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gi|63252913|ref|NP_001738.2|-----MYTAIQSGSPFPGSVDPGLHWVRVEKLPVVAQENQGVFFSGDSYLVLHNGPEEVSHLHLWIGQOSSRDEQGACAVLAVHLNLLGERPVQHREVCGNESDL 150
gi|114578496|ref|XP_001166228.1|-----MYTAIQSGSPFPGSVDPGLHWVRVEKLPVVAQENQGVFFSGDSYLVLHNGPEEVSHLHLWIGQOSSRDEQGACAVLAVHLNLLGERPVQHREVCGNESDL 150
gi|73980918|ref|XP_540197.2|-----MYTISLQSGSPFPGSVDPGLHWVRVEKLPVVAQENQGVFFSGDSYLVLHNGPEELSHLHLWIGQOSSRDEQGACAVLAVHLNLLGERPVQHREVCGNESDL 150
gi|110227377|ref|NP_001035999.1|-----MYTPIQSGSPFPASVDPGLHWVRVEKLPVVAQENQGVFFSGDSYLVLHNGPEEASHLHLWIGQOSSRDEQGACAVLAVHLNLLGERPVQHREVCGNESDL 150
gi|61556900|ref|NP_001013104.1|-----MYTPIQSGSPFPASVDPGLHWVRVEKLPVVAQENQGVFFSGDSYLVLHNGPEEASHLHLWIGQOSSRDEQGACAVLAVHLNLLGERPVQHREVCGNESDL 150
gi|30466254|ref|NP_848669.1|-----MYSPIQSGSPFPPTIVKLPGLHWVRVEKLPVVAQENQGVFFSGDSYLVLHNGPEELSHLHLWIGQOSSRDEQGACAVLAVHLNLLGERPVQHREVCGNESDL 150
gi|48762660|ref|NP_001001594.1|-----MQPFAAGQFGDEVKQPLGLYCWVRKMKAVPLNQAQVGAFFNGDSYLVLDNRGDGADLHMWIGEKSSRDEQVACAMLATQLDNLFLGGDPVQHREVCGYESSPE 150
gi|292613749|ref|XP_693782.2|MQSHALLPYLTPNLQSGPPPLSGSSSEPHHTLKPQTSYLLFLLFLRMLNLRRAQSQTHEVREPLWVVRVEKMKAVLLDSQRGIFVNGDAYIVLSNRKDGSDLHMWMEKSSPDEQGACAMLATQLDNLFLGGDPVQHREVCGYESSPE 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi|63252913|ref|NP_001738.2|FMSYFPRGLKYQEGGVESAFHKTSTGAPAA-IKKLYQVKGKKNIRATERALNWDSEFNTGDCFILDGQNIFAWCGGKSNILERNKARDLALAIRDSERQGAQVEIVTDGEEPAEMIQVLGPKPKALKEGNPEEDLTADKANAAQAALYKV 300
gi|114578496|ref|XP_001166228.1|FMSYFPRGLKYQEGGVESAFHKTSTGAPAA-IKKLYQVKGKKNIRATERALNWDSEFNTGDCFILDGQNIFAWCGGKSNILERNKARDLALAIRDSERQGAQVEIVTDGEEPAEMIQVLGPKPKALKEGNPEEDLTADKANAAQAALYKV 300
gi|73980918|ref|XP_540197.2|FMSYFPRGLKYQEGGVESAFHKTSPGATAAP-IKKLYQVKGKKNIRATERALNWDSEFNTGDCFILDGQNIFAWCGGKSNILERNKARDLALAIRDSERQGAQVEIVTDGEEPAEMIQVLGPKPKALKEGNPEEDLTADRINAQAALYKV 300
gi|110227377|ref|NP_001035999.1|FMSYFPRGLKYREGGVESAFHKTTSGATPAAIRKLYQVKGKKNIRATERALSWDSEFNTGDCFILDGQNIFAWCGGKSNILERNKARDLALAIRDSERQGAQVEIITDGEPAEMIQVLGPKPKALKEGNPEEDITADQINAQAALYKV 300
