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                                 * :                                                  :*:           . *.: :.* . :.*::*. : * *:          ::*::    * * ::*   .  **:
gi|10048460|ref|NP_065232.1|     -------MEPPDARAG-------------------------------------------LLWLTLLLSGY-------SGAQAELHVSVPPRVEVMRGEQVALDCTP-REHPEHYVLEWFLVDGTGARHRLASVEPQGSEFLGTVH-SLG   150
gi|13929056|ref|NP_113940.1|     -------MEPPDARAG-------------------------------------------LLWLTLLLSGY-------SGAQAELHVSVPPRVEVMRGEQIALDCTP-REHPENYVLEWLLVDASGARHRLASVEPQGSEFLGTIHNSRG   150
gi|31543106|ref|NP_005572.2|     -------MEPPDAPAQARGAPR-------------------------------------LLLLAVLLAAH-------PDAQAEVRLSVPPLVEVMRGKSVILDCTP-TGTHDHYMLEWFLTDRSGARPRLASAEMQGSELQVTMHDTRG   150
gi|114677742|ref|XP_001161836.1| -------MEPPDAPAQARGAPR-------------------------------------LLLLAVLLAAH-------PDAQAEVRLSVPPLVEVMRGNSVILDCTP-TGTHDHYMLEWFLTDRSGARPRLASAEMQGSELQVTMHDTRG   150
gi|73948194|ref|XP_541571.2|     MPGIAGSKETKVARTGPARGKRKKDGIGETNPRHQSGPTPPLLGPAWARESWASPLFYSEGMHLTRFLAPSKRLRGQGAGAQAEVRLSVPSLVEVMKGEPVALNCTP-LGTHDHFVLEWFLADRSGVRHRLASAELQGSELQGRVLDSRG   150
gi|27807439|ref|NP_777166.1|     -------MEPPDARAGARRAPR-------------------------------------LLVLALLLAAP-------PGSKAEVRLSVPPLVEVMRGESVTLDCSP-LGTHDYFMLEWFLVDRSGARHRLASAELRGSELRDKELNSRG   150
gi|115495543|ref|NP_001070095.1| ---------MKRAISGP-------------------------------------------FWICCTLLAVVL------QVCLASVTVKVNPEMHVLKGDTVMLPCTYTTSAEAAVAVQWFIEFADGGRKQVAYKSSVGSDAG-------T   150
                                 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150

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gi|10048460|ref|NP_065232.1|     RVPPYEVDSRGRLVIAKVQVGDGRDYVCVVKAGAAGTSEATSSVRVFATPEDTEVSPN--KGTLSVMDQFAQEIATCSSNNGNPVPRITWYRNGQRLEVPMEVNQKGYITIRTVREASGLYSLTSTLYLRLHKDDRDANFHCAAHYDLPS   300
gi|13929056|ref|NP_113940.1|     RRPPYKIDSLGRLVIAEAQVGDERDYVCVVKAGAAGTSEATSSVRVFATPEATEVAPN--KGTLSVMEQFAQEIATCSSNNGNPVPRITWYQNGQRLDVPMELNSKGYMTSRTVREASGLYSLTSTLYLRLHKEDRDASFHCAAHYDLPS   300
gi|31543106|ref|NP_005572.2|     RSPPYQLDSQGRLVLAEAQVGDERDYVCVVRAGAAGTAEATARLNVFAKPEATEVSPN--KGTLSVMEDSAQEIATCNSRNGNPAPKITWYRNGQRLEVPVEMNPEGYMTSRTVREASGLLSLTSTLYLRLRKDDRDASFHCAAHYSLPE   300
gi|114677742|ref|XP_001161836.1| RSPPYQLDSQGRLVLAEAQVGDERDYVCVVRAGAAGTAEATARLNVFAKPEATEVSPN--KGTLSVMEDSAQEIATCNSRNGNPAPKITWYRNGQRLEVPVEMNPEGYMTSRTVREASGLLSLTSTLYLRLRKDDRDASFHCAAHYSLPE   300
