

gi | 22328958 | ref | NP_194417.2 | -----MVGSEVLEECGKIKKESKRAAKLEKLLRQREBEAT--SSLSLEEEDES-----CSSNYGDVTTNELQ-- 150
gi | 30688949 | ref | NP_194847.3 | -----MSSE-----SEIPLSSSTAABESGKIKKAAKKAALKLEKLRQBEATRRTASISLEENDE-----FSNNYGDVTTLELQSSADPKAGKW 150
gi | 115447981 | ref | NP_001047770.1 | -----MSSEPPDAAAAAASSAGDLAADLSSATSKKQLKDKARKAEKAEKASQRQQQ-----QPADADDP-----FAANYGDVVEETQ-- 150
gi | 6323011 | ref | NP_013083.1 | -----MSQDEN--IVKVAEES-AEPAQVILGEDGKPLSKKALKKQKEQEKQRKKEERALLQEAEREAREKKAASADT-----AKDNYG--KLPLTQSR 150
gi | 50306525 | ref | XP_453236.1 | -----MSDEVK--KDPVEEIS-EGVECVILGEDGKPLSKKALKKQKEQEKQRKKEERERLQAAEAREKKAASANDT-----AKENYG--KAPLTIOS 150
gi | 45187834 | ref | NP_984057.1 | -----MSEQVEQVADKVAELS-TKEETVILGEDGKPLSKKALKKQKEQEKQRKKEERAAQLAAEAREKKAASADT-----ARDNYG--ALPLTIOS 150
gi | 19075852 | ref | NP_588352.1 | -----MSMEMEKVENLSLEAKNEKPKVEILGEDGKPLSKKALKKLEKEREKQKRRERAREAEKKKRE--ANEYD-----SAGKYG--DLPLNRS 150
gi | 17136276 | ref | NP_476609.1 | -----MVED--KEQ--VANGEOVSKGAKKLAAKKAQKAEIN-ASTAANNAGG--DSABDH-----AAGRYG--LSEMIOS 150
gi | 158294413 | ref | XP_315584.3 | -----MVTETIKPEPVGAGABAESKKAAKKAADAEKAAKAEHKAASAAAAGTGG--AVADDTGADGVD--SAGRYG--TMPMIOS 150
gi | 45439306 | ref | NP_001340.2 | -----MPSASARSKSOK--PREIM--DAAEEDY-----AKERYG--TSSMIOS 150
gi | 114581044 | ref | XP_515810.2 | -----MPSASARSKSOK--PREIM--DAAEEDY-----AKERYG--TSSMIOS 150
gi | 73984263 | ref | XP_848666.1 | -----MPSASARSKSOK--PREIM--DAAEEDY-----AKERYG--YSSMIOS 150
gi | 78045531 | ref | NP_001030257.1 | -----MPSANASRRSOK--PREIM--DAAEEDY-----AKERYG--YSSMIOS 150
gi | 21703998 | ref | NP_663482.1 | -----MPSANASRRSOK--PREIM--DAAEEDY-----AKERYG--YSSMIOS 150
gi | 16758642 | ref | NP_446251.1 | -----MPSANASRRSOK--PREIM--DAAEEDY-----AKERYG--YSSMIOS 150
gi | 55741590 | ref | NP_00106528.1 | -----MPSANASRRSOK--PREIM--DAAEEDY-----AKERYG--YSSMIOS 150
gi | 117606291 | ref | NP_001071079.1 | -----MPSANASRRSOK--PREIM--DAAEEDY-----AKERYG--YSSMIOS 150
