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                                                  *: *:  * :*:  : ::* *****:     :.  : :*.*:*:*.** *:: *:*****  ** .      . :  :                .*:***.** :** **  .  :  :  .     ::*:*****
gi|15229522|ref|NP_189023.1|      --MALLVEKTSSGREYKVKDMSQADFGRLEIELAEVEMPGLVSCVTEFGPSQPLKGARITGSLHMTIQTAVLIETLTALGAEVRWCSCN-IFSTQDHAAAAIARDS-AAVFAWKGETLQEYWWCTERALD-WGPGG--GPDLIVDDGGDA   150
gi|15236376|ref|NP_193130.1|      --MALLVEKTSSGREYKVKDMSQADFGRLEIELAEVEMPGLMACRTEFGPSQPFKGARITGSLHMTIQTAVLIETLTALGAEVRWCSCN-IFSTQDHAAAAIARDS-AAVFAWKGETLQEYWWCTERALD-WGPGG--GPDLIVDDGGDA   150
gi|115485403|ref|NP_001067845.1| CHGALPGEDLVGERSTKLKDLSQADFGRLEIELAEVEMPGLMACRAEFGPSQPFKGARISGSLHRTIQAAVLIETLTALGRRGPLVLLQHLLHAGPRRRPPSPRDS-AAVFAWKGETLEEYWWCTERCLD-WGVGA--GPDLIVDDGGDA   150
gi|6320882|ref|NP_010961.1|       --------MSAPAQNYKIADISLAAFGRKEIELAEHEMPGLMAIRKAYGDVQPLKGARIAGCLHMTIQTAVLIETLVALGAEVTWSSCN-IYSTQDHAAAAIAASG-VPVFAWKGETEEEYLWCIEQQLFAFKDNK--KLNLILDDGGDL   150
gi|45198761|ref|NP_985790.1|      --------MSIPAQNYKVADLSLAAFGRKEIELSEHEMPGLMAIRKAYGDAQPLKGARIAGCLHMTIQTAVLIETLVALGAEVTWTSCN-IYSTQDHAAAAIAASG-VPVFAWKGETEEEYLWCIEQQLFAFKDGK--KLNLILDDGGDL   150
gi|50302237|ref|XP_451052.1|      --------MSAPAHNYKVADISLAAFGRKEIELAEHEMPGLIAIREAYGAEQPLKGARIAGCLHMTIQTAVLIETLVALGAEVTWSSCN-IYSTQDHAAAAIAASG-VPVFAWKGETEEEYLWCIEQQLFAFKDDK--KLNLILDDGGDL   150
gi|39940170|ref|XP_359622.1|      --------MAAPAHKFKVADLSLAAFGRKEIELAENEMPGLMQTREKYAADQPLKGARIAGCLHMTIQTAVLIETLTALGAEVTWTSCN-IFSTQDHAAAAIAAAG-VPVFAWKGETEEEYNWCLEQQLLAFKDGK--KLNLILDDGGDL   150
gi|32416316|ref|XP_328636.1|      --------MSAPAHKFKVADLSLAAFGRKEIELAENEMPGLMATRKKYAADQPLKGARIAGCLHMTIQTAVLIETLTALGAEVTWSSCN-IFSTQDHAAAAIAAAG-VPVFAWKGETEEEYQWCLEQQLIAFKDNK--KLNLILDDGGDL   150
gi|19112372|ref|NP_595580.1|      ----------MATQNYKVADISLAAFGRKELEIAENEMPGLIAVREKYAKSQPLKGARIAGCLHMTIQTAVLIETLVALGAEVTWSSCN-IYSTQDHAAAAIAATG-VPVFAWKGETEEEYLWCIEQQLKSFPSGK--PLNMILDDGGDL   150
gi|24642172|ref|NP_511164.2|      ----------MSKPSYKVADISLAEWGRKAIIIAENEMPGLMACRKKYGPSKPLKGARITGCLHMTVQTAVLIETLVELGAQVQWSSCN-IFSTQDNAAAAIAATG-VPVYAWKGETDEEYMWCIEQTLV-FPDGQ--PLNMILDDGGDL   150