gi|73948194|ref|XP_541571.2|     RSPPYQLDSRGRLVLTEAQVGDEQNYVCVVRAGAAGTAEATTRLQMFAKPEATEVSPN--RGILSVVDDSAQEIATCNSRNGNPAPQITWYRNGQPLEVPLEVNTEGYMTIRTVREASGLQSLTSTLYLRLHKADRDASFHCSVRYHLPT   300
gi|27807439|ref|NP_777166.1|     RSPPYQLDSQGRLVLPEAQVGDERDYVCVVKAGAAGTAEATARLKVFAKPEAPEVSPN--KGILSVMDDFAQEIATCSSRNGNPAPQIMWYRNGQPLAVPLEVNSEGYMTTRTVREASGLLSLTSTLYLRLHKPDREASFHCSVHYYLPA   300
gi|115495543|ref|NP_001070095.1| FTDRYTIEKDMSLNISQVTVDDHKKFICQVTAGPVGTAESATEVKVFSAPEKPMVVPNPQKIFVDSSISSSAEVGKCISRNGHPEPRIIWFKDDNPLPEEKKKTEKTYMIHFLVKEASGLYTLTSMLYMHLTKADAKSVYHCIVEYTMPD   300
                                 .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300

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gi|10048460|ref|NP_065232.1|     GQHGRLDSHTFRLTLHYPTEHVEFWVGSPSTTEGWVREGDAVQLLCQGDGSPSPEYSFFRQQGTQEEQLNVNLKGNLTLERVHRNQSGIYGCRVEDYDADEEVQLVKKLKLHVAYLDPLELSVPEELFVFLNSSSTVVNCSARGLPTPTV   450
gi|13929056|ref|NP_113940.1|     GQHGRLDSHTFRLTLHYPTEHVEFWVGSPSTTEGWVREGDAVQLLCQGDGSPSPEYSFFREQGNQEEQLNVNLKGNLTLEGVHRSQSGIYGCRVEDYDADEEVQLVKKLKLHVAYLDPLELSVPEEFSVFLNSSGTVVNCSARGLPAPIV   450
gi|31543106|ref|NP_005572.2|     GRHGRLDSPTFHLTLHYPTEHVQFWVGSPSTPAGWVREGDTVQLLCRGDGSPSPEYTLFRLQDEQEEVLNVNLEGNLTLEGVTRGQSGTYGCRVEDYDAADDVQLSKTLELRVAYLDPLELSEGKVLSLPLNSS-AVVNCSVHGLPTPAL   450
gi|114677742|ref|XP_001161836.1| GRHDRLDSPTFHLTLHYPTEHVQFWVGSPSTPAGWVREGDTVQLLCRGDGSPSPEYTLFRLQDEQEEVLNVNFEGNLTLEGVTRGQSGTYGCRVEDYDAADDVQLSKTLELRVAYLDPLELSEGKVLSLPLNSS-AVVNCSVHGLPTPAL   450
gi|73948194|ref|XP_541571.2|     GQHGRLDSPAFHLTLHYPTERVQFWVGSPSTTEGWVREGDSVQLFCRGDGSPSPEYTFFRLQDKQEDVLKTNLERNLTLEGVGRG---------------DRLEGSRTLASRETNLDPLELSTGEELSLHLGNS-TAVNCSVQGLPTPAL   450
gi|27807439|ref|NP_777166.1|     GQHGRLDGPSFSLTLHYPTEHVLFWLGSQSTAEGWVREGDSVQLLCQGDGSPTPEYTFFWLQDKQEDVLKTSLEGNLTLERVQRNQSGTYGCRVEDFDVPEDAELSKTLELRVAYLDSLELSAGEELSLPLHNS-TTVTCSARGLPTPTL   450
gi|115495543|ref|NP_001070095.1| NQIKQESSDNFNISLQYSTENVFFKVKN----EGPIKEGDDVVMQCETDGNPQPQFDFFK-----GEKLLEGLGGTLKKKSITREDSGTYKCEAMDYEADSKVQLHKTLNINVHYIDITVEPEG--PLVVSKGDHVELQCKAKASEAHTL   450
                                 .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450

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gi|10048460|ref|NP_065232.1|     RWTKDSVTLADGPMLSLQSVTFDSAGTYTCEASTPTVPLLSRTQSFQLIVQGAPELKPNEIMPKSGNSWTEGDEVMLTCSARGFPEPKLTWSQRGD-TPAEPPFEGRGWKSSSLMVKVTSALSREGVSCEASNIHGKKGHVFHFGSVAPQ   600
