

FIG. 1

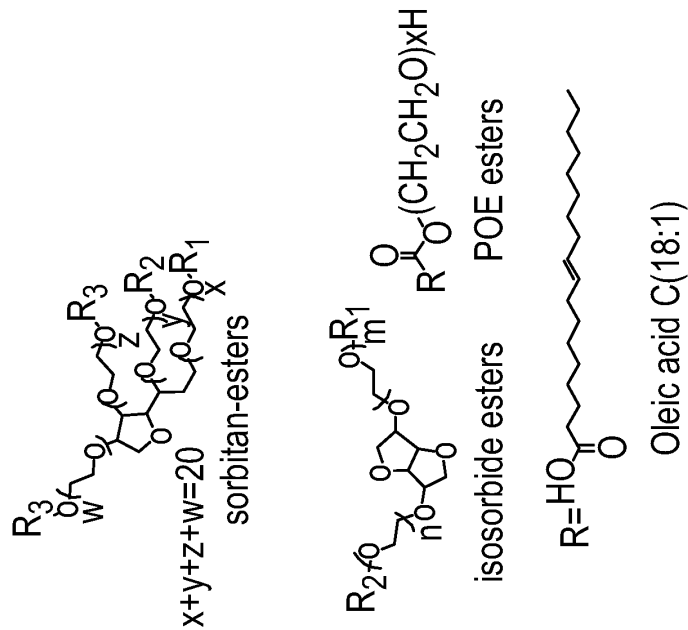
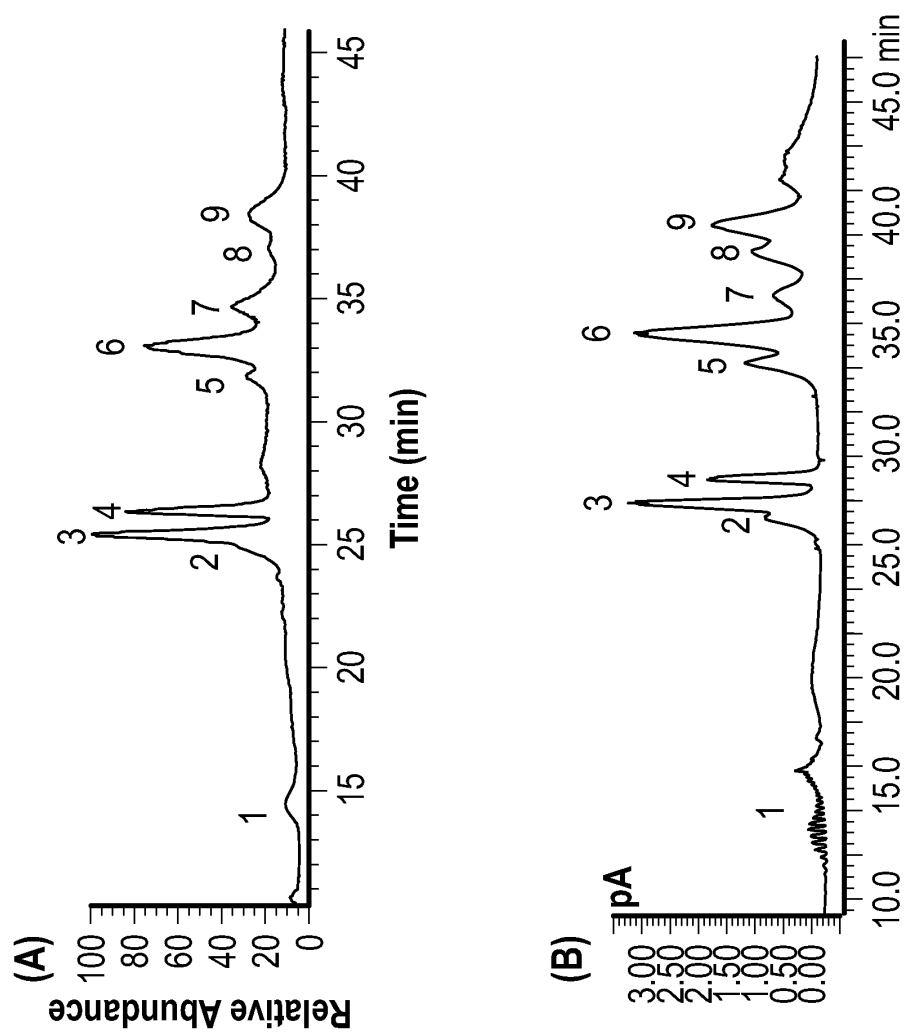


