

gi	124494251	ref	NP_004314.4	-----MAQRGG-----ARRPRGDRERLGRSLR-ALRPGREPROSEPPAQRGPPPGRPPPARSTASGHRDPTRGAAAGARRPRMCKKTRRRSTRSE-----ELTRSE--	90
gi	114624364	ref	XP_520528.2	-----MGIKTGWVLAGQSDGVRGSLVCGVNRDLGNRDEGEKSRPSVARSFSA-----TARSTASRHRDPTRGAAAGARRPRMCKKTRRRSTRSE-----ELTRSEET	94
gi	73971741	ref	XP_854585.1	MRRRKAPIGASRLFFRVFRAAFRGRSASRAGRGGKARNSAPTAGWSTASGLAERGGARRPRGDRERLGRSLR-APRPGREPROSVLPAERGGPPPGQRSSARGAARGHAGSTRGAAAGARRSRVKKVR-PRRARSE-----DVARSO	139
gi	194676497	ref	XP_001250235.2	-----MATAKLS-----QTVPAIRATP-----VESVTRGHAGSTRGAAACARRPRVKKKTPRRARSE-----EVCRES-----	59
gi	34398362	ref	NP_033866.3	-----MAGRSA-----ARRPRGDRERLGRSLR-APRPAAREPROSEIIRAEERGLPPQRSSVRSAAAGHRDSTRGAPAGACKPRVKKKVRPRSSQSEKVGSSSRRLTRSKKV	99
gi	62648811	ref	XP_216377.3	-----	

1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi	124494251	ref	NP_004314.4	---ELT---LSEEAWSSEEAQSEEAQCEEMNRSQEVTRDEESTRESEVTRREEMAAAGLTVVTHSNKHDLVTSQSGSEPVVQDLAQVVEEVIGVPSQFKLIFKPKSLKEMETPLSALGIQDGCVRMLIGKKNSPQEEVELKKLK	234
gi	114624364	ref	XP_520528.2	TRSEELT---LSEEAWSSEEAQSEEAQCEEMNRSQEVTRDEESTRESEVTRREEMAAAGLTVVTHSNKHDLVTSQSGSEPVVQDLAQVVEEVIGVPSQFKLIFKPKSLKEMETPLSALGIQDGCVRMLIGKKNSPQEEVELKKLK	242
gi	73971741	ref	XP_854585.1	-----EVTRSEEVVAQSEEVTEQEVVAPSE-----EMAAAGLSVTVTHSNKHDLVTSQSGSEPIVQDLAQVVEEATGVPLPFQKLIKFKGKSLKEMETPLSALGIQNGCRVMLIGKKNSPQEEVELKKLK	260
gi	194676497	ref	XP_001250235.2	-----EMSRSEEVVAPSEEVVAPSEEVVAPSEEVVAPSE-----EMAAAGLSVTVTHSNKHDLVTSQSGSEPIVQDLAQVVEEATGVPLPFQKLIKFKGKSLKEMETPLSALGIQNGCRVMLIGKKNSPQEEVELKKLK	186
gi	34398362	ref	NP_033866.3	TRSKNVIGTQVEEVTKIEEATQIEEVTVAEVETQIDNMAKTEEMVOT-----EEMETPRLSVIVTHSNERYDLLVTPQSGSEPIVQDLAQVVEEATGVPLPFQKLIKFKGKSLKEMETPLSALGMONGCRVMLIGKKNSPQEEVELKKLK	244
gi	62648811	ref	XP_216377.3	-----MAOTEEMVOT-----EEMETPRLSVIVTHSNERYDLLVTPQSGSEPIVQDLAQVVEEATGVPLPFQKLIKFKGKSLKEMETPLSALGMONGCRVMLIGKKNSPQEEVELKKLK	108

.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi	124494251	ref	NP_004314.4	HLEKSVKEIADOLEELNKKELTGIOGFLPKDLQAEALCKLDRRVKATIEQFMKILEEIDTLILPENFKDSRLKRRKGLVKKVQAFLAECDTVEQNICQETERLOSTNLFALAE	345
gi	114624364	ref	XP_520528.2	HLEKSVKEIADOLEELNKKELTGIOGFLPKDLQADALCKLDRRVKATIEQFMKILEEIDTLILPENFKDSRLKRRKGLVKKVQAFLAECDTVEQNICQETERLOSTNLFALAE	353
gi	73971741	ref	XP_854585.1	DLEKSVKEIADOLEELNKKELTGIOGFLAKDLQAEALCKLDRRVKATIEQFMKILEEIDTLILPENFKDSRLKRRKGLVKKVQAFLAECDTVEQNICQETERLOSTNLFALAE	371
gi	194676497	ref	XP_001250235.2	DLEKSVKEIADOLEELNKKELTGIOGFLAKDLQAEALCKLDRRVKATIEQFMKILEEIDTLILPENFKDSRLKRRKGLVKKVQAFLAECDTVEQNICQETERLOSTNLFALAE	297
gi	34398362	ref	NP_033866.3	DLEVSAEKIANHLEELNKKELSGIOGFLAKELQAEALCKLDRRVKATIEQFMKILEEIDTMVLPENFKDSRLKRRKGLVKKVQAFLAECDTVEQNICQETERLOSTNLFALAE	355
gi	62648811	ref	XP_216377.3	DLEVSAEKIANHLEELNKKELSGIOGFLAKELQAEALCKLDRRVKATIEQFMKILEEIDTMVLPENFKDSRLKRRKGLVKKVQAFLAECDTVEQNICQETERLOSTNLFALAE	219

.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410

