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                                                                                                :**...  .   * : *.*********** ***:.:*.:**:**:****** ****::::*.::**:***:**.:*: ::::***::
gi|4826798|ref|NP_004972.1|      ------------------------------------------------------------MHGHSRNGQAHVPRRKRRNRFVKKNGQCNVYFANLSNKSQRYMADIFTTCVDTRWRYMLMIFSAAFLVSWLFFGLLFWCIAFFHGDLEASP   150
gi|114686380|ref|XP_525593.2|    ------------------------------------------------------------MHGHSRNGQAHVPRRKRRNRFVKKNGQCNVYFANLSNKSQRYMADIFTTCVDTRWRYMLMIFSAAFLVSWLFFGLLFWCIAFFHGDLEASP   150
gi|73969634|ref|XP_538374.2|     ------------------------------------------------------------MHGHSRNGQAHVPRRKRRNRFVKKNGQCNVYFANLSNKSQRYMADIFTTCVDTRWRYMLMIFSAAFLVSWLFFGLLFWCIAFFHGDLEAGP   150
gi|46358362|ref|NP_032453.2|     ------------------------------------------------------------MHGHNRNGQAHVPRRKRRNRFVKKNGQCNVYFANLSNKSQRYMADIFTTCVDTRWRYMLMIFSAAFLVSWLFFGLLFWWIAFFHGDLEASP   150
gi|76881824|ref|NP_446322.2|     ------------------------------------------------------------MHGHSRNGQAHVPRRKRRNRFVKKNGQCNVYFANLSNKSQRYMADIFTTCVDTRWRYMLMIFSAAFLVSWLFFGLLFWCIAFFHGDLEPSP   150
gi|118082716|ref|XP_416263.2|   MGSVRVNREESRRENRDSQPYTVPGPKCCSSRTSVCSFSSRYSIVSTEEDGHKVSALGSMNGHSRNGKGHTPRRKHRNRFVKKNGQCNVYFANLSNKSQRYMADIFTTCVDTRWRYMLMIFSAAFLVSWLFFGFLFWCIAFFHGDLN---   150
gi|189540843|ref|XP_001922242.1| ---------------------------------MGTNRANRYSIVSPDEERLKIATLGLHNGHGNGKISTSGRSQLRSRFVKKNGQCNVVFANMEDKPRRYLADLFTTCVDIRWRYLMLVFCSTFLLSWLLFGVIFYSVSLLHGDFQKEH   150
                                 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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                                                  ***::**:.*:******:*********:********:*:::*********:******************* ***:**::***::***************:*************:**:* ***::**:
gi|4826798|ref|NP_004972.1|      GVPAAG---GPAAGGGGAAPVAPKPCIMHVNGFLGAFLFSVETQTTIGYGFRCVTEECPLAVIAVVVQSIVGCVIDSFMIGTIMAKMARPKKRAQTLLFSHHAVISVRDGKLCLMWRVGNLRKSHIVEAHVRAQLIKPYMTQEGEYLPLD   300
gi|114686380|ref|XP_525593.2|    GVPAAG---GPAAGGGGAAPVAPKPCIMHVNGFLGAFLFSVETQTTIGYGFRCVTEECPLAVIAVVVQSIVGCVIDSFMIGTIMAKMARPKKRAQTLLFSHHAVISVRDGKLCLMWRVGNLRKSHIVEAHVRAQLIKPYMTQEGEYLPLD   300
gi|73969634|ref|XP_538374.2|     AAAAAAAAAGAPTGSGAAAPTAPKPCIMHVNGFLGAFLFSVETQTTIGYGFRCVTEECPLAVIAVVVQSIVGCVIDSFMIGTIMAKMARPKKRAQTLLFSHHAVISVRDGKLCLMWRVGNLRKSHIVEAHVRAQLIKPYMTQEGEYLPLD   300
gi|46358362|ref|NP_032453.2|     SVPAVG---GPGGNGG-ESPNAPKPCIMHVNGFLGAFLFSVETQTTIGYGFRCVTEECPLAVIAVVVQSIVGCVIDSFMIGTIMAKMARPKKRAQTLLFSHHAVISVRDGKLCLMWRVGNLRKSHIVEAHVRAQLIKPYMTQEGEYLPLD   300
gi|76881824|ref|NP_446322.2|     SGPTAG---GPGGNGGGAAPTAAKPCIMHVNGFLGAFLFSVETQTTIGYGFRCVTEECPLAVIAVVVQSIVGCVIDSFMIGTIMAKMARPKKRAQTLLFSHHAVISVRDGKLCLMWRVGNLRKSHIVEAHVRAQLIKPYMTQEGEYLPLD   300
gi|118082716|ref|XP_416263.2|    -APVVG-----------GSPSLLKPCIMHVNSFLGAFLFSVETQTTIGYGFRCVTEECPLAIMAVVVQSIVGCVIDSFMIGTIMAKMARPKKRAQTLLFSHHAVISVRDGKLCLMWRVGNLRRSHIVEAHVRAQLIKPYMTEEGEYLPLD   300
