

gi | 73947202 | ref | XP\_533562.2 | -----MVKVVARVQCPFFLLKEIIPEDRRIKESKGRGWKSEDDLAYRNMVVKASMKFAGLLCVLLLVIFOTDFGQNEETPRKORRRYYRRLKSS-SPRRSSROLGIQOT-V 150  
gi | 77736141 | ref | NP\_001029769.1 | -----MKFSSLYCFLLLLIFOTDFGQNEETSRKORRRMYHRRRLKSS-LSTHRSVROPGIQOMKI 150  
gi | 4557543 | ref | NP\_001384.1 | -----MKIAYLVCFLLIFOTDFGQNEETPRKORRIYHRRRLKSSSTSHKHSRNOLGIQOTTV 150  
gi | 114625602 | ref | XP\_001148362.1 | MLILLMLFGDYHIPAECCNQVLGHNNHVCNNKGVQOILFNIPCFPFVFKESSEDFVFSAGDLNDRKQSLLSLDLKLKLAGG---KKSNNMKIAYLVCFLLIFOTDFGQNEETPRKORRIYHRRRLKSSSTSHKHSRNOLGIQOTTV 150  
gi | 59858563 | ref | NP\_001012324.1 | -----MKLAVLFCFILLIVLQTDCEG---TRRORRRMHORRRRLKSS--SFHLRANROLEVOQTAA 150  
gi | 50754246 | ref | XP\_414297.1 | -----MRHRGLRRLSS---MAGRFLRQPRMKL 150  
gi | 125850016 | ref | XP\_686507.2 | -----MPLCLIPQGSVMRPNLILAMSLACLTFSLANEQRRRLVQKRRGVGPKRKRKQTSNLSLQCGRI 150  
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi | 73947202 | ref | XP\_533562.2 | VTIPIAT-IPVLNLDYSIEEKDSEFLSILGVSESSYNVLPKGGKGLVNGMIMYNRAVWSPEPCTTCLCNGRVLDEMTCHPLTCPQTVRPEGECCSVCSDA-----ETEPINSPHQ-----VEMDQALQKE 300  
gi | 77736141 | ref | NP\_001029769.1 | VTPAAK-LPIINLDYSIEENFESFLVPGVESYVNLPGKGGKGLANGMIMYNKAVWSPEPCTTCLCLNGKVLDEMTCKHPQMCPTIIPGECCPVCNSI-----EOREPNTLPHKQSPFWEEMNRALRKE 300  
gi | 4557543 | ref | NP\_001384.1 | FTPVAR-LPIVNFVDSMEEFKESFSPFVGVSESSYNVLPKGGKGLVKGIMYNKAVWSPEPCTTCLCDGRVLCDEMTMCHPQRCPTQTVIPEGECCPVCNSIIVSYLLSGIALNDRNEFGDSEOREPNTLLHKQLPPPQVGMDIRVKE 300  
gi | 114625602 | ref | XP\_001148362.1 | FTPVAR-LPIVNFVDSMEEFKESFSPFVGVSESSYNVLPKGGKGLVKGIMYNKAVWSPEPCTTCLCDGRVLCDEMTMCHPQRCPTQTVIPEGECCPVCNSIIVSYLLSGIALNDRNEFGDSEOREPNTLLHKQLPPPQVGMDIRVKE 300  
gi | 59858563 | ref | NP\_001012324.1 | -APPAR-LPIANSVSEENIESLLNVLGVSESSYVLPKGGKGVCFVKGIMYNKAVWSPEPCTTCLCNGRVLDEMTCHPKACPVIIPGECCPVCNSI-----EQUESTNKLKQVPPPMEMDQVAIKE 300  
gi | 50754246 | ref | XP\_414297.1 | PAPAAPSIPILNIDDGVMGVDFSLIQLGHESSYNVLPKGGKGLVNGMIMYFDKAVWSPKPCITCLCSKGEVICDTMCHPLKCPQTIIPAGECCPVCSDTVSPLDEN-----IVSLDDITELSGDSPEPNDLNNPNVLP 300  
gi | 125850016 | ref | XP\_686507.2 | PESNGQ-----DRSVF--MESYKKEKPKNFVETAGKSENCFVRFIMYDQTAWSKPKVSLCSKGEVVCQILCPTLQQLKQFPMGECCPVCSDTVSPLDEN-----DLADPILTEISNRRKDKRLKKEEERV 300  
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi | 73947202 | ref | XP\_533562.2 | ELQFEENEELKEDKDKQKK-----KILGPGGQGRSLAEEQER--GAAGRPRAVGRPAHQGHAPAREEAEDEKE-----AEEEEEEAEEEEEG-TIRGDMFRV-----WSRPRGPPPPR 450  