gi | 17551876 | ref | NP_499089.1 | -----MPSANASRRSOK--PREIM--DAAEEDY-----AKERYG--YSSMIOS 150
gi | 124505695 | ref | XP_001350961.1 | -----MPSAAGRGQKDRRDNBEQ--PAADY-----AKERYG--YSSMIOS 150
-----MTKENVCGGGEEQQAQSKKALKKQKEKAEKAAKAEKAKLASEEQE--TEEDDF-----AKDRYG--ICPMVOS 150
-----MADAAEGEQPLSKKELNKLARKAKAEKAGKGGQQQAAM--QEDA-----SKDFYG--SYGLVNE 150
MTNCLLQNLGRLNVLKRYLLLLNLFNLKNDINFLVLRKGLFVCGLRKMKDDVVSSTPAATEEAVMNDKKKCKKAKLAKELKLAELRENKNEAAKVLVYVCD--INKDNYGYTKVSLQKYADSIMELVNLLEDIVNFFV 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi | 22328958 | ref | NP_194417.2 | -----AVEGKELDVSNLV-EEIVG-----SEVSIIRGLRHKRNLVGTGL-FVILLRESGFTVCV--BETRVGANMIKRVKQLSRESVVELIGVVSHPKPLTGT--QVEIHVRKMFCLRSLEPLVVEDAAR-----SESDI 300
gi | 30688949 | ref | NP_194847.3 | -----IHAEGKEWIDVSDLV-EEMLG-----SEVLIRGRVHNRPTSNKLGFLVLRRESSTVCCVVSQSEKTKVGNMVKYKQLSRESFVDVIGVVTLKPKPLTGT--QVEIQVRKVCINKSLAKPLSVEDAAR-----SEADI 300
gi | 115447981 | ref | NP_001047770.1 | -----KTISGRVWTEIGGLD-EAAG-----SEVLIRGAQAIRPVSKMAFVLRRESMSTVQCVLVSADAGVTQMRVFATSLSKESIVDVEGVVSLPKPLKAT--QVEIQVRKVCINKRAIPLPILNEDASR-----SEADI 300
gi | 6323011 | ref | NP_013083.1 | -----DSDRTGQKRVKFLDRAKSD--KEVLFRRVHNRQAGATLAFLLRQOASLIQGLVKANKEGHSIKNMVWAGSLNLESIVLVRGVVKKVDEPIKSAIVONLEIHTIKYIIEETPEALPILNEDASRSE-----AEA 300
gi | 50306525 | ref | XP_453236.1 | -----TTKSGVERILFEDLRESKDDG--REVVFRARVHNSRQAGATLAFLLRQOASLIQGLVKANKEGHSIKNMVWAGSLNLESIVLVRGVVKKVDEPIKSAIVONLEIHTIKYIIEETPEALPILNEDASRSE-----AEA 300
gi | 45187834 | ref | NP_984057.1 | -----ASRTGKRIQFALR-ABDEG-----KEVLLRSRVHNSRQAGATLAFLLRQOASLIQGLVKANKEGHSIKNMVWAGSLNLESIVLVRGVVKKVDEPIKSAIVONLEIHTIKYIIEETPEALPILNEDASRSE-----AEA 300
gi | 19075852 | ref | NP_588352.1 | -----TARPCRTYQISDIS--AKNDG-----QTVLLRARVYTSRQGNKMCFFELRQKYDTICILAVVND--ISKQMVKCGSISLESIVLVEGIVKKSPEIKRSATVODAEIHSISIVVIFSIKKNLPLVEDAGRSEBEQIRSE 300
gi | 17136276 | ref | NP_476609.1 | -----KDKRSERNFVPSELS-GVYKG-----GLVWVGRVHNSRAKG-KCFLVLRQOSTVQICLAVGDV--ISKQMVKFAINPKESIIDIQAKPVAVSSKIESCTEESLELSVEQIFVQAKAQPLQIATEDASR-----PHNAD 300
