```
                                 *  .  .  : . :    .  :   . ::         ..:              :  ::*********:***.*** ************************:****************:********* *******************
gi|14916494|ref|NP_000956.2|     MFDCMDVLSVSPGQ-ILDFYTASPSSCMLQEKALKACFSGLT------QTEWQHRHTAQSIETQSTSSEELVPSPPSPLPPPRVYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMIYTCHRDKNCVINKVTRNRCQYCRLQKCFE   143
gi|73989935|ref|XP_862280.1|     MFDCMDVLSVSPGQ-ILDFYTASPSSCMLQEKALKACFSGLT------QTEWQHRHTAQSIETQSTSSEELVPSPPSPLPPPRVYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMIYTCHRDKNCVINKVTRNRCQYCRLQKCFE   143
gi|114585741|ref|XP_001164404.1| MFDCMDVLSVSPGQ-ILDFYTASPSSCMLQEKALKACFSGLT------QTEWQHRHTAQSIETQSTSSEELVPSPPSPLPPPRVYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMIYTCHRDKNCVINKVTRNRCQYCRLQKCFE   143
gi|45593124|ref|NP_035373.1|     MFDCMDVLSVSPGQ-ILDFYTASPSSCMLQEKALKACLSGFT------QAEWQHRHTAQSIETQSTSSEELVPSPPSPLPPPRVYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMIYTCHRDKNCVINKVTRNRCQYCRLQKCFE   143
gi|45384512|ref|NP_990657.1|     MTTSSRTCPVPAVNGHMTHYPAAPYPLLFPPVIGGLSLPSLHGLQSHPPTSGCSTPSPATVETQSTSSEELVPSPPSPLPPPRVYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMVYTCHRDKNCVINKVTRNRCQYCRLQKCFE   150
gi|24308525|ref|NP_571414.1|     MFDCMEALGMGPRQ---LYDVTNRGACMLRKASP--FYAGLD------PFAWTGTASVRSVETQSTSSEEMVPSSPSPPPPPRVYKPCFVCQDKSSGYHYGVSSCEGCKGFFRRSIQKNMVYTCHRDKNCQINKVTRNRCQYCRLQKCFE   139
                                 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
```

```
                                 ******:**********: ..:   .*.**:.:**:.*.:*: ******************:                 :.:  *   .:************:***************** ***********:******:*******
gi|14916494|ref|NP_000956.2|     VGMSKESVRNDRNKKKKETSKQEC-TESYEMTAELDDLTEKIRKAHQETFPSLCQLGKYTTN------------------SSADHR---VRLDLGLWDKFSELATKCIIKIVEFAKRLPGFTGLTIADQITLLKAACLDILILRICTRY   270
gi|73989935|ref|XP_862280.1|     VGMSKESVRNDRNKKKKEPSKQEC-TESYEMTAELDDLTEKIRKAHQETFPSLCQLGKYTTKQGQGGEPVLCARPPALAGATGSPARPPWFRLDLGLWDKFSELATKCIIKIVEFAKRLPGFTGLTIADQITLLKAACLDILILRICTRY   292
gi|114585741|ref|XP_001164404.1| VGMSKESVRNDRNKKKKETSKQEC-TESYEMTAELDDLTEKIRKAHQETFPSLCQLGKYTTN------------------SSADHR---VRLDLGLWDKFSELATKCIIKIVEFAKRLPGFTGLTIADQITLLKAACLDILILRICTRY   270
gi|45593124|ref|NP_035373.1|     VGMSKESVRNDRNKKKKEPSKQEC-TESYEMTAELDDLTEKIRKAHQETFPSLCQLGKYTTN------------------SSADHR---VRLDLGLWDKFSELATKCIIKIVEFAKRLPGFTGLTIADQITLLKAACLDILILRICTRY   270
gi|45384512|ref|NP_990657.1|     VGMSKESVRNDRNKKKKEPTKQES-TENYEMTAELDDLTEKIRKAHQETFPSLCQLGKYTTN------------------SSADHR---VRLDLGLWDKFSELATKCIIKIVEFAKRLPGFTSLTIADQITLLKAACLDILILRICTRY   277
gi|24308525|ref|NP_571414.1|     VGMSKEAVRNDRNKKKKDVKDEVIPPESYELSGELEELVNKVSKAHQETFPSLCQLGKYTTN------------------SSSDHR---IQLDLGLWDKFSELSTKCIIKIVEFAKRLPGFTTLTIADQITLLKSACLDILMLRICTRY   267
                                 .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
```

```
                                 ********************************:**.************************ ***** :**:************ *:***.******:.********.**:*****.*********.*****:*****.*..*  : ::
                                                                                                                                                                                                  .
