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gi | 91598939 | ref | NP_001035149.1 | -----MRLAVICFCLLGIICAI PVKQADSGSSEEEK-----NAVSEETNDFKQE-----TLPSKSNESHDMDDDEDDDD--DHVDSQDSIDSND 81
gi | 114595077 | ref | XP_001159723.1 | -----MRLAVICFCLLGIICALPVKQADSGSSEEEK-----NAVSEETNDFKQE-----TLPSKSNESHDMDDVDEDDDD--DHVDSQDSIDSND 81
gi | 74002217 | ref | XP_535649.2 | MSYPAGRRKONQICGLKSLSETLPSCGTLELEPEESCGKLTMR IAVICFCLLGIAYAIPIKHADSGSSEEEKQLNKKYPGAVATWLPKDPSPKOTFLALG-----TFSSKSNES---HDDVDEDDGD--DVSQDSVDSNDL 131
gi | 27806401 | ref | NP_776612.1 | -----MRLAVICFCLLGIASALPVKPTSSGSSEEEKQLNKKYPDAVAIWLKPDPSKOTFLTPONSVSSEETDDNKONLPSKSNESPEQTHDDLDDDDNSQDVNSNDSDDAETI 109
gi | 6678113 | ref | NP_033289.1 | -----MRLAVICFCLFGIASSSLPVKVDSSGSSEEEK-LYSLHDPPIAIFWVPDPSKQNL LAPONAVSSEEEKDDFKQETLPSNSNES---HDHMDDDDDDD--DDDGDHAESEDS 103
gi | 6981580 | ref | NP_037013.1 | -----MRLAVVCLCLFGLASCLPVKVAEFGSGSSEEKAHYSKHSDAVATWLPKDPSPKQNL LAPONAVSSEETDDFKQETLPSNSNES---HDHMDDDDDDD--DDD-GDHAESEDS 103
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi | 91598939 | ref | NP_001035149.1 | DDVDDTDDSHQSDSHHSDESDELVDLFPDLPAIEVFTPVVPTVDIYDGRGDSVVYGLRSKSKKFRRPDIQYPAIDEDITSHMSEELNGAYKAIPVAQDLNAPSDDWDSRGKDSYETSQQLDDQSAETHSHKQSRLYKRRKANDES--- 227
gi | 114595077 | ref | XP_001159723.1 | DDVDDTDDSHQSDSHHSDESDELVDLFPDLPAIEVFTPVVPTVDIYDGRGDSVVYGLRSKSKKFRRPDIQYPAIDEDITSHMSEELNGAYKAIPVAQDLNAPSDDWDSRGKDSYETSQQLDDQSAETHSHKQSRLYKRRKANDES--- 227
gi | 74002217 | ref | XP_535649.2 | D--DSSNESDESDE-----LVNDFPTDIPALOLFPAVPIRGSYDGRGDSVAYGLRSKSKKSHRYEVOYPPDSEEDFTSLVKSASMEDDFNAVLLSRTVVRGTEDRDHAKDQETSQQLDDHSMETKGRKHSQEKLRASDES--- 266
gi | 27806401 | ref | NP_776612.1 | DDPDHSDSHHSDES-----DEVDFPTDIPTIAVFTPIPIESANDGRGDSVAYGLRSKSKKFRRNVOQSPDATEEDFTSHIESEEMHDAP-----KKTSQLTDHSEKINSELSKELTPKAKDK--- 224
gi | 6678113 | ref | NP_033289.1 | VDSDESDESHHSDES-----DEFTASTQADLFTPIVPTVDPNGRGDSLAYGLRSKRSFQVSDQYPAIDEDLTSRMKSEESDEAIRVTPVAQLLSMPSDQDNNKGKSHESQQLDEPSELETHRLEHSEKSE--- 233
gi | 6981580 | ref | NP_037013.1 | VNSDESDESHHSDES-----DEFTASTQADLFTPIVPTVDPNGRGDSLAYGLRSKRSFQVSDQYPAIDEDLTSRMKSEESDEAIRVTPVAQLLSMPSDQDNNKGKSHESQQLDEPSELETHRLEHSEKSE--- 243
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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gi | 91598939 | ref | NP_001035149.1 | -----NEHSDVIDSQELSKVSRFHSHEFHSHEDMLVVDPKSKKEEDKHLKFRISHELDASSEVN 287
gi | 114595077 | ref | XP_001159723.1 | -----NEHSDVIDSKELSKVSRFHSHEFHSHQDMLVVDPKSKKEEDKHLKFRISHELDASSEVN 287
gi | 74002217 | ref | XP_535649.2 | -----NMHSHEIGSQENSSEVSSSELVQLQSHHEKELIVDSKSEEDKHLKFRHSHELDASSEIN 326
gi | 27806401 | ref | NP_776612.1 | -----NKHSNLIESQENSKLSQEFH-----SLEDKLDLHKSEE-DKHLKIRISHELDASSEVN 278
gi | 6678113 | ref | NP_033289.1 | -----SADQSDVIDSQASSKASLEHQSHKHFHSHKDKLVLDPKSKEDDRYLKFRISHELSSSEVN 294
gi | 6981580 | ref | NP_037013.1 | DAIDSAAEKPDAIDSAAERSDAIDSQAASSKASLEHQSHKHFHSHEDKLVLDPKSKEDDRYLKFRISHELSSSEVN 317
.....310.....320.....330.....340.....350.....360.....370.....

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