

gi | 18643383 | ref | NP_079470.1 | MRRCPCRGSLNEAEAGALPAAARMGLAEPGRRRPPGQORPPGAGAPAGRPEGGGPWARTEGSSLLHSEPERAGLGPAPGTEPQAEFWTDGQTEPAAAGLVGVEERPKQKTEPDRSSLRTHLEW--WSELETTCLWTEGTGDLGWD 148
gi | 114677357 | ref | XP_524271.2 | MRRCPCRGSLSEAEAGALPAAARMGLAEPGRRRPPGQORPPGAGAPAEERPEGGGPWARTEGSSLLHSEPERAGLGPAPGTEPQAEFWTDGQTEPAAAGLVGVEERPKQKTEPDRSSLRTHLEW--WSELETTCLWTEGTGDLGWD 148
gi | 73948314 | ref | XP_855312.1 | -----MLHLKNGR--AAGLVTEGVEAKLVTRG-----CSLHTEPERVGLGPEPG-----TDGGEPEAAAGLVGDTTERPKRTEPKSSLRICPERSHSHWSEQETAGPWTETGTDGFWTD 103
gi | 115496544 | ref | NP_001069479.1 | MRRCPCRGSLSEAEAGALPAAARMGLAEPGRRRPPGQORPPGAGGVPGRPEGGGPRAWIESSLLHSEAEERLDLEPAPCPNPGQAESCGDGHAECEAAGLVVASEKPRNKELDGSNLOTHPRRNPLVEMEMAGSW---TDGFRTD 141
gi | 31712006 | ref | NP_853624.1 | MRRCPCRGSLSEAEAGALPAAARMGLAEPGRRRPPGQORPPGAGGVPGRPEGGGPRAWIESSLLHSEAEERLDLEPAPCPNPGQAESCGDGHAECEAAGLVVASEKPRNKELDGSNLOTHPRRNPLVEMEMAGSW---TDGFRTD 146
gi | 30017415 | ref | NP_835195.1 | MRRCPCRGSLSEAEAGALPAAARMGLAEPGRRRPPGQORPPGAGGVPGRPEGGGPRAWIESSLLHSEAEERLDLEPAPCPNPGQAESCGDGHAECEAAGLVVASEKPRNKELDGSNLOTHPRRNPLVEMEMAGSW---TDGFRTD 146



gi | 18643383 | ref | NP_079470.1 | PHSRDLQFOPBEASFWTPQGVHGPWTELETHG-SQTQPERV-KSWADNLWTHQNSSSLQTHPEGACPKPEPSADGSKWELKLYTDGSRQODIEGPPWEPYTDGSKKQDTEAARKQPGTGGFQIQDIDGSWTQPSIDGSOIAPGTDCLLG 296
gi | 114677357 | ref | XP_524271.2 | PHSRDLQFOPBEASFWTPQGVHGPWTELETHG-SQTQPERV-RSWADNLWTHQNSSSLQTHPEGACPKPEPSADGSKWELKLYTDGSRQODIEGPPWEPYTDGSKKQDTEAARKQPGTGGFQIQDIDGSWTQPSIDGSOIAPGTDCLLG 296
gi | 73948314 | ref | XP_855312.1 | PHSRDLQSGSERASLWTRQGVSPWTELETHG-SQTQPERA-KIWAHNLWTHNRRNLRQPEGGRTTEPNAGG-----SWKELVTDGSGIQDIDGTEARTQVGTDFGFTQDIDGSWTQPSIDGSOIAPGTDCLLG 233
gi | 115496544 | ref | NP_001069479.1 | PHRIDLQSQPQRNLWACPGVDGPWTELEKYG-SQTQSERA-KPRADNLCTQN-RSSVTRQPEGVPLTERSDSSWKPQFTEGSRQKGTEDSWTELEHIDGSGIQDIDTEAWKQDIDGSGFPPIQDIDGLWSQPGTDPGQTEPRIDCLLG 287
gi | 31712006 | ref | NP_853624.1 | LHSRDLQSRPKRSLCTOPGFDESWELEDRSDMWQTLPERDNKPRVDNLRTHGVSKLQTHP--VCLSPESADNSGKLSADASRTPHDIDGFWIESQIDDSLKGPSQTACROPDGSDFSS-KDTEALTOPGT---DGLRDSVVLG 289
gi | 30017415 | ref | NP_835195.1 | LHRPDLQARPKRSLCTOPGFDESWELEDRSELWQTLPERD-KPVDHLRTHGDMERLQTHP--ACPEPESAGTSCCKELSDGSRTPHDIDGFWIESQIDDSLKGPSQTACROPANDGSA-QDIDGTLTOPGT---DGPVWVSVLE 289



