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gi |27886557|ref|NP_002440.2| MASPSKGNLDFSPDEEGPAVVAGPGPGGGAEGAAEERRVKVSSLPFSVEALMSDKKPKPEASPLPAESASAGATL--RPLLLSGHGAREAHSP-GPLVK-PFETASVKSENS--EDGAAWMOEPGRYSPPPRHMSPTTCTLRKHKHTNR 150
gi |118601824|ref|NP_001073082.1| MASPSKGNLDFSSDEEGPAMVAGPGPGGGAEGAAEERRVKVSSLPFSVEALMSDKKPKETSPPRPAESASAGATL--RPLLLPGHGAREAHSP-GPLVK-PFETASVKSENS--EDGAAWMOEPGRYSPPPRHMSPTTCTLRKHKHTNR 150
gi |50978788|ref|NP_001003098.1| MASPSKGSDFSSDEEGPAALAGPGPGGGAEGAAEERRVKVSSLPFSVEALMSDKKPKGASPRPADSASAGAAL--RPLLLPGHGAREAHSP-GPPGK-PFEAASVKSENS--EDGAAWMOEPGRYSPPPRHMSPTTCTLRKHKHTNR 150
gi |114326504|ref|NP_038629.2| MASPTKGGDLFSSDEEGPAVLAGPGPGGGAEGSAEERRVKVSSLPFSVEALMSDKKPKESPAVPPDCASAGAVL--RPLLLPGHGVRDAHSP-GPLVK-PFETASVKSENS--EDGAPWIOEPGRYSPPPRHMSPTTCTLRKHKHTNR 150
gi |45383057|ref|NP_989890.1| MASPSKAKEVFSSDEEGP-----AAGAEHHKVKVSSLPFSVEALMSDKKPKELPLAAGGSADGATVGTSRNLLLPGHGSRDAHSPGALTK-TFDTASVKSENS--EDGTSWIOEAGRYSPPPRHLSPTTCTLRKHKHTNR 150
gi |6981226|ref|NP_037114.1| -----MEQRKTKVSSHFPFSVEELISSHKTNKDFERRREIVSDFQACT-----EIRDSCGSAGIPKHFMLQTSFVKSESPELDCISWVMN-SRYS-QTRQESF-CPLRKHHTNR 150
gi |82697600|ref|NP_571351.2| 1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi |27886557|ref|NP_002440.2| KPRTPFTTSQLLALERKFRQKQVLSIAERAEFSSSLNLTETQVKIWFQNRRAKAKRLQEALEKLEKMAAKPMLPSGFSLPFPISPLQ-AASIYGASYPFHRPVLPIPPVGLYATPVGYGMYHLS 275
gi |118601824|ref|NP_001073082.1| KPRTPFTTSQLLALERKFRQKQVLSIAERAEFSSSLNLTETQVKIWFQNRRAKAKRLQEALEKLEKMAAKPMLPSGFSLPFPINSPLQ-AASIYGASYPFHRPVLPIPPVGLYATPVGYGMYHLS 275
gi |50978788|ref|NP_001003098.1| KPRTPFTTSQLLALERKFRQKQVLSIAERAEFSSSLNLTETQVKIWFQNRRAKAKRLQEALEKLEKMAAKPMLPSGFSLPFPINSPLQ-AASIYGASYPFHRPVLPIPPVGLYATPVGYGMYHLS 275
gi |114326504|ref|NP_038629.2| KPRTPFTTSQLLALERKFRQKQVLSIAERAEFSSSLNLTETQVKIWFQNRRAKAKRLQEALEKLEKMAAKPMLPSGFSLPFPINSPLQ-AASIYGASYPFHRPVLPIPPVGLYATPVGYGMYHLS 275
gi |45383057|ref|NP_989890.1| KPRTPFTTSQLLALERKFRQKQVLSIAERAEFSSSLNLTETQVKIWFQNRRAKAKRLQEALEKLEKMAAKPMLPSGFSLPFPINSPLQ-AASLYGTSYPFHRPVLPIPPVGLYATPVGYSMYHLS 275
gi |6981226|ref|NP_037114.1| KPRTPFTTSQLLALERKFRQKQVLSIAERAEFSSSLNLTETQVKIWFQNRRAKAKRLQEALEKLEKMAAKPMLPSGFSLPFPINSPLQ-AASIYSASYPFHRPVLPIPPVGLYATPVGYGMYHLS 275
gi |82697600|ref|NP_571351.2| KPRTPFTTSQLLALERKFRQKQVLSIAERAEFSSSLTLETQVKIWFQNRRAKAKRLQEALEKPKLTKAPALHPNFSPLPLPLGLQLHSAVSLYQSYVYQRPVLPVAVGLYGTPLGYSMYHLA 275
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....

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