

gi |157419154|ref|NP\_002996.2| MANCQIAI-----LYQRFQRVVFG--ISLLLCFSAIISLITNC 36  
gi |114565270|ref|XP\_001137240.1| MANCQKAI-----LYQRFQRVVFG--ISLLLCFSAIISLITNC 36  
gi |73961386|ref|XP\_537202.2| MASCLKAI-----RNRFRQVIFFT--SAKLLCFSVLIFELIK 36  
gi |6755456|ref|NP\_035477.1| MAGCPKGS-----WTPRLRSVILG--GAOLIWFSAIISLITNC 36  
gi |6981524|ref|NP\_037246.1| MAGCPKGS-----WTPRLRSVILG--GAOLIWFSAIISLITNC 36  
gi |118094064|ref|XP\_422207.2| MSPCPGGCRRCPGRCLRYRQRLQGTGCVRVHLILFRPLSVAADMGTPVGGHCARRMVALSSCGVCCGLGIAAFICGVV 79  
gi |189533210|ref|XP\_001336824.2| MVHNEVFNALKEKLPKLSAPYYWIGMKKINDTMMWVANGAADYINWAEIENPNNRLSEENCVEMVYIISLSKSGNWNDDSCENPKYFVCHKVVSCPHLSITFKGWMECSGLYGNYSLDLSDKCFSCAAGYKIKGIAELNCSGAWNAPL 150



gi |157419154|ref|NP\_002996.2| --KEVAAWTYHYSIK-AYSWNIERKVCQNYRDLVAIQNKNEIDYLNKVLPPYSSYYWIGIRKNNKTTWVGTKKALINEAEWADNEPNNKRNEDCVEIYIKSPAPGKWNDEHCLKKKHALCYTASCODMCSKJGECLEIIGNYTC 183  
gi |114565270|ref|XP\_001137240.1| --KEVAAWTYHYSIK-AYSWNIERKVCQNYRDLVAIQNKNEIDYLNKVLPPYSSYYWIGIRKNNKTTWVGTKKALINEAEWADNEPNNKRNEDCVEIYIKSPAPGKWNDEHCLKKKHALCYTASCODTDCSKJGECLEIIGNYTC 183  
gi |73961386|ref|XP\_537202.2| --KEVAGWTYNYSTK-AYSWNYSRIFCQHYDLVAIQNKKEIAYLNDVIPYNSYYWIGIRKINDKWTWVGTKKLLEAEWADNEPNNKRNEDCVEIYIKSLAPGKWNDEPCWKRKRALCYTASCODMCSKJGECIEIIGNYTC 183  
gi |6755456|ref|NP\_035477.1| --KEVAAWTYNYSTK-AYSWNNRVRFCRRHFDDLVAIQNKNEIAHLNDVIPFNYSYYWIGIRKINKNTWVGTNKTLTEAEWADNEPNNKRNEDCVEIYIKSNAPGKWNDEPCFKRRKRALCYTASCODMCSNQGECIEIIGSYTC 183  
gi |6981524|ref|NP\_037246.1| --KKVATWYNYSTK-AYSWNNRVRFCRRHFDDLVAIQNKNEIAHLNDVIPYNSYYWIGIRKINKNTWVGTNKTLTEAEWADNEPNNKRNEDCVEIYIKSNAPGKWNDEPCFKRRKRALCYTASCODMCSNQGSRIEIIGSYTC 183  
gi |118094064|ref|XP\_422207.2| --MVGAWTYNYSEK-DYEWDEARAYCKTFFDDLVAIQNKQIEIYLRITLPYHNKYYWIGIRKQKGTWVGTNKTLTKBATWAAAREPNNRSGNDCVEIYIKRPSAAGKWNDEPCTKKKALCYKASCQPLLGLHGDCVVIQSVK 226  
gi |189533210|ref|XP\_001336824.2| PSCAVNAWYHYNIIDSKLDWTAARQWCTHFDLVAIQNKAEIAYLNEILPFHRAYYWIGIRKIDGHWTWVGTKKRLTVEAAWATNEPNNQGTGEDCVEIYIKRNKDTAKWNDERCSKKKATVCYLASCIEIISCSSEHARCVIEIGNYTC 300



gi |157419154|ref|NP\_002996.2| SCYPGFYGP-----ECEYVREGGELELPOHVLNCSHPLGNFNSQCSFHCTDGYOVNGPSSKLECLASGIWTKPPOCLAAQCPPLKIPERGNM 273  
gi |114565270|ref|XP\_001137240.1| SCYPGFYGP-----ECEYAREGGELELPOHVLNCSHPLGNFNSQCSFHCTDGYOVNGPSSKLECLASGIWTKPPOCLAAQCPPLKIPERGNM 273  
gi |73961386|ref|XP\_537202.2| SCYFGFYGS-----ECEYAREGGELELPOHVLNCSHPLGNFNSQCSFHCTDGYOVNGPSSKLECLASGIWTKPPOCLAAQCPPLKIPERGNM 273  
gi |6755456|ref|NP\_035477.1| SCYFGFYGP-----ECEYVKECGKVINIPHVLNCSHPLGDFEFSQCFSCAEGVELDGGEGELQCLASGIWTKNPPKDAVQCSLEAPFHGM 273  
gi |6981524|ref|NP\_037246.1| SCYFGFYGP-----ECEYVQECGKFDIPHVLNCSHPLGDFEFSQCFSCAEGVELDGGEGELQCLASGIWTKNPPKDAVQCSLEAPFHGM 273  
gi |118094064|ref|XP\_422207.2| ECHPGFEGD-----NCENAVTTPVLSAPBEHGLNCSHLGNFNFNSCDFSCQPGFELTGPQSRRECIAGVGNWTEIPCKAIKSCPVLSAPBEHGL 316  
gi |189533210|ref|XP\_001336824.2| QCDAGFMGPRFVQCQPVENPQGLVCKDGAFFGNFNSSCQFOCATGFNLVGAERHCLTGHWNITLIPVQAVKQAIIDAPRGWITMCTHPLSMNFSNSCEFECKEGFELNGSKTWCWDTGHWDKAPTCTVTVTCNPLLAPANSFL 450



