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                                 *::: :**:*.***:*********************** ****** .*****:********:: ** :************:**:**::*.:**:*** :****. ** *:* ** **: *  :**::* **::*: ***:*
gi|154759283|ref|NP_055418.2|    MRRAAGMEDFSAEEEESWYDQQDLEQDLHLAAELGKTLLERNKELEGSLQQMYSTNEEQVQEIEYLTKQLDTLRHVNEQHAKVYEQLDLTARDLELTNHRLVLESKAAQQKIHGLTETIERLQAQVEELQAQVEQLRGLEQLRVLREKRE   150
gi|114670381|ref|XP_523717.2|    MRRAAGMEDFSAEEEESWYDQQDLEQDLHLAAELGKTLLERNKELEGSLQQMYSTNEEQVQEIEYLTKQLDTLRHVNEQHAKVYEQLDLTARDLELTNHRLVLESKAAQQKIHGLTETIERLQAQVEELQAQVEQLRGLEQLRVLREKRE   150
gi|124286868|ref|NP_001074398.1| MRRAAGMEDYSAEEEESWYDHQDLEQDLHLAAELGKTLLERNKELEESLQQMYSTNEEQVHEIEYLTKQLDTLRLVNEQHAKVYEQLDLTARDLELTNQRLVMESKAAQQKIHGLTETIERLQSQVEELQAQVEQLRGLEQLRIRREKRE   150
gi|109489379|ref|XP_340934.3|    ------MEEYSAEEEESWYDHQDLEQDLHLAAELGKTLLERNKELEESLQQMYSTNEEQVQEIEYLTKQLDTLRLVNEQHAKVYEQLDLTARDLELTNQRLVLESKAAQQKIHGLTETIERLQSQVEELQAQVEQLRGLEQVRVRREKRE   150
gi|73965050|ref|XP_540425.2|     MRRAAGMEDFSTEEEEPWYDQQDLEQDLHLAAELGKTLLERNKELEESLQQMYSTNEEQVQEIEYLTKQLDTLRHMNEQHAKVYEQLDLTARDLELTNQKLVLESKAAQQKIHGLTETIERLQAQVEELQAQVEQLRGLEQLRVRREKRE   150
gi|194675699|ref|XP_869616.3|    MRRAARMEDFTAEEEEPWYDQQDLEQDLHLAAELGKTLLERNKELEESLQQMYSTNEEQVQEIEYLTKQLDTLRHVNEQHAKVYEQLDLAARDLELTNQKLVLESKVAQQKIHGLTETIERLQTQVEELQAQVEQLRDLEQLRVRREKRE   150
gi|118099932|ref|XP_426243.2|    ------MEEFQSEEEEPWYDQQDLEQDLHLAAELGKTLLERNKELEESLQQMYATNEEQVQEIEYLTKQLEMLRQMNEQHAKVYEQLDLTARDLELANQKLVLESKTSQQKIQCLTETIEGLQNQVEELQKQVEEMRSLEQLRIRREKRE   150
gi|45387559|ref|NP_991127.1|     ------MDEFVTEEDEPWYDQRDLEQDLHLAAELGKTLLERNKELEDSLQQMYINNEEQVQEIEYLTKQMEMLREMNEQHAKVYEQLDVTARELEITNEKLVLESKGSQQKIDRLTGTMEMLQGQVDTLTARVEELRTLEELRVRREKKE   150
                                 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150

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gi|154759283|ref|NP_055418.2|    RRRTIHTFPCLKELCTSPRCKDAFRLHS-SSLELGP-RPLEQENERLQTLVGALRSQVSQERQRKERAEREYTAVLQEYSELERQLCEMEACRLRVQELEAELLELQQMKQAKTYLLGPDDHLAEALLAPLTQAPEADDPQPGRGDDLGA   300
gi|114670381|ref|XP_523717.2|    RRRTIHTFPCLKELCTSPRCKDAFRLHS-SSLELGP-RPLEQENERLQTLVGALRSQVSQERQRKERAEREYTAVLQEYSELERQLCEMEACRLRVQELEAELLELQQMKQAKTYLLGPDDHLAEALLAPLTQAPEADDPQPGRGDDSGA   300
gi|124286868|ref|NP_001074398.1| RRRTIHTFPCLKELCTSSRCEDAFRLHS-SSLELGP-RPLEQENERLQTLVGVLRSQVSQERQRKERAEREYTVVLQEYTELERQLCEMEGCRLRVQELEAELLELQQMKQAKTYLLAREEHLAEALLAPLTQAPEADDPQPGSGDDSNA   300
gi|109489379|ref|XP_340934.3|    RRRTIHTFPCLKELCTSPRCEDAFRLHS-SSLELGP-RPLEQENERLQTLVGVLRSQVSQERQRKERAEREYTLVLQEYTELERQLCEMEGCRLRVQELEAELLELQQMKQAKTYLLARDEHLAEALLAPLTQAPEADDPQPGSGDDPNA   300
gi|73965050|ref|XP_540425.2|     RRRTIHTFPCLKELCTSPRCEDAFRLHS-SSLELGP-RPLEQENERLQTLVGVLRSQVSQERQRKERAEREYAAVLQEYSELERQLCEMEGCRLRVQELEAELLELQQMKQAKTYLLGREDHLAEALLAPLTQAPEADDPQPGSGDDSAA   300
gi|194675699|ref|XP_869616.3|    RRRTIHTFPCLKELCTSPRCEDAFRLHS-SSLELGP-RPLEQENERLQTLVGVLRSQVSQERQRKERAEREYAAVLQEYSELERQLCEMEGCRFRVQELEAELLELQQMKQAKTYLLGREDHLAEALLAPLTQAPEADDPQPGIGDDSGP   300
gi|118099932|ref|XP_426243.2|    RRRTIHTFPCLKELCSSPRYEDAFQVHN-SSTEFNQ-KPLEQENERLQAMVDSLRSQVNQEKQRKERVEREYSSVIQEYSDLEQRVCEMEHCKLRIKELEAELLELQQMKQVKKYLLSREDNLSEALLEPLNNAPEADYIDLS--EEEGG   300
gi|45387559|ref|NP_991127.1|     RRKTVHSFPCLKELCTAPRYEDSFMVSDPGSGDLEECQPADEENEHLRVMVSSLRAAVAAERGRREAAERECAAVLQEFERLEQRLLGAESCQRRVHELEAELQEMQQLRKSRVCLLSGEEGLEQTLLN---CAPETDTPDEA----VMA   300
                                 .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300

