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gi | 19922446 | ref | NP_611218.1 | -----MQSR-WLCC--IFVIVLAHWTRANPILSHPKVALEFILLHNDMHARFDQTSVNSCTCPPEDVHTKCYGGRVAHEVRKRYRKEAQEGGTVLVYLNAGDTYTGTSWFTIFKDKIASAFLNKLKPDAT 150
gi | 19922444 | ref | NP_611217.1 | -----MLPARGLLIGSCCLLALLIHPVQPNP LAPRAEVAAEFILLHNDMHARFEQTSVSTGCTSCKEBANLDQCYGGRFARVAHEVRKRYRKEAEEGTIPVFLYNAGDTYTGTAWFTVYKDKIASAFLNKLKSPDAT 150
gi | 118784010 | ref | XP_313394.3 | -----GTMARRTHIP---LVAVILASVCSLAAPKAG--GLFLIILLHNDMHARFEQTSVNDQCPDVAENRQCYGGRFARVAHEVRKRYRKEAEASGGLPVLYLNAGDTYTGTPWFSVFKDNI TAAPLNILKPDAT 150
gi | 28573524 | ref | NP_725682.2 | -----MHSLLPQWFFPLS---LILFFLDNIS-----GFKFTLLHNDMHARSFDPISDTGGRCRTVDDAMGICFGGGRVAEVAASAANTATD---PVIYLNAGDSFQGTWFSVYRGMVARMNLPLADPM 150
gi | 41055552 | ref | NP_957226.1 | -----MMMMNVL SALLLLFIHQCL-----CWSADFLTLHNDVHARVEETNKDSGKCSKPPC-----FAGVSRRSIKIKIRSKSKN-----VLLLDAGDQYOGTIVWFNYYKGAEAAYFMNQLKYDAM 150
gi | 292624509 | ref | XP_002665677.1 | -----MMMMNVL SALLLLFIHQCL-----CWSADFLTLHNDVHARVEETNKDSGKCSKPPC-----FAGVSRRSIKIKIRSKSKN-----VLLLDAGDQYOGTIVWFNYYKGAEAAYFMNQLKYDAM 150
gi | 4505467 | ref | NP_002517.1 | -----MCPRAARAPATL LLLALGAVL---WPAAGAWELTLLHNDVHSRLEQTSDDSSKCVNASR---CMGGVARLFTKVQGIIRRAEPN-----VLLLDAGDQYOGTIWFTVYKGAEVAHFMMNLRKYDAM 150
gi | 114608462 | ref | XP_518619.2 | -----MCPRAARAPATL LLLALGAVL---WPAAGAWELTLLHNDVHSRLEQTSDDSSKCVNASR---CMGGVARLFTKVQGIIRRAEPN-----VLLLDAGDQYOGTIWFTVYKGAEVAHFMMNLRKYDAM 150
gi | 99028963 | ref | NP_776554.2 | -----MNPGAARTPALRILALGALL---WPAARPWELTLLHNDVHSRLEQTSDDSSKCVNASR---CVGGVARLFTKVQGIIRRAEPN-----VLLLDAGDQYOGTIWFTVYKGTVAHFMMNLRKYDAM 150
gi | 6754900 | ref | NP_035981.1 | -----MRPAAAKV PKWLLLLALSALLPQWPAASAWELTLLHNDVHSRLEQTSDDSKCVNASL---CVGGVARLFTKVQGIIRKEEPPN-----VLLLDAGDQYOGTIWFTVYKGAEVAHFMMNLRKYDAM 150
gi | 11024643 | ref | NP_067587.1 | -----MRPAAATA PKWLLLLALSALLPLWP TAKSWELTLMHNDVHSRLEQTSDDSKCVNASL---CVGGVARLFTKVQGIIRKEEPPN-----VLLLDAGDQYOGTIWFTVYKGAEVAHFMMNLRKYDAM 150
gi | 73973882 | ref | XP_532221.2 | -----MGYARR-----PKEEGAEGLSGEVAGMACFVRVPLGEAARQSGGPF---EPNGTSRSEEWERAKKVG-----GAG-----VFENQLPIAS---PVLGQ----- 150