gi|58381447|ref|XP_311257.2|      ----------MAKPAYKVADISLAEFGRKEIVLAENEMPGLMACRQKYGPLKILKGARIAGCLHMTIQTAVLIETLIELGAEVQWSSCN-IFSTQDHAAAAMAKAG-VPVYAWKGETDEEYMWCIRQTLI-FPDGK--PLNMILDDGGDL   150
gi|9951915|ref|NP_000678.1|       ---------MSDKLPYKVADIGLAAWGRKALDIAENEMPGLMRMRERYSASKPLKGARIAGCLHMTVETAVLIETLVTLGAEVQWSSCN-IFSTQDHAAAAIAKAG-IPVYAWKGETDEEYLWCIEQTLY-FKDG---PLNMILDDGGDL   150
gi|114681558|ref|XP_514594.2|     ---------MSDKLPYKVADIGLAAWGRKALDIAENEMPGLMRMRERYSASKPLKGARIAGCLHMTVETAVLIETLVTLGAEVQWSSCN-IFSTQDHAAAAIAKAG-IPVYAWKGETDEEYLWCIEQTLY-FKDG---PLNMILDDGGDL   150
gi|61098092|ref|NP_057870.2|      ---------MSDKLPYKVADIGLAAWGRKALDIAENEMPGLMRMREMYSASKPLKGARIAGCLHMTVETAVLIETLVALGAEVRWSSCN-IFSTQDHAAAAIAKAG-IPVFAWKGETDEEYLWCIEQTLH-FKDG---PLNMILDDGGDL   150
gi|8392878|ref|NP_058897.1|       ---------MADKLPYKVADIGLAAWGRKALDIAENEMPGLMRMREMYSASKPLKGARIAGCLHMTVETAVLIETLVALGAEVRWSSCN-IFSTQDHAAAAIAKAG-IPVFAWKGETDEEYLWCIEQTLH-FKDG---PLNMILDDGGDL   150
gi|77735583|ref|NP_001029487.1|   ---------MSDKLPYKVADISLAAWGRKALDLAENEMPGLMHMREMYSASKPLKGARIAGCLHMTVETAVLIETLVALGAEVRWSSCN-IFSTQDHAAAAIAKAG-IPVYAWKGETDEEYLWCIEQTLY-FKDG---PLNMILDDGGDL   150
gi|73991635|ref|XP_534388.2|      ---------MSDKLPYKVADISLASWGRKALDIAENEMPGLMRMREMYSASKPLKGARIAGCLHMTVETAVLIETLVALGAEVRPSVFS-VGGTSGEGQVLMCCPTPPPVYAWKGETDEEYLWCIEQTLY-FKDG---PLNMILDDGGDL   150
gi|118100510|ref|XP_417331.2|     ---------MSDRLPYKVADISLADWGRKAIEIAENEMPGLMKMREMYGASKPLKGARIAGCLHMTVQTAVLIETLIKLGAEVQWSSCN-IFSTQDHAAAAIAKAG-IPVFAWKGETDEEYLWCIEQTLY-FKDGQ--PLNMILDDGGDL   150
gi|40363541|ref|NP_954688.1|      ---------MSEKLPFKVADISLAEWGRKAIEIAENEMPGLMKMRELYGQSKPLKGARIAGCLHMTLQTAVLIETLTALGAEVQWSSCN-IFSTQDHAAAAIAKTG-VPVYAWKGETDEEYVWCIEQTIY-FKDGQ--PLNMILDDGGDL   150
gi|17506425|ref|NP_491955.1|      --------MAQSKPAYKVADIKLADFGRKEIILAENEMPGLMAMRSKYGPSQPLKGARIAGCLHMTIQTAVLIETLTALGAEVQWSSCN-IFSTQDHAAAAIAQTG-VPVYAWKGETDEEYEWCIEQTIV-FKDGQ--PLNMILDDGGDL   150
gi|124506339|ref|XP_001351767.1| ----------MVENKSKVKDISLAPFGKMQMEISENEMPGLMRIREEYGKDQPLKNAKITGCLHMTVECALLIETLQKLGAQIRWCSCN-IYSTADYAAAAVSTLENVTVFAWKNETLEEYWWCVESALT-WGDGDDNGPDMIVDDGGDA   150
