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gi|6679695|ref|NP_031982.1|      MTMTLHTKASGMALLHQIQGNELEPLNRPQLKMPMERALGEVYVDNSKPTVFNYPEGAAYEFNAAAAAAAA-ASAPVYGQSGIAYGPGSE---AAAFSANSLGAFPQLNSVSPSPLMLLHPPPQ-LSPFLHPHG------QQVPYYLENE   150
gi|6978815|ref|NP_036821.1|      MTMTLHTKASGMALLHQIQGNELEPLNRPQLKMPMERALGEVYVDNSKPAVFNYPEGAAYEFNAAAAAAAAGASAPVYGQSSITYGPGSE---AAAFGANSLGAFPQLNSVSPSPLMLLHPPPH-VSPFLHPHG------HQVPYYLENE   150
gi|170295804|ref|NP_001116214.1| MTMTLHTKASGMALLHQIQGNELEPLNRPQLKIPLERPLGEVYLDSSKPAVYNYPEGAAYEFNAAAA-----ANAQVYGQTGLPYGPGSE---AAAFGSNGLGGFPPLNSVSPSPLMLLHPPPQ-LSPFLQPHG------QQVPYYLENE   150
gi|47824866|ref|NP_001001443.1|  MTMTLHTKASGMALLHQIQANELEPLNRPQLKIPLERPLGEVYMDSSKPAVYNYPEGAAYDFNAAAP-----ASAPVYGQSGLPYGPGSE---AAAFGANGLGAFPPLNSVSPSPLVLLHPPPQPLSPFLHPHG------QQVPYYLENE   150
gi|73945701|ref|XP_533454.2|     --MTLHTKASGMALLHQIQGPELDSLNRPQLKIPLERPLGEVYVDSSKPAVYNYPEAGAYDFNAAPA-----APAPLYGQSGLGYGPGSEAVAAAAFGANGLGGFPPLNSMSPSPPVLLHPPPQ-LSSFLHPHG------QQVPYYLENE   150
gi|45383986|ref|NP_990514.1|     MTMTLHTKASGVTLLHQIQGTELETLSRPQLKIPLERSLSDMYVESNKTGVFNYPEGATYDFG---------TTAPVYGSTTLSYAPTSE-----SFGSSSLAGFHSLNNVPPSPVVFLQTAPQ-LSPFIHHHS------QQVPYYLENE   150
gi|23308675|ref|NP_694491.1|     --MYPKEEHSAGGISSSVN----------------------YLDG----AYEYPN-PTQTFG---------TSSPAEPAS-VGYYPAPP--------DPHEEHLQTLGGGSSSPLMFAPSSPQ-LSPYLSHHGGHHTTPHQVSYYLDSS   150
                                 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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gi|6679695|ref|NP_031982.1|      PS-AYAVRDTGPPAFYRSNSDNRRQNGRERLSSSNEKGNMIMESAKETRYCAVCNDYASGYHYGVWSCEGCKAFFKRSIQGHNDYMCPATNQCTIDKNRRKSCQACRLRKCYEVGMMKGGIRKDRRGGRMLKHKRQRDDLEGRNEMGASG   300
gi|6978815|ref|NP_036821.1|      PS-AYAVRDTGPPAFYRSNSDNRRQNGRERLSSSSEKGNMIMESAKETRYCAVCNDYASGYHYGVWSCEGCKAFFKRSIQGHNDYMCPATNQCTIDKNRRKSCQACRLRKCYEVGMMKGGIRKDRRGGRMLKHKRQRDDLEGRNEMGTSG   300
gi|170295804|ref|NP_001116214.1| PS-GYTVREAGPPAFYRPNSDNRRQGGRERLASTNDKGSMAMESAKETRYCAVCNDYASGYHYGVWSCEGCKAFFKRSIQGHNDYMCPATNQCTIDKNRRKSCQACRLRKCYEVGMMKGGIRKDRRGGRMLKHKRQRDDGEGRGEVGSAG   300
gi|47824866|ref|NP_001001443.1|  SS-GYAVREAGPPAYYRPNSDNRRQGGRERLASTSDKGSMAMESAKETRYCAVCNDYASGYHYGVWSCEGCKAFFKRSIQGHNDYMCPATNQCTIDKNRRKSCQACRLRKCYEVGMMKGGIRKDRRGGRMLKHKRQRDDGEGRNEAVPSG   300
gi|73945701|ref|XP_533454.2|     PS-GYAVRQAGPPAFYRPNSDNRRQGGRERLASTSDKGNMAMESAKETRYCAVCNDYASGYHYGVWSCEGCKAFFKRSIQGHNDYMCPATNQCTIDKNRRKSCQACRLRKCYEVGMMKGGIRKDRRGGRMLKHKRQRDDGEGRNEVGSSG   300
gi|45383986|ref|NP_990514.1|     QG-SFGMREAAPPAFYRPSSDNRRHSIERMSSTNEKGSLSMESTKETRYCAVCNDYASGYHYGVWSCEGCKAFFKRSIQGHNDYMCPATNQCTIDKNRRKSCQACRLRKCYEVGMMKGGIRKDRRGGEMMKQKRQREEQDSRNGEASST   300
gi|23308675|ref|NP_694491.1|     SSTVYRSSVVSSQQAAVGLCEELCSATDRQELYTGSRAAGGFDSGKETRFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYVCPATNQCTIDRNRRKSCQACRLRKCYEVGMMKGGIRKDR-GGRSVRRERRRSSNEDRDKSSSDQ   300
                                 .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
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gi|6679695|ref|NP_031982.1|      DMRAANLWPSPLVIKHTKKN--SPALSLTADQMVSALLDAEPPMIYSEYDPSRPFSEASMMGLLTNLADRELVHMINWAKRVPGFGDLNLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEIFDMLLATS   450
gi|6978815|ref|NP_036821.1|      DMRAANLWPSPLVIKHTKKN--SPALSLTADQMVSALLDAEPPLIYSEYDPSRPFSEASMMGLLTNLADRELVHMINWAKRVPGFGDLNLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEIFDMLLATS   450