gi | 118088842 | ref | XP_419855.2 | -----MAYGLSALCLWLWLN---AAAGLRLLTLHNDVHARVHAEARG---CAEGPRG---CFGGVARRAARVAEAAERAAQRN-----VLLLDAGDQYOGSVVWFSRFKQGEAAVHFMNLRKYDAM 150
gi | 145612976 | ref | XP_001412525.1 | -----MSRLLQVA-LCALPFGVSVSAEDVLHS--RRLNKRFLDDEGHYNI SFYHINDVHAHLDFSSSGDCTNPAGG---CYGGYARVKHVVDLTPREDHPD---SLFLNAGDEFGQTLFYSYGGKEIAELNLQGFDCM 150
gi | 85091076 | ref | XP_958725.1 | -----MASLQKLLTAGL LLLGSHGLMASAEDHLISERKLSKRFIDDEKGNVNI SFYHINDVHAHLDFSSSGDCTNPAGG---CYGGYARVKHILINETRFPSHKD---SLVNLGDEFGQTLFYSYGGKEIAELNLQGFDCM 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi | 19922446 | ref | NP_611218.1 | -----SLGNHEFFERVEGLIP-FLNEVTFPVLANL L DLSKVPQLKAWHLANSALLENGTKVGVIGIYLPDKKILN-MDVEFNEEVEINVEAKLKAQ-GIKIITIALGHSGLYKD 300
gi | 19922444 | ref | NP_611217.1 | -----SLGNHEFFQNVGGLVP-FLNAVEFPVLACNLNLTDPVEMAQAQANSTILERNGKVVGVIGIYLPDKKILAFR-NKVEEBEIVINAEAAKLAQ-GIITIALGHSGLYKD 300
gi | 118784010 | ref | XP_313394.3 | -----SLGNHEFFDLGVEGLVP-FLNEVDFPVLVNL DLSKTPEMOFSRQLQRSIIFTKAGVRIGVIGIYLPDKKQLAPLNTVEFLDEIEEINKKATSLKQ-GVNIITIALGHSGLERD 300
gi | 28573524 | ref | NP_725682.2 | -----ALGVHELDDGADALAE-FLNITTFPMVSSNINLINEPKLAENANLVTSLVITKGNRKIGIVGIRPDKERTQP-SNVIFKRVPAINKETKRLKQ-GIDITIALGHSGLYKD 300
gi | 41055552 | ref | NP_957226.1 | -----ALGNHEFFDNGV DGLLPPFLQEVNCTVLSANIKADETLAPRISGYFFPYKIFTLGSEKVVGVIGIYLPDKKILN-MDVEFNEEVEINVEAKLKAQ-GIKIITIALGHSGLYKD 300
gi | 292624509 | ref | XP_002665677.1 | -----ALGNHEFFDNGV DGLLPPFLQEVNCTVLSANIKADETLAPRISGYFFPYKIFTLGSEKVVGVIGIYLPDKKILN-MDVEFNEEVEINVEAKLKAQ-GIKIITIALGHSGLYKD 300
gi | 4505467 | ref | NP_002517.1 | -----ALGNHEFFDNGV DGLLPPFLQEVNCTVLSANIKADETLAPRISGYFFPYKIFTLGSEKVVGVIGIYLPDKKILN-MDVEFNEEVEINVEAKLKAQ-GIKIITIALGHSGLYKD 300
gi | 114608462 | ref | XP_518619.2 | -----FQVLPFGHCLLQVKKRFGCSRDVLLVLEMMWGMGRALGNHEFFDNGV DGLLPPFLQEVNCTVLSANIKADETLAPRISGYFFPYKIFTLGSEKVVGVIGIYLPDKKILN-MDVEFNEEVEINVEAKLKAQ-GIKIITIALGHSGLYKD 300
gi | 99028963 | ref | NP_776554.2 | -----ALGNHEFFDNGV DGLLPPFLQEVNCTVLSANIKADETLAPRISGYFFPYKIFTLGSEKVVGVIGIYLPDKKILN-MDVEFNEEVEINVEAKLKAQ-GIKIITIALGHSGLYKD 300
