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                                 : * .* ****** .::  :.* *.**   **  **: :  .*:*.*:* :      * * *  . :*  :      * ::  :  ::            :*.*    *.:: :
gi|23510335|ref|NP_695005.1|     MCVCQTMEVGQYGKNASRAGDRGVLLEPFIHQVGGHSSMMRYDDHTVCKPLISREQRFYESLPPEMKEFTPEYKGVVSVCFEGDSDGYINLVAYPYVESETVEQDDTTEREQPRRKHSRRSLHRSGSGSDHKEEKASLSLETSES---SQ   147
gi|114586927|ref|XP_516467.2|    MCVCQTMEVGQYGKNASRAGDRGVLLEPFIHQVGGHSSMMRYDDHTVCKPLISREQRFYESLPPEMKEFTPEYKGVVSVCFEGDSDGYINLVAYPYVESETVEQDDTPEREQPRRKHSRRSLHRSGSGSDHKEEKASLSLETSES---SQ   147
gi|40254568|ref|NP_038813.2|     MCVCQTMEVGQYGKNASRAGDRGVLLEPFIHQVGGHSSMMRYDDHTVCKPLISREQRFYESLPPEMKEFTPEYKGVVSVCFEGDSDGYINLVAYPYVESETVEQDDTPEREQPRRKHSRRSLHRSGSGSDHKEEKASLSFETSES---SQ   147
gi|25742635|ref|NP_445768.1|     MCVCQTMEVGQYGKNASRAGDRGVLLEPFIHQVGGHSSMMRYDDHTVCKPLISREQRFYESLPPEMKEFTPEYKGVVSVCFEGDSDGYINLVAYPYVESETVEQDDTPEREQPRRKHSRRSLHRSGSGSDHKEEKASLSFETSES---SQ   147
gi|73985495|ref|XP_861842.1|     MCVCQTMEVGQYGKNASRAGDRGVLLEPFIHQVGGHSSMMRYDDHTVCKPLISREQRFYESLPPEMKEFTPEYKGVVSVCFEGDSDGYINLVAYPYVESETVEQDDTPEREQPRRKHSRRSLHRSGSGSEHKEERASLSLETSESSFSSQ   150
gi|115496522|ref|NP_001069478.1| MCVCQTMEVGQYGKNASRAGDRGVLLEPFIHQVGGHSSMMRYDDHTVCKPLISREQRFYESLPPEMKEFTPEYKGVVSVCFEGDSDGYINLVAYPYVESETVEPDDTPEREQPRRKHSRRSLHRSGSGSDHKEEKASLPLETSES---PQ   147
gi|125851271|ref|XP_692904.2|    MCVPHTMEAGKHSASQGQGSCGGVPLEPFIHQVGGHTSMMRYDDHTVCKPLITREQRFYESLPPEMKEFTPEYKGVVLVCFEGDSDGYINLVAYPYEESEGLDHEELSERDQPRRKHSRRSLHRSSS--EHKEDRHAHDSDGNDN---LQ   145
gi|32564658|ref|NP_492519.2|     ----------------------MELTAFRHQVGGHFGILLCNGH-VAKPSNLREMAFYKVMNSELKHFSPAF------CKEVDVRATVNPSTG-QIVVETLEKLDCHKK-------------KSSS----KHERSSTGFR---------   93
                                 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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                                 *  *..  ::**   ***:  *: : :.** .* :      ******** *:. **:****:********** .*  **: **.:****:***** ***:*: :*  *   :*  ** :.  ***  : :::
gi|23510335|ref|NP_695005.1|     EAKSPKVELHSHSEVPFQMLDGNSGLSSEKISHNPWSLRCHKQQLSRMRSESKDRKLYKFLLLENVVHHFKYPCVLDLKMGTRQHGDDASAEKAARQMRKCEQSTSATLGVRVCGMQVYQLDTGHYLCRNKYYGRGLSIEGFRNALYQYL   297
gi|114586927|ref|XP_516467.2|    EAKSPKVELHSHSEVPFQMLDGNSGLSSEKISHNPWSLRCHKQQLSRMRSESKDRKLYKFLLLENVVHHFKYPCVLDLKMGTRQHGDDASAEKAARQMRKCEQSTSATLGVRVCGMQVYQLDTGHYLCRNKYYGRGLSIEGFRNALYQYL   297
gi|40254568|ref|NP_038813.2|     EAKSPKVELHSHSDVPFQMLDSNSGLSSEKISYNPWSLRCHKQQLSRMRSESKDRKLYKFLLLENVVHHFKYPCVLDLKMGTRQHGDDASAEKAARQMRKCEQSTSATLGVRVCGMQVYQLDTGHYLCRNKYYGRGLSIEGFRNALYQYL   297
gi|25742635|ref|NP_445768.1|     ETKSPKVELHSHSDVPFQMLDSNSGLSSEKISYNPWSLRCHKQQLSRMRSESKDRKLYKFLLLENVVHHFKYPCVLDLKMGTRQHGDDASAEKAARQMRKCEQSTSASLGVRVCGMQVYQLDTGHYLCRNKYYGRGLSIEGFRNALYQYL   297
gi|73985495|ref|XP_861842.1|     EAKSPKVELHSHSDVPFQMLDGNSGLSSEKISHNPWSLRCHKQQLSRMRSESKDRKLYKFLLLENVVHHFKYPCVLDLKMGTRQHGDDASAEKAARQMRKCEQSTSATLGVRVCGMQVYQLDTGHYLCRNKYYGRGLSTEGFRNALYQYL   300
