

Additional file 12 - Clustal format Mafft (v6.857b) alignment for lipoprotein Blast matches to LP1.

Nearly identical sequences were excluded (C7A8A2, see Fig. S3; Q0VJU3_MANSE is C-terminally longer by two amino acids than VITM_MANSE (P19616) and was retained for comparison to *Bombyx mori* sequences). Marked in yellow: sequence identities with LP1. Marked in green: sequences identities with L302. Marked in pink: sequence identities with LP3. Accession numbers in red represent related proteins from *Manduca sexta* and *Pseudaletia separata*.

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sp|P09334|LP1_M-----
tr|Q17185|_M-----
sp|Q00801|L302_M-----
tr|A7LIK7|_M-----
sp|P09335|LP2_M-----
sp|P09338|LP5_M-----
sp|P09337|LP4_M-----
tr|Q0VJU3|_M-----
tr|Q05432|_M-----
tr|Q75RW3|_M-----
tr|E5EVW2|_M-----
tr|D4QGC0|_-----
tr|D4QGB9|_-----
tr|C7A8A3|_M-----
sp|Q00802|L301_M-----
sp|P09336|LP3_M-----
tr|Q6Q0S8|_-----
tr|Q2PQU4|_MTTSFSHSQVKTPSEEKWEAASEPDYHTNEDLLYPYSPIPYFGMYHLVKIPIG-RGLVHH
tr|B5BSX5|_M-----MDPQDKLPNYVTNVDLKYPYSDLPHYIGQYKLLKLPFT-GKLIEH
tr|Q76IB6|_M-----RSLTIWKLAQRPNFNTNINKQFPYSETPYQGDYYLEKIPISLNNLIQH
tr|E5EVW3|_M-----
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sp P09334	LP1	-----	RLTL
tr Q17185		-----	RLTL
sp Q00801	L302	-----	K
tr A7LIK7		-----	K
sp P09335	LP2	-----	K
sp P09338	LP5	-----	K
sp P09337	LP4	-----	K
tr Q0VJU3		-----	LR
tr Q05432		-----	K
tr Q75RW3		-----	K
tr E5EVW2		-----	K
tr D4QGC0		-----	
tr D4QGB9		-----	
tr C7A8A3		-----	K
sp Q00802	L301	-----	K
sp P09336	LP3	-----	K
tr Q6Q0S8		-----	
tr Q2PQU4		VDYWGEKGKVTNLDRVRGFRRSYNVNEQFALVSKGHSKQIPNRI PVVSVDSDTSSYIR	
tr B5BSX5		VDYWGEGSIVNGGLYSGFRNCYNVNRQYQEVSNQPDMDGRKIPNRI PVRDENDCDTRAYIK	
tr Q76IB6		VDYWGEKGKVVTEEGVRGFSNCYNVNHQYQLVSSGPDKDRKIPNRI PVRSEDEDCDTSSYIK	
tr E5EVW3		-----	

sp P09334	LP1	FAFVLAVCALASN	-----
tr Q17185		FAFVLAVCALASN	-----
sp Q00801	L302	FLVVFASCVLAVS	-----
tr A7LIK7		LLVVFAMCMLAAS	-----
sp P09335	LP2	LLVVFAMCVPAAS	-----
sp P09338	LP5	FLVVFVAVVRACVT	-----
