

gi|32455244|ref|NP_859050.1| MAGASELCTGPGAAGGDDSLYPIAVLIDELRNEDVQLRLNSIKKLSITIALALGVERTRELLPFLDITYDEDEVLLALAEOLGNFTGLVGGPDFAHCLLPPLLENLAIVETVVRDKAVESLRQISQEHPTVALEAHFVPLVKRLASG 150
gi|114640311|ref|XP_522178.2| -MTFTSLFEGKG-----LPVHEHLQPLSGWQ--SKLLRAFVYVFLSDYTVVYNYTILKP-----RKAKQIRKKSQVTTAWRPPKCLLPLENLAIVETVVRDKAVESLRQISQEHPTVALEAHFVPLVKRLASG 124
gi|73954805|ref|XP_850884.1| MAGAAGPCTGPGAAGGDDSLYPIAVLIDELRNEDVQLRLNSIKKLSITIALALGVERTRELLPFLDITYDEDEVLLALAEOLGNFTGLVGGPDFAHCLLPPLLENLAIVETVVRDKAVESLRQISQEHPTVALEAHFVPLVKRLASG 150
gi|194673192|ref|XP_001788645.1| MAGAAGPATGSGAAGGDDSLYPIAVLIDELRNEDVQLRLNSIKKLSITIALALGVERTRELLPFLDITYDEDEVLLALAEOLGNFTGLVGGPDFAHCLLPPLLENLAIVETVVRDKAVESLRQISQEHPTVALEAHFVPLVKRLASG 150
gi|77539770|ref|NP_001029257.1| MAGAAGPGSGPGAAGGDDSLYPIAVLIDELRNEDVQLRLNSIKKLSITIALALGVERTRELLPFLDITYDEDEVLLALAEOLGNFTGLVGGPDFAHCLLPPLLENLAIVETVVRDKAVESLRQISQEHPTVALEAHFVPLVKRLASG 150
gi|70794752|ref|NP_001020589.1| MAGAAGPCTVPGAAGGDDSLYPIAVLIDELRNEDVQLRLNSIKKLSITIALALGVERTRELLPFLDITYDEDEVLLALAEOLGNFTGLVGGPDFAHCLLPPLLENLAIVETVVRDKAVESLRQISQEHPTVALEAHFVPLVKRLASG 150
gi|53933248|ref|NP_001005590.1| MAGAEG-----DLSYPIAVLIDELRNEDVQLRLNSIKKLSITIALALGVERTRELLPFLDITYDEDEVLLALAEOLGSGFVLVGGPEFVHCLLPPLLENLAIVETVVRDKAVESLRQISQEHPTVALEAHFVPLVKRLASG 138
gi|118105147|ref|XP_001236602.1| -----
gi|15222601|ref|NP_173920.1| MAMVDEP-----LYPIAVLIDELKNDIQLRLNSIRRLSTIARALGEEERTRKELIPFLFENSDDDEVLLAMAEELGVFIFVGGIEFAHVLLPPLSELCTVVEETCVREKAVESLCKIGSOMKENDLVEFVPLVKRLASG 136
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi|32455244|ref|NP_859050.1| DWFTSRTSACGLFVVCYPRASNVAKAEIRQFRSLCSDDTPMVRRAAASKLGEFAKVELDQVSKSEIVPLFTSLASDEQDSVRLLAVEACVIAQLLSQDDLELVMPTLRQAAEDKSWRVRYMVAADRFSSELOKAMGPKITLNDLIPAFG 300
gi|114640311|ref|XP_522178.2| DWFTSRTSACGLFVVCYPRASNVAKAEIRQFRSLCSDDTPMVRRAAASKLGEFAKVELDQVSKSEIVPLFTSLASDEQDSVRLLAVEACVIAQLLSQDDLELVMPTLRQAAEDKSWRVRYMVAADRFSSELOKAMGPKITLNDLIPAFG 274
gi|73954805|ref|XP_850884.1| DWFTSRTSACGLFVVCYPRASNVAKAEIRQFRSLCSDDTPMVRRAAASKLGEFAKVELDQVSKSEIVPLFTSLASDEQDSVRLLAVEACVIAQLLSQDDLELVMPTLRQAAEDKSWRVRYMVAADRFSSELOKAMGPKITLNDLIPAFG 300
gi|194673192|ref|XP_001788645.1| DWFTSRTSACGLFVVCYPRASNVAKAEIRQFRSLCSDDTPMVRRAAASKLGEFAKVELDQVSKSEIVPLFTSLASDEQDSVRLLAVEACVIAQLLSQDDLELVMPTLRQAAEDKSWRVRYMVAADRFSSELOKAMGPKITLNDLIPAFG 300
