

```

gi|24663653|ref|NP_648625.1|  --MVNFVHPEEMYLEFVESIRPFVEVGSFKWLEVHEMILGLSQAALELQNRREEVKEFLISRDKLRVLVHEAYCVTLWKRTRVLP---HLLLEIDP-NPQANFL-----IYTVLYHEAALVALLDVCLYHPSGCETLQES 130
gi|158287575|ref|XP_309572.4|  -----RWIEQHEVLEKLCQQAIFEAATKQEEVVKQLILEDKIPLLVHELYSVLWVWTEVLP---RLLALK--NPDASFV-----LYSVVIYHEANVCSLLETIVFYHRSGCCAALGSN 101
gi|31982595|ref|NP_444483.2|  MGDLELLLPGAEAVLVRGLRSLFQLRMGSEGWVQOHEHLEKLNMQAILDANISQAEPIDQLLTHGKIPPLVBEELIAYEMWKKQVFP---VLCRLLEDFKPONTFF-----IYMVVHHEASIIINLLETIVFFHKVCEESADDK 133
gi|51948538|ref|NP_001004284.1| MGDLELLLPGAEAVLVRGLRSLFQLRMGSEGWVQOHEHLEKLNMQAILDANISQAEPIDQLLTHGKIPPLVBEELIAYEMWKKQVFP---VLCRLLEDFKPONTFF-----IYMVVHHEASIIINLLETIVFFHKVCEESADDK 133
gi|37594444|ref|NP_056980.2|  MGDLELLLPGAEAVLVRGLRSLFQLRMGSEGWVQOHEHLEKLNMQAILDANISQAEPIDQLLTHGKIPPLVBEELIAYEMWKKQVFP---VFCRVEDFKPONTFF-----IYMVVHHEASIIINLLETIVFFHKVCEESADDK 133
gi|114587053|ref|XP_516479.2|  MGDLELLLPGAEAVLVRGLRSLFQLRMGSEGWVQOHEHLEKLNMQAILDANISQAEPIDQLLTHGKIPPLVBEELIAYEMWKKQVFP---VFCRVEDFKPONTFF-----IYMVVHHEASIIINLLETIVFFHKVCEESADDK 133
gi|57101210|ref|XP_533818.1|  MGDLELLLPGAEAVLVRGLRSLFQLRMGSEGWVQOHEHLEKLNMQAILDANISQAEPIDQLLTHGKIPPLVBEELIAYEMWKKQVFP---VLCRLLEDFKPONTFF-----IYMVVHHEASIIINLLETIVFFHKVCEESADDK 133
gi|94966893|ref|NP_001035638.1| MGDLELLLPGAEAVLVRGLRSLFQLRMGSEGWVQOHEHLEKLNMQAILDANISQAEPIDQLLTHGKIPPLVBEELIAYEMWKKQVFP---VLCRLLEDFKPONTFF-----IYMVVHHEASIIINLLETIVFFHKVCEESADDK 133
gi|41055327|ref|NP_956691.1|  MD--SVLLHGEAEGVIQSLKEMSLREIGSRPRWFRQHEFELEKLNMQAVLNASANQEEPIKDLFVSLGKIPIPLVHAMILTEVWKKHVVFP---IICKLQDFNPKSIFL-----IYMVVHHEASIIINLLETIVFFHKVCEESADDK 131
gi|86170672|ref|XP_966061.1|  ---MNIISDIEFLNHTVNIKNMIDLQFSDKDMMIYHEHIVYINVLNHNKDIIDIIQDERMNIILKKFELILRDLIKIYFIRFLVYFKKBEENISILNKNKEKQVQENMMDEDTLNHRISSYILMVMHELKLLNLEFIFLYSDHVYVHIEITY 146
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

```



```

gi|24663653|ref|NP_648625.1|  VLDLIDYCAQAIISQVIGLVSMGYHENETKLDVD---EAVLTELERQKRFDIYKIGLRCSVNLNYIADNVTFLHLSAARRLLVTHDIPWLMADVLSFRPWQRKTSKG-IQKFIDEKWT--NVDDVTIKIVKPEAQAWFCVQRLLNLPIME 273
gi|158287575|ref|XP_309572.4|  ALDLIDYCAQAAGRLIGLLANGYNDREDDPPDELLESIAEEVVRMGRIMDFRIGVSKLGIIVSYLVEGLDQLPLSAATRLVVRVHDFPCLIAEVLHAKPWLRRNREGVFEKVRNGSWIPAHGDAILKVEEBAQWFCVLRLLFGDLMR 251