gi|14916494|ref|NP_000956.2|     TPEQDTMTFSDGLTLNRTQMHNAGFGPLTDLVFTFANQLLPLEMDDTETGLLSAICLICGDRQDLEEPTKVDKLQEPLLEALKIYIRKRRPSKPHMFPKILMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGHEPLTPSS   420
gi|73989935|ref|XP_862280.1|     TPEQDTMTFSDGLTLNRTQMHNAGFGPLTDLVFTFANQLLPLEMDDTETGLLSAICLICGDRQDLEEPTKVDKLQEPLLEALKIYIRKRRPSKPHMFPKILMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGHEPLTPSS   442
gi|114585741|ref|XP_001164404.1| TPEQDTMTFSDGLTLNRTQMHNAGFGPLTDLVFTFANQLLPLEMDDTETGLLSAICLICGDRQDLEEPTKVDKLQEPLLEALKIYIRKRRPSKPHMFPKILMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGHEPLTPSS   420
gi|45593124|ref|NP_035373.1|     TPEQDTMTFSDGLTLNRTQMHNAGFGPLTDLVFTFANQLLPLEMDDTETGLLSAICLICGDRQDLEEPTKVDKLQEPLLEALKIYIRKRRPSKPHMFPKILMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGHEPLTPSS   420
gi|45384512|ref|NP_990657.1|     TPEQDTMTFSDGLTLNRTQMHNAGFGPLTDLVFTFANQLLPLEMDDTETGLLSAICLICGDRQDLEEPMKVDKLQEPLLEALKIYIRKRRPNKPHMFPKILMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGHEPLTPTS   427
gi|24308525|ref|NP_571414.1|     TPEQDTMTFSDGLTLNRTQMHNAGFGPLTDLVFAFAGQLLPLEMDDTETGLLSAICLICGDRMDLEEPERVDRLQEPLLEALKIYARRRRPNKPHMFPRMLMKITDLRGISTKGAERAITLKMEIPGPMPPLIREMLENPEAFEDQSEAT   417
                                 .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450
```

```
                                 . :   ..*: .*              * . :.. . **  :
gi|14916494|ref|NP_000956.2|     SGNTAEHSPSISP---------------SSVENSGVSQSPLVQ-------------------------------------   448
gi|73989935|ref|XP_862280.1|     SGNPAEHSPSISP---------------SSVENSGVSQSPLVQ-------------------------------------   470
gi|114585741|ref|XP_001164404.1| SGNTAEHSPSISP---------------SSVENSGVSQSPLVQ-------------------------------------   448
gi|45593124|ref|NP_035373.1|     SGNIAEHSPSVSP---------------SSVENSGVSQSPLLQ-------------------------------------   448
gi|45384512|ref|NP_990657.1|     NGNTAEHSPSISP---------------SSVDNSSVSQSPMVQ-------------------------------------   455
gi|24308525|ref|NP_571414.1|     EKKPEPEPPAPPPPALLTMKKEQEDEDDSWATENGSEPSPEEEDDDDEDGEEERGTDSDGEAWGGQEPNADVSRKSHGGRAQ   499
                                 .......460.......470.......480.......490.......500.......510.......520.......530..
```