

gi 114205408 ref NP_598823.1 |-----MIVFRQENVDDYDTEGELGSGQFAVVKKCREKSTGLQYAAKFIKRRRTKSSRRGVSREDIEREVSILKEIR--HPNVITLHEVYENKTDVILILELVAGGELFDFLAEKESLTFEEATEFLKQILNGVYYLHSLG 134
gi 62663156 ref XP_225138.3 |-----MIVFRQENVDDYDTEGELGSGQFAVVKKCREKSTGLQYAAKFIKRRRTKSSRRGVSREDIEREVSILKEIR--HPNVITLHEVYENKTDVILILELVAGGELFDFLAEKESLTFEEATEFLKQILNGVYYLHSLG 134
gi 89363047 ref NP_004929.2 |-----MIVFRQENVDDYDTEGELGSGQFAVVKKCREKSTGLQYAAKFIKRRRTKSSRRGVSREDIEREVSILKEIQ--HPNVITLHEVYENKTDVILILELVAGGELFDFLAEKESLTFEEATEFLKQILNGVYYLHSLG 134
gi 114625378 ref XP_001140200.1 |-----MIVFRQENVDDYDTEGELGSGQFAVVKKCREKSTGLQYAAKFIKRRRTKSSRRGVSREDIEREVSILKEIQ--HPNVITLHEVYENKTDVILILELVAGGELFDFLAEKESLTFEEATEFLKQILNGVYYLHSLG 134
gi 73946538 ref XP_541259.2 |-----MIVFRQENVDDYDTEGELGSGQFAVVKKCREKSTGLQYAAKFIKRRRTKSSRRGVSREDIEREVSILKEIQ--HPNVITLHEVYENKTDVILILELVAGGELFDFLAEKESLTFEEATEFLKQILNGVYYLHSLG 134
gi 194669620 ref XP_613544.4 |-----MIVFRQENVDDYDTEGELGSGQFAVVKKCREKSTGLQYAAKFIKRRRTKSSRRGVSREDIEREVSILKEIQ--HPNVITLHEVYENKTDVILILELVAGGELFDFLAEKESLTFEEATEFLKQILNGVYYLHSLG 134
gi 118104165 ref XP_425037.2 |-----MIVFRQENVDDYDTEGELGSGQFAVVKKCREKSTGLQYAAKFIKRRRTKSSRRGVSREDIEREVSILKEIQ--HPNVITLHEVYENKTDVILILELVAGGELFDFLAEKESLTFEEATEFLKQILNGVYYLHSLG 134
gi 153792613 ref NP_001093460.1 |-----MIVFNLENVEDYDEIGGELGSGQFAVVKKCRKHSKGVYAAKFIKRRRTKSSRRGVSREDIEREVSILKEIQ--HPNVITLHDVFENKHEVILILELVAGGELFDFLAEKESLTFEEATEFLKQILDGVSYLHSLK 134
gi 115533596 ref NP_490840.2 |MSDDVNSSATSTSSSTVHFDDTPEFDVYIEIETELGSGQFAVVRVRDRKIGEKYAAKFIKRRRTKSSRRGVSREDIEREVRVLRKIRGNSVVELLHAYVETASDVIIVLELVSGGELFDFVCAKECLDEVEAAAFIKQILLAVRHLSLH 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi 114205408 ref NP_598823.1 |IAHFDLKPENIMLLDRNVKPKRIKIIDFLGAKHIDFGNEFKNIFGTFPEFVAPEIVNYEPLGLEADMWIGVITYILLSGASPLFGDTKQETLANVSAVNYDFEEFFRNTSLAKDFIRRLLVKDPKKRMTIQDSLQHPWIKPKDTPQOAL 284
gi 62663156 ref XP_225138.3 |IAHFDLKPENIMLLDRNVKPKRIKIIDFLGAKHIDFGNEFKNIFGTFPEFVAPEIVNYEPLGLEADMWIGVITYILLSGASPLFGDTKQETLANVSAVNYDFEEFFRNTSLAKDFIRRLLVKDPKKRMTIQDSLQHPWIKPKDTPQOAL 284
