

gi | 5031681 | ref | NP\_005855.1 | .....\*:\*.....\*:\*:\*:\*:\* \*  
gi | 114652142 | ref | XP\_509854.2 | -----MAIATSQALARALYDNTAESPOELSFRRGDVLRVLOREGAGGLDQWCLCSLHGQOQIVPANRVKLLPAGPAPKPSLCPASPAQPG-SPYF 150  
gi | 73962629 | ref | XP\_537374.2 | -----MAIATSQALARALYDNTAESPOELSFRRGDVLRVLOREGAGGLDQWCLCSLHGQOQIVPANRVKLLPAGPAPKPSLCPASPAQPG-SPYF 150  
gi | 149642919 | ref | NP\_001092380.1 | -----MRABQDETCKEIVGRGHTIEGPTTRPRIRRRSRGPPWPGAAAAEVSETELGLEQAAREAKAMAVATSAQLARALYDNTAESPOELSFRRGDVLRVLOREGAGGLDQWCLCSLHGQOQIVPANRVKLLPAGTAPQPSLQVPPAPQPG-SPYF 150  
gi | 31981787 | ref | NP\_034242.2 | -----MAIATSQALARALYDNTAESPOELSFRRGDVLRVLOREGAGGLDQWCLCSLHGQOQIVPANRVKLLPAGPAPKPSLCPASPAQPG-SPYF 150  
gi | 62661467 | ref | XP\_237944.3 | -----MAIATSQALARALYDNTAESPOELSFRRGDVLRVLOREGAGGLDQWCLCSLHGQOQIVPANRVKLLPAGPAPKPSLCPASPAQPG-SSCP 150  
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi | 5031681 | ref | NP\_005855.1 | .....\*:\*.....\*:\*:\*:\*:\* \*  
gi | 114652142 | ref | XP\_509854.2 | -----APDSNEDQEVYVPPARPCPTSGPPAGPCPPSPDLLYKIPRASGQLAARPDALQEVYDVPPTALRVSSGGPYDCPASFSHPLTRVAPQPPGEDDAPYDVLFPKPPAELEPDLEWEGGREGPPPIYAAPSNLKRASALLNLYEAPPEEL 300  
gi | 73962629 | ref | XP\_537374.2 | -----APDSNEDQEVYVPPARPCPTSGPPAGPCPPSPDLLYKIPRASGQLAARPDALQEVYDVPPTALRVSSGGPYDCPASFSHPLTRVAPQPPGEDDAPYDVLFPKPPAELEPDLEWEGGREGPPPIYAAPSNLKRASALLNLYEAPPEEL 300  
gi | 149642919 | ref | NP\_001092380.1 | -----APEHGNEDQEVYVPPARPCPTSGPPAGPCPPSPDLLYKIPRASGQLAARPDALQEVYDVPPTALRVSSGGPYDCPASFSHPLTRVAPQPPGEDDAPYDVLFPKPPAELEPDLEWEGGREGPPPIYAAPSNLKRASALLNLYEAPPEEL 300  
gi | 31981787 | ref | NP\_034242.2 | -----APEHGNEDQEVYVPPARPCPTSGPPAGPCPPSPDLLYKIPRASGQLAARPDALQEVYDVPPTALRVSSGGPYDCPASFSHPLTRVAPQPPGEDDAPYDVLFPKPPAELEPDLEWEGGREGPPPIYAAPSNLKRASALLNLYEAPPEEL 300  
gi | 62661467 | ref | XP\_237944.3 | -----TPERGCEQEVYVPPARPCPTSGPPAGPCPPSPDLLYKIPRASGQLAARPDALQEVYDVPPTALRVSSGGPYDCPASFSHPLTRVAPQPPGEDDAPYDVLFPKPPAELEPDLEWEGGREGPPPIYAAPSNLKRASALLNLYEAPPEEL 300  
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