FIG. 2

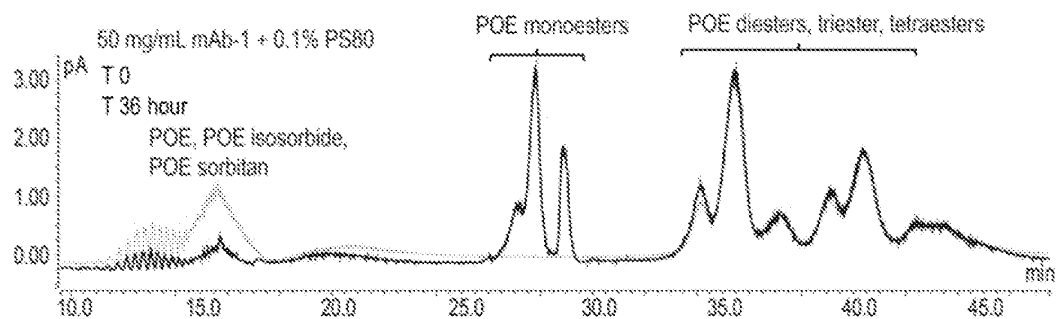
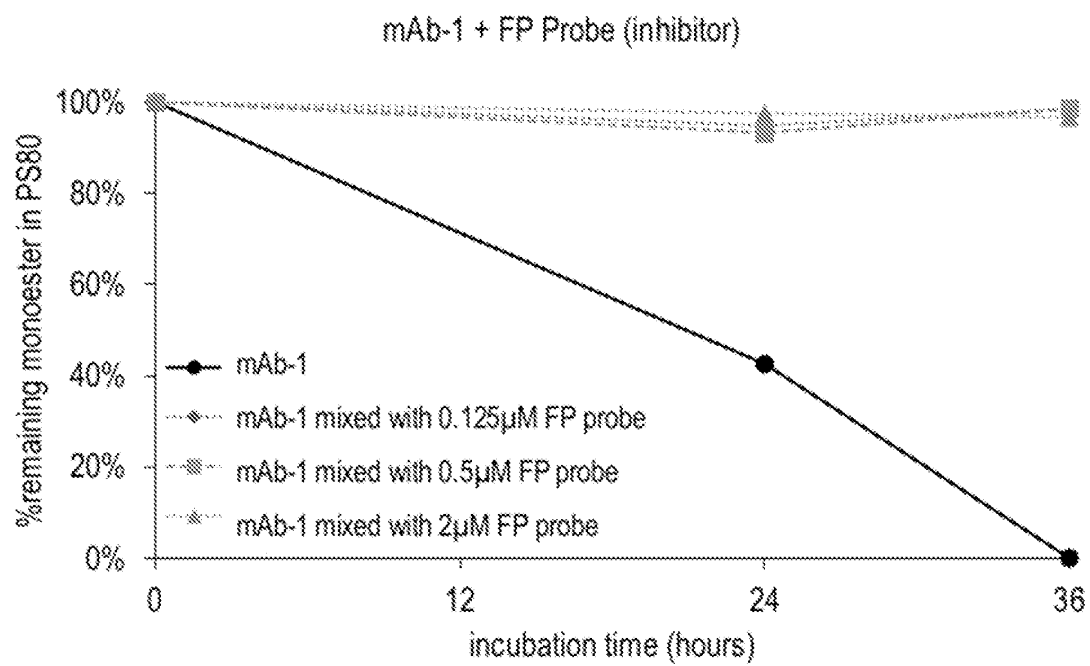


