

gi | 145608852 | ref | XP_369806.2 | ... LMFPSSTIGPSS ... NLPGYLRPEAQQFLNFAKLLLEYNQDMPFASASIGKSYRNEISPRGGLLRVREFLMAEIEHFVDPKSGKHPFAEVAADIELELLDREQLSGKTITKKVAIGKAVKD 323
gi | 32403756 | ref | XP_322491.1 | ... LMFQTAIGPSSG ... NLAGYMRPEAQQFLNFAKLLLEYNAGNMPFASASIGKSYRNEIAPRGGLLRVREFLMAEIEHFVDPAGHKKHERFHEVADIELEALLDRNVQSGQTHVTKMTITGSAVKQ 322
gi | 19114847 | ref | NP_593935.1 | ... LMFETAIQIPSSG ... GLKGYLRPEAQQFLNFRLLLEFNKGVPPFASAMVGFARNEISPRGGLLRVREFLMAEIEHFVDPK-NKEHDRFDEVSHMPLRLLRGVLQEGKTDILEMPTIGDAVKK 321
gi | 6319597 | ref | NP_009679.1 | ... LMFETAIGPSSG ... QLKGYLRPEAQQFLNFRLLLEFNKSTPPFASASIGKSYRNEISPRAGLLLRVREFLMAEIEHFVDDL-DKSHPKFNEIKDKLSFLPRDVOEAGSTPIVTKVTGSAVAS 328
gi | 50303953 | ref | XP_451926.1 | ... LMFETAIGPSSG ... QYKGYLRPEAQQFLNFRLLLEFNKSTPPFASASIGKSYRNEISPRGGLLRVREFLMAEIEHFVDPN-DKSHKRFQDKDKLKLFLPREVQSGSTVPLLEKVTGSAVAT 328
gi | 45187500 | ref | NP_983723.1 | ... LMFETAIGPSSG ... QLKGYLRPEAQQFLNFRLLLEFNKSTPPFASASIGKSYRNEISPRGGLLRVREFLMAEIEHFVDPD-NKNHHPFDEVKNLKLFKPKQVQEGARTPEPIESTVADAVS 325
gi | 24664462 | ref | NP_730022.1 | ... LMFETAIGPSSG ... LVKGFRLPEAQQGIFVNFKRLLEFNQGLKLPFAAAGIGNSFRNEISPRGGLLRVREFLMAEIEHFCDPQ-LKDHHPKFGNFKSEKLLVYACNIMDG-KHBAQVQITGSAVAS 430
gi | 158293345 | ref | XP_557743.2 | ... LMFETAIGPSSG ... LVKGFRLPEAQQGIFVNFKRLLEFNQGLKLPFAAAGIGNSFRNEISPRGGLLRVREFLMAEIEHFCDPQ-AKNHHPKFENVAIDVIMLYLSACNIMDG-KBAQVQITGSAVAS 368
gi | 17554996 | ref | NP_498093.1 | ... LMFETAIGPSSG ... DFKAFRLPEAQQGIFVNFKRLLEFNQGLKLPFAAAGIGNSFRNEISPRGGLLRVREFLMAEIEHFVDPD-DKSLAKFAKVAQDKLVLFACNLDG-AFAQVQITGSAVAK 408
gi | 93102417 | ref | NP_851009.2 | ... LMFQTAIGPSSG ... NMPGYLRPEAQQGIFLNFKRLLEFNQGLKLPFAAAGIGNSFRNEISPRGGLLRVREFLMAEIEHFVDPD-EKDHHPKQSVADLCLVLYLSAKAQVGT-QSARKMRLGDAVEQ 388
gi | 109472087 | ref | XP_216152.4 | ... LMFQTAIGPSSG ... NMPGYLRPEAQQGIFLNFKRLLEFNQGLKLPFAAAGIGNSFRNEISPRGGLLRVREFLMAEIEHFVDPD-EKDHHPKQSVADLCLVLYLSAKAQVGT-QSARKMRLGDAVEQ 448