gi|31982595|ref|NP_444483.2|  VLDLVDYCHRKLILLVARKGGGDLSEEEFQDSSTP---MQELQKQAEEMMEFEISLKALSVLRYITDCVDSLSTLNRMLRTHNLPCLLVELLEHSPWRRR-VGGKLOHFESEGRWQTVAPSEQQKLNKLDGOVWIALYNLLLSPEARA 277
gi|51948538|ref|NP_001004284.1| VLDLVDYCHRKLILLVARKGGGDLSEEEFQDSSTP---MQELQKQAEEMMEFEISLKALSVLRYITDCVDSLSTLNRMLRTHNLPCLLVELLEHSPWRRR-VGGKLOHFESEGRWQTVAPSEHQKLNKLDGOVWIALYNLLLSPEART 277
gi|37594444|ref|NP_056980.2|  VLDLVDYCHRKLILLVAQSGCGGPPPEGESQDSSTP---MQELQKQAEELMEFEIALKALSVLRYITDCVDSLSTLNRMLRTHNLPCLLVELLEHSPWRRR-VGGKLOHFESEGRWQTVAPSEQQKLNKLDGOVWIALYNLLLSPEAQA 277
gi|114587053|ref|XP_516479.2|  VLDLVDYCHRKLILLVAQSGCGGPPPEGESQDSSTP---MQELQKQAEELMEFEIALKALSVLRYITDCVDSLSTLNRMLRTHNLPCLLVELLEHSPWRRR-VGGKLOHFESEGRWQTVAPSEQQKLNKLDGOVWIALYNLLLSPEAQA 277
gi|57101210|ref|XP_533818.1|  VLDLVDYCHRKLILLVAQSGRGAPPEEESQDSSTP---IQELQKQAEELMEFEIALKALSVLRYITDCVDSLSTLNRMLRTHNLPCLLVELLEHSPWRRR-VGGKLOHFESEGRWQTVAPSEHQKLNKLDGOVWIALYNLLLSPEART 276
gi|94966893|ref|NP_001035638.1| VLDLVDYCHRKLILLVAQSGRGAPPEEESQDSSTP---IQELQKQAEELMEFEIALKALSVLRYITDCVDSLSTLNRMLRTHNLPCLLVELLEHSPWRRR-VGGKLOHFESEGRWQTVAPSEHQKLNKLDGOVWIALYNLLLSPEART 189
gi|41055327|ref|NP_956691.1|  VLDLVDYCHRKLILLVGRSVSGETPTDRITHQISGTSASVQDLQKQSDMLEFEIISIKALSVLCYITDVEVSLSLSVLSRMLCTHNMPCVVLVQLVNCPWKR---GTQEKVTEGKWRAVLPEDQLKSKKHGQVWIALYNLLMCKPDCQR 277
gi|86170672|ref|XP_966061.1|  MIIIIISVYVSNLVSFLGTSQYFVKIISSEMLINE--MVLDEEDNTNIDKLIKIYLNINILRNITDRHLLNNTVNVN-KIVDYDMLLILPLIEKKPWRHQ---NYVFEKNEWIR---DDHTLCSVKEKQLWLLIYTLIILSDSCQQ 284
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

```



```

gi|24663653|ref|NP_648625.1|  NYAFNEARCKQLHLKLLGLMHEPLLDLPPLIEIKVFLSRLTSL---GNTAKTOPLLLEDIPQIQEELLDKVEENGG-----FYQIAQDQDSVFLSKNKENICALATRLSKAVGTDLLCELQNMDDLKMGBAKDAGAGGDDG 407
gi|158287575|ref|XP_309572.4|  DYEINGYRHRREIGKCGIGLMNQLDLPALIPKQHLCLQLQITNEAGGGTGGSTASALLLEPEVVRDRILMQAARTG-----WDQIVEKQRKIFIDLEHHDVEMAKRIGAAANTDLLERYTFQEKRRKQGENYASA----- 384
gi|31982595|ref|NP_444483.2|  RYCLTSFAKGLLLKQAPLTDITLLDLPNLAHLKGFSLAHLSLA---ETQPPKDLVLEQIPEIWRDLEREN---KGG---WQATAKHQLQHVFSLEKDLRQQAQRWAETVRLDVLVAVAPERPR----- 393
