```
                                                   **:***                                                                                  *:*****:***** ****:*: ::*.    * :.:*. .
gi|118766339|ref|NP_001073136.1| --------MWSGGSGKARGWEAAAGGRSSPGRLSRRRIMSMSPK-------------------------------------------------------------HTTPFSVSDILSPLEESYKKVGMEGGGLGAPLAAYRQGQ   150
gi|114652691|ref|XP_509911.2|    --------MWSGGSGKARGWEAAAGGRSSPGRLSRRRIMSMSPK-------------------------------------------------------------HTTPFSVSDILSPLEESYKKVGMEGGGLGAPLAAYRQGQ   150
gi|40254605|ref|NP_033411.2|     -------------------------------------MSMSPK-------------------------------------------------------------HTTPFSVSDILSPLEESYKKVGMEGGGLGAPLAAYRQGQ   150
gi|109478242|ref|XP_216720.4|    -------------------------------------MSMSPK-------------------------------------------------------------HTTPFSVSDILSPLEESYKKVGMEGGGLGAPLAAYRQGQ   150
gi|50979060|ref|NP_001003260.1|  -------------------------------------MSMSPK-------------------------------------------------------------HTTPFSVSDILSPLEESYKKVGMEGGGLGAPLAAYRQGQ   150
gi|119913929|ref|XP_880071.2|    --------MWSGGSGKARGWEAAAGGRSGPGRLSRRRIMSMSPK-------------------------------------------------------------HTTPFSVSDILSPLEESYKKVGMEGGGLGAPLAAYRQGQ   150
gi|45382925|ref|NP_989947.1|     -------------------------------------MSMSPK-------------------------------------------------------------HTTPFSVSDILSPWEESYKKVGMEGSNLGAPLSAYRQSQ   150
gi|18859487|ref|NP_571851.1|     -------------------------------------MSMSPK-------------------------------------------------------------HTTPFSVSDILSPLEESYKKVSMEGNNLGAPLASYRQPQ   150
gi|62862652|ref|NP_001015473.1|  MSSHGLAYTTRIERKSYRELQINRDQYFVTAPNEEDLVMSLSPKDTLIHTAISQHHQVDTSTKLNTNETSTQNTVSTAAAAAVAHHHHNLSSIHHLQNLHSQHQSTLFNSNHSTPFSVTDILSPIEESYRKLELNGN----PPSPFRSNS   150
                                 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150

                                  : .        :.  *::.::   .. .:  * *:  :  ** *  .*:*    * * **.*::   ***:.. **** :***:*.::: .*. *. :..*.  . .   :  : ********:**************:******
gi|118766339|ref|NP_001073136.1| AAPPTAAMQQHAVGHHGAVTAAYHMTAAGVPQLSHS-AVGGYCNGNLGNMSELPPYQDTMRNSASGPGWYGANP-DPRFPAISRFMGPASGMNMSGMGGLGSLGDVSKNMAP---LPSAPRRKRRVLFSQAQVYELERRFKQQKYLSAPE   300