gi | 116805340 | ref | NP_002038.2 | ... LMFQTAIGPSSG ... NMPGYLRPEAQQGIFLNFKRLLEFNQGLKLPFAAAGIGNSFRNEISPRGGLLRVREFLMAEIEHFVDPD-EKDHHPKQSVADLCLVLYLSAKAQVGT-QSARKMRLGDAVEQ 398
gi | 114612672 | ref | XP_519025.2 | ... LMFQTAIGPSSG ... NMPGYLRPEAQQGIFLNFKRLLEFNQGLKLPFAAAGIGNSFRNEISPRGGLLRVREFLMAEIEHFVDPD-EKDHHPKQSVADLCLVLYLSAKAQVGT-QSARKMRLGDAVEQ 398
gi | 73976563 | ref | XP_532502.2 | ... LMFQTAIGPSSG ... NMPGYLRPEAQQGIFLNFKRLLEFNQGLKLPFAAAGIGNSFRNEISPRGGLLRVREFLMAEIEHFVDPD-EKDHHPKQSVADLCLVLYLSAKAQVGT-QSARKMRLGDAVEQ 400
gi | 147902079 | ref | NP_001091035.1 | ... LMFQTAIGPSSG ... NMPGYLRPEAQQGIFLNFKRLLEFNQGLKLPFAAAGIGNSFRNEISPRGGLLRVREFLMAEIEHFVDPD-EKDHHPKQSVADLCLVLYLSAKAQVGT-QSARKMRLGDAVEQ 398
gi | 71895709 | ref | NP_001026681.1 | ... LMFQTAIGPSSG ... NMPGYLRPEAQQGIFLNFKRLLEFNQGLKLPFAAAGIGNSFRNEISPRGGLLRVREFLMAEIEHFVDPD-EKDHHPKQSVADLCLVLYLSAKAQVGT-QSARKMRLGDAVEQ 344
gi | 189536638 | ref | XP_692410.3 | ... LMFQTAIGPSSG ... NMPGYLRPEAQQGIFLNFKRLLEFNQGLKLPFAAAGIGNSFRNEISPRGGLLRVREFLMAEIEHFVDPD-EKDHHPKQSVADLCLVLYLSAKAQVGT-QSARKMRLGDAVEQ 423
gi | 18397278 | ref | NP_564337.1 | ... LMFQTAIGPSSG ... LIPGYMRPEAQQGIFVNFKRLLEFNQGLKLPFAAAGIGNSFRNEISPRGGLLRVREFLMAEIEHFVDPD-NKSHHPKSDVAKLEFLMFPREEVMSG-QSARKMLGSAVAK 395
gi | 115477547 | ref | NP_001062369.1 | ... LMFQTAIGPSSG ... LNVGYMRPEAQQGIFVNFKRLLEFNQGLKLPFAAAGIGNSFRNEISPRGGLLRVREFLMAEIEHFVDPD-DKSHHPKQSVADLCLVLYLSAKAQVGT-QSARKMLGSAVAK 363
gi | 124808643 | ref | XP_001348371.1 | ... LMFQTAIGPSSG ... LNVGYMRPEAQQGIFVNFKRLLEFNQGLKLPFAAAGIGNSFRNEISPRGGLLRVREFLMAEIEHFVDPD-DKSHHPKQSVADLCLVLYLSAKAQVGT-QSARKMLGSAVAK 536



gi | 145608852 | ref | XP_369806.2 | ... GLVDNETLGYFLARIHLFLEKIGVDKSKLRFROHMANEMAHYADCWDAEILLTSYGWIECVGCADRSDAYDLTVSHAKTKNAPLIVRRLPEPKIIVEEWTVEVDKPKFKPKKDAKAVETVLELNDQIRGKLEKLDNGSITVDVPGVG 473
gi | 32403756 | ref | XP_322491.1 | ... KLVNDNETLGYFLARIHLFLEKIGVDQSKIRFRHMGNEAMAHYADCWDAEILLTSYGWIECVGCADRSDAYDLTVSHAKTKNAPLIVRRLPEPKIIVEEWTVEVDKPKFKPKKDAKAVETVLELNDQIRGKLEKLDNGSITVDVPGVG 472