gi | 6754900 | ref | NP_035981.1 | -----ALGNHEFFDNGV DGLLPPFLQEVNCTVLSANIKADETLAPRISGYFFPYKIFTLGSEKVVGVIGIYLPDKKILN-MDVEFNEEVEINVEAKLKAQ-GIKIITIALGHSGLYKD 300
gi | 11024643 | ref | NP_067587.1 | -----ALGNHEFFDNGV DGLLPPFLQEVNCTVLSANIKADETLAPRISGYFFPYKIFTLGSEKVVGVIGIYLPDKKILN-MDVEFNEEVEINVEAKLKAQ-GIKIITIALGHSGLYKD 300
gi | 73973882 | ref | XP_532221.2 | -----ALGNHEFFDNGV DGLLPPFLQEVNCTVLSANIKADETLAPRISGYFFPYKIFTLGSEKVVGVIGIYLPDKKILN-MDVEFNEEVEINVEAKLKAQ-GIKIITIALGHSGLYKD 300
gi | 118088842 | ref | XP_419855.2 | -----ALGNHEFFDNGV DGLLPPFLQEVNCTVLSANIKADETLAPRISGYFFPYKIFTLGSEKVVGVIGIYLPDKKILN-MDVEFNEEVEINVEAKLKAQ-GIKIITIALGHSGLYKD 300
gi | 145612976 | ref | XP_001412525.1 | -----ALGNHEFFDNGV DGLLPPFLQEVNCTVLSANIKADETLAPRISGYFFPYKIFTLGSEKVVGVIGIYLPDKKILN-MDVEFNEEVEINVEAKLKAQ-GIKIITIALGHSGLYKD 300
gi | 85091076 | ref | XP_958725.1 | -----ALGNHEFFDNGV DGLLPPFLQEVNCTVLSANIKADETLAPRISGYFFPYKIFTLGSEKVVGVIGIYLPDKKILN-MDVEFNEEVEINVEAKLKAQ-GIKIITIALGHSGLYKD 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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gi | 19922446 | ref | NP_611218.1 | -----LEIAKNCPEVDIVIGGHTNIFLYTG-----AQPDAEHIDGYPYIMVQKNSGKEVPVQAYAYTKYLGLKLVQFDADGNLIQWDDGSPILLNASSVAQEQDLDLLEVFVRNTRLEKSVVGHKQVHLEGNKVAECRAEENLGLIAD--AM 450
gi | 19922444 | ref | NP_611217.1 | -----QEIAMNCP EVDIVIGGHTNIFLYTG-----TDSDEAVRGPYPTVVQASGKQVVPVQAYAYTKYLGLKLVQFDADGNLIEFDGAPILLNASSVAQEQDLDLLEVFVRNTRLEKSVVGHKQVHLEGNKVAECRAEENLGLIAD--AM 450
gi | 118784010 | ref | XP_313394.3 | -----KEIAACPDVDLVIIGGHTNIFLYSG-----TAPDVEDPAGPYPMVKNAAGKEVPVQAYAYTKYLGLKLVQFDADGNLIEFDGAPILLNASSVAQEQDLDLLEVFVRNTRLEKSVVGHKQVHLEGNKVAECRAEENLGLIAD--AM 450
gi | 28573524 | ref | NP_725682.2 | -----MEIARKCPDVDIVVGGHTNIFLYSG-----KAPKKEVSEGPYPPIIVVFKDGRKVPVQAYAYTKYLGLKLVQFDADGNLIEFDGAPILLNASSVAQEQDLDLLEVFVRNTRLEKSVVGHKQVHLEGNKVAECRAEENLGLIAD--AM 450
gi | 41055552 | ref | NP_957226.1 | -----QMIARKVQGV DVVIGGHTNIFLYTG-----DPPSTEVPAGPYPLMVKSDGGRQVVPVQAYAFGKYLGLKLVQFDADGNVLESTGNPILLNASSVPEPDIQAKVDSWRMNLANYSSQVQGLVFLNGTFEECRFRECNGNLICD--AM 450
gi | 292624509 | ref | XP_002665677.1 | -----QMIARKVQGV DVVIGGHTNIFLYTG-----DPPSTEVPAGPYPLMVKSDGGRQVVPVQAYAFGKYLGLKLVQFDADGNVLESTGNPILLNASSVPEPDIQAKVDSWRMNLANYSSQVQGLVFLNGTFEECRFRECNGNLICD--AM 450
