

Supplemental Files

Lipid transfer particle from silkworm, *Bombyx mori* is a novel member of the apoB/large lipid transfer protein family.

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Supplemental Files

Supplemental TABLE 1. Accession numbers of sequences of the large lipid transfer protein (LLTP) superfamily.

LLTP sequences were collected from the National Center for Biotechnology Information (NCBI* <http://www.ncbi.nlm.gov>) protein sequence database. Lipid transfer particle (LTP) from silkworm, *B. mori*, is a novel member of the apoB/large lipid transfer protein family.

Supplemental Fig. 1. cDNA structure of *Bombyx mori apoLTP-II/I*.

The column (*apoLTP-II* and *apoLTP-I* cDNA) indicated the ORF of apoLTP-II/I cDNA. PCR primers used for determination of the cDNA sequence are indicated above the column. All sequences from 5'-RACE, 3'-RACE, and RT-PCR methods were combined into the full-length cDNA sequence of *B. mori apoLTP-II/I*. For details on the determination of cDNA, see the Materials and Methods.

Supplemental Fig. 2. Alignment of conserved motifs in the large lipid transfer (LLT) module of the large lipid transfer protein (LLTP) superfamily.

Twenty-two conserved motifs, N1-N22, are indicated below the alignment. The allowed conservative substitution were as follows: A, G; S, T; E, D; R, K, H; Q, N; V, I, L, M; Y, F, W; P; and C. Gaps are indicated by dashes; $\geq 50\%$ identical amino acid residues are boxed in gray.

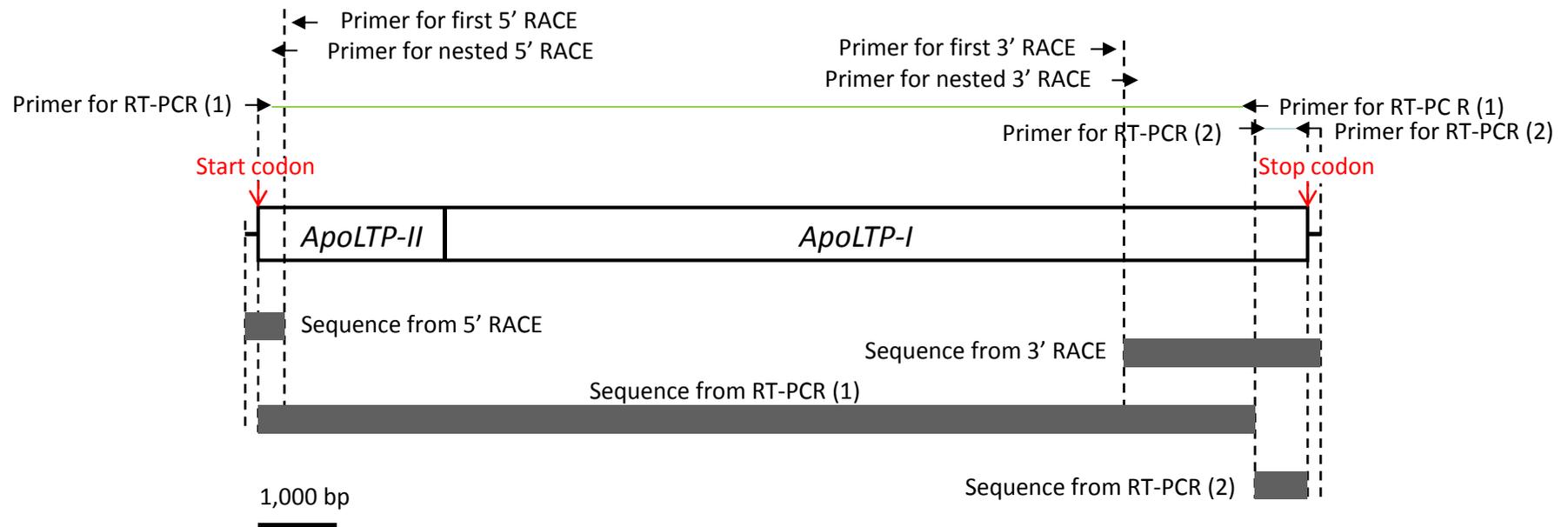
Supplemental Fig. 3. Multiple alignment of *Bombyx mori* apoLTP-III and similar proteins collected from the NCBI protein database.

The predicted JHBP superfamily domain is indicated by a dotted line above the alignment. The allowed conservative substitutions were as follows: A, G; S, T; E, D; R, K, H; Q, N; V, I, L, M; Y, F, W; P; and C. Gaps are indicated by dashes; $\geq 50\%$ identical amino acid residues are boxed in gray.

Supplemental Table 1. Accession numbers of amino acid sequences of LLTPs

Sequence name	Species	Protein accession number
Vtg1_Nematode	<i>Caenorhabditis elegans</i>	NP_509305.1
Vtg5_Nematode	<i>Caenorhabditis elegans</i>	NP_508589.1
MTP_Chicken	<i>Gallus gallus</i>	NP_001103254.1
MTP_Human	<i>Homo sapiens</i>	P55157.1
MTP_Zebrafish	<i>Danio rerio</i>	NP_998135.1
apoB_Chicken	<i>Gallus gallus</i>	NP_001038098.1
apoB_Human	<i>Homo sapiens</i>	AAA35549.1
Vtg_Crayfish	<i>Cherax quadricarinatus</i>	AAG17936.1
Vtg_Shrimp	<i>Metapenaeus ensis</i>	AAM48287.1
apoB_Zebrafish	<i>Danio rerio</i>	XP_694827.4
Vtg6c_Nematode	<i>Caenorhabditis elegans</i>	NP_001023276.1
MTP_Fruitfly	<i>Drosophila melanogaster</i>	NP_610075.2
CG15828_Fruitfly	<i>Drosophila melanogaster</i>	CG15828
LTP_Silkmoth	<i>Bombyx mori</i>	AB700597 *
similar_to_CG15828_Honeybee	<i>Apis mellifera</i>	XP_394269.4
apoLp_Fruitfly	<i>Drosophila melanogaster</i>	AAC47284.1
apoLp_HornWorm	<i>Manduca sexta</i>	Q25490.1
apoLp_Locust	<i>Locusta migratoria</i>	Q9U943.2
apoLp_Silkmoth	<i>Bombyx mori</i>	BAK82317.1
M-177_Mite	<i>Euroglyphus maynei</i>	AAF14270.1
Vtg1_Zebrafish	<i>Danio rerio</i>	NP_001038362.2
Vtg2_Chicken	<i>Gallus gallus</i>	AAA49139.1
Vtg_Lamprey	<i>Ichthyomyzon unicuspis</i>	Q91062.1
Vtg_GalaxyCoral	<i>Galaxea fascicularis</i>	BAD74020.2
Vtg_PacificOyster	<i>Crassostrea gigas</i>	BAC22716.1
Vtg1_Cockroach	<i>Periplaneta americana</i>	Q9U8M0.1
Vtg_Beetle	<i>Tenebrio molitor</i>	AAU20328.2
Vtg_SilkMoth	<i>Bombyx mori</i>	NP_001037309.1
Vtg_WaterFlea	<i>Daphnia magna</i>	BAD05137.1
CP_SignalCrayfish	<i>Pacifastacus leniusculus</i>	AAD16454.1
CP_TigerShrimp	<i>Penaeus monodon</i>	Q9U572.1
MEP_Fruitfly	<i>Drosophila melanogaster</i>	NP_732076.1
MEP_Beetle	<i>Tenebrio molitor</i>	BAB03250.1
MTP_Nematoda	<i>Caenorhabditis elegans</i>	NP_499903.3

