

Both isoforms of *Drosophila* ApoLpp (ApoB) cross the blood–brain barrier in adults

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Human ApolipoproteinB (ApoB) exists in two isoforms that are packaged into low density lipoprotein particles and are major contributors to atherosclerosis. Alternatively, *Drosophila* Apolipoprotein Lipophorin (ApoLpp) also exists in two isoforms packaged into lipoprotein particles that cross the blood–brain barrier (BBB) in second instar larvae where they deliver lipids to neuroblasts. To extend our understanding of ApoLpp function to adult brains and suggest new hypotheses for human ApoB, we document evolutionary conservation between the two N-terminal isoforms human ApoB48 and fly ApoLppII. Then our tissue-specific analyses including rescue of *apolpp* lethality and *apolpp* RNAi showed that *apolpp* expression in the fat body is both necessary and sufficient for survival to adulthood. Our imaging studies of ApoLpp in the adult brain employed endogenous isoform-specific tagged proteins generated by the Fourth Chromosome Resource Project. Images revealed that both ApoLpp isoforms are present in the adult brain with ApoLppII accumulation prominent near glia. Nanobody morphotrap experiments that blocked tagged ApoLpp at the BBB demonstrated that ApoLpp detected inside the adult brain is exogenous. An N- and C-terminal tagged ApoLpp transgene expressed solely in the fat body facilitated tracking of each isoform from fat body secretion to the BBB and then inside the adult brain. Overall, our data suggest that the known role of ApoLpp in lipid delivery to larval brains likely continues in adults. Strong conservation between ApoLppII and ApoB48 supports the hypothesis that ApoB48 may have a role in the brain outside the circulatory system.

Keywords: cortex; glia; medulla; morphotrap; myoglianin; phylogenetics

Introduction

The Apolipoprotein (Apo) family, in humans and other species is not a traditional protein family where all members share sequence similarity derived from a common ancestor. Instead, Apo is a family that investigators defined based on the ability to bind lipids. As organisms utilize lipids in a myriad of ways, this function originated multiple times during the course of life on earth. Thus, except for recent gene duplications, Apo proteins in a single species are only tenuously connected to each other in intraspecific trees. However, a homologous relationship that is actively maintained by selection for a specific function should be visible in interspecific trees.

The APOB gene is unique among human Apo family members. Its 14 kb mRNA encodes the largest human Apo family member by an order of magnitude, a 4,563 amino acid isoform called ApoB100. Another novel feature of APOB is that its mRNA undergoes editing to convert cytosine to uracil at nucleotide 6,538. Editing converts a normally translated CAA codon to a stop codon, creating an N-terminal 2,180 amino acid isoform called ApoB48. Editing occurs in the liver where ApoB48 is the exclusive form and in the gut where ApoB100 and ApoB48 are generated (Higuchi et al. 1988). Both ApoB isoforms are secreted into the bloodstream where ApoB100 is the primary protein in very low

density lipoproteins and ApoB48 the primary in ultralow density lipoproteins. In colloquial terms, ApoB isoforms contribute to two types of “bad cholesterol.” Heterozygosity for pathogenic mutations in APOB is the cause of 5% to ~10% of cases of familial hypercholesterolemia (Beheshti et al. 2020). No roles for ApoB outside the circulatory system are known.

However, evidence of potential roles for human ApoB outside the circulatory system is accumulating. In humans, mutations in APOB and circulating levels of ApoB have been associated with cognitive impairment: (i) loss of function mutations in APOB are among the causes of familial Alzheimer's disease (Aumont-Rodrigue et al. 2024), (ii) high serum ApoB levels are connected to greater risk of dementia (Gong et al. 2022), and (iii) a high ratio of ApoB/ApoA1 in circulation predicts the extent of diminished mental capacity in stroke patients (Lee et al. 2023). In rodents, studies of adult rat brains showed ApoB in a complex with the Low Density Lipoprotein (LDL) receptor on glia (Jung-Testas et al. 1992) and in an in vitro model the mouse LDL receptor was shown to transcytose the blood–brain barrier (BBB) (Dehouck et al. 1997). These studies suggest the hypothesis that ApoB transits the BBB to perform an unknown role in brain. Upstream of APOB, the brain has a role with glucagon like peptide-1 (GLP-1) signals from the hypothalamus regulating ApoB liver and gut expression and secretion (Farr et al. 2015).

The possibility that studies of Apolipoprotein Lipophorin (ApoLpp) can be employed to suggest hypotheses for ApoB is based on known similarities between the two. Among these are that ApoLpp is also large (3,350 amino acid) and subdivided, in this case by furin cleavage, to create N-terminal (ApoLppII) and C-terminal (ApoLppI) isoforms. ApoB48 and ApoLppII N-terminal isoforms both contain a Vitellogenin domain (pfam09172). In humans and flies the N-terminal isoform and full length proteins are incorporated into circulating lipoprotein particles. However, to date only in fly second instar larvae do particles containing ApoLpp cross the BBB to deliver lipids to neuroblasts (Brankatschk and Eaton 2010). Particles containing the ApoLpp sibling Apolipoprotein Lipid Transfer Particle (ApoLTP) also cross the BBB during second instar to deliver lipids to insulin producing neurons (Brankatschk et al. 2014).

To extend our understanding of ApoLpp brain function to adults and perhaps provide evidence for a hypothesis that human ApoB has a role in the brain, we established an evolutionary connection between the N-terminal isoforms ApoB48 and ApoLppII. Then our rescue studies showed that ApoLpp from the fat body, an organ functionally analogous to the ApoB expressing liver (Ugur et al. 2016; Meschi and Delanoue 2021), is necessary and sufficient for flies to survive beyond the *apolpp* mutant embryonic lethal phenotype. Imaging studies of ApoLpp indicated that both N- and C-terminal isoforms are present in the adult brain. Morphotrap studies with tagged ApoLpp blocked at the BBB demonstrated that the ApoLpp in the adult brain is exogenous. Utilizing an N- and C-terminal tagged version of ApoLpp expressed solely in the fat body, we tracked both isoforms from fat body secretion to the BBB and into the adult brain. Overall, the fly data suggest that the previously known role of ApoLpp in second instar lipid delivery to the brain persists through third instar to adulthood. Our phylogenetic data connecting ApoLppII and ApoB48, supports the hypothesis that ApoB can transit the BBB to perform a function in the brain.

Materials and methods

Phylogenetics of human, fly and nematode Apolipoproteins

Human sequences

Twenty-three human Apo proteins were identified by name in Uniprot (uniprot.org). Reference sequences were downloaded (ncbi.nlm.nih.gov/refseq) and their structural domains retrieved (pfam-legacy.xfam.org). The ApoB sequence was divided and analyzed separately as ApoB48 (Higuchi et al. 1988) and the remainder of ApoB100 that we named ApoB52. Microsomal Triglyceride Transfer Protein (MTTP) was chosen as the outgroup since it has a similar function but not the Apo name. Splitting ApoB plus the outgroup yielded 25 human sequences.

Fly sequences

Eight fly Apo proteins were identified via the DIOPT function in Flybase, the longest reference sequence downloaded and structural domains retrieved. The ApoLpp and ApoLTP sequences were divided and analyzed separately as isoforms generated by furin cleavage. Isoform naming followed Brankatschk and Eaton (2010) with N-terminal isoforms ApoLppII and ApoLTPII, and C-terminal isoforms ApoLppI and ApoLTPI. Fly Microsomal triacylglycerol transfer protein (Mtp) was recovered by BLASTp as the homolog of human MTTP and employed as the outgroup. Splitting ApoLpp and ApoLTP plus the outgroup yielded 11 fly sequences.

Nematode sequences

Nine nematode Apo proteins were identified via structural domains in WormBase, the longest reference sequence downloaded and structural domains retrieved. Each of the Vit-1 through Vit-6 sequences was divided as predicted by a furin consensus cleavage site conserved in ApoLpp and ApoLTP. The naming convention for ApoLpp was applied. For example, for Vit-1 the N-terminal region was named Vit-1II and the C-terminal region was named Vit-1I. The outgroup was Microsomal triacylglycerol transfer protein (Dsc-4) due to its similar function, but it is not the homolog of either the human or fly outgroup by reciprocal BLASTp. Splitting of Vit-1 through Vit-6 plus the outgroup yielded 16 nematode sequences.

Phylogenetics

Analyses were conducted in MEGAX (Kumar et al. 2018). Protein sequences were aligned with default settings using MUSCLE (Edgar 2004). Complete Deletion, the most conservative method for handling gaps was employed with the alignments for each species and the two species pairs (human-fly and fly-nematode) for best-fit model selection (lowest Bayesian Information Criterion) then Maximum Likelihood tree building. With Complete Deletion, a position is considered noninformative and removed from consideration if even one sequence in the alignment has a gap at that position. For the alignment of all three species, the Partial Deletion method was employed with an 80% cutoff for best-fit model selection (lowest Bayesian Information Criterion) and Maximum Likelihood tree building. With Partial Deletion, a position that has a gap in up to 19% of the aligned sequences was still considered informative and retained. In all trees, non-parametric bootstrapping was applied with 500 replicates to assess the relative strength of each node.

We took into account the fact that the absence of common ancestry violates two equality assumptions of the maximum likelihood algorithm (equal rates of substitution in all sequences and equal constraints on branch length; Dhar and Minin 2016). Note these are not the core independence assumptions of the algorithm (individual substitutions in a single sequence are independent of all other substitutions in that sequence and substitutions in one sequence are independent of substitutions in all other sequences; Felsenstein 2004). Violations of the independence assumptions would completely undermine the algorithm. The impact of equality assumption violations is less severe and we counterbalanced the impact by consistently applying independent node validation. Validation methods such as reciprocal BLASTp and identifying shared structural domains were routine.

Stocks, mutagenesis, tissue-specific rescue of *apolpp* lethality and RNAi

Stocks

Three UAS *apolpp* cDNA clones were obtained from Marko Brankatschk (Biotec TU-Dresden; Brankatschk and Eaton 2010) then injected by BestGene (www.thebestgene.com). Transformant lines were obtained and mapped to a chromosome. Stocks designated as UAS. *ApoLpp.wt* contain a wild type *apolpp* cDNA. UAS.5'-HA-*ApoLpp-Myc-3'* stocks contain a double tagged *apolpp* cDNA. UAS.5'-HA-*ApoLpp-Myc* furin-resistant stocks contain the doubled tagged *apolpp* cDNA with a mutation in the furin cleavage site. Five GAL4 stocks were utilized in rescue crosses: Repo.GAL4 glia (BL#7415), CG.GAL4 fatbody/hemocytes (Asha et al. 2003, BL#7011), Mhc82.GAL4 muscle (Schuster et al. 1996), NPC1b.GAL4 gut (BL#95257) and R4.GAL4 fat body specific (Lee and Park 2004,

BL#33832). *apolpp*¹⁰² is a 29 base pair (bp) deletion that removes the initiator methionine (Tanaka et al. 2021). UAS.*apolpp*.RNAi (BL#3388) was validated with ubiquitous expression employing Da.GAL4 (Wodarz et al. 1995, BL#55851) to recreate the *apolpp* loss of function lethal phenotype. Elav.GAL4 with neuronal specific expression (Luo et al. 1994, BL#458) was crossed to *apolpp*.RNAi as a control for off target effects that showed there were none. Three fourth chromosome balancers were: adult eye like Glazed from a lethal insertion in *Gat* (Ti[GMR-HMS04515]*Gat*^{eyw}), fourth longitudinal wing vein truncation from a lethal inversion in *In(4)ci^D* (both in BL#90852) and a lethal neural GFP enhancer trap (*P{w+; ActGFP}unc-13^G*; BL#4759).

Mutagenesis

For generation of new *apolpp* mutants, two gRNAs roughly 2.3 kb apart on opposite sides of the furin cleavage site were selected using CRISPR Optimal Target Finder (<https://flycrispr.org/target-finder>) and cloned into pU6-BbsI (Gratz et al. 2013). Plasmids expressing these gRNAs were injected into a *vasa*.Cas9-expressing stock (BL#5491) by GenetiVision (genetivision.com). Fifteen G⁰ males were crossed to *P{w+; ActGFP}unc-13^G/In(4)ci^D*. Ten F¹ males of the genotype mutant?*/In(4)ci^D* from each G⁰ male were backcrossed to *P{w+; ActGFP}unc-13^G/In(4)ci^D* flies. After mating, each F¹ male was subject to PCR with primers covering the gRNA targets. Sequencing identified 2 new mutant alleles.

gRNA 1 (C-terminal): 5'-CTTCAATGGGCTGACGAAACCACG-3'

gRNA 2 (N-terminal): 5'-CTTCGGAATAGAAGCGGAACATG-3'

PCR *apolpp* 1 (C-terminal) forward: 5'-CTTCAATGGGCTGACGAAACCACG-3'

PCR *apolpp* 1 reverse: 5'-AAACCGTGGTTTCGTCAGCCCATT-3'

PCR *apolpp* 2 (N-terminal) forward: 5'-CTTCGGAATAGAAGCGGAACATG-3'

PCR *apolpp* 2 reverse: 5'-AAACCATGTTCCGCTTCTATTCCC-3'

Lethal phase analysis

To determine the lethal phase of *apolpp* transheterozygous loss of function mutants, *apolpp*^{70A}/*P{w+; ActGFP}unc-13^G* females were crossed to *apolpp*^{32B}/*P{w+; ActGFP}unc-13^G* males and eggs collected on apple juice agar plates for 6 h. Fifty GFP-negative eggs were picked and placed in rows on another agar plate. Twenty-five of these eggs (*apolpp*^{70A}/*apolpp*^{32B}) hatched into first instar larvae but died shortly thereafter without an increase in size. Of the 25 that did not hatch, five were subsequently noted as GFP-positive and thus *P{w+; ActGFP}unc-13^G* heterozygotes that were mispicked. The remaining 20 *apolpp*^{70A}/*apolpp*^{32B} eggs appeared normal but failed to hatch.

Tissue specific rescue of lethality

For the rescue experiment, males were employed with one of the five GAL4 transgenes listed above on chromosome two over CyO *P{w+; ActGFP}JMR1* or on chromosome three over TM3 *P{w+M/C} = ActGFP}JMR2 Ser* and with *apolpp*¹⁰² on chromosome four over *P{w+; ActGFP}unc-13^G*. These were crossed to females with one of the three UAS.ApoLpp transgenes on chromosome three over TM6B *P{w+; Ubi-GFP.S65T}PAD2 Tb* with *apolpp*^{70A} on chromosome four over *P{w+; ActGFP}unc-13^G*. Three days after mating, eggs were collected on apple juice agar plates for six hours. Two hundred eggs were picked and placed on a gridded plate, then the eggs and agar grid were transferred to a culture bottle with media. This was done twice more for each GAL4/UAS combination. Adults were scored over a 15-day period and GFP-negative individuals considered rescued with a genotype of GAL4 on

chromosome two or three, UAS on chromosome three and *apolpp*¹⁰²/*apolpp*^{70A} on chromosome four.

Tissue specific RNAi phenocopy of *apolpp* lethal phase

Twenty females carrying one of four GAL4 transgenes, Da.GAL4, CG.GAL4, R4.GAL4 and Elav.GAL4 were crossed to 10 males with UAS.*apolpp*.RNAi over TM6B *P{w+; Ubi-GFP.S65T}PAD2 Tb*. After three passes in clear glass vials progeny (>100 third instar larvae that became >100 adults) were scored as larvae and again as adults for the presence or absence of the TM6B Tb phenotype with surviving UAS.*apolpp*.RNAi individuals expected to show a wild type phenotype at both stages.

Immunohistochemistry of larval and adult gene and protein expression

Stocks *apolpp*

Three stocks with a distinct transgene in the *apolpp* locus were created by the Fourth Chromosome Resource Project (FCRP). The N-terminal tagged ApoLppII N-enhanced Green Fluorescent Protein (eGFP) and transcriptional reporter *apolpp* T2A.GAL4 are DoubleHeader conversions of an *apolpp* second intron CRIMIC (CR70471-BL#9179; Stinchfield et al. 2024). ApoLppII N-eGFP (BL#97744; Kyoto#118965) allows ApoLppII to be visualized. *apolpp* T2A.GAL4 includes an in-frame stop codon that terminates translation of the endogenous *apolpp* mRNA and a downstream internal ribosome entry site that initiates the translation of GAL4 mRNA in the expression pattern of the endogenous *apolpp* mRNA. When crossed to flies carrying UAS.GFP, the progeny express GFP in the pattern of the *apolpp* mRNA. The ApoLppII N-eGFP and *apolpp* T2A.GAL4 transgenes are homozygous lethal and balanced over *Gat* (Ti[GMR-HMS04515]*Gat*^{eyw}). ApoLppI C-eGFP was created by the Gene Disruption Project via a scarless CRISPR exon swap of the last coding exon that leaves behind the endogenous *apolpp* 3' UTR (gift of Oguz Kanca and Hugo Bellen; Kanca et al. 2022). The ApoLppI C-eGFP transgene is homozygous viable.

Stocks *myo*

Two stocks with a distinct transgene in the *myoglianin* (*myo*) locus were created. Myo eGFP (BL#600215; Kyoto#118960) and *myo* T2A.GAL4 were generated by the FCRP via DoubleHeader conversion of a *myo* second intron CRIMIC (CR02262; BL#92207). The Myo eGFP and *myo* T2A.GAL4 transgenes are homozygous lethal. Additional stocks were 9-137.GAL4 (DeSalvo et al. 2014), UAS.CD8.RFP (BL#27398) and UAS.nls.GFP (BL#4775).

Brain expression assays

Brains, fat body and body wall muscle from third instar larvae and adults were dissected in cold phosphate-buffered saline (PBS) buffer, fixed in 4% formaldehyde for 20 min, dehydrated in methanol then stored -20 °C. They were then exposed to primary antibodies to detect eGFP from an ApoLpp or Myo transgene, to detect UAS.GFP driven by either *apolpp* or *myo* T2A.GAL4, or to detect the HA or Myc tagged ApoLpp isoforms. Detection of UAS.RFP driven by 9-137.GAL4 was via direct luminescence without antibodies. Brains were counterstained with antibodies against Repo that identifies all glial nuclei or against Vvl that identifies BBB glial nuclei. Antibody detection for eGFP in expression studies employed a modified TSA reaction (Stinchfield et al. 2024). Antibody detection of eGFP in morphotrap employed only antibodies as described (Goldsmith and Newfeld 2023). In tracking experiments with UAS.5'-HA-ApoLpp-Myc-3', HA was detected with Roche rat 3F10, Myc detected with DSHB monoclonal mouse 9E

–10, Vvl as described (previously known as Drifter; [Tran et al. 2018](#)) and DAPI in staining solution at 300 μ M in PBS. Brains were imaged on a Leica SP8 confocal microscope with slices acquired every 2 μ m and analyzed in FIJI. Scale bars are provided.

Larval and adult morphotrap

Stocks

The primary morphotrap was *M[w[+mC]=lexAop-UAS-morphotrap.ext.mCh]ZH-35B/CyO* ([Harmansa et al. 2015](#), BL#68170). This transgene encodes an UAS controlled fusion of the external portion of the transmembrane protein CD8 to a nanobody against GFP. We call this experimental morphotrap CD8-morpho. This transgene effectively traps nearby GFP-tagged secreted proteins at the outer membrane of any expressing cell. CD8-morpho was driven in the BBB by 9-137.GAL4 and tracked by co-expression of UAS.CD8.RFP, a combination that we call 9-137:RFP. As a negative control, we employed another morphotrap *M[w[+mC]=lexAop-UAS-morphotrap.ext.mCh]ZH-86Fb* ([Harmansa et al. 2017](#), BL#68173). This transgene encodes a nanobody to GFP fused to the external portion of the transmembrane protein Nrv1 that only inserts into the membrane on the basolateral surface of polarized epithelia. We call this control morphotrap Nrv-morpho. This is a negative genotype control since the BBB is a squamous epithelia providing no appropriate location for nanobody insertion.

Morphotrap genotypes and brain expression

Stocks homozygous for chromosome two insertions of CD8-morpho with either ApoLppII N-eGFP or ApoLppI C-eGFP or *apolpp*^{81D} balanced over *Tl[GMR-HMS04515]Gat^{eya}* on chromosome four were created. Companion stocks containing chromosome two with 9-137:RFP balanced over CyO plus either ApoLppII N-eGFP or ApoLppI C-eGFP or *apolpp*^{81D} balanced over *ln(4)ci^D* on chromosome four. Crosses produced progeny that were CD8-morpho transheterozygotes with 9-137:RFP on chromosome two and *apolpp* transheterozygotes on chromosome four. Four distinct CD8-morpho genotypes were generated to allow for morphotrap of either ApoLppII N-eGFP or ApoLppI C-eGFP or both. One genotype was transheterozygous for ApoLppII N-eGFP/*apolpp*^{81D}. The second was homozygous for ApoLppI C-eGFP. The third was transheterozygous for ApoLppI C-eGFP/*apolpp*^{81D}. The fourth was transheterozygous for ApoLppI C-eGFP/ApoLppII N-eGFP. eGFP and Repo detected as above.

Results

Human ApoB48 is conserved in flies and nematodes

Sequence conservation as revealed by phylogenetics has successfully predicted multiple conserved functions and regulatory mechanisms for cell signaling pathways (e.g. [Konikoff et al. 2008](#) predicted [Dupont et al. 2009](#)). These studies employed alignments and trees with human, fly and nematode proteins as their evolutionary focus. We employed the same approach. Conservation across these three species reveals the value of a protein for organismal survival such that natural selection maintained it during the 700 million years since these species last common ancestor ([Kumar et al. 2022](#)).

There are 23 human Apo proteins in the Uniprot database ([Supplementary Table 1](#)). They range in size from 99 amino acids (ApoC3) to 4,563 amino acids (ApoB), with all but ApoB below 450 amino acids. Similar variability exists in their subcellular location: 16 are secreted, four are cytoplasmic, three are transmembrane

including two in the mitochondrial inner membrane while one remains a prediction. Family members are ApoA through ApoOL and include the multi-member subfamilies ApoA, ApoC, and ApoL. Note that ApoP is an apoptotic protein and excluded. Four defined structural domains are found in multiple Apo proteins: (i) pfam04711 in ApoA2 and ApoD, (ii) pfam01442 in ApoA1/A4/A5 and ApoE, (iii) pfam09769 in ApoO and ApoOL, and (iv) pfam05461 in ApoL1-6. The ApoL proteins reside contiguously on chromosome 22q11.2. Two other Apo chromosomal contigs contain proteins from multiple groups. These are: (i) ApoE, ApoC1, ApoC4, ApoC2 on 19q13.32, and (ii) ApoA1, ApoC3, ApoA4, ApoA5 on 11q23.3.

We examined paralogous relationships via an alignment ([Supplementary Fig. 8](#); note all alignments are at the end of supplementary material) and an intraspecific tree ([Fig. 1](#)). Since strong protein clusters suggest a level of sequence similarity that implies similar ancestry, we examined the tree for informative clusters. The tree shows that only ApoL proteins resemble an ancestry-based subfamily (pfam05461). All members cluster together and exclude other Apo proteins with three recent duplications evident. This fits well with the chromosomal contiguity of ApoL proteins. For ApoC proteins, only ApoC2 and ApoC4 are a recent duplication with ApoC3 and ApoC1 divergent. This is distinct from ApoC1 contiguity on the chromosome with ApoC2 and ApoC4, suggesting divergent selection on the older ApoC1. For ApoA proteins, ApoA2 is divergent in the tree and does not cluster with ApoA1, ApoA4 and ApoA5 on the chromosome. The strength of the node linking ApoA2 and ApoD (reinforced by results from reciprocal BLASTp) indicates that they are a recent duplication and that perhaps ApoA2 should be called ApoD2. The presence of only ApoL as a true subfamily underscores the non-ancestral nature of the human Apo protein family.

