

gi|6678339|ref|NP_033404.1| MLGIFFLGVLAPASLG-----LSALAKLQPTGSOVEHECFALFQGPATFLDASQACORLQGHLMTVRSSVAADVI SLLLSQSSMD--LGPWIGLQLPQGGDDPVHLGPLRGFQWVTGDNHTSYSRWARPNQ-TAPLCGFLCVTVSTA 150
gi|13929084|ref|NP_113959.1| MLGVFLGVLAPAGLG-----LSALAKLQPKGSQCVGNECFALFQDPVTFLDASQACORLQGHLMTVRSSVAADVI SLLVSDSSMD--SRPWIGLQLPQGGDDPVHLGPLRGFQWVTGDNHTSYSRWARPNQ-SPPLCGFLCVTVSTA 150
gi|4507483|ref|NP_000352.1| MLGVFLGVLAPAGLG-----FPAPAEPPGGSQCVHEHDCFALYFPGPATFLNASQICDGLRGLHMTVRSSVAADVI SLLLNQGGVGRRLWIGLQLPQGGDDPKRLGPLRGFQWVTGDNHTSYSRWARLDLN-GAPLCGFLCVAVSAA 150
gi|114681254|ref|XP_525283.2| MLGVFLGVLAPAGLG-----FPAPAEPPGGSQCVHEHDCFALYFPGPATFLNASQICDGLRGLHMTVRSSVAADVI SLLLNQGGVGRRLWIGLQLPQGGDDTKRLGPLRGFQWVTGDNHTSYSRWARLDLN-GAPLCGFLCVAVSAA 150
gi|55741805|ref|NP_001006954.1| MLRVLLGVLAPAGLG-----LPTPAQPPRPSQCMEDHCFQFRGPATFLAASQICEGLGHLMTVRSSVAADVI SLLLSGDDGDPRLWIGLQLRQSGSDPQGGGFLRGFQWVTGDNHTSYSRWARFHVGPAGFPAPLCVAVSAA 150
gi|119905421|ref|XP_610749.3| MLRVLLGVLAPAGLG-----LPAPPEPPLGGQCVLDLDFAVRGPATFLAASRVCRERLQGHLMTVRSSVAADVI SLLLSGDDG---PRLWIGLQRPFGCDDPEHSGPLRGFQWVTGDNHTSYSRWARFHVGPAGFPAPLCVAVSAA 150
gi|118087552|ref|XP_426101.2| MRRLLLPLLAGLGLGLGLVGLGEPFPAPSGAQCLEHDCFAVFWTPGPFAAASACERHGGHLMTVRSTVAEDAIELLRKRGG---RLWGLRLPTLCTEPAR--RLRGFQWVTGDTGIDYDNWVF---SGRRCQLCVTVSRE 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi|6678339|ref|NP_033404.1| T-EAAPGEPAAWEEKPCETEKGFLCEFYFAASCRPLTVNTRDPEAAHISSTYINPLFGVSGADFOITLPGSSAAVEPLGLELVCRAPPGTSEGHWAWEATGAWNCSEVENGGCEYLGNRSINPRCLCPMDLQADGRSCARPVVGSNCEL 300
gi|13929084|ref|NP_113959.1| T-EAAPGEPAAWEEKPCENEKGFCEFYFAAFCRPLRVNTRDPEGAHISSTYINPLFGVSGADFOITLPGSSAAVEPLGLELVCRAPPGTSEGHWAWEATGAWNCSEVENGGCEYLGNRSINPRCLCPMDLQADGRSCAKPVAIGLCEL 300
gi|4507483|ref|NP_000352.1| E-ATVPSEPIWEEQQCEVKADGFLCEFHFPATCRPLAVEPGAAAAA-VSIIYGTFFAARGADFOALPVGSSAAVAPLGLQLMCTAPPGAVQGHWAREAPGAWDCSEVENGGCEHACNAIPGAPRCQCPAGAALQADGRSCTASATQSCNDL 300
gi|114681254|ref|XP_525283.2| E-ATVPSEPIWEEQQCDVKADGFLCEFHFPATCRPLAVEPGAAAAA-VSIIYGTFFAARGADFOALPVGSSAAVAPLGLQLMCTAPPGAVQGHWAREAPGAWDCSEVENGGCEHACNAIPGAPRCQCPAGAALQADGRSCTAPATQSCNDL 300
gi|55741805|ref|NP_001006954.1| A-APAPGEPAAWEEQRCAEADGFLCEFHFAASCRPLLVDAARAAAAGVSVIYISYTFGARGADFOALPVGSSAAVAPFVGLCAAPRGEAARWRGEPAGAWDCSEVENGGCQRACSAAGAPRCLCPADATYLQADGRSCATFAEHSQHL 300
gi|119905421|ref|XP_610749.3| AGALAPGEPAAWEEPCDAEADGFLCEFHFAASCRPLAVDPGATAAAGLSIITYGTFGARGADFOALPLGSTAAVAPLGVLECAAPQGETGRWSREAPGAWACVGERGGCQHEKGSAGASLCPADAALQADGRSCGLPAEHPHQHL 300
gi|118087552|ref|XP_426101.2| L-----SWEERRCDEPADGFLCEYVYVSDGCRPLISPSDGL-----ASLIVYRPFGAAGGDFLALPHGSTAFVSPMGLQLLCEAAADSCKMRWRSEPGAWFCRLDNGCCGSGCELDGTFSCACPAKCKLQPDGRSCVSPFCAG--AA 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi|6678339|ref|NP_033404.1| CEHFCVSNAEVPGSYSCMCEICGYQLAADGHRCEVDVDDCKGPNPFCPLCVNTEKGFECFCYDGYELVDGECVEQLDPCFRSKCEYOCQPVNSIHYNCICAEGFAPKLDPPDRCEMFCNEISCPADCDPNSPFCQCPGEGFILLDEG---S 450
