

gi	145615522	ref	XP_360277.2	-----MDDFVSEESDYASYWRDWFISSRGNEVFCEIDEDYITDRFNLTGLNEQVPHVROALDMILD-LFP	150
gi	164427743	ref	XP_001728406.1	-----MDDFVSEESDYASYWRDWFISSRGNEVFCEIDEDYITDRFNLTGLNEQVPHVROALDMILD-LFP	150
gi	19115518	ref	NP_594606.1	-----MDDFVSEESDYASYWRDWFISSRGNEVFCEIDEDYITDRFNLTGLNEQVPHVROALDMILD-LFP	150
gi	73972260	ref	XP_532075.2	MAGATSVLGLLGLHFFPAFAAPDPWRLRVALSPSPISPISTHTAPRPPPRYFACRGRVRLRCSRRLSLEAATPLPHPGGPGPRPAADVMS	150
gi	114326228	ref	NP_001039919.1	-----MSSSE--EVSWSISWFCGLRGNEFFCEVEDEYIQDKFNLTGLNEQVPHVROALDMILD-LFP	150
gi	7106277	ref	NP_034105.1	-----MSSSE--EVSWSISWFCGLRGNEFFCEVEDEYIQDKFNLTGLNEQVPHVROALDMILD-LFP	150
gi	23503295	ref	NP_001311.3	-----MSSSE--EVSWSISWFCGLRGNEFFCEVEDEYIQDKFNLTGLNEQVPHVROALDMILD-LFP	150
gi	78214347	ref	NP_001030315.1	-----MSSSE--EVSWSISWFCGLRGNEFFCEVEDEYIQDKFNLTGLNEQVPHVROALDMILD-LFP	150
gi	292624283	ref	XP_002665575.1	-----MSSSE--EVSWSISWFCGLRGNEFFCEVEDEYIQDKFNLTGLNEQVPHVROALDMILD-LFP	150
gi	18858421	ref	NP_571262.1	-----MSSSE--EVSWSISWFCGLRGNEFFCEVEDEYIQDKFNLTGLNEQVPHVROALDMILD-LFP	150
gi	45554910	ref	NP_996415.1	-----MSSSE--EVSWSISWFCGLRGNEFFCEVEDEYIQDKFNLTGLNEQVPHVROALDMILD-LFP	150
gi	17508229	ref	NP_492254.1	-----MSSSE--EVSWSISWFCGLRGNEFFCEVEDEYIQDKFNLTGLNEQVPHVROALDMILD-LFP	150
gi	15232283	ref	NP_191584.1	-----MSSSE--EVSWSISWFCGLRGNEFFCEVEDEYIQDKFNLTGLNEQVPHVROALDMILD-LFP	150
gi	15224934	ref	NP_181996.1	-----MSSSE--EVSWSISWFCGLRGNEFFCEVEDEYIQDKFNLTGLNEQVPHVROALDMILD-LFP	150
gi	50309855	ref	XP_454941.1	-----MSSSE--EVSWSISWFCGLRGNEFFCEVEDEYIQDKFNLTGLNEQVPHVROALDMILD-LFP	150
gi	45185773	ref	NP_983489.1	-----MSSSE--EVSWSISWFCGLRGNEFFCEVEDEYIQDKFNLTGLNEQVPHVROALDMILD-LFP	150
gi	6324613	ref	NP_014682.1	-----MSSSE--EVSWSISWFCGLRGNEFFCEVEDEYIQDKFNLTGLNEQVPHVROALDMILD-LFP	150