gi | 158294413 | ref | XP_315584.3 | -----AKRAERFVNVFDLS-HCQKD-----ALVWVGRVHNSRAKG-KCFLVLRQOSTVQICLAVGDV--VSKQMVKFSGSTIPRESIIDLAKVVPVEERIESCTEOTLELHVLELFLLAARQAQLPQIATEDASR-----PEKSD 300
gi | 45439306 | ref | NP_001340.2 | -----QEK-PDRVLRVRDLT-IQKAD-----EVVWVRRVHNSRAKG-KCFLVLRQOQFNVALVAVGDH--ASKQMVKFAANINKESIIVDEGVVRRKVNKIGSCTQODVELHVQIKIYVLSAEFRLPQLDDAVR-----PEAEG 300
gi | 114581044 | ref | XP_515810.2 | -----QEK-PDRVLRVRDLT-IQKAD-----EVVWVRRVHNSRAKG-KCFLVLRQOQFNVALVAVGDH--ASKQMVKFAANINKESIIVDEGVVRRKVNKIGSCTQODVELHVQIKIYVLSAEFRLPQLDDAVR-----PEAEG 300
gi | 73984263 | ref | XP_848666.1 | -----QEK-PDRVLRVRDLT-IQKAD-----EVVWVRRVHNSRAKG-KCFLVLRQOQFNVALVAVGDH--ASKQMVKFAANINKESIIVDEGVVRRKVNKIGSCTQODVELHVQIKIYVLSAEFRLPQLDDAVR-----PEVEG 300
gi | 78045531 | ref | NP_001030257.1 | -----QEK-PDRVLRVRDLT-IQKAD-----EVVWVRRVHNSRAKG-KCFLVLRQOQFNVALVAVGDH--ASKQMVKFAANINKESIIVDEGVVRRKVNKIGSCTQODVELHVQIKIYVLSAEFRLPQLDDAVR-----PEVEG 300
gi | 21703998 | ref | NP_663482.1 | -----QEK-PDRVLRVRDLT-IQKAD-----EVVWVRRVHNSRAKG-KCFLVLRQOQFNVALVAVGDH--ASKQMVKFAANINKESIIVDEGVVRRKVNKIGSCTQODVELHVQIKIYVLSAEFRLPQLDDAIR-----PEVEG 300
gi | 16758642 | ref | NP_446251.1 | -----QEK-PDRVLRVRDLT-IQKAD-----EVVWVRRVHNSRAKG-KCFLVLRQOQFNVALVAVGDH--ASKQMVKFAANINKESIIVDEGVVRRKVNKIGSCTQODVELHVQIKIYVLSAEFRLPQLDDAIR-----PEVEG 300
gi | 55741590 | ref | NP_00106528.1 | -----QEK-PDRVLRVRDLT-IQKAD-----EVVWVRRVHNSRAKG-KCFLVLRQOQFNVALVAVGDH--ASKQMVKFAANINKESIIVDEGVVRRKVNKIGSCTQODVELHVQIKIYVLSAEFRLPQLDDAIR-----PEVEG 300
gi | 117606291 | ref | NP_001071079.1 | -----QEK-PDRVLRVRDLT-IQKAD-----EVVWVRRVHNSRAKG-KCFLVLRQOQFNVALVAVGDH--ASKQMVKFAANINKESIIVDEGVVRRKVNKIGSCTQODVELHVQIKIYVLSAEFRLPQLDDAIR-----PEVEG 300
gi | 17551876 | ref | NP_499089.1 | -----QEK-PDRVLRVRDLT-IQKAD-----EVVWVRRVHNSRAKG-KCFLVLRQOQFNVALVAVGDH--ASKQMVKFAANINKESIIVDEGVVRRKVNKIGSCTQODVELHVQIKIYVLSAEFRLPQLDDAIR-----PEVEG 300