gi 89363047 ref NP_004929.2 |IAHFDLKPENIMLLDRNVKPKRIKIIDFLGAKHIDFGNEFKNIFGTFPEFVAPEIVNYEPLGLEADMWIGVITYILLSGASPLFGDTKQETLANVSAVNYDFEEFFRNTSLAKDFIRRLLVKDPKKRMTIQDSLQHPWIKPKDTPQOAL 284
gi 114625378 ref XP_001140200.1 |IAHFDLKPENIMLLDRNVKPKRIKIIDFLGAKHIDFGNEFKNIFGTFPEFVAPEIVNYEPLGLEADMWIGVITYILLSGASPLFGDTKQETLANVSAVNYDFEEFFRNTSLAKDFIRRLLVKDPKKRMTIQDSLQHPWIKPKDTPQOAL 284
gi 73946538 ref XP_541259.2 |IAHFDLKPENIMLLDRNVKPKRIKIIDFLGAKHIDFGNEFKNIFGTFPEFVAPEIVNYEPLGLEADMWIGVITYILLSGASPLFGDTKQETLANVSAVNYDFEEFFRNTSLAKDFIRRLLVKDPKKRMTIQDSLQHPWIKPKDTPQOAL 284
gi 194669620 ref XP_613544.4 |IAHFDLKPENIMLLDRNVKPKRIKIIDFLGAKHIDFGNEFKNIFGTFPEFVAPEIVNYEPLGLEADMWIGVITYILLSGASPLFGDTKQETLANVSAVNYDFEEFFRNTSLAKDFIRRLLVKDPKKRMTIQDSLQHPWIKPKDTPQOAL 284
gi 118104165 ref XP_425037.2 |IAHFDLKPENIMLLDRNVKPKRIKIIDFLGAKHIDFGNEFKNIFGTFPEFVAPEIVNYEPLGLEADMWIGVITYILLSGASPLFGDTKQETLANVSAVNYDFEEFFRNTSLAKDFIRRLLVKDPKKRMTIQDSLQHPWIKPKDTPQOAL 284
gi 153792613 ref NP_001093460.1 |IASHFDLKPENIMLLDRNVKPKRIKIIDFLGAKHIDFGNEFKNIFGTFPEFVAPEIVNYEPLGLEADMWIGVITYILLSGASPLFGDTKQETLANVSAVNYDFEEFFRNTSLAKDFIRRLLVKDPKKRMTIQDSLQHPWIKPKDTPQOAL 284
gi 115533596 ref NP_490840.2 |IVHLDIKPENVMKQR--GDSQIKIIDFLGSLREIEPGAVVDMVGTPEFVAPEIVNYEPLGLEADMWIGVITYILLSGASPLFGDNRDTEFSNITIRVRIHFSDRYFKNSKHAQDFIYRFRVDRVDQRAIVVECLQHPWIRGPEGNALD 298
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi 114205408 ref NP_598823.1 |SRKASAVNMEKFKKFAARKKWKQSVRLISLCQRLSRSLFRSNMNSVARSDDTLDEEDSFVMKAIITHAINDDNVPGLOHLLGSLSSYDVNQPKNKGTPLLLIAAGCGNIQIOLLIKRGSRIDVODKGGSNAYWAARHGVDTLKFLNEN 434
gi 62663156 ref XP_225138.3 |SRKASAVNMEKFKKFAARKKWKQSVRLISLCQRLSRSLFRSNMNSVARSDDTLDEEDSFVMKAIITHAINDDNVPGLOHLLGSLSSYDVNQPKNKGTPLLLIAAGCGNIQIOLLIKRGSRIDVODKGGSNAYWAARHGVDTLKFLNEN 434
gi 89363047 ref NP_004929.2 |SRKASAVNMEKFKKFAARKKWKQSVRLISLCQRLSRSLFRSNMNSVARSDDTLDEEDSFVMKAIITHAINDDNVPGLOHLLGSLSSYDVNQPKNKGTPLLLIAAGCGNIQIOLLIKRGSRIDVODKGGSNAYWAARHGVDTLKFLNEN 434
gi 114625378 ref XP_001140200.1 |SRKASAVNMEKFKKFAARKKWKQSVRLISLCQRLSRSLFRSNMNSVARSDDTLDEEDSFVMKAIITHAINDDNVPGLOHLLGSLSSYDVNQPKNKGTPLLLIAAGCGNIQIOLLIKRGSRIDVODKGGSNAYWAARHGVDTLKFLNEN 434
