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gi | 115497340 | ref | NP_001068728.1 | MKLFTGLILCSLVLGVHS-QWMSFFGEAYEGAKDMWRAYS DMREANYKGADKYFHARGNYDAAQRGPGGAWAAKVIS DARENIQRFTDPLFKGTTSGGQGEDSRADQAANEWGRSGKDPNHFRPAGLPDKY 130
gi | 194679780 | ref | XP_873089.3 | MKLFTGLILCSLVLGVHS-QWMSFFGEAYEGAKDMWRAYS DMREANYKGADKYFHARGNYDAAQRGPGGAWAAKVIS DARENIQRFTDPLFKGTTSGGQGEDSRADQAANEWGRSGKDPNHFRPAGLPDKY 130
gi | 40316912 | ref | NP_000322.2 | MKLLTGLVFCSLVLGVSSRSFFSFLGEAFDGARDMWRAYS DMREANYIGSDKYFHARGNYDAAQRGPGGAWAAEVIS DARENIQRFF-----GHGAEDSLADQAANEWGRSGKDPNHFRPAGLPDKY 122
gi | 76691395 | ref | XP_875660.1 | MNLSFGIIFCFLILGVSSQGWGTFLEKAGQGAKDMWRAYQDMKEANYKGADKYFHARGNYDAAQRGPGGAWAAKVIS NARETIQGITDPLFKGMTIRDQVREDSKADQAANEWGRSGKDPNHFRPAGLPDKY 131
gi | 38566696 | ref | NP_851359.2 | MNLSFGIIFCFLILGVSSQRWGTFLKEAGQGAKDMWRAYQDMKEANYRGADKYFHARGNYDAAQRGPGGAWAAKVIS NARETIQGITDPLFKGMTIRDQVREDSKADQFANEWGRSGKDPNHFRPAGLPDKY 131
gi | 57102730 | ref | XP_534081.1 | MKLLVGILLCSLVLGVSSQRWLTFLKEAGQGRDMWRAYS DMREANYKNSDKYFHARGNYDAAQRGPGGAWAAKVIS DARENSORITD-RLKFGDSGHGAEDSKADQAANKWGRSGKDPNHFRPAGLPDKY 130
gi | 73988894 | ref | XP_537868.2 | MKLLVGILLCSLVLGVSSQRWLTFLKEAGQGRDMWRAYS DMREANYKNSDKYFHARGNYDAAQRGPGGAWAAKVIS DAREKSORITD-LFKFGDSGHGVEDSKADQAANEWGRSGKDPNHFRPAGLPDKY 130
gi | 6755396 | ref | NP_035445.1 | MKPSIAIILCILILGVDSQRWVQFMKEAGQGSRDWRAYS DMKKANWKNSSDKYFHARGNYDAAQRGPGGAWAAKVIS DAREAVQKFT-----GHGAEDSRADQFANEWGRSGKDPNHFRPAGLPDKY 122
gi | 53933260 | ref | NP_001005599.1 | MKLLLAVLVMFMVVEAQA-QWYRFPEAAGGAKDMWRAYQHMKEANWKNSSDKYFHARGNYEAAQRGPGGYWAAKVIS DGREALQGLIR-----RGNDAADQFANLWGRNGGDPNKYRPKGLPIKY 121
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.

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