* deduced amino acid sequence of apoLTP-II/I determined in this study



Supplemental Fig. 1

Supplemental Fig. 2

<p>Vtg2_Chicken Vtg1_Zebrafish Vtg_Lamprey Vtg1_Nematode Vtg5_Nematode Vtg6c_Nematode Vtg_WaterFlea Vtg1_Cockroach Vtg_SilkMoth Vtg_Beetle Vtg_PacificOyster Vtg_GalaxyCoral MEP_Fruitfly MEP_Beetle CP_SignalCrayfish CP_TigerShrimp apoCr_Shrimp apoCr_Crayfish M-177_Mite apoLp_Locust apoLp_Fruitfly apoLp_Silkmoth apoLp_HornWorm apoB_Human apoB_Chicken apoB_Zebrafish LTP_Silkmoth CG15828_Fruitfly similar_to_CG15828_Honeybee MTP_Human MTP_Chicken MTP_Zebrafish MTP_Nematoda MTP_Fruitfly</p>	<pre> 1 FNSRRSYLYNYEGSMNGFEYSS--GR--IGNIYAPEDCPDLCVNIIVRGILNMFQMEBAGIGGICHARYVIVVTRTVDL 73 1 FAHDKTYVYKYEALLLGGFYAN--GV--VGKVFAPAGVSPVVMNLHRLNLNLEAGAGQGVCRTHYVIVTKSKDL 73 1 FQPGKYRYRYSDAFSISGFDYSA--GR--IGDIYAPPQVTDTAVNIIVRGILNLFQLETVGEGICQTTYVVVVTKDL 73 1 FEPKIDYHYKFDGLVLSGAQLRN--GL--IAELQFDKEDAWSKNMRAVVMNMFSEKTELEGGCQVAVYVITKSNF 73 1 FSPKSEYVYKFDGLLSGAQIRN--GL--ISEIQFSSEDAEWSKNAKRSLLNLFSLSEKTEMEGGCEVAYTYTKSVNF 73 1 FRAGREYRYLNFNGQLSAGFDYEH--GL--VREIRFAENDQPSWENIKRAVINMLQVETLEGECEVLYTVWAKSNF 73 1 WMAGYTYEYDYGAWTSTGVKVFVS--GK--VETVAIGKEEPLWIVNFKRALAAQOLEGVSVTGECQTWYHIIVKNRDL 73 1 WDPNRQYVYKVESRAFTAILQN--GH--IVNVKVKDSTPNWAVNMLKGLLSLITQLETTITTEGCEVEYDVIEKTONF 73 1 WQVQYRYEYVTSRFLAHIEIDG--GR--IVSLDFPSTVVPVQENLIKGLLSALQLETTVTDGCEYLYTVVTKSTNY 73 1 WEENKLYTYEVRGRSFASIELNK--GA--IRDIFVEKKMRNWEVMVKGIVSQLEBETVTVGVAETLYEIVVKKHNY 73 1 YESNKEYLYEYEQALTGFYVR--GN--VKDIHHEADDPWSVNVKGLLSLMEPEPSIVGCEYLYRIITKVRNY 73 1 YQKEQRYTYSYQTEASQAFSFKVQDS--LKEISAHPNDSSEWSLNIKRGILNLFQLESPQOSVTAQVVYVILLTKVMNY 75 1 IGLNKQMLYEGNVLVGIALTGD--GA--ISHVVFKEGDPISVMNFKRAIASLQFELGHTGRTTEYFVIRKTPEV 74 1 SPWDKEVYVYKALVKAGIYDTK--GL--AIGIVTEAQEKEFSRNLIKKAITATIFQMEHSIYGHFDVDTIVHKLHDM 74 1 LHSNLEYQYRYSGRVASGALPGE--QR--GEEHLVGPAPPAWITNLIKALIVRAFISIGTFIHGDVWCVYSMMSRTVDF 73 1 LQPGLEYQYRYRSARVASGVIMNE--SH--VPSYMEGPEEPIWISNVRKGFVNIIVRVEETLVGRQONWYTSVRRTTDF 73 1 YEPGKYTYAYSGSKVQVAVAE--GR--VQHVCAHPEDQPAWNLKKGVASALQNETDVIKQPPNTKVVTEKEKH 73 1 YQPGKYTYEYSGKSRIQVAVTD--GK--VHVCSHPDDDTWSINLKKGVASAFQNETDVGKCPTRYEVMIKEKNH 73 1 INPKAQSTYVYSLDAKTVFGYFN--GR--ILGVCNPANDQDWSLNVKKAIVSALQVETDFTSGTCTEYRKMEKRD 73 1 YQKGQTYTYSEFETTLTASNFK---GSSINKQLCSEGDGNQSSLNLIKRAILLSLQTEVDVFGICPTNVRHISKTRNL 74 1 YIPGNYDYVYSDSILITIGFTLVS--GI--LEPQICSDSDLDYSINIKRAVVSILQSEVDVFGICPTHTSTITKARNL 74 1 FQAGQTYNYGVEGYSVTFIFGYQD--GK--IQEQICABEDDTQWSINIKRAILLSLQNLQVDVFGICPTVSTVHRSRD 74 1 FAAGQYNYGVEGTVSVYFSYQD--GR--VGPEICAAEDDSRRSLNIKRAILLSLQAQVDVFGVCFTEVSSLHRSRD 74 1 FKHLRKYTYNYEAESSSGLAIPPE--GK--QVFLYPEKDEPTYIINIKRGIISALLVLDTVYGNCSHTFTVISTERDL 73 1 FKSLRKYVYLYEAESSSGFTSQD--GT--KVKLYPEKDEPLNVLNLIKRGIISALLAMDTVYGKCDSEVEFISINRNL 73 1 FKNLRKYVYQYTAESKNGFVVDQ--VT--SVSIYPEEDEPENIINIKRGIISALLVMSTIHGICKTEVTVSVVRDL 73 1 YLSDIVYTYEYRVNVEFLAFHND--GL--ITEICPDEKEEDVILNFKRAILLALQNEQDIGHGTONVDYSVLVKRRDL 73 1 NYGEQYLYKYQYTVAVRTEFAFHD--GL--ISEVCFQEQETPWLNLKKGILSAFQNETDVGQCVQYALIRKTKDI 73 1 PVEMQYRYSVDVSTNLGNSFTFDD--GQ--IDELCPDKREPWALNLIKRGVLSLQFNEVDVNGICDTSYHFVKKKKDL 73 1 LNNDRLYKLYSTEVLLDLHLIH--GK--VKEFYSYQNEAVAIENIKRGLASLQTEVDISGNCKVTYQAVIKIKAL 73 1 LSNDRLYRFAYTAEVYVDLELAR--GK--VQNFYSYENEPGFTQNLKRGLASLQLEVDISGKNVTYQVVTIKIKAL 73 1 LDNGKLYRYSYGTEVGLNVLWKM--GK--IRSLYQKAEPATVKNLIKRGVASSLMEPADASGKCLVEYKVVIRTKHL 73 1 LDEIKKLRKHGPDYKNIAFRQ--GGNNAEHILKASDES DATWFLYAIVNTIYTVDTIYGRCFVNFGRKRFRRI 75 1 NNSQQIFKIQNVILQELISLVR--GQ--PDKVIAHTSKDQSLNLERGIASLQLELDVSGICRVSYNVTKVEKTK 73 </pre>
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<p>Vtg2_Chicken Vtg1_Zebrafish Vtg_Lamprey Vtg1_Nematode Vtg5_Nematode Vtg6c_Nematode Vtg_WaterFlea Vtg1_Cockroach Vtg_SilkMoth Vtg_Beetle Vtg_PacificOyster Vtg_GalaxyCoral MEP_Fruitfly MEP_Beetle CP_SignalCrayfish CP_TigerShrimp apoCr_Shrimp apoCr_Crayfish M-177_Mite apoLp_Locust apoLp_Fruitfly apoLp_Silkmoth apoLp_HornWorm apoB_Human apoB_Chicken apoB_Zebrafish LTP_Silkmoth CG15828_Fruitfly similar_to_CG15828_Honeybee MTP_Human MTP_Chicken MTP_Zebrafish MTP_Nematoda MTP_Fruitfly</p>	<pre> 74 NNCQMEARQQLTFLFL-EVVLQCRIANADNLESISAVSASSTTETLTKFLKRNRILOQVACLGYSSVVNRYCREDKMKLA 149 74 SHCQMEAKQTLAFFV-QLVQLLRVASLEKLEAIDALPAVGTPIVILKFIKEKFLREVVMGEGYSLIAKYQDIPEITLA 149 74 NNCDIESRQKLIIFLFL-RLTAFLRNVDAGVLQSIDAVPAMATSEALLFLKRTLLRKTAVLGYGSLVFRYQDEEBIVLA 149 74 DKCTTETRSLVLEFLARLVRIFRITSTTSQLEIHALAIAGTKNTIQHILVHIVRQSAWLAAGSVVRGIVTTEYKILA 150 74 DKCISETRAKVTFLIARVFRMCTIEBLKVTTLAVAGTKNTIQHLIHHFLRQSAWLAAGSVVRGIVTTEYKILA 150 74 DKCTAFTLNTMELTVARIVKLRCENEQLEQINTLALAGTRVTIQQFVDKVLRSQWLTGYAIVNGVCTRYEKVLA 150 74 DNCRGLTVQHLTLIN-MLRRALASLDYNELMGFDALMLSGTNPSSLMLVREYILKITTALSLSRVLYQACDAGERMAF 149 74 SNCKIVSRVNVITILM-MMRDIVRTMTAKQLQKADMVSESTHPALEELSIIWVNSTGLLALATLHRQVHNRPKIQVI 149 74 GHCHVYSHVHMELLS-KFNILVRLTASMSTEQLDGVTOAGTLPAPKQIQSWIINSSALMAATKILNQLQDSTKAQVY 149 74 TY-SVNTKLTTLTFLV-TLMSLVRTMDHEEVNKVDVAQOSTSPALLNIKEWIIILSKPYVNESAILSYTDDTRKIHV 148 74 QHCLTYLNQTLNLLM-SLLEBRITADESRLAVGHPSICGTTSTATEVLDVSLKRAAFLCLGSLVAGMLRVFDDKILS 149 76 EKCSVTTRQTLQFFA-VAVQBLRKNQDTRMERIDALSFVGTREAFQVLQKQVCRQCLSLSLYLYKGSQEDRILTF 151 75 KTC-INSELLNFDSTLSDVIKLLSEMDFDSLEIIPRIGTKASVFLTHHLVVRQAAIISFATLHNVYDFDQKMLY 149 75 HD--IPVNSMHLVN-RVQRLQFFSLTKLEELHILPLVGTKSSTLFIKQLIVRKAVALSFASLVQHSYDYKVMQTY 148 74 DSCEI STFTNTQTLMS-TLVDAASILSRPEALEELVVTAGTEPAIRYLDKIFKMTLLNLASLAKQLCSLWIRLVY 149 74 DMCEVDFTFTNTQLIG-RLMEAVANLDYPYIQTLOLVIHAGTEPAVNFVAVDNLHHSGLGMNFATLAHDAQVWQRLIY 149 74 RHCTANQESTLRFVD-KALHMLRSVPAEVVEVDVAVFVHESGAVKVMVEEI-KPTLMLAASMVNKYCAEBEIVAA 148 74 RQCKAKMSTLYKYVA-RAIQFLRMVPEEAVEQTEFVSVFDEPGAVKVMVKELMPYPT-LAASSVMNNYITVQAAIT 148 74 NLCDLMCRMTLKDFH-KLVQDKLRYLSAEEATVDAFAFASDGSIRTLVKAHTIRPMLLGFSLVVRRYDPSERTMI 149 75 NRYAVETKLTLSFR-TLVSVLRQSSTTDILKVDAL-FRTSTGDAVEVIARLLPTEAFGLIGSFIGRYCGENRAIAA 149 75 NSCSVVTILKLNKAK-KVFEFIRLLRQSDSETLDGL-FRTSTAESARVILKQAPKELYAVGNLVAKYCEEBERIVYI 149 75 SRCSVHTKLTLTGFA-QLVRIILRRTEKEDLVKVDALLRAGTGDSEASLILILLPKDQVYLGAGALAGAYCEDTVVAV 150 75 SRCAVHTKLTLSGFA-QLVRIIMRTSSKDDLMRIDALLRAGTGESTEASIQILLPKEVYLGAGALGAYCEDTVVAV 150 74 GCDVVTQTLKLEDFN-KLVTELRGLSDEAVTSLQALVQCGPQCSTHIIQLWLRSLRATLYALSHAVNHHDEDTYLI 149 74 KACDVNQTLEDFY-KFVSGRLSLHNSTLGSQALIQCGTPECYSAVILKRSRATFVGLSHAVTKFYDAELTYLT 149 74 SDCSVKQSLTLQDFH-KLVSEVRGLKNETLSGAQTLFQCGTDECTSAIMQILPSKPIYALANTVKQLPDEDSTFLT 149 74 SECTVVDLVLSIG-RFVRAARPLDFPSLSQIDALPYIASTGSMELIKMINDKVVSVFVSSMVHSYCRDNIVIA 149 74 NSCRSTSRLKLDGFT-NFLQTSKSLDYKTLVLESPLPFGTSTASYKVMRDQILDAEYTGATAVVHSFCTRRERMVIL 149 74 SNCDSTATLRLIEFT-AFIQSAARYLDYPSLSQNALPFGTSSAALNVMRDLMSETFILSYSATYAFCAIKETLEA 149 74 DSCKIVSKQKLELFL-AFIQHLRTAKKEELIQDAVTSAGTSDSLEAILDFLIRETVMIITGTIVRKLCKEDTRMY 149 74 DTCEIVSKQKLELFL-SFIQIRKATKEELIQDAITSAQTPASLEAILBFLIRETVLVMIGELLRKLCKDDNVRMY 149 74 ETCKVLSRQSLTFLFL-TLVHSLRKSSEKSEITLDAVTSAGTPSSLSAILEFLIKESVVIIMGALLRKLCESEVQMY 149 76 EKODSRTHVEITNYS-QIAQEARLAKRQDWAASALGGVCTAESITTAREVLEYKVVANTIATVLNKRCGGVEVRV- 150 74 RDCSSSLIQHVSIV-KLILPLARITRQEQFEDIDILGAVQTFDAHNATFGFLRESVIQTVATLFRQSGTSKEPTLY 149 </pre>
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Vtg2_Chicken	150	LKCI	GNM	GEPAS	LKRILK	FLIQ	DAIT	AL	LKKI	IAWKD	VQGY	LI	QQL	-ADQSL	PP	EV	RM	MACAVI	FET	PALALIT	TAN	225																																																					
Vtg1_Zebrafish	150	LKVM	GNAGH	PSS	LKPIMK	LLVQ	DAIT	AL	LRNI	IAKKE	VQPV	ALQ	LV	-LDRAL	HP	EV	RM	VACIVL	FET	PS	VALISS	LAG	225																																																				
Vtg_Lamprey	150	LKAL	GNAG	QPN	SI	KKI	QRFV	QAE	AT	ML	LRNI	IAKRD	VQEI	VL	IF	-LN	VA	IK	SEL	IR	SCIV	FF	ES	PS	VALV	SM	VAV	225																																															
Vtg1_Nematode	151	LKSI	GNAG	L	DIS	VN	QLNE	I	IV	RKEA	IDL	RLL	KD	MI	QK	VL	LP	LY	-KN	QY	EP	IR	MI	AL	WR	MM	HT	PE	ES	LL	VQ	VVS	226																																										
Vtg5_Nematode	151	LKTL	GNAG	I	DLS	VY	ELVQ	I	IR	TEA	VD	AL	RLL	KD	VM	IQ	VL	PVY	-KN	RQ	NP	KP	EL	RM	AAL	WR	MM	HT	PE	EP	VL	LA	HS	226																																									
Vtg6c_Nematode	151	LKTL	ANAG	L	DLS	VY	LEKI	I	IR	TEA	ES	FR	RL	RT	QMI	QV	TL	MPVY	-LN	RQ	Q	PH	IR	MS	AL	LH	QI	IY	TE	PE	WS	VL	SG	IGN	226																																								
Vtg_WaterFlea	150	LIT	AL	GN	I	GHEI	I	V	FP	VP	KP	FV	IR	AK	I	F	AL	ST	LAV	Q	T	Q	VT	L	M	P	F	-FN	K	AE	TE	IR	LA	L	H	QI	IY	TE	PE	WS	VL	SG	IGN	225																															
Vtg1_Cockroach	150	IR	AL	GN	T	GN	KR	I	LN	Y	LE	PY	ER	LL	M	V	T	S	L	D	I	L	A	E	I	N	A	R	Q	V	L	N	V	-I	N	I	G	E	N	H	E	L	R	C	A	S	V	I	L	M	R	T	P	P	A	M	L	Q	R	M	A	E	225												
Vtg_SilkMoth	150	IQ	AI	GN	I	G	H	R	E	I	L	K	V	F	A	P	Y	L	R	T	H	I	V	K	N	L	T	L	A	K	L	R	V	R	A	V	L	S	T	L	-R	N	T	A	B	P	P	V	R	V	A	A	I	Q	S	I	F	I	S	P	T	G	E	M	M	Q	A	M	A	E	225				
Vtg_Beetle	149	IR	AL	GN	V	Q	O	O	I	L	E	A	F	E	P	Y	L	R	T	H	I	V	K	N	L	T	L	A	K	L	R	V	R	A	V	L	S	T	L	-R	N	T	A	B	P	P	V	R	V	A	A	I	Q	S	I	F	I	S	P	T	G	E	M	M	Q	A	M	A	E	224					
Vtg_PacificOyster	150	F	K	T	I	G	N	A	G	L	W	E	M	I	P	T	I	R	T	Y	I	L	R	T	Q	A	I	Y	S	L	R	K	L	A	R	H	Y	I	Q	T	L	L	P	L	-F	D	Q	S	E	K	E	B	E	R	I	G	S	Y	L	V	M	T	F	P	S	R	Q	L	L	E	M	V	A	Q	225
Vtg_GalaxyCoral	152	I	K	T	L	G	N	A	G	S	P	D	A	Q	E	Q	L	K	I	L	T	R	V	E	C	V	W	L	R	R	I	T	R	Q	A	T	Y	P	C	L	I	S	I	F	-A	D	R	Q	E	N	P	E	L	R	M	A	T	F	V	Q	L	N	T	P	N	F	V	I	L	Q	A	L	T	N	227
MEP_Fruitfly	150	LQ	G	L	N	N	I	Q	L	G	N	V	A	N	L	E	P	I	V	L	K	F	Q	A	A	W	T	L	A	L	A	D	R	R	I	E	V	Y	W	P	I	F	-E	S	R	N	A	S	I	E	L	R	V	A	A	V	T	L	L	I	S	P	T	A	A	R	L	I	S	H	R	225			
MEP_Beetle	149	L	M	G	L	O	M	R	L	H	S	I	K	H	L	P	A	V	L	S	L	W	A	V	-S	T	A	V	V	E	E	R	D	V	I	E	T	W	P	I	F	-T	N	V	D	E	L	T	E	M	R	T	A	F	Y	F	I	M	T	P	N	D	S	R	L	T	N	M	F	N	225				
CP_SignalCrayfish	150	I	Q	A	L	A	N	I	G	I	P	O	T	I	D	V	L	K	H	F	A	L	R	T	N	A	I	L	G	S	V	Y	L	P	E	V	G	I	L	M	P	V	F	-E	N	T	G	E	H	N	E	V	R	A	V	A	L	A	M	T	F	P	S	L	A	W	B	E	R	A	I	225			
CP_TigerShrimp	150	LQ	A	L	S	N	I	G	T	P	O	T	I	D	V	L	K	H	F	A	L	R	T	N	A	I	L	G	S	V	Y	L	P	E	V	G	I	L	M	P	V	F	-E	N	T	G	E	H	N	E	V	R	A	V	A	L	A	M	T	F	P	S	L	A	W	B	E	R	A	I	225				
apoCr_Shrimp	149	LK	AL	GN	M	G	V	V	T	P	A	V	T	S	A	A	V	T	I	R	V	A	A	A	E	V	F	R	Q	A	K	--	C	A	V	E	K	L	V	D	I	A	-T	H	P	D	F	T	E	V	R	I	V	S	Y	L	A	A	I	K	C	A	E	M	D	L	E	K	I	N	222				
apoCr_Crayfish	149	LK	AL	GN	M	G	V	M	T	P	A	V	T	S	V	L	R	I	R	V	A	A	A	A	Q	A	F	R	K	A	K	--	C	S	T	G	R	L	V	G	Y	A	-L	S	R	K	T	T	E	V	R	I	A	S	Y	I	A	A	V	R	C	A	B	K	W	D	F	E	K	I	V	E	222		
M-177_Mite	150	V	R	A	L	E	N	I	N	V	N	T	E	D	V	D	N	M	I	N	A	L	R	A	A	V	N	L	P	S	D	A	--	S	R	Y	K	S	L	V	M	---	D	E	S	M	P	N	E	A	R	I	A	A	F	H	K	M	Q	N	G	M	T	H	I	K	D	L	F	A	220				
apoLp_Locust	150	LK	AL	GN	I	R	H	L	N	N	A	L	G	E	K	V	K	Q	V	R	V	A	A	L	E	V	I	Q	S	D	P	--	C	I	Q	A	A	L	Q	I	L	-R	D	Q	V	E	S	E	L	R	I	K	A	Y	L	A	V	V	E	C	P	D	N	V	V	K	T	I	S	N	223				
apoLp_Fruitfly	150	LK	G	L	GN	A	K	S	L	SG	N	T	V	A	A	L	S	E	I	R	V	A	L	H	A	F	S	K	V	K	--	C	L	Q	S	K	S	L	E	L	L	-K	N	R	N	E	S	E	L	R	I	E	A	Y	L	S	A	I	S	C	P	N	A	E	V	A	N	Q	I	S	E	223			
apoLp_Silkmoth	151	LK	G	I	R	N	I	R	H	L	E	N	S	L	I	E	K	L	V	R	I	R	A	A	V	L	E	A	F	H	A	D	P	--	C	V	K	K	I	S	L	D	I	L	-K	N	R	Q	L	D	S	E	I	R	I	K	A	Y	L	A	V	I	E	C	P	C	H	S	A	N	E	N	224		
apoLp_HornWorm	151	LK	G	I	R	N	I	R	H	L	E	N	S	L	I	E	K	L	V	H	V	R	A	V	L	E	A	F	H	A	D	P	--	C	H	K	T	A	M	D	I	M	-K	N	R	Q	L	D	S	E	I	R	I	K	A	Y	L	A	V	I	E	C	P	C	H	S	A	S	E	L	K	N	224		
apoB_Human	150	L	R	V	I	G	N	M	G	T	M	E	Q	L	T	P	E	L	K	S	I	Q	K	A	A	I	Q	A	L	R	K	M	--	P	D	Q	E	V	L	L	Q	T	F	-L	D	D	A	S	P	G	D	K	R	L	A	A	Y	L	M	L	M	R	S	P	S	O	A	D	I	N	K	I	V	Q	223
apoB_Chicken	150	L	R	A	I	G	N	M	G	A	V	M	E	K	A	K	P	S	L	K	A	V	Q	K	A	I	Q	A	F	R	K	M	T	--	I	D	R	S	A	L	L	K	E	F	-Q	E	G	D	A	P	T	D	K	R	L	A	T	Y	L	I	M	K	N	P	S	P	A	D	L	A	K	I	M	R	223
apoB_Zebrafish	150	L	R	V	I	G	N	M	G	K	Y	M	E	G	F	P	S	L	K	S	V	Q	K	A	I	Q	A	F	R	L	M	E	--	M	V	R	S	A	L	I	Q	O	Y	-Q	N	V	E	A	P	A	Q	K	R	I	A	A	Y	L	M	L	M	R	N	P	E	V	A	E	--	N	V	L	R	221	
LTP_Silkmoth	150	I	K	AL	GN	I	G	F	K	L	E	F	A	D	V	L	M	S	I	R	L	T	A	I	D	A	F	R	R	T	P	--	C	R	E	Y	F	L	E	T	Y	-R	E	D	F	V	N	I	E	V	R	I	A	S	Y	I	Q	V	M	R	C	P	D	L	T	T	V	R	T	I	F	H	222		
CG15828_Fruitfly	150	LK	G	L	GN	I	G	V	S	S	A	F	A	E	Q	L	W	I	R	L	H	G	I	L	A	F	R	R	V	D	--	C	R	S	Y	F	L	D	N	Y	-Q	N	Y	T	L	N	S	E	L	R	I	Y	S	L	Q	A	M	R	C	P	D	I	S	V	G	V	I	K	S	222					
similar_to_CG15828_Honeybee	150	LK	AL	GN	M	G	L	E	T	E	R	L	L	K	L	K	E	I	R	V	A	S	I	D	A	H	R	R	M	P	--	S	D	L	Y	F	L	N	Y	-R	N	F	S	L	D	E	L	R	I	A	S	Y	L	Q	V	M	R	C	P	D	N	V	V	K	T	I	K	H	222						
MTP_Human	150	L	L	A	L	K	N	A	L	L	P	E	G	I	P	S	L	L	K	Y	A	L	A	T	T	A	L	Q	R	Y	D	L	P	F	I	T	D	V	K	K	T	N	R	I	Y	H	Q	N	R	K	V	H	-E	V	R	T	A	A	A	I	I	L	N	P	S	Y	M								