gi | 4505467 | ref | NP_002517.1 | -----KLIQAKVQGV DVVVGGHTNIFLYTG-----NPPSKEVPAGKYPIFIVTSDGGRKVPVQAYAFGKYLGLKLVQFDADGNVLESTGNPILLNASSVPEPDIQAKVDSWRMNLANYSSQVQGLVFLNGTFEECRFRECNGNLICD--AM 450
gi | 114608462 | ref | XP_518619.2 | -----KLIQAKVQGV DVVVGGHTNIFLYTG-----NPPSKEVPAGKYPIFIVTSDGGRKVPVQAYAFGKYLGLKLVQFDADGNVLESTGNPILLNASSVPEPDIQAKVDSWRMNLANYSSQVQGLVFLNGTFEECRFRECNGNLICD--AM 450
gi | 99028963 | ref | NP_776554.2 | -----KLIQAKVQGV DVVVGGHTNIFLYTG-----NPPSKEVPAGKYPIFIVTSDGGRKVPVQAYAFGKYLGLKLVQFDADGNVLESTGNPILLNASSVPEPDIQAKVDSWRMNLANYSSQVQGLVFLNGTFEECRFRECNGNLICD--AM 450
gi | 6754900 | ref | NP_035981.1 | -----KLIQAKVQGV DVVVGGHTNIFLYTG-----NPPSKEVPAGKYPIFIVTSDGGRKVPVQAYAFGKYLGLKLVQFDADGNVLESTGNPILLNASSVPEPDIQAKVDSWRMNLANYSSQVQGLVFLNGTFEECRFRECNGNLICD--AM 450
gi | 11024643 | ref | NP_067587.1 | -----KLIQAKVQGV DVVVGGHTNIFLYTG-----NPPSKEVPAGKYPIFIVTSDGGRKVPVQAYAFGKYLGLKLVQFDADGNVLESTGNPILLNASSVPEPDIQAKVDSWRMNLANYSSQVQGLVFLNGTFEECRFRECNGNLICD--AM 450
gi | 73973882 | ref | XP_532221.2 | -----KLIQAKVQGV DVVVGGHTNIFLYTG-----NPPSKEVPAGKYPIFIVTSDGGRKVPVQAYAFGKYLGLKLVQFDADGNVLESTGNPILLNASSVPEPDIQAKVDSWRMNLANYSSQVQGLVFLNGTFEECRFRECNGNLICD--AM 450
gi | 118088842 | ref | XP_419855.2 | -----KLIQAKVQGV DVVVGGHTNIFLYTG-----NPPSKEVPAGKYPIFIVTSDGGRKVPVQAYAFGKYLGLKLVQFDADGNVLESTGNPILLNASSVPEPDIQAKVDSWRMNLANYSSQVQGLVFLNGTFEECRFRECNGNLICD--AM 450
gi | 145612976 | ref | XP_001412525.1 | -----KRLAEQVSGLHLIMGGHSHFLVGDMP-----GAEQPYPIATINRKGDEEVFVTA YRWGEVLYGIDVTYDSBGLLILAYHGAPILHTNQTEPELQAOIDAWRAPFAEFAAEVVGFNVELDQI--TCRTRCRLLDGLMAD--AM 450
gi | 85091076 | ref | XP_958725.1 | -----QRLAKEITGLYLIMGGHSHFLVGDMP-----GAVQPYPIATINRKGDEEVFVTA YRWGEVLYGIDVTYDSBGLLILAYHGAPILHTNQTEPELQAOIDAWRAPFAEFAAEVVGFNVELDQI--TCRTRCRLLDGLMAD--AM 450
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450

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gi |19922446|ref|NP_611218.1|VFSRLMEEQGG-DFWTDAAISIMQGGIRSSIETKRS-DGAITDNDILSVLPWKNLYMVPTMG---IRRALEHGAALRGKDSDGGFLQVE-GIRVVFNNKPEGQRVVSVQVRAACRVPTYSDLNDTAINVNVLGEFLLDGGDHVM 600