gi | 19114847 | ref | NP_593935.1 | ... GLVDNETLGYFLARIHLFLEKIGVDKSKLRFROHMANEMAHYADCWDAEILLTSYGWIECVGCADRSDAYDLTVSHAKTKNAPLIVRRLPEPKIIVEEWTVEVDKPKFKPKKDAKAVETVLELNDQIRGKLEKLDNGSITVDVPGVG 471
gi | 6319597 | ref | NP_009679.1 | ... RMVDNETLGYFLARIYQFLIKIGVDPERLRFROHMANEMAHYADCWDAEILLTSYGWIECVGCADRSDAYDLTVSHAKTKNAPLIVRRLPEPKIIVEEWTVEVDKPKFKPKKDAKAVETVLELNDQIRGKLEKLDNGSITVDVPGVG 478
gi | 50303953 | ref | XP_451926.1 | ... KLVNDNETLGYFLARIYQFLIKIGVDPERLRFROHMANEMAHYADCWDAEILLTSYGWIECVGCADRSDAYDLTVSHAKTKNAPLIVRRLPEPKIIVEEWTVEVDKPKFKPKKDAKAVETVLELNDQIRGKLEKLDNGSITVDVPGVG 478
gi | 45187500 | ref | NP_983723.1 | ... GMIDNETLGYFLARIYQFLIKIGVDDEKLRFRHMGNEAMAHYADCWDAEILLTSYGWIECVGCADRSDAYDLTVSHAKTKNAPLIVRRLPEPKIIVEEWTVEVDKPKFKPKKDAKAVETVLELNDQIRGKLEKLDNGSITVDVPGVG 475
gi | 24664462 | ref | NP_730022.1 | ... KLVANETLGYFLARIYQFLIKIGVDPECLRFROHMGNEAMAHYADCWDAEILLTSYGWIECVGCADRSDAYDLTVSHAKTKNAPLIVRRLPEPKIIVEEWTVEVDKPKFKPKKDAKAVETVLELNDQIRGKLEKLDNGSITVDVPGVG 577
gi | 158293345 | ref | XP_557743.2 | ... GLVANETLGYFLARIYQFLIKIGVDPERLRFROHMGNEAMAHYADCWDAEILLTSYGWIECVGCADRSDAYDLTVSHAKTKNAPLIVRRLPEPKIIVEEWTVEVDKPKFKPKKDAKAVETVLELNDQIRGKLEKLDNGSITVDVPGVG 515
gi | 17554996 | ref | NP_498093.1 | ... KLVANETLGYFLARIYQFLIKIGVDDEKLRFRHMGNEAMAHYADCWDAEILLTSYGWIECVGCADRSDAYDLTVSHAKTKNAPLIVRRLPEPKIIVEEWTVEVDKPKFKPKKDAKAVETVLELNDQIRGKLEKLDNGSITVDVPGVG 555
gi | 93102417 | ref | NP_851009.2 | ... GVINNSVLGYFGRIRIYLYLTKVGISPDKLRFROHMANEMAHYADCWDAEILLTSYGWIECVGCADRSDAYDLTVSHAKTKNAPLIVRRLPEPKIIVEEWTVEVDKPKFKPKKDAKAVETVLELNDQIRGKLEKLDNGSITVDVPGVG 535
gi | 109472087 | ref | XP_216152.4 | ... GVINNSVLGYFGRIRIYLYLTKVGISPDKLRFROHMANEMAHYADCWDAEILLTSYGWIECVGCADRSDAYDLTVSHAKTKNAPLIVRRLPEPKIIVEEWTVEVDKPKFKPKKDAKAVETVLELNDQIRGKLEKLDNGSITVDVPGVG 595
