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gi |8923665|ref|NP_060419.1| MTSLFRSSSSGSG---GGGAGARGG---GGTAAPQELNNSRPARVRRLEFNQAMDDFKTFMFMNDYDIECVLRANS GAVDAIDQLLQMNLEGGSSGGVYEDSSDSEDSIPPEILERTLEPSSDEEPPPVYSPPAYHMHVDFRP 144
gi |114669506|ref|XP_511904.2| MTSLFRSSSSGSGGGGAGARGG---GGTAAPQELNNSRPARVRRLEFNQAMDDFKTFMFMNDYDIECVLRANS GAVDAIDQLLQMNLEGGSSGGVYEDSSDSEDSIPPEILERTLEPSSDEEPPPVYSPPAYHMHVDFRP 146
gi |149642935|ref|NP_001092534.1| MTSLFRSSSS---GGGAAGARGA---GAGAAASQELNNSRPARVRRLEFNQAMDDFTTFMFMNDYDIECVLRANS GAVDAIDQLLQMNLEAGG---GGVYEDSSDSEDSIPPEILERTLEPSSDEEPPPVYSPPAYHMHVDFRP 139
gi |37574104|ref|NP_932130.1| MTSLFRSSSSGSG---GGGATGARGAGTGAGDGSTAPQELNNSRPARVRRLEFNQAMDDFKTFMFMNDYDIECVLRANS GAVDAIDQLLQMNLEAGG---GSAYEDSSDSEDSIPPEILERTLEPSSDEEPPPVYSPPAYHMHVDFRP 146
gi |62078671|ref|NP_001013993.1| MTSLFRSSSSGSG---GGGATGARGAGTGAGDGSAAPQELNNSRPARVRRLEFNQAMDDFKTFMFMNDYDIECVLRANS GAVDAIDQLLQMNLEAGG---VSAYEDSSDSEDSIPPEILERTLEPSSDEEPPPVYSPPAYHMHVDFRP 146
gi |148233231|ref|NP_001082842.1| MTSLFRSSNS---NGGSR---GGGSAAGELNNSRPNRQVRRLEFNQAMDDFKTFMFMNDYDIECVLRANS GAVDAIDQLLQMSIDGQG---SDDSDSDSIPPEILERTLEPSSDEEPPPVYSPPAYDMHIYDRK 131
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi |8923665|ref|NP_060419.1| YPLAPP PPRIDALGSGAPTSORRYRNWNPPLLGNLPDDFLRILPQQLDSIQG-NAGGPKPGSGEGCPP-----AMAGPGP--GDQSRWKQYLEDERIALFLQNEEFMKELQRNRDFLLALERDRLKYESQKSKSSSVAVGNDFG 283
gi |114669506|ref|XP_511904.2| YPLAPP PPRIDALGSGAPTSORRYRNWNPPLLGNLPDDFLRILPQQLDSIQG-NAGGPKPGSGEGGPP-----AMAEPGP--RDQSRWKQYLEDERIALFLQNEEFMKELQRNRDFLLALERDRLKYESQKSKSSSVAVGNDFG 285
gi |149642935|ref|NP_001092534.1| YPLAPP PPRIDVLGSAAPSSORRYRNWNPPLLGNLPEDFLRILPQQLDSIQG-A-TSRGSKLITFEGSLP-----PAAGPEP--RDQSRWKQYLEDERIALFLQNEEFMKELQRNRDFLLALERDRLKYESQKSTSSSVAVGNDFD 278
gi |37574104|ref|NP_932130.1| YLMAPP PPRIDVPGSGQPASORRYRNWNPPLLGSLPDDFLRILPQQLDSIQG-HPGGSKPMSGEGGPP-----PAPGPMA--CDQSRWKQYLEDERIALFLQNEEFMKELQRNRDFLLALERDRLKYESQKSKSNYAAVGNDDG 285
gi |62078671|ref|NP_001013993.1| YLTAPP PPRIDVLGSGQPASQSRRYRNWNPPLLGNLPDDFLRILPQQLDSIQG-HPGGSKPMSGEGVPP-----VAPGPMA--CDQSRWKQYLEDERIALFLQNEEFMKELQRNRDFLLALERDRLKYESQKSKSSNVAVGSDVG 285
gi |148233231|ref|NP_001082842.1| YPEAPPVPPRFQAQPPGHRQVGGYKNWNPPLLGNLPDDFLRILPQQLDSIQGQSSTSNPSSSTSSSSTTIAQKVVAAGTAAGATEERKLRWKQYLEDERIALFLQNEEFMKELQRNREFLIALERDRLKYESKSKSSHSASMEN- 280
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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gi |8923665|ref|NP_060419.1| FSSVPVPGTGDANPAVSEDALFRDKLKHMGKSTRRKLFLARAFSEKTKMRKSKRKHLLKHQSLGAAASTANLLDDVEGHACDEDFRGRROEAPKVEEGLREGC- 386
gi |114669506|ref|XP_511904.2| FSPVPGTGDANPAVSEDALFRDKLKHMGKSTRRKLFLARAFSEKTKMRKSKRKHLLKHQSLGAAASTANLLDDVEGHACDEDFRGRROEAPKVEEGLREGC- 388
gi |149642935|ref|NP_001092534.1| FSPVPGNSDASPAVSEDALFRDKLKHMGKSTRRKLFLARAFSEKTKMRKSKRKHLLKHQSLGAAASTANLLDDVEGHAYEEDFRGRROEVPVVEEALKEGC- 381
gi |37574104|ref|NP_932130.1| FSSVPGTSEINPVSSEDALFRDKLKHMGKSTRRKLFLARAFSEKTKMRKSKKHLPKLQSLGAAASTANLLDDVEGHAYEEDFRGRROEVPKVEEALREGC- 388
gi |62078671|ref|NP_001013993.1| FSSVPGINDINPVSSEDALFRDKLKHMGKSTRRKLFLARAFSEKTKMRKSKKHLPKLQSLGAAASTANLLDDVEGHAYEEDFRGRROEVPKVEEALREGC- 388
gi |148233231|ref|NP_001082842.1| -SSGDHYAGSVEASTDDALFRDKLKHMGKSTRRKLFLARAFSEKTKMRKSKRKHLLRHHLGIANSTANLLDDVEGNPCDEERQLRRFAAQEEEPQKEPL- 383
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400

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