gi|77539770|ref|NP_001029257.1| DWFTSRTSACGLFVVCYPRASNVAKAEIRQFRSLCSDDTPMVRRAAASKLGEFAKVELDQVSKSEIVPLFTSLASDEQDSVRLLAVEACVIAQLLSQDDLELVMPTLRQAAEDKSWRVRYMVAADRFSSELOKAMGPKITLNDLIPAFG 300
gi|70794752|ref|NP_001020589.1| DWFTSRTSACGLFVVCYPRASNVAKAEIRQFRSLCSDDTPMVRRAAASKLGEFAKVELDQVSKSEIVPLFTSLASDEQDSVRLLAVEACVIAQLLSQDDLELVMPTLRQAAEDKSWRVRYMVAADRFSSELOKAMGPKITLNDLIPAFG 300
gi|53933248|ref|NP_001005590.1| DWFTSRTSACGLFVVCYPRVYSVVAKAEIRQFRSLCSDDTPMVRRAAASKLGEFAKVELDQVSKSEIVPLFTSLASDEQDSVRLLAVEACVIAQLLSQDDLELVMPTLRQAAEDKSWRVRYMVAADRFSSELOKAMGPKITLNDLIPAFG 288
gi|118105147|ref|XP_001236602.1| -----
gi|15222601|ref|NP_173920.1| EWFARVYVACGIFVAVYQCTDVLKTELRAVYSQLCKDDMPMVRRAAASNLGKFAITVVESTFLIAEIMTMFDLTKDDQDSVRLLAVEGCAALGKLEPQDCVARILPVIVNFSQDKSWRVRYMVAANLYELCEAVGPDCTRTDLVPAV 286
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi|32455244|ref|NP_859050.1| NLLKDCEAEVRAAAAHKVKELGENLPIDRETIIMNQILPYIKELVSDTNQHVKSALASVIMGLSTILGKENTIEHLLPLFLAQLKDECPVRLNIIISNLDVCVNEVIGIRQLSQSLLPAIVELAEDAKWRVRLAIEYMPLLAGOLGV 450
gi|114640311|ref|XP_522178.2| NLLKDCEAEVRAAAAHKVKELGENLPIDRETIIMNQILPYIKELVSDTNQHVKSALASVIMGLSTILGKENTIEHLLPLFLAQLKDECPVRLNIIISNLDVCVNEVIGIRQLSQSLLPAIVELAEDAKWRVRLAIEYMPLLAGOLGV 424
gi|73954805|ref|XP_850884.1| NLLKDCEAEVRAAAAHKVKELCENLPTEGRETIIMNQILPYIKELVSDTNQHVKSALASVIMGLSTILGKENTIEHLLPLFLAQLKDECPVRLNIIISNLDVCVNEVIGIRQLSQSLLPAIVELAEDAKWRVRLAIEYMPLLAGOLGV 450
gi|194673192|ref|XP_001788645.1| NLLKDCEAEVRAAAAHKVKELCENLPMEGRETIIMNQILPYIKELVSDTNQHVKSALASVIMGLSTILGKENTIEHLLPLFLAQLKDECPVRLNIIISNLDVCVNEVIGIRQLSQSLLPAIVELAEDAKWRVRLAIEYMPLLAGOLGV 450
gi|77539770|ref|NP_001029257.1| SLLRDCEAEVRAAAAHKVRLEENLPAEGRETIIMNQILPYIKELVSDTNQHVKSALASVIMGLSTILGKENTIEHLLPLFLAQLKDECPVRLNIIISNLDVCVNEVIGIRQLSQSLLPAIVELAEDAKWRVRLAIEYMPLLAGOLGV 450
gi|70794752|ref|NP_001020589.1| SLLRDCEAEVRAAAAHKVRLEENLPAEGRETIIMNQILPYIKELVSDTNQHVKSALASVIMGLSTILGKENTIEHLLPLFLAQLKDECPVRLNIIISNLDVCVNEVIGIRQLSQSLLPAIVELAEDAKWRVRLAIEYMPLLAGOLGV 450
gi|53933248|ref|NP_001005590.1| NLLKDCEAEVRAAAANKVKFCENLPEDSRETIIMTHILPCVKELVSDTNQHVKSALASVIMGLSTILGKENTIEHLLPLFLAQLKDECPVRLNIIISNLDVCVNEVIGIRQLSQSLLPAIVELAEDAKWRVRLAIEYMPLLAGOLGV 438
gi|118105147|ref|XP_001236602.1| -----CPVRLNIIISNLDVCVNEVIGIRQLSQSLLPAIVELAEDAKWRVRLAIEYMPLLAGOLGV 58
gi|15222601|ref|NP_173920.1| RLLRDNEAEVRIAAAGKVTKFCRLN---PELATQHILPCVKELSDSSEHVSALASVIMGMAPILGKDSIEHLLPIFLSLKDEFPVRLNIIISNLDVCVNEVIGIRQLSQSLLPAIVELAEDAKWRVRLAIEYMPLLAGOLGV 432