gi | 124505695 | ref | XP_001350961.1 | -----QEK-PDRVLRVRDLT-IQKAD-----EVVWVRRVHNSRAKG-KCFLVLRQOQFNVALVAVGDH--ASKQMVKFAANINKESIIVDEGVVRRKVNKIGSCTQODVELHVQIKIYVLSAEFRLPQLDDAIR-----PEVEG 300
-----KSK-EDCENEKREICVDNKGVDKDAYNEEILLGKKKIWRGRIHDIRSKG-SIAFIIILRHKLYSLQCILDIKNN--NNDKNMKNVSNLSLECIYDIYKIKPEIPIDSN--IKVEIHTINKIFLKTMKLPLFLKDNAP-----KET 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi | 22328958 | ref | NP_194417.2 | -----EKSQKDGKQAARVLDLRLNLRVLDLRTIPANQAIIFRIQCOVQIAFREYLQSKGFLEIHTPKLIAGSSEGGSAVFRLEYKQPACLAQSPQLHKQMAICGDMRRVFEVGPVFRABDFTHRHLCFVGLDVEIMERMHYSSEIMDLVGLHFLF 450
gi | 30688949 | ref | NP_194847.3 | -----EASLQTESPAARVNDLRLNLRVLDLRTIPANQAIIFRIQCOVQIAFREYLQSKGFLEIHTPKLIAGSSEGGSAVFRLEYKQPACLAQSPQLHKQMAICGDMRRVFEVGPVFRABDFTHRHLCFVGLDVEIMERMHYSSEIMDLVGLHFLF 450
gi | 115447981 | ref | NP_001047770.1 | -----EKAEQAGEKLVVGLDRLNLRVLDLRTIPANQAIIFRIQCOVQIAFREYLQSKGFLEIHTPKLIAGSSEGGSAVFRLEYKQPACLAQSPQLHKQMAICGDMRRVFEVGPVFRABDFTHRHLCFVGLDVEIMERMHYSSEIMDLVGLHFLF 450
gi | 6323011 | ref | NP_013083.1 | -----HAAG-----LQVNVLDLRLDNRVIDLRTIPANQAIIFRIQAGVCELFRYFLYKFTVHHPKLLGAPSEGGSSVFEVYFYGKSYLAQSPQLYKQMAIADDFERFVEVAPVFRABDFTHRHLCFVGLDVEIMERMHYSSEIMDLVGLHFLF 450
gi | 50306525 | ref | XP_453236.1 | -----HAAG-----LQVNVLDLRLDNRVIDLRTIPANQAIIFRIQAGVCELFRYFLYKFTVHHPKLLGAPSEGGSSVFEVYFYGKSYLAQSPQLYKQMAIADDFERFVEVAPVFRABDFTHRHLCFVGLDVEIMERMHYSSEIMDLVGLHFLF 450
gi | 45187834 | ref | NP_984057.1 | -----HAAG-----LQVNVLDLRLDNRVIDLRTIPANQAIIFRIQAGVCELFRYFLYKFTVHHPKLLGAPSEGGSSVFEVYFYGKSYLAQSPQLYKQMAIADDFERFVEVAPVFRABDFTHRHLCFVGLDVEIMERMHYSSEIMDLVGLHFLF 450
gi | 19075852 | ref | NP_588352.1 | -----NAAEGDSK-FVRVNLRLDNRVIDLRTIPANQAIIFRIQAGVCELFRYFLYKFTVHHPKLLGAPSEGGSSVFEVYFYGKSYLAQSPQLYKQMAIADDFERFVEVAPVFRABDFTHRHLCFVGLDVEIMERMHYSSEIMDLVGLHFLF 450
gi | 17136276 | ref | NP_476609.1 | -----DAGEGLN-----IRVNDLRLDNRVIDLRTIPANQAIIFRIQAGVCELFRYFLYKFTVHHPKLLGAPSEGGSSVFEVYFYGKSYLAQSPQLYKQMAIADDFERFVEVAPVFRABDFTHRHLCFVGLDVEIMERMHYSSEIMDLVGLHFLF 450