gi | 77736141 | ref | NP\_001029769.1 | ELQLEDEEEVKQDENREQKK-----KIFRPGDWGRINEGQERE-GKAQRPEEGRQAHRNPARNEEDDE-----EEDDDDEEEDDDEETIRGDMFRM-----PPRLPIPATPR 450  
gi | 4557543 | ref | NP\_001384.1 | ALQSEDEE--VKEDTQQR-----EIPESRNCCQLYSQDGRGDRKQRPKERRLAHQQRQGR-EEEEDEE-----EEGEGEDEDEE-DFVRGDMFRM-----PFRSLPAPPR 450  
gi | 114625602 | ref | XP\_001148362.1 | ALQSEDEE--VKEDTQQR-----EIPESRNCCQLYSQDGRGDRKQRPKERRLAHQQRQGR-EEEEDEE-----EEGEGEDEDEE-DFVRGDMFRM-----PFRSLPAPPR 450  
gi | 59858563 | ref | NP\_001012324.1 | ALQSEDEE--IAEGHKEHK-----EISVPTK-----IHGDGERTERKLRPEKGRSAHQPLYHGRREESKEET-----EREGEEEEEEEDAIRGDMFRM-----SBR-VIPGTPR 450  
gi | 50754246 | ref | XP\_414297.1 | SRTQTEKGE-LLRTEVVEIKE-----NEVHKDEKRRKKGKKNRQYKAHQKEKPDGRKDEERRRLFEBELQLE-----KELIRKRGVTRTRERDESEYESDED-----DGTFFIPVPTI 450  
gi | 125850016 | ref | XP\_686507.2 | KKDAERKQRKQKKEAERQKLLKKAKEAKEKEAQRRLREEEEEKAAAEERKKMEERORRAEERARRLEMEQREMMRALBEAAERAEGLRGDEATDEEDIVWLRGDVFOMSLVQPKAEPILLPLPEPSEFVEDTETEGEGDVE 450  
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi | 73947202 | ref | XP\_533562.2 | -----GMPVSPGCSLSYRTISCSISAGLLOIPPLTGPETISLELSGNSITATPDEAFNGLPNLERLDLSKNNITSSGIGPKAFKRLKRLMRLNLDGNLAEIIPSELPSALEELKINENGLQAVSEESLSDNLQVLTLEGNLSETNV 600  
gi | 77736141 | ref | NP\_001029769.1 | -----GIPSLPSCLSYRTISCSISADLTQIPPLTAPETISLELDNSITSPDEAFNGLPNLERLDLSKNNITSSGIGPKAFKFLKRLMRLNMDGNLVTIPSELPSALEELKINENKLVQVIDEESLSDNLQVLTLEGNLSETNV 600  
gi | 4557543 | ref | NP\_001384.1 | -----GTLRLPSCLSYRTISCSINAMLTQIPPLTAPETISLELTGNSIASIPDEAFNGLPNLERLDLSKNNITSSGIGPKAFKLLKRLMRLNMDGNLVTIPSELPSALEELKINENKLVQVIDEESLSDNLQVLTLEGNLSEANV 600  
gi | 114625602 | ref | XP\_001148362.1 | -----GTLRLPSCLSYRTISCSINAMLTQIPPLTAPETISLELTGNSIASIPDEAFNGLPNLERLDLSKNNITSSGIGPKAFKLLKRLMRLNMDGNLVTIPSELPSALEELKINENKLVQVIDEESLSDNLQVLTLEGNLSEANV 600  
gi | 59858563 | ref | NP\_001012324.1 | -----GRPRLPSCLSYRTISCVHADFTIIPPLTAPETISLELVGNSIISIPDEAFNGLPNLERLDLSKNNITSSGIGPKAFKLLKRLMRLNMDGNLVTIPSELPSALEELKINENKLVQVIDEESLSDNLQVLTLEGNLSEINV 600  
gi | 50754246 | ref | XP\_414297.1 | -----EAPPLPAACSTSESIVSCINAKLTQIPPLTAPETISLELDLGNITTTISNEAFNGLPNLEWLDLSKNNITSSGIGPHAFKTLKRLKRLYLDGNLVTIPSELPSALEELKINENKLVQVIDEESLSDNLQVLTLEGNLSEANV 600  
gi | 125850016 | ref | XP\_686507.2 | EEESEMVTTLPPGCTISDVIVTCENAKLMGIPPLTIPPELKSLLNQGNEIKTPAGAFNGLPNLEWLDLGNITSSGIGPHAFKLLKRLKRLYLDGNLVTIPSELPSALEELKINENKLVQVIDEESLSDNLQVLTLEGNLSEANV 600  
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



