

gi | 24663889 | ref | NP\_648660.1 | -----MNRFAIVEARELSPNESFVSRDNRVKIYDGDQR-IDFEDGEVVLVTHRLFWGRP----- 52  
gi | 158297929 | ref | XP\_554602.2 | -----MNRFEYCQARLFENESFVAKDRNKIYDGDQR-INYEDGEVVLVTHRLWGRN----- 52  
gi | 30794416 | ref | NP\_081614.1 | -----MDRFVWTSGLLEINTELVIQQRGVRYDGEER-IKFDAGTLLLSHTRLIWR----- 50  
gi | 34879118 | ref | XP\_214382.2 | -----MDRFVWTSGLLEINTELVIQQRGVRYDGEER-IKFDAGTLLLSHTRLIWR----- 50  
gi | 71051598 | ref | NP\_057159.2 | -----MDRFVWTSGLLEINTELVIQQRGVRYDGEER-IKFDAGTLLLSHTRLIWR----- 50  
gi | 114649836 | ref | XP\_509796.2 | -----MDRFVWTSGLLEINTELVIQQRGVRYDGEER-IKFDAGTLLLSHTRLIWR----- 50  
gi | 73993160 | ref | XP\_534484.2 | -----MDRFVWTSGLLEINTELVIQQRGVRYDGEER-IKFDAGTLLLSHTRLIWR----- 50  
gi | 149642887 | ref | NP\_001092409.1 | -----MDRFVWTSGLLEINTELVIQQRGVRYDGEER-IKFDAGTLLLSHTRLIWR----- 50  
gi | 50730915 | ref | XP\_417077.1 | -----MDRFVWTSGLLEINTELVIQQRGVRYDGEER-IKFDAGTLLLSHTRLIWR----- 50  
gi | 41053913 | ref | NP\_956271.1 | -----MDRFVWTSGLLEINTELVIQQRGVRYDGEER-IKFDAGTLLLSHTRLIWR----- 50  
gi | 71990236 | ref | NP\_505798.2 | -----MNRFSWYTPGES-TEELLCAQAGVGIYEGDLRQNFQGTASLQMORIIWA----- 50  
gi | 15238374 | ref | NP\_196112.1 | MASGSSSIAIGGLFENAEVTTSGRPVLRNVEVECFLLSSIDIDEDDPPRFALRSGNLLILTHRLIWIH----- 70  
gi | 115440641 | ref | NP\_001044600.1 | -----MSAAAADWLPAADVTAAGRFLVAGEVERHLVAGDVEPEESP-RLGPLRARLLVLTSHRLIHLF----- 64  
gi | 145613365 | ref | XP\_363778.2 | -----MFLKNLDTLTALRPSVLPDEDLFVDMVGLYEGKYKLPNQNGQVYLLSHRICHVDKTEPRKYSAALDLKDIERYEYFAGFLKSFKPKITLVPKANKRASLPSPRNGNAIPAQRVDSFPFRAPPVDLPPASSAWATI 137  
gi | 164425008 | ref | XP\_962337.2 | -----MEYWHYVETSSGQPLLRREGKDIIFDQSVGLYHGKSKILQRQRGRIFLTSQRRIINIDDAKPTQNSLGLLEDDLAYVNYSSGFLTRSPRLLILFKD-PSKDELGKSAETASAD-----VVFTWVCPICMVSNEI 129  
gi | 6323449 | ref | NP\_013521.1 | -----MGSIVNYLSYQYAEATASGHPIRLREGERDIYVQDVGLYHGKIKILNKQKRCRYLTSQRRIIVDDLFAKESVSIELDDVEKARINAKFLKRAKTVLFLK--PNSKHSLGGKASRQNVDKFKFRIVEKSGWTCAICMAHNEI 143  
gi | 45190698 | ref | NP\_984952.1 | -----MSAGFIYWHVPIEIASGGQPIRLNERDIYVQSVGLYHGKIKILNKQKRCRYLTSQRRIIVDDLFAKESVSIELDDVEKARINAKFLKRAKTVLFLK--ELSQNEAPITEEKQKQVH-----TQWNCPICGVENRI 131  
gi | 50303407 | ref | XP\_451645.1 | -----MAFYLETTPSNLPVLDPEEILLVDDQVGLYFGDEKSPFRHNGTLYLKKHIFVDSVDPKKNLSLKIKISDTRDVOHTSRVFRSPKIRLSLR----- 93  
