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gi|6996932|ref|NP_034996.1| MELLSPPLRDIDLGGPDGSLCSFETADDFYDDPCFDSDLRFFEDLDPRLVHVGALLKPEEHAHFTAVHPGPGAREDEHVRAPSGHHQAGRCLLWACKACKRKTINADRRKAATMRERRRLSKVNEAFETLKRCTSSNPQORLPKVEIL 150
gi|28570184|ref|NP_788268.1| MELLSPPLRDIDLGGPDGSLCSFATRDDFYDDPCFDSDLRFFEDLDPRLVHVGALLKPEEHAHFTAVHPGPGAREDEHVRAPSGHHQAGRCLLWACKACKRKTINADRRKAATMRERRRLSKVNEAFETLKRCTSSNPQORLPKVEIL 150
gi|23111009|ref|NP_002469.2| MELLSPPLRDVLDLAPDGLSCLSFATDDFYDDPCFDSDLRFFEDLDPRLMHVGALLKPEEHSHPAAVHPAPGAREDEHVRAPSGHHQAGRCLLWACKACKRKTINADRRKAATMRERRRLSKVNEAFETLKRCTSSNPQORLPKVEIL 150
gi|114636406|ref|XP_508311.2| MELLSPPLRDVLDLAPDGLSCLSFATDDFYDDPCFDSDLRFFEDLDPRLMHVGALLKPEEHSHPAAVHPAPGAREDEHVRAPSGHHQAGRCLLWACKACKRKTINADRRKAATMRERRRLSKVNEAFETLKRCTSSNPQORLPKVEIL 150
gi|73988888|ref|XP_854756.1| MELLSPPLRDVLDLGGPDGSLCNFASADDFYDDPCFDSDLRFFEDLDPRLVHVGALLKPEEHSHPAAVHPAPGAREDEHVRAPSGHHQAGRCLLWACKACKRKTINADRRKAATMRERRRLSKVNEAFETLKRCTSSNPQORLPKVEIL 150
gi|113205976|ref|NP_001035568.2| MELLSPPLRDVLDLGGPDGSLCNFATADDFYDDPCFDSDLRFFEDLDPRLVHVGALLKPEEHSHPAAVHPAPGAREDEHVRAPSGHHQAGRCLLWACKACKRKTINADRRKAATMRERRRLSKVNEAFETLKRCTSSNPQORLPKVEIL 150
gi|45383692|ref|NP_989545.1| MDLLGP-----MEMTSGSLCSFETADDFYDDPCFNTSDMHFFEDLDPRLVHVGALLKAEHHPHTRAPPRE---PTEEHVRAPSGHHQAGRCLLWACKACKRKTINADRRKAATMRERRRLSKVNEAFETLKRCTSSNPQORLPKVEIL 150
gi|112982794|ref|NP_571337.2| -----MELSD-IPFPFIPSAADDFYDDPCFNTNDMHFFEDLDPRLVHVS-LLKPEEHH-----IDEHVRAPSGHHQAGRCLLWACKACKRKTINADRRKAATMRERRRLSKVNEAFETLKRCTSSNPQORLPKVEIL 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi|6996932|ref|NP_034996.1| RNAIRYIEGLQALLRDQDAAPPQ-AAAFYAPGGLPPGRGSEHYSGSDASSPRNSCDGMMDYSGPPGPRRONGYDANYSEAVR-ESRPGKSAAVSSLDCLSSIVERISTDSPAAPALLLADAPPE-SPPGPPPEGASLSDTQ-GTQ 300
gi|28570184|ref|NP_788268.1| RNAIRYIEGLQALLRDQDAAPPQ-AAAFYAPGGLPPGRGSEHYSGSDASSPRNSCDGMMDYSGPPGPRRONGYDANYSEAVR-ESRPGKSAAVSSLDCLSSIVERISTDSPAAPALLLADAPPE-SPPGPPPEGASLSDTQ-GTQ 300
gi|23111009|ref|NP_002469.2| RNAIRYIEGLQALLRDQDAAPPQAAAFYAPGGLPPGRGSEHYSGSDASSPRNSCDGMMDYSGPPGARRRNCYEGAYNEAPE-EPRPGKSAAVSSLDCLSSIVERISTE SPAAPALLLADVPSE-SPPRRQEAAPSEGESGDPT 300
gi|114636406|ref|XP_508311.2| RNAIRYIEGLQALLRDQDAAPPQAAAFYAPGGLPPGRGSEHYSGSDASSPRNSCDGMMDYSGPPGARRRNCYEGAYNEAPE-EPRPGKSAAVSSLDCLSSIVERISTE SPAAPALLLADVPSE-SPPRRQEAAPSEGESGDPT 300
gi|73988888|ref|XP_854756.1| RNAIRYIEGLQALLRDQDAAPPQAAAFYAPGGLPPGRGSEHYSGSDASSPRNSCDGMMDYSGPPGARRRNCYDRTYYS EAPN-EPRPGKSAAVSSLDCLSSIVERISTE SPAAPALLLADAPPE-SPPGPEAAQSDAER-GAPT 300
gi|113205976|ref|NP_001035568.2| RNAIRYIEGLQALLRDQDAAPPQAAAFYAPGGLPPGRGSEHYSGSDASSPRNSCDGMMDYSGPPGARRRNCYDRTYYS EAPN-EPRPGKSAAVSSLDCLSSIVERISTE SPAAPALLLADAPPE-SPPGPEAAQSDAER-GAPT 300
gi|45383692|ref|NP_989545.1| RNAIRYIEGLQALLRDQ-----EDAYYP-----VLEHYSGSDASSPRNSCDGMMEYSGPPCSSRRRNSYDSYVYTESPN-DPKHGKSSVSSLDCLSSIVERISTDNSICPILPPAEVAEGSPCSPQEGNLSDSGAQIPSP 300
gi|112982794|ref|NP_571337.2| RNAISSVIEGLQALLRSQ-----EDNYYP-----VLEHYSGSDASSPRNSCDGMDFMGPTCQTRRRNSYDSYVYTESPN-DPKHGKSSVSSLDCLSSIVERISTEIPACPVLVPEGHEE-SPCSPHEGNSVLSDTGTAPSP 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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gi|6996932|ref|NP_034996.1| PFPDAAPQCPAGSNP-NAIYQVL 323
gi|28570184|ref|NP_788268.1| PFPDSTPQCPAGSKP-NPIYQVL 323
gi|23111009|ref|NP_002469.2| QFPDAAPQCPAGANP-NPIYQVL 323
gi|114636406|ref|XP_508311.2| QFPDAAPQCPAGANP-NPIYQVL 323
gi|73988888|ref|XP_854756.1| PFPDAAPQCPAGANP-NPIYQVL 323
gi|113205976|ref|NP_001035568.2| PFPDTAPQGLAGANP-NPIYQVL 323
gi|45383692|ref|NP_989545.1| TNCTPLPQESSSSSNPIYQVL 323
gi|112982794|ref|NP_571337.2| TFC---PQQQAEET---IYQVL 323
.....310.....320...

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