                                  1.......10........20........30........40........50........60........70........80........90........100.......110.......120.......130.......140.......150
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gi|15229522|ref|NP_189023.1|      TLLIHEGVKAEEIFAKNGTFPDPTSTDNPEFQIVLSIIKDGLQVDPKKYHKMKERLVGVSEETTTGVKRLYQMQETGALLFPAINVNDSVTKSKFDNLYGCRHSLPDGLMRATDVMIAGKVAVICGYGDVGKGCAAAMKTAGARVIVTEI   300
gi|15236376|ref|NP_193130.1|      TLLIHEGVKAEEIFEKTGQVPDPTSTDNPEFQIVLSIIKEGLQVDPKKYHKMKERLVGVSEETTTGVKRLYQMQQNGTLLFPAINVNDSVTKSKFDNLYGCRHSLPDGLMRATDVMIAGKVAVICGYGDVGKGCAAAMKTAGARVIVTEI   300
gi|115485403|ref|NP_001067845.1| TLLIHEGVKAEEEFEKSGKVPDPESTDNAEFKIVLTIIRDGLKSDPSKYRKMKERLVGVSEETTTGVKRLYQMQETGALLFPAINVNDSVTKSKFDNLYGCRHSLPDGLMRATDVMIAGKVAVVCGYGDVGKGCAAALKQAGARVIVTEI   300
gi|6320882|ref|NP_010961.1|       TTLVHE----------------------------------------KHPEMLEDCFGLSEETTTGVHHLYRMVKEGKLKVPAINVNDSVTKSKFDNLYGCRESLVDGIKRATDVMLAGKVAVVAGYGDVGKGCAAALRGMGARVLVTEI   300
gi|45198761|ref|NP_985790.1|      TTLVHE----------------------------------------KYPEMLDDCFGVSEETTTGVHHLYRMLKEGKLKVPAINVNDSVTKSKFDNLYGCRESLVDGLKRATDVMLAGKVAVVAGYGDVGKGCAAALRGMGARVIVTEI   300
gi|50302237|ref|XP_451052.1|      TSLVHD----------------------------------------KYPDMLMDCFGLSEETTTGVHHLYRMVKENKLKVPAINVNDSVTKSKFDNLYGCRESLIDGIKRATDVMLAGKVAVVAGYGDVGKGCAAALRGFGARVIVTEI   300
gi|39940170|ref|XP_359622.1|      THLVHD----------------------------------------KYPEMLADCYGVSEETTTGVHHLYKMLKEGKLLVPAINVNDSVTKSKFDNLYGCRESLVDGIKRATDVMIAGKIAVVAGYGDVGKGCAMALHGMGARVIVTEI   300
gi|32416316|ref|XP_328636.1|      THLVHT----------------------------------------KYPEMLEDCFGVSEETTTGVHHLYRMLKEGKLLVPAINVNDSVTKSKFDNLYGCRESLVDGIKRATDVMIAGKIAVVAGFGDVGKGCAMALSGMGARVIVTEV   300
gi|19112372|ref|NP_595580.1|      TALVHE----------------------------------------RHPELLVDIRGISEETTTGVHNLYKMFKENKLKVPAINVNDSVTKSKFDNLFGCKESLVDGIKRATDVMIAGKVAVVAGFGDVGKGCSTSLRSQGARVIVTEV   300
gi|24642172|ref|NP_511164.2|      TNLVHE----------------------------------------KFPQYLKNIKGLSEETTTGVHNLYKMFKEGRLGVPAINVNDSVTKSKFDNLYGCRESLIDGIKRATDVMIAGKVCCVAGYGDVGKGCAQALKGFGGRVIVTEV   300