sp P09337	LP4	FVVVFASCVLAVS	-----
tr Q0VJU3		TTVVLLTLAAIAF	-----
tr Q05432		FLVFFSTCVLAAS	-----
tr Q75RW3		TLAVLALCLVAAS	-----
tr E5EVW2		PVIVILCLFVASI	-----
tr D4QGC0		-----	-----
tr D4QGB9		-----	-----
tr C7A8A3		PAIVILCLFVASI	-----
sp Q00802	L301	PAIVILCLFVASI	-----
sp P09336	LP3	PAIVILCLFVASI	-----
tr Q6Q0S8		-----	-----
tr Q2PQU4		DGGVKTVTISTGP-ISKRCAADVARI	VNASEGLVVAYGYSENSDDIQNLERELGKKGLYY
tr B5BSX5		DDSVKIVTLM SAP-IIPNSARDITRIVNERVGMVVIY	GMPVESQGIKLLAAELKSKLLLY
tr Q76IB6		DNSVLTVTVAEASRITSSCAKDIARI	INSDHGKVIVYGVQGNSQEISELAVELRKKGLTP
tr E5EVW3		-----	-----

sp P09334 LP1	-----A-----TLAPRTDDVLAEQLYMSVVIGEYETAIACSEYLKEKKGE-V
tr Q17185	-----A-----TLAPRTDDVLAEQLYMSVVIGEYETAIACSEYLKEKKGE-V
sp Q00801 L302	-----A--GVAEMSAVSMSSSNKELEEKLYNSILTG DYDSAVRQSLEYENQGKGS-I
tr A7LIK7	-----A--GVVELSA---DTSNQDLEEKLYNSILTG DYDSAVRQSLEYESQGKGS-I
sp P09335 LP2	-----A--GVVELSADSMSPSNQDLEDKLYNSILTG DYDSAVRKSLEYESQGQGS-I
sp P09338 LP5	-----P--ACAEMSAVSMSSSNKELEEKLYNSILTG DYDSAVRQSLEYESQGKGS-I
sp P09337 LP4	-----A--GVTEMSAASMSSSNKELEEKLYNSILTG DYDSAVRQSLEYENQGKGS-I
tr Q0VJU3	-----AAPTSDDIYNNVVIGDIDGAVAKSKELQKQKQKGD-I
tr Q05432	-----A--GLIDLDINILSAPTR-AETRLVDAITTTADYNTAVSLILLLEKQSSGS-I
tr Q75RW3	-----ATPSIDGDDRYPIHAPSG-YEDIVTNATITRNYEAAASMTVQLKRRSSGR-Y
tr E5EVW2	-----YAADSDVPNDILEEQLYNSIVVADYDSAVEKSKHLYEEKKSE-V
tr D4QGC0	-----SDVPNDILEEQLYNSIVVADYDSAVEKSKHLYEEKKSE-V
tr D4QGB9	-----SDVPNDILEEQLYNSV VVADYDSAVEKSKHLYEEKKSE-V
tr C7A8A3	-----YAADSDVPNDILEEQLYNSV VVADYDSAVEKSKHLYEEKKSE-V
sp Q00802 L301	-----YAADSDVPNDILEEQLYNSV VVADYDSAVEKSKHLYEEKKSE-V
sp P09336 LP3	-----YAADSDVPNDILEEQLYNSV VVADYDSAVEKSKHLYEEKKSE-V
tr Q6Q0S8	-----ADSDVPNDILEEQLYNSV VVADYDSAVEKSKHLYGEKKSE-V
tr Q2PQU4	GAGYELPADLKTQTEFSTKMVFADARSINDHLYNLVTGGDYINAVKTVRSLDDNQGS-G-V
tr B5BSX5	CPDYELPDYLQEPTMMDSHVAFLNKQLLMDLLFKCVSTGDYDKAVTITKSLQDDNVGF-M
tr Q76IB6	SPNAALPRELQGLTYYN SHVAFLDNHNFEEEVYNSVINGDYDAAVNMAQSYGVASNSE-F
tr E5EVW3	-----SVEASDSGKSDRKLYNSVITADYDDATKRCEQLQSEPDGSI

