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gi | 73982066 | ref | XP_533144.2 | MRLOHTSPGRIPDAQTRGSPAGSPKGRITGCDHOALGTGPGRRRRTRRAPTSGNLSLGEAQTPLPSSRPQIWAIPPALFFPGHACASPREMMONKVDVVRGAPLSTAPATTTVINVPVETVVPDHVVVSLFNTIFLNWFCCLGFVAF 150
gi | 73982064 | ref | XP_540515.2 | -----MHGR-----NVLEAGGPPLPALPSSRPHLGATWPPALFFPGHACASPREMMONKVDVVRGALLSTAPATTTVINVPETVVPDHVVVSLFNTIFLNWFCCLGFVAF 100
gi | 57099775 | ref | XP_540516.1 | -----MDQCYKVPETGAPQSMVPTTTVINIRSDTVVPDHVVVSLFNTIFMNVCCCLGIVAF 57
gi | 150010589 | ref | NP_003632.3 | -----MHKEHEVAVLGAPPSTILLPRSTVINIHSEISVDPDHVVVSLFNTIFLNWCCCLGFIAF 57
gi | 34861201 | ref | XP_215117.2 | -----MPKEQEVVILGGPHTSISATTTINMPAISISVDPDHVVVSLFNTIFMNVCCCLGFIAF 57
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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*****:*****:*****:*** * **
gi | 73982066 | ref | XP_533144.2 | VYSVKARDRKMVGDLTGAQSFASARCLNIWALVGLLLIIIVLLGMAYAAAYGALLOAMOESGRYH 219
gi | 73982064 | ref | XP_540515.2 | VYSVKARDRKMVGDLTGAQSFASARCLNIWALVGL---IIIVLLGMAYAAAYGALLOVMOESGRYH 165
gi | 57099775 | ref | XP_540516.1 | AYSVKARDRKMVGDLTGAQSFASARCLNISALVVGIIILGIIIVLLRIAFGAAYWALLOVMOESRYH 126
gi | 150010589 | ref | NP_003632.3 | AYSVKSRRDRKMVGDVTGAQAYASTAKCLNIWALILGILMIIIFILLLVFQSVTVVHIMLCIIIEKRGY- 125
gi | 34861201 | ref | XP_215117.2 | SYSVKSRRDRKMVGDVTGAKTYASTAKCLNISVIFITILMAILIILLYA-----KRT-- 109
.....160.....170.....180.....190.....200.....210.....

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