gi | 18643383 | ref | NP_079470.1 | EP-EDGPLEEPEPGELLTHLYSHLKCSPLCVPRLLIIPETPEPEAQPVGPPSRVEGGSGGFSASSFDESEDDVAGGGGASDPEDRSGSKPWKLLKTVLKYSFFVVSFRKHY-PWVQLSGHAGNFQAGEDGRILKRFCQCEQRSLQL 444
gi | 114677357 | ref | XP_524271.2 | EP-EDGPLEEPEPGELVTHLYSHLKCSPLCVPRLLIIPETPEPEAQPVGPPSRVEGGSGGFSASSFDESEDDVAGGGGASDPEDRSGSKPWKLLKTVLKYSFFVVSFRKHY-PWVQLSGHAGNFQAGEDGRILKRFCQCEQRSLQL 444
gi | 73948314 | ref | XP_855312.1 | ESKQDGPLEEPEPGELVTHLYSHLKCSPLCVPRLLIIPETPEPEAQPVGPPSRVEGGSGGFSASSFDESEDDVAGGGGASDPEDRSGSKPWKLLKTVLKYSFFVVSFRKHY-PWVQLSGHAGNFQAGEDGRILKRFCQCEQRSLQL 382
gi | 115496544 | ref | NP_001069479.1 | EPNQDSDLSEPEHRELVTHLYSHLEGLLTPVPRLLIIPETPEPEAQPVGPPSRVEGGSGGFSASSFDESEDDVAGGGGASDPEDRSGSKPWKLLKTVLKYSFFVVSFRKHY-PWVQLSGHAGNFQAGEDGRILKRFCQCEQRSLQL 436
gi | 31712006 | ref | NP_853624.1 | ESNQNDPLDSEPEGELVTHLYSHLKCSPLCVPRLLIIPETPEPEAQPVGPPSRVEGGSGGFSASSFDESEDDVAGGGGASDPEDRSGSKPWKLLKTVLKYSFFVVSFRKHY-PWVQLSGHAGNFQAGEDGRILKRFCQCEQRSLQL 439
gi | 30017415 | ref | NP_835195.1 | KNGDDPLMEPEPRDLVNLCSHLECSLCPVPRLLIIPETPEPEAQPVGPPSRVEGGSGGFSASSFDESEDDVAGGGGASDPEDRSGSKPWKLLKTVLKYSFFVVSFRKHY-PWVQLSGHAGNFQAGEDGRILKRFCQCEQRSLQL 439



gi | 18643383 | ref | NP_079470.1 | MKDPLRPFVPAIYGMVLDGQTFNQMEDLLADFEGPSIMDCMKGSRTYLEELVKARERPRPRKDMYEKMAVDPGAPTPEEHAQAVTKPRYMWRETVSSTSTLGFRIEIKKADGTCNTNFKKIQALEQVTKVLEDFVGDHVLILK 594
gi | 114677357 | ref | XP_524271.2 | MKDPLRPFVPAIYGMVLDGQTFNQMEDLLADFEGPSIMDCMKGSRTYLEELVKARERPRPRKDMYEKMAVDPGAPTPEEHAQAVTKPRYMWRETVSSTSTLGFRIEIKKADGTCNTNFKKIQALEQVTKVLEDFVGDHVLILK 594
gi | 73948314 | ref | XP_855312.1 | MNDPLRPFVPAIYGMVLDGQTFNQMEDLLADFEGPSIMDCMKGSRTYLEELVKARERPRPRKDMYEKMAVDPGAPTPEEHAQAVTKPRYMWRETVSSTSTLGFRIEIKKADGTCNTNFKKIQALEQVTKVLEDFVGDHVLILK 532
gi | 115496544 | ref | NP_001069479.1 | MRDPLRPFVPAIYGMVLDGQTFNQMEDLLADFEGPSIMDCMKGSRTYLEELVKARERPRPRKDMYEKMAVDPGAPTPEEHAQAVTKPRYMWRETVSSTSTLGFRIEIKKADGTCNTNFKKIQALEQVTKVLEDFVGDHVLILK 586
gi | 31712006 | ref | NP_853624.1 | MGDPLRPFVPAIYGMVLDGQTFNQMEDLLADFEGPSIMDCMKGSRTYLEELVKARERPRPRKDMYEKMAVDPGAPTPEEHAQAVTKPRYMWRETVSSTSTLGFRIEIKKADGTCNTNFKKIQALEQVTKVLEDFVGDHVLILK 589
gi | 30017415 | ref | NP_835195.1 | MGDPLRPFVPAIYGMVLDGQTFNQMEDLLADFEGPSIMDCMKGSRTYLEELVKARERPRPRKDMYEKMAVDPGAPTPEEHAQAVTKPRYMWRETVSSTSTLGFRIEIKKADGTCNTNFKKIQALEQVTKVLEDFVGDHVLILK 589



gi | 18643383 | ref | NP_079470.1 | VVARLEELREALEISPFKTHEVVGSSLLFVHDHTGLAKVWMIIDFGKTVLDPHQMLSHRLLPWAEGNREDGYLWGLDNMLICLLGGLAQS 683
gi | 114677357 | ref | XP_524271.2 | VVARLEELREALEISPFKTHEVVGSSLLFVHDHTGLAKVWMIIDFGKTVLDPHQMLSHRLLPWAEGNREDGYLWGLDNMLICLLGGLAQS 683
gi | 73948314 | ref | XP_855312.1 | VVARLEELREALEISPFKTHEVVGSSLLFVHDHTGLAKVWMIIDFGKTVLDPHQMLSHRLLPWAEGNREDGYLWGLDNMLICLLGGLAQS 621
gi | 115496544 | ref | NP_001069479.1 | VVARLEELREALEISPFKTHEVVGSSLLFVHDHTGLAKVWMIIDFGKTVLDPHQMLSHRLLPWAEGNREDGYLWGLDNMLICLLGGLAQS 675
gi | 31712006 | ref | NP_853624.1 | VVARLEELREALEISPFKTHEVVGSSLLFVHDHTGLAKVWMIIDFGKTVLDPHQMLSHRLLPWAEGNREDGYLWGLDNMLICLLGGLAQS 678
gi | 30017415 | ref | NP_835195.1 | VVARLEELREALEISPFKTHEVVGSSLLFVHDHTGLAKVWMIIDFGKTVLDPHQMLSHRLLPWAEGNREDGYLWGLDNMLICLLGGLAQS 678