gi |19922444|ref|NP_611217.1|IYSRVLENKGG-EFWTDAIAFMQGGIRSGSVDKD-DGVINGATLLAVLPPFENNLYVTRILGS---ILLAALEHSASVRLQDSNGGFLQM-GLRVVYNNNEQGKRVVSAQALCASCAVPTYKSINETALYQVIVPQFLLEGGGDGYTL 600
gi |118784010|ref|XP_313394.3|IYATTIREQSND-GFWTDAAIGFIQGG---ILLAALEHSASVRLQDSNGGFLQM-GLRVVYNNNEQGKRVVSAQALCASCAVPTYKSINETALYQVIVPQFLLEGGGDGYTL 600
gi |28573524|ref|NP_725682.2|VYARVVQTMADRSSWTDASIGLINAGAIRASIDPGE-TGAITEADVVTVLPFGQDLYYTRISGS---QLMKALEHSAQMRSKHMSAHLOVE-GLRLKFNHSLPKGERIEIRALCSDCQIPHYEAVDINGYYGVVVTSFLLNGGEGYSF 600
gi |4105552|ref|NP_957226.1|VHNLIKYADEL--QWNHVSSCILNGGGIRGPIDERNNRNGSITMEDLIAVLPFGGTFDLVQLNGS---ILLEAFEHSVRRHG-GNTGEFLQVE-GFQVVYDLSKAPGSRVKSVKVLCTQCRVPHYEPLVENKVYKVVLSYLVDGGDGFTM 600
gi |292624509|ref|XP_002665677.1|VHNLIKYADEL--QWNHVSSCILNGGGIRAPIDERNNRNGSITMEDLIAVLPFGGTFDLVQLNGS---ILLEAFEHSVRRHG-GNTGEFLQVE-GFQVVYDLSKAPGSRVKSVKVLCTQCRVPHYEPLVENKVYKVVLSYLVDGGDGFTM 600
gi |4505467|ref|NP_002517.1|INNLRHRHDADEM--FWNHVSMCILNGGGIRSPIDERN-NGTITWENLAAVLPFGGTFDLVQLKGS---ILLKAFEHSVHRYG-QSTGEFLQVG-GIHVVYDLSRKPGDRVVKLDVLCTQCRVPSYDLKMDEVYKVILENFLANGGDGFQM 600
gi |114608462|ref|XP_518619.2|INNLRHRHDADEM--FWNHVSMCILNGGGIRSPIDERN-NGTITWENLAAVLPFGGTFDLVQLKGS---ILLKAFEHSVHRYG-QSTGEFLQVG-GIHVVYDLSRKPGDRVVKLDVLCTQCRVPSYDLKMDEVYKVILENFLANGGDGFQM 600
gi |99028963|ref|NP_776554.2|INNLRHRHDADEM--FWNHVSMCILNGGGIRSPIDERN-NGTITWENLAAVLPFGGTFDLVQLKGS---ILLKAFEHSVHRYG-QSTGEFLQVG-GIHVVYDLSRNPGDRVVKLEVLCTQRVPSYEFLRMDKVYKVILSFLVSGDGDFQM 600
gi |6754900|ref|NP_035981.1|INNLRHRHDADEM--FWNHVSMCILNGGGIRSPIDERN-NGTITWENLAAVLPFGGTFDLVQLKGS---ILLKAFEHSVHRYG-QSTGEFLQVG-GIHVVYDLSRNPGDRVVQLEVLCTQRVPSYEFLRMDKVYKVILSFLVSGDGDFQM 600
gi |11024643|ref|NP_067587.1|INNLRHRHDADEM--FWNHVSMCILNGGGIRSPIDERN-NGTITWENLAAVLPFGGTFDLVQLKGS---ILLKAFEHSVHRYG-QSTGEFLQVG-GIHVVYDLSRKPWDRVVQLVLCTQCRVPIYEFLEMDKVYKVILSFLVSGDGDFQM 600
gi |73973882|ref|XP_532221.2|INNLRHRHDADEM--FWNHVSMCILNGGGIRSPIDERN-NGTITWENLAAVLPFGGTFDLVQLKGS---ILLKAFEHSVHRYG-QSTGEFLQVG-GIHVVYDLSRKPGNRVVKLDVLCTQCRVPSYEPLVENKVYKVVLSFLANGGDGFQM 600
gi |118088842|ref|XP_419855.2|LYENVRRPDRK--SWNHVSLCILNGGGIRASIDERNANGTITWEDLSVLPFGGRFDLVLTLKGS---ILLKAFEHSVHRYG-RGTGELLQVG-GIHVVYDLSRAPGHRAVSIEVLCTQACRVPAYVPLEMDEVYNVTLSYMLFGGDGYM 600
