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gi |18858733|ref|NP_571286.1| MEVSP-----EQRRVWVTHHT---VGQHPETHHPGLG-----HSYMDPSQYQLAEDVDVLFNIDG-----GSNHP--YYGNPVRA-VOR---YPPPHSSQMCRPSLLHGSLPWLDDGGS 150
gi |189518178|ref|XP_001918794.1| MEVSP-----EQRRVWVTHHT---VGQHPETHHPGLG-----HSYMDPSQYQLAEDVDVLFNIDG-----GSNHP--YYGNPVRA-VOR---YPPPHSSQMCRPSLLHGSLPWLDDGGS 150
gi |4503929|ref|NP_002042.1| MEVTA-----DQPRVSHHHPAVLNGQHPDTHHPGLS-----HSYMDAAQYPLPEEVDVLFNIDG-----GQNHVPPYYGNSVRAIVOR---YPTHGSOVCRPPLLHGSLPWLDDGKA 150
gi |114629290|ref|XP_001149347.1| MEVTA-----DQPRVSHHHPAVLNGQHPDTHHPGLS-----HSYMDAAQYPLPEEVDVLFNIDG-----GQNHVPPYYGNSVRAIVOR---YPTHGSOVCRPPLLHGSLPWLDDGKA 150
gi |6679951|ref|NP_032117.1| MEVTA-----DQPRVSHHHPAVLNGQHPDTHHPGLG-----HSYME-AQYPLTEEVDVLFNIDG-----GQNHVPPYYGNSVRAIVOR---YPTHGSOVCRPPLLHGSLPWLDDGKA 150
gi |18959228|ref|NP_579827.1| MEVTA-----DQPRVSHHHPAVLNGQHPDTHHPGLG-----HSYMDPAQYPLPEEVDVLFNIDG-----GQNHVPPYYGNSVRAIVOR---YPTHGSOVCRPPLLHGSLPWLDDGKA 150
gi |73949082|ref|XP_858152.1| MEVTA-----DQPRVSHHHPAVLNGQHPDTHHPGLG-----HSYMDPAQYPLPEEVDVLFNIDG-----GQNHVPPYYGNSVRAIVOR---YPTHGSOVCRPPLLHGSLPWLDDGKA 150
gi |116003829|ref|NP_001070272.1| MEVTA-----DQPRVSHHHPAVLNGQHPDTHHPGLG-----HSYMDPAQYPLPEEVDVLFNIDG-----GQNHVPPYYGNSVRAIVOR---YPTHGSOVCRPPLLHGSLPWLDDGKA 150
gi |56605890|ref|NP_001008444.1| MEVST-----DQPRVSHHHPAVLNGQHPDTHHPGLG-----HTYMDPTQYPLAEEVDVLFNIDG-----GQNVFPVPPYYGNSVRAIVOR---YPTAHGSOVCRPPLLHGSLPWLDDGKA 150
gi |24644977|ref|NP_731211.1| MDMSTAAEAARSWYDSPRLGGGGSGGGNGGGVSPQTNGLGSSAGSSLAHSHSLSSGASSAGSSVGVGSAALGGGGSGLDTSDMSEAFVALESNGHRRRYTPSYHQHTSR---MPSATHASPOVCRPHFHTPLSPWLSTSEH- 150
gi |158291624|ref|XP_562743.3| MDMSTAAEAARSWYDSPRLGGGGSGGGNGGGVSPQTNGLGSSAGSSLAHSHSLSSGASSAGSSVGVGSAALGGGGSGLDTSDMSEAFVALESNGHRRRYTPSYHQHTSR---MTSSHHVSPQVCRPHFGPLSLWLDGPP- 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi |18858733|ref|NP_571286.1| IGPHHSTSPWNLGPFPKTSLHSSSPGPLSVYPPASSSSLSAGHSSPHLFTFPPTPKKDVSPDPAISTSGSGSSVROEDKEKCIKYOVSLAESMKLDSAHSR-SMASIGAGASSAHHPIATYPSVVPDYGPGLFPPSSLLIGGSSSYGSKTR 300
gi |189518178|ref|XP_001918794.1| IGPHHSTSPWNLGPFPKTSLHSSSPGPLSVYPPASSSSLSAGHSSPHLFTFPPTPKKDVSPDPAISTSGSGSSVROEDKEKCIKYOVSLAESMKLDSAHSR-SMASIGAGASSAHHPIATYPSVVPDYGPGLFPPSSLLIGGSSSYGSKTR 300
gi |4503929|ref|NP_002042.1| LGSHTASPWNLSPFKTSLHSSSPGPLSVYPPASSSSLSAGHSSPHLFTFPPTPKKDVSPDPAISTSGSAGSARODEKECKLYQVPLPDSMKLESSHRSMTALGGASSSTHHPITTYPPVPEYSSGLFPPSSLLGGSPTFGCKSR 300