gi | 116805340 | ref | NP_002038.2 | ... GVINNSVLGYFGRIRIYLYLTKVGISPDKLRFROHMANEMAHYADCWDAEILLTSYGWIECVGCADRSDAYDLTVSHAKTKNAPLIVRRLPEPKIIVEEWTVEVDKPKFKPKKDAKAVETVLELNDQIRGKLEKLDNGSITVDVPGVG 545
gi | 114612672 | ref | XP_519025.2 | ... GVINNSVLGYFGRIRIYLYLTKVGISPDKLRFROHMANEMAHYADCWDAEILLTSYGWIECVGCADRSDAYDLTVSHAKTKNAPLIVRRLPEPKIIVEEWTVEVDKPKFKPKKDAKAVETVLELNDQIRGKLEKLDNGSITVDVPGVG 545
gi | 73976563 | ref | XP_532502.2 | ... GVINNSVLGYFGRIRIYLYLTKVGISPDKLRFROHMANEMAHYADCWDAEILLTSYGWIECVGCADRSDAYDLTVSHAKTKNAPLIVRRLPEPKIIVEEWTVEVDKPKFKPKKDAKAVETVLELNDQIRGKLEKLDNGSITVDVPGVG 545
gi | 147902079 | ref | NP_001091035.1 | ... GVINNSVLGYFGRIRIYLYLTKVGISPDKLRFROHMANEMAHYADCWDAEILLTSYGWIECVGCADRSDAYDLTVSHAKTKNAPLIVRRLPEPKIIVEEWTVEVDKPKFKPKKDAKAVETVLELNDQIRGKLEKLDNGSITVDVPGVG 545
gi | 71895709 | ref | NP_001026681.1 | ... GVINNSVLGYFGRIRIYLYLTKVGISPDKLRFROHMANEMAHYADCWDAEILLTSYGWIECVGCADRSDAYDLTVSHAKTKNAPLIVRRLPEPKIIVEEWTVEVDKPKFKPKKDAKAVETVLELNDQIRGKLEKLDNGSITVDVPGVG 491
gi | 189536638 | ref | XP_692410.3 | ... GVINNSVLGYFGRIRIYLYLTKVGISPDKLRFROHMANEMAHYADCWDAEILLTSYGWIECVGCADRSDAYDLTVSHAKTKNAPLIVRRLPEPKIIVEEWTVEVDKPKFKPKKDAKAVETVLELNDQIRGKLEKLDNGSITVDVPGVG 570
gi | 18397278 | ref | NP_564337.1 | ... GVINNSVLGYFGRIRIYLYLTKVGISPDKLRFROHMANEMAHYADCWDAEILLTSYGWIECVGCADRSDAYDLTVSHAKTKNAPLIVRRLPEPKIIVEEWTVEVDKPKFKPKKDAKAVETVLELNDQIRGKLEKLDNGSITVDVPGVG 542
gi | 115477547 | ref | NP_001062369.1 | ... GVINNSVLGYFGRIRIYLYLTKVGISPDKLRFROHMANEMAHYADCWDAEILLTSYGWIECVGCADRSDAYDLTVSHAKTKNAPLIVRRLPEPKIIVEEWTVEVDKPKFKPKKDAKAVETVLELNDQIRGKLEKLDNGSITVDVPGVG 510
gi | 124808643 | ref | XP_001348371.1 | ... NLIANBALAYFLARITLFLKCGINKDGRHOHLKTEMAHYADCWDAEILLTSYGWIECVGCADRSDAYDLTVSHAKTKNAPLIVRRLPEPKIIVEEWTVEVDKPKFKPKKDAKAVETVLELNDQIRGKLEKLDNGSITVDVPGVG 686



gi | 145608852 | ref | XP_369806.2 | ... ---DKGVQVEKDLVSIITWTKRNRREFIPNVIEPSFGIGRILYCLLEHNYVTRASDGGDEARGVLSFTTPVAVPQKVLVPLSRHDDVFPVQVQIKISQKLRVSVSSRVDDSSAIGRRYARNDELGPFGLITDFDQVTK---DGTITLRLD 617
