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gi|73988894|ref|XP_537868.2|MKLLVGILLCSLVLGVSSORWLTFLKEAGQGRDMWRAYSDMREANYKNSDKYFHARGNYDAAQRGPGGAWAAKVISDAREKSORITD-LFKFGDSGHGVEDSKADQAAEWGRSGKDPNHFRPAGLPDKY 130
gi|57102730|ref|XP_534081.1|MKLLVGILLCSLVLGVSSORWLTFLKEAGQGRDMWRAYSDMREANYKNSDKYFHARGNYDAAQRGPGGAWAAKVISDARENSORITD-LFKFGDSGHGAEKSKADQAAEWGRSGKDPNHFRPAGLPDKY 130
gi|6755396|ref|NP_035445.1|MKPSIAIILCILILGVDSORWVQFMKEAGQGRDMWRAYS DMKKANWKN S DKYFHARGNYDAAQRGPGGAWAAKVISDAREAVQKFT-----GHGAEDSRADQFANEWGRSGKDPNHFRPAGLPDKY 122
gi|115497340|ref|NP_001068728.1|MKLFTGLILCSLVLGVHS-QWMSFFGEAYEGAKDMWRAYS DMREANYK GADKYFHARGNYDAAQRGPGGAWAAKVISDARENIQRFTDPLFKGTTSGQGQEDSRADQAAEWGRSGKDPNHFRPAGLPDKY 130
gi|194679780|ref|XP_873089.3|MKLFTGLILCSLVLGVHS-QWMSFFGEAYEGAKDMWRAYS DMREANYK DADKYFHARGNYDAAQRGPGGAWAAKVISDARENIQRFTDPLFKGTTSGQGQEDSRADQAAEWGRSGKDPNHFRPAGLPDKY 130
gi|40316912|ref|NP_000322.2|MKLLTGLVFCSLVLGVSSRSFFSFLGEAFDGMWRAYS DMREANYIGS DKYFHARGNYDAAQRGPGGAWAAEVISDARENIORFF-----GHGAEDSLADQAAEWGRSGKDPNHFRPAGLPDKY 122
gi|76691395|ref|XP_875660.1|MNLSFGIIFCFLILGVSSQGWGTFLEKAGQGAKDMWRAYQDMKEANYK GADKYFHARGNYDAAQRGPGGAWAAKVISNARETIQGITDPLFKGMTTRDQVREDSKADQAAEWGRSGKDPNHFRPAGLPDKY 131
gi|38566696|ref|NP_851359.2|MNLSTGIIFCFLILGVSSORWGTFLKEAGQGAKDMWRAYQDMKEANYR GADKYFHARGNYDAAQRGPGGAWAAKVISNARETIQGITDPLFKGMTTRDQVREDSKADQFANEWGRSGKDPNHFRPAGLPDKY 131
gi|53933260|ref|NP_001005599.1|MKLLLAVLVMFMVVEAQA-QWYRFPGEAAGGAKDMWRAYQHMKEANWKN S DKYFHARGNYEAAQRGPGGYWAAKVISDGREALQGLIR-----RGNSDAADQEAANLWGRNGGDPNKYRPGKLPDKY 121
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.

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