gi 73946538 ref XP_541259.2 |SRKASAVNMEKFKKFAARKKWKQSVRLISLCQRLSRSLFRSNMNSVARSDDTLDEEDSFVMKAIITHAINDDNVPGLOHLLGSLSSYDVNQPKNKGTPLLLIAAGCGNIQIOLLIKRGSRIDVODKGGSNAYWAARHGVDTLKFLNEN 434
gi 194669620 ref XP_613544.4 |SRKASAVNMEKFKKFAARKKWKQSVRLISLCQRLSRSLFRSNMNSVARSDDTLDEEDSFVMKAIITHAINDDNVPGLOHLLGSLSSYDVNQPKNKGTPLLLIAAGCGNIQIOLLIKRGSRIDVODKGGSNAYWAARHGVDTLKFLNEN 434
gi 118104165 ref XP_425037.2 |SRKASAVNMEKFKKFAARKKWKQSVRLISLCQRLSRSLFRSNMNSVARSDDTLDEEDSFVMKAIITHAINDDNVPGLOHLLGSLSSYDVNQPKNKGTPLLLIAAGCGNIQIOLLIKRGSRIDVODKGGSNAYWAARHGVDTLKFLNEN 434
gi 153792613 ref NP_001093460.1 |SRKESAVNMEKFKKFAARKKWKQSVRLISLCQRLSRSLFRSNMNSVARSDDTLDEEDSFVMKAIITHAINDDNVPGLOHLLGSLSSYDVNQPKNKGTPLLLIAAGCGNIQIOLLIKRGSRIDVODKGGSNAYWAARHGVDTLKFLNEN 434
gi 115533596 ref NP_490840.2 |IRKASCTITISHISFKTRQWRKCVLEVMVLLKASKSRRIGDGRFDEEDMVASCTLI CAEENLRALHKLKSLALHKLKLPNAIRKSLKSFSEPNAGATAMHCAAKYGHAEVFNIFHMKGGNICARDNNGDTPLHVACRFAQHTVAGYVANE 448
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi 114205408 ref NP_598823.1 |KCPDVDKDSGETALHVAARYGHADVVOVLLCSFGSNPFDQKBEETPLHCAAWHGYSVAKALCEAGCNVNIKNREGETPLLLASARGYHDIVECLAEGADLNASDKDGHIALHLAVRRCQMEVIKLLGHGSGVDFODRHGNTPLHVA 584
gi 62663156 ref XP_225138.3 |KCPDVDKDSGETALHVAARYGHADVVOVLLCSFGSNPFDQKBEETPLHCAAWHGYSVAKALCEAGCNVNIKNREGETPLLLASARGYHDIVECLAEGADLNASDKDGHIALHLAVRRCQMEVIKLLGHGSGVDFODRHGNTPLHVA 584
gi 89363047 ref NP_004929.2 |KCPDVDKDSGEMALHVAARYGHADVVOVLLCSFGSNPFDQKBEETPLHCAAWHGYSVAKALCEAGCNVNIKNREGETPLLLASARGYHDIVECLAEGADLNACDKDGHIALHLAVRRCQMEVIKLLSGCCFVYQDRHGNTPLHVA 584
gi 114625378 ref XP_001140200.1 |KCPDVDKDSGETALHVAARYGHADVVOVLLCSFGSNPFDQKBEETPLHCAAWHGYSVAKALCEAGCNVNIKNREGETPLLLASARGYHDIVECLAEGADLNASDKDGHIALHLAVRRCQMEVIKLLSGCCFVYQDRHGNTPLHVA 584
gi 73946538 ref XP_541259.2 |KCPDVDKDSGETALHVAARYGHADVVOVLLCSFGSNPFDQKBEETPLHCAAWHGYSVAKALCEAGCNVNIKNREGETPLLLASARGYHDIVECLAEGADLNASDKDGHIALHLAVRRCQMEVIKLLSGCCFVYQDRHGNTPLHVA 584
gi 194669620 ref XP_613544.4 |KCPDVDKDSGETALHVAARYGHADVVOVLLCSFGSNPFDQKBEETPLHCAAWHGYSVAKALCEAGCNVNIKNREGETPLLLASARGYHDIVECLAEGADLNASDKDGHIALHLAVRRCQMEVIKLLSGCCFVYQDRHGNTPLHVA 584
gi 118104165 ref XP_425037.2 |KCPDVDKDSGETALHVAARYGHADVVOVLLCSFGSNPFDQKBEETPLHCAAWHGYSVAKALCEAGCNVNIKNREGETPLLLASARGYHDIVECLAEGADLNASDKDGHIALHLAVRRCQMEVIKLLSGCCFVYQDRHGNTPLHVA 584
