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gi | 4506841 | ref | NP_002973.1 | MKVSAALLCLLLIAATFIPOGLAQPDAINAPVTCCYNFTNRKISVORLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWQDSMDHLDKQT--QTPKT---- 105
gi | 114668180 | ref | XP_001174551.1 | MKVSAALLCLLLIAATFIPOGLAQPDAINAPVTCCYNFTNRKISVORLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWQDSMDHLDKQT--QTPKT---- 105
gi | 50979120 | ref | NP_001003297.1 | MKVSAALLCLLLIAAALTTOVLTQPDAAISPVTCYTLTNKKISIQRLASYKRVTSKCPKEAVIFKTVLNKEICADPKQKWQDSMAHLDKKSTQTAKP---- 105
gi | 27806711 | ref | NP_776431.1 | MKVSAALLCLLLVAAFSTEVLQPDAINSQVACCYTFNSKKISMORLMNYRRVTSKCPKEAVIFKTIILGKELCADPKQKWQDSINYLNKKN--QTPKP---- 105
gi | 119226206 | ref | NP_035461.2 | MKIS--TLLCLLLIATTTISPOVLAGPDAVSTPVTCCYNVVKQKIHVRKLLKSYRRITSSQCPREAVIFRTILDKEICADPKEKWVKN SINHLDKTSTQFILEPSCLG 105
gi | 27674225 | ref | XP_213425.1 | MKIS--TLLCLLLIAAAISPOVLAGPDSVFTPVTCCYNVAKQKIHRRLLKSYRKITSSQCPREAVIFRTVLDKELCADPKEKWVKDSMNHLDKKSTRT--QHP---- 105
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....

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