FIG. 3



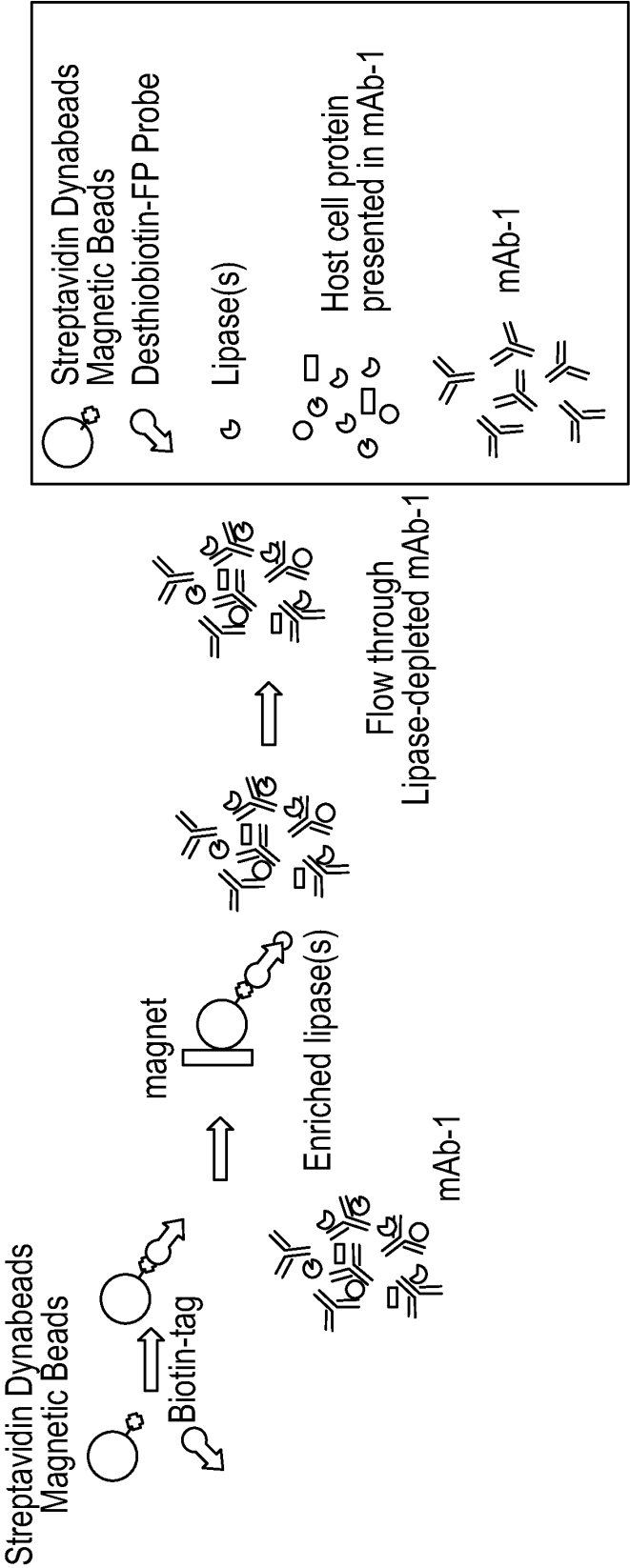
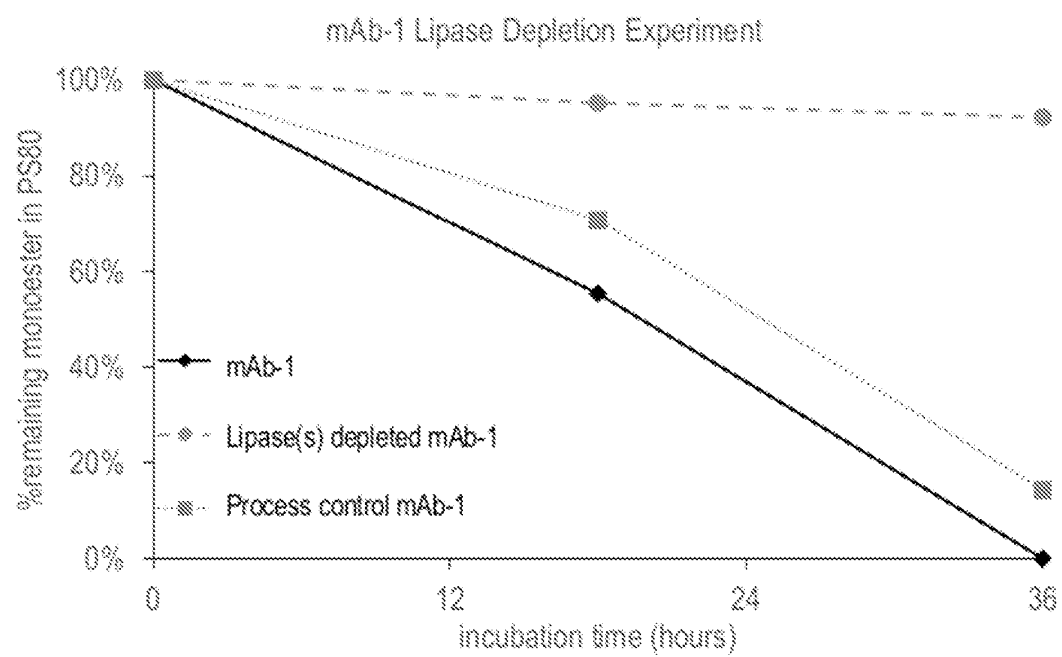


