNIEALWGIRYHQPVEVSVQELLDCGRCGDGCKGGFTWDAFITVLNNSGLASAKDYPFLGNTKPHRCLAKKYKKVAWIQDFIMLQGNEQAIAWYLATKGPITVTINMKLLQHYQKGVIQATHTTCDPQRVDHSVLLVGFGK   300
                                 .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
```

```
                                 *   *  :    *:   :  :. ***********.***:*****:**.****::*:*.**:*:    *  .****
gi|31981819|ref|NP_034115.2|     EK--EGMQTGTVLSHS-RKRRHSSPYWILKNSWGAHWGEKGYFRLYRGNNTCGVTKYPFTAQVDSPVKKARTSCPP   371
gi|66730453|ref|NP_001019413.1|  EK--GGMQTGTLLSHS-RKPRRSTPYWILKNSWGAEWGEKGYFRLYRGNNTCGIAKYPITARVDRPVKKAPVSCPP   371
gi|23110964|ref|NP_001326.2|     VKSEEGIWAETVSSQSQPQPPHPTPYWILKNSWGAQWGEKGYFRLHRGSNTCGITKFPLTARVQKPDMKPRVSCPP   376
gi|114638622|ref|XP_001170363.1| VKSEEGIWAERVSSQSQPQPPHPTPYWILKNSWGAQWGEKGYFRLHRGSNTCGITKFPLTARVQKPDMKPRVSCPP   376
gi|73983670|ref|XP_540846.2|     SKSVAGKQAEGGSSR--PRPHHPIPYWILKNSWGAEWGEEGYFRLHRGNNTCGITKYPVTARVDLRVKKRLVSCPP   374
                                 .......310.......320.......330.......340.......350.......360.......370......
```