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gi|67782365|ref|NP_005547.3|      MSIHFSSPVFTSRSAAFSGRGAQVRLSSARPGGLGSS-SLYGLGASRPRVAVRSAYGGPVGAGIREVTINQSLLAPLRLDADPSLQRVRQEESEQIKTLNNKFASFID---KVRFLEQQNKLLETKWTLLQEQKSAKSSRLPDIFEAQIA   150
gi|114644593|ref|XP_522383.2|     MGSEVERRPWSTLVESQP-RGSSVHQADLLPG------SLCAVSG-------------------------------------------------------------------------------AAEQAQKSAKSSRLPDIFEAQIA   150
gi|114051856|ref|NP_001039876.1|  MSLHFGSQVFSSRSAAFPGRGTQVRLSSVRPGGFGSSSSLYGLGASRPRVAARSSYGAPVGTGIRAVTINQSLLTPLQVDIDPSIQQVRQEEREQIKTLNNKFASFID---KVRFLEQQNKLLETKWALLQEQKSAKSNRLPGIFEAQIA   150
gi|73996579|ref|XP_534795.2|      MSIHLGSQVFSSRSAAFPGRGLQVRLSSARPGGFGSR-SLLGLGASRPRVAVRSASGGPGGAGIRQVTVNQSLLAPLRVDIDPAIQQVRREEREQIKTLNNRFASFSTGEPRVRFLEQQNKLLETKWALLQEQRSARSSCLPSIFEAHIA   150
gi|14861854|ref|NP_149064.1|      MSIHFS-----SRSTAYPGRGAQVRLSSGRAS-FGSR-SLYGLGSSRPRVAVRSAYGGPVGAGIREITINQSLLAPLSVDIDPTIQQVRQEEREQIKTLNNKFASFID---KVRFLEQQNKMLETKWALLQEQKSAKSSQLPRIFEAQIA   150
gi|34868200|ref|XP_217035.2|      MSIHFS-----SRSTAYPGRGAQVRLSSGRAG-FGSR-SLYGLGTSRPRVAVRSAYGGPVGAGIREITINQNLLAPLSVDIDPTIQQVRQEEREQIKTLNNKFASFID---KVRFLEQQNKMLETKWALLQDQKSAKSSQLPRIFEAQIA   150
gi|125849603|ref|XP_696736.2|     ----------MSLRSKRISSSSSVRSSGKMGGYGYSSLSGISLGASAPSFSTSSAYLGPP---IASVSVNKSLLAPLNLEIDPNIQMVRTQEKEQIKSLNNRFATFID---KVRFLEQQNKMLETKWELLQTQTPGRSNVEP-MFEAYMA   150
                                  1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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gi|67782365|ref|NP_005547.3|      GLRGQLEALQVDGGRLEAELRSMQDVVEDFKNKYEDEINHRTAAENEFVVLKKDVDAAYMSKVELEAKVDALNDEINFLRTLNETELTELQSQISDTSVVLSMDNSRSLDLDGIIAEVKAQYEEMAKCSRAEAEAWYQTKFETLQAQAGK   300
gi|114644593|ref|XP_522383.2|     GLRGQLEALQVDGGRLEAELQSMQDVVEDFKNKYEDEINRRAAAENEFVVLKKDVDAAYMSKVELEAKVDALNDEINFLRTLNETELTELQSQISDTSVVLSMDNSRSLDLDGIIAEVKAQYEEMAKCSRAEAEAWYQTKFETLQAQAGK   300
gi|114051856|ref|NP_001039876.1|  GLRKQLEALQLDGGRLEVELRNMQDVVEDFKNKYEDEINHRTAAENEFVVLKKDVDVAYMNKVELEAKVDTLNDEINFLRTLYEQELKELQSEVSDTSVVLSMDNNRSLDLDSIIAEVKAQYEEIANRSRAEAEACYQTKFETLQAQAGK   300
gi|73996579|ref|XP_534795.2|      GLRRHLEGLQTDGGRLEVELRNMQDVLEDFKNKYEDEINRRTAAENEFVVLKKDVDAAYMSKVELEAKVEALNDEINFFKTLYETELAELQSQISDTSVVLSMDNSRSLDLDGIIAEVKAQYEEMANRSRAETETMYQSKFETLQAQAGK   300
gi|14861854|ref|NP_149064.1|      GLRQQLETLQLDGGRLEVELRNMQDVVEDFKNKYEEEINRRTAAENEFVLLKKDVDAAYTNKVELEAKADSLQDEINFLKTLHETELAELQSQISDTSVVLSMDNSRSLDLDGIIADVKAQYEEMANHSRAEAEAWYQTKFETLQAQAGK   300
gi|34868200|ref|XP_217035.2|      GLRQQLEALQLDGGRLEVELRSMQDVVEDFKNKYEEEINRRTAAENEFVLLKKDVDAAYTNKVELEAKADSLQDKINFLKTLHETELAELQSQISDTCVVLSMDNSRSLDLDGIIADVKAQYEEMANHSQAEAEAWYQTKFETLQAQAGK   300
gi|125849603|ref|XP_696736.2|     NLRRQMDVVNNDRTKLDGELRNMQGLVEDFKHKYEDEINKRNNLENDFVILKKDVDSAYLVKADLEDKVGALTDEINFLRTIYDEELRELQASIQDTSVVVQMDNSRNLNMDHIVAEVKSQYEEIAARSREEAESWYKSKFDQMASQANQ   300
                                  .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
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                                  :.*:*:***.**.::** :.:**:**: :* **:**  **:**:**:::*:*:.:  ::* ***:.***:.* *******:..**.****************.*:  :    ***..:  . .                : * *.:   .