FIG. 4

FIG. 5



6/7

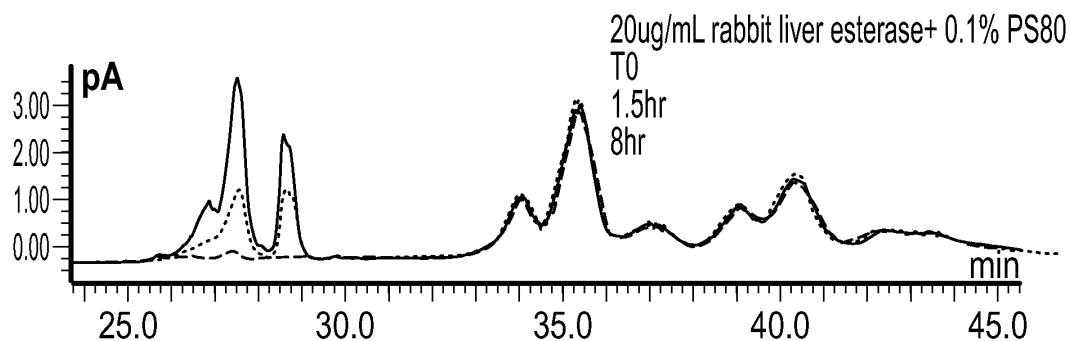


FIG. 6A

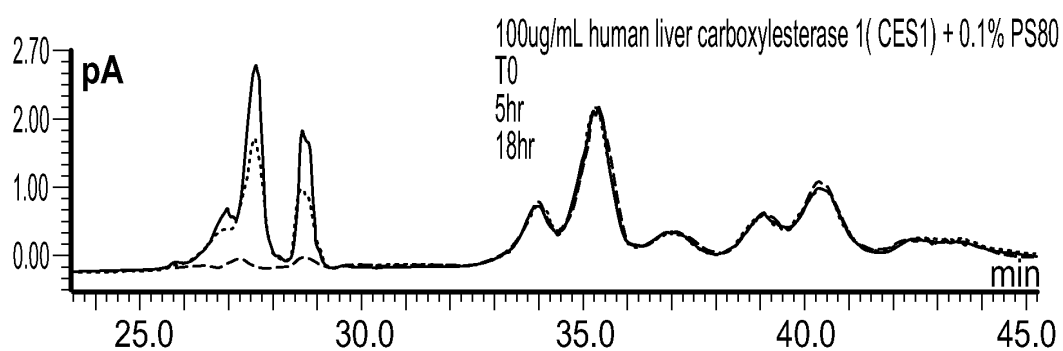


FIG. 6B

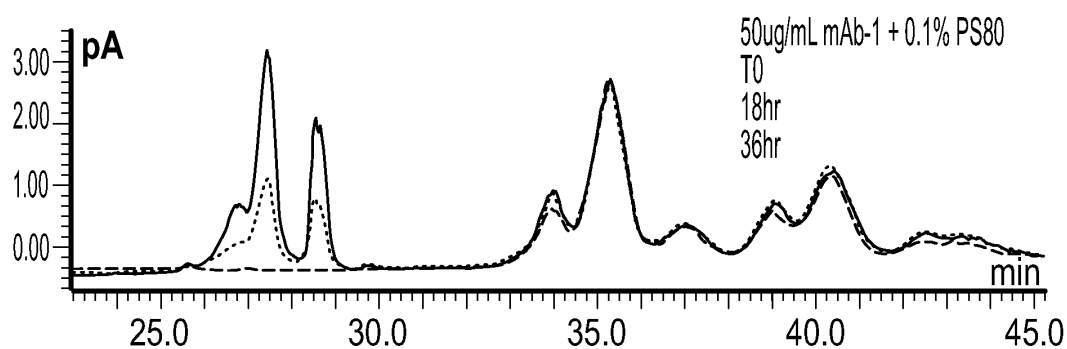


FIG. 6C

TR	A0A061I7X9		A0A061I7X9_CRIGR	-MCLQALFLVLQAICMVWGHPSPPVNTVHGKVLGRYISLEGFSQPVAVFLGVFPAKP	59
TR	A0A061IFE2		A0A061IFE2_CRIGR	MMWLCTFVLTLTACLYQGHPSPPIVDTVHGKVLGKYVSLEGTQPVAIFLGVFPAKP	60
SP	P23141 EST1	_	HUMAN	-MWLRAFILATLSASAAGHPSPPVVDTVHGKVLGKFVSLEGFAPVAIFLGIPFAKP	59
				* * : . : * : : * * * * : * : * : * : * : * : * : * : *	
TR	A0A061I7X9		A0A061I7X9_CRIGR	LGLSLRFAPPQPAEPWSFVKNATSYPMCSQDAVRGQKINDLTNRKEIHLEFSEDCLYL	119
TR	A0A061IFE2		A0A061IFE2_CRIGR	LGLSLRFAPPQSAEPWSFVKNATSYPMCSQDPAAGQMLSALTNRKETIPTLFSEDCLYL	120
SP	P23141 EST1	_	HUMAN	LGPLRLFTPPQPAEPWSFVKNATSYPMCQTQDPKAGQLSELFTRNKENIPLKLSIEDCLYL	119
				** ** ** : * * * * * : * * * * * : * * * * * : * * * * *	
TR	A0A061I7X9		A0A061I7X9_CRIGR	NIYTPANLTRSSRLPAARCMIRKARTV-----SGTK-----SFLLPQKI	158
TR	A0A061IFE2		A0A061IFE2_CRIGR	NIYTPADLTKSSRLPVMVWIHGGGLVDG-ASTYDGLPLSAHENVVVVTIQYRLGTWGFFS	179
SP	P23141 EST1	_	HUMAN	NIYTPADLTCKNRLPVMVWIHGGGLMVGAASTYDGLALAHENVVVVTIQYRLGTWGFFS	179
				* * * * * : * * * * * : * * * * * : * * * * *	
TR	A0A061I7X9		A0A061I7X9_CRIGR	TGDEHSQGNWGHLDQVAALHWVQDNIAFYEGGDPGSVTI FGESAGGSVSVLVLSPLAKNL	218
TR	A0A061IFE2		A0A061IFE2_CRIGR	TQDEHSRGNWGHLDQVAALHWVQDNIANFGGDPGSVTI FGESAGGASVSVLVLSPLAKNL	239
SP	P23141 EST1	_	HUMAN	TGDEHSRGNWGHLDQVAALRWVQDNIA SF GGN PG SV TI FG ES AG GE SV SV LV LS PL AK NL	239
				* * * * * : * * * * * : * * * * * : * * * * *	