gi|115496522|ref|NP_001069478.1| EAKSPKVELHSHSDVPFQMLDGNSGLSSEKISHNPWSLRCHKQQLSRMRSESKDRKLYKFLLLENVVHHFKYPCVLDLKMGTRQHGDDASAEKAARQMRKCEQSTSATLGVRVCGMQVYQLDTGHYLCRNKYYGRGLSIEGFRNALYQYL   297
gi|125851271|ref|XP_692904.2|    ELKSPLLDLQLHSDVPFQMLDSNSGLSSEKISHNPWSLRCHKQQLSRMRSESKDRKLYKFLLLENVVHHFKYPCILDLKMGTRQHGDDASEEKAARQMKKCEQSTSATLGVRVCGMQVYQMDTGHYLCRNKYYGRSLSIDGFRQALFQFM   295
gi|32564658|ref|NP_492519.2|     -----------------QTTDGRVTVDTEKQ-WNPWAAGCQCKVVERMLKELEPT---PFLLLENVVAHYTRPCVLDLKIGTRQHGDDASESKRHRQLMKCRHSTSATLGVRVVGMQLYEAETKSYSYVEKQEGRRIDAAGFRGYVKRFI   222
                                 .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
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                                 :     *   :.  **** .* * :*    ***:*:*:*: ::                                    :    .   .   *.* :********.** :*  .:.*.*.* ::**:.::. :: : .::
gi|23510335|ref|NP_695005.1|     HNGLDLRRDLFEPILSKLRGLKAVLERQASYRFYSSSLLVIYDGKECRAESCLDRRSEMRLKHLDMVLPEVASSCGPSTSPSNTSPEAGPSSQPKVDVRMIDFAHSTFKGFRDDPTVHDGPDRGYVFGLENLISIMEQMRDENQ------   441
gi|114586927|ref|XP_516467.2|    HNGLDLRRDLFEPILSKLRGLKAVLERQASYRFYSSSLLVIYDGKECRAESCLDRRSEMRLKHLDMVLPEVASSCGPSTSPSNTSPEAGPSSQPKVDVRMIDFAHSTFKGFRDDPTVHDGPDRGYVFGLENLISIMEQMRDENQ------   441
gi|40254568|ref|NP_038813.2|     HNGLDLRRDLFEPILSKLRGLKAVLERQASYRFYSSSLLVIYDGKECR--------SELRLKHVDMGLPEVPPPCGPSTSPSSTSLEAGPSSPPKVDVRMIDFAHSTFKGFRDDPTVHDGPDRGYVFGLENLISIMEQMRDENQ------   433
gi|25742635|ref|NP_445768.1|     HNGLDLRRDLFEPILSKLRGLKAVLERQASYRFYSSSLLVIYDGKECR--------SELRLKHVDMGLPEVPPLCGPSTSPSNTSLEAGPSSPPKVDVRMIDFAHSTFKGFRDDPTVHDGPDRGYVFGLENLISIMEQMRDENQ------   433
gi|73985495|ref|XP_861842.1|     HNGLDLRRDLFEPILSKLRGLKAVLERQASYRFYSSSLLVIYDGRECRAESFLDRRAEMRLKHLDTGLPEGAPPCGPSTSPNSTSPEAGPSSPPKVDVRMIDFAHSTFKGFRDDPTVHDGPDRGYVFGLENLISIMEQMRDENQ------   444
gi|115496522|ref|NP_001069478.1| HNGLDLRRDLFEPILSKLRGLKAVLERQASYRFYSSSLLVIYDGKECRSESYLDRRSEMRMKHLDTSLPEVAPPCSPSTSLSSTSPEAGPFSPPKVDVRMIDFAHSTFKGFRDDPTVHDGPDRGYVFGLENLISIMEQMRDENQ------   441
gi|125851271|ref|XP_692904.2|    HNGTLLRKDLFEPVLSKLCSLKAVLERQASYRFYSSSLLIIYEGKDPES-------ADSWQKPSE--LPSAKENQATSSENPAASELHTPPQVLNVDVRMIDFAHSTFKGFRDDQTVHDGPDRGYVFGLESLINILQEIREENQ------   430
gi|32564658|ref|NP_492519.2|     KCCGRSRAARIRQKLSKLRSLLAEFEG---YRFFSASILIAFD-------------------------------------AEAADSSSDDAVKVCIIDFAHSTFSGFFED-LAYSGADEGCLLGLDSIVEAMEPIVSKDPVTPSSS   327
                                 .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450
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gi|23510335|ref|NP_695005.1|     -----   441
gi|114586927|ref|XP_516467.2|    -----   441
gi|40254568|ref|NP_038813.2|     -----   433
gi|25742635|ref|NP_445768.1|     -----   433
gi|73985495|ref|XP_861842.1|     -----   444
gi|115496522|ref|NP_001069478.1| -----   441
gi|125851271|ref|XP_692904.2|    -----   430
gi|32564658|ref|NP_492519.2|     FEKKK   332
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