gi | 158294413 | ref | XP_315584.3 | -----DPEALK-----IRVNDLRLDNRVIDLRTIPANQAIIFRIQAGVCELFRYFLYKFTVHHPKLLGAPSEGGSSVFEVYFYGKSYLAQSPQLYKQMAIADDFERFVEVAPVFRABDFTHRHLCFVGLDVEIMERMHYSSEIMDLVGLHFLF 450
gi | 45439306 | ref | NP_001340.2 | -----EEEGR-----ATVNDLRLDNRVIDLRTIPANQAIIFRIQAGVCELFRYFLYKFTVHHPKLLGAPSEGGSSVFEVYFYGKSYLAQSPQLYKQMAIADDFERFVEVAPVFRABDFTHRHLCFVGLDVEIMERMHYSSEIMDLVGLHFLF 450
gi | 114581044 | ref | XP_515810.2 | -----EEEGR-----ATVNDLRLDNRVIDLRTIPANQAIIFRIQAGVCELFRYFLYKFTVHHPKLLGAPSEGGSSVFEVYFYGKSYLAQSPQLYKQMAIADDFERFVEVAPVFRABDFTHRHLCFVGLDVEIMERMHYSSEIMDLVGLHFLF 450
gi | 73984263 | ref | XP_848666.1 | -----EEEGR-----ATVNDLRLDNRVIDLRTIPANQAIIFRIQAGVCELFRYFLYKFTVHHPKLLGAPSEGGSSVFEVYFYGKSYLAQSPQLYKQMAIADDFERFVEVAPVFRABDFTHRHLCFVGLDVEIMERMHYSSEIMDLVGLHFLF 450
gi | 78045531 | ref | NP_001030257.1 | -----EEEGR-----ATVNDLRLDNRVIDLRTIPANQAIIFRIQAGVCELFRYFLYKFTVHHPKLLGAPSEGGSSVFEVYFYGKSYLAQSPQLYKQMAIADDFERFVEVAPVFRABDFTHRHLCFVGLDVEIMERMHYSSEIMDLVGLHFLF 450
gi | 21703998 | ref | NP_663482.1 | -----EEEGR-----ATVNDLRLDNRVIDLRTIPANQAIIFRIQAGVCELFRYFLYKFTVHHPKLLGAPSEGGSSVFEVYFYGKSYLAQSPQLYKQMAIADDFERFVEVAPVFRABDFTHRHLCFVGLDVEIMERMHYSSEIMDLVGLHFLF 450
gi | 16758642 | ref | NP_446251.1 | -----EEEGR-----ATVNDLRLDNRVIDLRTIPANQAIIFRIQAGVCELFRYFLYKFTVHHPKLLGAPSEGGSSVFEVYFYGKSYLAQSPQLYKQMAIADDFERFVEVAPVFRABDFTHRHLCFVGLDVEIMERMHYSSEIMDLVGLHFLF 450
gi | 55741590 | ref | NP_00106528.1 | -----EEEGR-----ATVNDLRLDNRVIDLRTIPANQAIIFRIQAGVCELFRYFLYKFTVHHPKLLGAPSEGGSSVFEVYFYGKSYLAQSPQLYKQMAIADDFERFVEVAPVFRABDFTHRHLCFVGLDVEIMERMHYSSEIMDLVGLHFLF 450
gi | 117606291 | ref | NP_001071079.1 | -----DEEGR-----ATVNDLRLDNRVIDLRTIPANQAIIFRIQAGVCELFRYFLYKFTVHHPKLLGAPSEGGSSVFEVYFYGKSYLAQSPQLYKQMAIADDFERFVEVAPVFRABDFTHRHLCFVGLDVEIMERMHYSSEIMDLVGLHFLF 450
gi | 17551876 | ref | NP_499089.1 | -----EQENQL-----AVVNLRLDNRVIDLRTIPANQAIIFRIQAGVCELFRYFLYKFTVHHPKLLGAPSEGGSSVFEVYFYGKSYLAQSPQLYKQMAIADDFERFVEVAPVFRABDFTHRHLCFVGLDVEIMERMHYSSEIMDLVGLHFLF 450
gi | 124505695 | ref | XP_001350961.1 | -----NDEIIT-----IKVNDLRLDNRVIDLRTIPANQAIIFRIQAGVCELFRYFLYKFTVHHPKLLGAPSEGGSSVFEVYFYGKSYLAQSPQLYKQMAIADDFERFVEVAPVFRABDFTHRHLCFVGLDVEIMERMHYSSEIMDLVGLHFLF 450