gi 153792613 ref NP_001093460.1 |KCPLDIQKDSGETALHVAARYGNVDVVOVLLCSITHANPDLIDREGETPLHCAAWHGYSVAKALCEAGCNVNIKNREGETPLLLASARGYHDIVECLLEHCAADMDSADKDGHIALLHLAVRRCQVIVVVCLLHHCVVVDODRHGNTPLHVA 584
gi 115533596 ref NP_490840.2 |KIDVDVINKKGETALHCAVESADTRVVRLLQLRRLPLPASGDDVHLHAADSINPRVPLLVCLAPPLHLRIRREPLHVAARGHVDVQVALLDANSFIDAVEQDKTALITALENGVNDIASLILNGCDINHADHGGDTALHVA 598
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



gi 114205408 ref NP_598823.1 |CKDGSAPVVVALCEASCNLDSNKYGRTPHLLAANNGLDVVRYLCLMGANVEALTDGKTAEDLAKAEQHEHVAGLLARLRKDTHRGLFTQDLRPTQNLQPRIKLLKFGHSGSGKSTLVEVSLKCGLLRSFFRRRRLPSSSTNSRFPPE 734
gi 62663156 ref XP_225138.3 |CKDGSAPVVVALCEASCNLDSNKYGRTPHLLAANNGLDVVRYLCLMGANVEALTDGKTAEDLAKAEQHEHVAGLLARLRKDTHRGLFTQDLRPTQNLQPRIKLLKFGHSGSGKSTLVEVSLKCGLLRSFFRRRRLPSSSTNSRFPPE 734
gi 89363047 ref NP_004929.2 |CKDGNMPVVVALCEANCLDSNKYGRTPHLLAANNGLDVVRYLCLMGASVEALTDGKTAEDLARSEQHEHVAGLLARLRKDTHRGLFTQDLRPTQNLQPRIKLLKFGHSGSGKSTLVEVSLKCGLLRSFFRRRRLPSSSTNSRFPPE 734
gi 114625378 ref XP_001140200.1 |CKDGNMPVVVALCEANCLDSNKYGRTPHLLAANNGLDVVRYLCLMGASVEALTDGKTAEDLARSEQHEHVAGLLARLRKDTHRGLFTQDLRPTQNLQPRIKLLKFGHSGSGKSTLVEVSLKCGLLRSFFRRRRLPSSSTNSRFPPE 734
gi 73946538 ref XP_541259.2 |CKDGNMPVVVALCEANCLDSNKYGRTPHLLAANNGLDVVRYLCLAGANVEALTDGKTAEDLARSEQHEHVAGLLARLRKDTHRGLFTQDLRPTQNLQPRIKLLKFGHSGSGKSTLVEVSLKCGLLRSFFRRRRLPSSSTNSRFPPE 734
gi 194669620 ref XP_613544.4 |CKDGNMPVVVALCEANCLDSNKYGRTPHLLAANNGLDVVRYLCLAGANVEALTDGKTAEDLARSEQHEHVAGLLARLRKDTHRGLFTQDLRPTQNLQPRIKLLKFGHSGSGKSTLVEVSLKCGLLRSFFRRRRLPSSSTNSRFPPE 734
gi 118104165 ref XP_425037.2 |CKDGNMPVVVALCEANCLDSNKYGRTPHLLAANNGLDVVRYLCLAGANVEALTDGKTAEDLARSEQHEHVAGLLARLRKDTHRGLFTQDLRPTQNLQPRIKLLKFGHSGSGKSTLVEVSLKCGLLRSFFRRRRLPSSSTNSRFPPE 734
gi 153792613 ref NP_001093460.1 |CKDANMPVVVQLCAAKANLDPNFKGRTPHLLAASNGGLEVRRHLCSGANTAEIINDGKTAEDLATAEQHEHVAVLLAKLKDNDNQLDQDLRPTQLRQRLKLLKFGHSGGAGKSTLVEVSLKCGILRSFFRRRRLPSSSTNSRFPPE 732
gi 115533596 ref NP_490840.2 |SKHGLLQAVQLCHCAVTVDSVANKKALHLLAAHYGHVDIIRVLLLRADVTLRQDDGLLAEVLVAVAAERLEAHSLLKMKVQSQETREYISQLVPLDTSLRRLIKLLGHSGSGKTRLVQHLHS 729