gi|51948538|ref|NP_001004284.1| RYCLTSFAKGLLLKQAPLTDITLLDLPNLAHLKGFSLAHLALV---ETQPPKDLVLEQIPEIWRDLEREN---KGG---WQATAKHQLQHVFSLEKDLRQQAQRWAETVRLDVLVAVAPERPR----- 393
gi|37594444|ref|NP_056980.2|  RYCLTSFAKGRLLKRAFLTDITLLDLPNLAHLQSFSLAHLTLT---ETQPPKDLVLEQIPEIWRDLEREN---RGG---WQATAKHQLQHVFSPEQDLRLQARRWAETVRLDVLVAVAPERPR----- 393
gi|114587053|ref|XP_516479.2|  HYCLTSFAKGRLLKRAFLTDITLLDLPNLAHLQSFSLAHLTLT---ETQPPKDLVLEQIPEIWRDLEREN---RGG---WQATAKHQLQHVFSPEQDLRLQARRWAETVRLDVLVAVAPERPR----- 393
gi|57101210|ref|XP_533818.1|  RYCVTSFAKGLLLKRAFLTDITLLDLPNLAHLQGFSLAHLALT---ETQPPKDLVLEQIPEIWRDLEREN---RGG---WQATAKHQLRHIFSPPEQDLRLQARRWAETVRLDVLVAVAPERPR----- 392
gi|94966893|ref|NP_001035638.1|  KYDFNSNKTQLLKLRFGLTDVVIDQLPNIPLDQKHFLSQAALT---DVPAPKDLILEQIPEIWNINVMEN---DKK-----WKATAKYQVTVNVPSPSESLREQASRLAQTNLDVMENTIIPDKPK----- 189
gi|41055327|ref|NP_956691.1|  KYEMINVRNRLKLRKVMNEHMYEQLPPIKSLHTFIEHLYISK---IFPDKKNSYLMIDVVPVPEIFDEIKNDVNLKNDIMSLFNRIKKELEKINSIDVYLCTYFDQENKRNKNSQNEBEKKMIKQEKELNETENKQND----- 393
gi|86170672|ref|XP_966061.1|  -----CGACGRTGVKRCRCQGEWVGNRECVKHWPKHKLSCNLMAEAFQKIQEEMKISS----- 448
ECVLCNNKELAELECSQCKKTYYSKKEQMKMDWINHRDVCNII----- 472
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450

```



```

gi|24663653|ref|NP_648625.1|  LDHTCALCQAKAKKCCCKKVHYCSRDCQKLDWPKHKLVCCLK----- 451
gi|158287575|ref|XP_309572.4|  -VKVCGNCGASAAKCCSCNMHVYYCSRDCQLQNWTDHKEKLCRQLK----- 428
gi|31982595|ref|NP_444483.2|  ---CGYCNAEASKRCSRCQNVVYCCRECVKHWKHKGTCLVLAAGDRAK----- 440
gi|51948538|ref|NP_001004284.1|  ---CAYCSAEASKRCSRCQKVVYCCRECVKHWKHKGTCLVLAAGDRAK----- 440
gi|37594444|ref|NP_056980.2|  ---CAYCSAEASKRCSRCQNEWYCCRECVKHWKHKGTCLVLAAGDRAK----- 440
gi|114587053|ref|XP_516479.2|  ---CAYCSAEASKRCSRCQNEWYCCRECVKHWKHKGTCLVLAAGDRAK----- 440
gi|57101210|ref|XP_533818.1|  ---CAYCSADASKRCSRCQNEWYCCRECVKHWKHKGACVLAAGNRAK----- 439
gi|94966893|ref|NP_001035638.1|  ----- 189
gi|41055327|ref|NP_956691.1|  ---CGACGRTGVKRCRCQGEWVGNRECVKHWPKHKLSCNLMAEAFQKIQEEMKISS----- 448
gi|86170672|ref|XP_966061.1|  ECVLCNNKELAELECSQCKKTYYSKKEQMKMDWINHRDVCNII----- 472
.....460.....470.....480.....490.....500.....

```

