

gi | 52138513 | ref | NP_056075.1 | MAHAGGSGGSGAGGPAAGRGLSGARWGR 28
gi | 114675954 | ref | XP_512485.2 | MAHAGGSGGSGG--GGPAGRGLSGARWGR 25
gi | 73986243 | ref | XP_852728.1 | MKHK 4
gi | 28212270 | ref | XP_852728.1 | MAHAGSG --GSAGRFGGSRWGR 21
gi | 118103322 | ref | XP_418257.2 | MPGRRLKGSPPKPMCFKPFGLCLALQPNRSRGRPRGPRAPVRNVPLRSPEPSRGAHPGQPHSLGLPRAHRRRRRRRRRGRKGRKQAVRAAPPAAAVVPLRAGFGRGAVRADADAPHALTGGARRRRLRLTIMAAGRRRPRSGTA 150
gi | 113678676 | ref | NP_001038410.1 | MAKIQAHSSSTAKQINQIQDKAYVVQKVCQQH 32



gi | 52138513 | ref | NP_056075.1 | SGAGHEKLPVHVEDALTYLDQVKIRFGSDPAIYNGFLEIMKEFKSQSIDPGVIRRVSQLFHHEHPDLIVGFNAFLPLGYRIDIPKNGKLNIOQSPLSQEN 129
gi | 114675954 | ref | XP_512485.2 | SGAGHEKLPVHVEDALTYLDQVKIRFGSDPAIYNGFLEIMKEFKSQSIDPGVIRRVSQLFHHEHPDLIVGFNAFLPLGYRIDIPKNGKLNIOQSPLSQEN 126
gi | 73986243 | ref | XP_852728.1 | -----KVEDALTYLDQVKIRFGSDPAIYNGFLEIMKEFKSQSIDPGVIRRVSQLFHHEHPDLIVGFNAFLPLGYRIDIPKNGKLNIOQSPSSQDS 94
gi | 28212270 | ref | NP_033214.1 | SGGGHEKLPVHVEDALTYLDQVKIRFGSDPAIYNGFLEIMKEFKSQSIDPGVIRRVSQLFHHEHPDLIVGFNAFLPLGYRIDIPKNGKLNIOQSPSSQDN 122
gi | 118103322 | ref | XP_418257.2 | AFPRDLRLPGALSAVGVSAEGLCRAPGLCPPGASAAASRPQVEDALSYLDQVKIRFGSDPAIYNGFLEIMKEFKSQSIDPGVIRRVSQLFHHEHPDLIVGFNAFLPLGYRIEIPKNGKLSIQSPLSQEN 280
gi | 113678676 | ref | NP_001038410.1 | FQKLVEDALSYLDQVKIRFGSDPAIYNGFLEIMKEFKSQSIDPGVINRVSQLFHGHHPDLIVGFNAFLPPGYRIEIPKNGMAFLQSPSSQVSPGAGRSVSSVVSASSAVV 146



gi | 52138513 | ref | NP_056075.1 | SHNHGDGAEDFKQOVFPYKEDKPOVPLESDS-----VEFNNAISYVVKIKTRFLDHPETIYRFLFLEILHTYQKEQLNTR-----GRPFRGMSSEEVFTEVANLFRGQEDLLSEFGQFLPEAKRSLFTGNGPC 249
gi | 114675954 | ref | XP_512485.2 | SHNHGDGAEDFKQOVFPYKEDKPOVPLESDS-----VEFNNAISYVVKIKTRFLDHPETIYRFLFLEILHTYQKEQLNTR-----GRPFRGMSSEEVFTEVANLFRGQEDLLSEFGQFLPEAKRSLFTGNGPC 246
gi | 73986243 | ref | XP_852728.1 | SHNHSDCAENFKQOMLYKEDKPOVPLESDS-----VEFNNAISYVVKIKTRFLDHPETIYRFLFLEILHTYQKEQLNTR-----GRPFRGMSSEEVFTEVANLFRGQEDLLSEFGQFLPEAKRSLFTGNGPC 214
gi | 28212270 | ref | NP_033214.1 | SHNHSDCGEDFKQMS--YKEDRGQVPLESDS-----VEFNNAISYVVKIKTRFLDHPETIYRFLFLEILHTYQKEQLNTR-----GRPFRGMSSEEVFTEVANLFRGQEDLLSEFGQFLPEAKRSLFTGNGPC 241
gi | 118103322 | ref | XP_418257.2 | SHNHSDCSEEFHQLPYKEDKQVPLESDS-----VEFNNAISYVVKIKTRFLDHPETIYRFLFLEILHTYQKEQLNTR-----GRPFRGMSSEEVFTEVANLFRGQEDLLSEFGQFLPEAKRSLFTGNGPC 400
gi | 113678676 | ref | NP_001038410.1 | EAAGPAQNEAVTSPESLASSGPPPEQSSKLSLPLNRESGQAPATVSPPTSEPSVPEVDSAISYVVKIKTRFLDHPETIYRFLFLEILHTYQKEQLNTR-----GRPFRGMSSEEVFTEVANLFRGQEDLLSEFGQFLPEAKRSLFTGNGPC 293