gi|13929084|ref|NP_113959.1| CEHFCVSNAEVPGSYSCMCEICGYQLAADGHRCEVDVDDCKGPNPFCPLCVNTEKGFECFCYDGYELVDGECVEQLDPCFRSKCEYOCQPVNSIHYNCICAEGFAPKLDPPDRCEMFCNEISCPADCDPNSPFCQCPGEGFILLDEG---S 450
gi|4507483|ref|NP_000352.1| CEHFCVNPDPQPGSYSCMCEICGYRLAADGHRCEVDVDDCILEPSPCPQRCVNTQGGFECFCYPNVLDVDEGCEVDPDFCFRANCEYOCQPLNQSYLVCVCAEGFAPIPHEPHRCQMFNQTACPADCDPNTQASCCPEGYILLDDG---F 450
gi|114681254|ref|XP_525283.2| CEHFCVNPDPQPGSYSCMCEICGYRLAADGHRCEVDVDDCILEPSPCPQRCVNTQGGFECFCYPNVLDVDEGCEVDPDFCFRANCEYOCQPLNQSYLVCVCAEGFAPIPHEPHRCQMFNQTACPADCDPNTQASCCPEGYILLDDG---F 450
gi|55741805|ref|NP_001006954.1| CEHFCIPNASVPGSYLQMCCEICGYQLAADGHRCEVDVDDCICVPSLCPCLCVNTRGAFECFCYDGYELVDNECEVDPDFCFGSKCEYOCQPVNSQDVCRCICAEGFAPVPHDHRQMFNQTACPADCDPNSPFCQCPGEGYILLDDG---F 450
gi|119905421|ref|XP_610749.3| CEHFCIHLHG--LGNVTCICEAGYQLAADGHRCEVDVDDCAGLPSPCQRCVNTQGGFECFCYDGYELVDGECVDPDFCFDNNCEYOCQPVNSQDVCRCICAEGFAPVPGAPHKQMFNQTACPADCDPNTQASCCPEGYILLDEG---S 450
gi|118087552|ref|XP_426101.2| CEHFCVDPDGE--GFHMCSEGYELGPDGSSQDQVDDCKVKEVEVCEVYCNTEKGFECFCYDGYELVDGECVDPDFCFDNNCEYOCQPVNSQDVCRCICAEGFAPVPGAPHKQMFNQTACPADCDPNTQASCCPEGYILLDEG---S 450
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi|6678339|ref|NP_033404.1| VCTDIDECISQGECEFNSECRNFPGSYECICGPDALAGQISKDCD---PIPVREDKKEEGSGEPPVS-PTPGSPH--GPPSARPVHSGVLIGISIASLSLVVALLALLCHLRKKQGAARAEYKCASS-AKEVVLQHVTRDRITLOKE 598
gi|13929084|ref|NP_113959.1| VCTDIDECISQGECEFNSECRNFPGSYECICGPDALAGQISKDCD---PIPVLEDS-EDGSGEHPSSNPTVVSTH--VPPSARPMHSGVLIGISIASLSLVVALLALLCHLRKKQGAARAEYKCTSS-AKEVVLQHVTRDRITLOKE 598
gi|4507483|ref|NP_000352.1| ICTDIDECENGFCISGVCNRLPGTFECICGPDALARHIGDCD---SGKVDGG---DSGSGEPPVS-PTPGSTL--PFAVGLVHSGLLIGISIASLCLVALLALLCHLRKKQGAARAKMEYKCAAP-SKEVVLQHVTRTERPQRL 598
gi|114681254|ref|XP_525283.2| ICTDIDECENGFCISGVCNRLPGTFECICGPDALARYIGNDCD---SGKVDGG---DSGSGEPPVS-PTPGSTL--PFAVGLVHSGLLIGISIASLCLVALLALLCHLRKKQGAARAKMEYKCAAP-SKEVVLQHVTRTERPQRL 598
gi|55741805|ref|NP_001006954.1| MCTDIDECENG-ECPEACRNLPGYECICGPDALAGQISKDCD---PIPVLEDS-EDGSGEHPSSNPTVVSTH--VPPSARPMHSGVLIGISIASLSLVVALLALLCHLRKKQGAARAEYKCTSS-AKEVVLQHVTRTERPQRL 598
gi|119905421|ref|XP_610749.3| ICTDINECDTN-ICPGQCHNLPGYECICGPDALAGQISKDCD---PIPVLEDS-EDGSGEHPSSNPTVVSTH--VPPSARPMHSGVLIGISIASLSLVVALLALLCHLRKKQGAARAEYKCTSS-AKEVVLQHVTRTERPQRL 598
gi|118087552|ref|XP_426101.2| LCVDIDECBSN-HCEHNTNITAGSYICHCQP---GYMPFDVN--HCIPISQEDNEDGYSQSGPPWVPSHIP---PKAEHLHPGALVGTIMVLCALVLLAVGYHLARKRCHPPSSMEYKCGSPREKEMGLQVSAQKRV--- 598
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590