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750



gi |114205408|ref |NP_598823.1| PLAAKPTVSVSINNLYPGCENVSVRSRSMFEPGLTKGMLVVFVAPSHHLCSTDDOSTKAIIDIONAYLNGVGFVWVFGNPNVVFCCYDYFAANDPTSIHIIIVFSLPEEYETIQLNOVIFWLSFLKSLVPEEPIAFGGKLNPLRVVL 884
gi |62663156|ref |XP_225138.3| PLATKPTVSVSINNLYPGCENVSVRSRSMFEPGLTKGMLVVFVAPSHHLCSTDDOSTKAIIDIONAYLNGVGFVWVFGNPNVVFCCYDYFAANDPTSIHIIIVFSLPEEYETIQLNOVIFWLSFLKSLVPEEPIAFGGKLNPLRVVL 884
gi |89363047|ref |NP_004929.2| PLASKPTVSVSINNLYPGCENVSVRSRSMFEPGLTKGMLVVFVAPTHHPHCSADDOSTKAIIDIONAYLNGVGFVWVFGNPNVVFCCYDYFAANDPTSIHVVFVSLPEEYETIQLNOVIFWLSFLKSLVPEEPIAFGGKLNPLRVVL 884
gi |114625378|ref |XP_001140200.1| PLASKPTVSVSINNLYPGCENVSVRSRSMFEPGLTKGMLVVFVAPTHHPHCSADDOSTKAIIDIONAYLNGVGFVWVFGNPNVVFCCYDYFAANDPTSIHVVFVSLPEEYETIQLNOVIFWLSFLKSLVPEEPIAFGGKLNPLRVVL 884
gi |73946538|ref |XP_541259.2| PLASKPAVSVSISNLYPGCEHVSVRSRSMFEPGLTRGTLGLVLPVAPPPLHCAADDOSTKAIIDIONAYLNGVGFVWVFGNPNVVFCCYDYFAANDPTSIHIIIVFSLPEEYETIQLNOVIFWLSFLKSLVPEEPIAFGGKLNPLRVVL 884
gi |194669620|ref |XP_613544.4| PLASKPAVSVSISNLYPGCENVSVRSRSMFEPGLTKGMLVVFVAPSHHPHCAADDOSTKAIIDIONAYLNGVGFVWVFGNPNVVFCCYDYFAANDPTSIHIIIVFSLPEEYETIQLNOVIFWLSFLKSLVPEEPIAFGGKLNPLRVVL 884

gi |118104165|ref |XP_425037.2| PVTSEKPAVSVSISNLYPGCENVSVRSRSMFEPGLTKGMLVVFVAPSHHPHCAADDOSTKAIIDIONAYLNGVGFVWVFGNPNVVFCCYDYFAANDPTSIHIIIVFSLPEEYETIQLNOVIFWLSFLKSLVPEEPIAFGGKLNPLRVVL 881
gi |153792613|ref |NP_001093460.1| FLESVTRRISDHYSPSSSMKDDGIHSTNGSFVSESNNSFFDLAAAAGSKYAPPHSYTRGIDVGTVNINGCEGFSVWVFGGYPMHTCYDFVFG-NADCTHLLILYRTSDPEVQKQILYWNMFLKGRVTFPEFICGCGFSRRSKVII 878
gi |115533596|ref |NP_490840.2|760.....770.....780.....790.....800.....810.....820.....830.....840.....850.....860.....870.....880.....890.....900



gi |114205408|ref |NP_598823.1| VATHADIMNIPRPAG-GEFYDKDTSLLKEIRNRFNDLHVSNKLFVLDAGASGSKDIKVLNRHLOEIRSOIVSGCSPMTHLCEKIIISTLPSWRKLNPNQMLSLQOFVYVDVODLNPLASEDDLRRIAOQLHSTGEINIMOSETVQ-DV 1032
gi |62663156|ref |XP_225138.3| VATHADIMNIPRPAG-GEFYDKDTSLLKEIRNRFNDLHVSNKLFVLDAGASGSKDIKVLNRHLOEIRSOIVSGCSPMTHLCEKIIISTLPSWRKLNPNQMLSLQOFVYVDVODLNPLASEDDLRRIAOQLHSTGEINIMOSETVQ-DV 1032