There are eight fly Apo proteins identified via DIOPT in Flybase ([Supplementary Table 2](#)). They range in size from 157 to 4,333 amino acids with two above 3,350 amino acids. The two largest (ApoLpp and ApoLTP) are subject to furin cleavage creating N-terminal (ApoLppII and ApoLTPII) and C-terminal isoforms (ApoLppI and ApoLTPI). Six proteins are secreted, one is cytoplasmic and one is in the mitochondrial inner membrane. Three structural domains shared with humans are: (i) pfam09172 Vitellogenin-N (ApoB with fly ApoLpp and Cv-d), (ii) pfam00061 Lipocalin (ApoM with fly CG31659/Fabp/Glaz/Nlaz), and (iii) pfam09769 ApoO (ApoO/ApoOL with fly Mic26-27).

We examined paralogous relationships via an alignment ([Supplementary Fig. 9](#)) and an intraspecific tree ([Supplementary Fig. 1](#)). In the tree two strong clusters stand out. Glaz and Nlaz are a recent duplication (as noted previously, [Liu et al. 2017](#)) and the N-terminal isoforms ApoLppII and ApoLTPII. The cluster of the C-terminal isoforms ApoLppI and ApoLTPI is distant and considerably weaker. This scenario suggests divergent selection on the N-terminal and C-terminal isoforms with the similarity of ApoLppII and ApoLTPII maintained by selection.

To identify conservation between human and fly Apo proteins we generated an interspecific alignment ([Supplementary Fig. 10](#)) and a tree ([Fig. 2](#)). The tree has only two clusters that contain human and fly proteins. Within one, ApoB48 (N-terminal region of human full length ApoB100) and the C-terminal region of ApoB100 (called here ApoB52 that is not a biological isoform) are linked. Intra-protein similarity between these regions was previously noted ([Chen et al. 1986](#)). The fly N-terminal regions, ApoLppII and ApoLTPII are also clustered together and both are linked with the ApoB48/ApoB52 cluster. The only other human and fly cluster is human ApoF with fly Fabp. The remaining

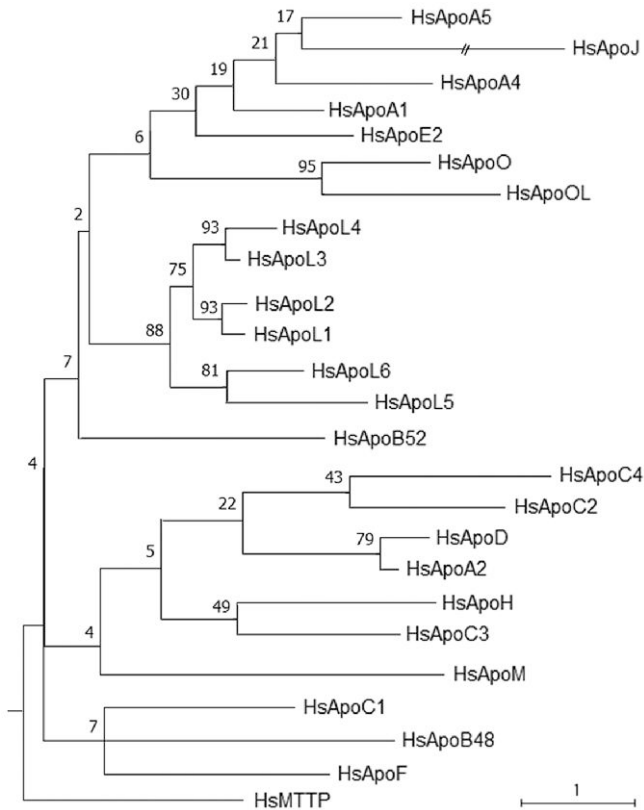


Fig. 1. Tree of 25 human Apolipoproteins. Maximum likelihood tree. The percentage of bootstrap replicates (out of 500) in which the associated node appeared is shown. Node values are for internal comparison only as they do not measure statistical confidence. Branch lengths are to scale and measured in the number of substitutions per site (a scale bar is provided). ApoB48 and ApoB52 (C-terminal sequence of ApoB100) are analyzed as separate sequences plus an outgroup. There are 171 informative positions in the underlying MUSCLE alignment (Supplementary Fig. 8). Among the named groups only ApoL and ApoO cluster unambiguously while ApoA and ApoC are dispersed.

proteins are in monospecific clusters suggesting only human ApoB and ApoF predate the human and fly divergence. One note of caution is that the similarity of human ApoA2 and ApoD from their recent duplication, obscures in our trees the previously noted similarity of human ApoD with fly Glaz and Nlaz. On the other hand, confidence in the tree is bolstered by clustering of the two outgroups that share pfam19444.

To further extend the reach of our evolutionary analysis, an interspecific tree of fly and nematode Apo proteins was generated. There are nine nematode Apo proteins identified via WormBase (Supplementary Table 3). The six Vit proteins are roughly 1,650 amino acids, while the other three are roughly 250 amino acids. All six Vit proteins contain a predicted furin cleavage site that is also present in ApoLpp and ApoLTP. Thus, Vit-1 through Vit-6 likely are split into isoforms to perform their function. We name the isoforms with the convention of ApoLpp (II is N-terminal and I is C-terminal). The Vit furin cleavage site is also present in the sole Vit protein in the distantly related nematode *Pristionchus pacificus*, called Vit-6 (KAF8354296) as it best matches Vit-6 in *Caenorhabditis elegans*. Further evidence that Vit-6 is the original Vit protein in *C. elegans* is that Vit-6 is on chromosome 4 while all the others are on the X chromosome. Vit structural domains shared with ApoLpp and ApoLTP are: pfam09172 Vitellogenin-N (in the N-terminal isoform) and pfam00094 von Willebrand type D (in the C-terminal isoform).

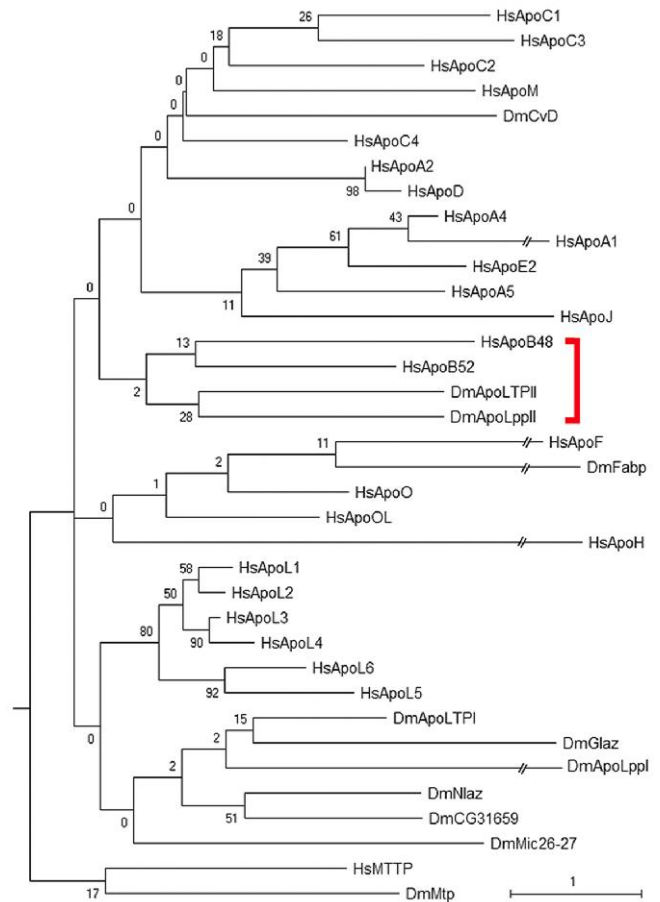


Fig. 2. Human ApoB48 and fly ApoLppII are conserved. Tree as in Fig. 1. There are 25 human (Hs) and 11 fly (Dm) sequences in the tree with both outgroups. The two isoforms of human ApoB, fly ApoLpp and fly ApoLTP are analyzed separately. There are 172 informative positions in the alignment (Supplementary Fig. 10). Deep nodes shown as zero are actually present one to four times (below the 1% bootstrap threshold for 500 replicates) and are the most frequent among the connected sequences. Confidence in the tree is bolstered by the clustering of the two outgroups at the bottom as the most divergent. Red bar indicates the cluster containing human ApoB48 and ApoB52, fly ApoLppII and ApoLTPII. The other interspecific cluster (human ApoF with fly Fabp) is shown directly underneath but is not related.

The interspecific alignment (Supplementary Fig. 11) and tree (Supplementary Fig. 2) with fly and nematode Apo proteins reveals that Vit-6II clusters with ApoLppII and ApoLTPII. The Vit-1II through Vit-5II isoforms are in two nearby clusters. Vit-1I through Vit-6I also cluster together, though at a distance from the VitII cluster. The Vit clustering pattern suggests multiple recent rounds of gene duplication in the *C. elegans* lineage. There are no other clusters of fly and nematode proteins indicating that ApoLppII and ApoLTPII alone in flies are conserved in nematodes, as Vit-6II.

The lack of common ancestry among Apo proteins in each species overwhelmed multiple approaches to constructing a tree from an alignment of humans, flies and nematodes (Supplementary Fig. 12). Neither a tree of human and nematode nor a tree of all three species was possible. Thus, by extension from the two interspecific trees, we suggest that among human Apo family members ApoB alone is conserved from a common ancestor with nematodes. In fairness, we are not the first to note a connection between ApoB and Vit proteins. This was suggested in a brief note nearly 40 years ago based

on conserved structural domains (Baker 1988). For our purposes, evidence of evolutionary conservation all the way to nematodes increases the likelihood that new information about fly ApoLppII will suggest hypotheses for ApoB48 in humans.

ApoLpp fat body expression is necessary and sufficient for survival to adult

Fly *apolpp* and human APOB are transcribed and secreted from the fat body (Palm et al. 2012) and liver (Higuchi et al. 1988), respectively. These are considered analogous tissues since they perform many of the same roles in triglyceride storage, metabolism and endocrine function (Ugur et al. 2016; Meschi and Delanoue 2021). We designed a pair of experiments to test the hypothesis that ApoLpp fat body expression alone is necessary and sufficient to rescue normally lethal *apolpp* mutant genotypes to adult.

Before embarking on these studies, we documented *apolpp* transcription and ApoLpp translation in the larval fat body utilizing *apolpp* T2A.GAL4 and ApoLppI C-eGFP transgenes (described below). Examining individual slices underlying the *apolpp* T2A.GAL4 image indicated that all larval fat body cells transcribe *apolpp* (Supplementary Fig. 3). The image of ApoLppI C-eGFP is consistent with all fat body cells translating *apolpp*. We then determined the stage of lethality for *apolpp* loss of function mutants. Three new lethal alleles of *apolpp* were generated by CRISPR: *apolpp*^{70A} (2 bp deletion leading to a truncation at amino acid 124 causing a severe shortening of ApoLppII and complete loss of ApoLppI), *apolpp*^{32B} (9 bp deletion within ApoLppII plus 39 bp deletion within ApoLppI) and *apolpp*^{81D} (2 single base pair substitutions leading to missense mutations plus a 9 bp deletion within ApoLppII). The stage of lethality assay showed that these alleles as transheterozygotes died either as embryos or first instar larvae.

The rescue studies were conducted with a more severe loss of function genotype: *apolpp*¹⁰²/*apolpp*^{70A} (*apolpp*¹⁰² has no initiator methionine; Tanaka et al. 2021). Expression of wild type ApoLpp in the fat body, with CG.GAL4, but no other tissue fully rescued *apolpp* loss of function mutants to adults (17.8% observed versus 12.5% expected; Table 1). Fat body expression of a double-tagged ApoLpp rescued roughly one-third of expected adults. Expression of a cleavage resistant form of ApoLpp did not rescue. However, CG.GAL4 is also expressed in hemocytes and the lymph gland, leading us to repeat the experiment with R4.GAL4 that is fat body specific (Lee and Park 2004). We again obtained full rescue

with wild type ApoLpp (12.1% observed versus 12.5% expected). These data show that fat body expression of ApoLpp is sufficient for survival of *apolpp* genomic loss of function mutants to adult.

In the complementary experiment, we employed UAS. *apolpp*.RNAi balanced over a chromosome with multiple larval and adult visible markers (Stubble, Tubby, and Humeral). First, to ascertain whether this transgene was capable of complete knock down we drove it ubiquitously with Da.GAL4. This combination was completely lethal prior to the third instar larval stage, thus recreating the lethal phase of *apolpp* loss of function mutants. Second, to test for off-target effects we expressed *apolpp*.RNAi in all neurons with Elav.GAL4 balanced over the marked chromosome. This combination had no effect on survival of experimental larvae or adult progeny, these were each present in their expected Mendelian proportions. Third, we drove *apolpp*.RNAi in the fat body with either CG.GAL4 or with R4.GAL4 to ascertain if expression in this specific tissue alone recreated the lethal phase of *apolpp* loss of function mutants. In both cases, no experimental third instar larvae were observed (Table 2). Failure to obtain larvae indicates that fat body expression of *apolpp* is necessary for survival of wild type flies. Taken together the rescue and RNAi data indicate that fat body expression is both necessary and sufficient for survival. The results further suggest that the fat body is the major source of ApoLpp.

To this point we know that ApoB and ApoLpp are: (i) both processed to create functional N-terminal isoforms (ApoB48 and ApoLppII), (ii) their N-terminal isoforms are highly conserved, and (iii) the tissues of origin for the N-terminal isoforms (liver and fat body, respectively) perform similar roles in homeostasis. These similarities add weight to our contention that new data on ApoLppII will suggest new hypotheses for ApoB48.

ApoLppII N-eGFP and ApoLppI C-eGFP are present in adult brains

Based on the second instar larval data that ApoLpp has a function in the brain (Brankatschk and Eaton 2010), we examined adult brains for the presence of ApoLpp utilizing three transgenes generated by the FCRP (Stinchfield et al. 2024). Two are endogenous eGFP tagged transgenes with ApoLppII N-eGFP tracking the N-terminal isoform and ApoLppI C-eGFP tracking the C-terminal isoform (possibly also full-length ApoLpp; Brankatschk and

Table 1. First instar lethality of *apolpp* mutants is rescued to adult only by fat body expression.

	CG.GAL4 (fat body)			Npc1.GAL4 (gut)			Mhc.GAL4 (muscle)			Repo.GAL4 (glia)		
	Adults	Rescue	% ^a	Adults	Rescue	%	Adults	Rescue	%	Adults	Rescue	%
UAS.ApoLpp.wt	236	42	17.8	311	0	0.0	72	0	0.0	103	0	0.0
UAS.5'-HA-ApoLpp-Myc-3'	288	13	4.5	100	0	0.0	210	0	0.0	92	0	0.0
UAS.HA-ApoLpp-Myc furin mutant	278	0	0.0	380	0	0.0	73	0	0.0	53	0	0.0

^aGiven the parental genotypes, the expected fraction of *apolpp* mutant progeny (*apolpp*¹⁰²/*apolpp*^{70A}) was one-eighth (12.5%) in all crosses.

Table 2. Fat body specific *apolpp*.RNAi phenocopies *apolpp* genomic loss of function.

	CG.GAL4 (fat body)			R4.GAL4 (fat body)			Da.GAL4 (ubiquitous)			Elav.Gal4 (neuron)		
	Adults	Not Tb	% ^a	Adults	Not Tb	%	Adults	Not Tb	%	Adults	Not Tb	%
UAS. <i>apolpp</i> .RNAi	140	0	0.0	131	0	0.0	127	0	0.0	147	50	34

^aGiven the parental genotypes, the expected fraction of *apolpp*.RNAi progeny (those not Tubby) was one-half for CG.GAL4 and one-third for the others.

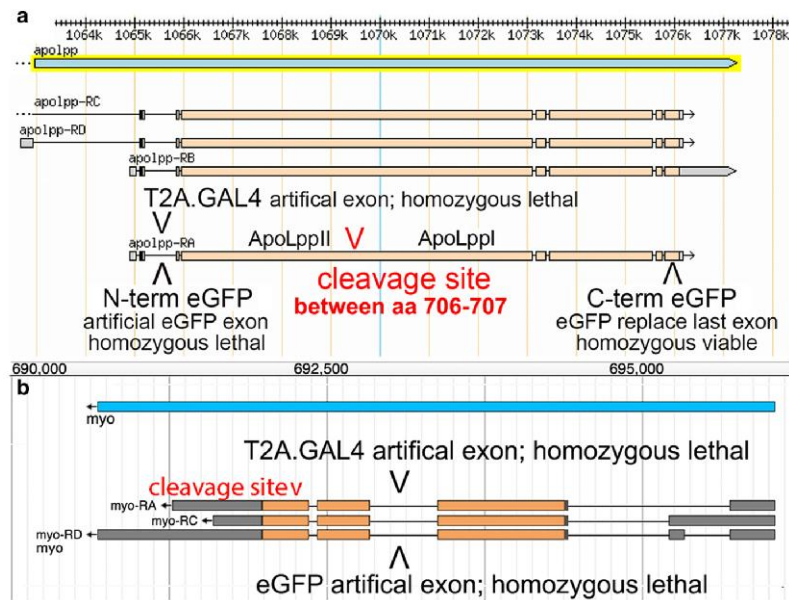


Fig. 3. Fourth chromosome transgenes for *apolpp* and *myo*. a) Number line depicts the sequence of the fourth chromosome polytene region 102F7-8. The *apolpp* gene and four transcripts (from the numbered strand left to right) that encode a single ApoLpp protein are shown. The bottom transcript/protein is annotated to show a furin cleavage site between amino acids 706 and 707 and the isoforms created by cleavage. Three artificial exons carried in transgenes are shown. In the first intron of the coding region are two FCRP DoubleHeader conversions of CR70471. The *apolpp* T2A.GAL4 and ApoLppII N-eGFP transgenes are homozygous lethal. A custom designed CRIMIC provided by Oguz Kanca (Kanca et al. 2022; Bellen lab, Baylor) replaced the last coding exon of *apolpp* with eGFP but retained the endogenous *apolpp* 3' UTR. The ApoLppI C-eGFP transgene is homozygous viable. b) Number line depicts the sequence of polytene region 102D4. The *myo* gene and three *myo* transcripts (from the opposite strand right to left) that encode a single Myo protein are shown. The transcripts/proteins are annotated to show a furin cleavage site between amino acids 476 and 477. In the first intron of the coding region are two FCRP DoubleHeader conversions of CR02262. The *myo* T2A.GAL4 and Myo eGFP transgenes are homozygous lethal. Note the Myo eGFP tag is in the prodomain but also tracks the receptor-binding ligand because the prodomain is attached to the ligand until released prior to receptor binding (Rifkin et al. 2022).

Eaton 2010). The third transgene, *apolpp* T2A.GAL4 tracks *apolpp* transcription (Fig. 3).

Examining eGFP in the adult brain revealed that ApoLppII N-eGFP is widely visible. Low magnification images from brains with glial cells marked by Repo show ApoLppII N-eGFP accumulation in the optic lobe cortex and medulla (Fig. 4). Higher magnification images reveal that ApoLppII N-eGFP is visible overlapping glial nuclei in the BBB. There is also ApoLppII N-eGFP in the underlying optic lobe cortex that contains both neurons and glia. Further medial in the optic lobe medulla, a high concentration of ApoLppII N-eGFP is present around three rows of medulla glia. In these rows are astrocytes (their projections tile neurons in specific area) and ensheathing glia (their projections are neuronal axon wrappers). ApoLppII N-eGFP is also visible apical and medial to the medulla in the lamina and lobula, respectively. In the BBB, cortex, and medulla ApoLppII N-eGFP overlaps a subset of Repo-expressing glial nuclei.

ApoLppI C-eGFP is also present in the adult brain, but appears more restricted than ApoLppII N-eGFP (Fig. 5). ApoLppI C-eGFP transits the BBB and enters the cortex where its deposition pattern resembles ApoLppII N-eGFP. ApoLppI C-eGFP maintains a presence in BBB glia though it does not overlap any nuclei. ApoLppI C-eGFP moves past the cortex into the medulla, but it appears to accumulate only near a single row of glia. In this row ApoLppI C-eGFP overlaps some but not all Repo-expressing medulla glial nuclei. Neither the lamina nor lobula show ApoLppI C-eGFP accumulation.

Then we analyzed adult brains for transcription utilizing *apolpp* T2A.GAL4 (Fig. 5). This transgene identifies cells transcribing the *apolpp* mRNA that leads to both ApoLppII and ApoLppI isoforms. We detect no transcription yet are confident the transgene is

functioning due to its ability to reveal *apolpp* transcription in the fat body (Supplementary Fig. 3). The absence of *apolpp* transcription in the adult brain is also consistent with a donor's note for the *apolpp* T2A.GAL4 parent stock (CR80040; BDSC #97179) that little or no GAL4 expression was detected in the larval brain. Taken together multiple lines of evidence suggest that ApoLppII and ApoLppI in the adult brain are exogenous.

ApoLppII, ApoLppI, and Myo are present in glia in adult brains

We then looked with more care at the accumulation patterns of both ApoLpp isoforms in the adult brain using Myoglianin (Myo) as a marker for a subset of glia in the BBB, cortex and medulla. Myo is a secreted protein in the TGF- β family (Wisotzkey and Newfeld 2020). We examined two *myo* transgenes created by the FCRP: *myo* T2A.GAL4 identifies cells transcribing *myo*, and Myo eGFP tracks the Myo protein (Fig. 3). *myo* is visible in many BBB glia, where its transcription appears similar to ApoLppII N-eGFP accumulation (Fig. 6). A closer view of the BBB and cortex reveals that *myo* transcription is so strong that UAS.nls.GFP overflows nuclei into glial projections. Subsequently, Myo eGFP is efficiently secreted from BBB and cortex glia as shown by the absence of accumulation in glial cells. Higher magnification views of ApoLppII N-eGFP and ApoLppI C-eGFP in the cortex show they appear ubiquitous like Myo eGFP. The overall impression is of similarity between Myo and ApoLpp in the BBB and in the cortex.