gi | 73947202 | ref | XP\_533562.2 | NPLAFKSLKLSYLRLGRNFRRIIPQGLPASIEELYLENHIEEITIEICFNHTRKINIVLRYNKEENRIAPLAWINQENLESIDLSNKLYHVPSYLPKSLHLVLLGNQIERIPGVVFGHMPEGLLEYLYLDFNRLSDDGVDQVSVFYG 750  
gi | 77736141 | ref | NP\_001029769.1 | NSLAFKPLKLSYLRLGRNFRRIIPQGLPASIEELYLENNQIEEITIEICFNHTRKINIVLRYNKEENRIAPLAWINQENLESIDLSNKLYHVPSYLPKSLVHLVLLGNQIERIPGVVFGHMPEGLLEYLYLDFNRLSDDGVDQVSVFYG 750  
gi | 4557543 | ref | NP\_001384.1 | NPLAFKPLKLSLAVLRLGKNFRRIIPQGLPGSIEELYLENNQIEEITIEICFNHTRKINIVLRYNKEENRIAPLAWINQENLESIDLSNKLYHVPSYLPKSLHLVLLGNQIERIPGVVFGHMPEGLLEYLYLDFNRLSDDGMDRVSFYG 750  
gi | 114625602 | ref | XP\_001148362.1 | NPLAFKPLKLSLAVLRLGKNFRRIIPQGLPGSIEELYLENNQIEEITIEICFNHTRKINIVLRYNKEENRIAPLAWINQENLESIDLSNKLYHVPSYLPKSLHLVLLGNQIERIPGVVFGHMPEGLLEYLYLDFNRLSDDGMDRVSFYG 750  
gi | 59858563 | ref | NP\_001012324.1 | DPLAFCSLESYLRLGRNFRRIIPQGLPASIEELYLENNQIEEITIEICFNHTRKIMLILRYNKEESRIAPLAWINQENLESIDLSNKLYHVPSYLPKSLHLVLLGNQIERIPGVVFGHMPEGLLEYLYLDFNRLSDDGVDVSVFYG 750  
gi | 50754246 | ref | XP\_414297.1 | SPLAFYPLKLSYLRLGRNFRRIIPQGLPTLIEELYLENNQIEEIVSEITIEICFNHTRKINIVLRYNKEEBSRIAPLAWINQENLESIDLSNKLYHVPSYLPKSLHLVLLGNQIERIPGVVFGHMPEGLLEYLYLDFNRLSDDGVDVSVFFG 750  
gi | 125850016 | ref | XP\_686507.2 | NPQAFKPLKELNLYLRLNRNHFRTIIPQGLPESLLEYLYLENNQIEDISEAFNHTINIVLRYNKEESRIAPLAWINQENLESIDLSNKLYHVPSYLPKSLVHLVLLGNQIERIPGVVFGHMPEGLLEYLYLDFNRLSDDGVDVSVFFG 750  
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750



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gi | 73947202 | ref | XP_533562.2 | AYHSLRRLFLDHDNLDKSIIPGVREMKALHFLRLNNNKIRNIIPEQIC-----NAEEDGDTLEHLHLENNYIKTREISSYAFSCIRSYSSIVLKPQNIK 857
gi | 77736141 | ref | NP_001029769.1 | AYHSLRRLFLDHDNLDKSIIPGVREMKALHFLRLNNNKIRNIIPEQIC-----NAEEDDDNLQHLHLENNYIKTREIPSYAFSCIRSYSSIVLKPQNIK 857
gi | 4557543 | ref | NP_001384.1 | AYHSLRRLFLDHDNLDKSIIPGIVREMKALHFLRLNNNKIRNIIPEEIC-----NAEEDDDNLQHLHLENNYIKIREIPSYTFSCIRSYSSIVLKPQNIK 857
gi | 114625602 | ref | XP_001148362.1 | AYHSLRRLFLDHDNLDKSIIPGIVREMKALHFLRLNNNKIRCVS-----DAVLETVTNRSDF--VAFPLW----- 857
gi | 59858563 | ref | NP_001012324.1 | AYHSLRRLFLDHDNDFKSIIPGIVDMKALHFLRLNNNKIRNIIHPEQIC-----NAEEDDESALEHLHLENNYIKRTREISSYAFSCIRLYSSIVLKPQHIIK 857
gi | 50754246 | ref | XP_414297.1 | AYHSLRRLFLDHDNLDKSVVPGIIEEMKLRFLRLNNNKIRTVPPERICRTHLHDDDVHYNSEDEGEDSRLEHVHLENNYINTRQLSPHSFSCIRSYCVVLPKPKTK 857
gi | 125850016 | ref | XP_686507.2 | TLNTMTLCLDHDNHLMAIPMGINEMTLLHFLRLNNNKIRHVPEQAIC-----DPLSEDDSHLVAVRLENNFIDPRKIPPTAFSCVRSYSSVVLKPKRIK 857

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