gi |89363047|ref |NP_004929.2| VATHADIMNIPRPAG-GEFYDKDTSLLKEIRNRFNDLHVSNKLFVLDAGASGSKDMKVLNRHLOEIRSOIVSGCSPMTHLCEKIIISTLPSWRKLNPNQMLSLQOFVYVDVODLNPLASEDDLRRIAOQLHSTGEINIMOSETVQ-DV 1032
gi |114625378|ref |XP_001140200.1| VATHADIMNIPRPAG-GEFYDKDTSLLKEIRNRFNDLHVSNKLFVLDAGASGSKDMKVLNRHLOEIRSOIVSGCSPMTHLCEKIIISTLPSWRKLNPNQMLSLQOFVYVDVODLNPLASEDDLRRIAOQLHSTGEINIMOSETVQ-DV 1032
gi |73946538|ref |XP_541259.2| VATHADIMNIPRPAG-GEFYDKDTSLLKEIRNRFNDLHVSNKLFVLDAGASGSKDMKVLNRHLOEIRSOIVSGCSPMTHLCEKIIISTLPSWRKLNPNQMLSLQOFVYVDVODLNPLAREGDLRRIAOQLHSTGEINIMOSETVQ-DV 1032
gi |194669620|ref |XP_613544.4| VATHADIVNLRPSAG-GEFYDKDTSLLKEIRNRFNDLHVSNKLFVLDAGASGSKDMKVLNRHLOEIRSOIVSGCSPMTHLCEKIIISTLPSWRKLNPNQMLSLQOFVYVDVODLNPLASEDDLRRIAOQLHSTGEINIMOSETVQ-DV 1032
gi |118104165|ref |XP_425037.2|910.....920.....930.....940.....950.....960.....970.....980.....990.....1000.....1010.....1020.....1030.....1040.....1050

gi |153792613|ref |NP_001093460.1| VATHADIVNLRPSAG-GEFSYDKERKLLKEVRNRFNDLHVSNKLFVLDAGASGSKDIKVLNRHLOEIRSOIVSGCSPMTHLCEKIIISTLPSWRKLNPNQMLSLQOFVYVDVODLNPLASEDDLRRIAOQLHSTGEINIMOSETVQ-DV 1029
gi |115533596|ref |NP_490840.2| VGIHATSFLPDMNQEGEYVSSDIEAMLNIVRLRFETHFMDHRLILLDDATNPSGIMKILKMLAKCRINILAKLLKPLAILDVTVNHLNLRKKNANFVPIIWPDFIQVLRNEINPLTGAHCRQIVQQLQILGELVLRNLDLADY 1028



gi |114205408|ref |NP_598823.1| LLLDPRWLCINVLGKLLSVETPRALHHYRGRYTMEDIQRLVPSDVEEELLOILDAMDICARDLSSGTMVDIPALIKTDSLQSWADEE---DEVMVYGGVRIVPEHLFPFCGIFHKVQVNLCRWIHQOOSAEGBDAD-IRLWVSGCIA 1177
gi |62663156|ref |XP_225138.3| LLLDPRWLCINVLGKLLSVETPRALHHYRGRYTMEDIQRLVPSDVEEELLOILDAMDICARDLSSGTMVDIPALIKTDSLQSWADEE---DEVMVYGGVRIVPEHLFPFCGIFHKVQVNLCRWIHQOOSAEGBDAD-IRLWVSGCIA 1177
gi |89363047|ref |NP_004929.2| LLLDPRWLCINVLGKLLSVETPRALHHYRGRYTMEDIQRLVPSDVEEELLOILDAMDICARDLSSGTMVDIPALIKTDSLQSWADEE---DEVMVYGGVRIVPEHLFPFCGIFHKVQVNLCRWIHQOOSAEGBDAD-IRLWVSGCKLA 1177
gi |114625378|ref |XP_001140200.1| LLLDPRWLCINVLGKLLSVETPRALHHYRGRYTMEDIQRLVPSDVEEELLOILDAMDICARDLSSGTMVDIPALIKTDSLQSWADEE---DEVMVYGGVRIVPEHLFPFCGIFHKVQVNLCRWIHQOOSAEGBDAD-IRLWVSGCKLA 1177