gi|114652691|ref|XP_509911.2|    AAPPAAAMQQHAVGHHGAVTAAYHMTAAGVPQLSHS-AVGGYCNGNLGNMSELPPYQDTMRNSASGPGWYGANP-DPRFPAISRFMGPASGMNMSGMGGLGSLGDVSKNMAP---LPSAPRRKRRVLFSQAQVYELERRFKQQKYLSAPE   300
gi|40254605|ref|NP_033411.2|     AAPPAAAMQQHAVGHHGAVTAAYHMTAAGVPQLSHS-AVGGYCNGNLGNMSELPPYQDTMRNSASGPGWYGANP-DPRFPAISRFMGPASGMNMSGMGGLGSLGDVSKNMAP---LPSAPRRKRRVLFSQAQVYELERRFKQQKYLSAPE   300
gi|109478242|ref|XP_216720.4|    AAPPAAAMQQHAVGHHGAVTAAYHMTAAGVPQLSHS-AVGGYCNGNLGNVSELPPYQDTMRNSASGPGWYGANP-DPRFPAISRFMGPASGMNMSGMGGLGSLGDVSKNMAP---LPSAPRRKRRVLFSQAQVYELERRFKQQKYLSAPE   300
gi|50979060|ref|NP_001003260.1|  AAPPAAAMQQHAVGHHGAVTAAYHMTAAGVPQLSHS-AVGGYCNGNLGNMSELPPYQDTMRNSASGPGWYGANP-DPRFPAISRFMGPASGMNMSGMGGLGSLGDVSKNMAP---LPSAPRRKRRVLFSQAQVYELERRFKQQKYLSAPE   300
gi|119913929|ref|XP_880071.2|    TAPPAAAMQQHAVGHHGAVTAAYHMTAAAVPQLSHS-AVGGYCNGNLGNMSELPPYQDTMRNSASGPGWYGANP-DPRFPAISRFMGPASGMNMSGMGGLGSLGDVSKNMAP---LPSAPRRKRRVLFSQAQVYELERRFKQQKYLSAPE   300
gi|45382925|ref|NP_989947.1|     VSQP--AMQQHPMGHNGTVTAAYHMTAAGVPQLSHA-TMGGYCNGNLGNMSELPPYQDTMRNSASATGWYGTNP-DPRFSSISRFMAPSSGMNMGGMGGLSSLGDVSKSMAP---LQSTPRRKRRVLFSQAQVYELERRFKQQKYLSAPE   300
gi|18859487|ref|NP_571851.1|     VTQA--AMQQHHMGHNGTVPAAYHMTAAGVSQLSHT-AMGGYCNGNLGNMSDLPAYQDGMRGSTTATSWYGTNP-DPRFSTISRFMGSSSGMNMGSMSTLSSLADVGKGMGP---LTSTPRRKRRVLFSQAQVYELERRFKQQKYLSAPE   300
gi|62862652|ref|NP_001015473.1|  SSSS--------INSPGTLTTSTMANPYAMGTLYHSPGVQTYC-GPTDNLSLAGHYTD-MRNSAS---WYGSTANDPRF-AISRLMSSSASGTMSHMGNMSGLAACSVSDSKPLQFPLAQRRKRRVLFTQAQVYELERRFKQQRYLSAPE   300
                                 .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300

                                 ******:****************** *****:*.   : *::                    .*****************..  .:   .   . :.                 .  : :      .  :    . :  *.. * .:
gi|118766339|ref|NP_001073136.1| REHLASMIHLTPTQVKIWFQNHRYKMKRQAKDKAAQQQLQQDSGGGGGGGG-TGCPQQQQAQQQSPRRVAVPVLVKDGKPCQA--GAPAPGAASLQGHAQQQAQHQAQAAQAAAAAISVGS---GGAGLGAHPGHQPGSAGQSPDLAHHA   450
gi|114652691|ref|XP_509911.2|    REHLASMIHLTPTQVKIWFQNHRYKMKRQAKDKAAQQQLQQDSGGGGGGGG-AGCPQQQQAQQQSPRRVAVPVLVKDGKPCQA--GAPAPGAASLQGHAQQQAQQQAQAAQAAAAAISVGS---GGAGLGAHPGHQPGSAGQSPDLAHHA   450
gi|40254605|ref|NP_033411.2|     REHLASMIHLTPTQVKIWFQNHRYKMKRQAKDKAAQQQLQQDSGGGGGGGGGAGCPQQQQAQQQSPRRVAVPVLVKDGKPCQA--GAPAPGAASLQSHAQQQAQQQAQAAQAAAAAISVGS---GGAVLGAHPGHQPGSAGQSPDLAHHA   450