gi|67782365|ref|NP_005547.3|      HGDDLRNTRNEISEMNRAIQRLQAEIDNIKNQRAKLEAAIAEAEERGELALKDARAKQEELEAALQRGKQDMARQLREYQELMSVKLALDIEIATYRKLLEGEESRLAGDGVGAVNISVMNSTGGSSSGGGIGLTLGGTMGSNALSFSSS   450
gi|114644593|ref|XP_522383.2|     HGDDLRNTRNEISEMNRAIQRLQAEIDNIKNQRAKLEAAIAEAEERGELALKDARAKQEELEAALQRAKQDMARQLREYQELMSVKLALDIEIATYRKLLEGEESRLAGDGVGAVNISVMNSTGGSSSGGGIGLTLGGTMGSNALSFSSS   450
gi|114051856|ref|NP_001039876.1|  HGDDLQNTRNEIADMNRAVQRLQAEIDSVKNQRSKLEAAIADAEQRGELAVKDARAKQEDLEAALQKAKQDMTRQLREYQELMNVKLALDIEIATYRKLLEGEESRLTGDGVGAVNISVVSSTGGSGS----LLTFGGTMGNNALRFSSG   450
gi|73996579|ref|XP_534795.2|      HGDDLRNTRNEIAEMNRAIQRLQAEIDNIKNQRTKLEAAIAEAEERGELALKDAHAKQEELEAALQRAKQDMARQLREYQELMNVKLALDIEIATYRKLLEGEESRLAGDGVGAVNISVVNSTGGGGS----GLSFGGTMGSNALSFSSG   450
gi|14861854|ref|NP_149064.1|      HGDDLRNTRNEIAEMNRSIQRLQAEIDTLKNQRAKLESSIAEAEEQGELAIKDAHAKQGELEAALQKAKQDVARQLREYQELLNTKLALDIEIATYRKLLEGEESRLSGDGMGPVNISVVNSTGGNGG----KLIFGGTMGSNALSFS--   450
gi|34868200|ref|XP_217035.2|      HGDDLRNTRNEIAEMNRSIQKLQAEIDTVKNQRAKLESSIAEAEEQGELALKDARAKLAEVEEALQKAKQDLARLLREYQELMNVKLGLDIEIATYRKLLEGEESRLSGDGMEPVNISVVNSTGANGS----RLTIGGTMGSNALSFS--   450
gi|125849603|ref|XP_696736.2|     YNDELRNTRGEIGDINRMISRLQSEIEVIKAQRANLENQIAEAEDRGEMTVKEAKGRIKDLEEALQRAKQDMARQLREYQELMNVKLALDIEIATYRKLLEGEEDRIGQQ--PIVNIQAVPNYN----------SKGMNGFQQNSS   450
                                  .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450
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                                   .*  :   : .*  ::   . :
gi|67782365|ref|NP_005547.3|      AGPGLLKAYSIRTASASRRSARD   473
gi|114644593|ref|XP_522383.2|     AGPGPLKAYSIRTASASRRSARN   473
gi|114051856|ref|NP_001039876.1|  GGPGTLKAYSMRTTSATSRSPRK   473
gi|73996579|ref|XP_534795.2|      GGPGAFRSYSIRTSAATHRSIRK   473
gi|14861854|ref|NP_149064.1|      GGPGALRAYSIKTTSTTRRGTHN   473
gi|34868200|ref|XP_217035.2|      GGPGVLRTYSIKTTSTARRGTHH   473
gi|125849603|ref|XP_696736.2|     PSPK-IVIKTTETRNSTRFSTH-   473
                                  .......460.......470...
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