gi |157419154|ref|NP\_002996.2| TCLHSAKAFQHQSSCSFSCCEGFALVGPVVOCTASGVWTAAPVCKAVQCOHLEAPSEGTMDCVHPLTAFAYGSSCKFECPQGYRVRGLDMLRCDISGHWSAPLPTCEAISCEPLESP-VHGSMDCSPLRAFQYDINCSFRCAEGFML 422  
gi |114565270|ref|XP\_001137240.1| TCLHSAKAFQHQSSCSFSCCEGFALVGPVVOCTASGVWTAAPVCKAVQCOHLEAPSEGTMDCVHPLTAFAYGSSCKFECPQGYRVRGLDMLRCDISGHWSAPLPTCEAISCEPLESP-VHGSMDCSPLRAFQYDINCSFRCAEGFML 422  
gi |73961386|ref|XP\_537202.2| NCLHSVEAFQHQSSCHFSCEEGFALVGPVVOCTASGMWTAAPVCEAVAGC-----PLKSP-VHGSMDCSPLRAFQYNTSFRCAEGFML 360  
gi |6755456|ref|NP\_035477.1| ACMHPIAAAFADSSCKFECPQGYRVRGSLDLCSTGSGWSEPLPTCEAIACE-----PPHPI-IRGSMDCVPSSTGTFGYNSSCFELCAEGFML 360  
gi |6981524|ref|NP\_037246.1| DCTHPLAAAFADSSCKFECPQGYRMRGSDILHCTDSGWSSEPLPTCEAIACE-----PLESP-LRGSMDCSPLRAFQYNTSFRCAEGFML 360  
gi |118094064|ref|XP\_422207.2| NCSHLHGSFTFNSTCDFSCQPGFELVGSISRECTATGNWTDGDSRCKAVTCTP-----VLSAP-EHGLNCSHLHGNFTFNSTCDFSCQPGFEL 403  
gi |189533210|ref|XP\_001336824.2| ACADPLGKSSFRSACNVVDEGYSKLRGAAALCQREGNWSAPLVEVVCDSLKPPIANGSYQCHDSVDFSVGSTCFWFKCDSGFVHNGTNSHCTKQGNWSHISPICHAVOCPPPLSDTFKIGSVYCVHPLSTNSYNSCEFFCEGLVL 600



gi |157419154|ref|NP\_002996.2| RGADIVRCNDNLGOWTAPAPVCOALQCODLPVNEARVNCSPHFGAFRYQSVCSFTCNEGLLLVGSASVLOCLATGNWNSVPPCOAIPCTPLLSPONGTMTVOPLGSSSYKSTCFICDEGYLSLSPERLDCITRSGRWTDSPPMCKAIC 572  
gi |114565270|ref|XP\_001137240.1| RGADIVRCNDNLGOWTAPAPVCOALQCODLPVNEARVNCSPHFGAFRYQSVCSFTCNEGLLLVGSASVLOCLATGNWNSVPPCOAIPCTPLLSPONGTMTVOPLGSSSYKSTCFICDEGYLSLSPERLDCITRSGRWTDSPPMCKAIC 572  
gi |73961386|ref|XP\_537202.2| EGADLVQCTDLGOWTAPAPACQALQCODLLAPNKAQVNCSPHFGAFRYQSVCSFTCDEGLLLVGSASVLOCLATGNWNSAPPPECOAMSCPTPLLSPHNGTMTVOPLGSSSYRSTCRFTCNEGFSLSPERLDCITRSGHWTDSPPMCKAIC 510  
gi |6755456|ref|NP\_035477.1| KGNDAIQCADSGOWTAPAPVCEALQCEPFPVPSKAQVNCSDPFGTLTYQSVCSFSDGESSLLVGSASVIRCLATGHWNAPPECOAVSCAPMLSPENGSMTCVOPLGNSYKSTCFQPMDCDEGYLSLSPERLDCITRSGHWTDSPPMCKAIC 510  
gi |6981524|ref|NP\_037246.1| MGNDAIHCADLGOWTAPAPVCEALQCEPFPVPSKAQVNCSDPFGTLTYQSVCSFSDGESSLLVGSASVIRCLATGHWSAPPECOAVSCPTPLLSPENGSMTCVOPLGNSYKSTCFQPMDCDEGYLSLSPERLDCITRSGHWTDSPPMCKAIC 510  
gi |118094064|ref|XP\_422207.2| AGPQSRCTAMGNWTDGTTQCKAISGSLVRAPEHGLNCSHLGNFTFNSTCDFSCQPGFELGPE-----QSP-----VTCVLSAPKHGELNCSHLHGNFTFNSTCDFSCQPGFELGPE-----SFTV 519  
gi |189533210|ref|XP\_001336824.2| RGTDSHGHDFHCHWNTAFICTAVACDPLVTPVNSNLTCANPLGKFSFRISCEVIQEVYKLRGDTLNLCSNGNWAAPTACKVIRCALESVHHGSHVCHDLLEEFYSQSEWLEAGFLNGTNSYTCISQKWKQELSVCAQCC 750