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



gi	145615522	ref	XP_360277.2	-----MRETIKESARHLVGLVHARYIVITRGLSKMLEKYYKGGDFGKCPRVHCGSHPLLPMLGMDIPSSPKVKLYCARCEDINPKSSRHAIDGAYFGTFFHNLIFQVYVFPALMPVKSAERIVPRCFGRVHAAASLVRWQSGRR	300
gi	164427743	ref	XP_001728406.1	LD---CDDDMRETIKESARHLVGLVHARYIVITRGLQKMFKEYKKAIDFGKCPRVHCGSHPLLPMLGMDIPSSPKVKLYCARCEDINPKSSRHAIDGAYFGTFFHNLIFQVYVFPALMPVKSAERIVPRCFGRVHAAASLVRWQSGRR	300
gi	19115518	ref	NP_594606.1	PD---LPEEVQDEVEASARHLVGLVHARYIVITRGLQKMFKEYKKAIDFGKCPRVHCGSHPLLPMLGMDIPSSPKVKLYCARCEDINPKSSRHAIDGAYFGTFFHNLIFQVYVFPALMPVKSAERIVPRCFGRVHAAASLVRWQSGRR	300
gi	73972260	ref	XP_532075.2	DEELEDNPNQSDLLIEQAAEMLYGLIHARYILNTRGIAQMLEKYQQGDFGYCPRVYCNENPMLPIGLSDIPGEAMVKLYCPKCMDVYTPKSSRHHHTDGAYFGTFFHNLIFQVYVFPALMPVKSAERIVPRCFGRVHAAASLVRWQSGRR	300
gi	114326228	ref	NP_001039919.1	DEELEDNPNQSDLLIEQAAEMLYGLIHARYILNTRGIAQMLEKYQQGDFGYCPRVYCNENPMLPIGLSDIPGEAMVKLYCPKCMDVYTPKSSRHHHTDGAYFGTFFHNLIFQVYVFPALMPVKSAERIVPRCFGRVHAAASLVRWQSGRR	300
gi	7106277	ref	NP_034105.1	DEELEDNPNQSDLLIEQAAEMLYGLIHARYILNTRGIAQMLEKYQQGDFGYCPRVYCNENPMLPIGLSDIPGEAMVKLYCPKCMDVYTPKSSRHHHTDGAYFGTFFHNLIFQVYVFPALMPVKSAERIVPRCFGRVHAAASLVRWQSGRR	300
gi	23503295	ref	NP_001311.3	DEELEDNPNQSDLLIEQAAEMLYGLIHARYILNTRGIAQMLEKYQQGDFGYCPRVYCNENPMLPIGLSDIPGEAMVKLYCPKCMDVYTPKSSRHHHTDGAYFGTFFHNLIFQVYVFPALMPVKSAERIVPRCFGRVHAAASLVRWQSGRR	300
gi	78214347	ref	NP_001030315.1	DEELEDNPNQSDLLIEQAAEMLYGLIHARYILNTRGIAQMLEKYQQGDFGYCPRVYCNENPMLPIGLSDIPGEAMVKLYCPKCMDVYTPKSSRHHHTDGAYFGTFFHNLIFQVYVFPALMPVKSAERIVPRCFGRVHAAASLVRWQSGRR	300
gi	292624283	ref	XP_002665575.1	DEELEDNPNQSDLLIEQAAEMLYGLIHARYILNTRGIAQMLEKYQQGDFGYCPRVYCNENPMLPIGLSDIPGEAMVKLYCPKCMDVYTPKSSRHHHTDGAYFGTFFHNLIFQVYVFPALMPVKSAERIVPRCFGRVHAAASLVRWQSGRR	300
gi	18858421	ref	NP_571262.1	DEELEDNPNQSDLLIEQAAEMLYGLIHARYILNTRGIAQMLEKYQQGDFGYCPRVYCNENPMLPIGLSDIPGEAMVKLYCPKCMDVYTPKSSRHHHTDGAYFGTFFHNLIFQVYVFPALMPVKSAERIVPRCFGRVHAAASLVRWQSGRR	300
gi	45554910	ref	NP_996415.1	DEELEDNPNQSDLLIEQAAEMLYGLIHARYILNTRGIAQMLEKYQQGDFGYCPRVYCNENPMLPIGLSDIPGEAMVKLYCPKCMDVYTPKSSRHHHTDGAYFGTFFHNLIFQVYVFPALMPVKSAERIVPRCFGRVHAAASLVRWQSGRR	300
gi	17508229	ref	NP_492254.1	EDLEEDNPNQSDLLIEQAAEMLYGLIHARYILNTRGIAQMLEKYQQGDFGYCPRVYCNENPMLPIGLSDIPGEAMVKLYCPKCMDVYTPKSSRHHHTDGAYFGTFFHNLIFQVYVFPALMPVKSAERIVPRCFGRVHAAASLVRWQSGRR	300
gi	15232283	ref	NP_191584.1	EDLEEDNPNQSDLLIEQAAEMLYGLIHARYILNTRGIAQMLEKYQQGDFGYCPRVYCNENPMLPIGLSDIPGEAMVKLYCPKCMDVYTPKSSRHHHTDGAYFGTFFHNLIFQVYVFPALMPVKSAERIVPRCFGRVHAAASLVRWQSGRR	300
gi	15224934	ref	NP_181996.1	EDLEEDNPNQSDLLIEQAAEMLYGLIHARYILNTRGIAQMLEKYQQGDFGYCPRVYCNENPMLPIGLSDIPGEAMVKLYCPKCMDVYTPKSSRHHHTDGAYFGTFFHNLIFQVYVFPALMPVKSAERIVPRCFGRVHAAASLVRWQSGRR	300
gi	50309855	ref	XP_454941.1	EDLEEDNPNQSDLLIEQAAEMLYGLIHARYILNTRGIAQMLEKYQQGDFGYCPRVYCNENPMLPIGLSDIPGEAMVKLYCPKCMDVYTPKSSRHHHTDGAYFGTFFHNLIFQVYVFPALMPVKSAERIVPRCFGRVHAAASLVRWQSGRR	300
gi	45185773	ref	NP_983489.1	EDLEEDNPNQSDLLIEQAAEMLYGLIHARYILNTRGIAQMLEKYQQGDFGYCPRVYCNENPMLPIGLSDIPGEAMVKLYCPKCMDVYTPKSSRHHHTDGAYFGTFFHNLIFQVYVFPALMPVKSAERIVPRCFGRVHAAASLVRWQSGRR	300
gi	6324613	ref	NP_014682.1	EDLEEDNPNQSDLLIEQAAEMLYGLIHARYILNTRGIAQMLEKYQQGDFGYCPRVYCNENPMLPIGLSDIPGEAMVKLYCPKCMDVYTPKSSRHHHTDGAYFGTFFHNLIFQVYVFPALMPVKSAERIVPRCFGRVHAAASLVRWQSGRR	300