gi | 32403756 | ref | XP_322491.1 | ... ---DKGVQVEKDLVLEWKKHINIREFIPNVIEPSFGIGRILYCLLEHNYVTRASDGGDEARGVLSFTTPVAVPQKVLVPLSRHDDVFPVQVQIKISQKLRVSVSSRVDDSSAIGRRYARNDELGPFGLITDFDQVTK---DGTITLRLD 613
gi | 19114847 | ref | NP_593935.1 | ... ---H---TVESDLVLEKRRKHEHRTYTPNVIEPSFGLGRILYVLMHEAYVTRP---EDVNRGVLSPFPAIAPKALVPLSRNAEFAPVVKLSAKLRNLGINSKIDDSNANIGRRYARNDELGPFGLITDFDQVTK---NETITLRLD 609
gi | 6319597 | ref | NP_009679.1 | ... ---G-EVELDDKLVKIEQRTVEHREVPVSVIEPSFGIGRILYVLFESHSFWRNP---EDNARVLSFPPVAVPQKVLVPLSRHDDVFPVQVQIKISQKLRVSVSSRVDDSSAIGRRYARNDELGPFGLITDFDQVTK---DGTITLRLD 618
gi | 50303953 | ref | NP_451926.1 | ... ---G-DVEVDKMSIEKVTNHEHREVPVSVIEPSFGIGRILYVLFESHSFWRNP---EDNARVLSFPPVAVPQKVLVPLSRHDDVFPVQVQIKISQKLRVSVSSRVDDSSAIGRRYARNDELGPFGLITDFDQVTK---DGTITLRLD 618
gi | 45187500 | ref | NP_983723.1 | ... ---G-DIELDKSFIIEHRTYTPNVIEPSFGIGRILYVLFESHSFWRNP---EDNARVLSFPPVAVPQKVLVPLSRHDDVFPVQVQIKISQKLRVSVSSRVDDSSAIGRRYARNDELGPFGLITDFDQVTK---DGTITLRLD 615
gi | 24664462 | ref | NP_730022.1 | ... D---GQSHDLGKDIISVKHSTKIVHVEEIPVSVIEPSFGIGRILYVLFESHSFWRNP---EDNARVLSFPPVAVPQKVLVPLSRHDDVFPVQVQIKISQKLRVSVSSRVDDSSAIGRRYARNDELGPFGLITDFDQVTK---DGTITLRLD 720
gi | 158293345 | ref | XP_557743.2 | ... ---GTDVKLNDLILAVKTTSKIVHVEEIPVSVIEPSFGIGRILYVLFESHSFWRNP---EDNARVLSFPPVAVPQKVLVPLSRHDDVFPVQVQIKISQKLRVSVSSRVDDSSAIGRRYARNDELGPFGLITDFDQVTK---DGTITLRLD 657
gi | 17554996 | ref | NP_498093.1 | ... ---GNYVALPEHLNKKYTKKIVHVEEIPVSVIEPSFGIGRILYVLFESHSFWRNP---EDNARVLSFPPVAVPQKVLVPLSRHDDVFPVQVQIKISQKLRVSVSSRVDDSSAIGRRYARNDELGPFGLITDFDQVTK---DGTITLRLD 698
gi | 93102417 | ref | NP_851009.2 | ... ---GKTFQLKDMVSKRQKILHVEEVPVSVIEPSFGLGRIMYVLFESHSFWRNP---EGDEQRFFSFPVAVPQKVLVPLSRHDDVFPVQVQIKISQKLRVSVSSRVDDSSAIGRRYARNDELGPFGLITDFDQVTK---DGTITLRLD 678
gi | 109472087 | ref | XP_216152.4 | ... ---GKTFQLKDMVSKRQKILHVEEVPVSVIEPSFGLGRIMYVLFESHSFWRNP---EGDEQRFFSFPVAVPQKVLVPLSRHDDVFPVQVQIKISQKLRVSVSSRVDDSSAIGRRYARNDELGPFGLITDFDQVTK---DGTITLRLD 738