TR	A0A061I7X9		A0A061I7X9_CRIGR	FHRAISESGVIFVPSLFTK-NPRTEATEKVAVTAGCKTTTSAVIVHCLRQKTEDELLEVMO	277
TR	A0A061IFE2		A0A061IFE2_CRIGR	FHRAISQSSVILNPCLFG-RDARPIAERVAALAGCKTTTSAMVHCLRQKTEDELLEITK	298
SP	P23141 EST1	_	HUMAN	FHRAISESGVALTSVLVKKGDVKPLAEQIAITAGCKTTTSAMVHCLRQKTEEEELLETL	299
				* * * * * : * * * * * : * * * * * : * * * * *	
TR	A0A061I7X9		A0A061I7X9_CRIGR	KMGVGFSENGMCSRCLDHAFVPTVL DGVLLPKAPEEILA EK NF NT VP Y I VG IN K Q E F GW LL	337
TR	A0A061IFE2		A0A061IFE2_CRIGR	KMKFGALDFLGDPRESYPFLTVIDGVLLPKTPPEEILA EK S FN TP Y M V G IN K Q E F G W SM	358
SP	P23141 EST1	_	HUMAN	KMKFLSLDLQGDGPRESQPLL GT VID GML L LT P EE LA ER NF HT VP Y M V G IN K Q E F G W LI	359
				* * : : : * * * * * : * * * * * : * * * * * : * * * * *	
TR	A0A061I7X9		A0A061I7X9_CRIGR	PTM-MRFPQPD---DKKMAIAL LQKFAPYFGMNEDVPVAIEKYVRGSNEPLKIRDGVLD	393
TR	A0A061IFE2		A0A061IFE2_CRIGR	PMW-IGFPLSEDKLDQKR T TS LL WQS Y PI LN IS E SL PA AE KY L SG TD N P IR KK D L L LD	417
SP	P23141 EST1	_	HUMAN	PMQLMSYPLSEGQLDQKTAMSLLWKSYP LVC IA KE LI PE A TE KY LG GT DD TV KK DL FL D	419
				* : : * : * : * * : * * : * * : * * : * * : * * : * * :	
TR	A0A061I7X9		A0A061I7X9_CRIGR	ILGDLTFGPSVIVSRGRHDTCASTMYMEFQYHPFSSSHMRPNKVVDGHDGEVYSVF GAP	453
TR	A0A061IFE2		A0A061IFE2_CRIGR	LMGDVMFGVPSVIVSRGRHDAGAPTMYMEFQYLPSEFSDMRPKTVKGDDHGLFSVWGAP	477
SP	P23141 EST1	_	HUMAN	LIADVMFGVPSVIVARNHRDAGAPTMYMEFQYRPSFSSDMKPKTVIGDHGDELFSVFGAP	479
				: : * : * : * * * * : * * * * * * * * * * * * * * * : * : * * *	
TR	A0A061I7X9		A0A061I7X9_CRIGR	ILRDGASEETNL SK MM KF WAN FAR NG NP NG EG L PH W PE Y D Q K E G Y L Q I GA TT Q O T Q RL	513