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



gi	145615522	ref	XP_360277.2	MRRRLRKMEVSESGFKDGADEIE---DDEEEDDEEDEDGEMKDEGMAVGLVD--AVPGDSMMQGV-----	373
gi	164427743	ref	XP_001728406.1	MRRRLRKLEVESGFKDAEAEALDDDEEEEEEEEEEEELAAAMDEAGAAQQAHAAGAATGGVAAGGEGVH	373
gi	19115518	ref	NP_594606.1	QKKRLQGAEAESKNKLAIT	373
gi	73972260	ref	XP_532075.2	SPVKTIIR	373
gi	114326228	ref	NP_001039919.1	SPVKTIIR	373
gi	7106277	ref	NP_034105.1	SPVKTIIR	373
gi	23503295	ref	NP_001311.3	SPVKTIIR	373
gi	78214347	ref	NP_001030315.1	SPVKTIIR	373
gi	292624283	ref	XP_002665575.1	SPVKTIIR	373
gi	18858421	ref	NP_571262.1	SPVKTIIR	373
gi	45554910	ref	NP_996415.1	MPLRAQRGPPPKDEEPEENNADTVPKRL	373
gi	17508229	ref	NP_492254.1	ANNVAAAQNNTPAGQQSGGFNNYGL	373
gi	15232283	ref	NP_191584.1	-----	373
gi	15224934	ref	NP_181996.1	-----	373
gi	50309855	ref	XP_454941.1	LEKLLITKGINLINESGGYQF	373
gi	45185773	ref	NP_983489.1	LERELIKGVDLTKNGGYKK	373
gi	6324613	ref	NP_014682.1	LVEKLESKVDLTKSGGFKT	373

.....310.....320.....330.....340.....350.....360.....370.....