Vtg2_Chicken	301	LGQEVAFININKELLVESCLGLPLEYGSPSLYVHTVATMGVNTTEYFOHA	349
Vtg1_Zebrafish	299	FGQEVAVVNFDKTIILPTAVGVPMEFWSWVALQTFVAVMGVNTAFIQAA	347
Vtg_Lamprey	299	HGQEVVFAELDKKMMQPVCIIGIPMDLNLTSMSQHAVAIMGLETTDLAKAG	347
Vtg1_Nematode	297	KDMDYAILFVDTLQIFPTLGLPLIVSGPSVAATHVYEMRMFTPLFEQG	345
Vtg5_Nematode	297	KEMDYIVLFPIDMETIIPITIGMPLTISGPTVATTHVTEMRFWYVPIEQG	345
Vtg6c_Nematode	297	RDMDYAFLPIDADSIPTMGLFVQFTSPRVASTHVLSLRVICPIAEVG	345
Vtg_WaterFlea	295	LDNYQRFFINPNTIIPBSAMGLAYTWASPVVVSVMSTRMLMVEPTPFSRAY	343
Vtg1_Cockroach	299	LGNDRFFSY-DKNDIFPNALGLPSLFTIPWKLGARSETSLTYSVKEMSK	346
Vtg_SilkMoth	298	MNNQRLFSFSESDLQFPEVASGMPFIFKYPSKDNKYEAMNIKDVQFTYA	346
Vtg_Beetle	298	NAWQEIFSF-DNHTLLPTALGLPFVYVYPRISTEGHIQKPDVHAEFEI	345
Vtg_PacificOyster	299	MGNELQYITLDGTLVIPSCEGLPLRLKLPSTVLFQLRGEMEMDAEYFKMG	347
Vtg_GalaxyCoral	302	YGNQEVKFMVVKQDVVLPVLAGIPLNIQFPSINTHVHAVVAIHTPFLRVG	350
MEP_Fruitfly	298	BGKTVLSYYLNQRMFVPTVLGTSSDVLVRSRSYNPFLNLDHEINREQG	346
MEP_Beetle	297	HGHIVNTYFFDQHSIIPITDLGIPALWEYPFVDVWQGVNRYHSYDAVWPL	345
CP_SignalCrayfish	298	TDPISLTPVLSSPENLPTDLGLPFMIHYPTKRKDFADLTLDPSQDNTLE	346
CP_TigerShrimp	298	DRLLIYVALQYHFMEGFPTETIGIPFSVLYTSGKMKVNVDFIPETSQVQFV	346
apoCr_Shrimp	296	MQQEVTYANIAETLKLPTIQGLHSRSPWGLSIHTTGFVGFDAFIKAG	344
apoCr_Crayfish	296	MQQEISFASLAGDLTFPTIQGTIPFKLKMPSLSVEVDGFVGYDCHISKTG	344
M-177_Mite	293	NGKNVYVTDVFDLKLPTITGLPLVYKFPFLVDMDIQKKEHSLLLRFNTK	341
apoLp_Locust	297	FGSELAWFNYDGKHEYPTNLGFPLKLAIPSAAVELTGKLLVDAYVVEGG	345
apoLp_Fruitfly	297	FGSELAFLSLGDNIPTPTSIGVPELVAPSVDINANVQIGFNAQVLSGTG	345
apoLp_Silkmoth	298	FGTDAVFLSFGDDKGYPTSTGLPLHLNLPSTDLLEIAGAFVLVDAYAVTTG	346
apoLp_HornWorm	298	FGTDAVFLSFGDDKGYPTSVGLEPLRLNLPSTDFEISGAFIIDADAFSTG	346
apoB_Human	297	LGEBELGFASLHDLQLLPTGAGLQIQISSPSVSVFVNTMGIIPDFARS	345
apoB_Chicken	297	LGEBELGYMKLSDFKLLPTGAGLQKFAIPSVAVEFVTHLGINMPEFARS	345
apoB_Zebrafish	291	FGTELGYLKTSDLKHLPTSAAGFPLKLTLPSTVGVFEITQMGVYIPEFVVA	339
LTP_Silkmoth	296	FGNEISYWSAEGDDEVPTGCGPLNMLNLPSTAVNVAAATMSVAVAGLSSS	344
CG15828_Fruitfly	295	LGYKLYDYNNPRAQVPLAVGLPLAIHAPSVSVDVITTMQTDMFWEQSG	343
similar_to_CG15828_Honeybee	296	FGNDLKYSTLNGDREVEMTTGLVRLDLPSTINVDTTGSMTVDAFYKTAG	344
MTP_Human	296	SGDPIISVVKGLILLINRVTVVITTDITVPEFRQFEKRYERLSTGRGYVSQ	344
MTP_Chicken	296	TGDPISVVKGLILLTNRIAMFVAGNAEVPFRHSVTKYESLPSGRRYTAR	344
MTP_Zebrafish	296	SGDPIINVVKGLILLTNRGALVVICNMTVPEFRETIVSKQEKLPQMFSTRK	344
MTP_Nematoda	294	DGRTHKAFEGHVPRYTSGLHLTASLYINQKTVVQDIQGHKKKTLNR	342
MTP_Fruitfly	293	SASDSTPAYQATTLSONTIGSAVLGHLAVLKQTNVRSVFLQSVDRPYAKH	341