gi |114629290|ref|XP_001149347.1| LGSHTASPWNLSPFKTSLHSSSPGPLSVYPPASSSSLSAGHSSPHLFTFPPTPKKDVSPDPAISTSGSAGSARODEKECKLYQVPLPDSMKLESSHRSMTALGGASSSTHHPITTYPPVPEYSSGLFPPSSLLGGSPTFGCKSR 300
gi |6679951|ref|NP_032117.1| LGSHTASPWNLSPFKTSLHSSSPGPLSVYPPASSSSLSAGHSSPHLFTFPPTPKKDVSPDPAISTSGSAGSARODEKECKLYQVPLPDSMKLESSHRSMTALGGASSSTHHPITTYPPVPEYSSGLFPPSSLLGGSPTFGCKSR 300
gi |18959228|ref|NP_579827.1| LGSHTASPWNLSPFKTSLHSSSPGPLSVYPPASSSSLSAGHSSPHLFTFPPTPKKDVSPDPAISTSGSAGSARODEKECKLYQVPLPDSMKLESSHRSMTALGGASSSTHHPITTYPPVPEYSSGLFPPSSLLGGSPTFGCKSR 300
gi |73949082|ref|XP_858152.1| LGSHTASPWNLSPFKTSLHSSSPGPLSVYPPASSSSLSAGHSSPHLFTFPPTPKKDVSPDPAISTSGSAGSARODEKECKLYQVPLPDSMKLESSHRSMTALGGASSSTHHPITTYPPVPEYSSGLFPPSSLLGGSPTFGCKSR 300
gi |116003829|ref|NP_001070272.1| LGSHTASPWNLSPFKTSLHSSSPGPLSVYPPASSSSLSAGHSSPHLFTFPPTPKKDVSPDPAISTSGSAGSARODEKECKLYQVPLPDSMKLESSHRSMTALGGASSSTHHPITTYPPVPEYSSGLFPPSSLLGGSPTFGCKSR 300
gi |56605890|ref|NP_001008444.1| LSSHSAAPWNLSPFKTSLHSSSPGPLSVYPPASSSSLSAGHSSPHLFTFPPTPKKDVSPDPAISTSGSAGSARODEKECKLYQVPLPDSMKLESSHRSMTALGGASSSTHHPITTYPPVPEYSSGLFPPSSLLGGSPTFGCKSR 300
gi |24644977|ref|NP_731211.1| -KFPAPASAWSMGQFACF---QEPQVEKHLQMGQS---HQTAAAGQSHFPFPTPKKDVSPDPAISTSGSAGSARODEKECKLYQVPLPDSMKLESSHRSMTALGGASSSTHHPITTYPPVPEYSSGLFPPSSLLGGSPTFGCKSR 300
gi |158291624|ref|XP_562743.3| -KFIASSAWGS-PPACF---QDP---QDKLQV---QIQGQGLHFLFPPTPKKDVSPDPAISTSGSAGSARODEKECKLYQVPLPDSMKLESSHRSMTALGGASSSTHHPITTYPPVPEYSSGLFPPSSLLGGSPTFGCKSR 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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gi |18858733|ref|NP_571286.1| PKTRSSSEGRECVNCGATSTPLWRRDGTGHYLCNACGLYHKMNGQNRPLIKPKRRL---SAARRAGTSCANCQTTTTLWRRNANGDPVCNACGLYYKLNINRPLTMKKEGIQTRNRKMSKSKKCKK---HDSMEDFS 450
gi |189518178|ref|XP_001918794.1| PKTRSSSEGRECVNCGATSTPLWRRDGTGHYLCNACGLYHKMNGQNRPLIKPKRRL---SAARRAGTSCANCQTTTTLWRRNANGDPVCNACGLYYKLNINRPLTMKKEGIQTRNRKMSKSKKCKK---HDSMEDFS 450
gi |4503929|ref|NP_002042.1| PKARSSTEGRECVNCGATSTPLWRRDGTGHYLCNACGLYHKMNGQNRPLIKPKRRL---SAARRAGTSCANCQTTTTLWRRNANGDPVCNACGLYYKLNINRPLTMKKEGIQTRNRKMSKSKKCKK---HDSLEDFF 450
gi |114629290|ref|XP_001149347.1| PKARSSTEGRECVNCGATSTPLWRRDGTGHYLCNACGLYHKMNGQNRPLIKPKRRL---SAARRAGTSCANCQTTTTLWRRNANGDPVCNACGLYYKLNINRPLTMKKEGIQTRNRKMSKSKKCKK---HDSLEDFF 450
gi |6679951|ref|NP_032117.1| PKARSSTEGRECVNCGATSTPLWRRDGTGHYLCNACGLYHKMNGQNRPLIKPKRRL---SAARRAGTSCANCQTTTTLWRRNANGDPVCNACGLYYKLNINRPLTMKKEGIQTRNRKMSKSKKCKK---HDALEDFF 450
gi |18959228|ref|NP_579827.1| PKARSSTEGRECVNCGATSTPLWRRDGTGHYLCNACGLYHKMNGQNRPLIKPKRRL---SAARRAGTSCANCQTTTTLWRRNANGDPVCNACGLYYKLNINRPLTMKKEGIQTRNRKMSKSKKCKK---HDALEDFF 450