gi |73946538|ref |XP_541259.2| LLLDPRWLCINVLGKLLSVETPRALHHYRGRYTMEDIQRLVPSDVEEELLOILDAMDICARDLSSGTMVDIPALIKTDSLQSWADEE---DEGRVYGGVRIVPEHLFPFCGIFHKVQVNLCRWIHQOOSAEGBDAD-IRLWVSGCKIA 1177
gi |194669620|ref |XP_613544.4| LLLDPRWLCINVLGKLLSVETPRALHHYRGRYTMEDIQRLVPSDVEEELLOILDAMDICARDLSSGTMVDIPALIKTDSLQSWADEE---DEARVYGGVRIVPEHLFPFCGIFHKVQVNLCRWIHQOOSAEGBDAD-IRLWVSGCKIA 1177
gi |118104165|ref |XP_425037.2| VLLDPRWLCINVLGKLLSVENPKALHHYRGRYTMEDIQRLVPSDVEEELLOILDAMDICARDLSSGTMVDIPALIKTDSLQSWADEE---DEVLVYGGVRIVPEHLFPFCGIFHKVQVNLCRWIHQOOSAEGBDAD-IRLWVSGKIM 220
gi |153792613|ref |NP_001093460.1| VLLDPRWLCINVLGKLLSIFPKAIHHYRGRYRVEELQLHVSSEGDIDELLQVLDAMDVCARDLANPQMVDPALIRTKGGLQHTDEEDVEGEDALLNGVVRMVEHLAEPFCGLFHKLQVNLCRWISQKPEVEADDVWSSGGARIC 1179
gi |115533596|ref |NP_490840.2| VVLNAEWFQTHILGQLLSAEFLSKASPNGSYHTSLAKIFPEIQSDMLTILEVLQLCAPDARTG-AHEFPVFQTEAPDSTWRPYSLKEKERDLYVGGVRIPLMRGMERSLHSPFRIOVALRRSINDYQPAKDTQ-LHQWSECskLV 1176
.....1060.....1070.....1080.....1090.....1100.....1110.....1120.....1130.....1140.....1150.....1160.....1170.....1180.....1190.....1200



gi |114205408|ref |NP_598823.1| NRGAEILLVLLVNHGGGIEVQVRGLETEKIKCCLLLDSVCSITIEVMATLPGLLTVKHYLSPQOLREHHEPVMYQPRDFFRAQTLKESLNTMGGYKESFSSITCFGCHDVYSQASLGMDIHASDLNLLTRRKLRLDPPDPGKDW 1327
gi |62663156|ref |XP_225138.3| NRGAEILLVLLVNHGGGIEVQVRGLETEKIKCCLLLDSVCSITIEVMATLPGLLTVKHYLSPQOLREHHEPVMYQPRDFFRAQTLKESLNTMGGYKESFSSITCFGCHDVYSQASLGMDIHASDLNLLTRRKLRLDPPDPGKDW 1327
gi |89363047|ref |NP_004929.2| NRGAEILLVLLVNHGGGIEVQVRGLETEKIKCCLLLDSVCSITIEVMATLPGLLTVKHYLSPQOLREHHEPVMYQPRDFFRAQTLKESLNTMGGYKESFSSIMCFGCHDVYSQASLGMDIHASDLNLLTRRKLRLDPPDPGKDW 1327
gi |114625378|ref |XP_001140200.1| NRGAEILLVLLVNHGGGIEVQVRGLETEKIKCCLLLDSVCSITIEVMATLPGLLTVKHYLSPQOLREHHEPVMYQPRDFFRAQTLKESLNTMGGYKESFSSIMCFGCHDVYSQASLGMDIHASDLNLLTRRKLRLDPPDPGKDW 1327
gi |73946538|ref |XP_541259.2| NRGAEILLVLLVNHGGGIEVQVRGLETEKIKCCLLLDSVCSITIEVMATLPGLLTVKHYLSPQOLREHHEPVMYQPRDFFRAQTLKESLNTMGGYKESFSSIMCFGCHDVYSQASLGMDIHASDLNLLTRRKLRLDPPDPGKDW 1327
gi |194669620|ref |XP_613544.4| NRGAEILLVLLVNHGGGIEVQVRGLETEKIKCCLLLDSVCSITIEVMATLPGLLTVKHYLSPQOLREHHEPVMYQPRDFFRAQTLKESLNTMGGYKESFSSIMCFGCHDVYSQASLGMDIHASDLNLLTRRKLRLDPPDPGKDW 1327