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sp P09334	LP1	IKEAVKRLIENGKRNTMDFAYQLW--TKDGKEIVKSYFPFIQFRVIFTEQT-VKLINKRDH
tr Q17185		IKEAVKRLIENGKRNTMDFAYQLW--TKDGKEIVKSYFPFIQFRVIFTEQT-VKLINKRDH
sp Q00801	L302	IQNVVNLIIDGSRNTMEYCYKLW--VGNGQHIVRKYFPYNFRLIMAGNF-VKLIYRNYN
tr A7LIK7		IQNVVNLIIDKRRNTMEYCYKLW--VGNGQEIVRKYFPPLNFRLIMAGNY-VKIIYRNYN
sp P09335	LP2	VQNVVNLIIDKRRNTMEYCYKLW--VGNGQDIVKKYFPPLSFRLIMAGNY-VKLIYRNYN
sp P09338	LP5	IQNVVNLIIDKRRNTMEYCYKLW--VGNGQEIVRKYFPPLNFRLIMAGNY-VKIIYRNYN
sp P09337	LP4	IQNVVNLIIDGSRNTMEYCYKLW--VGNGQHIVRKYFPYNFRLIMAGNF-VKLIYRNYN
tr Q0VJU3		ITEAVNRLIRDSQRNTMEYAYQLW--SLEARDIVKERFPFIQFRMMLGEHS-IKLINKRDN
tr Q05432		IEDTVNNLIRDGNRNVLEFAYKLW--IGEGKEIVKHYPVQFRQVLSESN-VKIINKRDN
tr Q75RW3		ITIIIVNRLIRENKRNICDLAYKLWDYMDSEQEIIVKEYFPVIFRQIFSENS-VKIINKRDN
tr E5EVW2		ITNVVNKLIRNNKMNCMEYAYQLW--LQGSKDIVRDCFPVEFRLIFAENA-IKLMYKRDG
tr D4QGC0		ITNVVNKLIRNNKMNCMEYAYQLW--LQGSKDIVRDCFPVEFRLIFAENA-IKLMYKRDG
tr D4QGB9		ITNVVNKLIRNNKMNCMEYAYQLW--LQGSKDIVRDCFPVEFRLIFAENA-IKLMYKRDG
tr C7A8A3		ITNVVSKLIRNNKMNCMEYAYQLW--LQGSKDIVRDCFPVEFRLIFAENA-IKLMYKRDG
sp Q00802	L301	ITNVVNKLIRNNKMNCMEYAYQLW--LQGSKDIVRDCFPVEFRLIFAENA-IKLMYKRDG
sp P09336	LP3	ITNVVNKLIRNNKMNCMEYAYQLW--LQGSKDIVRDCFPVEFRLIFAENA-IKLMYKRDG
tr Q6Q0S8		ITNVVNKLIRSNKMNCMEYAYQLW--LQGSKDIVRDCFPVEFRLIFAENA-IKLMYKRDG
tr Q2PQU4		CRDVVSRLVSQGIKNAMSFAYKLW--HEGHKDIVEDYFPSEFQLILDQKR-IKLIGNHYN
tr B5BSX5		IEELIDRLLRAREPNVFAYADKLW--SAGHHDIVNDFFPSEVKLITKQER-VKIIIGRYN
tr Q76IB6		TNRIVTRLMTAFPRKLMSFAYKLW--HGAKEIVRNHFPKAFQHIFNEDA-VTIVNKQYQ
tr E5EVW3		IKNTVTELLNNAESNTINF SYKLW--TTGHQNIIVQSCFPLEFRLILDDKKDCIKIINKHDD
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sp P09334	LP1	HALKLID--QQNHNKIAFGDSKD--KTSKKVSWKFTPV-LENNRVYFKIMSTEDKQYLKL
tr Q17185		HALKLID--QQNHNKIAFGGSKD--KTSKKVSWKFTPV-LENNRVYFKIMSTEDKQYLKL
sp Q00801	L302	LALKLGPTLDPANERLAYGDGKE--KNSDLISWKFITL-WENNRVYFKIHNTKYNQYLKL
tr A7LIK7		LALKLGSTTNPSNERIAYGDGVD--KHTELVSWKFITL-WENNRVYFKIHNTKYNQYLKM
sp P09335	LP2	LALKLGSTTNPSNERIAYGDGVD--KHTDLVSWKFITL-WENNRVYFKAHNTKYNQYLKM
