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                                 ***: :   .  .*                *:**. .  : : . ..     .  :: *****..****** ::** *  * **: : *.       ..  . *: :   .:***. * *:*:**: ***** *:**:**:******* :*
gi|4885653|ref|NP_005420.1|      MHLLGFFSVACSLLAAALLPGPREAP-AAAAAFESGLDLSDAEPD-AGEATAYASKDLEEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGGWQHNREQANLNSRTEETIKFAAAHYNTEILKSIDNEWRKTQCMPREVCIDVGKEFGVAT   150
gi|55623542|ref|XP_526740.1|     MHLLGFFSVACSLLAAALLPGPREAP--AAAAFESGLDLSDAEPD-AGEATAYASKDLEEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGGWQHNREQANLNSRTEETIKFAAAHYNTEILKSIDNEWRKTQCMPREVCIDVGKEFGVAT   150
gi|6678565|ref|NP_033532.1|      MHLLCFLSLACSLLAAALIPSPREAP-ATVAAFESGLGFSEAEPD-GGEVKAFEGKDLEEQLRSVSSVDELMSVLYPDYWKMYKCQLRKGGWQ----QPTLNTRTGDSVKFAAAHYNTEILKSIDNEWRKTQCMPREVCIDVGKEFGAAT   150
gi|16758992|ref|NP_446105.1|     MHLLCFLSLACSLLAAALIPGPREAP-ATVAAFESGLGFSEAEPD-GGEVKGFEGKDLEEQLRSVSSVDELMSVLYPDYWKMYKCQLRKGGWQ----QPSLNMRTGDTVKLAAAHYNTEILKSIDNEWRKTQCMPREVCIDVGKEFGAAT   150
gi|27806191|ref|NP_776913.1|     MHLLGFCSVACSLLAAALLPGPRRAPAAAAAAFESGLGFSDTEPD-AGENKAYAGKEMEEQLRSVSSVDELMTVLYPEYWKMYKCQLRKGGWQHSTEQANTNIRTGETLKFAAAHYNTEILRSIDNEWRKTQCMPREVCIDVGKEFGAAT   150
gi|73979612|ref|XP_540047.2|     MHLLGFWSLACSLLAAALLPGPRDAP-AAAAAFESGLGFSDAEPD-AGEAQAYAGKDLEEQLRSASSVDELMTVLYPEYWKMYKCQLRKGGWQRNKEQPNISARTEETIKFAAAHYNAEILKSIDNEWRKTQCIPREVCIDVGKEFGAAT   150
gi|50746517|ref|XP_420532.1|     MHLLEMLSLGCCLAAGAVLLGPRQPP--VAAAYESGHGYYEEEPG-AGEPKAHASKDLEEQLRSVSSVDELMTVLYPEYWKMFKCQLRKGDWQHNREHSSSDTRSDDSLKFAAAHYNAEILKSIDTEWRKTQCMPREVCVDVGKEFGATT   150
gi|45387875|ref|NP_991297.1|     MHLFGFSVFCLALFYAN-------------LAFESSHDYYEYDQDQADAMQEHSEPDLVEQLRSAGSVDELMRIVYPTYRIMLKCRSKMGSRLLRREPSSTETRSEE-ASFAAAFINLELLKSIEIEWRKTLCMPRQVCLDVGKEFG-AT   150
                                 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150

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gi|4885653|ref|NP_005420.1|      NTFFKPPCVSVYRCGGCCNSEGLQCMNTSTSYLSKTLFEITVPLSQGPKPVTISFANHTSCRCMSKLDVYRQVHSIIRRSLPATLPQCQAANKTCPTNYMWNNHICRCLAQEDFMFSSDAGD-DSTDGFHDICGPNKELDEETCQCVCRA   300
gi|55623542|ref|XP_526740.1|     NTFFKPPCVSIYRCGGCCNSEGLQCMNTSTSYLSKTLFEITVPLSQGPKPVTISFANHTSCRCMSKLDVYRQVHSIIRRSLPATLPQCQAANKTCPTNYMWNNHICRCLAQEDFMFSLDAGD-DSTDGFHDICGPNKELDEETCQCVCRA   300
gi|6678565|ref|NP_033532.1|      NTFFKPPCVSVYRCGGCCNSEGLQCMNTSTGYLSKTLFEITVPLSQGPKPVTISFANHTSCRCMSKLDVYRQVHSIIRRSLPATLPQCQAANKTCPTNYVWNNYMCRCLAQQDFIFYSNVED-DSTNGFHDVCGPNKELDEDTCQCVCKG   300