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gi | 114652142 | ref | XP\_509854.2 | -----LADGEGGTDDEGIYDVPPLGPEAPPSPPEPPGALASHDQDTLQALLARSPPPPHRPRLPSAESLRRRLPALPVPEAPSPSPVPSAPAGRKGSIQDRPLPPPPPLPGYGGPKVEGDPGEGREDDPAGHHNEYEGIPMAEYDVVHLKGM 450  
gi | 73962629 | ref | XP\_537374.2 | -----LADGEGGTDDEGIYDVPPLGPEAPPSPPEPPGALASHDQDTLQALLARSPPPPHRPRLPSAESLRRRLPALPVPEAPSPSPVPSAPAGRKGSIQDRPLPPPPPLPGYGGPKVEGDPGEGREDDPAGHHNEYEGIPMAEYDVVHLKGM 450  
gi | 149642919 | ref | NP\_001092380.1 | -----LADGEGGTDDEGIYDVPPLGPEAPPSPPEPPGASANDLDTLQALLARSPPPPHRPRLPSAESLRRRLPALPVPEAPSPSPVPSAPAGRKGSIQDRPLPPPPPLPGYGGPKVEGDPGEGREDDPAGHHNEYEGIPMAEYDVVHLKGM 450  
gi | 31981787 | ref | NP\_034242.2 | -----LADGEGGADDEGIYDVPPLGPEAPPSPPEPPGASANDLDTLQALLARSPPPPHRPRLPSAESLRRRLPALPVPEAPSPSPVPSAPAGRKGSIQDRPLPPPPPLPGYGGPKVEGDPGEGREDDPAGHHNEYEGIPMAEYDVVHLKGM 450  
gi | 62661467 | ref | XP\_237944.3 | -----LANGESRDADDEGIYDVPPLGPEAPPSPPEPPGASANDPDTVAQLLRSPPPPHRPRLPSAESLRRRLPALPVPEAPSPSPVPSAPAGRKGSIQDRPLPPPPPLPGYGGPKVEGDPGEGREDDPAGHHNEYEGIPMAEYDVVHLKGM 450  
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi | 5031681 | ref | NP\_005855.1 | .....\*:\*:\*:\*:\*:\*:\*:\*:\*.....\*:\*:\*:\*:\* \*  
gi | 114652142 | ref | XP\_509854.2 | -----DKACGSRPPDQACTGDPPELPERGMPAPQEALSPGEPVLVSTGDLQLLYFYVAGQCQSHYSALQAAVAALMSTQANQPPRLFVPHSKRVVVAHRLLVVFVGDTLGRLAASAPLRAQVRAAGTALGOALRAIVLAVKGAALGYSPSPAIQEMV 600  
gi | 73962629 | ref | XP\_537374.2 | -----DKACGSRPPDQACTGDPPELPERGMPAPQEALSPGEPVLVSTGDLQLLYFYVAGQCQSHYSALQAAVAALMSTQANQPPRLFVPHSKRVVVAHRLLVVFVGDTLGRLAASAPLRAQVRAAGTALGOALRAIVLAVKGAALGYSPSPAIQEMV 600  
gi | 149642919 | ref | NP\_001092380.1 | -----DKVQEARPPDKASPGDPEQLEREPPQEQEALSPGEPVLVSTGDLQLLYFYVAGQCQSHYSALQAAVAALMSTQANQPPRLFVPHSKRVVVAHRLLVVFVGDTLGRLAASAPLRAQVGAAGTALGOALRAIVLAIKGAALGYSPSPAEBEMA 600  
gi | 31981787 | ref | NP\_034242.2 | -----DTACGSRPLDKAFVVDPELLERGLARKEALSPPEPLVLTGDLQLLYFYVAGQCQSHYSALQAAVAALMSTQANQPPRLFVPHSKRVVVAHRLLVVFVGDTLGRLAASAPLRAQVGAAGTALGOALRAIVLAVKGAALGYSPSDTAVQEMA 600  
gi | 62661467 | ref | XP\_237944.3 | -----DKACGSRPLDNFADPELLERGLVQKEALSPPEPLVLTGDLQLLYFYVAGQCQSHYSALQAAVAALMSTQANQPPRLFVPHSKRVVVAHRLLVVFVGDTLGRLAASAPLRAQVGAAGTALGOALRAIVLAVKGAALGYSPSDTAVQEMA 600  
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



gi | 5031681 | ref | NP\_005855.1 | .....\*:\*:\*:\*:\*.....\*:\*:\*:\*.....\* \*  
gi | 114652142 | ref | XP\_509854.2 | -----QCVTELQALQFVTLTLLSLAP 622  
gi | 73962629 | ref | XP\_537374.2 | -----QCVTELQALQFVTLTLLSLAP 622  
gi | 149642919 | ref | NP\_001092380.1 | -----QVADLQALQFVTLTLLSLAP 622  
gi | 31981787 | ref | NP\_034242.2 | -----RCVAELQALRFVTLTLLGSLP 622  
gi | 62661467 | ref | XP\_237944.3 | -----RCVAELQALRFVTLTLLGSLP 622  
.....610.....620.....