Within the medulla, Myo eGFP appears in a subset of all three rows of ensheathing glia and astrocytes (Fig. 7). Looking next at *myo* transcription, this is also visible in a subset of all three rows of medulla glia. Comparing Myo eGFP to ApoLppII N-eGFP in the

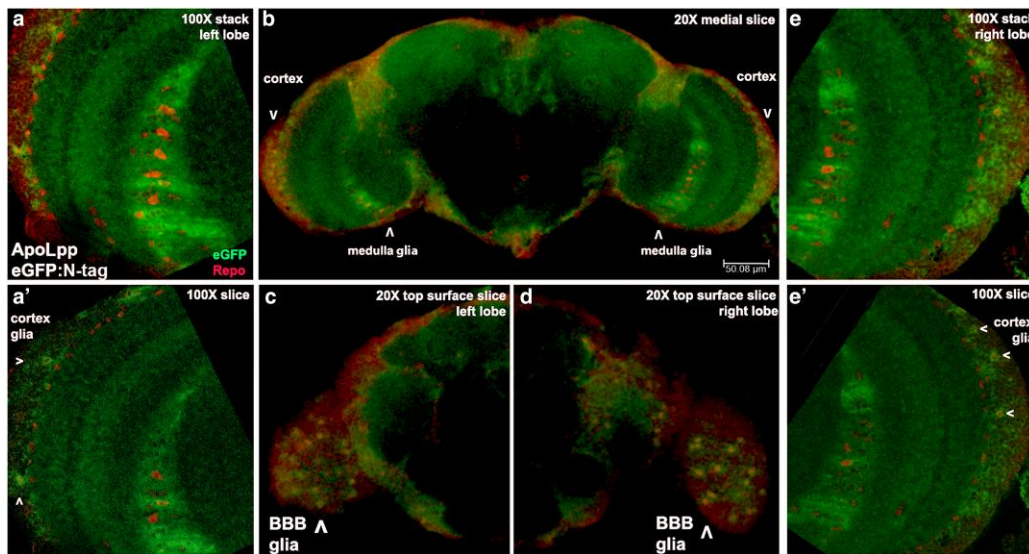


Fig. 4. ApoLppII N-eGFP accumulates near BBB, cortex and medulla glia of adult brains. a') Confocal stack and medial slice of the left optic lobe of an ApoLppII N-eGFP adult male brain ($n = 4$) displaying eGFP (green) and Repo (red). ApoLppII N-eGFP is present throughout the lobe, including near the nuclei of cortex glia (arrowheads in a') and medulla glia at the right. b) Medial slice of the same brain revealing left-right symmetry for ApoLppII N-eGFP near cortex (down arrowheads) and medulla glia nuclei (up arrowheads). c and d) Slice of the left and right optic lobe anterior surfaces revealing that ApoLppII N-eGFP overlaps the nuclei of BBB glia in both locations (up arrowheads). e-e') Confocal stack and medial slice of the right optic lobe indicates the same ApoLppII N-eGFP accumulation pattern as the left including the association with the nuclei of cortex (arrowheads in e') and medulla glia at the left.

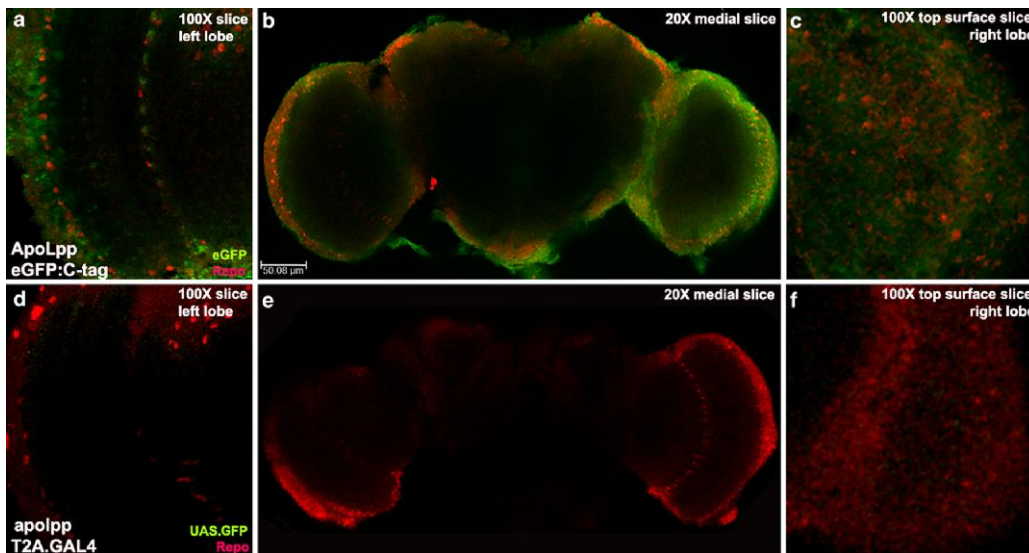


Fig. 5. ApoLppI C-eGFP accumulates near BBB, cortex and medulla glia but *apolpp* is not transcribed in adult brains. a to c) ApoLppI C-eGFP adult female brain ($n = 5$) displaying eGFP (green) and Repo (red). a) Medial slice of the left optic lobe showing ApoLppI C-eGFP is prominent in the cortex while modest in the medulla. b) Medial slice of the whole brain revealing left-right symmetry for ApoLppI C-eGFP. c) Slice of the right optic lobe anterior surface showing that ApoLppI C-eGFP is present in BBB glia though not overlapping nuclei like ApoLppII N-eGFP. d to f) *apolpp* T2A.GAL4 heterozygous adult female brain ($n = 4$) expressing UAS.nls.GFP (green) and Repo (red). No GFP is visible. Functionality of *apolpp* T2A.GAL4 was verified via rescue of a transheterozygote with *apolpp*^{32B} with two copies of wild type UAS.ApoLpp. The absence of *apolpp* transcription in the adult brain indicates that ApoLppI C-eGFP and ApoLppII N-eGFP in the adult brain are exogenous.

medulla reveals a strikingly similar accumulation pattern. ApoLppII N-eGFP is visible in the cortex and medulla with the highest abundance near the three rows of medulla glia. Similarity between these 2 eGFP transgenes also exists outside the medulla with Myo eGFP visible in the lamina and lobula similar to ApoLppII N-eGFP. On the other hand, ApoLppI C-eGFP in the medulla appears restricted to the serpentine row, with faint expression in the lamina and lobula.

BBB morphotrap confirms that both isoforms of ApoLpp in the adult brain are exogenous

Taken together the data thus far suggest the hypothesis that ApoLpp isoforms in the adult brain are not expressed there but are instead derived from the fat body after crossing the BBB. We tested this hypothesis in morphotrap experiments. A morphotrap transgene encodes an UAS controlled fusion of a nanobody against GFP to the external portion of the transmembrane protein CD8,

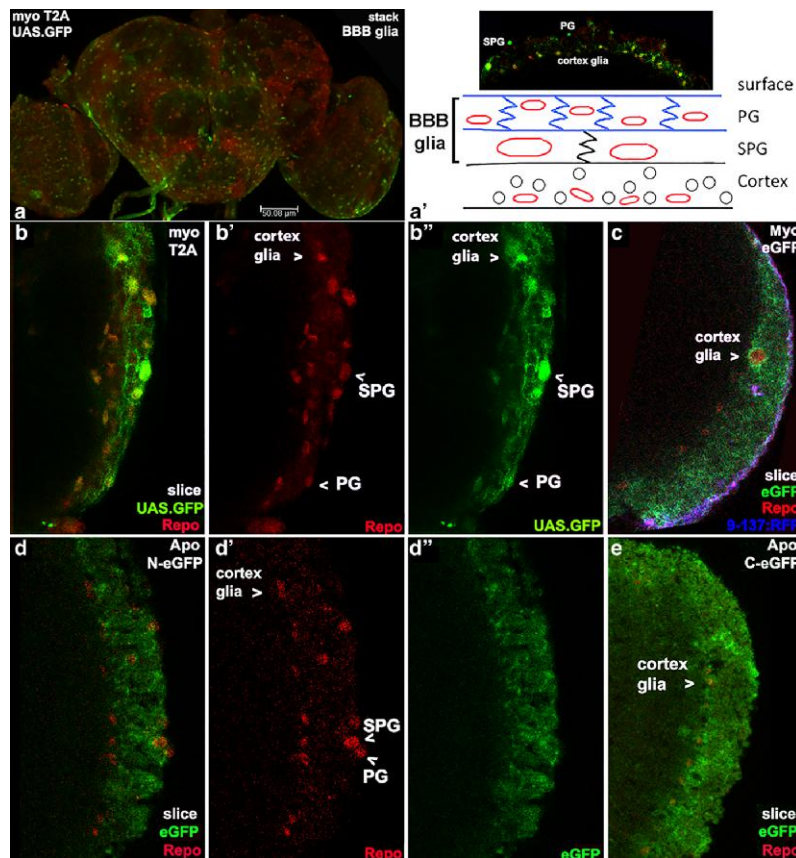


Fig. 6. ApoLppII N-eGFP, ApoLppI C-eGFP and Myo are abundant in BBB and cortex glia. a) Confocal stack at low magnification of a *myo T2A.GAL4* adult female brain ($n = 4$) displaying UAS.nls.GFP (green) with Repo (red). *myo* transcription is visible in many BBB glia. a') Schematic below a confocal slice of the BBB plus cortex in cross-section from the same brain. The BBB consists of two distinct rows of glia packed tightly together. The perineural glia row (pg) is apical and in contact with the circulation. Medial is the subperineural glia (spg). These two rows can be distinguished empirically by their nuclei size and spacing as shown. Medial to the BBB is the cortex containing primarily neurons with glia; black circles represent neuronal and red circles glial nuclei without cell delineation. In the image many BBB and cortex glia transcribe *myo*. b–b'') Single slice at high magnification of the BBB and cortex from the right brain lobe of same brain in two colors and single channels. Strong *myo* transcription is visible in cortex, perineural and subperineural glia such that nls.GFP overflows into cell projections. c) Slightly lower magnification slice of a *Myo eGFP* adult female right brain lobe ($n = 4$) displaying eGFP (green), Repo (red) and 9-137:RFP (blue) that marks perineural glia. *Myo eGFP* is ubiquitous in the cortex reflecting efficient glial secretion. d–d'') Same view of the cortex in a slice from a *ApoLppII N-eGFP* adult female brain ($n = 5$) reveals abundant eGFP. e) Same view of an *ApoLppI C-eGFP* adult female brain ($n = 2$) also reveals abundant eGFP.

that we call CD8-morpho. This transgene effectively traps nearby GFP-tagged secreted proteins at the outer membrane of any expressing cell, thus preventing the secreted protein from traveling further. In our hypothesis test, CD8-morpho was driven in the BBB by 9-137:GAL4 to block ApoLppII N-eGFP and/or ApoLppI C-eGFP at the BBB. CD8-morpho BBB expression was tracked by co-expression of UAS.CD8.RFP. A similar approach employing CD8-morpho and 9-137:RFP was reported in the analysis of an adult BBB enriched drug efflux pump (Hindle et al. 2017). We examined the brains of third instar larvae as well as adult females.

We confirmed that 9-137:RFP expression was restricted to BBB membranes in third instar larvae and adults by examining brain expression in otherwise wild type flies (Supplementary Fig. 4). Then to be sure CD8-morpho driven by 9-137:RFP was able to trap eGFP effectively in third instar larvae we examined ApoLppI C-eGFP homozygotes with and without CD8-morpho. Control larvae without CD8-morpho exhibited eGFP on the BBB and inside the brain. Larvae with CD-8 morpho displayed eGFP on the BBB but no eGFP inside the brain (Supplementary Fig. 5). Based on these observations, CD8-morpho should be effective at blocking eGFP from entering the adult brain.

Examination of one day old virgin female brains expressing CD8-morpho in the BBB and ApoLppII N-eGFP as a heterozygote with *apolpp*^{81D} showed ApoLppII N-eGFP uniformly on the surface but not inside the brain (Supplementary Fig. 6). This is the same phenotype seen in larval brains homozygous for ApoLppI C-eGFP with CD8-morpho in the BBB (Supplementary Fig. 5). Data from one day old females is promising but perhaps not conclusive given the extent of neural development and vitellogenesis that occur immediately after eclosion in females (Zhang et al. 2022; Li et al. 2024). As a control, to ensure the exclusion of ApoLppII N-eGFP from the brain was due to CD8-morpho in the BBB, we substituted Nrv-morpho for CD8-morpho. Nrv-morpho is only effective in a polarized epithelium as Nrv is specifically inserted in the basolateral membrane (Harmansa et al. 2017). The BBB is a squamous epithelium and Nrv is not inserted in the membrane. All other features of the genotype were identical to CD8-morpho. In larvae and adults with Nrv-morpho, both ApoLppII N-eGFP and ApoLppI C-eGFP are detected inside the brain (Supplementary Fig. 7).

We then analyzed CD8-morpho brains from ten day old virgin females to represent aged adults that were expressing ApoLppII N-eGFP in a heterozygote with *apolpp*^{81D} or homozygous for ApoLppI C-eGFP (Fig. 8). A low magnification confocal stack shows

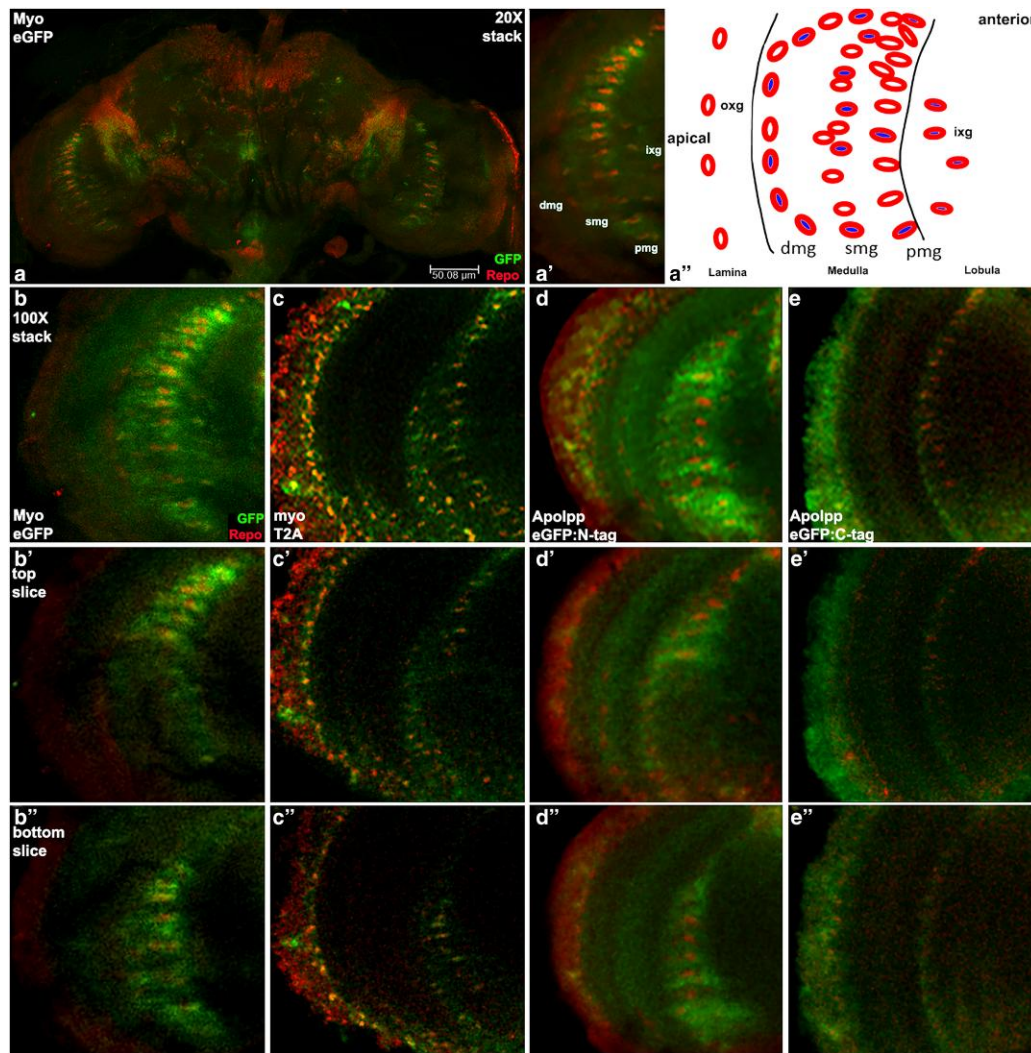


Fig. 7. ApoLppII N-eGFP and ApoLppI C-eGFP are near medulla glia expressing Myo. a) Confocal stack at low magnification of a Myo eGFP female brain ($n = 4$) displaying eGFP (green) with Repo (red). Myo eGFP presence is strongest in glia of the medulla but also visible in the lamina and lobula. a') Single slice at high magnification of the left brain lobe reveals that Myo eGFP is present in a subset of all three rows of medulla glia. a'') Schematic of glial subtypes in the medulla. Three roughly parallel rows of glia (red circles) are aligned from anterior to posterior (image top to bottom). The rows are bunched at the ends and well separated in between. These rows are named from left to right distal (dmgl), serpentine (smgl) and proximal (pmgl). Each row contains two classes of glia. One class (blue center) is astrocytes with projections that tile the neurons in a specific area and function in neuron homeostasis. The other class (white center) is ensheathing glia with nuclei arrayed at the medulla boundary and projections that extend into the medulla where they act as neuronal axon wrappers. Apical to the medulla in the lamina there is an anterior-posterior row of glia called the outer chiasm glia (oxg). Medial to the medulla in the lobula there is a roughly triangular set of glia pointing toward the central brain called the inner chiasm glia (ixg). b-b'') Confocal stack at high magnification with two slices from a Myo eGFP female brain expressing eGFP (green) and Repo (red). b') In the dorsal slice, at the top of the medulla glia rows the diffuse nature of Myo eGFP suggests astrocyte expression. b'') In the ventral slice, in the middle of the medulla glia rows Myo eGFP emanates apically in a linear shape suggesting ensheathing glia expression. c-c'') Stack with two slices from a myo T2A.GAL4 female brain ($n = 4$) expressing UAS.nls.GFP (green) and Repo (red). myo is transcribed in cortex glia and a subset of all three rows of medulla glia. d-d'') Stack with two slices from a ApoLppII N-eGFP male brain ($n = 4$) expressing eGFP (green) and Repo (red). ApoLppII N-eGFP is visible in the cortex, lamina, medulla and lobula with highest abundance near glia in the cortex and medulla. The pattern of ApoLppII N-eGFP medulla expression is similar to Myo eGFP. e-e'') Stack with two slices from a ApoLppI C-eGFP female brain ($n = 2$) expressing eGFP (green) and Repo (red). ApoLppI C-eGFP is strong in the cortex but restricted to the serpentine row of medulla glia.

ApoLppII N-eGFP uniformly on the surface. Low magnification slices reveal that ApoLppII N-eGFP is not visible inside the brain. The impression is reinforced by high magnification stacks and slices of ApoLppI C-eGFP that reflect the same distribution. Taken together the one and ten day old virgin female data suggest that ApoLppII N-eGFP and ApoLppI C-eGFP visible inside the brain in our previous experiments were exogenous.

Brains from mature ten day old mated CD8-morpho females (mated for three days then gender segregated), were consistent with those of ten day old virgins (Fig. 9). Images from adults

expressing ApoLppII N-eGFP in a heterozygote with *apolpp*^{81D} or homozygous for ApoLppI C-eGFP or both were examined. Low magnification confocal stacks of brains from ApoLppII N-eGFP or ApoLppI C-eGFP mated females show the same phenotype as their virgin siblings, with eGFP uniformly distributed on the surface. A high magnification confocal stack of a ten day old mated female with ApoLppII N-eGFP and ApoLppI C-eGFP looks virtually identical to the one from a ten day old virgin female, with eGFP uniformly distributed on the surface. A high magnification slice (Fig. 9d) shows that a very small amount of ApoLpp eGFP

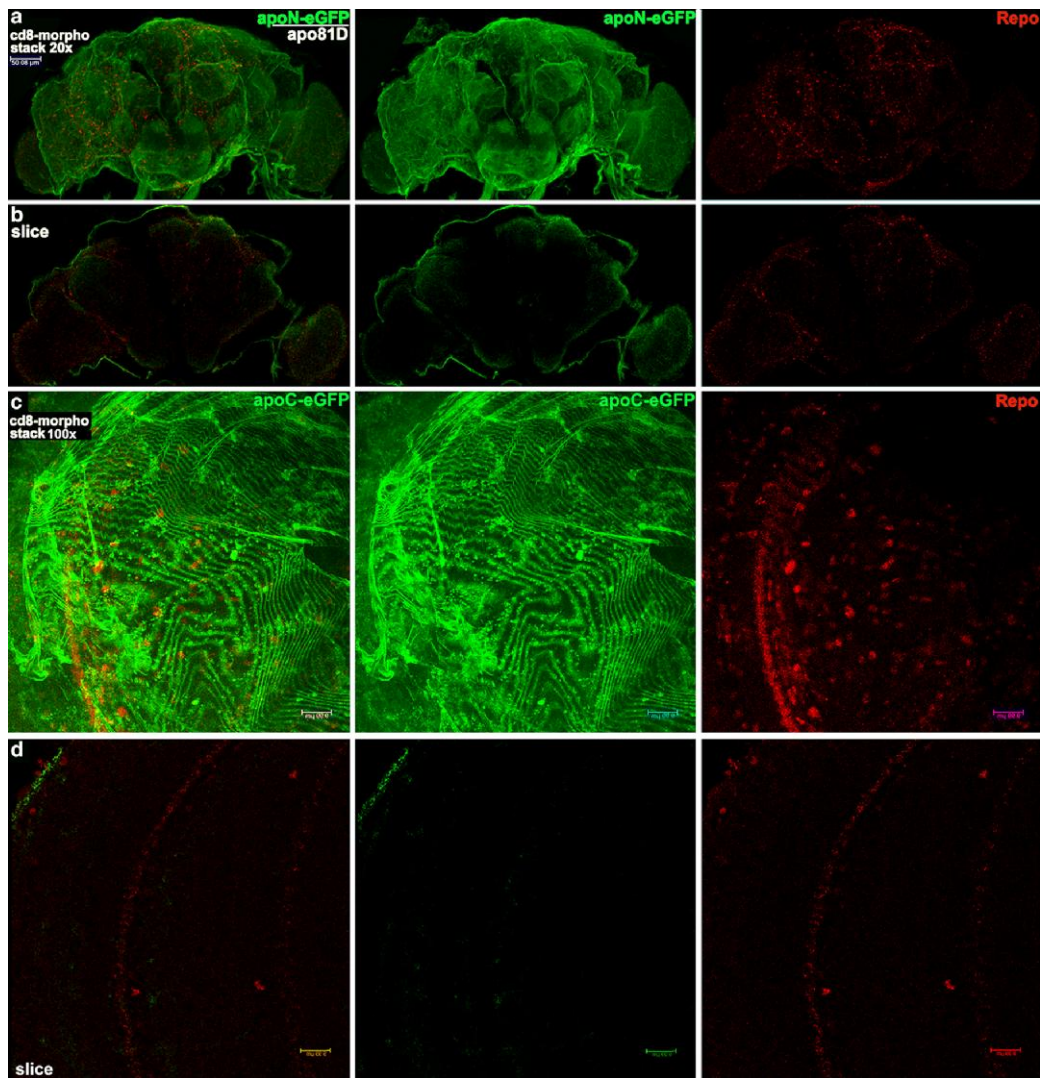


Fig. 8. BBB morphotrap in ten day old unmated females shows that ApoLppII N-eGFP and ApoLppI C-eGFP in the adult brain are exogenous. Aged adult female brains ($n = 3$) with CD8-morpho driven by 9-137.GAL4 in the BBB displaying either ApoLppII N-eGFP in a heterozygote with *apolpp*^{81D} or homozygous ApoLppI C-eGFP (as indicated in green) and Repo (red) in two colors (left column) and single channels. a) Low magnification confocal stack reveals ApoLppII N-eGFP uniformly distributed on the brain surface. b) Single slice from the same brain shows that ApoLppII N-eGFP is restricted to the brain surface. c) High magnification stack ($n = 3$) from the left brain lobe reveals that ApoLppI C-eGFP is uniformly distributed on the brain surface. d) Single slice from the same lobe shows that ApoLppI C-eGFP is restricted to the brain surface.

penetrates a short distance into the brain with most ApoLpp eGFP at the BBB adjacent to perineural glia. The insert shows that perineural glial nuclei are embedded in ApoLpp eGFP. Moving one slice dorsal (Fig. 9e) shows ApoLpp eGFP is barely visible for just a short distance inside the brain with most ApoLpp eGFP at the BBB adjacent to subperineural glia. The insert shows the asymmetric distribution of ApoLpp around subperineural glia with considerably more apically than medially.