gi|170295804|ref|NP_001116214.1| DMRAANLWPSPLMIKRSKKN--SLALSLTADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRVPGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEIFDMLLATS   450
gi|47824866|ref|NP_001001443.1|  DMRAANLWPSPIMIKHTKKN--SPVLSLTADQMISALLEAEPPIIYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRVPGFVDLALHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEIFDMLLATS   450
gi|73945701|ref|XP_533454.2|     DVRTSSLWPSPLLIKHTKKN--SPALSLTADQMVSALLEAEPPIIYSDYDPSRPFSEASMMGLLTNLADRELVHMINWAKRVPGFVDLSLHDQVHLLECAWLEILMIGLVWRSMEHPGKLFFAPNLLLDRNQGKCVEGIVEIFDMLLATS   450
gi|45383986|ref|NP_990514.1|     ELRAPTLWTSPLVVKHNKKN--SPALSLTAEQMVSALLEAEPPIVYSEYDPNRPFNEASMMTLLTNLADRELVHMINWAKRVPGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEIFDMLLATA   450
gi|23308675|ref|NP_694491.1|     CSRAGVRTTGPQDKRKKRSGGVVSTLCMSPDQVLLLLLGAEPPAVCSRQKHSRPYTEITMMSLLTNMADKELVHMIAWAKKVPGFQDLSLHDQVQLLESSWLEVLMIGLIWRSIHSPGKLIFAQDLILDRSEGECVEGMAEIFDMLLATV   450
                                 .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450
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                                 :*** ::*: *******:***:***.::* **.:.. * :.  :: :**:*.*:**: ::*:* :** * :* *****:***:************ ***** *************:*:::      .  : :  .     ..:  :*::.
gi|6679695|ref|NP_031982.1|      SRFRMMNLQGEEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITDTLIHLMAKAGLTLQQQHRRLAQLLLILSHIRHMSNKGMEHLYNMKCKNVVPLYDLLLEMLDAHRLHAPASRMGVPPE-EPSQTQLATTSSTSAHSLQT   600
gi|6978815|ref|NP_036821.1|      SRFRMMNLQGEEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKINDTLIHLMAKAGLTLQQQHRRLAQLLLILSHIRHMSNKGMEHLYNMKCKNVVPLYDLLLEMLDAHRLHAPASRMGVPPE-EPSQSQLTTTSSTSAHSLQT   600
gi|170295804|ref|NP_001116214.1| SRFRMMNLQGEEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITDTLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEMLDAHRLHAPTSRGGASVE-ETDQSHLATAGSTSSHSLQK   600
gi|47824866|ref|NP_001001443.1|  SRFRMMNLQGEEFVCLKSIILLNSGVYTFLSSTLRSLEEKDHIHRVLDKITDTLIHLMAKAGLTLQQQHRRLAQLLLILSHFRHMSNKGMEHLYSMKCKNVVPLYDLLLEMLDAHRLHAPANFGSAPPE-DVNQSQLAPTGCTSSHSLQT   600
gi|73945701|ref|XP_533454.2|     SRFRMMNLQGEEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRILDKITDTLIHLMAKAGLTLQQQHRRLAQLLLILSHIRHMSNKGMEHLYNMKCKNVVPLYDLLLEMLDAHRLHAPASRGGVPME-ETNQSQLATTGPTSSHSLQT   600
gi|45383986|ref|NP_990514.1|     ARFRMMNLQGEEFVCLKSIILLNSGVYTFLSSTLKSLEERDYIHRVLDKITDTLIHLMAKSGLSLQQQHRRLAQLLLILSHIRHMSNKGMEHLYNMKCKNVVPLYDLLLEMLDAHRLHAPAARSAAPME-EENRNQLTTAP-ASSHSLQS   600
gi|23308675|ref|NP_694491.1|     ARFRSLKLKLEEFVCLKAIILINSGAFSFCSSPVEPLMDNFMVQCMLDNITDALIYCISKSGASLQLQSRRQAQLLLLLSHIRHMSNKGMEHLYRMKCKNRVPLYDLLLEMLDAQRFQSSGKVQRVWSQSEKNPPSTPTTSSSSSNNSPR   600
                                 .......460.......470.......480.......490.......500.......510.......520.......530.......540.......550.......560.......570.......580.......590.......600
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                                           :  .   :
gi|6679695|ref|NP_031982.1|      YYIPP-EAEGFPNTI----   619
gi|6978815|ref|NP_036821.1|      YYIPP-EAEGFPNTI----   619
gi|170295804|ref|NP_001116214.1| YYITG-EAEGFPATV----   619
gi|47824866|ref|NP_001001443.1|  YYITG-EAENFPSTV----   619
gi|73945701|ref|XP_533454.2|     YYITE-EAGNFPTTV----   619
gi|45383986|ref|NP_990514.1|     FYINSKEEESMQNTI----   619
gi|23308675|ref|NP_694491.1|     GGAAAIQSNGACHSHSPDP   619
                                 .......610.........
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