

gi	73970139	ref	XP_538481.2	MGTKKEQETDSQDOSQGGSEROTDLOAPVHAASFQALLRKCKIKENIINKGVLEGLLISGNKESRRNFHAFSDIRKHSKLDKLPITIAAYVKNFMEGPISPRSQVRSRAASGRRKIPFFDFLGGHESRRISRFPOPTA	145
gi	78369402	ref	NP_001030367.1	-----MAPPOVLA-----FG	10
gi	218505670	ref	NP_002345.2	-----MAP-----POVLA-----FG	10
gi	114577430	ref	XP_515458.2	-----MALGGGGQPPNGVATRFPAAEFVPRALAPLPRFG	38
gi	112293275	ref	NP_032558.2	-----MAG-----FKALA-----FG	10
gi	25742698	ref	NP_612550.1	-----MAP-----FKALA-----FG	10
gi	60302776	ref	NP_001012582.1	-----MELLRG-----AA	8
gi	62955155	ref	NP_001017593.1	-----MKVLVA-----LFV	9

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



gi	73970139	ref	XP_538481.2	LPRAGGAP-----AAAPPAS-----CPPPPAGACICENYKLTINCSLNNINCCCTSIG-AONSVICSKLAKCLVMKAEMT-----GTKSG	224
gi	78369402	ref	NP_001030367.1	LLVAAATAA-----VAADDE-----GCVCENYKLTINCSVNALGCOCTSVG-TQHSVICTKLAKCLVMKAEMN-----HSKSG	79
gi	218505670	ref	NP_002345.2	LLLLAAATAA-----FAAAC-----EBCVCENYKLAIVNCFVNNRHCOCTSVG-AONTVICSKLAAKCLVMKAEMN-----GSKLG	79
gi	114577430	ref	XP_515458.2	VDLGFQNSPSSRWSLCHRDRARPCCSGRMNWASGGDRCPDGGLCGRYAPARRPGLHRECGCFPFKDHMSNAKLIVGNAELIIVKRCVCENYKLAIVNCFVNNRHCOCTSVG-AONTVICSKLAAKCLVMKAEMN-----GSKLG	181
gi	112293275	ref	NP_032558.2	LLLVAVTAA-----LAAAQ-----RDCVCDNYKLAISGLNBYGECCTSYG-FONTVICSKLASKLAMKAEMT-----HSKSG	79
gi	25742698	ref	NP_612550.1	LLLVAVTAA-----LAAAQ-----KDCVCNYYKLTISRVEYENGCCTSYG-FONTVICSKLASKCLVMKAEMT-----HSKSG	79
gi	60302776	ref	NP_001012582.1	LLLLLCAA-----CAQDS-----CTCTKNKRWANCRLLDN-VCHCNIG-SSVFNCEILTCKLLMKAEMA-----NTKSG	74
gi	62955155	ref	NP_001017593.1	VALVDVVT-----CACKTKMWAN-----CDDSGCSLTLHESSTQTLNCSKLVKPCFLMQAEMYRACNHQDTRSG	76