N20

N21

N22

Supplemental Fig. 3

B.mori LTP-III

D.plexippus (EHJ73751.1) 0 ----- 0
D.plexippus (EHJ73750.1) 0 ----- 0
D.ponderosae (ABE62911.1) 0 ----- 0
T.castaneum (XP_972731.1) 0 ----- 0
A.florea (XP_003697952.1) 0 ----- 0
A.mellifera (XP_395658.4) 0 ----- 0
B.impatiens (XP_003492016.1) 0 ----- 0
M.rotundata (XP_003708008.1) 0 ----- 0
N.vitripennis (XP_001606118.1) 0 ----- 0
S.invicta (EFZ14465.1) 1 ----- MLHRCVP 7
A.echinatior (EGI63413.1) 0 ----- 0
H.saltator (EFN76863.1) 0 ----- 0
C.floridanus (EFN74421.1) 0 ----- 0
A.aegypti (XP_001654113.1) 1 ----- MHRQNTAGSGVEVPTTESPKVNTQSL LCKLTHPAQTDTIISDDLRSVSVIIPK 53
A.aegypti (XP_001653919.1) 0 ----- 0
C.quinquefasciatus (XP_001863022.1) 0 ----- 0
A.gambiae (XP_312626.4) 0 ----- 0
A.darlingi (EFR25164.1) 0 ----- 0
D.virilis (XP_002052633.1) 0 ----- 0
D.mojavensis (XP_002002021.1) 0 ----- 0
D.grimshawi (XP_001989184.1) 0 ----- 0
D.willistoni (XP_002064455.1) 0 ----- 0
D.simulans (XP_002078032.1) 0 ----- 0
D.sechellia (XP_002045314.1) 0 ----- 0
D.melanogaster (NP_608781.2) 0 ----- 0
D.melanogaster (AAL68365.1) 0 ----- 0
D.melanogaster (AAL48116.1) 0 ----- 0
D.erecta (XP_001968564.1) 0 ----- 0
D.yakuba (XP_002087828.1) 0 ----- 0
D.ananassae (XP_001965094.1) 0 ----- 0
D.pseudoobscura (XP_001356411.1) 0 ----- 0
A.pisum (XP_001945904.1) 1 MKTTVAVVAIALSLCGLFPFVTVVALPVPGDQNESVAAATELQTTTVLPVDTTTEVSVPATVPTDT 67
A.pisum (XP_001948728.2) 0 ----- 0
P.humanus corporis (XP_002425163.1) 0 ----- 0
D.pulex (BFX77001.1) 0 ----- 0

B.mori LTP-III

D.plexippus (EHJ73751.1) 1 ----- MKIALCIVLVILFQFRNCQEIPEEVSSSEDE----- 30
D.plexippus (EHJ73750.1) 1 ----- MFNKIVVIVLFLCSSVLGDLQDV----- TT 25
D.plexippus (EHJ73750.1) 1 ----- MCIVRLTLLLLITIVKSQDENEYFESTDSDEFF----- ET 35
D.ponderosae (ABE62911.1) 1 ----- MTRTVVLLLLLGGWLVGGAP----- 21
T.castaneum (XP_972731.1) 1 ----- MRSGLIFLLLLSLNFCHSEVRNA----- 23
A.florea (XP_003697952.1) 1 ----- MKLLKLEFFVLFYFIKINQCDIKISTV----- KN 28
A.mellifera (XP_395658.4) 1 ----- MKVLKLEFFVLFYFIKIGQCDIKISTV----- KN 28
B.impatiens (XP_003492016.1) 1 ----- MVVHFDRMSKPEMHLPKLFLFSFFIAIGQCDVQNSIG----- KD 40
M.rotundata (XP_003708008.1) 1 ----- MQFSKLEFVYFAYCTLVCFCDVQQSFG----- KN 28
N.vitripennis (XP_001606118.1) 1 ----- MAREALVVFASTLLLLLILSCQSARSDEAPA----- AT 32
S.invicta (EFZ14465.1) 8 GSAKKGINMQCETRSERVYAMVFLVMCCFLCSPCAGEE--PKPNVSSPSID----- N 58
A.echinatior (EGI63413.1) 1 ----- MRCKTRLEMRVYAVVFLIVCCFLCSCCASEE-LKTNNA-STSID----- K 43
H.saltator (EFN76863.1) 1 ----- MQIYAAFLVVVCCFLCPLCAGDD-LKLDASSSSISK----- SK 38
C.floridanus (EFN74421.1) 1 ----- MRAAILLVCCFLCCLCAGDESKKLNDISSSSIN----- DK 36
A.aegypti (XP_001654113.1) 54 KTDVETCPQTIETVMFRARLLIALLLFNCLLISTVR-----CDEDKSSSAB-----ESSPED 105
A.aegypti (XP_001653919.1) 1 ----- MDRERIHPPQYLACSSVVMIMLFCGIIYFILQVII--LHVS PGR-----SQ 44
C.quinquefasciatus (XP_001863022.1) 1 ----- MTKPRWKRLTALLINCTLLALISNVR-----CDDKSSSGE-----DSTSD 43
A.gambiae (XP_312626.4) 1 ----- MTMAKAVIALLWINLICLISVVV-----CTTDAWP-----NNGG 34
A.darlingi (EFR25164.1) 1 ----- MDDPQSEVPLTRHFEHFAAIRLIRC--TLFERSS--CSGHAWTIVSVQTESRGQCRTKSVG 57
D.virilis (XP_002052633.1) 1 ----- MKSLIVLLVALLILAY-----NVPAQAQDEN-----EAEGG 31
D.mojavensis (XP_002002021.1) 1 ----- MKVLIIVFLVAYLILG-----SVRAQDENAE-----ANDEN 30
D.grimshawi (XP_001989184.1) 1 ----- MKALIVILVAIALIH-----CSSAQDVN-----EADDE 28
D.willistoni (XP_002064455.1) 1 ----- MYNLIIVILMGIGLLAHGTAAIQRELNEIPGAMDQD-----AGNET 40
D.simulans (XP_002078032.1) 1 ----- MKPLIVVVLVGLLASGCHIVH---SQEPGDAVEQ-----EASES 36
D.sechellia (XP_002045314.1) 1 ----- MKPLIVVVLVGLLASGCHIVH---SQEPGDAVEQ-----EASES 36
D.melanogaster (NP_608781.2) 1 ----- MKPLIVVVLVGLMASGCHIVH---SQEPGDAVEQ-----EASES 36
D.melanogaster (AAL68365.1) 1 ----- MKPLIVVVLVGLMASGCHIVH---SQEPGDAVEQ-----EASES 36
D.melanogaster (AAL48116.1) 1 ----- MKPLIVVVLVGLMASGCHIVH---SQEPGDAVEQ-----EASES 36
D.erecta (XP_001968564.1) 1 ----- MKPLIVVLVGLLASGCHIVH---SQDPGEVVEQ-----EASES 36
D.yakuba (XP_002087828.1) 1 ----- MKPLIVFVLVGLLASGCHIVH---SQEPGEAVEQ-----EASES 36
D.ananassae (XP_001965094.1) 1 ----- MMKPLIIIAWL--MATSCYLVS--SQES-EAAEQ-----EVEKS 34
D.pseudoobscura (XP_001356411.1) 1 ----- MKPLIGFLLVGLLMCAQQTQ--PQDVDAIVEQ-----EAGET 35
A.pisum (XP_001945904.1) 68 TTEIVNETTAEPLLETTNDVVPPTTTEVVVPTTTEVVVPTTTEVVVPTTNDVVPVPTLELATSEATTAV 134
A.pisum (XP_001948728.2) 1 ----- MKTNIILVIIFMLNTKCLCQFYAFD-----DDV 28
P.humanus corporis (XP_002425163.1) 1 ----- MfvNSNDKFTIN----- 12
D.pulex (BFX77001.1) 1 ----- MKWLSVFFLVFLCASGTEIEPGDPEDIGDPAPQGTAPPQTSDLEETK----- 49