gi|16758992|ref|NP_446105.1|     NTFFKPPCVSVYRCGGCCNSEGLQCMNTSTGYLSKTLFEITVPLSQGPKPVTISFANHTSCRCMSKLDVYRQVHSIIRRSLPATLPQCQAANKTCPANYVWNNYMCQCLAQQDFIFYSNVED-DSSNGFHDVCGPNKELDEDTCQCVCKG   300
gi|27806191|ref|NP_776913.1|     NTFFKPPCVSVYRCGGCCNSEGQQCMNTSTSYLSKTLFEITVPLSQGPKPVTISFANHTSCRCMSKLDVYRQVHSIIRRSLPAALPQCQAANKTCPADYIWNNHVCRCLAQHDFIFSPSAGD-DSADGFHDICGPNKELDEETCQCVCKG   300
gi|73979612|ref|XP_540047.2|     NTFFKPPCVSVYRCGGCCNSEGLQCMNTSTSHLSKTLFEITVPLSQGPKPVTISFANHTSCRCMSKLDVYRQVHSIIRRSLPATLPQCQAANKTCPTNYIWNNHLCRCLAQQDFIFASNSGD-DSTDGFHDICGPNKELDEETCQCVCRG   300
gi|50746517|ref|XP_420532.1|     NTFFKPPCVSIYRCGGCCNSEGLQCMNISTNYISKTLFEITVPLSHGPKPVTVSFANHTSCRCMSKLDVYRQVHSIIRRSLPATQTQCHVANRTCPKNHIWNNQICRCLAQHDFGFSSHLGDSDTSEGFH-ICGPNKELDEETCQCVCKG   300
gi|45387875|ref|NP_991297.1|     NTFYKPPCVSVYRCGGCCNSEELQCRNISTSYISKTLFEITVPVKQGTKPVTISFANHTSCSCLSKQNLYRQQHSIIRR----ALTECHVANKTCPKNHSWSNHLCKCVLLPDTLHSKPHSDFET-----DFCGPDKELDEETCQCECRK   300
                                 .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300

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gi|4885653|ref|NP_005420.1|      GLRPASCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKRTCPRNQPLNPGKCACECTESPQKCLLKGKKFHHQTCSCYRRPCTN--RQKACEPGFSYSEEVCRCVPSYWKRPQMS   424
gi|55623542|ref|XP_526740.1|     GLRPASCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKRTCPRNQPLNPGKCACECTESPQKCLLKGKKFHHQTCSCYRRPCTN--RQKACEPGFSYSEEVCRCVPSYWKRPQMS   424
gi|6678565|ref|NP_033532.1|      GLRPSSCGPHKELDRDSCQCVCKNKLFPNSCGANREFDENTCQCVCKRTCPRNQPLNPGKCACECTENTQKCFLKGKKFHHQTCSCYRRPCAN--RLKHCDPGLSFSEEVCRCVPSYWKRPHLN   424
gi|16758992|ref|NP_446105.1|     GLRPSSCGPHKELDRDSCQCVCKNKLFLNSCGANREFDENTCQCVCKRTCPRNQPLNPGKCACECTENTQKCFLKGKKFHHQTCSCYRRPCTN--RLKHCDPGLSFSEEVCRCVPSYWKRPHLN   424
gi|27806191|ref|NP_776913.1|     GLQASSCGPHKELDRDSCQCVCKNKLFPSSCGANREFDENTCQCICKKTCPRNQPLNPGKCACECTENPQKCFLKGKKFQHQTCSCYRRPCTN--RVKHCEQGLSFSEEVCRCVPSYWKRPHVN   424
gi|73979612|ref|XP_540047.2|     GLRPSSCGPHKELDRNSCQCVCKNKLLPNSCGANREFDENTCQCVCKRTCPRNQPLNPGKCACECTENSQKCFLKGKKFQHQTCSCYRRPCTN--RLRHCEQGLIFSEEVCRCVPSYWKRPQMN   424
gi|50746517|ref|XP_420532.1|     DVRPSSCGSHKELDRASCQCMCKNKLLPTSCGPNKEFDEEKCQCVCKKTCPKHHPLNPAKCICECIESPNKCFLKGKRFHHQTCSCYRPPCTV--RTKRCDAGFYFSEEVCRCVPTYWKRPLMN   424
gi|45387875|ref|NP_991297.1|     ELRKAGCGPHHYLDKNTCQCVCKAQ--PSSCGPQQSFNRDTCQCTCAKVCPRSQPLNRTKCVCECTESPNKCFLKGRRFHPATCSCVRPPCNVDPKRRKCKENEYFSEELCHCIPTYWGRLD--   424
                                 .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420....
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