gi | 116805340 | ref | NP_002038.2 | ... ---GKTFQLKDMVSKRQKILHVEEVPVSVIEPSFGLGRIMYVLFESHSFWRNP---EGDEQRFFSFPVAVPQKVLVPLSRHDDVFPVQVQIKISQKLRVSVSSRVDDSSAIGRRYARNDELGPFGLITDFDQVTK---DGTITLRLD 688
gi | 114612672 | ref | XP_519025.2 | ... ---GKTFQLKDMVSKRQKILHVEEVPVSVIEPSFGLGRIMYVLFESHSFWRNP---EGDEQRFFSFPVAVPQKVLVPLSRHDDVFPVQVQIKISQKLRVSVSSRVDDSSAIGRRYARNDELGPFGLITDFDQVTK---DGTITLRLD 690
gi | 73976563 | ref | XP_532502.2 | ... ---GKTFQLKDMVSKRQKILHVEEVPVSVIEPSFGLGRIMYVLFESHSFWRNP---EGDEQRFFSFPVAVPQKVLVPLSRHDDVFPVQVQIKISQKLRVSVSSRVDDSSAIGRRYARNDELGPFGLITDFDQVTK---DGTITLRLD 688
gi | 147902079 | ref | NP_001091035.1 | ... ---GKTFQLKDMVSKRQKILHVEEVPVSVIEPSFGLGRIMYVLFESHSFWRNP---EGDEQRFFSFPVAVPQKVLVPLSRHDDVFPVQVQIKISQKLRVSVSSRVDDSSAIGRRYARNDELGPFGLITDFDQVTK---DGTITLRLD 688
gi | 71895709 | ref | NP_001026681.1 | ... ---GKTFQLKDMVSKRQKILHVEEVPVSVIEPSFGLGRIMYVLFESHSFWRNP---EGDEQRFFSFPVAVPQKVLVPLSRHDDVFPVQVQIKISQKLRVSVSSRVDDSSAIGRRYARNDELGPFGLITDFDQVTK---DGTITLRLD 634
gi | 189536638 | ref | XP_692410.3 | ... ---GKTFQLKDMVSKRQKILHVEEVPVSVIEPSFGLGRIMYVLFESHSFWRNP---EGDEQRFFSFPVAVPQKVLVPLSRHDDVFPVQVQIKISQKLRVSVSSRVDDSSAIGRRYARNDELGPFGLITDFDQVTK---DGTITLRLD 713
gi | 18397278 | ref | NP_564337.1 | ... TL---KKSVMNKKMVISKKEKKEHQRFVSVIEPSFGIGRILYCLLEHNYVTRASDGGDEARGVLSFTTPVAVPQKVLVPLSRHDDVFPVQVQIKISQKLRVSVSSRVDDSSAIGRRYARNDELGPFGLITDFDQVTK---DGTITLRLD 684
gi | 115477547 | ref | NP_001062369.1 | ... TL---GKDVITKDMVISKKEKKEHQRFVSVIEPSFGIGRILYCLLEHNYVTRASDGGDEARGVLSFTTPVAVPQKVLVPLSRHDDVFPVQVQIKISQKLRVSVSSRVDDSSAIGRRYARNDELGPFGLITDFDQVTK---DGTITLRLD 652
gi | 124808643 | ref | XP_001348371.1 | ... TL---GKDVITKDMVISKKEKKEHQRFVSVIEPSFGIGRILYCLLEHNYVTRASDGGDEARGVLSFTTPVAVPQKVLVPLSRHDDVFPVQVQIKISQKLRVSVSSRVDDSSAIGRRYARNDELGPFGLITDFDQVTK---DGTITLRLD 834



gi | 145608852 | ref | XP_369806.2 | RDITVQVRADQDKIVEAIQELVSGNKVWKDVQDELPAFEGQIEIVASR----- 665