gi |73949082|ref|XP_858152.1| PKARSSTEGRECVNCGATSTPLWRRDGTGHYLCNACGLYHKMNGQNRPLIKPKRRL---SAARRAGTSCANCQTTTTLWRRNANGDPVCNACGLYYKLNINRPLTMKKEGIQTRNRKMSKSKKCKK---HDTLEDFF 450
gi |116003829|ref|NP_001070272.1| PKARSSTEGRECVNCGATSTPLWRRDGTGHYLCNACGLYHKMNGQNRPLIKPKRRL---SAARRAGTSCANCQTTTTLWRRNANGDPVCNACGLYYKLNINRPLTMKKEGIQTRNRKMSKSKKCKK---HDALEDFF 450
gi |56605890|ref|NP_001008444.1| PKARSSTEGRECVNCGATSTPLWRRDGTGHYLCNACGLYHKMNGQNRPLIKPKRRL---SAARRAGTSCANCQTTTTLWRRNANGDPVCNACGLYYKLNINRPLTMKKEGIQTRNRKMSKSKKCKK---HDNLEDFF 450
gi |24644977|ref|NP_731211.1| PKQ--REGRECVNCGATSTPLWRRDGTGHYLCNACGLYHKMNGQNRPLIKPKRRLTLQSLQSAARRAGTSCANCQTTTTLWRRNANGDPVCNACGLYYKLNINRPLTMKKEGIQTRNRKMSKSKKCKKGLGGGLPIGGHLMGDFK 450
gi |158291624|ref|XP_562743.3| PKQ--REGRECVNCGATSTPLWRRDGTGHYLCNACGLYHKMNGQNRPLIKPKRRLVSSLQSAARRAGTSCANCQTTTTLWRRNANGDPVCNACGLYYKLNINRPLTMKKEGIQTRNRKMSKSKKCKKIPGSLPIGGHLMGDFK 450
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450

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gi |18858733|ref|NP_571286.1| KSLMEKNSSFS---PAALSRH---MISFP---PFSHSGHMLTTPPMHPPSSSLP---FA---SHHP---SSMVYAMG--- 539
gi |189518178|ref|XP_001918794.1| KSLMEKNSSFS---PAALSRH---MISFP---PFSHSGHMLTTPPMHPPSSSLP---FA---SHHP---SSMVYAMG--- 539
gi |4503929|ref|NP_002042.1| K---NSSFN---PAALSRH---MSSLSHI---PFSHSHMLTTPPMHPPSSSLP---FG---PHHP---SSMVYAMG--- 539
gi |114629290|ref|XP_001149347.1| K---NSSFN---PAALSRH---MSSLSHI---PFSHSHMLTTPPMHPPSSSLP---FG---PHHP---SSMVYAMG--- 539
gi |6679951|ref|NP_032117.1| K---SSSFN---PAALSRH---MSSLSHI---PFSHSHMLTTPPMHPPSSSLP---FG---PHHP---SSMVYAMG--- 539
gi |18959228|ref|NP_579827.1| K---SSSFN---PAALSRH---MSSLSHI---PFSHSHMLTTPPMHPPSSSLP---FG---PHHP---SSMVYAMG--- 539
gi |73949082|ref|XP_858152.1| K---SSSFN---PAALSRH---MSSLSHI---PFSHSHMLTTPPMHPPSSSLP---FG---PHHP---SSMVYAMG--- 539
gi |116003829|ref|NP_001070272.1| K---SSSFN---PAALSRH---MSSLSHI---PFSHSHMLTTPPMHPPSSSLP---FG---PHHP---SSMVYAMG--- 539
gi |56605890|ref|NP_001008444.1| K---SSSFN---PAALSRH---MSSLSHI---PFSHSHMLTTPPMHPPSSSLP---FG---PHHP---SSMVYAMG--- 539
gi |24644977|ref|NP_731211.1| P---LDPKPFGAFPGSMGQSHLSGGLHPAHHMHGQWYTGGMALGASGLQGGFSIAGSLSGAVVPHSQPYHGLGSMGTWRTDLY 539
gi |158291624|ref|XP_562743.3| P---LDHKPFGAFPGSMGQSHLSGGLHPAHHMHGQWYTGGMALGASGLQGGFSIAGSLSGAVVPHSQPYHGLGSMGTWRTDLY 539
.....460.....470.....480.....490.....500.....510.....520.....530.....

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