B.mori LTP-III
D.plexippus (EHJ73751.1) 31 ---KLSEGEKKLSHNILAIIEHYKQDPDTGLPGAKLPDFYVPVDPVKQSLTLG-TMHFKNIALYGTN 92
D.plexippus (EHJ73750.1) 26 TTESQLAKGEEKMSEYILKVLVLEHFQKQNFVGLPGAKVDFHKKVDMKHSVSIIG-TLYFKNTSVYGIS 91
D.plexippus (EHJ73750.1) 36 TTISQLKDGEOKMSEYILKVIIEHYKQPNPEGLPGVGS-QEYSVDPDRKSVGLFSSIDFIDTEVYGIN 101
D.ponderosae (ABE62911.1) 22 -----DGEQKLSSETLLAIVIEHYKQKDPVGVPGAPIPDFLPIPPMNHSSFSVG-KMNFDRMDLYGLK 80
T.castaneum (XP_972731.1) 24 QOKQIIEKQEKKISEYILQIIDLHYKDDPVGIPGAPIPDFLLIPELAHSFSLG-KMNFENVKLYGLS 89
A.florea (XP_003697952.1) 29 DTAALGALGKRELDHVRRAILKHYQSDPVGVLPGAPIPDFMSAPDMKYSFSMY-TMNFQKMNLYGLS 94
A.melifera (XP_395658.4) 29 DTAALGAVGKRELDHVRRAILKHYQSDPVGVLPGAPIPDFMSAPDMKYSFSMY-TMNFQKMNLYGLS 94
B.impatiens (XP_003492016.1) 41 DTTAALGALGKRELDHVRRAIVKHYQSDPVGVLPGAPIPDFMPVDMKHSFSMY-TMNFQKMNLYGLS 106
M.rotundata (XP_003708008.1) 29 DTAALGALGKRELDHVRRAIVKHYQSDPVGVLPGAPIPDFMPVDMKHSFSMY-TMNFQKMNLYGLS 94
N.vitripennis (XP_001606118.1) 33 STSAQIAQGEKRLGDIIRAILKHYQSDPVGVLPGAPIPDFMDVPMKQSFMSF-TMNLNSIKVYGLS 98
S.invicta (EFZ14465.1) 59 NKTTQMAAGEQRLGDIIRAILKHYQKDDPVGVLPGAPIPDFMSVDMKHSFSMY-TMNFQKISVSGLS 124
A.echinator (EGI63413.1) 44 KTAALGAAAGEQRLGDIIRAILKHYQKDDPVGVLPGAPIPDFMPVDMKHSFSIN-TINLKKISVYGLS 109
H.saltator (EFN76863.1) 39 ADQAGMAAGEQRLGDIIRAILKHYQKDDPVGVLPGAPIPDFMPVDMKHSFSMY-TMHFKQINVYGLA 104
C.floridanus (EFN74421.1) 37 NKAALGAAAGEQRLGDIIRAILKHYQKDDPVGVLPGAPIPDFMSVDMKHSFSY-TMHFKQINVYGLS 102
A.aegypti (XP_001654113.1) 106 VDKHNQOVGSESLISALNNAVIDLYKQEDPVGVLPGATVPDFMPIPEIKQSFSA-KMHMKNVLAYGLS 171
A.aegypti (XP_001653919.1) 45 YRFQKTPRYDRRFSTQLFHVLEFYKQDDPVGVLPGASIPDFLSIPDFRQSIQFT-AMEMRDLYTYGLS 110
C.quinquefasciatus (XP_001863022.1) 44 ADDHAKATGESLISALFAIIDLYKQEDPVGVLPGATVPDFMPIPEIKQSFSA-KMHMKNVLAYGLS 109
A.gambiae (XP_312626.4) 35 RSTVDQELGSEMLTKQLFAIIDLYKQDDPVGVLPGASIPDFMPIPEIKQSFSA-KMLHKNVLAGMS 100
A.darlingi (EFR25164.1) 58 DRARKQETGALSDQLFAIIDLYKQEDPVGVLPGATVPDFMPIPEIKQSFSA-TYMTKMYVYGLS 123
D.virilis (XP_002052633.1) 32 DEAQEIEASKNKLAQIEALIEHYKQEDPVGVLPGAPIPDFIEVDMAKNMGIS-NLNMMKKVAYGLS 97
D.mojavensis (XP_002002021.1) 31 DEAHNIEAQNRAVAQIEGLEHYKQEDPVGVLPGAPIPDFMDVPMKSLGMA-NLNMLKVKAYGLS 96
D.grimshawi (XP_001989184.1) 29 TDAHNIIEVSKNRVAQIEAVLEHYKQKDPVGLPGAPIPDFVDVPTDTSNSLGMA-NLNMRKVKAYGLS 94
D.willistoni (XP_002064455.1) 41 NEDHNINASQNRVAQIEAVLEHFQKADPVGVLPGVVPDFMEVDMKKS LGMA-NLNMMKVRAYGLS 106
D.simulans (XP_002078032.1) 37 DDALKIKESQASIAAQVEAMLVHFQEDPQGLPGVVPDFLEVPNVKKS MGMA-NLDMKQVKAYGLS 102
D.sechellia (XP_002045314.1) 37 DEALKIKESQASIAAQVEAMLVHFQEDPQGLPGVVPDFLEVPNVKKS MGMA-NLDMKQVKAYGLS 102
D.melanogaster (NP_608781.2) 37 DDALKIKESQASIAAQVEAMLVHFQEDPQGLPGVVPDFLEVPNVKKS MGMA-NLDMKQVKAYGLS 102
D.melanogaster (AAL68365.1) 37 DDALKIKESQASIAAQVEAMLVHFQEDPQGLPGVVPDFLEVPNVKKS MGMA-NLDMKQVKAYGLS 102
D.melanogaster (AAL48116.1) 37 DDALKIKESQASIAAQVEAMLVHFQEDPQGLPGVVPDFLEVPNVKKS MGMA-NLDMKQVKAYGLS 102
D.erecta (XP_001968564.1) 37 DDALKIKESQANIAAQVEAMLVHFQEDPQGLPGVVPDFLEVPNVKKS MGMA-NLDMKQVKAYGLS 102
D.yakuba (XP_002087828.1) 37 DDALKIKESQAKIAAQVEAMLVHFQEDPQGLPGVVPDFLEVPNVKKS MGMA-NLDMKQVKAHGLS 102
D.ananassae (XP_001965094.1) 35 NDEHNIEVSKNRVAQIEAVLEHFQKADPVGVLPGAAIPDFIEVDAKKNLGMA-TLDMKHKVAYGSS 100
D.pseudoobscura (XP_001356411.1) 36 DEEHNIEATQNRMAAQVEAVLEHFQKADPVGVLPGVVPDFIDVDPVKKNMFG-NLDMKQVKAYGLS 101
A.pisum (XP_001945904.1) 135 NNTLPEVEVVKDKLSEQIRKILKHYQHDPVGFPGAPIPDFLSIPPMNKDFGVA-FMTFKNMTVHGLS 200
A.pisum (XP_001948728.2) 29 PSLSEADERIINLTLTKNVLEHYQNDPVGVLPEAVPEYSDPEIPDNETPL--WSMHNSTMKGHS 93
P.humanus corporis (XP_002425163.1) 13 --HHEQLLFQKKISEQLIQILNHYKQEDPVGVLPGAPIPDFMAIPDMKHSFVA-TMNFKNSSVHGLS 76
D.pulex (BFX77001.1) 50 -----IELSLDARIRQLIEHYKQDDPGLPIPGVPIPEMPIDPEGDFPAA-KIKFSEABLQOLS 107

B.mori LTP-III
D.plexippus (EHJ73751.1) 93 EFRNLVYKADIGAMEAHAVMTLEKLOARQNYTFATWFNSVRGP-FTVHITGLRVTAAGLOVERDGK 158
D.plexippus (EHJ73750.1) 92 KFRILNINAEIGAMEVHAALADKLOAKGNYTMTWLNRVQGP-YTVDTIGIKVMKAKANLGVVERDGK 157
D.plexippus (EHJ73750.1) 102 KFRVIYVNLIDENMEGRAALEIDNLHIRGRYALNAFLNSNYGG-FTANITGIKITALTTLGVVERDGK 167
D.ponderosae (ABE62911.1) 81 KFRIEHVTLDVAALRLQAALLIDVMDVGLNYTLKTFWSSAQGP-FTVKLSGVFVQATATLEVLNDGR 146
T.castaneum (XP_972731.1) 90 KFRITHIKADITAMKVEAALTIKTLQVKNYTLRTFMSSAKGP-FTVKLTDDVYVKAATLEVERNGQ 155
A.florea (XP_003697952.1) 95 KFRIVNAESLALMQVSVTLNIESLDIRGFYTLSSWLSRSAGN-FTMKLMGVNVKIGRLEVASDGK 160
A.melifera (XP_395658.4) 95 KFRIVNAESLALMQVSVTLNIESLDIRGFYTLSSWLSRSAGN-FTMKLMGVNVKIGRLEVASDGK 160
B.impatiens (XP_003492016.1) 107 KFRIVNMESELALMQVSVTLNKNLNRGFRYTLSSWLSRSAGN-FTVKLSGVNVKIGRLEVASDGK 172
M.rotundata (XP_003708008.1) 95 KFRIVHMESELALMQVSVTLNIESLDIRGLYTLSSWLSRSAGN-FTVKLTENIQGIARLEVADDGK 160
N.vitripennis (XP_001606118.1) 99 KFRIEHIRSELALMQVSVGLDIEENLDIKGLYTLSSWISSAGD-FTVKLTGVKVEGLAKLEVGNDGK 164
S.invicta (EFZ14465.1) 125 KFRITHVESLALMQVSVAVRIDNLNMRGLYTLSSWLSRSAGD-FTVNLTDDVNVKIGARLEVGNDGK 190
A.echinator (EGI63413.1) 110 KFRIEHMESELALMQVSVAVRIDLDIRGLYTLSSWISSRSEG-FMVKLTGVKVEGIARLEVNTDGK 175
H.saltator (EFN76863.1) 105 KFRIEHVESLALMQVSVAVRIDLDIRGLYTLSSWLSKAGD-FSVKLTGVNVKIGARLEVNTDGK 170
C.floridanus (EFN74421.1) 103 KFRIEHVESLALMQVSVAVRIDSLVHGLYTLSSWLSRSTGN-FTSKLTGVNVKIGARLEVNTDGK 168
A.aegypti (XP_001654113.1) 172 KFRIKMFKTELTNTMKVQGTGVQIDEMLVKGNYSSTFFNRAEGP-FTVVLTKNVMTKGNVSLVDRDGK 237
A.aegypti (XP_001653919.1) 111 RLRIRLFQAKLSSMVLRLVLSVDELLVNGSYAIN--MGSSGP-FWLKMKNVRTMGNVSLGVDRDGI 173
C.quinquefasciatus (XP_001863022.1) 110 KFRIKLKFTELTNTMKVQGTGVQIDEMLVKGNYSSTFFNRAEGP-FTVVLTKNVMTKGNVSLVDRDGK 175
A.gambiae (XP_312626.4) 101 RFRIRYFHTELSRMSVTLVAVIDEITVNGNYTMTSTFFNRAEGP-FNVVMRNVLTKANVSLAVERDGT 166
A.darlingi (EFR25164.1) 124 RFRIRYFHTELSRMSVTLVAVIDEITVNGNYTMTSTFFNRAEGP-FTVNMKNVLTKANVSLAVERDGL 189
D.virilis (XP_002052633.1) 98 KFRIASINADFKEMMAKAGIQIDEMLVKGNYSSTFFSKTNGP-FTVVLTKNVYVRSVATLGVVERDGH 163
D.mojavensis (XP_002002021.1) 97 KFRISTVDVDFKMKKAEAGIQIDQMLVKNYSSTFFSKANGP-FTVVLTKNVYVRCVSTLGVVERDGH 162
D.grimshawi (XP_001989184.1) 95 KFRIASINADFKEMMEVAGITIDEMLVKGDYTLSSFFTKANGP-FTVVLTKNVYVTSASLIVKRDGH 160
D.willistoni (XP_002064455.1) 107 KFRITATINADFKDLQVQKAGIQIDEMNVKGNYSSTFFSKANGP-FTVVLTKNVYVVEATATLAVERDGH 172
D.simulans (XP_002078032.1) 103 KFRIDKMNLDLKEKRFNGGLQIDQMLVKGQYTLSSFFSKANGP-FTVVLTKNVYAEATAFLAVERDQ 168
D.sechellia (XP_002045314.1) 103 KFRIDKMNLDLKEKRFNGGLQIDQMLVKGQYTLSSFFSKANGP-FTVVLTKNVYAEATAFLAVERDQ 168
D.melanogaster (NP_608781.2) 103 KFRIDKMNLDLKEKRFNGGLQIDQMLVKGQYTLSSFFSKANGP-FTVVLTKNVYAEATAFLAVERDQ 168
D.melanogaster (AAL68365.1) 103 KFRIDKMNLDLKEKRFNGGLQIDQMLVKGQYTLSSFFSKANGP-FTVVLTKNVYAEATAFLAVERDQ 168
D.melanogaster (AAL48116.1) 103 KFRIDKMNLDLKEKRFNGGLQIDQMLVKGQYTLSSFFSKANGP-FTVVLTKNVYAEATAFLAVERDQ 168
D.erecta (XP_001968564.1) 103 KFRIDKMNLDLKEKRFNGGLQIDQMLVKGQYTLSSFFSKANGP-FTVVLTKNVYAEATAFLAVERDQ 168
D.yakuba (XP_002087828.1) 103 KFRIDKMNLDLKEKRFNGGLQIDQMLVKGQYTLSSFFSKANGP-FTVVLTKNVYAEATAFLAVERDQ 168
D.ananassae (XP_001965094.1) 101 QFRIDKLSADFKEMKINGGLQIDQMTVKGQYTLSSFFSKANGP-FTVVLTKNVYAEATAFLAVERDGH 166
D.pseudoobscura (XP_001356411.1) 102 KFRIDTVADADLKSMMKIKGGVQIDEMLVKGNYSSTFFSKANGP-FTVVLTKNVYAEATAFLAVERDGH 167
A.pisum (XP_001945904.1) 201 KFKVENVNTDLKNMRYVLLKIKRMYVGLNYTLRSWLSRPSAGPENVTLIDVEAAAEALPEADGN 267
A.pisum (XP_001948728.2) 94 KFRILKLYVNLVDLQLEFGISIDTLVVVGNYSYWKMYD---GYNVTLQLHIDGHLSSLOVSESGH 156
P.humanus corporis (XP_002425163.1) 77 IFRIEKIESNVADMEVVLVAMSTEQLLIKGQYTMSTWFSRQGGD-FNVTLSSGLIKGLASMEVNVQNGQ 142
D.pulex (BFX77001.1) 108 QFRINIVVRTDLKDLKVIWIGMTFDITLQVGRYRMSWFS-TSSGDFNVTLIRVHAEGFAGLVVDSGL 173