Taken together morphotrap data shows that at larval and adult stages both isoforms of ApoLpp eGFP inside the brain are exogenous. This finding is consistent with prior results suggesting that the fat body is an essential source of ApoLpp in larvae and adults.

ApoLpp expressed in the fat body is secreted then visible on the BBB and inside the brain

We then directly tested the hypothesis that ApoLpp protein in the larval and adult brain is not expressed there but is instead derived from the fat body after crossing the BBB. For these studies we employed three transgenes from the rescue crosses. There are the fat body

drivers CG.GAL4, R4.GAL4 and UAS.5'-HA-ApoLpp-Myc-3'. This cDNA rescued *apolpp* mutants at roughly one-third of the Mendelian expectation (Table 2), indicating the tags do not fully interfere with function. This transgene can produce both isoforms: HA tagged ApoLppII N-terminal (5'-HA-ApoLppII) and Myc tagged ApoLppI C-terminal (ApoLppI-Myc-3'). The double-tagged protein tracking experiment was conducted in third instar larvae and adults.

High magnification single color views of dissected larval fat body with R4.GAL4 driving the double-tagged ApoLpp, revealed both 5'-HA-ApoLppII and ApoLppI-Myc-3' are present in every cell (Fig. 10). Same view of a dissected body wall muscle stained similarly plus Dapi showed the highest concentration of 5'-HA-ApoLppII and ApoLppI-Myc-3' along the exterior surface of the muscle. There is a small amount of diffuse accumulation of each inside the muscle near the right side cut site. The distribution of 5'-HA-ApoLppII and ApoLppI-Myc-3' on the muscle suggests that both isoforms of ApoLpp were secreted by the fat body into the circulation then traveled to the muscle exterior surface.

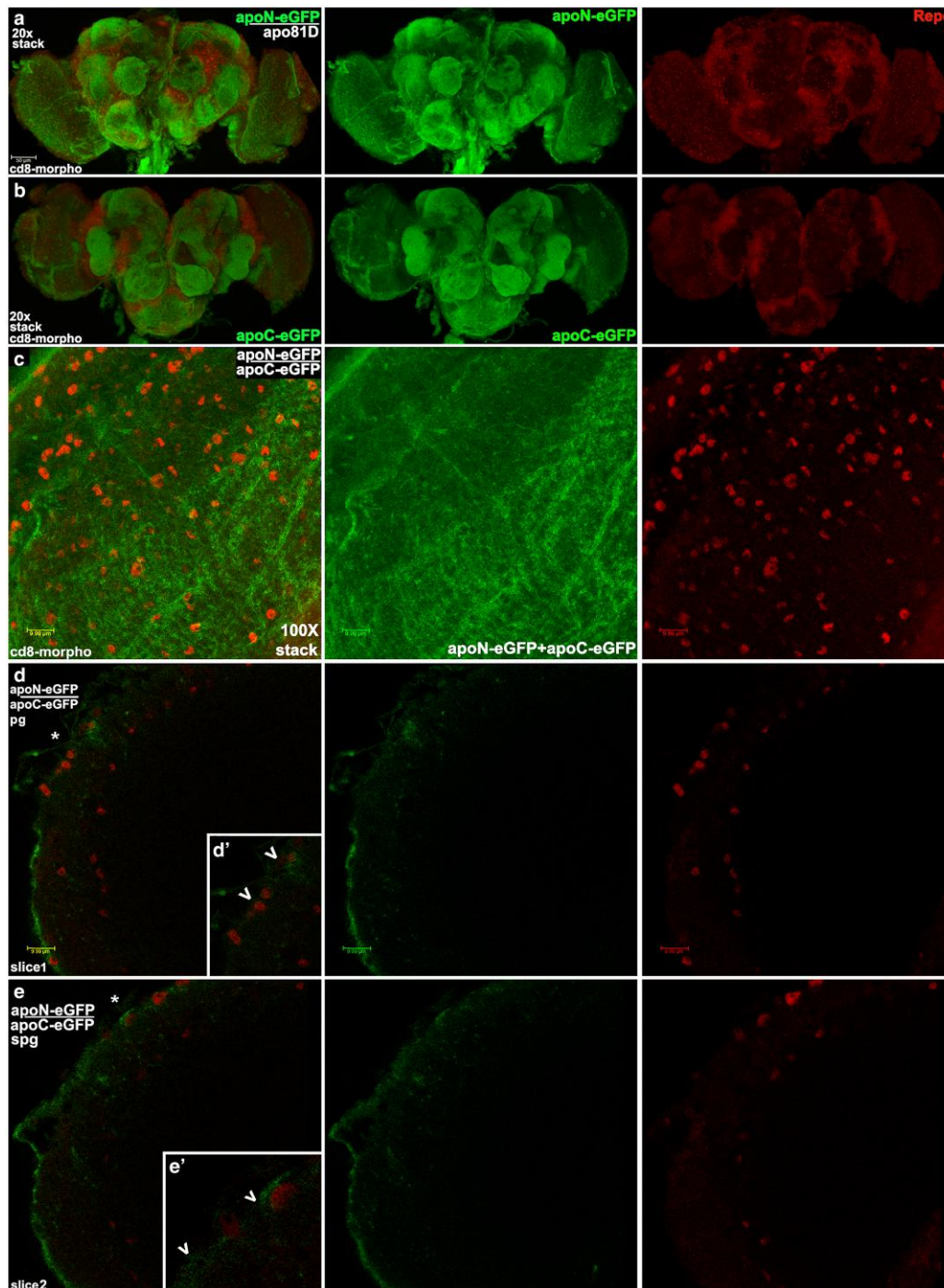


Fig. 9. BBB morphotrap in ten day old mated females shows that exogenous ApoLppII N-eGFP and ApoLppI C-eGFP are blocked at the subperineural glia. Aged adult female brains with CD8-morpho driven by 9-137.GAL4 in the BBB displaying isoforms of ApoLpp eGFP as indicated. a and b) Low magnification stacks show that ApoLppII N-eGFP in a heterozygote with *apolpp*^{81D} (*n* = 3) and homozygous ApoLppI C-eGFP (*n* = 3) are uniformly distributed on the brain surface. c) High magnification stack of the left lobe of a brain with ApoLppII N-eGFP over ApoLppI C-eGFP (*n* = 3) shows them uniformly distributed on the brain surface. d) Single slice of the same lobe focused on the structural layer of perineural glia (pg). The slice suggests that eGFP is largely restricted to the brain surface but can be seen medial to the perineural glia layer. Starred area shown as an inset. d') Arrowheads indicate perineural glia whose Repo expressing nuclei are surrounded by eGFP. e) Single slice, dorsal to the previous slice, focused on the subperineural glia row (spg), that constitutes the BBB barrier layer underneath the perineural glia. Starred area shown as an inset. e') Arrowheads indicate subperineural glia whose Repo expressing nuclei have eGFP primarily on their apical side with modest visibility medially.

Low magnification stack of a larval brain lobe stained with 5'-HA-ApoLppII and Dapi contains 5'-HA-ApoLppII accumulation on the surface and inside the brain. The distribution of 5'-HA-ApoLppII appears similar to ApoLppII N-eGFP in the larval brain. A high magnification confocal slice of an adult brain lobe

reflecting ApoLppI-Myc-3' and the BBB glial nuclear marker Vvl contains ApoLppI-Myc-3' accumulation on the surface and inside the brain. The distribution of ApoLppI-Myc-3' appears similar to ApoLppI C-eGFP in the adult brain. The double-tagged ApoLpp tracking data, together with the morphotrap, rescue and RNAi

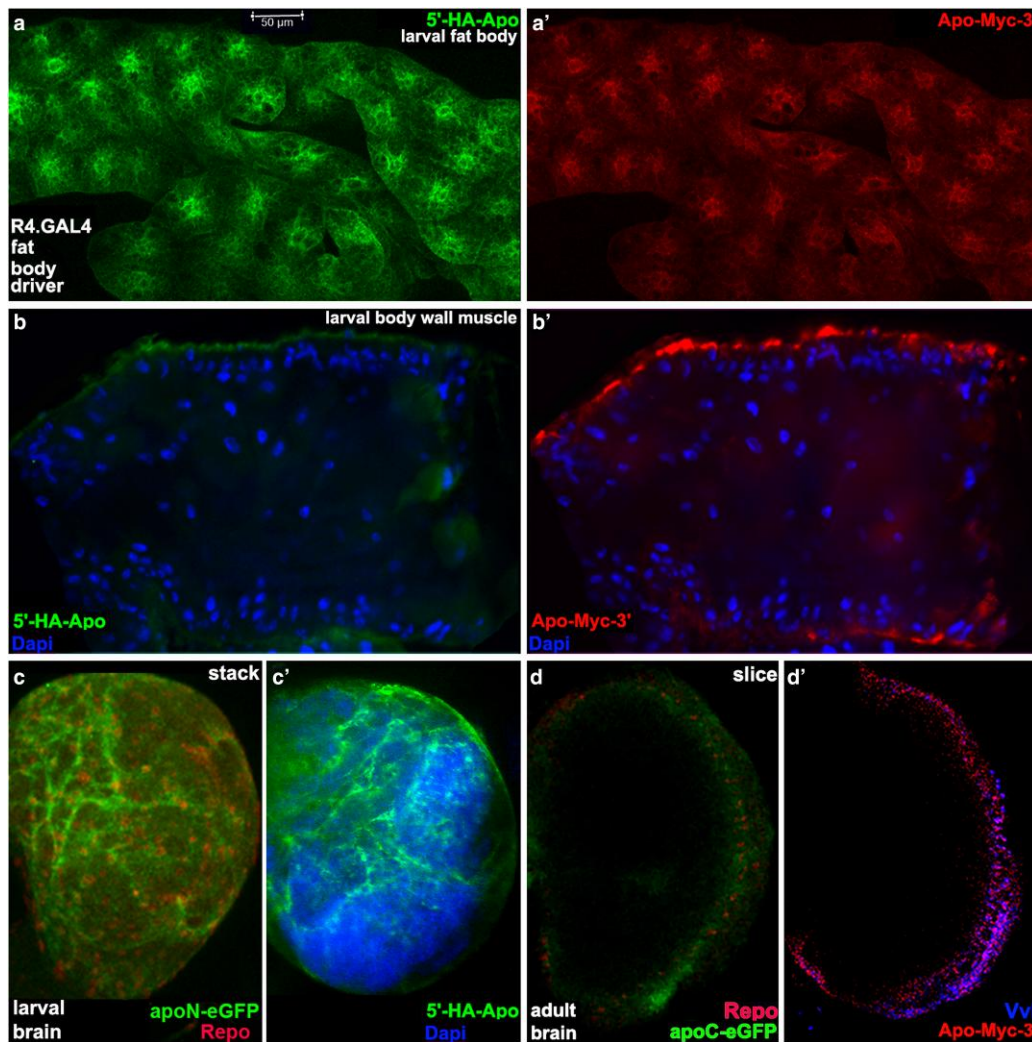


Fig. 10. Double tagged ApoLpp tracked from fat body secretion to the BBB then inside the larval and adult brain. a and a') Dissected larval fat body ($n = 3$) reflecting R4.GAL4 driven UAS.5'-HA-ApoLpp-Myc-3' shown as single channels. Every cell expresses 5'-HA-ApoLppII (green) and ApoLppI-Myc-3' (red). b-b') Dissected larval body wall muscle ($n = 4$) with multinucleated cells. 5'-HA-ApoLppII and ApoLppI-Myc-3' are visible on the surface with diffuse accrual at the open end (right). c-c') Larval brain left lobe stacks. c) ApoLppII N-eGFP (green) and Repo (red) displaying ApoLppII N-eGFP at the surface and inside the brain ($n = 4$). c') CG.GAL4 driven 5'-HA-ApoLppII (green) and Dapi (blue) displaying 5'-HA-ApoLppII at the surface and inside the brain ($n = 6$) similar to ApoLppII N-eGFP. d-d') Adult brain right lobe slices. d) R4.GAL4 driven ApoLppI C-eGFP (green) and Repo (red) displaying ApoLppI C-eGFP at the surface and inside the brain ($n = 5$). d') ApoLpp-Myc-3' (red) and Vv1 (blue; marks BBB glial nuclei) displaying ApoLpp-Myc-3' at the surface and inside the brain ($n = 3$) similar to ApoLppI C-eGFP.

data strongly support the hypothesis that ApoLpp protein in the larval and adult brain is not expressed there but is instead derived from the fat body after crossing the BBB.

Discussion

The Apolipoprotein (Apo) family, in humans and other species is not a traditional protein family where all members share sequence similarity derived from a common ancestor. As a result, the evolutionary relationships between Apo proteins overall and between ApoB and ApoLpp have not been clearly established. Our interspecific tree connected two human Apo proteins to fly proteins (ApoB48 with ApoLppII/ApoLTPII and ApoF with Fabp). This connection indicated that these proteins were conserved since the last common ancestor of mammals and flies. A second interspecific tree connected fly ApoLppII/ApoLTPII to nematode Vit-6II. Together the interspecific trees suggest a connection between human ApoB48, fly ApoLppII and nematode Vit6II in their common ancestor nearly 700 million years ago.

To extend our understanding of ApoLpp in flies beyond second instar and suggest new hypotheses for human ApoB, we conducted a series of experiments with new stocks from the FCRP to visualize endogenous *apolpp* transcription and ApoLpp isoform specific protein accumulation. In the rescue experiments, UAS.ApoLpp expressed in the fat body in an *apolpp* lethal genotype rescued these individuals to adulthood. Companion *apolpp*.RNAi experiments employing the same fat body drivers, eliminated larval survival. Taken together these experiments indicate that the fat body is a necessary and sufficient source of *apolpp* for survival to adult. Studies of *apolpp* transcription are consistent, with no expression seen in the larval or adult brain. Nevertheless, both isoforms of ApoLpp eGFP were visible in the larval and adult brain. ApoLpp brain accumulation resembled *myo* transcription/translation in the adult BBB, cortex and medulla suggesting an association of ApoLpp eGFP with adult brain glia and *myo*.

We directly tested the hypothesis that ApoLpp protein in the larval and adult brain is not expressed there but is instead derived from the fat body after crossing the BBB in two sets of experiments. The first set

employed a morphotrap expressed in the BBB to block circulating ApoLppII N-eGFP or ApoLppI C-eGFP from entering the brain. When the morphotrap was present, neither ApoLppII N-eGFP nor ApoLppI C-eGFP were visible in third instar or adult brains, confirming that ApoLpp protein in the larval and adult brain is exogenous. The second set showed that the source of the exogenous ApoLpp protein in the brain is the fat body. Double-tagged UAS.5'-HA-ApoLpp-Myc-3' was expressed exclusively in the fat body and tracked. Imaging showed both isoforms were expressed in the fat body, secreted into the circulation, then visible on the BBB surface and inside the brain. Double tagged ApoLpp results confirm the hypothesis that ApoLpp protein in the larval and adult brain is not expressed there but is instead derived from the fat body after crossing the BBB.

Our ApoLpp adult data extends the prior ApoLpp functional study in second instar (Brankatschk and Eaton 2010). Our adult data showing accumulation of ApoLpp near glia is consistent with a recent report employing RNAi to suggest that ApoLpp from the fat body enters the adult brain where it plays a role in glial phagocytosis in response to neuronal debris created by physical injury (Allassaf et al. 2025). Our adult data adds a third signal to recent reports of fat body/gut to brain signaling. Two examples are Vaha (a secretory lipase) and Neuropeptide F that are secreted by the gut, then cross the adult BBB to target insulin producing neurons (Chen et al. 2024; Singh et al. 2024).

The possibility that ApoLpp is a fat body to brain signal, in addition to delivering lipids, suggested two potential relationships between ApoLpp and *myo* in brain glia. Perhaps ApoLpp delivers lipids to *myo* expressing glia and/or *myo* expressing glia receive an ApoLpp signal from the fat body. In the latter case, it is tempting to speculate that Myo secreted by brain glia then plays the role of GLP-1 in signaling from the hypothalamus to the liver and gut, to regulate ApoB48 expression/secretion (Farr et al. 2015). Since we have shown ApoLpp travels from the fat body to the brain, if Myo from the brain then fulfilled the role of GLP-1 in signaling back to the fat body, it would suggest a feedback loop regulates ApoLpp, and perhaps also ApoB, expression/secretion.

Taken together our ApoLpp experimental data and evidence of conservation between ApoB48 and ApoLppII suggest the new hypothesis that human ApoB48 exits the circulation to fulfill a function in the brain. This hypothesis is supported by several circumstantial factors. First, there are many established similarities between the fly and mammal BBB (e.g. Desalvo et al. 2014; Contreras and Klämbt 2023). Second, ApoB mutations or serum levels are associated with features of cognitive impairment that are not readily connected to atherosclerosis. Third, studies of rodent cells in culture suggest a possible mechanism for ApoB BBB transit via LDL receptor transcytosis. This mechanism is similar to reports of ApoLTP passage through the BBB via endocytosis of its transporters LRP1 and LRP2 (Li et al. 2023; Singh et al. 2024).

Experimental evidence of ApoB inside the brain of a vertebrate derives from two studies in zebrafish, an organism that recapitulates human ApoB physiology including exclusive expression in the liver/gut (Schlegel 2016). The first paper employed a luciferase enzyme fused to endogenous ApoBb.1 to monitor accumulation in live larvae with specific genetic backgrounds under defined nutritional regimes. The authors noted ApoBb.1 presence in the brains of both wild type and experimental larvae (Thierer et al. 2019). The second paper employed the photoconvertible fluorophore Dendra2 fused to endogenous ApoBb.1 to monitor ApoBb.1 half-life in circulation in live wild type and juveniles with the same set experimental regimes. The authors again noted ApoBb.1 accumulation in the brain. Further, the photoconversion state of ApoBb.1 in the brain suggested to the authors that an LDL binding

domain protein was capturing ApoBb.1 after BBB transit (Moll et al. 2025). Reports from humans, rodents, zebrafish and now flies are consistent with the hypothesis that ApoB (or perhaps only ApoB48) crosses the BBB to fulfill a function in the brain.

In summary, we advance our knowledge of ApoLpp function to third instar and adult brains while demonstrating strong conservation with ApoB. Imaging studies in the adult brain employed new tagged proteins to reveal that both ApoLpp isoforms are present near glia. Morphotrap traps that block tagged ApoLpp at the BBB demonstrated that ApoLpp in the adult brain is exogenous. A double tagged version of ApoLpp expressed solely in the fat body was tracked from fat body secretion to the BBB and into the adult brain. Overall, our data suggest that the previously documented role of ApoLpp in second instar larval brain lipid delivery is likely operating in third instar and adults. Strong conservation between ApoLppII and ApoB48 supports the hypothesis that ApoB48 may have a role in the brain outside the circulatory system.

Data availability

Strains are available at the Bloomington Drosophila Stock Center (Cook and Parks 2022) and described in Flybase (Öztürk-Çolak et al. 2024). The authors affirm that all data underlying the conclusions are present within the article, figures, tables and supplementary material.

Supplemental material available at [GENETICS](https://doi.org/10.1101/2025.01.07.422482) online.

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Conflicts of interest

The author(s) declare no conflicts of interest..

Author contributions

MJS, SRG, MBO, and SJN designed experiments, collected & analyzed data. MJS, MBO, and SJN generated new reagents. SJN conceived the project and wrote the paper.

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Supplemental Data: Three Tables and Eleven Figures

Table S1. Twenty-three human Apo family members identified by name in Uniprot.					
Protein	Longest RefSeq	HGNC	Size	Secreted?	pfam structural domains
ApoA1	NP_001412021	600	158	Secreted	pfam01442 - A1/A4/E family
ApoA2	NP_001634	601	100	Secreted	pfam04711 - ApoA2 family
ApoA4	NP_000473	602	396	Secreted	pfam01442 - A1/A4/E family
ApoA5	NP_001358833	17288	366	Secreted	pfam01442 - A1/A4/E family
ApoB ^a	NP_000375	603	4563	Secreted Secreted	N-term: pfam09172 - Vitellogenin-N C-term: pfam06316 - Porin channels
Two true isoforms with common N-term; ApoB48 is 2180aa and ApoB100 is full length Alignments and trees employ the two parts of ApoB100 as distinct sequences (ApoB48 and ApoB52)					
ApoC1	NP_001366616	607	129	Secreted	pfam04691 - ApoC1 family
ApoC2	NP_000474	609	101	Secreted	pfam05355 - ApoC2 family
ApoC3	NP_000031	610	99	Secreted	pfam05778 - ApoC3 family
ApoC4	NP_001637	611	127	Secreted	pfam15119 - ApoC4 family
ApoD	AAB32200	612	266 ^b	Secreted	pfam04711 - ApoA2 family
ApoE2	NP_000032	613	317	Secreted	pfam01442 - A1/A4/E family
ApoF	NP_001629	615	326	Secreted	pfam15148 - ApoF family
ApoH	NP_000033	616	345	Secreted	pfam09014 - Sushi2 (6Cys-CCP)
ApoJ	NP_001822	2095	449	Secreted	pfam01093 - Clusterin
ApoL1	NP_001130012	618	398	Secreted	pfam05461 - ApoL family
ApoL2	NP_663612	619	337	Cytoplasm	pfam05461 - ApoL family
ApoL3	NP_001380522	14868	331	Cytoplasm	pfam05461 - ApoL family
ApoL4	XP_054181922	14867	348	Predicted	pfam05461 - ApoL family
ApoL5	NP_085145	14869	433	Cytoplasm	pfam05461 - ApoL family
ApoL6	NP_085144	14870	343	Cytoplasm	pfam05461 - ApoL family
ApoM	NP_061974	13916	188	Secreted-Membrane	pfam00061 - Lipocalin
ApoO	NP_077027	28727	198	Mito Inner Membrane	pfam09769 - ApoO (MICOS 26)
ApoOL	NP_940852.	24009	268	Mito Inner Membrane	pfam09769 - ApoO (MICOS 27)
ApoP	an apoptotic protein				
outgroup (similar function but not Apo name)					
MTP	NP_000244	7467	894	Secreted-ER	pfam19444 - MTP lipid-binding

a. Red indicates that ApoB48 (N-terminal) has the same Vitellogenin-N domain as fly ApoLppII.

b. AAB32200 does not contain the first 20 amino acids. These came from CAG33119.

Table S2. Eight fly Apo family members identified via DIOPT in Flybase.				
Protein	Longest RefSeq	Size	Secreted?	pfam structural domains
ApoLpp^a	NP_001284721	3351	Secreted-Cleaved	N-term: pfam09172 - Vitellogenin-N C-term: pfam00094 - vonWillebrand typeD Two isoforms separated by furin cleavage @ 706/707aa: ApoLppII is N-term and ApoLppI is C-term Alignments and trees utilized each isoform as a distinct sequence
ApoLTP	NP_995670	4333	Secreted-Cleaved	N-term: pfam09172 - Vitellogenin-N C-term: pfam00094 - vonWillebrand typeD Two isoforms separated by furin cleavage @ 779/780aa: ApoLTPII is N-term and ApoLTPI is C-term Alignments and trees utilized each isoform as a distinct sequence
Cv-d	NP_732076	1470	Secreted	N-term: pfam09172 - Vitellogenin-N No obvious furin cleavage site C-term: pfam00061 - Lipocalin
Glaz	NP_523727	212	Secreted	pfam00061 - Lipocalin
Nlaz	NP_001259867	245	Secreted	pfam00061 - Lipocalin
CG31659	NP_722702	192	Secreted	pfam00061 - Lipocalin
Fabp	NP_001027179	157	Cytoplasm	pfam00061 - Lipocalin
Mic26-27	NP_650523	226	Mito Inner Membrane	pfam09769 - ApoO
outgroup (homolog of human outgroup by BLASTp)				
Mtp	NP_610075	886	Secreted-ER	pfam19444 - MTP lipid-binding

a. Red indicates that ApoLppII alone contains the same N-terminal Vitellogenin-N domain as ApoB48.