gi |118104165|ref |XP_425037.2| NRGAEILLVLLVNHGGGIEVQVRGLETEKIKCCLLLDSVCSITIDNLIATLPGLLTVKHYLSPQOLREHHEPVMYQPRDFFRAQTLKESLNTMGGYKESFSSITCFGCHDVYSQASLGMDIHASDLNLLTRRKLRLDPPDPGKDW 370
gi |153792613|ref |NP_001093460.1| LGGVEALLVLLVNHGGGMEVLRGPDLPKRCVALLDLCGMAEGLLAATLPGLLTVKHYLSPQOLREHHEPVMYQPRDFFRAQTLKESLNTMGGYKESFSSIVALGCHIVYKQCNLGGEVAVAVSLLARRKLRLDPPDPGKDW 1329
gi |115533596|ref |NP_490840.2| SDRREAVIRMV--GDVAEIRARRGPSESA-SMFFYFMDLNLNVEHAAAEVGGPSLSLRHFISPKHLKEHREHPALFPPESEMMEQRESLVKQD-EEELFQDVVCFGSRDVARHLTGDVQVADLQMASRCCELACLDDPPHAMGRDW 1323
.....1210.....1220.....1230.....1240.....1250.....1260.....1270.....1280.....1290.....1300.....1310.....1320.....1330.....1340.....1350



gi |114205408|ref |NP_598823.1| CLLAMNGLPDMVAKHN--VNRASRD--FLPSPVHALLOEWTSY--ESTVGIILSKLRELGRDAADFLKASSVFKINLDGNGQ--EAYASSCNSG-TSYNSISSVSR 1430
gi |62663156|ref |XP_225138.3| CLLAMNGLPDMVAKHN--VNRASRD--FLPSPVHALLOEWTSY--ESTVGIILSKLRELGRDAADFLKASSVFKINLDGNGQ--EAYASSCNSG-TSYNSISSVSRDASHAWPLDYD 1442
gi |89363047|ref |NP_004929.2| CLLAMNGLPDLVAKYN--TNNGAPKD--FLPSPVHALLEWTTYP--ESTVGTILMSKRELGRDAADFLKASSVFKINLDGNGQ--EAYASSCNSG-TSYNSISSVSR 1430
gi |114625378|ref |XP_001140200.1| CLLAMNGLPDLVAKYN--TNNGAPKD--FLPSPVHALLEWTTYP--ESTVGTILMSKRELGRDAADFLKASSVFKINLDGNGQ--EAYASSCNSG-TSYNSISSVSR 1430
gi |73946538|ref |XP_541259.2| CLLAMNGLPDLVAKYN--TNNGAPKE--FLPSPVHALLEWTTYP--ESTVGTILMSKRELGRDAADFLKASSVFKINLDGNGQ--ETVSSCNSG-TSYNSISSVSR 1430
gi |194669620|ref |XP_613544.4| CLLAMNGLPDLVAKYN--TNNGAPKE--FLPSPVHALLEWTTYP--ESTVGTILMSKRELGRDAADFLKASSVFKINLDGNGQ--EAYASSCNSG-TSYNSISSVSR 1430
gi |118104165|ref |XP_425037.2| CLLAMNGLPDLVAKYN--TNNGTQND--FLSPPVHALLEWTTYP--ESTVGTILMSKRELGRDAADFLKASSVFKINLDGNGQ--EAYASSCNSG-TSYNSISSVSR 473
gi |153792613|ref |NP_001093460.1| CLLAMNGLSELAAKYSINGITFPADPLSPLSPVHALLEWTTYP--DSTIGVLAKLRELGRDAADFLRAAPVFRVNLLEITGPEPSPFCVCGGTSYNSISSVSR 1439
gi |115533596|ref |NP_490840.2| SILAVKQLTQVDPV--STGSS--LSRDQLLNWATHHPQASVGNLCRILVLRGCDARDALYRTPVLYVAPLEDQFLLETNDSGVVSGHSSEHNFINI 1425
.....1360.....1370.....1380.....1390.....1400.....1410.....1420.....1430.....1440.....1450.....1460.....1470.....