B.mori LTP-III 159 IRAENIVMDLISASNIIVAVNLENA --- EIIISGFINTIGPFI FDSIKFVYLKEAYATIKTTMNEKIDEV 221
D.plexippus (EHJ73751.1) 158 LRAQDIKIDISFSTISMNFNENAGFFGMLQGVNSIGTFLFDSIKFVYLKEAYTKAREEINKKLDEV 224
D.plexippus (EHJ73750.1) 168 LRAHDIITMDVNFNNIAVNFENSGLLVGLLQGLFNSIGTILFESIKFNLLKEAYTNMRTIEINKKLDQV 234
D.ponderosae (ABE62911.1) 147 LEAQDIAMDVTFKDMALDFQGLGFFASMFQGVNSVGFVFDSDIKFVYLSEANANIRREVNKQAARM 213
T.castaneum (XP_972731.1) 156 LEAQDMDMDITFKGIAMDFKGLGFFANMFOGVNSVGTFFI FDSIKFVYLREVTNLRNDVNVKQVKKV 222
A.florea (XP_003697952.1) 161 LQAQNI DMDLTFENIAMDFKNLGFLGSLVQSTINSVGSFIFDSIKFVYLKEINTKARGIANKQISQL 227
A.mellifera (XP_395658.4) 161 LQAQNI DMDLTFENIAMDFKNLGFLGSLVQSTINSVGSFIFDSIKFVYLKEINTKARGIANKQISQL 227
B.impatiens (XP_003492016.1) 173 LQAQNI DDLITFEKIDMDFKNLGFLGSLVQSMINSVGTFFI FDSIKFVYLKEINTKARGEANKQISQL 239
M.rotundata (XP_003708008.1) 161 LQAQDI DMDLTFDKIDMDFKNLGFLGSLVQGVINSIGTFFI FDSIKFVYLKEVNTNIRGEVNVKQISQL 227
N.vitripennis (XP_001606118.1) 165 LHAQDI VMDLTFENIDLDFKNLGFFASLFOGVNSVGSFVFDSDIKFVYLQEVNTNVRGEVNVKHISTL 231
S.invicta (EFZ14465.1) 191 LQAQDI DDLNLFFDKIQLNFNENLGLGSLVQFQIINSVGTFFI FDSIKFVYLKEVNTNVRGEVNVKQISQL 257
A.echinator (EGI63413.1) 176 LQAQNI DMDLTFDKIDLDFKNLGFLGSLVQGVINSVGSFIFDGIKFPVYLKEVNTNIRGEVNVKQISQL 242
H.saltator (EFN76863.1) 171 LQAQDI DMDLTFDKIDLDFKNLGFLGSLVQGVINSIGTFMFDSDIKFPVYLKEVNMNVRGEVNVKQISQL 237
C.floridanus (EFN74421.1) 169 LQATNI DMDLTFDKIDLDFKNLGFLATVFOGVNSIGSFLFDSIKFPVYLKEVNTNMRGEVNVKHISTL 235
A.aegypti (XP_001654113.1) 238 VRTQDI SLDIADFDDMSMDFQNLGFMGSI FQSVVNSASNLVFDITIKPFMLSEAYTKIRAEIDTRVENM 304
A.aegypti (XP_001653919.1) 174 LRTQDI ELDLDFGFMAMDFQNLGFWGRVFOGLANAAPNMVFDVYKPYMLSEAYTKIRAEIDTRVENM 240
C.quinquefasciatus (XP_001863022.1) 176 VRTQDI SLDIADFDDMSMDFQNLGFMGSI FQSVVNSASNLVFDITIKPFMLSEAYTKIRAEIDTRVENM 242
A.gambiae (XP_312626.4) 167 LRTQDI ELDLADFDDMSMDFQNLGFMGSI FQSVVNSASNLVYDITIKPFMLSEAYTKIRAEIDTRVENM 233
A.darlingi (EFR25164.1) 190 LHTDNI ELDLDFEEMAMDFQNLGFMGSI FQSVVNSASNLVYDITIKPFMLSEAYTKIRAEIDTRVENM 256
D.virilis (XP_002052633.1) 164 LTTTEQIKMDITFGEMAMDFQNLGFLGSLVQSMINSAPNVVFDAMKPFMLQEQADKQLRTEINAFIEKN 230
D.mojavensis (XP_002002021.1) 163 LTTTEHIDMDITFGEMAMDFQNLGFLGSLVQFQIINSAPNLVFDAMKPFMLQEQADKQMRGEINTRIEKF 229
D.grimshawi (XP_001989184.1) 161 LTTTDRIKMDISFGEMAMDFQNLGFLGSLVQGLINSAPNLVFDAMKPFMLQEQADKQLRTEINAFIEKN 227
D.willistoni (XP_002064455.1) 173 LTTTDSIKMDITFGEMAMDFQNLGFLGSLVQFQIINSAPNLVFDAMKPFMLQEQADKQLRGEINENIEKL 239
D.simulans (XP_002078032.1) 169 LATDRIKIDITFSDMTDFQNLGLVGSVFOGVNSVGNAPNLVFDAMKPFMLQEQADKQLRGEINVMIQKT 235
D.sechellia (XP_002045314.1) 169 LATDRIKIDITFSDMTDFQNLGLVGSVFOGVNSVGNAPNLVFDAMKPFMLQEQADKQLRGEINVMIQKT 235
D.melanogaster (NP_608781.2) 169 LATDRIKIDITFSDMTDFQNLGLVGSVFOGVNSVGNAPNLVFDAMKPFMLQEQADKQLRGEINVMIQKT 235
D.melanogaster (AAL68365.1) 169 LATDRIKIDITFSDMTDFQNLGLVGSVFOGVNSVGNAPNLVFDAMKPFMLQEQADKQLRGEINVMIQKT 235
D.melanogaster (AAL48116.1) 169 LATDRIKIDITFSDMTDFQNLGLVGSVFOGVNSVGNAPNLVFDAMKPFMLQEQADKQLRGEINVMIQKT 235
D.erecta (XP_001968564.1) 169 LATDRIKIDITFSDMTDFQNLGLVGSVFOGVNSVGNAPNLVFDAMKPFMLQEQADKQLRGEINVMIQKT 235
D.yakuba (XP_002087828.1) 169 LATDRIKIDITFSDMTDFQNLGLVGSVFOGVNSVGNAPNLVFDAMKPFMLQEQADKQLRGEINVMIQKT 235
D.ananassae (XP_001965094.1) 167 LATDRIKIDITFSDMTDFQNLGLVGSVFOGVNSVGNAPNLVFDAMKPFMLQEQADKQLRGEINVMIQKT 233
D.pseudoobscura (XP_001356411.1) 168 LTTTDRIKIDITFRDMDMDFQNLGFMGSI FQGVNSVGNAPNLVFDAMKPFMLQEQADKQLRGEINVMIQKT 234
A.pisum (XP_001945904.1) 268 LQATDTEMDMQFKDCELDKFLGFAASMMQGVISSMGSLVLEGIKFFIINEVNTNLRADVNAQVKAI 334
A.pisum (XP_001948728.2) 157 LETNINLNMNMYDSLHMDTDKLN - - IFFYDSFVNSFTHFVQTIKPIIMKLVNMIKEELNQMCKHF 221
P.humanus corporis (XP_002425163.1) 143 LEAQNI DMDITFQNIAMNFQNLGFMGSI FQGVINSVGTFFI FDSIKFVYLSEANANIRREVNKQAARM 209
D.pulex (BFX77001.1) 174 MQATNI TFDVGFKDIITMDFKFNLFGLGSLVQFQIINSVGTFFI FDSIKFVYLSEANANIRREVNKQAARM 240