gi|58381447|ref|XP_311257.2|      TNLVHA----------------------------------------EHPELLKEIRGLSEETTTGVHNLYKMFREGRLGMPAINVNDSVTKSKFDNLYGCRESLLDGIKRATDVMIAGKVCVVAGYGDVGKGCAQALRGSGGRVLITEI   300
gi|9951915|ref|NP_000678.1|       TNLIHT----------------------------------------KYPQLLPGIRGISEETTTGVHNLYKMMANGILKVPAINVNDSVTKSKFDNLYGCRESLIDGIKRATDVMIAGKVAVVAGYGDVGKGCAQALRGFGARVIITEI   300
gi|114681558|ref|XP_514594.2|     TNLIHT----------------------------------------KYPQLLPGIRGISEETTTGVHNLYKMMANGILKVPAINVNDSVTKSKFDNLYGCRESLIDGIKRATDVMIAGKVAVVAGYGDVGKGCAQALRGFGARVIITEI   300
gi|61098092|ref|NP_057870.2|      TNLIHT----------------------------------------KYPQLLSGIRGISEETTTGVHNLYNMMSNGILKVPAINVNDSVTKSKFDNLYGCRESLIDGIKRATDVMIAGKVAVVAGYGDVGKGCAQALRGFGARVIITEI   300
gi|8392878|ref|NP_058897.1|       TNLIHT----------------------------------------KHPQLLSGIRGISEETTTGVHNLYKMMANGILKVPAINVNDSVTKSKFDNLYGCRESLIDGIKRATDVMIAGKVAVVAGYGDVGKGCAQALRGFGARVIITEI   300
gi|77735583|ref|NP_001029487.1|   TNLIHT----------------------------------------KYPQLLSGIRGISEETTTGVHNLYKMMAKGILKVPAINVNDSVTKSKFDNLYGCRESLIDGIKRATDVMIAGKVAVVAGYGDVGKGCAQALRGFGARVIITEI   300
gi|73991635|ref|XP_534388.2|      TNLIHT----------------------------------------KYPQLLSGIRGISEETTTGVHNLYKMMANGKLKVPAINVNDSVTKSKFDNLYGCRESLIDGIKRATDVMIAGKVAVVAGYGDVGKGCAQALRGFGARVIITEI   300
gi|118100510|ref|XP_417331.2|     TNLVHT----------------------------------------KYPQLLKGIRGISEETTTGVHNLYKMKANGTLKVPAINVNDSVTKSKFDNLYGCRESLIDGIKRATDVMIAGKVAVVAGYGDVGKGCAQALRSFGARVIITEI   300
gi|40363541|ref|NP_954688.1|      TNLVHQ----------------------------------------KYPKLLAGIKGISEETTTGVHNLYKMLKSGELKVPAINVNDSVTKSKFDNLYGCRESLIDGIKRATDVMIAGKVAVVAGYGDVGKGCVQALRGFGARVIVTEI   300
gi|17506425|ref|NP_491955.1|      TNLVHA----------------------------------------KYPQYLAGIRGLSEETTTGVHNLAKMLAKGDLKVPAINVNDSVTKSKFDNLYGIRESLPDGIKRATDVMLAGKVAVVAGYGDVGKGSAASLKAFGSRVIVTEI   300
gi|124506339|ref|XP_001351767.1| TLLVHKGVEYEKLYEEKNILPDPEKAKNEEERCFLTLLKNSILKNPKKWTNIAKKIIGVSEETTTGVLRLKKMDKQNELLFTAINVNDAVTKQKYDNVYGCRHSLPDGLMRATDFLISGKIVVICGYGDVGKGCASSMKGLGARVYITEI   300