gi | 52138513 | ref | NP_056075.1 | EMHGVOKNEHDKTPEHSRKRSRPSSLRPPVSAPAKKKMLRGTKDLSIAAVGKYGTLOEFSFFDKVRRVLKSOEYVENFLRCIALFNOELVSGSELLQLVSPFLGKFPFELFAQFKSFLGVKELSFAPP--MSDRSGDGISREIDVASCRRIG 398
gi | 114675954 | ref | XP_512485.2 | EMHGVOKNEHDKTPEHSRKRSRPSSLRPPVSAPAKKKMLRGTKDLSIAAVGKYGTLOEFSFFDKVRRVLKSOEYVENFLRCIALFNOELVSGSELLQLVSPFLGKFPFELFAQFKSFLGVKELSFAPP--MSDRSGDGISREIDVASCRRIG 395
gi | 73986243 | ref | XP_852728.1 | EMNSVOKSEHEKNLEHKKRSPSSLRPPVSAPAKKKMLRGTKDLSIAAVGKYGTLOEFSFFDKVRRVLKSOEYVENFLRCIALFNOELVSGSELLQLVSPFLGKFPFELFAQFKSFLGVKELSFAPP--MSDRSGDGISREIDVASCRRIG 363
gi | 28212270 | ref | NP_033214.1 | EMNSGOKNE--EKSLEHKKRSPSSLRPPVSAPAKKKMLRGTKDLSIAAVGKYGTLOEFSFFDKVRRVLKSOEYVENFLRCIALFNOELVSGSELLQLVSPFLGKFPFELFAQFKSFLGVKELSFAPP--MSDRSGDGISREIDVASCRRIG 389
gi | 118103322 | ref | XP_418257.2 | EVNSVOKTEHEKNLEHKKRSPSSLRPPVSGPAKKKMLRGTKDLSIAAVGKYGTLOEFSFFDKVRRVLKSOEYVENFLRCIALFNOELVSGSELLQLVSPFLGKFPFELFAQFKSFLGVKELSFAPP--LSDRSGDGMSREIDVASCRRIG 549
gi | 113678676 | ref | NP_001038410.1 | SLPLKVEEELNKQTKKRPRMILLPHMTLLKKKMKYSCSKDPSFASVGHGVLREFTFFDKVRRVLKSOEYVENFLRCIALFNOELVSGAELLQLVTPFLGKFPFELFAQFKSFLGVKELSFAPP--SDRYMEGGGREVDVASCRRIG 442