gi|13929056|ref|NP_113940.1|     RWTKDSVTVADGPILSLDSVTFDSAGTYTCEASTPTVPLLSRTQSFQLVVQGAPELKPNEIKPKSGTSWTEGDEVMLTCSARGFPEPKLTWSQRGDTTPAEPPFEGRGWMSSSLTLKVTSALSREGVSCEASNIHGKNGHVFHFGSVAPQ   600
gi|31543106|ref|NP_005572.2|     RWTKDSTPLGDGPMLSLSSITFDSNGTYVCEASLPTVPVLSRTQNFTLLVQGSPELKTAEIEPKADGSWREGDEVTLICSARGHPDPKLSWSQLGG-SPAEPIPGRQGWVSSSLTLKVTSALSRDGISCEASNPHGNKRHVFHFGTVSPQ   600
gi|114677742|ref|XP_001161836.1| RWTKDSTPLGDGPMLSLSSITFDSNGTYVCEASLPTVPVLSRTQNFTLLVQGSPELKTAEIEPKADGSWREGDEVTLICSPPGHPDPKLI-----------------------------------------------------   600
gi|73948194|ref|XP_541571.2|     RWTKDSVPLGTGPTLSLSSITFDAAGTYICEASMPTVPLLSRTQSFRLLVQGPPQLRAEETQPKTEGSWMEGEEVRLVCSARGYPEPKLSWSQLGG-SPAEPALQGQGWVSSSLTLKVTSALSRDGVSCEASNPHGKKQHVFHFGSVTPQ   600
gi|27807439|ref|NP_777166.1|     YWTKDSAPMGEDPTLSLHSVTFDSAGTYTCEAYMPRIPLLSRTRSFRLLVQGTPELKAKETQPKAEGSWTEGDEVTLICYARGYPKPKLTWSQLGG-SPTEPAPGGQGWVSSSLTLKVTSALSQDGVSCEASNPLGNTHHVFHFGTVAPQ   600
gi|115495543|ref|NP_001070095.1| QWTKDSKELSNTGVFAKESVTLADGGVYVCVGAVPSVPGLQKQVNITVNVKGQPEIDAPVKGLVD----KEGGMVTLNCSALGHPAPQFIWTPSGK----ESVTVKGNRVISTVILEATAAVLKDGVICEAYNTHGRDSKNFEVKLDQAK   600
                                 .......460.......470.......480.......490.......500.......510.......520.......530.......540.......550.......560.......570.......580.......590.......600

gi|10048460|ref|NP_065232.1|     TAQAGVAVMAVAVSVGLLLLVVAAFYCMRRKGRPGCCRRAEKGAPPAREPELSHSGSERPEHTGLLMGGPSGGGRGGSGGFGDEC   685
gi|13929056|ref|NP_113940.1|     TAQAGVAVMAVAVSVGLLLLVVAAFYCMRRKGRPGCCQRAEKGAPPAREPELSHSGSERPEHTGLLMGGPSGGGRGGNGGFGDEC   685
gi|31543106|ref|NP_005572.2|     TSQAGVAVMAVAVSVGLLLLVVAVFYCVRRKGGPCCRQRREKGAPPPGEPGLSHSGSEQPEQTGLLMGGASGGARGGSGGFGDEC   685
gi|114677742|ref|XP_001161836.1| ---------------------------------------------------------------------------------   685
gi|73948194|ref|XP_541571.2|     TAQAGVAVMAVAVSVGLLLLVVAAFYCMRRKGRPGCCRRGEKGTPPAGEPELSHSGSERPEQTGLLMGGASGGARHGSGGFGDEC   685
gi|27807439|ref|NP_777166.1|     TSQAGVAVMAVAISVALLLLVVAVFYCMRRKGRPGCCQWGEKGSPPPGEPKLSHSGSQRPEQTGLLMGSASGGAKHGSGGFGDEC   685
gi|115495543|ref|NP_001070095.1| PTPANSDRGRHLSQLSLLLLSFSGLFLVHTL-------------------------------------------------   685
                                 .......610.......620.......630.......640.......650.......660.......670.......680.....
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