gi | 19113459 | ref | NP\_596667.1 | 1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi | 24663889 | ref | NP\_648660.1 | -----GEIARAAVTLCLPLSYVISVSEETIASN-----FFGKRTRIIMHLYPP-----SDKGGPGL-----DTSRAITHIKLSGKNGLSVFHSALRETLNAR 135  
gi | 158297929 | ref | XP\_554602.2 | -----GEIARAGSCLALKLYVLSVDEEASSM-----LFGKRRKIILRLGSL-----ASDKMPGPM-----DHCSTFVVLKSGRNGVEVAFVQALHSTLSAR 135  
gi | 30794416 | ref | NP\_081614.1 | -----DKNNECCMAIPLSQIVFIEEQAAG-----IGKSAKIVVHLHPA-----PSNKEPGPF-----QSSKNSYIKLSFKEHGOIEFVRRLSEEMTOR 129  
gi | 34879118 | ref | XP\_214382.2 | -----DKNNECCMAIPLSQIVFIEEQAAG-----IGKSAKIVVHLHPA-----PPNKEPGPF-----QSSKNSYIKLSFKEHGOIEFVRRLSEEMTOR 129  
gi | 71051598 | ref | NP\_057159.2 | -----DKNNECCMAIPLSQIVFIEEQAAG-----IGKSAKIVVHLHPA-----PPNKEPGPF-----QSSKNSYIKLSFKEHGOIEFVRRLSEEMTOR 129  
gi | 114649836 | ref | XP\_509796.2 | -----DKNNECCMAIPLSQIVFIEEQAAG-----IGKSAKIVVHLHPA-----PPNKEPGPF-----QSSKNSYIKLSFKEHGOIEFVRRLSEEMTOR 129  
gi | 73993160 | ref | XP\_534484.2 | -----DKNNECCMAIPLSQIVFIEEQAAG-----IGKSAKIVVHLHPA-----PSNKEPGPF-----QSSKNSYIKLSFKEHGOIEFVRRLSEEMTOR 129  
gi | 149642887 | ref | NP\_001092409.1 | -----DKNNECCMAIPLSQIVFIEEQAAG-----IGKSAKIVVHLHPA-----ASNKEPGPF-----QSSKNSYIKLSFKEHGOIEFVRRLSEEMTOR 129  
gi | 50730915 | ref | XP\_417077.1 | -----DKNNECCIAIPLSQVVFIEEQAAG-----IGKSAKIVVHLHPA-----SPNKEPGPF-----QSSKNSYIKLSFKEHGOIEFVRRLSEEMTOR 129  
gi | 41053913 | ref | NP\_956271.1 | -----DKNNECCICIPLSQIVFIEEQAAG-----IGKSAKIVVHLHPA-----PSNKEPGPF-----QSSKNSYIKLSFKEHGOIEFVRRLSEEMTOR 129  
gi | 71990236 | ref | NP\_505798.2 | -----SSDPPRRLLVHLSVISMKEKHKS-----MFSKGGKIVVLEKPP-----KAGN-IGPV-----NSHYELRLVFRHGGEDDFPKVEDAVRRK 129  
gi | 15238374 | ref | NP\_196112.1 | -----SSNESVSSIPLSAVTHIYS-HKKS-----IKSMFHS-----PRIRFQAD-----PGSIVTVIFVRKGFDFGLSKLWECWRGR 140  
gi | 115440641 | ref | NP\_001044600.1 | -----EFSRS--ARALPLAAVVHAYPPHRKHG-----NPLRSIFSSSSSSS-----HHPVRVLQISL-----PPSRSEVVAVVSKGQADVFYGRLLAVRAR 148  
gi | 145613365 | ref | XP\_363778.2 | -----SNATSROPGGGPAIYPLPDRSKQGSSESAPATQASPFPFQADAS--ASFQCPRCTFLNPPSLMSCEMCGGPLISNDLPAELMQRRRETSPGPVLSLAP-----KSEALEVVKISFRGGGKIFVRLKGSMTOR 268  