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi|32455244|ref|NP_859050.1| FDEKLSLCAWLVVDHVYAIREAATNMLKLVKQFGTEWAQNTIVPKVLVMANDPNYLHRMTTLFCINALSEACGQEIITKQMLPVLVKMAGDOVANVRFNVAKSLOKIGPILDTNALQGEVKPVLOKLGODEMDVKYFAOEAI SVVA 600
gi|114640311|ref|XP_522178.2| FDEKLSLCAWLVVDHVYAIREAATNMLKLVKQFGTEWAQNTIVPKVLVMANDPNYLHRMTTLFCINALSEACGQEIITKQMLPVLVKMAGDOVANVRFNVAKSLOKIGPILDTNALQGEVKPVLOKLGODEMDVKYFAOEAI SVLAL 574
gi|73954805|ref|XP_850884.1| FDEKLSLCAWLVVDHVYAIREAATNMLKLVKQFGTEWAQNTIVPKVLVMANDPNYLHRMTTLFCINALSEACGQEIITKQMLPVLVKMAGDOVANVRFNVAKSLOKIGPILDTNALQGEVKPVLOKLGODEMDVKYFAOEAI SAVAG 600
gi|194673192|ref|XP_001788645.1| FDEKLSLCAWLVVDHVYAIREAATNMLKLVKQFGTEWAQNTIVPKVLVMANDPNYLHRMTTLFCINALSEACGQEIITKQMLPVLVKMAGDOVANVRFNVAKSLOKIGPILDTNALQGEVKPVLOKLGODEMDVKYFAOEAI SAMAG 600
gi|77539770|ref|NP_001029257.1| FDEKLSLCAWLVVDHVYAIREAATNMLKLVKQFGTEWAQNTIVPKVLVMANDPNYLHRMTTLFCINALSEACGQEIITKQMLPVLVKMAGDOVANVRFNVAKSLOKIGPILDTNALQGEVKPVLOKLGODEMDVKYFAOEAI SVVA 600
gi|70794752|ref|NP_001020589.1| FDEKLSLCAWLVVDHVYAIREAATNMLKLVKQFGTEWAQNTIVPKVLVMANDPNYLHRMTTLFCINALSEACGQEIITKQMLPVLVKMAGDOVANVRFNVAKSLOKIGPILDTNALQGEVKPVLOKLGODEMDVKYFAOEAI SVLAL 600
gi|53933248|ref|NP_001005590.1| FDEKLSLCAWLVVDHVYAIREAATNMLKLVKQFGTEWAQNTIVPKVLVMANDPNYLHRMTTLFCINALSEACGQEIITKQMLPVLVKMAGDOVANVRFNVAKSLOKIGPILDTNALQGEVKPVLOKLGODEMDVKYFAOEAI SVLAL 588
gi|118105147|ref|XP_001236602.1| -----
gi|15222601|ref|NP_173920.1| FDDKLGALCMOWLQDKVYSIREAAANLKRLEAEFGEPEWAMQHLVLPVLDLDMVNNPHYLHRMMLRAISLMAVPMGSEIICSKFLPVVVEASKDRVPIKFNVAKLLSILIFIVDQSVVDKTIROCLVDSLDDPVDVRYFANALNSIDG 582
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



gi|32455244|ref|NP_859050.1| RLRKLEFPVKDSGEPVPRADKNHFRPPTVPGEDMGK-GPVYQLRGDTRDTLAQLGIAELVHFSQSTD---- 667
gi|114640311|ref|XP_522178.2| A----- 575
gi|73954805|ref|XP_850884.1| RLRKLDLFPVKDSSEPSGPGADKNHFLRPRGPGEDTGK-GPAYQLVHVTET-----HLPNWKLQ-- 658
gi|194673192|ref|XP_001788645.1| RLRKLDLFPVKDSSEPSIPGDKNHFLRPRGPGEDTGK-GPAYQLVHVTET-----HLPNWKLQ-- 672
gi|77539770|ref|NP_001029257.1| RLRKLDLFPVKDSSEPSIPGDKNHFLRPRGPGEDTGKFLPLMSRHRETER-----LQWLPRRQ-- 658
gi|70794752|ref|NP_001020589.1| A----- 601
gi|53933248|ref|NP_001005590.1| A----- 589
gi|118105147|ref|XP_001236602.1| ----- 58
gi|15222601|ref|NP_173920.1| SAAQS----- 588
.....610.....620.....630.....640.....650.....660.....670.....