Table S3. Nine nematode Apo family members identified via Wormbase.				
Protein	Longest RefSeq	Size	Secreted?	pfam structural domains
Vitellogenin-1	NP_001367671	1616	Secreted predicted.	N-term: pfam09172- Vitellogenin-N C-term: pfam00094 - vonWillebrand typeD predicted furin cleavage @ 740-741aa: RGR^R
For all Vit proteins, alignments and trees employ each predicted isoform as a distinct sequence				
Vit-2	NP_508868	1613	Secreted predicted.	N-term: pfam09172 - Vitellogenin-N C-term: pfam00094 - vonWillebrand typeD predicted furin cleavage @ 738-739aa: RGR^R
Vit-3	NP_001367903	1603	Secreted predicted	N-term: pfam09172- Vitellogenin-N C-term: pfam00094 - vonWillebrand typeD predicted furin cleavage @ 735-736 aa: RSR^R
Vit-4	NP_508612	1603	Secreted predicted.	N-term: pfam09172 - Vitellogenin-N C-term: pfam00094 - vonWillebrand typeD predicted furin cleavage @ 735-736aa: RSR^R
Vit-5	NP_508589	1603	Secreted predicted.	N-term: pfam09172 - Vitellogenin-N C-term: pfam00094 - vonWillebrand typeD predicted furin cleavage @ 735-736aa: RSR^R
Vit-6^a	NP_001023274	1650	Secreted predicted.	N-term: pfam09172 - Vitellogenin-N C-term: pfam00094 - vonWillebrand typeD predicted furin cleavage @ 766-767aa: RGK^R site is conserved in <i>Pristionchus pacificus</i> Vit-6
Moma-1	NP_497275	201	Mito Inner Membrane	pfam09769 - ApoO (MICOS 27)
ApoL1	NP_740988	265	Cytoplasm	pfam05461 - ApoL (not likely homolog as human ApoL1 is secreted)
ApoL3-like	NP_001379858	318	Cytoplasm	pfam05461 - ApoL (possible homolog as human ApoL3 is cytoplasmic)
outgroup (similar function but not homolog of either human or fly outgroup by reciprocal BLASTp)				
Dsc-4	NP_499903	892	Secreted-ER	pfam19444 - MTP lipid-binding

a. Red indicates that BLASTp shows Vit-6 is the original member of the Vit family in *C. elegans* with the other Vit proteins derived from serial duplications. As a result, all six *C. elegans* Vit proteins contain a predicted furin cleavage site conserved in ApoLpp and ApoLTP that creates two isoforms and their N-terminal isoforms contain the same Vitellogenin-N domain as ApoLppII and ApoB48.

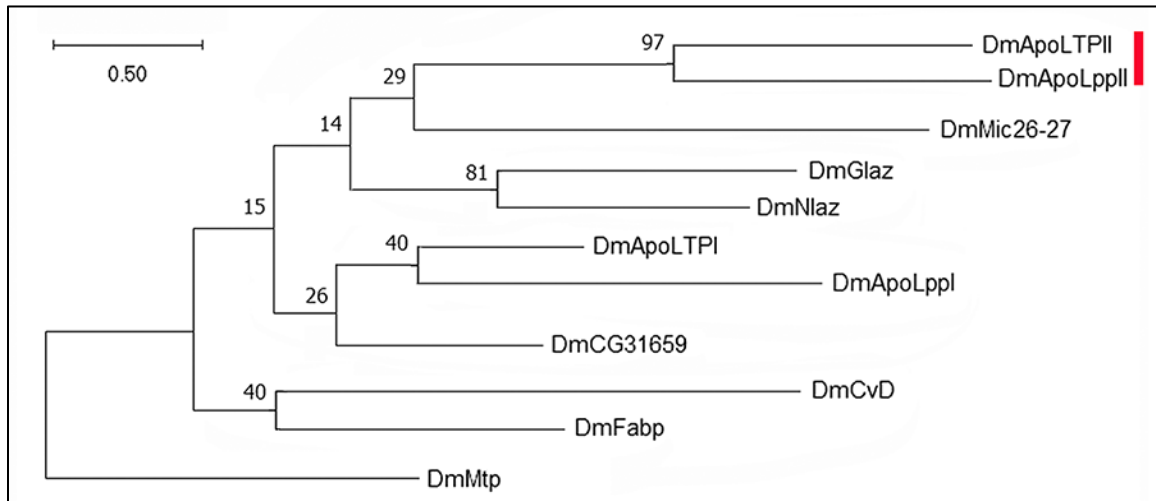


Fig. S1. Tree of 11 fly sequences with isoforms of ApoLpp and ApoLTP separated plus an outgroup. Maximum Likelihood tree with the highest log likelihood is shown as in **Fig. 1**. There are 194 informative positions in the MUSCLE alignment. Red bar indicates the strong grouping of ApoLppII with ApoLTPII. At a distance ApoLppI and ApoLTPI cluster together. The distinct placement of the ApoLpp/ApoLTP isoforms on the tree suggests divergent selection on the N-terminal versus the C-terminal isoforms in ApoLpp prior to the duplication creating ApoLTP.

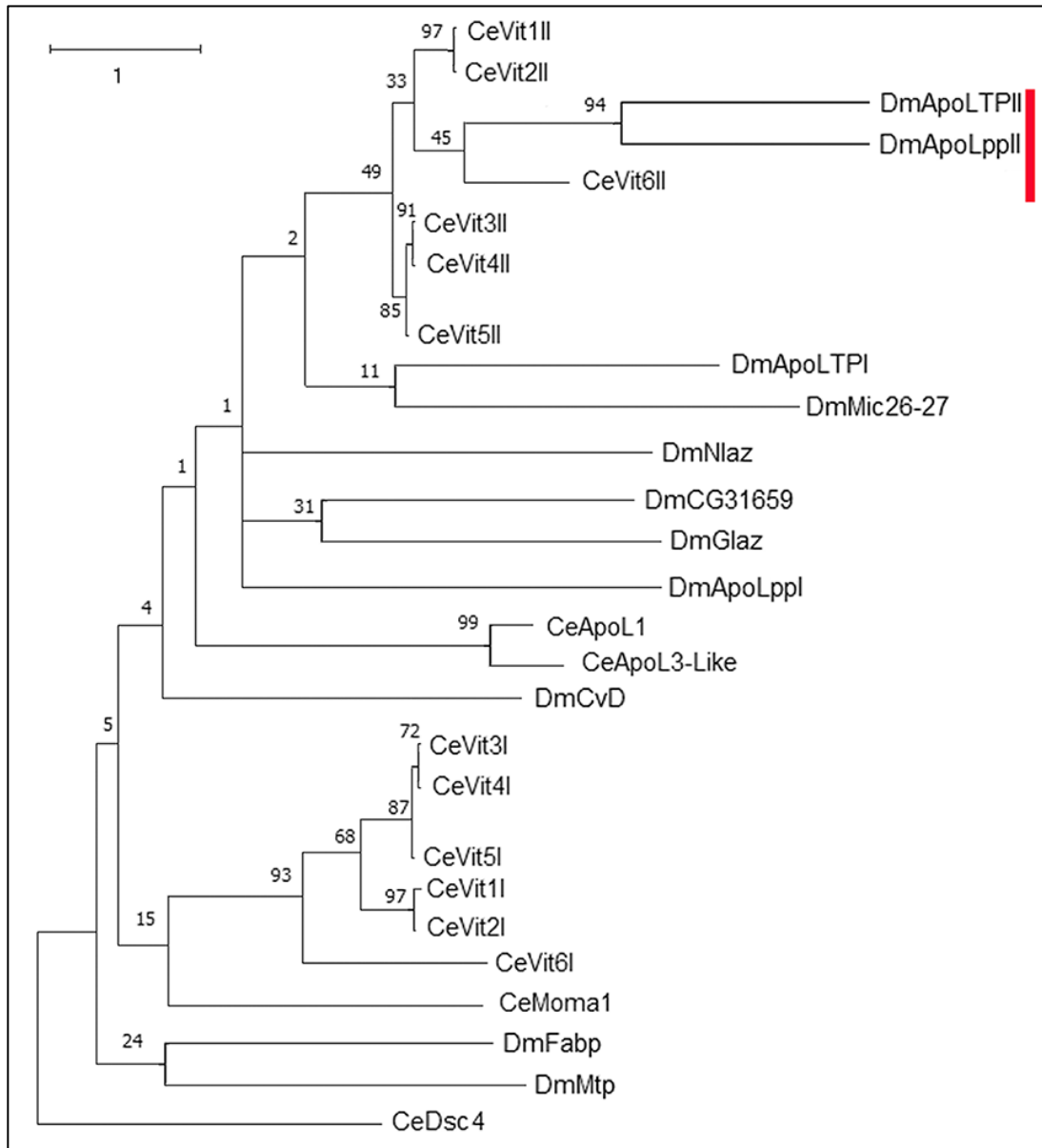


Fig. S2. Fly ApoLppII and nematode Vit-6II are conserved. Maximum Likelihood tree with the highest log likelihood is shown as in **Fig. 1**. There are 11 fly (Dm) and 16 nematode (Ce) sequences in the tree with the nematode outgroup. The two isoforms of ApoLpp, ApoLTP and Vit-1 through Vit-6 are shown separately. There are 279 informative positions in the MUSCLE alignment. Red bar indicates the cluster of Vit-6II with ApoLppII and ApoLTPII (all N-terminal domains). This cluster plus the cluster of the N-terminal domains ApoLppII and ApoLTPII with human ApoB48 in **Fig. 2** reveals that ApoB and Vit6 likely descended from a common ancestor.

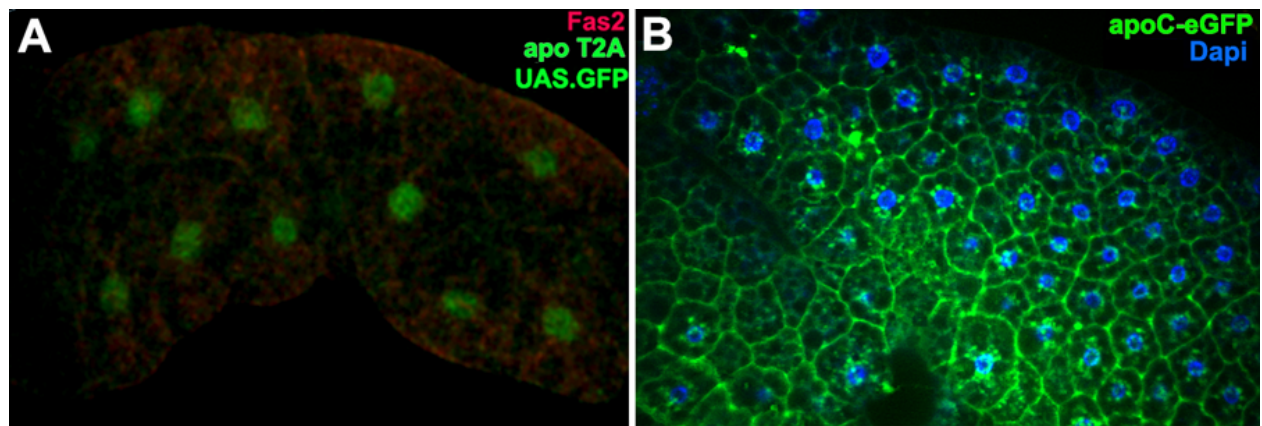


Fig. S3. *apolpp* T2A.GAL4 and ApoLppI C-eGFP are visible in the larval fat body. A,B) Confocal stacks of larval female fat bodies (n=2 each) with green displaying either UAS.nls-GFP driven by *apolpp* T2A.GAL4 (green) with FasII (red) or ApoLppI C-eGFP (green) with DAPI (blue). As FasII is a neuronal membrane protein, no expression is expected but a low level of background staining is visible outlining the tissue. **In both views**, GFP is visible in many if not all cells.

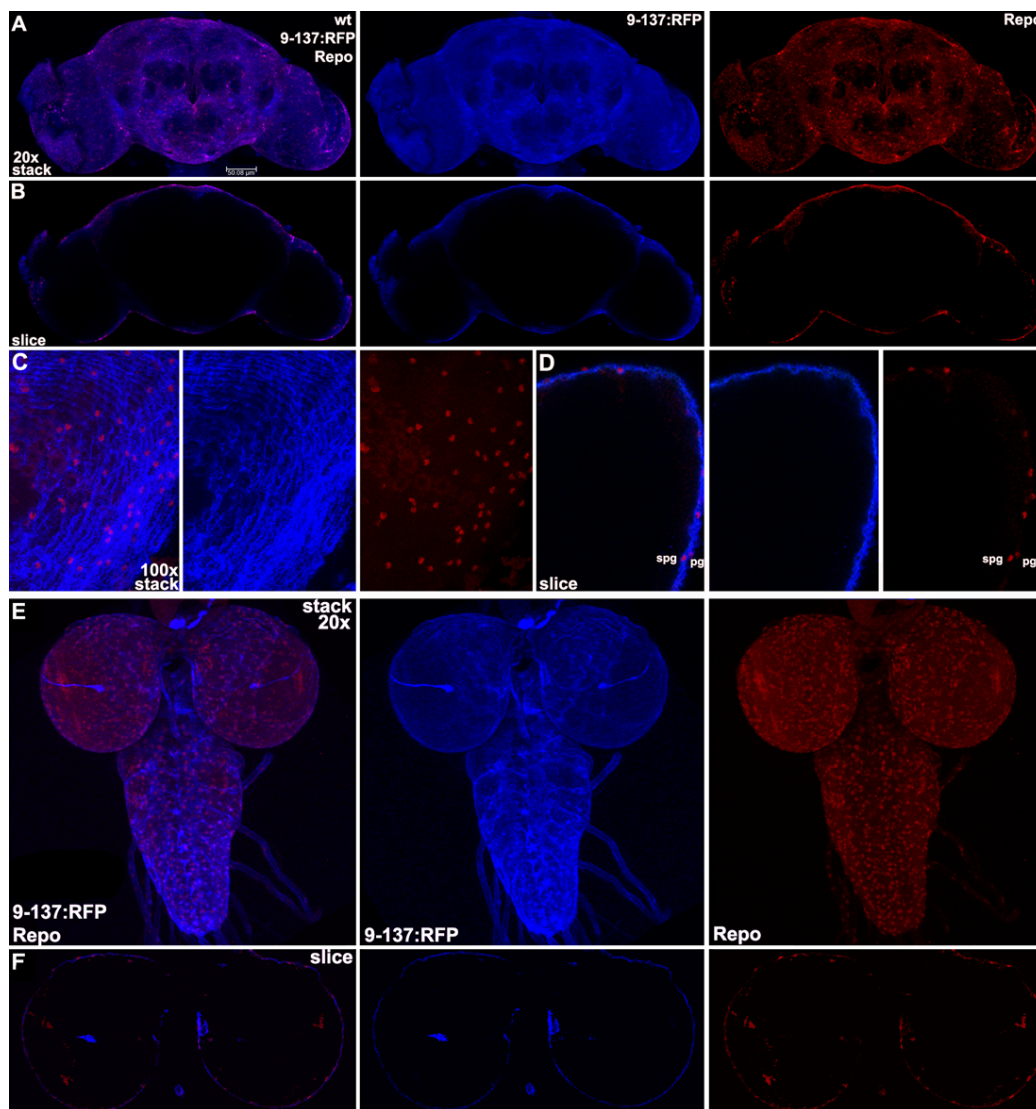


Fig. S4. 9-137.GAL4 driving UAS.CD8-RFP is BBB specific in adult and larval brains. A-D) Ten day old mated female adult brain (n=10) displays 9-137:RFP (blue) with Repo (red). A) Low magnification stack shows 9-137:RFP is uniformly visible. B) Single slice shows that 9-137:RFP is restricted to the BBB. C) High magnification stack of one brain lobe reveals 9-137:RFP is uniformly visible. D) Single slice demonstrates that 9-137:RFP is restricted to BBB glia (apical row of pg and medial row of spg nuclei are indicated). E,F) Female third instar larval brain (n=7) as above. E) Low magnification stack shows 9-137:RFP is uniformly visible. The transformation marker 3xP3-RFP seen in Bolwig's organ in the center of the optic lobes is unrelated to 9:137:RFP in the BBB and does not interfere with morphotrap experiments. F) Single slice of the brain lobes at low magnification indicates that 9-137:RFP is restricted to BBB glia.

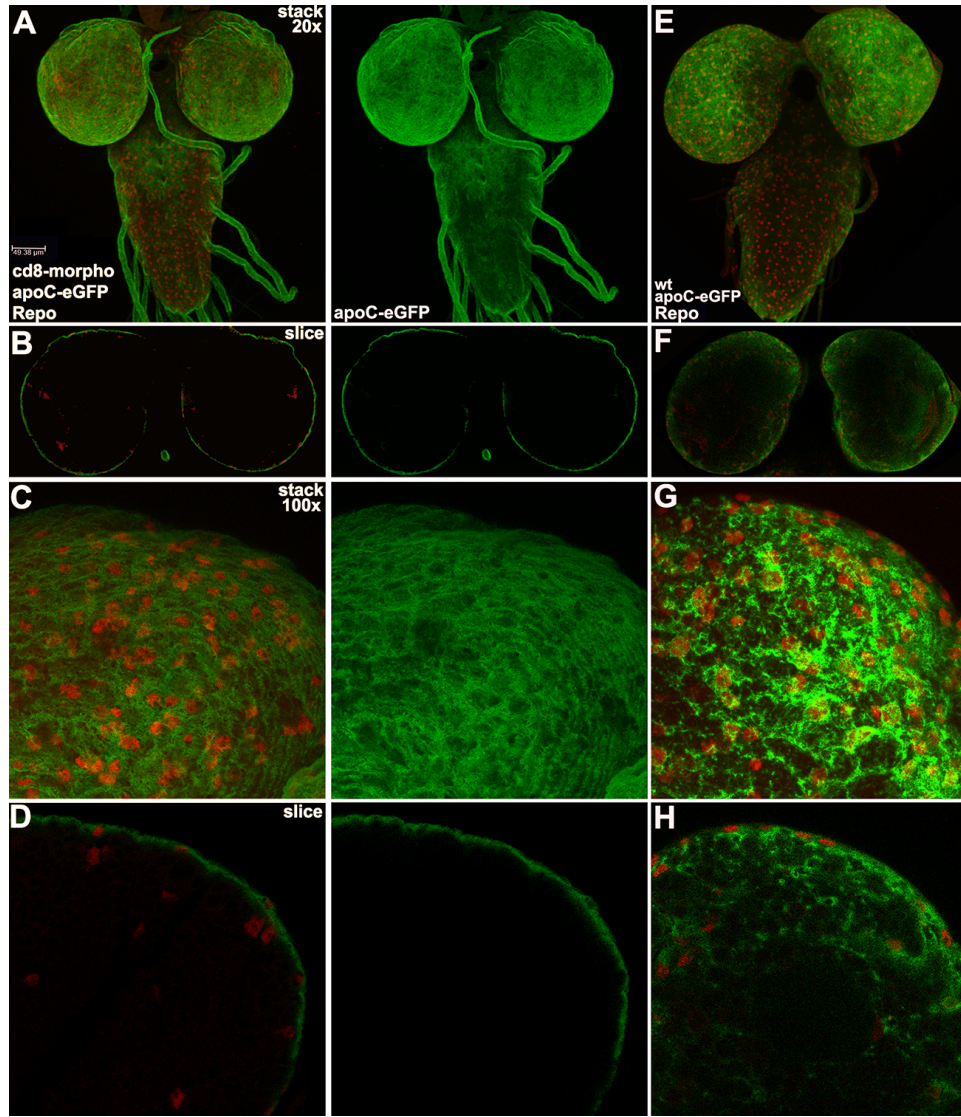


Fig. S5. BBB morphotrap in a third instar larva shows that ApoLppI C-eGFP in the brain is exogenous A-D) Female brain (n=6) with ApoLppI C-eGFP and CD8-morpho as shown in Fig. 8. A) ApoLppI C-eGFP is uniformly distributed on the brain surface. B) Single slice shows that ApoLppI C-eGFP is restricted to the brain surface. C) High magnification stack indicates ApoLppI C-eGFP is uniformly distributed on the brain surface. D) Single slice demonstrates that ApoLppI C-eGFP is restricted to the brain surface. E-H) Female brain (n=4) with ApoLppI C-eGFP but without CD8-morpho. E) ApoLppI C-eGFP is uniformly distributed on the brain surface. F) Single slice shows ApoLppI C-eGFP is present on the surface and inside the brain. G) High magnification stack of one optic lobe reveals ApoLppI C-eGFP is uniformly distributed on the brain surface. H) Single slice of the same lobe reveals ApoLppI eGFP is present on the surface and inside the brain.

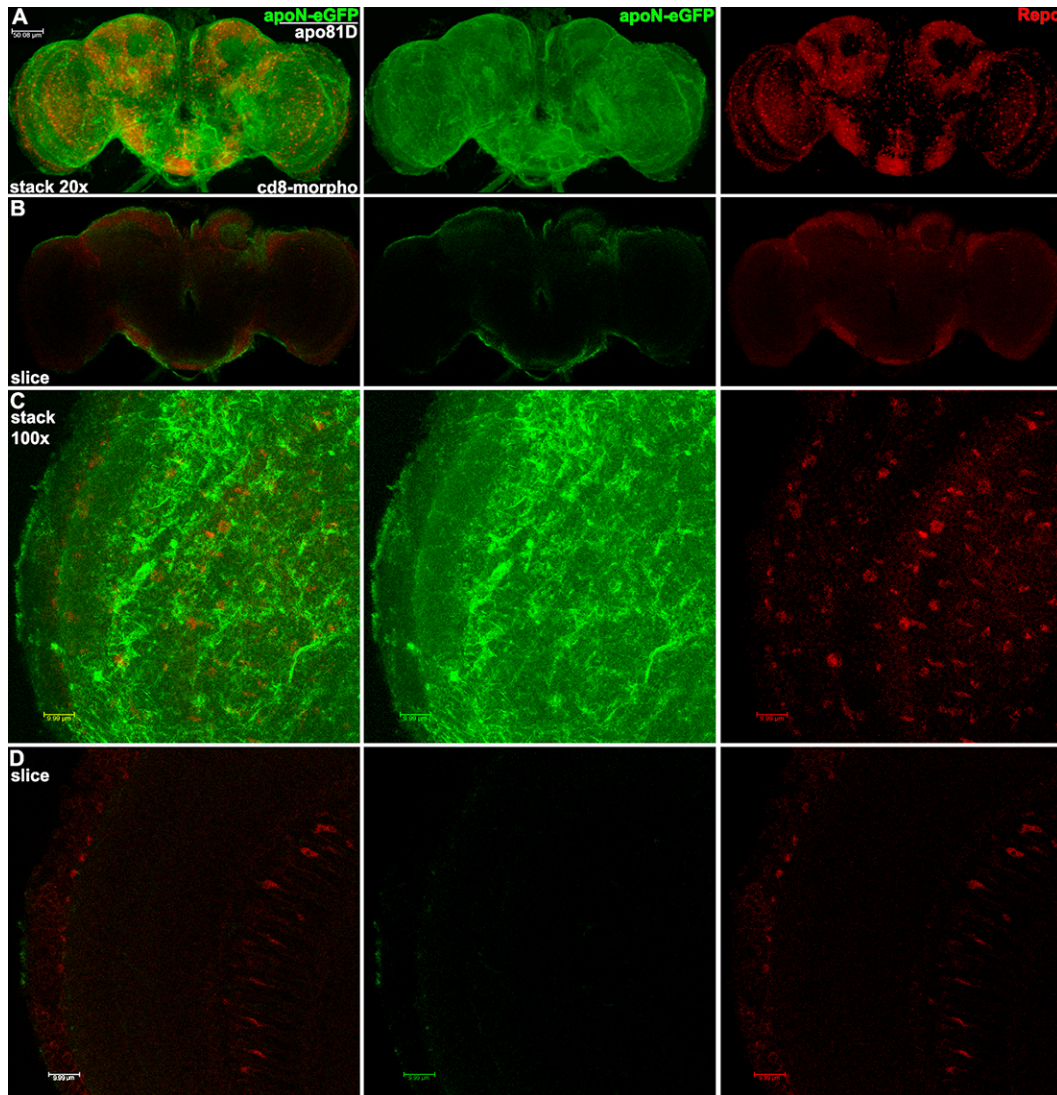


Fig. S6. BBB morphotrap in a one day old unmated adult female shows that ApoLppII N-eGFP in the brain is exogenous. One day old adult virgin female brain (n=3) as shown in Fig. 8 displaying ApoLppII N-eGFP (green) and Repo (red). A) Low magnification stack as two color and individual channels. ApoLppII N-eGFP is uniformly distributed. B) Single slice of the same brain indicates that ApoLppII N-eGFP is restricted to the surface. C) High magnification stack of one brain lobe shows that ApoLppII N-eGFP is uniformly distributed. D) Single slice of the same lobe demonstrates ApoLppII N-eGFP is restricted to the surface.