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



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gi | 22328958 | ref | NP_194417.2 | FIFTKIE--ERCPKELSVRKQVPPFSLKFL--PQLRLRTFAEGIQMLKEAG--EVD-----PLGDLNTESEERKLGQVLVLEKYKTEFYMLHRYPSAVRPFYTMPYENDSNYSNSFDVFIERGEIISGAQRIDPE 600
gi | 30688949 | ref | NP_194847.3 | FIFTSLN--ERCKKELAVGKQVPPFPLKFL--PKTLRLTFEEGVQMLKEAG--VEVD-----PLGDLNTESEERKLGQVLVLEKYNTTEFYILHRYPKAVRPFYTMTCADNPLYSNSFDVFIERGEIISGAQRVHIPE 600
gi | 115447981 | ref | NP_001047770.1 | AIFKHLN--ENCKKELTINRQVPPFPLKYL--EKTLRLTFEEGIQMLKEAG--TEIE-----PMGDLNTEAEKLLGRLVLEKYVTEFFYILRYPLAVRPFYTMPYDNPAYSNSFDVFIERGEIISGAQRIDPE 600
gi | 6323011 | ref | NP_013083.1 | FIFSEL--KRFAGEIELVRKQVPEEFKLPKDGKVMRLTYKEGIEMLRAG--KEIG-----DFEDLSTENEKLLGRLVLEKYVTEFFYILDKFPLAIRPFYTMPDPANPKYSNSYDFMFRGEEIISGAQRIDHA 600
gi | 50306525 | ref | XP_453236.1 | FIFSQLK--TRYAKEIALVRKQVPEEFKLPKDGKVMRIPFKEGIALLRAG--KDVD-----DFEDLSTENEKLLGRLVLEKYVTEFFYILDKFPLAIRPFYTMPDAEDPRYSNSYDFMFRGEEIISGAQRIDAD 600
gi | 45187834 | ref | NP_984057.1 | FIFTELK--KRFAREIAQVRKQVPEEFKFPADGKVMILHYKEGIAMLRAG--KEIG-----DFDLDSTENERFLGRLVLEKYVTEFFYILDKFPAELRPFYTMPDPADPRYSNSYDFMFRGEEIISGAQRIDPE 600
gi | 19075852 | ref | NP_588352.1 | YIFKTIIR--EKYAKQVAVRQVPSDFDILP--DADRIRFHFKDAVKLLKEAGYR--KQLVPGQKVPDEEFHYCEDPFFDFTPEERALGQIVREKYVTEFFYILDKYVPSVVRPFYTMPDPEPRYSNSYDFMFRGEEIISGAQRIDPE 600
gi | 17136276 | ref | NP_476609.1 | SIFKGLR--DKYAKEIESVGOQVYKVDAFKFL--EPPLILQFADGVAMLRAG--VEIG-----DEEDLSTPNEKLLGRLVLEKYVTEFFYILDKFPLAIRPFYTMPDNNFVYSNSYDFMFRGEEIISGAQRIDPE 600
gi | 158294413 | ref | XP_315584.3 | EMFKGLR--DHYAKEIAAVGQVNVPEPFKFL--EPPLKLEFAQAVAMLRAG--VQMD-----DEEDLSTPNEKLLGRLVLEKYVTEFFYILDKFPLAIRPFYTMPDPANAKYSNSYDFMFRGEEIISGAQRIDPE 600
gi | 45439306 | ref | NP_001340.2 | QIFKGLQ--ERFQTEIQTVNKQVPCPEPFKFL--EPTLRLEYCEALAMLRAG--VEMG-----DEEDLSTPNEKLLGRLVLEKYVTEFFYILDKYPLAVRPFYTMPDPRNPKQSNYSYDFMFRGEEIISGAQRIDPE 600