gi|109478242|ref|XP_216720.4|    REHLASMIHLTPTQVKIWFQNHRYKMKRQAKDKAAQQQLQQDSGGGGGGGGGAGCPQQQQAQQQSPRRVAVPVLVKDGKPCQA--GAPAPGAASLQGHAQQQAQQQAQAAQAAAAAISVGS---GGAGLGAHPGHQPGSAGQSPDLAHHA   450
gi|50979060|ref|NP_001003260.1|  REHLASMIHLTPTQVKIWFQNHRYKMKRQAKDKAAQQQLQQDSGGGGGGGG-AGCPQQQQAQQQSPRRVAVPVLVKDGKPCQA--GAPAPGAGSLQGHAQQQAQQQAQAAQAAAAAISVGS---GGPGLGAHPGHQPGSAGQSPDLAHHA   450
gi|119913929|ref|XP_880071.2|    REHLASMIHLTPTQVKIWFQNHRYKMKRQAKDKAAQQQLQQDSGGGGGAG--CQQQQQQAQQQSPRRVAVPVLVKDGKPCQA--GAPAPGATSLQGHAQQQAQQQAQAAQAAAAAISVGS---GGPGLGAHPGHQPGSAGQSPDLAHHA   450
gi|45382925|ref|NP_989947.1|     REHLASMIHLTPTQVKIWFQNHRYKMKRQAKDKAAH-EMQQENG---------SCQQ-----QQSPRRVAVPVLVKDGKPCQA--GSNTP-TAAIQSHPQQ-----------AATTITVAT---NGNSLGQHQSHQTNSAGQSPDMGQHS   450
gi|18859487|ref|NP_571851.1|     REHLASMIHLTPTQVKIWFQNHRYKMKRQAKDKVSQQQMQQDNG---------SCQQQ----QQSPRRVAVPVLVKDGKPCQG--SSHTP-NTGVQNHHHQ-----------GGNVMFMTN---TSLSMSQHQSQQVGSAGQSLDLGQHA   450
gi|62862652|ref|NP_001015473.1|  REHLASLIHLTPTQVKIWFQNHRYKCKRQAKEKAMAEQNQHNQP------------------ASSPRRVAVPVLVKDGKPCSGNNSSSQSQQHGTNSTSAGNNTGSANNGNANSGIVSVTANVSGGLNLITGDAPNSHSPDTSSSLLASY   450
                                 .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450

                                 .:      . **     .     **   *            *.    * **:*
gi|118766339|ref|NP_001073136.1| ASP-----AALQGQVSSLSHLNSSGSDYG----------TMSCS--TLLYGRTW   504
gi|114652691|ref|XP_509911.2|    ASP-----AALQGQVSSLSHLNSSGSDYG----------TMSCS--TLLYGRTW   504
gi|40254605|ref|NP_033411.2|     ASP-----AGLQGQVSSLSHLNSSGSDYG----------AMSCS--TLLYGRTW   504
gi|109478242|ref|XP_216720.4|    ASP-----AALQGQVSSLSHLNSSGSDYG----------AMSCS--TLLYGRTW   504
gi|50979060|ref|NP_001003260.1|  ASP-----AALQGQVSSLSHLNSSGSDYG----------TMSCS--TLLYGRTW   504
gi|119913929|ref|XP_880071.2|    ASP-----AALQGQVSSLPHLNSSGSDYG----------TMSCS--TLLYGRTW   504
gi|45382925|ref|NP_989947.1|     ASP-----SSLQSQVSSLSHLNSSTSDYGT---------AMSCS--TLLYGRTW   504
gi|18859487|ref|NP_571851.1|     ASP-----PSLQTQVPGLSHLNSSGSEYGA---------ALPCS--ALLYGRTW   504
gi|62862652|ref|NP_001015473.1|  GTVGGSNVAMLQQPCNNTLMSNSLAMAYRNQNNFISNGHQQQCGGYLPLQGRAW   504
                                 .......460.......470.......480.......490.......500....
```