B.mori LTP-III 222 AGD--LQFPNSISPL-DMVIA D VRKKVHQMDMPYKIKDYNTSVSV--FVVTLADTWVMGIISSFORV 283
D.plexippus (EHJ73751.1) 225 AGD--VQFPNSISPL-DKVIADLRKKVRIINMDPYQINDYNSTVSI--FTVSLTHTWITGIISSFORV 286
D.plexippus (EHJ73750.1) 235 VGD--IEFPNITITPL-DMVIVDARKNIRDKVMDPLRIDDYNTSAGW--VNIYLNKNTWLYGLSTINRV 296
D.ponderosae (ABE62911.1) 214 P----QRFPNSIAPC-DQVVAQARSMVRARGYDFYRVKALNTSISGL--ADVQLTHTWLYGAASFHRT 273
T.castaneum (XP_972731.1) 223 P----QKFPNSISPF-DQLITLDIRHKIRKAQDFYKVNVDYNTSVGV--FDIYMRHTWLYGLSSITHRV 282
A.florea (XP_003697952.1) 228 P----QYFPNSISPF-DMAI AELRKYISQMGYDFFKVNDYSQTVGI--FTVTSTHTWITGLASFYRM 287
A.mellifera (XP_395658.4) 228 P----QYFPNSISPF-DMAI AELRKYISQMGYDFFEVNDYSQTVGI--FTVTSTHTWITGLANIRYI 287
B.impatiens (XP_003492016.1) 240 P----QYFPNSISPF-DMLITLIRROISEKGYDFFKVKDYSQTVGI--FTVTSTHTWITGLGSMYRM 299
M.rotundata (XP_003708008.1) 228 P----QYFPNSISPF-DMAVAEARKVQSGLGYDFFKVQDYSQSVGM--FTVTSTHTWITGLASFYRM 287
N.vitripennis (XP_001606118.1) 232 P----NYFPNSISPF-DMAVAEARKVQSDMGYDFFKVKDYSQSMGM--FTVTSSHTWITGLASFYRM 291
S.invicta (EFZ14465.1) 258 P----QYFPNSISPF-DMAI AEARKEYSEMGYDFYKLDYTSQVGI--FTVTSSHTWITGLASFYRM 317
A.echinator (EGI63413.1) 243 P----QYFPNSISPF-DMAI AEARKEYVSMGYDFYKLDYTSQVGI--FTMTSSHTWITGLASFYRM 302
H.saltator (EFN76863.1) 238 P----QYFPNSISPF-DMAVAEARKVRLMGYDFYRVQDYTSAGV--FTVTSSHTWITGLASFYRM 297
C.floridanus (EFN74421.1) 236 P----QYFPNSISPF-DMAVAEARKVSEMGYDFYKLDYTSQVGI--FTVTSTHTWITGLASFYRM 295
A.aegypti (XP_001654113.1) 305 TTEYNIVFPNSISPL-DMAI GEARTLVRNKKFDPYLI PDYNTTLAGI--FGMHTSHTWIRGVSSFYRY 368
A.aegypti (XP_001653919.1) 241 VDKRAIVLANSVPL-DLMI SEARFLMRTKGFDFYHLPDYRNSLSI--FNFLFLSGTRLRGLSNFYRS 304
C.quinquefasciatus (XP_001863022.1) 243 TTEHRILFPNSISPL-DMAI GEARTLVRNKKFDPYLI PDYNTTLAGI--FGMQTTHTWIRGVSSFYRY 306
A.gambiae (XP_312626.4) 234 TVENQFTLNSIAPL-DMAI GEMRRIVRNKKLDFQVDPDYNNTAGI--FGMQTSSHTWISGGSSFYRY 297
A.darlingi (EFR25164.1) 257 TLEHDFILNSITPL-DMAI GEMRAVVRNKKGLDFLVPDYNNTAGI--FGMRTMTHTWIKGSSFYRY 320
D.virilis (XP_002052633.1) 231 MGDR--RMPNSITPL-DSAI AEGRKLVRQKGLDFYHVADMNRTMGV--FSVQLSNTWINGISSFYRV 292
D.mojavensis (XP_002002021.1) 230 MGDR--RMPNSITPL-DSAI AGLRKMVRKGYDFYRLEDKNRTMGV--FSVQLTNTWITGCSFYRV 291
D.grimshawi (XP_001989184.1) 228 LGDR--RMPNSITPL-DSVIA EGRKLVRQNGYDFYHLPDMNRTMGV--FSVQLANTWISGVSFYRV 289
D.willistoni (XP_002064455.1) 240 MGDR--RLNSITPL-DSAI AEARKKVRAMGYDFYHVPDMNRTMGV--FSVQLSHTWINGISSFYRV 301
D.simulans (XP_002078032.1) 236 LGDR--RLNSITPL-DSAI AMARKMVRQGGYDFYHLPDMNRTMGV--FSVQLAHTWINGISSFYRV 297
D.sechellia (XP_002045314.1) 236 LGDR--RLNSITPL-DSAI AARKMVRQGGYDFYHLPDMNRTMGV--FSVQLAHTWINGISSFYRV 297
D.melanogaster (NP_608781.2) 236 LGDR--RLNSITPL-DSAI AMARKMVRQKGFDFYHLPDMNRTMGV--FSVQLAHTWINGISSFYRV 297
D.melanogaster (AAL68365.1) 236 LGDR--RLNSITPL-DSAI AMARKMVRQKGFDFYHLPDMNRTMGV--FSVQLAHTWINGISSFYRV 297
D.melanogaster (AAL48116.1) 236 LGDR--RLNSITPL-DSAI AMARKMVRQKGFDFYHLPDMNRTMGV--FSVQLAHTWINGISSFYRV 297
D.erecta (XP_001968564.1) 236 LGDR--RLNSITPL-DSAI AMARKMVRKGYDFYHLPDMNRTMGV--FSVQLAHTWINGISSFYRV 297
D.yakuba (XP_002087828.1) 236 LGDR--RLNSITPL-DSAI AMARKMVRKGYDFYHLPDMNRTMGV--FSVQLANTWINGISSFYRV 297
D.ananassae (XP_001965094.1) 234 MGDR--KLPNSITPL-DSAI AARKMVRKGYDFYKLDQDMNRTMGV--FSVQLSNTWISGVSFYRV 295
D.pseudoobscura (XP_001356411.1) 235 MGDR--RLNSITPL-DSAI AEGRKKVRQMGYDFYHLPDMNRTMGV--FSVQLSHTWINGISSFYRV 296
A.pisum (XP_001945904.1) 335 T----SKLPKMTVPVPDLAVAEGRKVVORMGYDFYHVADRHIDEGP--LNFTITELTVSGLSSFHRT 395
A.pisum (XP_001948728.2) 222 K----RFNITIPV-DLLI ABSRQIKSMGFDFYRVDLVNAVNFNIFSLDVNEIWIWISGLSSITVRL 282
P.humanus corporis (XP_002425163.1) 210 P----QRFPNSISPL-DMFISEMRKFAIKKFDYKIDYNNNSAGI--FTVELTNTWITGLASFYRV 269
D.pulex (BFX77001.1) 241 N----HILPDSVAPL-DMAMA GRABEQENGMDFEIPYETSILITG-VVVKIFNGTMHGLSTIHRV 301

B.mori LTP-III
D.plexippus (EHJ73751.1) 284 GNISLIMENNNAVADFEIGTQKLEGGTQKWEISATS-GLLSRAGTASFSVEYISARIIILGQPLDTRKK 349
D.plexippus (EHJ73750.1) 287 GNITLKLENNNTVIADFEIGTQRLGGTQWDVSAIS-GLLSRAGTASFSVEYISGRMILAQPLDTRKK 352
D.plexippus (EHJ73750.1) 297 GNVSLKVENKTVVADFSIGTEMLGSTDWEISGCR-GLISSFGTSSFSVKYIRGHFILLVQPLDTRKR 362
D.ponderosae (AEE62911.1) 274 RALVVAMRNNTLHALIEVGTQRLGLGTHWEVALVS-GVLSRAGTASFSVEYLRVQVNASOSMDTROR 339
T.castaneum (XP_972731.1) 283 GDIITFEIKKNSVYAVLEVGTQRMGGTSHWEVSLIA-GFMSKAGTASFSVEYLRVQVNASOSMDTRNP 348
A.florea (XP_003697952.1) 288 GNVITLGIKNGTVYATVDAGTQBLEGKTHWEVSVIG-GFLSRAGTASFTTQYFRAQVNLSSQPLDTRKR 353
A.mellifera (XP_395658.4) 288 GNVITLGIENGTVYATIDAGTQBLEGKTHWEVSVIG-GFLSRAGTASFTTQYFRAQVNLSSQPLDTRKR 353
B.impatiens (XP_003492016.1) 300 GNVITLGIENGTVYATIDAGTQBLEGKTHWEVSVIG-GFLSRAGTASFTTQYFRAQVNLSSQPLDTRKR 365
M.rotundata (XP_003708008.1) 288 GNITLSMENGTVYALIDVGTQBLEGRTHWEVSVIG-GFLSRAGTASFTTQYFRVQIKFGQPLDTRKK 353
N.vitripennis (XP_001606118.1) 292 GNITLSMENGTVYAVMDIGTQBLEGRTHWDVSVIG-GVLSRAGTASFTTVEYFRVQNLSSQPLDTRKR 357
S.invicta (EFZ14465.1) 318 GNITVSMENGTVYALVDIGTQBLEGKTHWEVSVIG-GFLSRAGTASFTTQYFRVQIKLGGQPLDTRKR 383
A.echinator (EGI63413.1) 303 GNITITMENGTVIYALLDVGTEBLEGKTHWEVSVIG-GFLSRAGTASFTTQYFRVQIKLGGQPLDTRKR 368
H.saltator (EFN76863.1) 298 GNITITMEKGNVYLLLDIGTQBLETGTKTHWEVSVIG-GFLSRAGTASFTTQYFRVQIKLGGQPLDTRKR 363
C.floridanus (EFN74421.1) 296 GNITITLENGTVYALLDVGTEKLGKTHWEVSVIG-GFLSRAGTASFTTQYFRVQIKLSSQPLDTRKR 361
A.aegypti (XP_001654113.1) 369 GAIIGILMONNTVVALTMQVGTQIRIMGSTQWEVSVGR-GMVSRAGQAQFTVEHIVKVSFEVQPLDTRKR 434
A.aegypti (XP_001653919.1) 305 GEMEITAVONKSMACITQVGTQIRIEGSTRWQLSVIR-DVLSRSGAIFFSVQVYRSLIKVQVPLDTRKR 370
C.quinquefasciatus (XP_001863022.1) 307 GDIIGILMONNTVSLTMQVGTQIRIMGSTQWEVSVGR-GMVTRAGQAQFTVEHIVKVSFEVQPLDTRKR 372
A.gambiae (XP_312626.4) 321 GDISITMONNTATVGMHVATORIVGSTQWTVSIGR-GMLSHPRGAQFTVEHIVKVSFEVQPLDTRKR 363
A.darlingi (EFR25164.1) 328 GAIISVTMONNTATVGLHVATORLGTSTHWEAGP-----SLRSSTSVQSSRS-----DSRLICDKK 375
D.virilis (XP_002052633.1) 293 GNITAAAMONNTVSLRLQVGTQOITGAGQWELGFG---LVTRVGHVQFTVQYIRATVEISQPLDTROR 356
D.mojavensis (XP_002002021.1) 292 GNVITAAAMHNTVISMRLQGTQOITGAGQWELGFG---LMTRVGHVQFTVQHIRATVEISQPLDTRKR 355
D.grimshawi (XP_001989184.1) 290 GNITAGMONNTVSLRVQVGTQOITGAGQWELGFG---LVTRVGHVQFTVQHIRATVEISQPLDTRKR 353
D.willistoni (XP_002064455.1) 302 GNMISAGIENNTVSLRVQIGTQOVTGAGQWELGFG---MMTRVGHVQFTVQHIRATVIGISQPLDTRKR 365
D.simulans (XP_002078032.1) 298 GNITAGMANKTVSVVLQIGTQOVTGAGQWELGFG---MMTRVGHVQFTVQHIRATVIGISQPLDTRKR 361
D.sechellia (XP_002045314.1) 298 GNITAGMANKTVSVVLQIGTQOVTGAGQWELGFG---MMTRVGHVQFTVQHIRATVIGISQPLDTRKR 361
D.melanogaster (NP_608781.2) 298 GNITAGMANKTVSVVLQIGTQOVTGAGQWELGFG---MMTRVGHVQFTVQHIRATVIGISQPLDTRKR 361
D.melanogaster (AAL68365.1) 298 GNITAGMANKTVSVVLQIGTQOVTGAGQWELGFG---MMTRVGHVQFTVQHIRATVIGISQPLDTRKR 361
D.melanogaster (AAL48116.1) 298 GNITAGMANKTVSVVLQIGTQOVTGAGQWELGFG---MMTRVGHVQFTVQHIRATVIGISQPLDTRKR 361
D.erecta (XP_001968564.1) 298 GNITAGMANKTVSAVLQIGTQOVTGAGQWELGFG---MMTRVGHVQFTVQHIRATVIGISQPLDTROR 361
D.yakuba (XP_002087828.1) 298 GNITAGMANKTVSVVLQIGTQOVTGAGQWELGFG---MMTRVGHVQFTVQHIRATVIGISQPLDTRKR 361
D.ananassae (XP_001965094.1) 296 GNITVGMANKTVSLNLHLGTQOVTGAGQWELGFG---MMTRVGHVQFTVQHIRALVGVSSQPLDTRKR 359
D.pseudoobscura (XP_001356411.1) 297 GNITALMANKTVSLVQVGTQOVTGAGQWELGFG---MMTRVGHVQFTVQHIRATVIGVSSQPLDTROR 360
A.pisum (XP_001945904.1) 396 GDITGLQIRGVPVQMSVHVITGAVNGSLRWVSYRLGLSKTFRRTGVSNFTVDHIVQVRAVNVQTLDIRNK 462
A.pisum (XP_001948728.2) 283 GDITHTISIQNTIISVHIHTQELKKGHCQWIKGAGG--VLKTTGVLVFSFIDYIQLBANVTQPMIDTRLA 347
P.humanus corporis (XP_002425163.1) 270 GNVITLTKKEKVLVYAGLHVGTINQLFGSCQWEIGVAG--LMSRAGTASFTTEYLQVNVTVAPLDRKR 334
D.pulex (BFX77001.1) 302 GDVIFNYENGLVVGAAQATQRLKGFHFNWQLDF---KVFAPRGKISLQIDHLDVKIGLSQVFNVOKK 365

