```
                                  ***** *:*.*******.:*********:******** ***  .:**.**:*.::*..*.  :   .** :*.  :.***:*.* .** : *************                                  :.
gi|74001795|ref|XP_544960.2|      MLAVGAMEGTRQSAFLLSSPPLAALHSMAEMKTPLYPAAYPPLPAGPPSSSSSSSSSSPSPPLGAHNPGSLKPPPAGGLSSLGSPPQQLSAATPHGINDILSRPSMPVASGAALPSASPSGSSSSSSSSTSASSASAAAAAAAAAAAA   150
gi|119894159|ref|XP_873269.2|     MLAVGAMEGPRQSAFLLSSPPLAALHSMAEMKTPLYPAAYPPLPAGPPSSSSSSSSSSPSPPLGAHNPGNLKPPAAGGLSALGSPPQQLSAATPHGINDILSRPSMPVASGAALPSASPSGSSSSSSSSTSAS---AAAAAAAAAAAA   147
gi|111120318|ref|NP_006159.2|     MLAVGAMEGTRQSAFLLSSPPLAALHSMAEMKTPLYPAAYPPLPAGPPSSSSSSSSSSPSPPLGTHNPGGLKPPATGGLSSLGSPPQQLSAATPHGINDILSRPSMPVASGAALPSASPSGSSSSSSSS-ASASSASAAAAAAAAAAAA   149
gi|21450629|ref|NP_659204.1|      MLAVGAMEGPRQSAFLLSSPPLAALHSMAEMKTPLYPAAYPPLPTGPPSSSSSSSSSSPSPPLGSHNPGGLKPPAAGGLSSLGSPPQQLSAATPHGINDILSRPSMPVASGAALPSASPSGSSSSSSSSASATSASAAAAAAAAAAAA   150
gi|13929036|ref|NP_113925.1|      MLAVGAMEGPRQSAFLLSSPPLAALHSMAEMKTPLYPAAYPPLPTGPPSSSSSSSSSSPSPPLGAHNPGGLKPPAAGGLSSLGSPPQQLSAATPHGINDILSRPSMPVASGAALPSASPSGSSSSSSSSASATSASAAAAAAAAAAAA   150
gi|50540018|ref|NP_001002475.1|   MLAVGQMDGSRQSAFLLNTPPLAALHSMTEMKTPLYP-AYPLSSTGPASSTSPTATSPNPGG-IPVSSPG-IKT--SSGLSALAS-AQQCAIATPHGINDILSRP----------------------------------------SV   101
                                  1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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                                  *.****:*:************** ************.. ******:***************** *****:**:***.*:*****************************************************************:*****
gi|74001795|ref|XP_544960.2|      ASSPAGLLAGLPRFSSLSPPPPPPGLYFSPSAAAVAAVGRYPKPLAELPGRTPIFWPGVMQSPPWRDARLACTPHQGSILLDKDGKRKHTRPTFSGQQIFALEKTFEQTKYLAGPERARLAYSLGMTESQVKVWFQNRRTKWRKKHAAEM   300
gi|119894159|ref|XP_873269.2|     ASSPAGLLAGLPRFSSLSPPPPPPGLYFSPSAAAVAAVGRYPKPLAELPGRTPIFWPGVMQSPPWRDARLACTPHQGSILLDKDGKRKHTRPTFSGQQIFALEKTFEQTKYLAGPERARLAYSLGMTESQVKVWFQNRRTKWRKKHAAEM   297
gi|111120318|ref|NP_006159.2|     ASSPAGLLAGLPRFSSLSPPPPPPGLYFSPSAAAVAAVGRYPKPLAELPGRTPIFWPGVMQSPPWRDARLACTPHQGSILLDKDGKRKHTRPTFSGQQIFALEKTFEQTKYLAGPERARLAYSLGMTESQVKVWFQNRRTKWRKKHAAEM   299
gi|21450629|ref|NP_659204.1|      ASSPAGLLAGLPRFSSLSPPPPPPGLYFSPSAAAVAAVGRYPKPLAELPGRTPIFWPGVMQSPPWRDARLACTPHQGSILLDKDGKRKHTRPTFSGQQIFALEKTFEQTKYLAGPERARLAYSLGMTESQVKVWFQNRRTKWRKKHAAEM   300
gi|13929036|ref|NP_113925.1|      ASSPAGLLAGLPRFSSLSPPPPPPGLYFSPSAAAVAAVGRYPKPLAELPGRTPIFWPGVMQSPPWRDARLACTPHQGSILLDKDGKRKHTRPTFSGQQIFALEKTFEQTKYLAGPERARLAYSLGMTESQVKVWFQNRRTKWRKKHAAEM   300
gi|50540018|ref|NP_001002475.1|   ACSPAGILSGLPRFSSLSPPPPP-GLYFSPSAAAVAVA-RYPKPLTELPGRTPIFWPGVMQSPHWRDARFACSPHQNSVLLDKDGKRKHTRPTFSGQQIFALEKTFEQTKYLAGPERARLAYSLGMTESQVKVWFQNRRTKWRKRHAAEM   249
                                  .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
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                                  *:**************:****::*************************.     ...*::*:** *.*
gi|74001795|ref|XP_544960.2|      ATAKKKQDSETERLKGASENEEEDDDYNKPLDPNSDDEKITQLLKKHKS---GGGGGLLLHASENESSS   366
gi|119894159|ref|XP_873269.2|     ATAKKKQDSETERLKGASENEEEDDDYNKPLDPNSDDEKITQLLKKHKSSGGGGGGGLLLHASETEGSS   366
gi|111120318|ref|NP_006159.2|     ATAKKKQDSETERLKGASENEEEDDDYNKPLDPNSDDEKITQLLKKHKSSS-GGGGGLLLHASEPESSS   367
gi|21450629|ref|NP_659204.1|      ATAKKKQDSETERLKGTSENEEDDDDYNKPLDPNSDDEKITQLLKKHKS----SGGSLLLHASEAEGSS   365
gi|13929036|ref|NP_113925.1|      ATAKKKQDSETERLKGTSENEEDDDDYNKPLDPNSDDEKITQLLKKHKS----SGGSLLLHASEAEGSS   365
gi|50540018|ref|NP_001002475.1|   ASAKKKQDSETERLKGASENEDDDDDYNKPLDPNSDDEKITQLLKKHKP-----NSALIIHTSENESS-   312
                                  .......310.......320.......330.......340.......350.......360........
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