                                  .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
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gi|15229522|ref|NP_189023.1|     DPICALQALMEGLQVLTLEDVVSEADIFCTTTGNKDIIMVDHMRKMKNNAIVCNIGHFDNEIDMLGLETYPGVKRITIKPQTDRWVFPDTNSGIIVLAEGRLMNLGCATGHPSFVMSCSFTNQVIAQLELWNEK------------SSG   450
gi|15236376|ref|NP_193130.1|     DPICALQALMEGLQVLTLEDVVSEADIFVTTTGNKDIIMVDHMRKMKNNAIVCNIGHFDNEIDMLGLETYPGVKRITIKPQTDRWVFPETKAGIIVLAEGRLMNLGCATGHPSFVMSCSFTNQVIAQLELWNEK------------ASG   450
gi|115485403|ref|NP_001067845.1| DPICALQALMEGLQVLTLEDVVSEADIFVTTTGNKDIIMVDHMRKMKNNAIVCNIGHFDNEIDMLGLETYPGVKRITIKPQTDRWVFPETNTGIIVLAEGRLMNLGCATGHPSFVMSCSFTNQVIAQLELWKEK------------STG   450
gi|6320882|ref|NP_010961.1|      DPINALQAAMEGYQVVTMEDASHIGQVFVTTTGCRDIINGEHFINMPEDAIVCNIGHFDIEIDVAWLKAN-AKECINIKPQVDRYLLSSGRH-VILLANGRLVNLGCATGHSSFVMSCSFSNQVLAQIALFKSNDKSFREKHIE-FQKTG   450
gi|45198761|ref|NP_985790.1|     DPINALQAAMEGYQVTTMDQCASYGQVFVTTTGCRDIIKKEHFLAMPEDAIVCNIGHFDIEIDVAWLKAN-AVEAVNIKPQVDRYLLSSGRH-VILLADGRLVNLGCATGHSSFVMSCSFSNQVLAQIALFKANDEAFRQKYIE-FQKTG   450
gi|50302237|ref|XP_451052.1|     DPINALQAAMEGYQVIPMEEAVSSGQVFVTTTGCRDIITKEHFLQMPEDAIVCNIGHFDIEIDVAWLKAN-ATEVINIKPQVDRYLLPSGKH-VILLADGRLVNLGCATGHSSFVMSCSFSNQVLAQIALFKAQDKAFREKYIE-FQKTG   450
gi|39940170|ref|XP_359622.1|     DPINALQAAMAGFQVTTMEKAASVGQIFVTTTGCRDILVGKHFEAMPNDAIVCNIGHFDIEIDVAWLKAN-AKSVQNIKPQVDRFLMANGRH-IILLAEGRLVNLGCATGHSSFVMSCSFTNQVLAQIMLYKNNDAAFGQKYVE-FAKSG   450
gi|32416316|ref|XP_328636.1|     DPINALQAAMAGYQVTTMEKAAPLGQIFVTTTGCRDILVGKHFEVMPNDAIVCNIGHFDVEIDVAWLKAN-AASVQNIKPQVDRFLMKNGRH-IILLAEGRLVNLGCATGHSSFVMSCSFTNQVLAQIMLYKANDEAFSNKYVE-FGKSG   450
gi|19112372|ref|NP_595580.1|     DPINALQAAMDGFEVTTMEEAVKEGQIFVTTTGCRDIIRGEHFNEMKEDSIVCNIGHFDVEIDVAWLKAN-AKDVVNIKPQVDRYELKNGRH-IILLADGRLVNLGCATGHPSFVMSCSFTNQVLAQIALWTDNTS--------------   450
gi|24642172|ref|NP_511164.2|     DPINALQAAMEGYEVTTMEEASKEASIFVTTTGCRDIITSVHLQQMPDDAIVCNIGHFDIEIDVDWLNAN-AKEKVNVKPQVDRYTMQSGKH-IILLAEGRLVNLGCAHGHPSFVMSNSFTNQVLAQIELWT--------------KSD   450
gi|58381447|ref|XP_311257.2|     DPINALQAAMEGYEVTTMEEASKEAQIFVTTTGCTDIIMGEHFLNMKDDSIVCNIGHFDCEINVTWLQEN-AVEKVNIKPQVDRYRLANGNH-IILLAEGRLVNLGCAMGHSSFVMSNSFTNQVLAQIELWT--------------NRE   450
