

gi|56786138|ref|NP_000610.2| MKYTSYILAFQLCIVLGSLSGCYCDPYPVKEAENLKKYFNAGHSDVADNGTFLFLGILKNWKEESDRKIMOSQIVSFYFKLFFKFKDDQSTQKSVETIKEDMNVKFFNSNKKKRDDFEKLIINYSVTDLNVORCAIHელიQVMAELSPAAKIG 150
 gi|114645729|ref|XP_001151968.1| MKYTSYILAFQLCIVLGSLSGCYCDPYPVKEAENLKKYFNAGHSDVADNGTFLFLGILKNWKEESDRKIMOSQIVSFYFKLFFKFKDDQSTQKSVETIKEDMNVKFFNSNKKKRDDFEKLIINYSVTDLNVORCAIHელიQVMAELSPAAKIG 150
 gi|50978906|ref|NP_001003174.1| MNYTSYILAFQLCIVLGSLSGCNCOAMFFKEIENLKEYFNASNPDVSDGGSLFVDILKKWREESDRKTIISQIVSFYFKLFFNFKDNOIQRSMDTIKEDMLGKFLNSSLTSKREDFLKLIIQIPVNDLOVORCAINELIKVMNDLSPKSNLR 150
 gi|31982949|ref|NP_776511.1| MKYTSYFLALLLCGLLGFSGSYGGQFFREIENLKEYFNASPPDVAKGGPLFSEILKNWDESDKKIISQIVSFYFKLFFENLKDNOVIQRSMDTIKQDMPQKFLNGSSEKLEDFKLLIIPVDDLOIQRCAINELIKVMNDLSPKSNLR 150
 gi|33468859|ref|NP_032363.1| MNAHCLLALQLF-LMAVSGCYCHGTVIESLESLSLNNYFNSSGIDVEE-KLFLDIWRNWQKDGDMKILQSIIISFYLRLEFVLKDNQAISSNNISVIESHLITFFFSNSKAKKDAFMSIAKFEVNNPQVORQAFNELIRVVHQLPESSLR 150
 gi|20302055|ref|NP_620235.1| MSATRRVLVQLC-LMALSGCYCOGLIESLESLSLNNYFNSSMDAMEGKSLLLDIWRNWQKDGNTKILESQIIISFYLRLEFVLKDNQAISSNNISVIESHLITFFFSNSKAKKDAFMSIAKFEVNNPQVORQAFNELIRVVHQLPESSLR 150
 1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



 gi|56786138|ref|NP_000610.2| KRKRSQLFRGRRASQ 166
 gi|114645729|ref|XP_001151968.1| KRKRSQLFRGRRASQ 166
 gi|50978906|ref|NP_001003174.1| KRKRSQLFRGRRASQ 166
 gi|31982949|ref|NP_776511.1| KRKRSQLFRGRRASQ 166
 gi|33468859|ref|NP_032363.1| KRKRRC----- 166
 gi|20302055|ref|NP_620235.1| KRKRRC----- 166
160.....

