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gi | 91598939 | ref | NP_001035149.1 | -----MRLAVICFCLLGIICAI PVKQADSGSSEEEK-----NAVSEETNDFKQE-----TLPSKSNESHDMDDMDEDDDD--DHVDSQDSIDSND 150
gi | 114595077 | ref | XP_001159723.1 | -----MRLAVICFCLLGIICALPVKQADSGSSEEEK-----NAVSEETNDFKQE-----TLPSKSNESHDMDDVDEDDDD--DHVDSQDSIDSND 150
gi | 74002217 | ref | XP_535649.2 | MSYPAGRRKONQICGLKSLSETLPSCGTLELEPEESCGKLTMR IAVICFCLLGIAYAIPIKHADSGSSEEEKQLNKKYPGAVALWIKPDPSPKOTFLALG-----TFSSKSNES---HDDVDEDDGD--DVVDSQDSVDSNDL 150
gi | 27806401 | ref | NP_776612.1 | -----MRLAVICFCLLGIASALPVKPTSSGSSEEEKQLNKKYPGAVALWIKPDPSPKOTFLTPONSVSSEETDDNKONTLPSKSNESPEQTDDLDDDDNSQDVNSNDSDDAETI 150
gi | 6678113 | ref | NP_033289.1 | -----MRLAVICFCLFGIASSLPVKVDSGSSEEEK-LYSLHDPPIAWPVPDPSPKQNL LAPONAVSSEEKDDFKQETLPSNSNES---HDHMDDDDDDD--DDDGDHAESEDS 150
gi | 6981580 | ref | NP_037013.1 | -----MRLAVVCLCLFGLASCLPVKVAEFGSSEEEKAHYSKHSDAVATWIKPDPSPKQNL LAPONAVSSEETDDFKQETLPSNSNES---HDHMDDDDDDD--DDD-GDHAESSEDS 150
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 | DDVDDTDDSHQSDSHHSDESDELVDFPDLPAIEVFPVVPVVDYDGRGDSVVYGLRSKSKKFRRPDIQYPAIDEDITSHMSEELNGAYKAIPVAQDLNAPSDWDSRGKDSYETSQQLDQSAETHSHKQSRLYKRRKANDES--- 300
gi | 114595077 | ref | XP_001159723.1 | DDVDDTDDSHQSDSHHSDESDELVDFPDLPAIEVFPVVPVVDYDGRGDSVVYGLRSKSKKFRRPDIQYPAIDEDITSHMSEELNGAYKAIPVAQDLNAPSDWDSRGKDSYETSQQLDQSAETHSHKQSRLYKRRKANDES--- 300
gi | 74002217 | ref | XP_535649.2 | D--DSSNESDESDE-----LVVDFPDLPAIEVFPVVPVVDYDGRGDSVVYGLRSKSKKSHRYEVOYPPDSEEDFTSLVKSASMEDDFNAVLLSRTVVRGTEDRDHAKDQETSQQLDHSMEIKGRKHSQEKLRASDES--- 300
gi | 27806401 | ref | NP_776612.1 | DDVDDSHSHHSDES-----DEVDFPDLPIPTIAVFPFIPESANDGRGDSVVYGLRSKSKKFRRNVOQPDATEDFTSHIESSEMHDAPE-----KKTSQLTDHSKENTSELSKELTPKAKDK--- 300
gi | 6678113 | ref | NP_033289.1 | VDSDESDESHHSDES-----DEVTASTQADLFTPIVPTVDPNGRGDSLAYGLRSKRSFQVSDQYPAIDEDLTSRMKSEESDEAIRVTPVAQLLSMPSDQDNNKGKSHESQQLDEPSELETHRLEHSEKSE----- 300
gi | 6981580 | ref | NP_037013.1 | VNSDESDESHHSDES-----DESFTASTQADVLTPIAPTVDVDPNGRGDSLAYGLRSKRSFVSDQYPAIDEDLTSRMKSEESDEAIRVTPVAQLLSMPSDQDNNGKTSHESSQQLDEPSELETHLEQSKYKQASHEHTEQSE 300
.....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 | -----NEHSDVIDSQELSKVSRFEFHSHEFHSHEDMLVVDPKSKKEEDKHLKFRISHELD SASSEVN 374
gi | 114595077 | ref | XP_001159723.1 | -----NEHSDVIDSKELSKVSRFEFHSHEFHSHQDMLVVDPKSKKEEDKHLKFRISHELD SASSEVN 374
gi | 74002217 | ref | XP_535649.2 | -----NMHSHEIGSQENSSEVSSSELVQLSQSHEKELIVDSKSEEDKHLKFRHVSHELD SASSEIN 374
gi | 27806401 | ref | NP_776612.1 | -----NKHSNLIESQENSKLSQEFH-----SLEDKLDLHKSEE--DKHLKIRISHELD SASSEVN 374
gi | 6678113 | ref | NP_033289.1 | -----SADQSDVIDSQASSKASLEHQSHKFKHSHKDKLVLDPKSKEDDRYLKFRISHELSSSEVN 374
gi | 6981580 | ref | NP_037013.1 | DAIDSAAEKPDAIDSAAERSDAIDSQASSKASLEHQSHKFKHSHEDKLVLDPKSKEDDRYLKFRISHELSSSEVN 374
.....310.....320.....330.....340.....350.....360.....370....

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