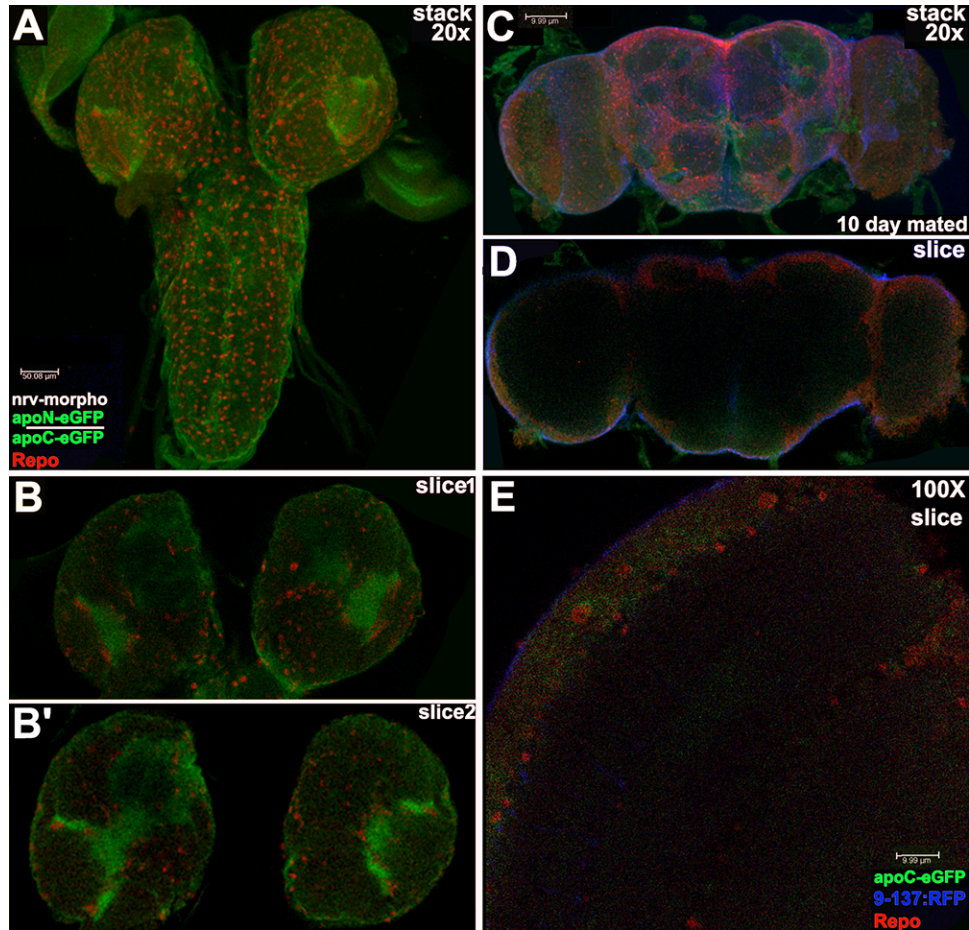


Fig. S7. ApoLpp eGFP is not trapped at the BBB by Nrv-morpho. A,B) Single female third instar larval brain (n=3) expressing Nrv-morpho with 9-137.GAL4 in the BBB that displays ApoLpp eGFP (green) and Repo (red). A) Low magnification confocal stack of the brain and cord (with an eye and wing disk) in two colors demonstrating that Nrv-morpho is not effective at restricting ApoLpp eGFP to the surface. B, B') Low magnification slices of the same brain show internal accumulation of eGFP near glia in the visual system. C-E) Single ten day old adult mated female brain expressing Nrv-morpho with 9-137.GAL4 displaying ApoLppI C-eGFP (green), 9-137:RFP (blue) and Repo (red). D,E) Low and high magnification of the same brain single slices show the wild type accumulation pattern of ApoLppI C-eGFP in the cortex and medulla.

Fig. S8. Alignment of 25 human sequences with ApoB48 and ApoB52 separated plus an outgroup.

HsApoA1	0	-----
HsApoA2	0	-----
HsApoA4	1	-----MFL
HsApoA5	0	-----
HsApoB48	1	-----MDPPRPALLALLALPALLLLLLLAGARAEEMELENVSLVCPKDATRFKHLRKYTYNYEAESSSGVPGTADSR
HsApoB52	1	FDQYIKDSYDLHDLKIAIANIIDEIIEKLKSLDEHYHIRVNLVKTIDHLHLFIENIDFNKSGSSTASWIQNVDTKYQIRIQIEKLQQLK
HsApoC1	0	-----
HsApoC2	0	-----
HsApoC3	0	-----
HsApoC4	0	-----
HsApoD	0	-----
HsApoE2	0	-----
HsApoF	0	-----
HsApoH	0	-----
HsApoJ	1	-----MM
HsApoL1	1	-----MEGAALLRVSVLCIWM
HsApoL2	0	-----
HsApoL3	0	-----
HsApoL4	0	-----
HsApoL5	0	-----
HsApoL6	0	-----
HsApoM	0	-----
HsApoO	0	-----
HsApoOL	0	-----
HsMTTP	1	-----MILLAVLFLCFISSYSASVKGHTTGLSLNDR
HsApoA1	1	-----MSKDLE-----
HsApoA2	0	-----
HsApoA4	4	KAVVLTALVAVAGARAESADQVATVMWDYFSQLSNNAKEAVEHLQKSELTQQLNALFQDKLGEVNTYAGDLQKKLVPFATELHERLAK
HsApoA5	1	-MASMAAVLTWALALLSAFSATQARKGFWDYFSQTSQDGRVEQIHQQKMAREPATL-----KDSLEQDLNNMNFLEKLRLPLSGS
HsApoB48	73	ATRINCKVELEVPQLCSFILKTSQCTLKEVYGFNPEGKALLKKTKNSEEFAAAMSRVELKLAIEGKQVFLYPEKDEPTYILNIKRGII
HsApoB52	91	RHIQNIDIQHLAGKLGKQHIEAIDVRVLLDQLGTTISFERINDILEHVKHVFVINLIGDFEVAEKINAFRAKVHELIEREYVDQIQVLM
HsApoC1	0	-----
HsApoC2	0	-----
HsApoC3	1	-----MQPRVLLVVALLAL-----
HsApoC4	0	-----
HsApoD	1	-----MVMLLLLLSALAGLFGAAEGQAFHLGKCPNPPVQENFDVNKY--LGRWYEIEKIPTTFENGRCIQ-----ANYSLMEN
HsApoE2	1	-----MKVLWAALLVTFLAGCQAKVEQAVETEPEPELRQQTEWQSGQWELALGRFWDYLRWVQTLSEQVQEELLSSQVTQELRALMDE
HsApoF	1	-MTGLCGYSAPDMRGLRLIMIPVELLLCYLLHLPVDATSYGKQTNVLMHFPLSLESQ-----TPSSDPLSCQFLHPKSLP
HsApoH	1	-----MISPVLIILFSSFLCHVAIAGRTCPKPDLPFSTVVPLKTF-----YEPGEEITYSCKP
HsApoJ	3	KTLLL FVGLLL TWESGQVLGDQTVSDNELQEMSNQGSKYVNKEIQNAVNGVKQIKTLIEKTNEERKTLLSNLEEAKKKKEDALNETRESE
HsApoL1	18	ALFLGVGVRAEEAGARVQQNVPSGTDGDPQSKPLGDWAAGTMDPESSIFIEDAIKY-----FKEKVSTQ
HsApoL2	1	-----MNPESSIFIEDYLYK-----FQDQVSRE
HsApoL3	1	-----MDSEKKRFTEEATKY-----FRERVSPV
HsApoL4	1	-----MGSWVQLITSVGVQQNHPGWTVAGQFQEKRFTEEIVIEY-----FQKKVSPV
HsApoL5	1	-MPCGKQGNLQVPGSKVLPGLGEGCKEMWLRKVIYGGVEVWGKSPPEFPLVNLCSWKINN-----
HsApoL6	1	-----MDNQAERESEAGVGLQRD-----
HsApoM	1	-----MFHQIWAALLYFY-----
HsApoO	1	-----MFKVIQRSVGPASLSLLTFKVYAAPKKDSPKNSVKVDELSLY-----
HsApoOL	1	-----MAAIRMGLTTMPAGLIYASVSVHAAKQEEKKQLVKPEQLPIY-----
HsMTTP	33	LYKLTYSTEVLLDRGKGKLDQSVGYRISSNVDAVLLWRNPDGDDQLIQITMKDVNVENVNQQRGEKSIFKGKSPSKIMKENLEALQRP
HsApoA1	6	-----
HsApoA2	0	-----
HsApoA4	94	DSEKLKEEIGKELE-----
HsApoA5	81	EAPRLPQDPVGMRRQLQEELE-----
HsApoB48	163	ALLVPPETEAKQVLFLDTVYGNCSHTFTVKTRKGNVATEISTERDLGQCDRFKPIRTGISPLALIKGMTRPLSTLISSSQSCQYTLDAK
HsApoB52	181	LVELAHQYKLKETIQKLSNVLQVQKIDYFEKLVGFIDDAVKKLNELSFKTFIEDVNKFLDMLIKKLKSFYDHFVDETDNKIREVTQRL
HsApoC1	0	-----
HsApoC2	0	-----
HsApoC3	14	-----
HsApoC4	0	-----
HsApoD	71	GKIKVL-----
HsApoE2	85	TMKELKAYKSELEEQLTPVAE-----
HsApoF	75	GF-----
HsApoH	54	GY-----
HsApoJ	93	TKLKELPGVCNETMMALWEECKPCLKQ-----
HsApoL1	83	NLLLLLTDNEAWNGFVAAAELPR-----
HsApoL2	24	NLLQLLTDDEAWNGFVAAAELPR-----
HsApoL3	24	HLQILLTNNEAWKRFVTAELPR-----
HsApoL4	48	HLKILLTSDEAWKRFVRAELPR-----
HsApoL5	61	-----
HsApoL6	18	-----
HsApoM	13	-----
HsApoO	43	-----
HsApoOL	44	-----
HsMTTP	123	TLLHLIHGKVKEFYSYQNEAVAIENIKRGLASLFQTQLSSGTTNEVDISGNCKVITYQAHQDKVIKIKALDSCKIARSGFTTPNQVLGVSS

HsApoA1	6	-----	
HsApoA2	0	-----	
HsApoA4	107	-----	
HsApoA5	101	-----	
HsApoB48	253	RKHVAAEAIckeQHlFLPFSYKNKYGMVAQVTQTlKLEdTPKINSRFFGEGTKKMGLAFESTKSTSPPKQAEAVLKTlQELKKLTISEQNl	
HsApoB52	271	NGEIQALELPQKAEALKlFLEETKATVAVYLESLQDTKITLIINWLQEALSSASLAHMKAKFRETLedTRDRMYQMDlQQELQRYLSLVG	
HsApoC1	0	-----	
HsApoC2	0	-----	
HsApoC3	14	-----	
HsApoC4	0	-----	
HsApoD	77	-----	
HsApoE2	105	-----	
HsApoF	76	-----	
HsApoH	55	-----	
HsApoJ	119	-----	
HsApoL1	105	-----	
HsApoL2	46	-----	
HsApoL3	46	-----	
HsApoL4	70	-----	
HsApoL5	61	-----	
HsApoL6	18	-----	
HsApoM	13	-----	
HsApo0	43	-----	
HsApo0L	44	-----	
HsMTTP	213	KATSVTTYKIEDSFVIaVLAEEThNFGLNFLQTIKGIvSKQKLElKtTEAGPRlMSGKQAAAIKAVDSKYTAIPVg-----	
HsApoA1	6	-----	-EVKAKVQPYLDDFQKKWQ
HsApoA2	0	-----	
HsApoA4	107	-----	-ELRARLLPHANEVSQKIG
HsApoA5	101	-----	-EVKARLQPYMAEAHELvG
HsApoB48	343	QRANLfnKlVTElRGLSDEAVTSLLPQLIEVSSPITlQALVQCGQPQCSTHIlQWLKRvHANPLlI-----	-DVVTYlVALIPEPSAQQL
HsApoB52	361	QVYSTLVTYISDWWTLAAKNLTDFAEQYSIQDWAKRMKAlVEQGFtVPEIKtIlGTMPAFEVSLQALQKATfQTPDFIVPLTDLRIPSVQ	
HsApoC1	0	-----	
HsApoC2	0	-----	
HsApoC3	14	-----	
HsApoC4	0	-----	
HsApoD	77	-----	-NQELRADGTvNQIEGEAT
HsApoE2	105	-----	-ETRARLSKELQAAQARlG
HsApoF	76	-----	-SHMAPlPKFlVSLALRNA
HsApoH	55	-----	-VSRGGMRFICPlTGLWP
HsApoJ	119	-----	-TCMKFYARVCRSGSGLvG
HsApoL1	105	-----	-NEADELRKAlDNLARQMI
HsApoL2	46	-----	-DEADELRKAlNKLASHMV
HsApoL3	46	-----	-DEADAlYEAlKKLRtYAA
HsApoL4	70	-----	-EEADAlYEAlKNLTpyVA
HsApoL5	61	-----	-LMSTVHSDEAGMlSYFlF
HsApoL6	18	-----	-EDDAPlCEDVELQDGDLS
HsApoM	13	-----	-GIILNSIYQCPEHSQlTT
HsApo0	43	-----	-SVPEGQSKYVEEARSQLE
HsApo0L	44	-----	-TAPPlQSKYVEEQPGHlQ
HsMTTP	291	-----	-QVFQSHCKGCPSlSELWR
HsApoA1	25	EEMELyRQKVEPlRAEL-----	-QEGARQKLHElQEKLSPlGEE-----
HsApoA2	1		-MKLLAATVLLlTICS-----
HsApoA4	126	DNLRELQQRLEPYADQLRTQVSTQ-----	-AEQLRRQLTPYAQRMERVLRE-----
HsApoA5	120	WNLEGLRQQLKPYTMDL-----	-MEQVALRVQELQEQLRVVGED-----
HsApoB48	427	REIFNMARDQRSrATLYAlSHAVNNYHKtN-PTGTQELlDIANYlMEQIQDDCTGDEDYTYlLRVIGNMGQTMEQLTPELKSSIlKCVQ	
HsApoB52	451	INFKDLKNIKIPSRFSTPEFTIlNTFHIPSFTIDfVEMKVKIIRtIDQMLNSELQWPVPDIYLRDLKVEDIPlARITlPDFRlPEIAIPE	
HsApoC1	1	-----	-MRLfLSlPVlVVVlSIVLEG-----
HsApoC2	1	-----	-MGTRlLPAlfVLlVLGfE-----
HsApoC3	14	-----	-LASARASEADASlLSFMQGY-----
HsApoC4	1	-----	-MSLLRNRLQAlPALClC-----
HsApoD	96	PVNlTEPAKlEVKfSWfM-----	-PSAPYWIlATDYENYAlVYSC-----
HsApoE2	124	ADMEDVCGRlVQYRGEVQAMlGQS-----	-TEELRVRLASHLRKlRKlRLR-----
HsApoF	95	LEEAGCQADVWAlQLQlY-----	-RQGGVNATQVlIQHlRGLQKG-----
HsApoH	74	INTlKCTPRVCPfAGlE-----	-NGAVRYTTfEYPNTISfSCNT-----
HsApoJ	138	RQlEEfLNQSSPFYfWMNGDRIDSlLENDRQ-----	-QTHMLDVMQDHfSRASSIIDE-----
HsApoL1	124	MKDKNWHDKGQQYRNWfLKE-----	-FPRLKSElEDNIRRLRALADG-----
HsApoL2	65	MKDKNRHDKDQQRQWfLKE-----	-FPRLKRElEDHlRKlRALAE-----
HsApoL3	65	IEDEYVQKDEQfREWfLKE-----	-FPQVKRKlQESIEKlRALANG-----
HsApoL4	89	IEDKDMQQKEQQfREWfLKE-----	-FPQlRWKlQESIERlRVIANE-----
HsApoL5	80	EELMRCDKDSMPDGnlSEEEKlFlSY-----	-FPlHKfELEQNIKELNTlADQ-----
HsApoL6	37	PEEKlFlRE-----	-FPRLKEDlKGNIIDKlRALADD-----
HsApoM	32	LGVDGKEfPEVHLGQWY-----	-FIAGAAPtKEELATfDPVDNI-----
HsApo0	62	ESISQLRHYPEYTTWCQETYSQT-----	-KPKMQSLVQWGLDSYDYLQNA-----
HsApo0L	63	MGFASIRtATGCYIGWCKGVYfVf-----	-KNGIMDTVQfGKDAYVYlKNP-----
HsMTTP	310	STRKYLQPDNLsKAEAVRNfLAF-----	-IQHLRTAKKEElQlLKMenK-----

HsApoA1	62	-----
HsApoA2	15	-----
HsApoA4	170	-----NADSLQASLRPHADELKAKID
HsApoA5	157	-----TKAQLLGGVDEA
HsApoB48	516	STKPSLMIQKAAIQALRKMEPKDKDQEVLLQTFLLDDASPGDKRLAAYLMLMRSPSQADINKIVQILPWEQNEQVKNFVASHIANILNSEE
HsApoB52	541	FIIPTLNLNDFQVPDLHIPEFQLPHISHTIEVPTFGKLYSILKIQSPLFTLDANADIGNGTTSANEAGIAASITAKGESKLEVLNFDQFA
HsApoC1	20	-----
HsApoC2	19	-----
HsApoC3	35	-----
HsApoC4	17	-----
HsApoD	135	-----
HsApoE2	168	-----
HsApoF	133	-----RSTERNVSVEALASA-
HsApoH	112	-----GFYLNAGDSAKCTEEGKWSPE
HsApoJ	189	-----LFQDRFFTREPQDTHYHLPFSLPHRRPHFFFPK
HsApoL1	164	-----VQKVHKGTTIANVVS GS
HsApoL2	105	-----VEQVHRGTTIANVVS NS
HsApoL3	105	-----IEEVHRGCTISNVVSSS
HsApoL4	129	-----IEKVHRGCVIANVVS GS
HsApoL5	126	-----VDTTHELLTKTSLVASS
HsApoL6	66	-----IDKTHKKFTKANMVATS
HsApoM	69	-----
HsApoO	106	-----
HsApoOL	107	-----
HsMTTP	353	-----EVL PQLVDAV TSAQTS DSLEAILDFLDFKSDS
HsApoA1	62	-----
HsApoA2	15	-----
HsApoA4	192	QNVEE-----
HsApoA5	170	WALLQG-----
HsApoB48	606	LDIQDLKKLVKEALKESQLPTVMDFRKFSRNYQLYKSVSLPSLD-
HsApoB52	631	NAQLSNPKINPLALKESVKFSSKYLRTHEHGSEMLFFGNAIEGKSNTVASLHTEKNTLELSNGVIVKINNQLTLDSENTKYFHKLNI PKLDF
HsApoC1	20	-----
HsApoC2	19	-----
HsApoC3	35	-----
HsApoC4	17	-----
HsApoD	135	-----
HsApoE2	168	-----
HsApoF	148	-----
HsApoH	134	LPVCAP-----
HsApoJ	223	SRIVR-----
HsApoL1	182	LSISSGILT-----
HsApoL2	123	VGTTSGILT-----
HsApoL3	123	TGAASGIMSL-----
HsApoL4	147	TGILSV-----
HsApoL5	144	SGAVSGVMNI-----
HsApoL6	84	TAVISGVMSL-----
HsApoM	69	-----
HsApoO	106	-----
HsApoOL	107	-----
HsMTTP	386	SIILQERFL-----
HsApoA1	62	-----
HsApoA2	15	-----
HsApoA4	196	-----LKGR LTPYADEFKVKIDQT-----
HsApoA5	175	-----LQSRVVHHTGRFKELFHPY-----
HsApoB48	649	-----PASAKIEGNL-----IFDPNNYLPKESMLKTTLTAFGFASADLIEIGLEGKGFEPTLEA
HsApoB52	721	SSQADLRNEIKTLLKAGHIAWTSSGKGSWKWACPRFSDEGTHESQISFTIEGPLTSFGLSNKINSKHLRVNQNLVYESGSLNFSKLEIQS
HsApoC1	20	-----
HsApoC2	19	-----
HsApoC3	35	-----
HsApoC4	17	-----VLVLACI-----
HsApoD	135	-----TCIIQLFHVDFAWILARNP-----
HsApoE2	168	-----DADDLQKRLAVY-----
HsApoF	148	-----LQLLAREQQSTGRVGRSLP-----
HsApoH	139	-----IICPPPSIPTFATLRVYKP-----SAGNNS
HsApoJ	227	-----SLMPFSPYEPLNFHAMFQP-----
HsApoL1	191	-----VGMGLAPFTEGGSLVLLEP-----GMELGI
HsApoL2	132	-----LGLGLAPFTEGISFVL LDT-----GMGLGA
HsApoL3	132	-----AGLV LAPFTAGTSLALTAA-----GVGLGA
HsApoL4	152	-----IGVMLAPFTAGLSLSITAA-----GVGLGI
HsApoL5	153	-----LGLALAPVTAGGSLMLSAT-----GTGLGA
HsApoL6	93	-----LGLALAPATGGGSLLLSTA-----GQGLAT
HsApoM	69	-----VFNMAAGSAPMQLHLRATIR-----
HsApoO	106	-----PPGFFPRLGVIGFAG-----
HsApoOL	107	-----PRDFLPKMGVITVSGL-----
HsMTTP	394	-----YACGFASHPN EELLRALISKFGSIGSSDIRETVMIITGTLVRK