gi |145612976|ref|XP_001412525.1|VAYRKAVTTE-----IDFALINGGVRATIPAGN---ITRGGVLTSFPFGNTIVDLTITASDLWLVLEGLVSGVNQFNQKPVTSYPQVSKEINIVDPSGPVGN---RLRKVTINGEPLKGDTSG-KVYHVILDFLAGGDNFV 600
gi |85091076|ref|XP_958725.1|LDYRLNASTDG-----LAPSFALINGGIRASIDVGP---ITRGEVLTAFPFGNAVEITLSGOLWDVLAGIVARNKANGKAVTSFLQVSRGIKIEYQPLNSPDNGVTLAAVTIGE---KLDMT--KQYKVVIDFVAGGDNFA 600
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600

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gi |19922446|ref|NP_611218.1|R-DSAHQPQRLQNDLEAVSQYLNQRDVYVYPEIEGRIIFINASST----LMGSAALLLISSLLLKIIA- 670
gi |19922444|ref|NP_611217.1|IEESDPFTESMQRNDLNATMEYLKQRHFVYPEIERIVIHEKADGSASGIVASISLLLLSLLTRFI-- 670
gi |118784010|ref|XP_313394.3|IEESDPFTESMQRNDLNATMEYLKQRHFVYPEIERIVIHEKADGSASGIVASISLLLLSLLTRFI-- 670
gi |28573524|ref|NP_725682.2|VDPKRPEVENMTILDRMAVIQYLQEHKVIYPEREDRQYVQHKHIANSGYMSLEPNLILSFLYFCHRFLVV 670
gi |4105552|ref|NP_957226.1|IKEKLKHDSGD-LDISVVAGIISERKRVHPAVEGRFQFSSCAGLRGYTSTVLLLWAVWMLV 670
gi |292624509|ref|XP_002665677.1|IKEKLKHDSGD-LDISVVAGIISERKRVHPAVEGRIQFSSCAGLRGYTSTVLLLWAVWMLV 670
gi |4505467|ref|NP_002517.1|IKDELLRHDSGD-QDINVVSTYISKMKVIYPAVEGRIKFTSGSHCHGSFSLIFLSLVAVIILYQ 670
gi |114608462|ref|XP_518619.2|IKDELLRHDSGD-QDINVVSTYISKMK-----GDECIGHD----- 670
gi |99028963|ref|NP_776554.2|IKDELLRHDSGD-QDINVVSGYISKMKVIYPAVEGRIQFSASHCCGSFLIFLSLVAVIILYQ 670
gi |6754900|ref|NP_035981.1|IKDELLRHDSGD-QDISVVSEYISKMKVIYPAVEGRIKFSAASHYQGSFPLVILSFWAMILILYQ 670
gi |11024643|ref|NP_067587.1|IKDELLRHDSGD-QDISVVSEYISKMKVIYPAVEGRIKFSAASHYQGSFPLILILSFWAVILVYQ 670
gi |73973882|ref|XP_532221.2|IKDEALRHDSGD-QDINVVSGYILKLKVIYPAVEGRIKFSASRCHGSFSLIFLLFLAVIIVYQ 670
gi |118088842|ref|XP_419855.2|LRDNHITYSKGE-PDIEVVSRYLDRMKRVYPAVEGRIKFSSGSLIQGSLLILSALLTVTFWHC 670
gi |145612976|ref|XP_001412525.1|ASSG-FALLDAQ---DVVLLEVLRDNNPIDIKLDGRIRTAS-CAAKRRTKRAAAL----- 670
gi |85091076|ref|XP_958725.1|EAISNLVVLDTL---DEVLVNYIKEKTPVDVELDGRIAPYSKCGGRKKSKKVRRER----- 670
.....610.....620.....630.....640.....650.....660.....670

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