gi | 32403756 | ref | XP_322491.1 | RDSTROVRAEEKIVDAIKALVEGSKTWQDVSELPFEGQLEIRPAEN----- 663
gi | 19114847 | ref | NP_593935.1 | RDSTKOVVRSQDEVIAALVSMVEGKSSPEDALAKFGEFKSTQE----- 652
gi | 6319597 | ref | NP_009679.1 | RDSTKOVVRSVENVIKAIKRDITVNGASWEEGTDLTPFIQAEEAETD----- 667
gi | 50303953 | ref | XP_451926.1 | RDSTKOVVRSVADVKAIREITVQGVSWEEGTDKDLAPFNSQAESE----- 663
gi | 45187500 | ref | NP_983723.1 | RDSTROVRSVTDIIRAIRDITVNGVTWEEGTSKSLTPFVSSSE----- 658
gi | 24664462 | ref | NP_730022.1 | RNTMKOVVRLGLEEVVGVVVDLSTARITWESVTEQVPLFEGQSEASK----- 765
gi | 158293345 | ref | XP_557743.2 | RDSMKOVVRLGLEEVANVIRDLATGRVSWAEVVEQKYPREFEQSEASAK----- 703
gi | 17554996 | ref | NP_498093.1 | AETMSQIRLEVSELGRLLISDLVAGRQWSDAQAKVPKFASATE----- 742
gi | 93102417 | ref | NP_851009.2 | RDSMROI RAEVSELPNVVRDLANGNITWADV EARVPLFEGQETGKKETVEE----- 729
gi | 109472087 | ref | XP_216152.4 | RDSMROI RAEVSELPVVRDLANGNITWADV EARVPLFEGQETGKKETVEE----- 789
gi | 116805340 | ref | NP_002038.2 | RDSMROI RAEVSELPVVRDLANGNITWADV EARVPLFEGQETGKKETVEE----- 739
gi | 114612672 | ref | XP_519025.2 | RDSMROI RAEVSELPVVRDLANGNITWADV EARVPLFEGQETGKKETVEE----- 739
gi | 73976563 | ref | XP_532502.2 | RDSMROI RAEVSELPVVCDLANGSITWADV EARVPVFEGQETGNRGIINLANSDDHLE----- 749
gi | 147902079 | ref | NP_001091035.1 | RDSMROI RAEVSELPVVRDLANGSITWADV EARVPVFEGQETGKKEAIEE----- 739
gi | 71895709 | ref | NP_001026681.1 | RDSMROI RAEVSELPALIRDLANGYLWADV EARVQVFEGQETGKKETVEE----- 685
gi | 189536638 | ref | XP_692410.3 | RDSMROI RAEVSELPETIIRDLANGAITWAEVSKYPIFEGQETSKKETVEE----- 764
gi | 18397278 | ref | NP_564337.1 | RDSKDQVRVTLLKKAASVSVSEGKMTWQVWATFPHSSAAADE----- 729
gi | 115477547 | ref | NP_001062369.1 | RDSKEQIRVGIDEVASVVKQLDQGSTWADV SFKYPSHIGPGDQE----- 698
gi | 124808643 | ref | XP_001348371.1 | RDSMLQIRISMHLVDIINSMLHAKKNWNEYIAQVGLFTQVLDL----- 879
.....910.....920.....930.....940.....950.....

