

gi|42544119|ref|NP\_059982.2| MVRGR---ISRLSVRVDVRFPTSLGGHGS DAMHTDPDYSAAYVVLETDAEDGKIGCGITFTLGKGT EKVVCVAVNALAHVHLNKDLKDIVGDFRFGFYROLTSDGQLRWIGPEKGVVHLAAVLA AVWDLWAKQEGKPVWVKLLVDM DPTLTV 150  
gi|114672465|ref|XP\_001149584.1| MVRGR---ISRLSVRVDVRFPTSLGGHGS DAMHTDPDYSAAYVVLETDAEDGKIGCGITFTLGKGT EKVVCVAVNALAHVHLNKDLKDIVGDFRFGFYROLTSDGQLRWIGPEKGVVHLAAVLA AVWDLWAKQEGKPVWVKLLVDM DPTLTV 150  
gi|73961860|ref|XP\_848625.1| MVRGR---ICSLLVSDVRFPTSLGGHGS DAMHTDPDYSAAYVVLETDAEDGKIGGYGTFITLGGGT EKVVCVAVNALAHVHLNKDLSDIVGDFRFGFYROLTSDGQLRWIGPEKGVVHLAAAILNA VWDLWAKQEGKPLWVKLLVMD PRTLL 150  
gi|114052721|ref|NP\_001040015.1| MVHGR---VSRLSVHVDVRFPTSLGGHGS DAMHTDPDYSAAYVVLETDAEDGKIGGYGTFITLGGGT EKVVCVAVNALA PHVNLKDLGEIVGDFRFGFYROLTSDGQLRWIGPEKGVVHLAAAVLN AVWDLWAKQEGKPLWVKLLVMD PRTLV 150  
gi|217272853|ref|NP\_001070210.2| MLAIK---IINVSVDVRFPTSLGQHGSDAMHTDPDYSAAYVVLETDAKAE-LKGYGLTFTVGRGT EIVVCVAVKALSTLVVGKTLLEIIISDFRFGFYRLSSDGQMRWIGPEKGVVHLATAAVLN AVWDLWAKVERKPLWVKLLVMD PAKLI 150  
gi|158285681|ref|XP\_001687931.1| MGKDRCLNII TLQAKDIRWPTSLGAHGSDAMHTDPDYSCVYVVIAT--ABGVTVGYGMTFTLGRGT DIVLLAVRAMKRRLVEGRTTTSIFERFGQFWRRLTSDQLRWIGPEKGVVHLAAAIINALWDLWGRIRNVVWQLLAEMPEEELV 150  
gi|145613870|ref|XP\_363374.2| MAAQE--IIITGWITRDVRFPTSLDKHGSDAMNAAGDYSSAACYILET-----DSEFGSGHGMT-----NRHLVNDV SOLRWIGPEKGVVHLALGAVVNALWDLWAKTLGKPVVRIVAEMTEPEEFV 150  
gi|164424530|ref|XP\_960329.2| MSDQE--IIITGWITRDVRFPTSLDKHGSDAMNAAGDYSSAACYILET--DSKYTGHGMTFTIGRGNDIVCSAINVHADRIIRGRTLSLNVANWQTVRHLVNDV SOLRWIGPEKGVVHLALGAVVNALWDLWAKVLGKPVVRISEMAPEEFV 150  
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi|42544119|ref|NP\_059982.2| SCIDFRYITDVLTEEDALEILQKGG I GKKEREKQMLAQ-GYPAYTTS CAWLGYSDDTLKQLCAALDKDGTFRFKVVKV GADLDDMRRCQIIRDMI GPE--KILMMDANQRWDVPEAVEWMSKLA FFKPLWIEEPTSPDDILGHATIISKAL 300  
gi|114672465|ref|XP\_001149584.1| SCIDFRYITDVLTEEDALEILQKGG I GKKEREKQMLAQ-GYPAYTTS CAWLGYSDDTLKQLCAALDKDGTFRFKVVKV GADLDDMRRCQIIRDMI GPE--KILMMDANQRWDVPEAVEWMSKLA FFKPLWIEEPTSPDDILGHATIISKAL 300  
gi|73961860|ref|XP\_848625.1| SCIDFRYITDVLTEEEAYEILQKGG I VGKKEREGQMLMH-GYPAYTTS CAWLGYSDDTLKQLCEALKGAWTRFKVKV GADLDDVRRCLIRNMI GPE--KILMMDANQRWDVPEAVKWSKLA FFKPLWIEEPTSPDDILGHATIISKAL 300  
gi|114052721|ref|NP\_001040015.1| SCIDFRYITDVLTEEEACEILRDS V GKKEREEQMLAH-GYPAYTTS CAWLGYSDDTLKQLCAALDKDGTFRFKVVKV GADLDDIRRCQLIRNMI GPE--KILMMDANQRWDVPEAVWMTKLA FFKPLWIEEPTSPDDILGHATIISKAL 300  
gi|217272853|ref|NP\_001070210.2| SCIDFRYITDALTEQEALDILVKGKKDKRSEREEQMLKE-GYPAYTTS CAWLGYTDQLLQALCNEALAAQGWTKFKVVKV GADLDDIRRCQLIRKLIGPN--NTLMIDANQRWDVNEAITWVTKLA FFKPLWIEEPTCPDDILGHATIISKAL 300  