HsApoA1	62	-----
HsApoA2	15	-----
HsApoA4	215	-----VEELRRSLAPY-----
HsApoA5	194	-----
HsApoB48	704	LFGKQGFFPDSVNKALYWVNGQVPDGVSKVLVDHFGYTKDDKHEQDMVNGIMLSVEKLIKDLKSKEVPEARAYLRILGEELGFASLHDLQ
HsApoB52	811	QVDSQHVGHSVLTAKGMALFGEKGAEFTGRHDAHLNGKVIIGTLKNSLFFSAQPFETASTNNEGNLKVRFPLRLTGKIDFLNNYALFLSP
HsApoC1	20	-----
HsApoC2	19	-----
HsApoC3	35	-----
HsApoC4	24	-----
HsApoD	154	-----NLPPETVDS-----
HsApoE2	180	-----
HsApoF	167	-----
HsApoH	165	LY-----RDTAVFECLPQHAMFG-----
HsApoJ	246	-----FLEMIHEAQQAMDIHFHSPAFAQHPPTFEFIREGD-----
HsApoL1	217	TA-----ALTGITSSTMDYGK-----
HsApoL2	158	AA-----AVAGITCSVVELVN-----
HsApoL3	158	AS-----AVTGITTSSIVEHSY-----
HsApoL4	178	AS-----ATAGIASSIVENTY-----
HsApoL5	179	AA-----AITNIVTNVL-----
HsApoL6	119	AA-----GVTSIVSGTLERSK-----
HsApoM	89	-----
HsApoO	121	-----
HsApoOL	123	-----
HsMTTP	439	LCQNEGCKLKAVVEAKKLILGGLKAEKKEDTRMYLLALKNALLPEGIPSLCLKYAEAGEGPISHLATTALQRYDLPFITDEVKKTLNRIY

HsApoA1	62	-----
HsApoA2	15	-----
HsApoA4	226	-----
HsApoA5	194	-----
HsApoB48	794	LLGKLLLMGARTLQGIPQMIGEVIRKGSKNDFFLHYIFMENAFELPTGAGLQLQISSSGVIAPGAKAGVKLEVANMQAELVAKPSVSVVEF
HsApoB52	901	SAQQASWQVSARFNQYKYNQNFSAAGNNENIMEAHVGINGEANLDFLNIPLTIPEMRLPYTIITTPPLKDFSLWEKTGLKEFLKTTKQSF
HsApoC1	20	-----
HsApoC2	19	-----
HsApoC3	35	-----
HsApoC4	24	-----
HsApoD	163	-----
HsApoE2	180	-----
HsApoF	167	-----
HsApoH	182	-----
HsApoJ	279	-----
HsApoL1	232	-----
HsApoL2	173	-----
HsApoL3	173	-----
HsApoL4	193	-----
HsApoL5	190	-----
HsApoL6	134	-----
HsApoM	89	-----
HsApoO	121	-----
HsApoOL	123	-----
HsMTTP	529	HQNRKVHEKTVRTAAAAIILNNNPSYMDVKNILLSIGELPQEMNKYM-----

HsApoA1	62	---MRDRARAHVDALRTHLAPYSDELR-----
HsApoA2	15	-LEGALVRRQAKEPCVESLSVQ-----
HsApoA4	226	-AQDTQEKLNHQLEGLTFQMKNNAEELK-----
HsApoA5	194	-AESLVSGIGRHHVQELHRSVAPHAPAS-----
HsApoB48	884	VTNMGIIIPDFARSGVQMNTNFFHESGLEAHVALKAGKLKFIIPSPKRPVKLLSGGNTLHLVSTTKTEVIPPLIENRQSWSVCKQVFPGL
HsApoB52	991	LSVKAQYKKKNKHRHSITNPLAVLCEFISQSIKSFDRHFENRNNALDFVTKSYNETKIKFDKYKAEKSHDELPRTFQIPGYTVPVNVVEV
HsApoC1	20	-----PAPAQGTDPDVSSALDKLKEFGN-----
HsApoC2	19	-VQGTQPPQQDEMPSPFTLTQVKESLSS-----
HsApoC3	35	-MKHATKTAKDALSSVQESQ-----
HsApoC4	24	-GACQPEAQEGTLSPPPCLKMSRWSLVR-----
HsApoD	163	-LKNILTSNNIDVKKMTVTDQVNCPKLSQ-----
HsApoE2	180	-QAGAREGAERGLSAIRERLGPLVEQGR-----
HsApoF	167	-TEDCENEKEQAVHNVVQLLPVGVT-----
HsApoH	182	-NDTITCTTHGNWTKLPECREVKCPF-----
HsApoJ	279	-DDRTVCREIRHNSTGCLRMKDQCDKCR-----
HsApoL1	232	-KWWTQAQAHDLVIKSLDKLKEVREFLG-----
HsApoL2	173	-KLARAQAARNLDQSGTNVAKVMKEFVG-----
HsApoL3	173	-TSSAAEAESRLTATSIDRLKVFKEVMR-----
HsApoL4	193	-TRSAELTASRLTATSTDQLEALRDILH-----
HsApoL5	190	-ENRSNSAARDKASRLGPLTTSHEAFGGINW-----
HsApoL6	134	-NKEAQARAEDILPTYDQEDREDEEEKA-----
HsApoM	89	-MKDGLCVPRKWIYHLTEGSTDLRTEGR-----
HsApoO	121	-----
HsApoOL	123	-AGLVSARKGSKFKKITYPGLATLGAT-----
HsMTTP	575	-LAIVQDILRFEMPASKIVRRVLKEMVAHNYDRFSRSG-----

HsApoA1	86	-----QRLAA-----
HsApoA2	36	-----
HsApoA4	253	-----ARISASAE-----
HsApoA5	221	-----ARLSRCVQLSRKLTAKALHAR-----
HsApoB48	974	NYCTSGAYSNASSTDSASYPLTGDTRLELELRPTGEIEQYSVSATYELQREDRALVDTLKFVTQAEGAKQTEATMTFKYNRQSM-----
HsApoB52	1081	SPFTIEMSAFGYVFPKAVSMPSFSILGSDVRVPSYTLILPSLELPVLHVPRNLKLSLPDF-KELCTISHIFIPAMGNITYDFSFKSSVIT
HsApoC1	42	-----
HsApoC2	46	-----
HsApoC3	54	-----
HsApoC4	51	-----
HsApoD	192	-----GRMKE-----
HsApoE2	207	-----AKEPCVESLVSQ-----
HsApoF	192	-----VRAATVGSAGQP-----
HsApoH	207	-----YNLGTALYYATQN-----
HsApoJ	306	-----PSRPDNGFVNYPAKPTLYYKDK-A-----
HsApoL1	259	-----EILSVDCSTNNPSQAKLRRELDE-----
HsApoL2	200	-----ENISNFLSLAGN-----
HsApoL3	200	-----GNTPNVLTIVDN-----
HsApoL4	220	-----DITPNLLSLLNN-----
HsApoL5	220	-----DITPNVLSFALD-----
HsApoL6	161	-----SEIEAAGFCVNK-----
HsApoM	116	-----DYVTAAGKIIYNLRN-----
HsApoO	121	-----PDMKTELFSSSCPGGIM-----
HsApoOL	150	-----VCYPVQSVIIAKVTAKKVYA-----
HsMTTP	612	-----SSSAYTGYIERSPRASTYSLDI-----
HsApoA1	91	-----RLEALKENG-----
HsApoA2	36	-----YFQTVTDYGK-----DLMEKVK-----
HsApoA4	262	-----LRQLAPLAE-----DVRGNLR-----
HsApoA5	245	-----IQQNLDQLRE-----ELSRFA-----
HsApoB48	1058	-----TLSSEVQIPDFDVLGTILRVNDESTEGKTSYRLTLDIQNKKITEVALMGHLSCDT-----
HsApoB52	1170	LNTNAELFNQSDIVAHLLSSSSVIDALQYKLEGTTRLTRKRGL-----KLATALSLSNKFVEGSHNSTVSLTTKNMEVSVATTTKAQIPIL
HsApoC1	42	-----TLEDKAR-----ELISRIK-----
HsApoC2	46	-----YWESAKTAAQ-----NLYEKTY-----
HsApoC3	54	-----VAQQARGWVT-----DGFSSLK-----
HsApoC4	56	-----LLETVVNRTR-----DGWQWFW-----
HsApoD	203	-----YFQTVTDYGK-----DLMEKVK-----
HsApoE2	220	-----LQERAQAWGE-----RLRARME-----
HsApoF	205	-----CLGKARERGR-----DGAIDL-----
HsApoH	230	-----TFGCHDGYSL-----DGPREE-----
HsApoJ	329	-----SLQVAERLTR-----KYNELLK-----
HsApoL1	271	-----TYQLTRGIGK-----DIRALRR-----
HsApoL2	212	-----WYQVTQGIGR-----NIRAIRR-----
HsApoL3	212	-----YYEATQTIGS-----EIRAIRQ-----
HsApoL4	232	-----FDEATKMIAN-----DVHTLRR-----
HsApoL5	232	-----CVKAIQGIK-----DLHAYQM-----
HsApoL6	176	-----TLKYAKKNVR-----AFWKLR-----
HsApoM	133	-----LNETGQGYQR-----
HsApoO	121	-----LIGLLLARGS-----KIKKLVY-----
HsApoOL	170	-----TSQQIFGAVK-----SLWTKSS-----
HsMTTP	635	-----LYSGSGILRRSNLIFQYIG-----
HsApoA1	101	-----
HsApoA2	53	-----
HsApoA4	279	-----
HsApoA5	262	-----
HsApoB48	1115	KEERKIKGVISIPRLQAEARSEILAHWSPAKLLLQMDSSATAYGSTVSKRVAWHYDEEKIEFEWNTGTNVDTKKMTSNFPVDSLSDYPKSL
HsApoB52	1257	RMNFKQELNGNTKSKPTVSSSMEFKYDFNSSMLYSTAKGAVDHKLSLESLSYFSIESSTKGDVKGSVLSREYSGTIASEANTYLNLSKST
HsApoC1	56	-----
HsApoC2	63	-----
HsApoC3	71	-----
HsApoC4	73	-----
HsApoD	219	-----
HsApoE2	237	-----
HsApoF	222	-----
HsApoH	247	-----
HsApoJ	346	-----
HsApoL1	288	-----
HsApoL2	229	-----
HsApoL3	229	-----
HsApoL4	249	-----
HsApoL5	248	-----
HsApoL6	193	-----
HsApoM	143	-----
HsApoO	138	-----
HsApoOL	187	-----
HsMTTP	655	-----

HsApoA1	101	-----
HsApoA2	53	-----
HsApoA4	279	-----
HsApoA5	262	-----
HsApoB48	1205	HMYANRLLDHRVPQTDMTFRHVGSKLIVAMSSWLQKASGSLPYTQTLQDHLNSLKEFNLQNMGLPDFHIPENLFLKSDGRVKYTLNKNSL
HsApoB52	1347	RSSVKLQGTSKIDDIWNLEVKENFAGEATLQRIYSLWEHSTKNHLQLEGLFFTNGEHTSKATLELSPWQMSALVQVHASQPSSFHDFPD
HsApoC1	56	-----
HsApoC2	63	-----
HsApoC3	71	-----
HsApoC4	73	-----
HsApoD	219	-----
HsApoE2	237	-----
HsApoF	222	-----
HsApoH	247	-----
HsApoJ	346	-----
HsApoL1	288	-----
HsApoL2	229	-----
HsApoL3	229	-----
HsApoL4	249	-----
HsApoL5	248	-----
HsApoL6	193	-----
HsApoM	143	-----
HsApoO	138	-----
HsApoOL	187	-----
HsMTTP	655	-----

HsApoA1	101	-----ARLAEYHAKATEHLSTLSEKAKPA-----
HsApoA2	53	-----SPELQAEAKSY-----
HsApoA4	279	-----GNTEGLQKSLAELGGHLDQQVEEFRRRVEPYGENFNKALVQQ-----
HsApoA5	262	-----GTGTEEGAGDPDQMLSEEVQRQLQAFRQDTYLQIAAF-----
HsApoB48	1295	KIEIPLPFGGKSSRDLMLETVRTPALHFKSVGFHLPSTREFQVPTFTTIPKLYQLQVPLLGVLDLSTNVYSNLWNWSASYSGGNTSTDHFS
HsApoB52	1437	GQEVALNANTKNQKIRWKNEVRIHSGSFQSQVELSNDQEKAHLDIAGSLEGLRFLKNIILPVYDKSLWDFLKLDDVTTSIGRRQHLRVST
HsApoC1	56	-----QSELSAKMRLEFPFGHGRAGVCFWVEPWQ-----
HsApoC2	63	-----LPAVDEKLRLDLYSKSTAAMSTYTGI-----
HsApoC3	71	-----DYWSTVKDK-----
HsApoC4	73	-----SPSTFRGMQTYDD-----
HsApoD	219	-----SPELQAEAKSY-----
HsApoE2	237	-----EMGSRTDRDLDEVKEQVAEVRAKLEEQAQQIRLQAEAFQ-----
HsApoF	222	-----YDLLMTMAGMSGGPMGLAISAAKPALRSGVQQLIQYYQDQKDN-----
HsApoH	247	-----CTKLGNWSAMPSCKASCKVPVKKATVVYQGER-----
HsApoJ	346	-----SYQWKMLNTSSLLEQLNEQFNWVSRLANLTQGEDQYYLR-----
HsApoL1	288	-----ARANLQSVPHASASRPRVTEPIAESGEQVERVNEPSILEMSRG-----
HsApoL2	229	-----ARANPQLGAYAPPPHVIGRISAEGGEQVERVVEGPAQAMSRG-----
HsApoL3	229	-----ARARARLPVTTWRISAGSGGQAERTIAGTTRAVSRG-----
HsApoL4	249	-----SKATVGRPLIAWRYVPINVVETLRTRGAPTRIVRVK-----
HsApoL5	248	-----AKSNSGFMAMVKNFVAKRHIPFWTARGVQRAFEGTTLAMTNG-----
HsApoL6	193	-----NPRLANATKRLLTTGQVSSRSRVQKAFAGTTLAMTKN-----
HsApoM	143	-----FLLYNRSPPHPEKCEVEFKSLTSC-----
HsApoO	138	-----PPGFMGLAASLYYPQQAIVFAQVSGER-----
HsApoOL	187	-----KEESLPKPKKTKLGSSEIEVPAKTTHV-----
HsMTTP	655	-----KAGLHGSQVVEIAQGLEALIAATPDEGEENLDSYAGMSAILFDVQ-----

HsApoA1	125	-----
HsApoA2	64	-----
HsApoA4	322	ME-----QLRQKLGPAGDVEGHLSF-----
HsApoA5	299	-----TRAIDQETEE-----
HsApoB48	1385	LRARYHMKADSVVDLLSYNVQSGGETTYDHKNFTTL-----
HsApoB52	1527	AFVYTKNPNGYSFSIPVKVLADKFIIPGLKLNDLNSVLVMPFTFHPFTDLQVPSCKLDFREIQIYKKLRTSSFALNPLTLPVKFPEVDV
HsApoC1	85	-----
HsApoC2	88	-----
HsApoC3	80	-----
HsApoC4	88	-----HLRDLGP-----
HsApoD	231	-----
HsApoE2	277	AR-----
HsApoF	267	-----ISQPETTKEGLRAISDVSD-----
HsApoH	279	-----VKIQEKFKNGMLHGDKVSF-----
HsApoJ	385	-----VTTVASHTSDSDVPSGVTE-----
HsApoL1	332	-----VKLTDVAPVSFFLVLDVVY-----
HsApoL2	271	-----TMIVGAATGGIILLLDVVS-----
HsApoL3	265	-----ARILSATTSGIFLALDVVN-----
HsApoL4	285	-----ARNLGKATSGVLVLDVVN-----
HsApoL5	290	-----AWVMGAAGAGFLLMKDMSS-----
HsApoL6	232	-----ARVLGGVMSAFSLGYDLAT-----
HsApoM	167	-----
HsApoO	165	-----
HsApoOL	216	-----
HsMTTP	701	LRPVTFNNGYSGLM---SKMLSASGDPISVVKGLIL---

HsApoA1	126	LEDLRQGLLPV-----	
HsApoA2	65	FEKSKEQLTPL-----	
HsApoA4	343	LEKDLRDK-----	
HsApoA5	310	VQQQLAPPPG-----	
HsApoB48	1421	SCDGLSRHKFLDSNIKFSHVEKL-----GNNPVSKGLLIFDASSSWGPMASVHLDSSKKKQHLFVKEVKIDGQFRVSSFYAKGT	
HsApoB52	1617	LTQYSQPEDSLIPFFEITVPESQLTVSQFTLPKSVSDGIAALDLNAVANKIADFELPTIIVPEQTIEIPSIKFSVPAGIVIPSQALTAR	
HsApoC1	86	MVQDEQIE-----	
HsApoC2	89	FTDQVLSV-----	
HsApoC3	81	FSEFWDLD-----	
HsApoC4	96	LTKAWFLE-----	
HsApoD	231	FEKSKEQLTPL-----	
HsApoE2	279	LKSWFEPL-----	
HsApoF	287	LEETTTLASFISEV-----	
HsApoH	299	FCKNKEKKCSY-----	
HsApoJ	405	VVVKLFDSDPI-----	
HsApoL1	352	LVYESKHL-----	
HsApoL2	291	LAYESKHL-----	
HsApoL3	285	LVYESKHL-----	
HsApoL4	305	LVQDSL DL-----	
HsApoL5	310	FLQSWKHL-----	
HsApoL6	252	LSKEWKHL-----	
HsApoM	168	LDKAFLLTP-----	
HsApoO	166	LYDWGLRGYIV-----	
HsApoOL	217	LKHSVPLPTL-----	
HsMTTP	734	LIDHSQELQLQ-----	
HsApoA1	136	-----	LESFKVSFLSA-LEEYTK
HsApoA2	75	-----	IKKAGTELVN--FLSYFV
HsApoA4	350	-----	VNSFFSTFKEKESQDKTL
HsApoA5	320	-----	HSFAPEFQQTDSGKVL
HsApoB48	1501	YGLSCQRDPNTGRLNGESNLRFNSSYLQGTNQITGTRYEDGTLSTSTSDLQSGIIKNTASLKYENYELTLKSDTNGKYKNFAT-SNMMDM	
HsApoB52	1707	FEVDSPVYNATWSASLKNKADYVETVLDSTCSSTVQFLEYELNVLGTHKIEDGTLASKTKGTFAHRDFSAEYEEDGKYEGLQEWEGKAHL	
HsApoC1	93	-----	KKTSPGEADNI-PLVTQL
HsApoC2	96	-----	LKGEE-----
HsApoC3	88	-----	PEVRPTSAVAA-----
HsApoC4	103	-----	SKDSLLKKTHS-LCPRLV
HsApoD	242	-----	IKKAGTELVN--FLSYFV
HsApoE2	286	-----	VEDMQRQWAGL-VEKVQA
HsApoF	300	-----	VSSAPYWGWAII-KSYDL
HsApoH	309	-----	TEDAQCIDGTI-EVPKCF
HsApoJ	415	-----	TVTVPVEVSRK-NPKFME
HsApoL1	359	-----	HEGAKSETAEE-LKKVAQ
HsApoL2	298	-----	LEGAKSESAAE-LKKRAQ
HsApoL3	292	-----	HEGAKSASAAE-LRRQAQ
HsApoL4	312	-----	HKGEKSESAAE-LRQWAQ
HsApoL5	317	-----	EDGARTETAEE-LRALAK
HsApoL6	259	-----	KEGARTKFAEE-LRAKAL
HsApoM	177	-----	RNQEACELSNN-----
HsApoO	176	-----	IEDLWKENFQK-PGNVKN
HsApoOL	227	-----	SSEAKTKSEST-SGATQF
HsMTTP	744	---SGLKANIEVQGGLAIDISGAMEFSLWYRESKTRVKNRVTVVITTDITVDSSFVKAGLETSTETEAGLEFISTVQFSQYPF-LVCMQM	
HsApoA1	154	KLNTQ-----	
HsApoA2	92	ELGTQPATQ-----	
HsApoA4	369	SLPELEQQQEQQQEQQEQVQMLAPLES-----	
HsApoA5	339	KLQARLDDLWEDITHSLHDQGHSHLGDP-----	
HsApoB48	1590	TFSKQNA-LLRSEYQADYESLRFFSLLSGSLNSHGLELNADILGTDKINSGAHKATLRIGQDGI STSATTNLKCSLLVLENELNAELGLS	
HsApoB52	1797	NIKSPAFTDLHLRYQDKKGISTSAASPAVGTVMGMDDEDDDFSKWNFFYSPQSSPDKKLTIFKTEL RVRESDEETQIKVNWEEEAASGL	
HsApoC1	111	DLKGVVFRDISESEGETQD-----	
HsApoC2	101	-----	
HsApoC3	99	-----	
HsApoC4	121	CGDKDQG-----	
HsApoD	258	ELGTQPATQ-----	
HsApoE2	304	AVGTS AAPVPSDNH-----	
HsApoF	318	DPGAGSLEI-----	
HsApoH	327	KEHSSLA-FWKTDASDVKPC-----	
HsApoJ	433	TVAEKALQEYRKKHREE-----	
HsApoL1	377	ELEEKLN-ILNNNYKILQADQEL-----	
HsApoL2	316	ELEGKLN-FLTKIHEMLQPGQDQ-----	
HsApoL3	310	ELEENLM-ELTQIYQRLNPCHTH-----	
HsApoL4	330	ELEENLN-ELTHIHQSLKAG-----	
HsApoL5	335	KLEQELD-RLTQHHRHLPQKASQTCSSSRGRAVRGSRVVKPEGSRSPLPVVEHQPR LGPGVALRTPKRTVSAPRMLGHQPAPPAPARK	
HsApoL6	277	ELERKLT-ELTQLYKSLQQKVRSRARGVGKDLTGTCETEAYWKELREHVMMWLWLCVCLCVCVYVQFT-----	
HsApoM	188	-----	
HsApoO	194	SPGTK-----	
HsApoOL	245	MPDPKLM-DHGQSHPEDIDMYSTRS-----	
HsMTTP	831	DKDEAPFRQFEKKYERLSTGRGVYSQKRKESVLAGECFPLHQENSEMCKVVFAPQPDSTSSGWF-----	

HsApoA1	158	-----
HsApoA2	100	-----
HsApoA4	396	-----
HsApoA5	366	-----
HsApoB48	1679	GASMKLTTNGRFREHNAKFSLDGKAALTELSLGSAYQAMILGVDSKNIFNFKVSQEGCLKLSNDMMGSYAEMKFDHTNSLNIAGLSLDFSS
HsApoB52	1887	LTSLKDNVPKATGVLYDYVNKYHWEHTGLTLREVSSKLRRNLQNNAEWVYQGAIHQIDDIDVRFQKAASGTTGTYYQEWKDKAQNLQYQELL
HsApoC1	129	-----
HsApoC2	101	-----
HsApoC3	99	-----
HsApoC4	127	-----
HsApoD	266	-----
HsApoE2	317	-----
HsApoF	326	-----
HsApoH	345	-----
HsApoJ	449	-----
HsApoL1	398	-----
HsApoL2	337	-----
HsApoL3	331	-----
HsApoL4	348	-----
HsApoL5	424	GRQAPGRHRQ-----
HsApoL6	343	-----
HsApoM	188	-----
HsApoO	198	-----
HsApoOL	268	-----
HsMTTP	894	-----