gi|61556900|ref|NP_001013104.1|FMSYFPRGLKYREGGVESAFHKTTSGTTPAAIRKLYQVKGKKNIRATERALSWDSEFNTGDCFILDGQNIFAWCGGKSNILERNKARDLALAIRDSERQGAQVEIITDGEPAEMIQVLGPKPKALKEGNPEEDITADQINAQAALYKV 300
gi|30466254|ref|NP_848669.1|FMSYFPHGLKYQEGGVESAFHKTSPGATPAAIKKLYQVKGKKNIRATERVLSWDSEFNTGDCFILDGQNIFAWCGKSNILERNKARDLALAIRDSERQGAQVEIVTDGEEPAEMIQVLGPKPKALKEGNPEEDLTADRINAQAALYKV 300
gi|48762660|ref|NP_001001594.1|FMKLFPRGVSQKEGGVESGFRRAS--GPGPVRORLYQIKGKRNIRAKEVDLSWQSFNKGDCFILDGQNIFAWCGGKSNILERNKARDLALAIRDSERQGAQVEIVTDGEEPAEMIQVLGPKPKALKEGNPEEDSKADASN--SASLYKV 300
gi|292613749|ref|XP_693782.2|FMGLFPKGVSKKEGGVESGFRRAS--RDPVKYLYQVKGKKNIRAREVEFSWGSFNKGDCEFILDGQNIFAWCGGKSNILERNKARDLALAIRDSERQGAQVEIVTDGEEPAEMIQVLGPKPKALKEGNPEEDSKADASN--SASLYKV 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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gi|63252913|ref|NP_001738.2|SDATGQMNLTQVADSSPFALLELLISDDCFVLDNGLCGKIYIWKGRKANERKAALQVAEGFISRMRQVAPN-TQVEILPQGRESPIFKOFFKDWK 395
gi|114578496|ref|XP_001166228.1|SDATGQMNLTQVADSSPFALLELLISDDCFVLDNGLCGKIYIWKGRKANERKAALQVAEGFISRMRQVAPN-TQVEILPQGRESPIFKOFFKDWK 395
gi|73980918|ref|XP_540197.2|SDATGQMNLTQVADSSPFALLELLISDDCFVLDNGLCGKIYIWKGRKANERKAALQVAEDFISRMRVAPN-TQVEILPQGRESPIFKOFFKDWK 395
gi|110227377|ref|NP_001035999.1|SDATGQMNLTQVADSSPFASELLIPDDCFVLDNGLCGKIYIWKGRKANERKAALQVADGFISSMRVSPN-TQVEILPQGRESPIFKOFFKNWK 395
gi|61556900|ref|NP_001013104.1|SDATGQMNLTQVADSSPFASELLIPDDCFVLDNGLCGKIYIWKGRKANERKAALQVADGFISSMRVSPN-TQVEILPQGRESPIFKOFFKDWK 395
gi|30466254|ref|NP_848669.1|SDATGQMNLTQVADSSPFALLELLIPDDCFVLDNGLCGKIYIWKGRKANERKAALQVAEDFITRMRVAPN-TQVEILPQGRESPIFKOFFKDWK 395
gi|48762660|ref|NP_001001594.1|SDATGSMKLTQVSEKSPFAKDLLVRDDCFILDNGANGKIFVWKGSGANAEKRVALKMADDFIQMNPKMKTQVEILPQGRESPIFKOFFKSWN 395
gi|292613749|ref|XP_693782.2|SNATGQMTLTKLCKDGPFGQELLEKDDCFILDNGANGKIYVWKGNGANAEKRVALKVADEFITMNPVPRMRTQVEILPQGRESVLFKOFFKSWN 395
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....

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