gi | 164425008 | ref | XP\_962337.2 | -----QGEFKDPLPPIGICNGPADYELTKSSINCSNAIDPNANPNQNFVNSENICPACTFANHPQIGNCEIGHRLPNASKVSKLNLNLFHDSRVHIELEKNSLARNKSSHSALSSSSSTGSETEFVLSFRKSDGVLFQALTERALENI 279  
gi | 6323449 | ref | NP\_013521.1 | -----NMETIQGYMPP--CVNCGIIVDFEMTSKSLTIVYADDAATAAKN-----KCPACTFDNHVMHNNCEMCGTRLPNMCPTALTRNQLGGDPRVHIELEGN-----PGFTSRDIPFVLSFRSDGSLFFPALCKLOEDW 268  
gi | 45190698 | ref | NP\_984952.1 | -----YSTLDSNGLNPPCGSCGVVDRDMVQNSIKVVDLEDETPEKN-----ICPVCTFINHPQIRNCEICGARLQKSRRTSKVK-----DSRVIRLLEK-----PSGEESSFAQLSPFRKTDGALFVETLVKLOEI 251  
gi | 50303407 | ref | XP\_451645.1 | -----HVEKMWACKICTFIVGDPINPCRCNGVANRFITIKPKSDARFSQGLCACTFQNYPLDN-----TCIEICGNQLK-----NVDNRQLIQLSFRGSSGSKFVEAKSSEIDEI 194  
gi | 19113459 | ref | NP\_596667.1 | .....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi | 24663889 | ref | NP\_648660.1 | -----VWEILLSEIILNGVASSPTLEPAND-----LARIQKRIGIGGIERHLEAKAKADENIALAFODLSVLMAMAKDMVGVSKTSSKIRKQ-----KGEIIDEIVR-----FKSYLLSLG-----IDDPVTRDNFT-SNAYVSSLAR 264  
gi | 158297929 | ref | XP\_554602.2 | -----IWIIVSDDGEQAQSQSDASAAAGPSAD-----ASRQLRIGIVGIERNLAEKQKQTDANINMAFKDLGRMLAMAKDMVAIINVVSAKIRER-----GGEISEDETVR-----FKSYLLSLG-----IDDPVTRDGTNR-SNAYVFLKLSRQ 263  
gi | 30794416 | ref | NP\_081614.1 | -----RWETVPVSSISLQTNK-----GPQPG-----RVRVAVGIERLLEKRRKEDKNISEAFEDLSKLMIKAKEMVELSKSIANKIKK-----QGDVTEDETIR-----FKSYLLSMG-----IANPVTRITYG-SGQYHMLAKQ 248  
gi | 34879118 | ref | XP\_214382.2 | -----RWETVPVSSISLQTKK-----GPQPG-----RIRAVGVIGIERLLEKRRKEDKNISEAFEDLSKLMIKAKEMVELSKSIANKIKK-----QGDVTEDETIR-----FKSYLLSMG-----IANPVTRITYG-SGQYHMLAKQ 248  
gi | 71051598 | ref | NP\_057159.2 | -----RWENMPVSSISLQNNR-----GPQPG-----RIRAVGVIGIERLLEKRRKEDKNISEAFEDLSKLMIKAKEMVELSKSIANKIKK-----QGDVTEDETIR-----FKSYLLSMG-----IANPVTRITYG-SGQYHMLAKQ 248  
gi | 114649836 | ref | XP\_509796.2 | -----RWENMPVSSISLQNNR-----GPQPG-----RIRAVGVIGIERLLEKRRKEDKNISEAFEDLSKLMIKAKEMVELSKSIANKIKK-----QGDVTEDETIR-----FKSYLLSMG-----IANPVTRITYG-SGQYHMLAKQ 248  
gi | 73993160 | ref | XP\_534484.2 | -----RWENMPVSSISLQNNR-----GPQPG-----RIRAVGVIGIERLLEKRRKEDKNISEAFEDLSKLMIKAKEMVELSKSIANKIKK-----QGDVTEDETIR-----FKSYLLSMG-----IANPVTRITYG-SGQYHMLAKQ 248  
gi | 149642887 | ref | NP\_001092409.1 | -----RWENMPVSSISLQNNR-----GPQPG-----RIRAVGVIGIERLLEKRRKEDKNISEAFEDLSKLMIKAKEMVELSKSIANKIKK-----QGDVTEDETIR-----FKSYLLSMG-----IANPVTRITYG-SGQYHMLAKQ 248  