gi|9951915|ref|NP_000678.1|      DPINALQAAMEGYEVTTMDEACQEGNIFVTTTGCIDIILGRHFEQMKDDAIVCNIGHFDVEIDVKWLNEN-AVEKVNIKPQVDRYRLKNGRR-IILLAEGRLVNLGCAMGHPSFVMSNSFTNQVMAQIELWT--------------HPD   450
gi|114681558|ref|XP_514594.2|    DPINALQAAMEGYEVTTMDEACQEGNIFVTTTGCIDIILGRHFEQMKDDAIVCNIGHFDVEIDVKWLNEN-AVEKVNIKPQVDRYRLKNGRR-IILLAEGRLVNLGCAMGHPSFVMSNSFTNQVMAQIELWT--------------HPD   450
gi|61098092|ref|NP_057870.2|     DPINALQAAMEGYEVTTMDEACKEGNIFVTTTGCVDIILGRHFEQMKDDAIVCNIGHFDVEIDVKWLNEN-AVEKVNIKPQVDRYWLKNGRR-IILLAEGRLVNLGCAMGHPSFVMSNSFTNQVMAQIELWT--------------HPD   450
gi|8392878|ref|NP_058897.1|      DPINALQAAMEGYEVTTMDEACKEGNIFVTTTGCVDIILGRHFEQMKDDAIVCNIGHFDVEIDVKWLNEN-AVEKVNIKPQVDRYLLKNGHR-IILLAEGRLVNLGCAMGHPSFVMSNSFTNQVMAQIELWT--------------HPD   450
gi|77735583|ref|NP_001029487.1|  DPINALQAAMEGYEVTTMDEACQEGNIFVTTTGCTDIILGQHFEQMKDDAIVCNIGHFDVEIDVKWLNEN-AVEKVNIKPQVDRYLLKNGRR-IILLAEGRLVNLGCAMGHPSFVMSNSFTNQVLAQIELWT--------------HPD   450
gi|73991635|ref|XP_534388.2|     DPINALQAAMEGYEVTTMDEACQEGNIFVTTTGCVDIILGRHFEQMKDDAIVCNIGHFDVEIDVKWLNEN-AVEKVNIKPQVDRYRLKNGRR-IILLAEGRLVNLGCAMGHPSFVMSNSFTNQVLAQIELWT--------------HPD   450
gi|118100510|ref|XP_417331.2|    DPINALQAAMEGYEVTTMEEACKEGNIFVTTTGCTDIVQGRHFEQMKDDAIVCNIGHFDVEVDAKWLNQN-AVEVVNVKPQVDRYKLRNGRH-IILLAEGRLVNLGCAMGHPSFVMSNSFTNQVLAQIELWT--------------NSD   450
gi|40363541|ref|NP_954688.1|     DPINALQAAMEGYEVTTMDEACKEGNIFVTTTGCEDILLGRHFEHMKDDSIVCNIGHFDCEIDMKWLNEH-AAKKINIKPQVDRYRMKNGRH-IIVLAEGRLVNLGCAMGHPSFVMSNSFTNQVLAQIELWK--------------NNS   450
gi|17506425|ref|NP_491955.1|     DPINALQAAMEGYEVTTLEEAAPKANIIVTTTGCKDIVTGKHFELLPNDAIVCNVGHFDCEIDVKWLNTN-ATKKDTIKPQVDRYTLKNGRH-VILLAEGRLVNLGCATGHPSFVMSNSFTNQVLAQVELWT------------KFGTPQ   450
gi|124506339|ref|XP_001351767.1| DPICAIQAVMEGFNVVTLDEIVDKGDFFITCTGNVDVIKLEHLLKMKNNAVVGNIGHFDDEIQVNELFNYKGIHIENVKPQVDRITLPNGNK-IIVLARGRLLNLGCATGHPAFVMSFSFCNQTFAQLDLWQNK------------DTN   450
                                 .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450
