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                          *.:*        :  .    :*    :*   *   :. .  :. .*.    *:**.****:**:***:.::***.*.**.***::*:::**:**   .    .  *:::.*..: * :*...  :**.*.:*******************
gi|5031759|ref|NP_005514.1|   -MDFDERGPCSSNMYLPSCTYYVSGPDFSSLPSFLPQTPSSRPMTYSYSSN-LPQVQPVREVTFREYAIEPATKWHPRGNLAHCYSAEELVHRDCLQAPSAAGVPGDVLAKSSANVYHHPTPAVSSNFYSTVGRNGVLPQAFDQFFETAY   150
gi|114612922|ref|XP_519012.2| -MGID---------FHVSLRLQIS----TSRIRFKEAAAVENHVKLGYCG--EPKVQPVREVTFREYAIEPATKWHPRGNLAHCYSAEELVHRDCLQAPSAAGVPGDVLAKSSANVYHHPTPAVSSNFYSTVGRNGVLPQAFDQFFETAY   150
gi|6754226|ref|NP_034580.1|   MMDFDERGPCSSNMYLPSCTYYVSGPDFSSLPSFLPQTPSSRPMTYSYSSN-LPQVQPVREVTFREYAIEPATKWHPRGNLAHCYSAEELVHRDCLQAPSAAGVPGDVLAKSSANVYHHPTPAVSSNFYSTVGRNGVLPQAFDQFFETAY   150
gi|45382911|ref|NP_989950.1|  MMDFDERVPCSSNMYLPSCTYYVSGPDFSSLPSFLPQTPSSRPMTYSYSSN-LPQVQPVREVTFREYAIDPSSKWHPRNNLPHCYSAEEIMHRDCLPSTTTASM-GEVFGKSTANVYHHPSANVSSNFYSTVGRNGVLPQAFDQFFETAY   150
gi|18858819|ref|NP_571222.1|  MMDFDERVPVGSNMYLPGCTYYVSGTDFSSLPPFLPQTPSSCPMTYSYSTSSLPQVQSVREVSFRDYAIDTSSKWHSRGNLPHCYATEDMVHRECLSNP---GTLGDMLSKNNS-VLYHSNSSHTSNVYGSVGRNGVLPQAFDQFFETAY   150
                          1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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                          *. **  .::* *:  .*.*                .* *.*:.           .:  .**    *. ****.***:.*:* ..*. **:*********************************************************
gi|5031759|ref|NP_005514.1|   GTPENLASSDYPGDKSAEKGPPAATATSAAA-AAAATGAPATSSSDSGGGGGCRETAAAAEEKERRRRPESSSSPESSSGHTEDKAGGSS-GQRTRKKRCPYTKYQIRELEREFFFSVYINKEKRLQLSRMLNLTDRQVKIWFQNRRMKE   300
gi|114612922|ref|XP_519012.2| GTPENLASSDYPGDKSAEKGPPAATATSAAA-AAAATGAPATSSSDSGGGGGCRETAAAAEEKERRRRPESSSSPESSSGHTEDKAGGSS-GQRTRKKRCPYTKYQIRELEREFFFSVYINKEKRLQLSRMLNLTDRQVKIWFQNRRMKE   300
gi|6754226|ref|NP_034580.1|   GTPENLASSDYPGDKNAEKGPQAAAATSAAAVAAAATGAPATSSSDGGGGGGCQE--AAAEEKERRRRPESSSSPESSSGHTEDKAGGSG-GQRTRKKRCPYTKYQIRELEREFFFSVYINKEKRLQLSRMLNLTDRQVKIWFQNRRMKE   300
gi|45382911|ref|NP_989950.1|  GTAENPSSADYPPDKSGEKAPAAAGAT------------AATSSSEGGCGG-----AAAAAGKERRRRPESGSSPESSSGNNEEKSGSSS-GQRTRKKRCPYTKYQIRELEREFFFSVYINKEKRLQLSRMLNLTDRQVKIWFQNRRMKE   300
gi|18858819|ref|NP_571222.1|  GNVEN-QPTEHPVDRATSKAPP----------------PAESGSDS---------CRGTDETER---CEETSSPEPSSGNNEDKFSGSSNGQKTRKKRCPYTKYQIRELEREFFFSVYINKEKRLQLSRMLNLTDRQVKIWFQNRRMKE   300
                          .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
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                          **:********:.:****
gi|5031759|ref|NP_005514.1|   KKINRDRLQYYSANPLL   317
gi|114612922|ref|XP_519012.2| KKINRDRLQYYSANPLL   317
gi|6754226|ref|NP_034580.1|   KKINRDRLQYYSANPLL   317
gi|45382911|ref|NP_989950.1|  KKINRDRLQYYSANPLL   317
gi|18858819|ref|NP_571222.1|  KKLNRDRLQYYTTNPLL   317
                          .......310.......
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