gi | 50730915 | ref | XP\_417077.1 | -----RWENMPAGOTTQVNN-----DPAQ-----RIRAVGVIGIERLLEKRRKEDKNISEAFEDLSKLMIKAKEMVELSKSIANKIKK-----QGDVTEDETIR-----FKSYLLSMG-----IANPVTRITYG-SGQYHMLAKQ 248  
gi | 41053913 | ref | NP\_956271.1 | -----RWENTPVSSIPITGT-----GPKAG-----RIRAVGVIGIERLLEKRRKEDKNISEAFEDLSKLMIKAKEMVELSKSIANKIKK-----QGDVTEDETIR-----FKSYLLSMG-----IANPVTRITYG-SGQYHMLAKQ 248  
gi | 71990236 | ref | NP\_505798.2 | -----TWNTSSSSGSSSSGSR-----ASN-----LSVGIISIERLLEKRRKEDKNISEAFEDLSKLMIKAKEMVELSKSIANKIKK-----QGDVTEDETIR-----FKSYLLSMG-----IANPVTRITYG-SGQYHMLAKQ 247  
gi | 15238374 | ref | NP\_196112.1 | -----AWEEEEKSSEETKSGSGTVAQGLYND-----GTVRM--VGLAGILRKEQWESDKSLQDAFDLINALMSKAKEMVSLAEKMRQKLLSAPSSNGSDDDEEMGSKEMQWMLSVG-----IISPVTKEBAG--ALYHOELSR 273  
gi | 115440641 | ref | NP\_001044600.1 | -----AWEVVAVAAPAG-GSSAAQGAPEED-----LAIRMPVVGVSGLIRMEAWESAGQNIQDAFDLINALMSKAKEMMELAEKMRQKLLTNSASNSND-EEEMGSKQMDQWLLSVG-----IYSPVTKEBAG--ALYHOELSR 281  
gi | 145613365 | ref | XP\_363778.2 | -----KWLLQDAPPIPRP-----LGGGTADPEGSSGRGTPN-----ERVKTAGTAGLEKRGIDLKRNNEILVGSFEDLEALMASAKDIVALAEFARQAN-SGGASS-EANAILAES-----ATQLGLVT-----TKDVTG-GSSS--EFLYISELARN 135  
gi | 164425008 | ref | XP\_962337.2 | -----KWLLQDAPPIPKSSNGLVGSGGGAGGGVGSAAQOPERVKTAGTAGLEKRGQSMRKNNEIVIGNAFEDLEALMASAKDIVALAEFARVAGGAGSSGSSEALLAES-----ASQLGLIA-----TKDIVSGGGG--DELVLSELART 409  
gi | 6323449 | ref | NP\_013521.1 | -----LLEKNKHFQNVQVSVNGVDMRKGASSH-EYNNVEVPIETKLSRIGISSLEKSRNQNNLNDILFNALTLNKLMSLATSIERLYKNINIMTKTKLNLQDESIVNEPKTR-----RPLLLIDREKFLN-----KELFLDEIARE 414  
gi | 45190698 | ref | NP\_984952.1 | -----ESDQKKHMFNQDLTKVNGVLET-----PIFEQDTRFSLGIASLEKSRBQQLKNNLILNKALTDLGNLAALASDIEKLYHDG-----E--APSNT-----NPLVLDREKFLS-----KFAFIDEIARE 378  
gi | 50303407 | ref | XP\_451645.1 | -----SRKESKHLFNQNLVSVNGVPTDF-----VIDDLVLSNDINLIGITALEKNEQQLKNNVMSNALSDLNLMALASDIEKMYQGN-----RKSKSN-----ESILLVDRKFLN-----KNVFLDEIARE 364  
gi | 19113459 | ref | NP\_596667.1 | -----EKQRYSNKYDKVLR-----KAILKES-----LRMGGIHDLECSHEMQLAKNRTLVHAFQDLDAFFSLAKDMSLADQFAEKMDGLTGTQSDKQVQLLNK-----SNQLGVLR-----GNHLDNVFVSANSRLVDIELCKS 317  
gi | .....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



