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**** .:** ***** : *.**.*.*.*.*****:***:*****:*.:.: * * :**:* ***** **.*: :*.:.:**: **.:**:* ** *:* *****:*. * :* *.* ***** .:** **:* **.* **
gi |50978922|ref|NP_001003182.1| -MAPFPALASGILLLLWVTAPSRACVCAPPHPOTALCNSQIVIRAKFVGTAEVNTDLNRRYEIKMTKMFKGFSAALGNASDIRFVDTPALESVCGYLHRSQNRSEEFVLVAGNLRDGHLOINICSFVAPWSLSLAORRGFTKTYAAGCEG 149
gi |27806161|ref|NP_776896.1| -MAPFPAPMASGILLLLWLTAPSRACVCVPPHPOTAFNCSDVIRAKFVGTAEVNETALYORYEIKMTKMFKGFSAALRDAPDIRFIYTPAMESVCGYFHRSONRSEEFLLIAGQLSNGLHITICSFVAPWNSLSLAORRGFTKTYAAGCEE 149
gi |4507509|ref|NP_003245.1| -MAPFPALASGILLLLWLTAPSRACVCVPPHPOTAFNCSDLVIRAKFVGTAEVNTTLYORYEIKMTKMFKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLLIAGKLDGGLHITICSFVAPWNSLSLAORRGFTKTYAAGCEE 149
gi |113205063|ref|NP_001037849.1| MMAPFASLASGILLLLSTIASKACSCAPPHPOTALCNSDLVIRAKFMGSPETNETTLYORYEIKMTKMLKGFKAAGNAADIRYAYTPVMSLGGYANKSONRSEEFLLITGRLRNGNLHISACSFVLPWRLLSPAQRAPSKTYSAGCGV 150
gi |16758666|ref|NP_446271.1| -MAPFASLASGILLLLSTIASKACSCAPTHPOTALCNSDLVIRAKFMGSPETNETTLYORYEIKMTKMLKGFDAVGNATGFRFAYTPAMESLCGYVHKSONRSEEFLLIAGRLRNGNLHITACSFVLPWHNLSLPAQRAPSKTYSAGCGV 149
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi |50978922|ref|NP_001003182.1| CTVFTCSIPCKLQSDTHCLWTDHFLTGSDDKGFQSRHLACLPREPGICTWOSLRPRMA----- 207
gi |27806161|ref|NP_776896.1| CTVFPSSIPCKLQSDTHCLWTDOLLTGSDDKGFQSRHLACLPREPGICTWOSLRQMA----- 207
gi |4507509|ref|NP_003245.1| CTVFPCLIPCKLQSGTHCLWTDOLLQSGSEKGFQSRHLACLPREPGICTWOSLRSQIA----- 207
gi |113205063|ref|NP_001037849.1| CTVFPCLIPCKLESSTHCLWTDQVLVGSSEYQSRHFACLPRNPGLCTWRSLGAR----- 205
gi |16758666|ref|NP_446271.1| CTVFPCLIPCKLESSTHCLWTDQILMGSEKGYQSDHFACLPRNPDLCTWQYLGVSMTSLPLAKAEA 217
.....160.....170.....180.....190.....200.....210.....

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