

mLPCAT3.seq	1	MASTADGMGETLEQMRGLWPGVEDLSLNKLATSLGASEQALRLTFSTFLGYPLALFYRH	60
mLPCAT4.seq	1	-----MATTSTTGSTLLQPLSNAVQLPIDQVNFVVCQLFALLAAVWFRF	44
mLPEAT1.seq	1	-----MAARPASLSYRTTGSTCLHPLSQLGLPILDQVNFVACQLFALSAAFVFRF	51
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mLPCAT3.seq	60	YLFY--KDSYLHFLHFTFTGLSIAYFNFGHGFYHSLLCVVLQFLTLRLMGRVTVAVITTL	118
mLPCAT4.seq	44	YVHSSKTSSFIRHVVATLLGLYLAFPCFGWYALHFLVQSGISYICIMIIAGVESMQCCFV	104
mLPEAT1.seq	51	YLHPGKASPEVRHTLATILGTYFVVFVFCGWYAVHLFVLVLMCYGVMMVTASVSNIHRSYFF	111
		**.....*.*.*.*.*.*.*.*.*.*.....*	
mLPCAT3.seq	118	CFQMayL----LAGYYTATGDYD[LKWTMPHCVLTlKlTGLCl]DYDYG--GKDGNSLTSEQ	173
mLPCAT4.seq	104	-FALGLSVCQITRVYIFDYDGYQASDFSGPMMIITQKITSLAYEIHDMGRKDEELTPSQ	163
mLPEAT1.seq	111	-VAMGYLTICHISR[YTFHYGILTDFSGPLMIVT]KITTLAFQVHDGLGRKAEDLSAEQ	170
		.....**.....*.*.*.*.*.*.*.*.*.*.....*	
mLPCAT3.seq	173	QKYAIRGVPSSLLEVAGFSYFYGAFLVGPQFSMNHMYMKLVRGQ-----LTDIPG	221
mLPCAT4.seq	163	RGLAVRRMPSLLEYVSYTCNFMGILAGLPCSYKYDIAFIEGRASHVAQPSEN--GKDEQHG	222
mLPEAT1.seq	170	HRLAVKAP[PSLCELYSLYHLNFMVSIAG]GPCNNFKDYVAFIEGRHIHMKLLEVNWTQRGFQS	230
		*.....*****.....*.*.*.*.*.*.*.*.....*	
mLPCAT3.seq	221	KM--PNSTIPALKRSL[GLVYLVGyTLLSPHITD]DYLLTEDYDNRPFWF--RCMYMLIWGKF	279
mLPCAT4.seq	222	KADPSNAAVEKELLVCGLSLFLHFLTISNMLPVEYNIDEHFQATASWPTKATYLYVSLLA	282
mLPEAT1.seq	230	LPEPSPMGAVIQKL[CVTLMSLLFLTLKSFPVTF]LDDVFWHKANFLSRLWLYVVMQA	290
		*.....*.*.*.*.*.*.*.*.....*	
mLPCAT3.seq	279	VLYK[YVTCWLVTEGVCTLSGLGF]NGFDENGTVRWDACANMKVWLFETTPRFN[ITASENI]	339
mLPCAT4.seq	282	ARPKYYFAWTLADAINNAAGFGFRGYDKNGVARWDLISNLRIQQIEMSTFKMFLDNWNI	342
mLPEAT1.seq	290	AKPKY[FAWTLADAVHNAAGFGFN]GMDTDGKSRWDLISNLRNIWKIETATSFKMYLENWNI	350
		*.*.*.*.....*.*.*.*.*.*.*.*.*.*.....*	
mLPCAT3.seq	339	[NTNAWVARYIF]KRLKFLGNKELSQL[SLFLALWHGLHSGYLICF]QMEFLIVIVEKQVSS	399
mLPCAT4.seq	342	QTALWLKRCYERATF----SPTIQTFFLSAIWH[GVYPGYLTFLTGLVMT]AARAVRN	397
mLPEAT1.seq	350	QTSTWLKVCYERVPW----YPTV[VLTFLLSALWHGVYPGYFTLGTVP]VTLAARAVRN	405
		*.*.*.*.....*.*.*.*.*.*.*.*.*.*.....*	
mLPCAT3.seq	399	LIRDS[PALSSLASITALQPFYYLV]QTIHFWLFGYSMTAFCLFTWDKWLKVYRS[CYFLGH]	459
mLPCAT4.seq	397	NFRH----YFLEPPQLKLFYD[LITWVATQITISYTVVVPFVLLSIR]PSFTFYSSWYCYLH	452
mLPEAT1.seq	405	NYRH----HFLSSKARKIAYD[VVTWAVTQLAVSYTAAPFVMLAV]EPTISLYK[SVFFFLH]	460
		*.*.....*.*.*.*.*.*.*.*.....*	
mLPCAT3.seq	459	[VFFLSLLETLPIY]HKAMVPRKEKLRKRE-----	487
mLPCAT4.seq	452	VCSILVLLLLPVK--KSQRRTSTQENVHL[SAQAKKFDERDNPLGQNSFSSTMMNVCNQNRDT	510
mLPEAT1.seq	460	[ITCLLITLFLPI]KPHQPQRQSRSPNSVKKKAD-----	492
		*.....**.....*	
mLPCAT3.seq	487	-----	487
mLPCAT4.seq	510	GSRHSSLTQ	519
mLPEAT1.seq	492	-----	492