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gi|15229522|ref|NP_189023.1|     KYEKKVYVLPKHLDEKVAALHLGKLGARLTKLTKDQSDYVSIPVEGPYKPVHYRY   505
gi|15236376|ref|NP_193130.1|     KYEKKVYVLPKHLDEKVALLHLGKLGARLTKLSKDQSDYVSIPIEGPYKPPHYRY   505
gi|115485403|ref|NP_001067845.1| KYEKKVYVLPKHLDEKVACLHLGKLGARLTKLSKSQG-----------------   505
gi|6320882|ref|NP_010961.1|      PFEVGVHVLPKILDEAVAKFHLGNLGVRLTKLSKVQSEYLGIPEEGPFKADHYRY   505
gi|45198761|ref|NP_985790.1|     PFDIGVHVLPKILDEAVAKFHLDKLGVKLTKLSSTQSEYLGIPEEGPFKADHYRY   505
gi|50302237|ref|XP_451052.1|     PFDIGVHVLPKILDEAVAKFHLDNLGVKLTKLSDVQSEYLGIPEEGPYKADHYRY   505
gi|39940170|ref|XP_359622.1|     KLEKKVYVLPKILDEEVAKLHLAHCNVELSTLTPVQAEYLSLPAEGPYKPEHYRY   505
gi|32416316|ref|XP_328636.1|     KLEKKVYVLPKILDEEVARLHLDHCNVELTQLSDVQAEYLGLATEGPYKSDHYRY   505
gi|19112372|ref|NP_595580.1|     -YPLGVHMLPKKLDEEVARLHLGKLGVKLTTLTSVQSDYLGIPVDGPYKADHYRY   505
gi|24642172|ref|NP_511164.2|     KYAVGVHVLPKILDEEVASLHLEKLGVKLTKLTEKQATYLGVSQTGPFKPDHYRY   505
gi|58381447|ref|XP_311257.2|     QYAIGVHVLPKKLDEEVAALHLDKLGVKLTKLSARQAEYLNLPAEGPYKPEHYRY   505
gi|9951915|ref|NP_000678.1|      KYPVGVHFLPKKLDEAVAEAHLGKLNVKLTKLTEKQAQYLGMSCDGPFKPDHYRY   505
gi|114681558|ref|XP_514594.2|    KYPVGVHFLPKKLDEAVAEAHLGKLNVKLTKLTEKQAQYLGMSCDGPFKPDHYRY   505
gi|61098092|ref|NP_057870.2|     KYPVGVHFLPKKLDEAVAEAHLGKLNVKLTKLTEKQAQYLGMPINGPFKPDHYRY   505
gi|8392878|ref|NP_058897.1|      KYPVGVHFLPKKLDEAVAEAHLGKLNVKLTKLTEKQAQYLGMPINGPFKPDHYRY   505
gi|77735583|ref|NP_001029487.1|  KYPVGVHFLPKKLDEAVAEAHLGKLNVKLTKLTEKQAQYLGVSREGPFKPDHYRY   505
gi|73991635|ref|XP_534388.2|     KYSVGVHFLPKKLDEAVAEAHLGKLNVKLTKLTEKQAQYLGLSRDGPFKPDHYRY   505
gi|118100510|ref|XP_417331.2|    KYSVGVHFLPKKLDEAVAAAHLDKLSVKLTKLSEKQAKYLGLSKDGPFKPDHYRY   505
gi|40363541|ref|NP_954688.1|     KYPLGVYFLPKKLDEEVAAAHLDKLGVKLTKLTEKQAKYLGLPSEGPFKPDHYRY   505
gi|17506425|ref|NP_491955.1|     EYKLGLYVLPKTLDEEVAYLHLAQLGVKLTKLSDEQASYLGVPVAGPYKPDHYRY   505
gi|124506339|ref|XP_001351767.1| KYENKVYLLPKHLDEKVALYHLKKLNASLTELDDNQCQFLGVNKSGPFKSNEYRY   505
                                 .......460.......470.......480.......490.......500.....
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