gi | 114581044 | ref | XP_515810.2 | QIFKGLQ--ERFQTEIQTVNKQVPCPEPFKFL--EPTLRLEYCEALAMLRAG--VEMG-----DEEDLSTPNEKLLGRLVLEKYVTEFFYILDKYPLAVRPFYTMPDPRNPKQSNYSYDFMFRGEEIISGAQRIDPE 600
gi | 73984263 | ref | XP_848666.1 | QIFKGLQ--KRFQTEIQTVNKQVPCPEPFKFL--EPTLRLEYCEALAMLRAG--IEMG-----DEEDLSTPNEKLLGRLVLEKYVTEFFYILDKYPLAVRPFYTMPDPRNPKQSNYSYDFMFRGEEIISGAQRIDPE 600
gi | 78045531 | ref | NP_001030257.1 | QIFKGLQ--KRFQTEIQTVNKQVPCPEPFKFL--EPTLRLEYCEALAMLRAG--IEMG-----DEEDLSTPNEKLLGRLVLEKYVTEFFYILDKYPLAVRPFYTMPDPRNPKQSNYSYDFMFRGEEIISGAQRIDPE 600
gi | 21703998 | ref | NP_663482.1 | QIFKGLQ--ERFQTEIQTVNKQVPCPEPFKFL--EPTLRLEYCEALAMLRAG--VEMD-----DEEDLSTPNEKLLGRLVLEKYVTEFFYILDKYPLAVRPFYTMPDPRNPKQSNYSYDFMFRGEEIISGAQRIDPE 600
gi | 16758642 | ref | NP_446251.1 | QIFKGLQ--ERFQTEIQTVNKQVPCPEPFKFL--EPTLRLEYCEALAMLRAG--VEMD-----DEEDLSTPNEKLLGRLVLEKYVTEFFYILDKYPLAVRPFYTMPDPRNPKQSNYSYDFMFRGEEIISGAQRIDPE 600
gi | 55741590 | ref | NP_001006528.1 | QIFKGLQ--ERFQAEIQTVNKQVPCPEPFKFL--EPTLRLEYREAVAMLRAG--IEMG-----DEEDLSTPNEKLLGRLVLEKYVTEFFYILDKYPLAVRPFYTMPDFVNPKNYSNSYDFMFRGEEIISGAQRIDPE 600
gi | 117606291 | ref | NP_001071079.1 | QIFKGLR--DRFQTEIQTVNKQVPSPEPFKFL--EPTLRLEYKEGLAMLRAG--VEMG-----DEEDLSTPNEKLLGRLVLEKYVTEFFYILDKYPLAVRPFYTMPDPRNPKQSNYSYDFMFRGEEIISGAQRIDHA 600
gi | 17551876 | ref | NP_499089.1 | QMFKGLQ--QNYQDEIAAVGNQVPAEPPQFC--EPPLILKVPDAIILLRENG--IEIG-----DEEDLSTPNEKLLGRLVLEKYVTEFFYILDKYPLAVRPFYTMPDAHDERYSNSYDFMFRGEEIISGAQRIDAD 600
gi | 124505695 | ref | XP_001350961.1 | HIFKELTNNENKNTFKIKIKNOVPSDDFVWL--DKTPIFTVEAIAIKLLIKNGKLFKKEED-----ILTVDLTDLEKELGKLIKLSNNTDYVYIINFPSSLRPFYTMPKEDDPKISNSYDFMFRGEEIISGQRIDMK 600
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600

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gi | 22328958 | ref | NP_194417.2 | LLEKRAECGIDV--KTIISTVIDAFRYGAPPHGGFGVGLERVVMLFCALNNIRKTSLFPRDSORLTP 667
gi | 30688949 | ref | NP_194847.3 | VLEQRAGECGIDV--KTIISTVIDSFRYGAPLHGGFGVGLERVVMLFCALNNIRKTSLFPRDPORLSP 667
