

gi 31560404 ref NP_062795.2	-----MALLAEHLKPF	150
gi 109496081 ref XP_213793.4	MTYQLGARMDQKLEPRARTEPLRWSVPDKPCITVPNLGAAHQVPDARASAKPRPPDQWRGCGGDELPLVERARRWAPITGRAAEGRGVLHGPGGLRAALSARCEARAEVATLASREAAGDSPGADALGAGWGITKGLDPEMALLAEHLKPF	150
gi 7705987 ref NP_057517.1	-----MALLAEHLKPF	150
gi 114636434 ref XP_521856.2	-----MALLAEHLKPF	150
gi 73995333 ref XP_854394.1	-----MALLAEHLKPF	150
gi 28461219 ref NP_786993.1	-----MALLAEHLKPF	150
gi 50770757 ref XP_427091.1	-----MALLAEHLKPF	150
gi 153792401 ref NP_001093458.1	-----MALLMEHOFRO	150
gi 71996318 ref NP_001022958.1	-----MTSSSPVVAVEPNDVADSPGHELVFAKPEHFFPH	150
	1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150	



gi 31560404 ref NP_062795.2	LPADKQIETGPFLAEVAHLPPFFDCLGSPVFTPIKADISGNIITRIKAVYDTPAKFKTLONILEVEKMGYGAEPKVGATLALLWLKRLRFIOVFLOSICDGERD--ENHPNLRVNAKAYEMALKKYHGWLVOKIFKAALYAAPYK	300
gi 109496081 ref XP_213793.4	LPADKQIETGPFLAEVAHLPPFFDCLGSPVFTPIKADISGNIITRIKAVYDTPAKFKTLONILEVEKMGYGAEPKVGATLALLWLKRLRFIOVFLOSICDGERD--ENHPNLRVNAKAYEMALKKYHGWLVOKIFKAALYAAPYK	300
gi 7705987 ref NP_057517.1	LPADKQIETGPFLAEVAHSLPPFFDCLGSPVFTPIKADISGNIITRIKAVYDTPAKFKTLONILEVEKMGYGAEPKVGATLALLWLKRLRFIOVFLOSICDGERD--ENHPNLRVNAKAYEMALKKYHGWLVOKIFKAALYAAPYK	300
gi 114636434 ref XP_521856.2	LPADKQIETGPFLAEVAHSLPPFFDCLGSPVFTPIKADISSNIITRIKAVYDTPAKFKTLONILEVEKMGYGAEPKVGATLALLWLKRLRFIOVFLOSICNEERD--ENHPNLRVNAKAYEMALKKYHGWLVO--IFQAALHAASCK	300
gi 73995333 ref XP_854394.1	LPADKQIETGPFLAEVAHSLPPFFDCLGSPVFTPIKADISGNIITRIKAVYDTPAKFKTLONILEVEKMGYGAEPKVGATLALLWLKRLRFIOVFLOSICDGERD--ENHPNLRVNAKAYEMALKKYHGWLVOKIFKAALYAAPYK	300
gi 28461219 ref NP_786993.1	LPADKQIETGPFLAEVAHSLPPFFDCLGSPVFTPIKADISGNIITRIKAVYDTPAKFKTLONILEVEKMGYGAEPKVGATLALLWLKRLRFIOVFLOSICDGERD--ENHPNLRVNAKAYEMALKKYHGWLVOKIFKAALYAAPYK	300
gi 50770757 ref XP_427091.1	-----KIRAVYDTPAKFKTLONILEVEKMGYGAEPKVGATLALLWLKRLRFIOVFLOSICDGERD--ENHPNLRVNAKAYEMALKKYHGWLVOKIFKAALYAAPYK	300
gi 153792401 ref NP_001093458.1	LPADKQVETRPFLAEVAHSLPPFFDCLGSAVFTPIKADISGNIITRIKAVYDTPAKFKTLONILEVEKMGYGAEPKVGATLALLWLKRLRFIOVFLOSICDGERD--ENHPNLRVNAKAYEMALKKYHGWLVOKIFKAALYAAPYK	300
gi 71996318 ref NP_001022958.1	LTDDGKIPLAQFLSACQGIADVFSFLG-ATFLVLRKDIQGNVDKVRVRFKQDEGQKYLQQLIDADLAEHGGKFG--IATTEGLLWLKRLRFIOVFLOSICDGERD--ENHPNLRVNAKAYEMALKKYHGWLVOKIFKAALYAAPYK	300
160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300	



gi 31560404 ref NP_062795.2	SDFLKALSKGQNVTEEECLEKIRLFLVNYTAITDAIYDMYTKMNAELDYTV	351
gi 109496081 ref XP_213793.4	SDFLKALSKGQNVTEEECLEKIRLFLVNYTAITDAIYEMYTEMNAELDYTV	351
gi 7705987 ref NP_057517.1	SDFLKALSKGQNVTEEECLEKIRLFLVNYTAITDVIYEMYTEMNAELNYKV	351
gi 114636434 ref XP_521856.2	SDFLKALSKGQNVTEEECLEKIRLFLVNYTAITDVIYERYTOMNAELNYKV	351
gi 73995333 ref XP_854394.1	SDFLKALSKGQNVTEEECLEKIRLFLVNYTAITDVIYEMYTEMNAELNYKV	351
gi 28461219 ref NP_786993.1	SDFLKALSKGQNVTEEECLEKIRLFLVNYTAITDVIYEMYTEMNAELNYKV	351
gi 50770757 ref XP_427091.1	-----	351
gi 153792401 ref NP_001093458.1	SDFLRALSKGREVKDEECLDKVRFQFLVNFATINDAIYEMYTEMNAELDYKV	351
gi 71996318 ref NP_001022958.1	RQILKAVALGQEGLDVCIHHI@CHLDNFRNLNVKILVDVYIEKKLDTDPDV	351
310.....320.....330.....340.....350	