gi | 52138513 | ref | NP_056075.1 | SSYRALPKTYQOPKCSGRTAI CKELDHWLLQGSWDDYCMSKFKNTCWIPGYSGVLDNTVWVSPSWSSEDSFVSSKKNPYEEQLHRCEDERFELDVVLETNLTATIRVLESVQKLSRMAPEDQKFRLLDSSLGGTSEVIQRRAIYRIY 548
gi | 114675954 | ref | XP_512485.2 | SSYRALPKTYQOPKCSGRTAI CKELDHWLLQGSWDDYCMSKFKNTCWIPGYSGVLDNTVWVSPSWSSEDSFVSSKKNPYEEQLHRCEDERFELDVVLETNLTATIRVLESVQKLSRMAPEDQKFRLLDSSLGGTSEVIQRRAIYRIY 545
gi | 73986243 | ref | XP_852728.1 | SSYRALPKTYQOPKCSGRTAI CKE-----VLDNTVWVSPSWSSEDSFVSSKKNPYEEQLHRCEDERFELDVVLETNLTATIRVLESVQKLSRMAPEDQKFRLLDSSLGGTSEVIQRRAIYRIY 481
gi | 28212270 | ref | NP_033214.1 | SSYRALPKTYQOPKCSGRTAI CKE-----VLDNTVWVSPSWSSEDSFVSSKKNPYEEQLHRCEDERFELDVVLETNLTATIRVLESVQKLSRMAPEDQKFRLLDSSLGGTSEVIQRRAIYRIY 507
gi | 118103322 | ref | XP_418257.2 | SSYRALPKTYQOPKCSGRTAI CKE-----VLDNTVWVSPSWSSEDSFVSSKKNPYEEQLHRCEDERFELDVVLETNLTATIRVLESVQKLSRLLEDQKFRLLDSSLGGTSEVIQRRAIYRIY 667
gi | 113678676 | ref | NP_001038410.1 | SSYRALPKTYQOPKCSGRTAI CKE-----VLDNTVWVSPSWSSEDSFVSSKKNPYEEQLHRCEDERFELDVVLETNLTATIRVLESVQKLSRLLEDQKFRLLDSSLGGTSEVIQRRAVYRIY 560



gi | 52138513 | ref | NP_056075.1 | GDKAPEIIESLKKNPVAVPVVVKRLKAKEEWEWAQQGFNKIWIWEQYKAYLKSLDHQAVNFKQNDTKALRSKSLLEIETSVYDEHOQHS-----GR-----SAPSSPHLIFVYEDRQILEDAAAALISYVVKRPAIQKEDQGTI 687
gi | 114675954 | ref | XP_512485.2 | GDKAPEIIESLKKNPVAVPVVVKRLKAKEEWEWAQQGFNKIWIWEQYKAYLKSLDHQAVNFKQNDTKALRSKSLLEIETSVYDEHOQHS-----GR-----SAPSSPHLIFVYEDRQILEDAAAALISYVVKRPAIQKEDQGTI 684
gi | 73986243 | ref | XP_852728.1 | GDKAPEIIESLKKNPVAVPVVVKRLKAKEEWEWAQQGFNKIWIWEQYKAYLKSLDHQAVNFKQNDTKALRSKSLLEIETSVYDEHOQHS-----GR-----SAPSSPHLIFVYEDRQILEDAAAALISYVVKRPAIQKEDQGTI 620
gi | 28212270 | ref | NP_033214.1 | GDKAPEVIESLKRNPATAVPVVVKRLKAKEEWEWAQQGFNKIWIWEQYKAYLKSLDHQAVNFKQNDTKALRSKSLLEIETSVYDEHOQHS-----GR-----SAPSSPHLIFVYEDRQILEDAAAALISYVVKRPAIQKEDQGTI 646
gi | 118103322 | ref | XP_418257.2 | GDKAPEIIESLKKNPVAVPVVVKRLKAKEEWEWAQQGFNKIWIWEQYKAYLKSLDHQAVNFKQNDTKALRSKSLLEIETSVYDEHOQHS-----GR-----SAPSSPHLIFVYEDRQILEDAASLISYVVKRPAIQKEDQGTI 806
gi | 113678676 | ref | NP_001038410.1 | GDKAPEIIEGLKRSFPAVAVPVVVKRLKAKEEWEWAQQGFNKIWIWEQYKAYLKSLDHQAVNFKQNDTKALRSKSLLEIETSVYDEHOQHS-----GR-----SAPSSPHLIFVYEDRQILEDAASLISYVVKRPAIQKEDQGTI 710



