

gi	57222272	ref	NP_001007568.1	MEAGRTAVLRVKKRRN-AEPAEALVLACKRPRSSVEVSAAR-ETPEGQEAARNVFQLVATVRSQEEPIQQLVRA-----ALRPFERSQLRIRRDLRASVREVRKEGRYRVVSSH-----SSGTSN-----LEFPQGSSEAVGD	130
gi	62665198	ref	XP_574233.1	MEAGRTAVLRVKKRRN-AEPAEALVLACKRRLRSGEVESAP-ETPEGQETG-AERNVFLVATVRSQEEPIQQLVRA-----ALRPFERSQLRIRRDLRASVREVRKEGRYRVVSSH-----SSGTSN-----LEFPQCVSEAVRD	129
gi	14149861	ref	NP_115554.1	MEAAARTAVLRVKKRRS-AEPAEALVLACKRRLRSDAVESAAQ-KHS-EDLERAENNVPFLVATVCSQEEPVQPLLRE-----VLRLERD-SQORVRRNLRASAREVRQEGRYRVLSRR-----LGTTSQGSSEYTPGNPEAAGN	133
gi	114663234	ref	XP_511054.2	-----MDIDFKIIFSK-----GTTT-----	15
gi	73957462	ref	XP_853763.1	MEAGRTAVLRVKKRRS-AEPAEALVLSCKRLRSSAVETAQ-KVPEEDLGERGPENNVPFLVATVRSQEEPVQALVRA-----ALRPFERSQQRIRRDLRASARENROEGRYRVISRR-----SSGIPSGGLESEDPGNPEAAED	134
gi	115497480	ref	NP_001069035.1	MEAGRTAVLRVKKRLG-TEPAEALVLACKRRLRSSAVELETP-KHSPEGLERAENNVPFLVATVRSQEEPVQPLLRA-----ALRPFQSQORIRHHLRASAREIROEGRYRVVFSRR-----SSGIPSDSLESEASGTAKAAD	134
gi	50753441	ref	XP_413987.1	--MERAALVLRVQRKRGGAEPAEALLLACKRRLRAEPGQGAP-----VERGVFKLVATVSSKNEPIQKLVQEGISKD-KAVQSLRPLSGTORVVQDLRSKIVRRKENRYRVVASHRP-----GSSGIAAALTDCFAVSDGGRSAPA	133
gi	55925217	ref	NP_001007345.1	--MDPSITLLRVRKRRG-TDPADALLLACKRIRPEATAAQPSDESEPEPQEPKIENSVFELVATVVSQDAPVQPHVREALARPLAHHLRPLQGSORIIIGDLRSVKWSTRREERYRILSSHRAGLPSEFAPAGGGGEENHDSHAEERD	148



gi	57222272	ref	NP_001007568.1	AG-----FOLLDLVHEE--ENPEAAATDCRKTSDPDVILCNSVELIRERLTVSEEDGSQVNHQEDPKHNDYVVDIYMEMAPPGWIENILSVOPYSQEWELVNDDEQ-SEDIYEDEDDENSENNWRNEYDDEE	256
gi	62665198	ref	XP_574233.1	GG-----FOLLDLVHEE--EDPEAAATDCRKTSDPDVILCNSVELIRERLTVSEEDGSQVHEQEBPKHSDDYVVDIYMEMAPPGWIENILSVOPYSQEWELVNDDEQ-PEDIYEDEDDENSENNWRNEYDDEE	255
gi	14149861	ref	NP_115554.1	SG-----FOLLDLVHEE--GEPEAASAGSCKTSDPDVILCNSVELIRERLTVSEEDGPGVRRQEBQKH--DDYVVDIYLETAIPGWIENILSVOPYSQEWELVNDDEQ-PEDIYDDEDDENSENNWRNEYPEEE	258
gi	114663234	ref	XP_511054.1	-----DPDVIILCNSVELIRERLTVSEEDGPGVRRQEBQKH--DDYVVDIYLETAIPGWIENILSVOPYSQEWELVNDDEQ-PEDIYDDEDDENSENNWRNEYPEEE	114
gi	73957462	ref	XP_853763.1	AS-----FOLFDLVHEEED-DPEAVATGGSSKTSDDVILCNSIELIRERLTVSEEDGPRIGHQEBQK--DDYVVDIYLEMAIPGWIENILSVOPYSQEWDLVNDVDDQ-PEDIYEDDDENSENNWRNEYPEEN	260
gi	115497480	ref	NP_001069035.1	AN-----FOLLDLVHEE--DAEVAAAATSCCKSDPDVILCNCVELIREGLNVSQCGPSSGHQEBQK--DDYVVDIYCLERATPGWIENILSVOPYSHEWELVNDVDDQ-PEDIYDDEDDENSENNWRNEYPEEN	258
gi	50753441	ref	XP_413987.1	AACDALQOESGAVDKSLDCGGNFOLFIVHEEEVVEDSSFLAANAQDTGDPDVIILCNAVEMIRERLNVSEDHNKVGHREK--DEYVVDIYVCMETSAFGWIONILSVOPYSQEWELVNDVDDQ-PAEIFEDEDDEDDNWRNDYDDEDE	278
gi	55925217	ref	NP_001007345.1	LPLG-----EVOVFDILHEE--EDVKVPGKVVSDPETIILCNSVKMIREKLSVSGAGLGEHREK--DDYVVDIYVQETATPGWIODILSVRPPYSQEGELVPEVAWEVEYVEDEDDENANWRNDYDDEE	273



gi	57222272	ref	NP_001007568.1	SDRDEDSRGSDEYNLSSEER-FCERLMWSKYPLDVQKEFDYDSPHG-----LDS	306
gi	62665198	ref	XP_574233.1	SDRDEDSRGSDEYNLSLDEER-FCRLVWSKYPLDVQKEFDYDSPHD-----LDS	305
gi	14149861	ref	NP_115554.1	SDGDEDSRGSADYNLSSEERGSRRQRMWSKYPLDVQKEFDYDSPHD-----LDS	309
gi	114663234	ref	XP_511054.2	SDGDEDSRGSADYNLSSEERGSRRQRMWSKYPLDVQKEFDYDSPHD-----LDS	165
gi	73957462	ref	XP_853763.1	TDEDEDSRGSDDYDSFSEERGNRQPMWSKYPLDVHKEFDYDSPHD-----LDS	311
gi	115497480	ref	NP_001069035.1	SDEDEDSRGS DNYS--SEERDNRQPMWSKYPLDVQKEFDYDSPHD-----LDS	307
gi	50753441	ref	XP_413987.1	FLAEDDEEKDSEESSDEDQ-CYRRRTWKNYRQEVLDQEFYDEIQD-----LDS	328
gi	55925217	ref	NP_001007345.1	---EGDEGEERYGGNSSEH-YSRRSRECYRRDMIDELENDKDEDEEREVNDSD	326