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



gi	73970139	ref	XP_538481.2	RRARPEGAFONNDGLYDPCDEKGLFKAKOCNGTTCWCVNTAGVRRITDK-DTEISCTERVRYWIIIEKHKTRRETPTDTSQALNALKETLKNRYOLDPKYITNLYEND--LITIDLQNSSSOKAONDVDIADVAYYFEKDVKDESIF	371
gi	78369402	ref	NP_001030367.1	RRGKPEGAIQNDGLYDPCDDKGLFKAKOCNGTSTCWCVNTAGVRRITDK-DSEISCEPVRTYWIIIEKHKTRKREKPYDLSLQALKDVIINRYOLDPKYITNLYEND--VITIDLQNSSSOKTQNDVDIADVAYYFEKDVKDESIF	226
gi	218505670	ref	NP_002345.2	RRAKPEGALQNDGLYDPCDESGLFKAKOCNGTSTCWCVNTAGVRRITDK-DTEITCSEVRVRYWIIIEKHKKAREKPYDGLSLRATLQKEITRYOLDPKFITNLYENN--VITIDLQNSSSOKTQNDVDIADVAYYFEKDVKDESIF	226
gi	114577430	ref	XP_515458.2	RRAKPEGALQNDGLYDPCDESGLFKAKOCNGTSTCWCVNTAGVRRITDK-DTEITCSEVRVRYWIIIEKHKKAREKPYDGLSLRATLQKEITRYOLDPKFITNLYENN--VITIDLQNSSSOKTQNDVDIADVAYYFEKDVKDESIF	328
gi	112293275	ref	NP_032558.2	RRIKPEGAIQNDGLYDPCDEQGLFKAKOCNGTTCWCVNTAGVRRITDK-DTEITCSEVRVRYWIIIEKHKKAREKPYDGLSLRATLQKEITRYOLDPKFITNLYENN--VITIDLQNSSSOKTQNDVDIADVAYYFEKDVKDESIF	226
gi	25742698	ref	NP_612550.1	RRMKPEGAIQNDGLYDPCDEQGLFKAKOCNGTTCWCVNTAGVRRITDK-DTEITCSEVRVRYWIIIEKHKKAREKPYDGLSLRATLQKEITRYOLDPKFITNLYENN--VITIDLQNSSSOKTQNDVDIADVAYYFEKDVKDESIF	226
gi	60302776	ref	NP_001012582.1	RREKPKDALQDGLYDPCENNGGLFKAKOCNGTTCWCVNTAGVRRITDK-DTEITCSEVRVRYWIIIEKHKKAREKPYDGLSLRATLQKEITRYOLDPKFITNLYENN--VITIDLQNSSSOKTQNDVDIADVAYYFEKDVKDESIF	221
gi	62955155	ref	NP_001017593.1	GKP-VETAFVDNDGIYDPCVCESDKFKAVCCNTEVWCVNSAGVRRITDKDKKNIKCEPAETVWVRVEMKHKSDVDFIDATKLRIGIENVLQQRVGLDKKLVSEVQYDKDRLIVVDVKKDKDRIT--DLSLMTYMEKDIKVLPLF	221

.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi	73970139	ref	XP_538481.2	HS-SKMDLRVNGEQLDLDPPGRITAIYYVDEKPPPEFSMOGLQAGIIAVIVVVVLAIVIAGIVVLVSRKRNMAKYEKAEIKEMGEMHRELNA	459
gi	78369402	ref	NP_001030367.1	HS-KRMDLRVNGEQLDLDPPGRITAIYYVDEKPPPEFSMOGLQAGIIAVIVVVVVAIAGIIVLVVSRKKSMTKYEKAEIKEMGEMHRELNA	314
gi	218505670	ref	NP_002345.2	HS-KKMDLTVNGEQLDLDPPGQTLIYYVDEKAPPEFSMOGLKAGVIAIVVVVIAVAVGIVVLVSRKRRMAKYEKAEIKEMGEMHRELNA	314
gi	114577430	ref	XP_515458.2	HS-KKMDLTVNGEQLDLDPPGQTLIYYVDEKAPPEFSMOGLKAGVIAIVVVVIAVAVGIVVLVSRKRRMAKYEKAEIKEMGEMHRELNA	416
gi	112293275	ref	NP_032558.2	HSSKSMDLRVNGEQLDLDPPGQTLIYYVDEKAPPEFSMOGLTAGIIAVIVVVVLAIVIAGIVVLVSTRKRSKAEKAEIKEMGEIHRELNA	315
gi	25742698	ref	NP_612550.1	HSSKSMDLRVNGEQLDLDPPGQTLIYYVDEKAPPEFSMOGLTAGIIAVIVVVVLAIVIAGIVVLVSTRKRSKAEKAEIKEMGEIHRELNA	315
gi	60302776	ref	NP_001012582.1	LN-NKLNMINIDNEELKFDN--MVYYVDEKPPPEFSMKSITAGVIAIVVVVLAIVAGIIGLVLSRRRK-GKYVKAEMKEMNHRELNA	306
gi	62955155	ref	NP_001017593.1	WNGPPEFVDVPGTKVSMEN--VLIYYVDDRAPFTMOKLITGGIIAVIVVVVLIIVIGFLVLPFLARRCKAQYSKAQAREMETIS----	303

.....460.....470.....480.....490.....500.....510.....520.....530.....