sp P09338	LP5	LALKLGSTTNPSNERIAYGDGVD--KHTELVSWKFITL-WENNRVYFKIHNTKYNQYLKM
sp P09337	LP4	LALKLGPTLDPANERLAYGDGKE--KNSDLISWKSHYLVGEQHSVLQDPPTLSYNQYLKL
tr Q0VJU3		LAMKLGVATDNSGDRIAYGAADD--KTSDRVAWKEVPL-SEDKRVYFKILNVQRGQYLKL
tr Q05432		LAIKLGAAADSDNDRIAYGDAND--KSSENVSWKLIPL-WENNRVYFKIYSVRRHQYLKL
tr Q75RW3		LAIKLGDALDSDNDRVAYGDAND--KTSDNVWAKLIPL-WDDNRVYFKIFS VHRNQIFEI
tr E5EVW2		LALTLSNDVHGN DGRLAFGDGKD--KTSPKVS WKFI AL-WENNKVYFKILNTERNQYLV L
tr D4QGC0		LALTLSNDVHGN DGRLAFGDGKD--KTSPKVS WKFI AL-WENNKVYFKILNTERNQYLV L
tr D4QGB9		LALTLSNDVQGDDGRPAYGDGKD--KTSPRVSWKLI AL-WENNKVYFKILNTERNQYLV L
tr C7A8A3		LALTLSNDVQGDDGRPAYGDGKD--KTSPRVSWKLI AL-WENNKVYFKILNTERNQYLV L
sp Q00802	L301	LALTLSNDVQGDDGRPRYGDGKD--KTSPRVSWKLI AL-WENNKVYFKILNTERNQYLV L
sp P09336	LP3	LALTLSNDVQGDDGRPAY--GKD--KTSPRVSWKLI AL-WENNKVYFKILNTERNQYLV L
tr Q6Q0S8		LAVTLSNDVQGDDGRPAYGDGKD--KTSPRVSWKLI AL-WENNKVYFKILNTERNQYLV L
tr Q2PQU4		QALKLDANVD RYKDR L TWGDGKD--YTSYRVSWRLISL-WENNNVIFKILNTEHEMYLKL
tr B5BSX5		QALKLDSNVDSYNNRLAWGDSKD--KTSHRVSWKFI PV-WENNKLLYKILNTEYTMYLKL
tr Q76IB6		QPLKLDVNTDSMNDR LAWGDHNQCKITSERLSWKILPM-WNRDGLTFKLYNVHRNMYLKL
tr E5EVW3		LYMTLSKDL DQNGDRDAYGDEDD--HKN---SWKFMSS-WESNRVYFKIFNPKNQRLKM
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sp P09334	LP1	DNTK-GSSD-DRIIYGDSTADTFKHHWYLEPS--MYESDVMFFVYNREYNS-VMTLDEDM
tr Q17185		DNTK-GSSD-DRIIYGDSTADTFKHQWYLEPS--MYESDVMFFVYNREYNS-VMTLDEDM
sp Q00801	L302	SSTT-DCNTQDRVIFGTNTADTTREQWFLOPT--KYENDVLFYIYNREYND-ALKLGRIV
tr A7LIK7		STTTCNCNSRDRVVYGGNSADSTREQWFFQPA--KYENDVLFYIYNRQFND-ALELGTIV
sp P09335	LP2	STSTCNCNARDRVVYGGNSADSTREQWFFQPA--KYENDVLFYIYNRQFND-ALELGTIV
sp P09338	LP5	STTTCNCNSRDRVVYGGNSADSTREQWFFQPA--KYENDVLFYIYNRQFND-ALELGTIV
sp P09337	LP4	SSTT-DCNTQDRIIFGTNTADTTREQWFLOPT--KYENDVLFYIYNREYVQRVALKLGRIV
tr Q0VJU3		GVET-DSDG-EHMAYASSGADTFRHQWYLQPA--KADGNLVFFIVNREYNH-ALKLGRSV
tr Q05432		GTGT-DGEN-DHSVYGDDRADTTHRHQWYLKPA--KLDNQVLFYIYNRQYNQ-ALKLSRSV
tr Q75RW3		RHTYLTVDN-DHGVYGGDDRADTTHRHQWYLNPA--ELENQVLFYIYNRQYDQ-ALKLGRNV