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gi|154759283|ref|NP_055418.2|    QDGVSSPAASPGHVVRKSCSDTALNAIVAKDPASRHAGNLTLHANSVRKRGMSILREVDEQYHALLEKYEELLSKCRQHGAGVRHAGVQTSRPISRDSSWRDLRGGEEGQG--------EVKAGEKSLSQHVEAVDKRLEQSQPEYKALF   450
gi|114670381|ref|XP_523717.2|    QDGVSSPAASPGHVVRKSCSDTALNAIVAKDPASRHAGNLTLHANSVRKRGMSILREVDEQYHALLEKYEELLSKCRQHGAGVRHAGVQTSRPISRDSSWRDLLGGEEGQG--------EVKAGEKSLSQHVEAVDKRLEQSQPEYKALF   450
gi|124286868|ref|NP_001074398.1| QDGVSSPAASPSHAVRKSCSDTALNAIVAKDPASRHAGNLTLHANSVRRRGMSILREVDEQYHALLEKYEELLSKCRQHGAGVRHAGVQTSRPISRDSSWRDLLGGEESPG--------EGKAGEKSLSQHVEAVDKRLEQSQPEYKALF   450
gi|109489379|ref|XP_340934.3|    QDGVSSPAASPSHAVRKSCSDTALNAIVAKDPASRHAGNLTLHANSVRRRGMSILREVDEQYHALLEKYEELLSKCRQHGAGVRHAGVQTSRPISRDSSWRDLLGGEESQG--------EGKAGEKSLSQHVEAVDKRLEQSQPEYKALF   450
gi|73965050|ref|XP_540425.2|     QDGVSSPAASPGHSVRKSCSDTALNAIVAKDPASRHAGNLTLHANSVRKRGMSILREVDEQYHALLEKYEELLSKCRQHGAGVRHAGVQTSRPISRDSSWRDLRGGEEGQG--------EARAGEKSLSQHVEAVDKRLEQSQPEYKALF   450
gi|194675699|ref|XP_869616.3|    QDGVSSPAASPGHAVRKSCSDTALNAIVAKDPASRHAGNLTLHANSVRKRGMSILREVDEQYHALLEKYEELLSKCRQHGAGVRHAGVQTSRPISRDSSWRDLRAGEEGLG--------ETKA-EKSLSQHVEAVDKRLEQSQPEYKALF   450
gi|118099932|ref|XP_426243.2|    KSHGPSMTPSPNHPVRKSCSDTALNAIVTKDAVSRHEGNYTLHANNVRKRGMSILREVDEQYHALLEKYEELLSKCRQHKDSVRHAGVQTSRPISRDSSFRDFRGEGFELE--------ERKSMEKTISKHVEAVDKRLEQSQPEYKALF   450
gi|45387559|ref|NP_991127.1|     QNGDANDGAAP---VRKSCSDTALDAISAVDASGRRKGSYALHANGVRKRGMSILREVDEQYHALLEKYEELLGKCRRHEESLRHAEVQTSRPVSRDPSMKECRVAEPQQPPPTPPQTPSTPEALEGISRQVEAVDKRLSQNTPEYKALF   450
                                 .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450

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gi|154759283|ref|NP_055418.2|    KEIFSRIQKTKADINATKVKTHSSK   475
gi|114670381|ref|XP_523717.2|    KEIFSRIQKTKADINATKVKTHSSK   475
gi|124286868|ref|NP_001074398.1| KEIFARIQKTKADINATKVKTHSSK   475
gi|109489379|ref|XP_340934.3|    KEIFARIQKTKADINATKVKTHSSK   475
gi|73965050|ref|XP_540425.2|     KEIFSRIQKTKADINATKVKTHSSK   475
gi|194675699|ref|XP_869616.3|    KEIFSRIQKTKADINATKVKTHSSK   475
gi|118099932|ref|XP_426243.2|    KEIFSRIQKTKADINATKVKNKSSK   475
gi|45387559|ref|NP_991127.1|     KEIFSRLQRTKSDINSTKGRKGGK-   475
                                 .......460.......470.....
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