B.mori LTP-III
D.plexippus (EHJ73751.1) 350 PQFRSLDLEVGNIQVRCNAGTLDYVVEFVFNILPNLLRYQIMDAIEGPKLKRRIQBELDKLDVEEMI 416
D.plexippus (EHJ73750.1) 353 PEFRLDLDLVGNIQVRFDDGAGTLDYVVEFAVNVLPNLLRYQIVDAIEGPIIEKIQQELNKNINVEEMI 419
D.plexippus (EHJ73750.1) 363 MMLKTLLELDVGNVQVRFDDGAGTLDYVVEFSTNLPNLLRYQIVDAIQNPKKWKLOBELDQLDLDEEAI 429
D.ponderosae (AEE62911.1) 340 PRLDDIQLQLGNVQVRFDDGAGTLDYVVELEAVNVLPNLLRYQIMDAIERPLRRIQIABLDKVDVERLI 406
T.castaneum (XP_972731.1) 349 PQLLEDIQLLELGNIQVRFDDGAGTLDYVVEFAVNVLPNLLRYQIMDAIEAPVKORIQBELNKNINVERMI 415
A.florea (XP_003697952.1) 354 PSMEBLELELGNIQVRIHGAGTLDYVVEASINILPNLLRYQIMDAIEGPKLKRRIQIFLNKVDVEKQI 420
A.mellifera (XP_395658.4) 354 PSMEBLELELGNIQVRIHGAGTLDYVVEASINILPNLLRYQIMDAIEGPKLKRRIQIFLNKVDVEKQI 420
B.impatiens (XP_003492016.1) 366 PNMEGLDLELGNIQVRIHGAGTLDYVVEASINILPNLLRYQIMDAIEGPKLKRRIQIFLNKVDVEKEI 432
M.rotundata (XP_003708008.1) 354 PRIEBLELELGNIQVRIHGAGTLDYVVEASINILPNLLRYQIMDAIEGPKLKRRIQIFLNKVDVEKLI 420
N.vitripennis (XP_001606118.1) 358 ATLEBLEDFELGNIQVRIHGAGTLDYVVEAGVNVLPNLLRYQIMDAIEGPIRRIQIDBLDKVNVKLI 424
S.invicta (EFZ14465.1) 384 ASLEBLELELGNIQVRIHGAGTLDYVVEASVNVLPNLLRYQIMDAIEGPKLKRRIQIDBLDKVNVKLI 450
A.echinator (EGI63413.1) 369 ALLEBLELELGNIQVRFHGARTLDYVVEASVNVLPNLLRYQIMDAIEGPKLKRRIQIBELDKLDVEKLI 435
H.saltator (EFN76863.1) 364 ASLEBLELELGNIQVRIHGAGTLDYVVEASVNVLPNLLRYQIMDAIEGPKLKRRIQIBELDKVNVKLI 430
C.floridanus (EFN74421.1) 362 ATLEBLELELGNIQVRIHGAGTLDYVVEAGVNVLPNLLRYQIMDAIEGPKLKRRIQIFLNKVDVEKLI 428
A.aegypti (XP_001654113.1) 435 PKLNDIQLLELGNIQVRCDDGAGTLDYVVEAVNVLPNLLRYQIMDAIENPLKTRVQEKLDCCINVEQMI 501
A.aegypti (XP_001653919.1) 371 PSLMDFQLELGNIQVIFSSGAGSMDYVVEAGVNVLPNLLRYQIMDAIERPLRRIQIREKLECNVEQV 437
C.quinquefasciatus (XP_001863022.1) 373 PKLNDIQLLELGNIQVRCDDGAGTLDYVVEAVNVLPNLLRYQIMDAIENPLKTRVQEKLDCCINVEQMV 439
A.gambiae (XP_312626.4) 364 LKLRDIQLLELGNIQVRSDDGAGTLDYVVEAVNVLPNLLRYQIMDAIENPLMRRIQEKLDCCINTEALV 430
A.darlingi (EFR25164.1) 376 LQKLDIQLLELGNIQVRFDDGAGTLDYVVEAVNVLPNLLRYQIMDAIENPLMRRIQEKLDCCINTEEMV 442
D.virilis (XP_002052633.1) 357 PQINDLQDFMGNIQVRCDDGAGTLDYVVEFAVNVLPNLLRYQIMDAIENPKIKRVQEKFNITDVEQVI 423
D.mojavensis (XP_002002021.1) 356 PQINDLQDFMGNIQVRCDDGAGTLDYVVEFVFNVLPNLLRYQIMDAIENPKIKRVQEKFNITDVEQVL 422
D.grimshawi (XP_001989184.1) 354 PQINDLQDFMGNIQVRCDDGAGTLDYVVEFAVNVLPNLLRYQIMDAIENPKIKRVQEKFNITDVEQAI 420
D.willistoni (XP_002064455.1) 366 PQINDLQDFMGNIQVRCDDGAGTLDYVVEFVFNVLPNLLRYQIMDAIENPKIKRVQEKFNITDVEQAI 432
D.simulans (XP_002078032.1) 362 AQITDLODFMGNIQVRCDDGAGTLDYVVEFAVNVLPNLLRYQIMDAIENPKIKRVQEKFNITDVEQVI 428
D.sechellia (XP_002045314.1) 362 AQITDLODFMGNIQVRCDDGAGTLDYVVEFAVNVLPNLLRYQIMDAIENPKIKRVQEKFNITDVEQVI 428
D.melanogaster (NP_608781.2) 362 AQITDLODFMGNIQVRCDDGAGTLDYVVEFAVNVLPNLLRYQIMDAIENPKIKRVQEKFNITDVEQVI 428
D.melanogaster (AAL68365.1) 362 AQITDLODFMGNIQVRCDDGAGTLDYVVEFAVNVLPNLLRYQIMDAIENPKIKRVQEKFNITDVEQVI 428
D.melanogaster (AAL48116.1) 362 AQITDLODFMGNIQVRCDDGAGTLDYVVEFAVNVLPNLLRYQIMDAIENPKIKRVQEKFNITDVEQVI 428
D.erecta (XP_001968564.1) 362 AQITDLODFMGNIQVRCDDGAGTLDYVVEFAVNVLPNLLRYQIMDAIENPKIKRVQEKFNITDVEQVI 428
D.yakuba (XP_002087828.1) 362 AQITDLODFMGNIQVRCDDGAGTLDYVVEFAVNVLPNLLRYQIMDAIENPKIKRVQEKFNITDVEQVI 428
D.ananassae (XP_001965094.1) 360 PQITDLODFMGNIQVRCDDGAGTLDYVVEFVFNVLPNLLRYQIMDAIENPKIKRVQEKFNITDVEQAI 426
D.pseudoobscura (XP_001356411.1) 361 PQITDLODFMGNIQVRCDDGAGTLDYVVEFAVNVLPNLLRYQIMDAIENPKIKRVQEKFNITDVEQAI 427
A.pisum (XP_001945904.1) 463 PVLDKLDIEVQKIEVQMRKEPLDYVVEIAVNSLPSLLRHITVDALIEPIKAKAQITLDDVQVEKLV 529
A.pisum (XP_001948728.2) 348 PFLNEFGLSVGNIQVRFDDGAGTLDYVVEALVNVLPNLLRYQIMDAIENPKIKRVQEKFNITDVEQAI 414
P.humanus corporis (XP_002425163.1) 335 PKIEDFNKLGNIQVRFVNGAGTLDYVVEFLVNVLPNLLRYQIMDAIENPKIKRVQEKFNITDVEQAI 401
D.pulex (BFX77001.1) 366 PRLVLEQVNLGNIQVRSSTGTSVDYVVEFAVNVLPNLLRYQIMDAIENPKIKRVQEKFNITDVEQAI 432

B.mori LTP-III	417	HEKLP EIDEMAESG-----FKLSS IIGKSEDEKDIRYDDDDFFN---	455
<i>D.plexippus</i> (EHJ73751.1)	420	KQELPKVDEM QETG-----FKLSALQIQNEDEE--SYGDDDDFFNF--	457
<i>D.plexippus</i> (EHJ73750.1)	430	KNELPRIDKIQEEG-----FQLAMLR FINKTGD--NYDEDEFFNF--	467
<i>D.ponderosae</i> (AEE62911.1)	407	QENAPKLDDPDG-----LTELTNLL-----	426
<i>T.castaneum</i> (XP_972731.1)	416	KENVDKIDNPES-----LKLL-----	431
<i>A.florea</i> (XP_003697952.1)	421	YEYIPSIIEKAR---QGMIPL EE-TNLE-LISFQDQDEQ-PFSESEENRGPS	466
<i>A.mellifera</i> (XP_395658.4)	421	YEYIPSIIEKAR---QGMIPL EE-ANLE-LISFQDQDEQ-PFSESEENRGPS	466
<i>B.impatiens</i> (XP_003492016.1)	433	YEHIPHIIEHATRH-IHGLVP EE-TILEGLMP EQDQDEQ-PFSESEENRGPS	482
<i>M.rotundata</i> (XP_003708008.1)	421	YEKIPNIEEQAR-Y-IQGLIP AE-TILEELIP EQDQDEQ-PFSESEEDRGPS	469
<i>N.vitripennis</i> (XP_001606118.1)	425	HEKIPDIEBRAKMLQGPPLEEBLEDDIVLEEVTPPEPDNEEPFSESEEEERGQS	477
<i>S.invicta</i> (EFZ14465.1)	451	DEKIPVIEEQARW--LHDLVP AE-TNLEEPTTHN-QDDLGP FSESEEEERGPS	499
<i>A.echinatior</i> (EGI63413.1)	436	DEKIPMIEEQARW--MQGLTP SE-TILEEPLP P NSQDDQTPFSESEEEERGPS	485
<i>H.saltator</i> (EFN76863.1)	431	DDKIPPEIEEQARW--MHGFKP AE-TILETPTP SPDEDSQVPFSESEENRGLS	480
<i>C.floridanus</i> (EFN74421.1)	429	DEKIPMIEEQVK---GLIPVEE-TILEESLLS-NQDDQIPFSESEENRGPS	474
<i>A.aegypti</i> (XP_001654113.1)	502	KKHVVVEYEKRGF-----DMEV-DFKLC-----	522
<i>A.aegypti</i> (XP_001653919.1)	438	KRHVADFERRGT-----NMVV-DWRLCERKLP EK-----	465
<i>C.quinquefasciatus</i> (XP_001863022.1)	440	KKHVVVEYEKRGF-----DMEL-DLKIC-----	460
<i>A.gambiae</i> (XP_312626.4)	431	RKYALEYKHHGI-----DIDLKDFELCEQQVPRGE-----	460
<i>A.darlingi</i> (EFR25164.1)	443	RKYATEFEEHGI-----DLDLQDFELCHS-----	466
<i>D.virilis</i> (XP_002052633.1)	424	KQQIEKNDHEGG-----NFAIDMNLFKMF-----	447
<i>D.mojavensis</i> (XP_002002021.1)	423	KVALEKYKKDGL-----NFIYBYKLDNLPFN-----	448
<i>D.grimshawi</i> (XP_001989184.1)	421	KQMAHKYEDEGS-----NFKFDLTQFKEYL-----	445
<i>D.willistoni</i> (XP_002064455.1)	433	KQLAQKYEAEGS-----NFSDFDKI-----	452
<i>D.simulans</i> (XP_002078032.1)	429	KTMAQN-----DFNFDPKLLGL-----	445
<i>D.sechellia</i> (XP_002045314.1)	429	KTMAKN-----DFNFDPKLLGL-----	445
<i>D.melanogaster</i> (NP_608781.2)	429	KTMAQN-----NFNFDPKLLGL-----	445
<i>D.melanogaster</i> (AAL68365.1)	429	KTMAQN-----NFNFDPKLLGL-----	445
<i>D.melanogaster</i> (AAL48116.1)	429	KTMAQN-----NFNFDPKLLGL-----	445
<i>D.erecta</i> (XP_001968564.1)	429	KTMAQN-----DFNFDPTLLGV-----	445
<i>D.yakuba</i> (XP_002087828.1)	429	KTMAEN-----NFNFDPKLLGI-----	445
<i>D.ananassae</i> (XP_001965094.1)	427	KTMAQNYKADGK-----NFD FDKTLGI-----	449
<i>D.pseudoobscura</i> (XP_001356411.1)	428	KQLAHKYETEGS-----NFTDFDKI-----	447
<i>A.pisum</i> (XP_001945904.1)	530	EDRLPELDRMVG D-----	542
<i>A.pisum</i> (XP_001948728.2)	415	EQRIPPIIDKMM EHN-----ITDIFKENEILHEDINIVSKEDF-----	452
<i>P.humanus corporis</i> (XP_002425163.1)	402	DEKLP TFFYELLA-----LNDTVNPEVNDIEF-----	427
<i>D.pulex</i> (EFX77001.1)	433	EEQLPKLSELKNDL-----	446