TR	A0A061IFE2		A0A061IFE2_CRIGR	FLKEGASEEEINLSKMVMKFWGNFARNGPNNGEGLPHWPEYDQKEGYLQIGVPTQAAHRL	537
SP	P23141 EST1	_	HUMAN	FLKEGASEEEIRLSKMVMKFWANFARNGPNNGEGLPHWPEYNQKEGYLQIGANTQAAQKL	539
				: * : * * * * * : * * * * * : * * * * * : * * * * * : * * : * *	
TR	A0A061I7X9		A0A061I7X9_CRIGR	KGEEVAFWTEILAKKHKPEH-NELSNKYLC---FELA IK ET RD SL HN PN AR D VF Q VL --	567
TR	A0A061IFE2		A0A061IFE2_CRIGR	KDKEVAFWTELRAKEPAERPTQRKHVMVWIHGGGLILGGASTYDGLALSAHENVVVA IQ	597
SP	P23141 EST1	_	HUMAN	KDKEVAFWTNLFAKKA VE KP QT EH IE L -----	567
				* : * * * * * : * * : * * : * * : * * : * * : * * : * * :	
TR	A0A061I7X9		A0A061I7X9_CRIGR	-KSASYCKGSIVRHPTSPPVVDTVHGKVLGKYVSLEG-----FAQPVAVFLGVPF----	616
TR	A0A061IFE2		A0A061IFE2_CRIGR	YRLSIWGFFS-----TGDEHSRGNWGHLDQVAALHWVQDNIANFGGDPGSVTI	645
SP	P23141 EST1	_	HUMAN	-----	
				-----AKPPLGSLRFAPPQPP-----EPWNFVK-----NATSYPPMCSQPD	652
TR	A0A061I7X9		A0A061I7X9_CRIGR	FGESAGGESVSVLMFSPLAKNLFHRAISESGVILVPLGFTKDSRIVTEKVAVTAGCKTT-	704
TR	A0A061IFE2		A0A061IFE2_CRIGR	-----	
SP	P23141 EST1	_	HUMAN	-----	
				VTGQIVNDLLTNRKENIPLQFSEDCLYLNITYTPSDLTRSD-----	692
TR	A0A061I7X9		A0A061I7X9_CRIGR	-TSATIVHCLRQKTEDELLEV MQ MN LF LKNV Q GD TK EN HA F V PT VL DG V LL PK A P EE IL	763
TR	A0A061IFE2		A0A061IFE2_CRIGR	-----	
SP	P23141 EST1	_	HUMAN	-----	
				-----RLPVSCGTSP-TF-----	704
TR	A0A061I7X9		A0A061I7X9_CRIGR	AEKNFNTPVIYVGINKQEFGWLLPTMMGFLQTDVKWDKKMAIAL LQKFAPYFCVQYGRPA	823
TR	A0A061IFE2		A0A061IFE2_CRIGR	-----	
SP	P23141 EST1	_	HUMAN	-----	
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