gi | 115447981 | ref | NP_001047770.1 | LLTKRATECGIDA--STISSYIESFSYGAPPHGGFGVGLERVVMLFCALNNIRKTSLFPRDPORLVP 667
gi | 6323011 | ref | NP_013083.1 | LLQERMKAHGLSPEDPGLKDYCDGFSYGCPPHAGGGI GLERVVMFYLDLKNIRRALFPRDPKRLRP 667
gi | 50306525 | ref | XP_453236.1 | LLKERMNAHEVHPEDPGLKDYCEAFYGCPPHAGGGI GLERVVMFYLDLKNIRRALFPRDPKRLRP 667
gi | 45187834 | ref | NP_984057.1 | LLRERMKHHGLQPEDAGFKDYCDAFYGCPPHAGGGI GLERVVMFYLDLKNIRRALFPRDPKRLRP 667
gi | 19075852 | ref | NP_588352.1 | LLVERMKALGVSP--DVGLQQYIDAFYAGCPPHAGGGI GLERVVMFYLDLKNIRRALFPRDPKRLRP 667
gi | 17136276 | ref | NP_476609.1 | YLIERAKHHGIDL--SKIAAYIDSFRYGCPPHAGGGI GMERVVMLYGLDNIRKTSMFPRDPKRLTP 667
gi | 158294413 | ref | XP_315584.3 | YLIERAKLHGIDL--SKIAAYIDAFRYGCPPHAGGGI GMERVVMLYGLDNIRKTSMFPRDPKRLTP 667
gi | 45439306 | ref | NP_001340.2 | LLTERALHHGIDL--EKIKAYIDSFRFGAPPHAGGGI GLERVMTMLFGLHNVRQTSMFPRDPKRLTP 667
gi | 114581044 | ref | XP_515810.2 | LLTERALHHGIDL--EKIKAYIDSFRFGAPPHAGGGI GLERVMTMLFGLHNVRQTSMFPRDPKRLTP 667
gi | 73984263 | ref | XP_848666.1 | LLTERALHHGIDL--EKIKAYIDSFRFGAPPHAGGGI GLERVMTMLFGLHNVRQTSMFPRDPKRLTP 667
gi | 78045531 | ref | NP_001030257.1 | LVTERALHHGIDL--EKIKAYIDSFRFGAPPHAGGGI GLERVMTMLFGLHNVRQTSMFPRDPKRLTP 667
gi | 21703998 | ref | NP_663482.1 | LLTERALHHGIDL--EKIKAYIDSFRFGAPPHAGGGI GLERVMTMLFGLHNVRQTSMFPRDPKRLTP 667
gi | 16758642 | ref | NP_446251.1 | LLTERALHHGIDL--EKIKAYIDSFRFGAPPHAGGGI GLERVMTMLFGLHNVRQTSMFPRDPKRLTP 667
gi | 55741590 | ref | NP_001006528.1 | LLTERAKHHGIDL--EKIKAYIDSFRFGAPPHAGGGI GLERVMTMLYGLHNVRQTSMFPRDPKRLTP 667
gi | 117606291 | ref | NP_001071079.1 | LLTERAMHHNIDL--EKIKAYIDSFRYGCPPHAGGGI GLERVMTMLYGLHNVRQTSMFPRDPKRLTP 667
gi | 17551876 | ref | NP_499089.1 | MLVERAKHHQVDL--AKIQSYIDSFKYGCPPHAGGGI GLERVMTMLFGLHNIRLALFPRDPKRLTP 667
gi | 124505695 | ref | XP_001350961.1 | LLENIKLFNLDL--NKLNFYIDSFAYSYPHSCGCI GLERVLMFLGLNNIRKTSLFPRDPKRLTP 667
.....610.....620.....630.....640.....650.....660.....

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