tr E5EVW2		GVGT-NPNG-DHMAFGVNSVDSFRAQWYLQPA--KYDKDNLFYIYNREYSK-ALTLSRTL
tr D4QGC0		GVGT-NPNG-DHMAFGVNSVDSFRAQWYLQPA--KYDKDNLFYIYNREYSK-ALTLSRTL
tr D4QGB9		GVGT-NWNG-DHMAFGVNSVDSFRAQWYLQPA--KYDNDVLFYIYNREYSK-ALTLSRTV
tr C7A8A3		GVGT-NWNG-DHMAFGVNSVDSFRAQWYLQPA--KYDNDVLFYIYNREYSK-ALTLSRTV
sp Q00802	L301	GVGT-NWNG-DHMAFGVNSVDSFRAQWYLQPA--KYDNDVLFYIYNREYSK-ALTLSRTV
sp P09336	LP3	GVGT-NWNG-DHMAFGVNSVDSFRAQWYLQPA--KYDNDVLFYIYNREYSK-ALTLSRTV
tr Q6Q0S8		GVGT-NWNG-DHMAFGVNSVDSFRAQWYLQPA--KYDNDVLFYIYNREYSK-ALTLSRTV
tr Q2PQU4		DVNV-DRYG-DRKTWGSNDSSEKRHTWYLYPV--KVGDQQLFLIENREYRQ-GLKLDANV
tr B5BSX5		DMNV-EEYG-DRKAWGSNNSNEKGHLWKLTTPV--VLETGNVLLIENHEYGQ-SLKLDHNV
tr Q76IB6		DASV-DSMG-DRQAWGSNNSNEDRHRYYLEPMISPHNGTLVFFIINYKYGQ-GLKLDAST
tr E5EVW3		GDPV--KDD-ERKVFSSDDATDSTSQWYLQAM--NHKGDLLFFIFNRRYSQ-ALKIGKDV
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sp P09334	LP1	_____	AANEDREALGHSGEVSGYPQLFAWYIVPY--
tr Q17185		_____	AANEDREALGHSGEVSGYPQLFAWYIVPY--
sp Q00801	L302	_____	DASGDRMAFGHDGEVAGLPDIFSWFVTPF--
tr A7LIK7		_____	YASGDRKAVGHDGEVAGLPDIYSWFITPF--
sp P09335	LP2	_____	NASGDRKAVGHDGEVAGLPDIYSWFITPF--
sp P09338	LP5	_____	NASGDRKAVGHDGEVAGLPDIYSWFITPF--
sp P09337	LP4	_____	DASGDRSGI-----WTRWMK--
tr Q0VJU3		_____	DSMGDRQVWGHNGNVIGNPELFGWSVVAFFV
tr Q05432		_____	DSDGDRRAYSSSSSVEGQPELFGWSISIL-N
tr Q75RW3		_____	DSDGDRRAYSSSSSVEGQPELYAWSISIL-N
tr E5EVW2		_____	ETSGNRMAWGYNGRVIGSPEHYAWGVKAF--
tr D4QGC0		_____	ETSGNRMAWGYNGRVIGSPEHYAWGVKAF--
tr D4QGB9		_____	EP SGHRMAWGYNGRVIGSPEHYAWGIKAF--
tr C7A8A3		_____	EP SGHRMSWGYNGRVIGSPEHYAWGIKAF--
sp Q00802	L301	_____	EP SGHRMAWGYNGRVIGSPEHYAWGIKAF--
sp P09336	LP3	_____	EP SGHRMAWGYNGRVIGSPEHYAWGIKAF--
tr Q6Q0S8		_____	EP SGHRMAWGHNGRVIGSPEHYAWGIKAF--
tr Q2PQU4		_____	DRYGDRLVWGNNGTVADNPEYYGFIIQPW-Q
tr B5BSX5		_____	DSYGDRLLWGNNGNVDGNPGYFGWVINAW-Q
tr Q76IB6		_____	DDIGDRLLWGHNGTVYNEYERFRWII SAW--
tr E5EVW3		_____	VN NEDFRIYGESEDAAEKPHYFGWLI EPM--

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