gi|158285681|ref|XP\_001687931.1| STIDFRYITDVAITPEEAIALMLKETE GGGADRICKDAENSRAVPA YTTTSAGNLG YGEEKMRALLEE TLAKGYKHFHLKVGGSIEQDRRLGIARDVIGHDRGN VLMVDANQVNSVPEAIEYMKALADF KPWFI EPTSPDDVLGHKAVREAL 300  
gi|145613870|ref|XP\_363374.2| RCIDFRYITDAITPEEAEMMLKETEKTKT ERICKDAENRAVPA YTTTSAGNLG YGEDKMRLLRE IMEKGYKHFHLKVGGSIEQDRRLGIAREVIGYDKGN VLMVDANQVNSVPEAIEYMKELKEFKPWFI EPTSPDDILGHKAVREAL 300  
gi|164424530|ref|XP\_960329.2| RCIDFRYITDAITPEEAEMMLKETEKTKT ERICKDAENRAVPA YTTTSAGNLG YGEDKMRLLRE IMEKGYKHFHLKVGGSIEQDRRLGIAREVIGYDKGN VLMVDANQVNSVPEAIEYMKELKEFKPWFI EPTSPDDILGHKAVREAL 300  
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi|42544119|ref|NP\_059982.2| VPLGIGIATGEQCHNRVIFKQLLQAKALQFLQIDSCR LGSVNEENLSVLLMAKKFEIPVCPHAGGVGLCEL VQHLIIFDYISVSASLENRVCEYVDH LHEHFKYPMVIRASVYMPKDPGYS TEMKEESVKKHQVY PDGE--VWKLLPAG E 450  
gi|114672465|ref|XP\_001149584.1| VPLGIGIATGEQCHNRVIFKQLLQAKALQFLQIDSCR LGSVNEENLSVLLMAKKFEIPVCPHAGGVGLCEL VQHLIIFDYISVSASLENRVCEYVDH LHEHFKYPMVIRASVYMPKDPGYS TEMKEESVKKHQVY PDGE--VWKLLPAG E 450  
gi|73961860|ref|XP\_848625.1| AFLGIGVATGEQCHNRVIFKQLLQAKALQFLQIDSCR LGSVNEENLSVLLMAKKFEIPVCPHAGGVGLCEL VQHLIIFDFISISASLONRMC EYVDH LHEHFRYPVVIKKASYMPPKDPAGYS TEMKEESVKKHQVY PDGE--VWKLLAAG E 450  
gi|114052721|ref|NP\_001040015.1| AFLGIGVATGEQCHNRVIFKQLLQAKALKFLQIDSCR LGSVNEENLSVLLMAKKFEIPVCPHAGGVGLCEL VQHLIIFDFISVSASLQDRMC EYVDH LHEHFKYVPLIREAAYMPPKDPAGYS TEMKEDSVKRHRYPDGE--VWKLLSAQ G 450  
gi|217272853|ref|NP\_001070210.2| AFLGIGVATGEQCHNRVIFKQLLQAKALQFLQIDSCR VGSVNEENLATILMAAKFNVPVCPHAGGVGLCEL VQHLIIFDYISVSASLNRMC EYVDH LHEHFKSPVIRNAKYIPPKDPGYSCEML EESVKKHQVY PEGE--VWRATKQK K 450  
gi|158285681|ref|XP\_001687931.1| REHSIGVATGEMCQNRVVFKQLLMSGALDVCQIDACR MGGVNEVLAVLLMARKFVGVIPVHSGGVGLPEYTOHLST IDYVVSQGKLS--LLEYVDHLHEHFLHPSVIKDFG YQTPTPEPGYSVEMKADSM DRFEYVSGE EGSWWKSEAKP 450  
gi|145613870|ref|XP\_363374.2| KEVYIGVATGEMCQNRVVFKQLLMSGALDVCQIDACR MGGVNEVLAVLLIAKKGVGVIPVHSGGVGLPEYTOHLST IDYVVSQGKLS--LLEYVDHLHEHFLHPSVIKDG YGYQTPTPEPGYSVEMKADSM DRFEYVSGE EGSWWKSEAKP 450  
gi|164424530|ref|XP\_960329.2| KEVYIGVATGEMCQNRVVFKQLLMSGALDVCQIDACR MGGVNEVLAVLLIAKKGVGVIPVHSGGVGLPEYTOHLST IDYVVSQGKLS--LLEYVDHLHEHFLHPSVIKDG YGYQTPTPEPGYSVEMKADSM DRFEYVSGE EGSWWKSEAKP 450  
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi|42544119|ref|NP\_059982.2| N----- 457  
gi|114672465|ref|XP\_001149584.1| N----- 457  
gi|73961860|ref|XP\_848625.1| N----- 457  
gi|114052721|ref|NP\_001040015.1| N----- 457  
gi|217272853|ref|NP\_001070210.2| ----- 457  
gi|158285681|ref|XP\_001687931.1| ----- 457  
gi|145613870|ref|XP\_363374.2| ILEGIKI 457  
gi|164424530|ref|XP\_960329.2| ILEGPKF 457  
.....