gi|189540843|ref|XP_001922242.1| G-------------------KLWKPCLLHVEGFVGAFLFSIETQTTIGYGWRCVTEECPVAIVTVVVQSIVGCIIDSFMIGTIMAKMARPKKRNQTLMFSQNAVIALRDGKLCLMWRVGNLRRSHIVEAHVRAQLIRPYVTAEGEFIPLE   300
                                 .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
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                                 * ******* * **:*****::*******:***:*:.: ***:::*************************: ***********:**::.:*:***::*******..** ***:**:*     *.    .. ********:** . :*:*
gi|4826798|ref|NP_004972.1|      QRDLNVGYDIGLDRIFLVSPIIIVHEIDEDSPLYGMGKEELESEDFEIVVILEGMVEATAMTTQARSSYLASEILWGHRFEPVVFEEKSHYKVDYSRFHKTYEVAGTPCCSARELQESKITVLPAPPPPPSAFCYENELALMSQEEEEM-   450
gi|114686380|ref|XP_525593.2|    QRDLNVGYDIGLDRIFLVSPIIIVHEIDEDSPLYGMGKEELESEDFEIVVILEGMVEATAMTTQARSSYLASEILWGHRFEPVVFEEKSHYKVDYSRFHKTYEVAGTPCCSARELQESKITVLPAPPPPPSAFCYENELALMSQEEEEM-   450
gi|73969634|ref|XP_538374.2|     QRDLNVGYDIGLDRIFLVSPIIIVHEIDEDSPLYGMGKEELESEDFEIVVILEGMVEATAMTTQARSSYLASEILWGHRFEPVVFEEKSHYKVDYSRFHKTYEVAGTPCCSARELQESKITVLPAPPPPPSAFCYENELALMSQEEEEM-   450
gi|46358362|ref|NP_032453.2|     QRDLNVGYDIGLDRIFLVSPIIIVHEIDEDSPLYGMGKEELESEDFEIVVILEGMVEATAMTTQARSSYLASEILWGHRFEPVVFEEKSHYKVDYSRFHKTYEVAGTPCCSARELQESKITVLPAPPPPPSAFCYENELALMSQEEEEM-   450
gi|76881824|ref|NP_446322.2|     QRDLNVGYDIGLDRIFLVSPIIIVHEIDEDSPLYGMGKEELESEDFEIVVILEGMVEATAMTTQARSSYLASEILWGHRFEPVVFEEKSHYKVDYSRFHKTYEVAGTPCCSARELQESKITVLPAPPPPPSAFCYENELALMSQEEEEM-   450
gi|118082716|ref|XP_416263.2|    QRDLNVGYDVGLDRIFLVSPIIIVHEIDEESPLYGIGKEELETENFEIVVILEGMVEATAMTTQARSSYLASEILWGHRFEPVVFEEKNHYKVDYSRFHKTYEVAGTPCCSARELQESKMTILPSPPPP-SAFCYENELALVSQDEDED-   450
gi|189540843|ref|XP_001922242.1| QTDLNVGYDDGTDRLFLVSPLVIVHEIDEDSPLWGMSRAELESDDFEIVVILEGMVEATAMTTQARSSYLSREILWGHRFEPVIFEDHDRYQVDYAHFHKTYEVPSTPGCSAKELHE-----LTRRRSSNSAFCYENEVALCCGEEDEEP   450
                                 .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450
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                                  ::           *  .:   . *  :: *:::.:::::: :::: :*** ::*: ** *
gi|4826798|ref|NP_004972.1|      EEEAAAAAAVAAGLGLEAGSKEEAG--IIRMLEFGSHLDLERMQAS-LPLDNISYRRESAI   511
gi|114686380|ref|XP_525593.2|    EEEAAAAAAVAAGLGLEAGSKEEAG--IIRMLEFGSHLDLERMQAS-LPLDNISYRRESAI   511
gi|73969634|ref|XP_538374.2|     EEEAAAAAAVAAGLGLEAGSKEEAG--IIRMLEFGSHLDLERMQAT-LPLDNISYRRESAI   511
gi|46358362|ref|NP_032453.2|     EEEAAAAAAVAAGLGLEAGSKEEAG--IIRMLEFGSHLDLERMQAATLPLDNISYRRESRI   511
gi|76881824|ref|NP_446322.2|     EEEAAAAAAVAAGLGLEAGSKEETG--IIRMLEFGSHLDLERMQAATLPLDNISYRRESAI   511
gi|118082716|ref|XP_416263.2|    DDE--------VGVALGGSTKEEGG--VIQMMDFGSHLDLERLQAT-LPLDTISYRRESAI   511
gi|189540843|ref|XP_001922242.1| PEDQINTIPSDFQKMLQDSAAVSSGSNMLCMLDMDNQIEFDILHST-IPLDPMTYKSESEI   511
                                 .......460.......470.......480.......490.......500.......510.
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