HsApoA1	158	-----
HsApoA2	100	-----
HsApoA4	396	-----
HsApoA5	366	-----
HsApoB48	1769	KLDNIYSSDKFYKQTVNLQLQPYSLVTTLNSDLKYNALDLTNGKLRLEPLKLHVAGNLKGAYQNNEIKHIYAISSAALSASYKADTVAK
HsApoB52	1977	TQEGQASFFQGLKDNVFDGLVRVTQEFHMKVKHLIDSLIDFLNFPFRQFPQKPGIYTREELCTMFIREVGTVLSQVYSKVHNGSEILFSYF
HsApoC1	129	-----
HsApoC2	101	-----
HsApoC3	99	-----
HsApoC4	127	-----
HsApoD	266	-----
HsApoE2	317	-----
HsApoF	326	-----
HsApoH	345	-----
HsApoJ	449	-----
HsApoL1	398	-----
HsApoL2	337	-----
HsApoL3	331	-----
HsApoL4	348	-----
HsApoL5	433	-----
HsApoL6	343	-----
HsApoM	188	-----
HsApoO	198	-----
HsApoOL	268	-----
HsMTTP	894	-----

HsApoA1	158	-----
HsApoA2	100	-----
HsApoA4	396	-----
HsApoA5	366	-----
HsApoB48	1859	VQGVFEFSHRLNTDIAGLASAIDMSTNYNSDSLHFSNVFRSVMAPFTMTIDAHTNGNGKLALWGEHTGQLYSKFLLKAEPLAFTFSHDYKG
HsApoB52	2067	QDLVITLPPFELRKHKLIDVISMYRELLKDLKSKEAQEVFKAIQSLKTTEVLRNLQDLLQFIFQLIEDNIKQLKEMKFTYLINYIQDEINTI
HsApoC1	129	-----
HsApoC2	101	-----
HsApoC3	99	-----
HsApoC4	127	-----
HsApoD	266	-----
HsApoE2	317	-----
HsApoF	326	-----
HsApoH	345	-----
HsApoJ	449	-----
HsApoL1	398	-----
HsApoL2	337	-----
HsApoL3	331	-----
HsApoL4	348	-----
HsApoL5	433	-----
HsApoL6	343	-----
HsApoM	188	-----
HsApoO	198	-----
HsApoOL	268	-----
HsMTTP	894	-----

HsApoA1	158	-----
HsApoA2	100	-----
HsApoA4	396	-----
HsApoA5	366	-----
HsApoB48	1949	STSHHLVSRKSISAALHKKVSALLTPAEQTGTWKLKTQFNNNEYSQDLDAYNTKDKIGVELTGRTLADLTLLDSPIKVPLLLSEPINIID
HsApoB52	2157	FSDYIPYVFKLLKENLCLNLHKFNEFIQNELQEASQELQQIHQYIMALREEYFDPSIVGWTVKYEELEEKIVSLIKNLLVALKDFHSEYI
HsApoC1	129	-----
HsApoC2	101	-----
HsApoC3	99	-----
HsApoC4	127	-----
HsApoD	266	-----
HsApoE2	317	-----
HsApoF	326	-----
HsApoH	345	-----
HsApoJ	449	-----
HsApoL1	398	-----
HsApoL2	337	-----
HsApoL3	331	-----
HsApoL4	348	-----
HsApoL5	433	-----
HsApoL6	343	-----
HsApoM	188	-----
HsApoO	198	-----
HsApoOL	268	-----
HsMTTP	894	-----

HsApoA1	158	-----
HsApoA2	100	-----
HsApoA4	396	-----
HsApoA5	366	-----
HsApoB48	2039	ALEMRAVEKPKQEFFIVAFVKYDKNQDVHSINLPFFETLQEYFERNRQTIIVVLENVQRNLKHINIDQFVRKYRAALGKLPQQANDYLN
HsApoB52	2247	VSASNFTSQLSSQVEQFLHRNIQEYLSILTDPDGKGKEKIAELSATAQEIIKSQAIATKKIISDYHQFQRYKLQDFSDQLSDYYEKFAE
HsApoC1	129	-----
HsApoC2	101	-----
HsApoC3	99	-----
HsApoC4	127	-----
HsApoD	266	-----
HsApoE2	317	-----
HsApoF	326	-----
HsApoH	345	-----
HsApoJ	449	-----
HsApoL1	398	-----
HsApoL2	337	-----
HsApoL3	331	-----
HsApoL4	348	-----
HsApoL5	433	-----
HsApoL6	343	-----
HsApoM	188	-----
HsApoO	198	-----
HsApoOL	268	-----
HsMTTP	894	-----

HsApoA1	158	-----
HsApoA2	100	-----
HsApoA4	396	-----
HsApoA5	366	-----
HsApoB48	2129	FNWERQVSHAKEKL TALT KKYRITENDIQIALDDAKINFNEKLSQLQTYMIQ
HsApoB52	2337	SKRLIDLSIQNYHTFLIYITELLKKLQSTTVMNPYMKLAPGELTIIL
HsApoC1	129	-----
HsApoC2	101	-----
HsApoC3	99	-----
HsApoC4	127	-----
HsApoD	266	-----
HsApoE2	317	-----
HsApoF	326	-----
HsApoH	345	-----
HsApoJ	449	-----
HsApoL1	398	-----
HsApoL2	337	-----
HsApoL3	331	-----
HsApoL4	348	-----
HsApoL5	433	-----
HsApoL6	343	-----
HsApoM	188	-----
HsApoO	198	-----
HsApoOL	268	-----
HsMTTP	894	-----

Fig. S9. Alignment of 11 fly sequences with ApoLpp and ApoLTP separated plus an outgroup.

DmApoLppI	1	-----SIVDDVSKISKYKMYGVKNVQDLNLDVSLKLFSGELAFSLSLGDNIPSS
DmApoLppII	0	-----
DmApoLTPI	1	RKAQEQRASEEEVDEDEDYFEESLEGNKQRKRDVSTTRKQEIDRNVDLSGYKLKYDYNPNRAQFGLRVFGNDLRYFNVES
DmApoLTPII	0	-----
DmCG31659	0	-----
DmCvD	0	-----
DmFabp	0	-----
DmGlaz	0	-----
DmMic26-27	0	-----
DmNlaz	0	-----
DmMtp	0	-----
DmApoLppI	50	LDDIINYFSTSFEEKAKQELSSFEKQFSSHHLFLDSDLAYPTSIGVPLELVAQGF-AATKVDLAVSL---DINAILEQNWQ
DmApoLppII	1	-----MARMKYNIALIGILASVLLTIAVNAENACNLGCPKSDNGLKYIPGNYDYDSFDSI
DmApoLTPI	81	LVEVMALAAKFNPFPQAKNVLSGKEFTYTKSRVFLDASYTVPLAVGLPLAIHAF-GASSIDLRVSG---NLDEMPPPTDW
DmApoLTPII	1	-----MGGLKPQAAIWLLLLIAHTQAVRENPLKDPRICGRPCQDSKSAKF--NYGEQLYKYQY
DmCG31659	1	-----MIKKWIFVPAILYLQSSMAMRAFHGACPSNMATAVG---DLDMDFRFGKW
DmCvD	1	-----MRLKCSVFVYLFILFDAGHAFSIIGLNKQMLYEGNVLVGAKPQD---EGHQAPPTTGW
DmFabp	1	-----MSFVGKKYKLDKSENFDEYMKELGVGLVTRKM-GNSLSP-----TVEVTLEGDTY
DmGlaz	1	-----MMSGQPLGSRVWLLSGVLLVTFAGTDAYGF-GRCPNYPSMP---KFNMSRVLGHW
DmMic26-27	1	-----MLRKTATMGIMAAVAVKAAPEPQKPASSAADCSLVCPSSELPYIG---SLRKTEPKPER
DmNlaz	1	-----MNHSSSHLLLLISVVFAGVVAHAQVP---FPGKCP-DVKLLD---TFDAEAYMGVW
DmMtp	1	-----MENKNKKCLRTLALLLALFLGLLEDGKTALIPNSQQIFKLQNQVILQELGRDSSSAETSY
DmApoLppI	126	KAKYRLKFV---PSVDINANVQIGFNAQVLSTGLRVVSSAHSATGSDITVAVISDGEFNVDELPREKLELINFNVDT
DmApoLppII	56	LTIGASSDV---PNDSDDTSLKVSQSAKIFAKGNCGYTLQLSSVKVTNTKESVEKKILNSIQKPV-----
DmApoLTPI	157	HFDVEGQFK---PSVSDVITTMQTDMFWEQSGIKVKSNLYSNSEL-VAKLKVRGRNLVSFSDLPDKNKEIFSVRSELL
DmApoLTPII	56	TVAVRTEFA---GSGDNSSDLLKSDLEIFFPKCEGYLRINDAKLYDTLDELNDNESDSSEKT-----
DmCG31659	46	YTHSIYPHL---SLRVEKCQST-----
DmCvD	58	IVRGKLTQ---RQSELVLAALVIDDVTLNNSGEKFLQNKEMYPYPKPF-----
DmFabp	49	TLTTTSTFK-----
DmGlaz	51	YEVEVSFYL---PEIASGCTTF-----
DmMic26-27	56	HPPQDSVLH---KNLEAGVRYV-----
DmNlaz	51	YEYAAYPFA---FEIGKKCIYA-----
DmMtp	60	TFETDLKINSVWSGDEDQLLEVFISGSKVDASGKARSITRIPDRPFYISLVR-----
DmApoLppI	203	LYVAEQDKQKAIALKGNKKNKNSQPSEICFNQLELVGLNICIKSSTSLSEVQAGNGNVAERGLSVSEKFHLSRPFNFAVY
DmApoLppII	118	-----
DmApoLTPI	233	VQKREEQLPQAGIANRSANSTCTWPV-----LDQAIGLQMCSHYSVPDLNATEIYPSLLLGLPLNFSILKKS
DmApoLTPII	117	-----
DmCG31659	65	-----
DmCvD	105	-----
DmFabp	58	-----
DmGlaz	70	-----
DmMic26-27	75	-----
DmNlaz	70	-----
DmMtp	112	-----
DmApoLppI	283	LTTERKFTFKGIHTQEAFSQKWKLDYSTPGSKVSHDTTVVYELGNPKPTFSRLSFDNSQCHFAVEGGINNDKNELVVGQ
DmApoLppII	118	-----
DmApoLTPI	302	DLSAKKYVFEYKWDQQEEDNNFSLVFTTPGSKVPR--VLVANVTKVPDAFNASVAFVNGPNRVSAAGSYDGNPDFRRLDI
DmApoLTPII	117	-----
DmCG31659	65	-----
DmCvD	105	-----
DmFabp	58	-----
DmGlaz	70	-----
DmMic26-27	75	-----
DmNlaz	70	-----
DmMtp	112	-----
DmApoLppI	363	YEQDKKEIKKSKIGF-----SKNGNEYKPLIEIQDNNGISNSINGYHADG
DmApoLppII	118	-----
DmApoLTPI	380	YLDTNGNRSLDLGMELRRHQDFTAWIYNPRMLLAINGVNITGLAGTVKVNEKNGIKQHDVDSFETKKLQAVIKGNVVQS
DmApoLTPII	117	-----KEYDYYDNLANEESQNYDNMHPK
DmCG31659	65	-----
DmCvD	105	-----
DmFabp	58	-----
DmGlaz	70	-----
DmMic26-27	75	-----
DmNlaz	70	-----
DmMtp	112	-----

DmApoLppI	407	KIVVKKNSNNIERYNFENFQVSNSNNAHVAVNGWSDVGTNSLTSELRLSDHQTFLLIKENLKLNGLYEAGFFINDE - HS
DmApoLppII	118	-----QFTLVSGILEPQICSDSSDLDSLNIKRAVVSLLQSGIEA-----EHEVDVFGMCPHTTSTSKV - GN
DmApoLTPI	460	EITTTNMTIKYRFQANKIEEINFAGKLVNNGDKSKTEYRGNMKLQTSAYPKLNFASESTWLSLQGHTEGMITYNNA - PD
DmApoLTPII	142	SSDFNVDLTKNLLRFAFHDGLISEVCPQEETPWVLNKKGILSAFQNTMMRFDVDANTTETDVSQGQCQVQYALEDTSS
DmCG31659	65	-----
DmCvD	105	-----KIALTKDGAISHVVFKEGDPIWSMNFKRAIASVLQFQMKSSGAFV - VDELGIHGTCRTEYFVSNR - TN
DmFabp	58	-----
DmGlaz	70	-----
DmMic26-27	75	-----
DmNlaz	70	-----
DmMtp	112	-----GQPDKVIAHTSKDQSLNLNLERGIASLLQLRLDASQ - - - EEELDVSGLCRVSYNVKSS - TK
DmApoLppI	486	PENIYGSSIHLLTIADQSYALKTNKAAAWSIGSDGSFNFQKLADSNSARAGSLVENVEIQYKNKQVGGIKIMSNFDVNKM
DmApoLppII	179	ANIITKARNLNSCSHREQINSGLV -
DmApoLTPI	539	YVNPNTSLVRLIFARSHSEDSFLDGTQTRASLELKLPRSKIDYRILVKHKEHIKN - - - GTEHNVIVGLKYTPEKEITGL
DmApoLTPII	222	YVTIRKTKDINSCRQRYATHSVLQ -
DmCG31659	65	-----
DmCvD	171	YISIRKTPEVKTCKPYSEAVHTTRSNVPPNTCEFDHQSVIIGNEAIYGMSPHNETGYL SMAHAKGTTLIHTFESTGEA
DmFabp	58	-----
DmGlaz	70	-----
DmMic26-27	75	-----
DmNlaz	70	-----
DmMtp	168	VEKTKRDCSLWDLRVNYPPEALGVTQQAQETVFYELSSGTLTLLHAESQENHRLNLAAPDVGSFVKSSLILQHVSQGSE
DmApoLppI	566	DVDVEISREQKIGSIIVKYESNQRHAQDYSLEASAKINKHSIDVISKCDFNGNVYVVDNSLVTSWGTLLSAKG - - - - -
DmApoLppII	203	-----
DmApoLTPI	616	FSVHLPRRNLFAIDAYMNVTVPEFNSCTASLKVNEKATKDYIIFINGSWFTGHSVAVKANYKDRSSRVQALHHLKMIVES
DmApoLTPII	246	-----
DmCG31659	65	-----
DmCvD	251	QFINSELLNLFNETPIDNPIDIETSMAAEPSNLELQRLDPNDPTGGR - - - - -
DmFabp	58	-----
DmGlaz	70	-----
DmMic26-27	75	-----
DmNlaz	70	-----
DmMtp	248	EVKQLQLGSL - - - - -
DmApoLppI	639	-----EIGQRYSAQDININIQGNVQISGDKVKTQWILKVIGTPDKTNSDFRIS
DmApoLppII	203	-----
DmApoLTPI	696	PSFNITSLNIIYRRKQLLIFYDIQAKYDQDPYGLTIQYASNAHNRNTNAEVRLLKVKERDYWINAKLLSEQPKLLQLEIHM
DmApoLTPII	246	-----
DmCG31659	65	-----
DmCvD	299	-----
DmFabp	58	-----
DmGlaz	70	-----
DmMic26-27	75	-----
DmNlaz	70	-----
DmMtp	258	-----
DmApoLppI	687	RDTSelikLTSESQHPQDKISFAKLNLIvKNQLTAKGEFRVAKNGKGDFtASIDTLKTEPKHKLEIESKFHIQSPKYDID
DmApoLppII	203	-----
DmApoLTPI	776	DKIRDVHIQVGLLNVDKRKELSLELKWdANRDPSQRLGLLAEYNSPGTKHYDGNLMITYPERTIHFGFNSFTGGPKYFGK
DmApoLTPII	246	-----
DmCG31659	65	-----
DmCvD	299	-----
DmFabp	58	-----
DmGlaz	70	-----
DmMic26-27	75	-----
DmNlaz	70	-----
DmMtp	258	-----
DmApoLppI	767	ASLTLDGKRKVHLKSE - - - - -
DmApoLppII	203	-----
DmApoLTPI	856	VHASWSINEVIEFEYEAGILPGHTLHNWVKAELRTPFDGWRVNSLDAGIYSLKNLILVNSTLFWADDQKLQVGYKSDYDV
DmApoLTPII	246	-----
DmCG31659	65	-----
DmCvD	299	-----
DmFabp	58	-----
DmGlaz	70	-----
DmMic26-27	75	-----
DmNlaz	70	-----
DmMtp	258	-----

DmApoLppI	783	-----NTIEKLFSTKNIGEANDKIIAFEANGSLKGE
DmApoLppII	203	
DmApoLTPI	936	NDQLMSFDVRFGINSTIRDIPTINVKVKHWMVKKVDTELYLGYSQGNDTFNTYSMDSSWEIEKNQRYNNYSGLVHLVSP
DmApoLTPII	246	
DmCG31659	65	-----
DmCvD	299	-----
DmFabp	58	-----
DmGlaz	70	-----
DmMic26-27	75	-----
DmNlaz	70	-----
DmMtp	258	-----
DmApoLppI	815	LRNGEIQGTFIFNAPDGRVIDGSINRKISTNAKSGLSQGNIDAQLSDTPF-----
DmApoLppII	203	
DmApoLTPI	1016	FKGYEKGLVAHFSLSDQRRVVSQAASLNFDLREFTLTMNGYVKKFTDNMLTVNITTPLEKFGTINARFGLNEKKRHAAVE
DmApoLTPII	246	
DmCG31659	65	-----
DmCvD	299	-----
DmFabp	58	-----
DmGlaz	70	-----
DmMic26-27	75	-----
DmNlaz	70	-----
DmMtp	258	-----
DmApoLppI	866	-----GSNKKRSISLIGKLDRLNTKTKEFSANS
DmApoLppII	203	
DmApoLTPI	1096	VRAPTAALGVEVLADIKNLLNFDVKLSVATPIESFQQAIFALFNPERVDMRGLWNNVTLGFTGVWHMQNITDFEYSYHV
DmApoLTPII	246	
DmCG31659	65	-----
DmCvD	299	-----
DmFabp	58	-----
DmGlaz	70	-----
DmMic26-27	75	-----
DmNlaz	70	-----
DmMtp	258	-----
DmApoLppI	894	NLVYTAFNGEKSEISYQIKQQPNGDAKNIDFSLKAYGNPLPQPFEIAFALGDYSAQHAVVSITSKYGEIFSVSANGNYNN
DmApoLppII	203	
DmApoLTPI	1176	FTPLAGFEENGFIQVQLLKRKEFVFQLHGKMSNYKLGVKINGEPKSDLVNQLGSNKMELEMLYDADFKPLNAETDYKPDAD
DmApoLTPII	246	
DmCG31659	65	-----
DmCvD	299	-----
DmFabp	58	-----
DmGlaz	70	-----
DmMic26-27	75	-----
DmNlaz	70	-----
DmMtp	258	-----
DmApoLppI	974	NQALEYGLQANIEIPKSTLKSLEINSHGKVLKSLIGNENAAYNVEFFLDSKTSLGQYARVNTVWNGTANDGSYDFAEQTN
DmApoLppII	203	
DmApoLTPI	1256	EEYFSYFTNFQVDTLVWPTIVGNVDIQEIIDFYLVVGHVELPQGKVEFKDRLHYPDYINVHLLTVTTTFAVAKNIKSIV
DmApoLTPII	246	
DmCG31659	65	-----
DmCvD	299	-----
DmFabp	58	-----
DmGlaz	70	-----
DmMic26-27	75	-----
DmNlaz	70	-----
DmMtp	258	-----
DmApoLppI	1054	NMESPLKFNGKYHRKQTGNIKDGLTGKQTYVLNAQYGAQYVKMDASLGYGAEKVDIAYVIDSSFDSVKDIKVNIRTFKP
DmApoLppII	203	
DmApoLTPI	1336	EYHVDLNFNAFYERVKFIVNDDKONTQELGFVFNYTALQDNVKPKAHDVQVTLTPYEMLHEIYVHGHIELDDNAYKGN
DmApoLTPII	246	
DmCG31659	65	-----
DmCvD	299	-----
DmFabp	58	-----
DmGlaz	70	-----
DmMic26-27	75	-----
DmNlaz	70	-----
DmMtp	258	-----

DmApoLppI	1134	LDDSTYVVTALFKQTDKSYGLDTTFYHSAHKKGVDIRLDLLKEKPPIISSIAELLGDRKGKVLFEILNLADLDIKINSEA
DmApoLppII	203	-----SGKVNEKAGITSSLLLQANYIKESRIVNHLIENVQLTETYKFIGNTKRNSDISA-----
DmApoLTPI	1416	SAVTAHTHLSMAASIENEDNFLETSGVIGLETDAIPHYGCQVYFKDFSAVDKAIDIRFEVTDNGTLNQLHISTDWHOTDP
DmApoLTPII	246	-----TTPYTFRDDKTIWPIILKSQSHCNLTIDNNVYKEIKCLETHLLVPFSNASSGALT-----
DmCG31659	65	-----DFIEKEENKFSVVARELNTQTGTVKM-----
DmCvD	299	-----SPQQQETLIAQAGTLLDSLAEALETTEFKFSEPYDSTLSDVIKLLSEMDFDSTLTKLYREVDIGTSY
DmFabp	58	-----TSAISFKLGVEFDEETLDGR-----
DmGlaz	70	-----QFEPYNKGEQSKFSNFKLAVAI-----
DmMic26-27	75	-----REEVQSGYKAVADQAGIVGHYVETA-----
DmNlaz	70	-----NYSLIDNSTVSVVN-----
DmMtp	258	-----DKAIQSLLEWYRVFELESVDGMISAIKEQTLEDQLKASLTQLSADVGKSSLALAYVKL-----
DmApoLppI	1214	SYV-----SIDEFYIIVNWSSKKLKDGYELEARAQSKNIKIQLKNE-----
DmApoLppII	257	-----KVVTILKLL-----
DmApoLTPI	1496	SYIVNANGRIKTTMLPLQMASTSVLVIQGNPHLNFNLNLSQNGQSIAYGARANKKKDVFNIIEVWTPMKNFRNISMHGT
DmApoLTPII	300	-----TSTSRLKLD-----
DmCG31659	91	-----RKADILNVE-----
DmCvD	365	R-----QETIRNIFHEIIPRIGTKASVFLTHHLVLNKLTKP-----
DmFabp	78	-----NVKSIITLD-----
DmGlaz	92	-----KNINRITGN-----
DmMic26-27	100	-----KAHTQSTID-----
DmNlaz	84	-----AANRFTGQ-----
DmMtp	318	-----IPLARITRQ-----
DmApoLppI	1256	-----NGIIFSGTATYALKKELNKTIIDGQGVQYQKALSGNFKLTRQHFDGTDREVGFSTYFMGNLGSK
DmApoLppII	266	-----
DmApoLTPI	1576	AIRSPRDPGRYDVSGFLYRNMATYEVGTAVRMTNSLPIDVVLRVQPKAGGRDGVIELNIHEAGPKKIRFSFSAIEDGKMC
DmApoLTPII	309	-----
DmCG31659	100	-----
DmCvD	401	-----
DmFabp	87	-----
DmGlaz	101	-----
DmMic26-27	109	-----
DmNlaz	93	-----
DmMtp	327	-----
DmApoLppI	1323	NGLGTLKITNKEFNTKFSVCEEKRQCTNLIVQSIVSIDEQ-----
DmApoLppII	266	-----
DmApoLTPI	1656	QMSGGYSVSKTNGAMDFSVLVESTEPEIARINFYGNLSPNSEGSLVGDLSLETPWKALGIDTVHLHSDVGFLNKGGHIVG
DmApoLTPII	309	-----
DmCG31659	100	-----
DmCvD	401	-----
DmFabp	87	-----
DmGlaz	101	-----
DmMic26-27	109	-----
DmNlaz	93	-----
DmMtp	327	-----
DmApoLppI	1363	-----KLD
DmApoLppII	266	-----
DmApoLTPI	1736	EYKIGQYIGRGSCLSWILAEQMQLVLENYLERPNAKPRIVHASAKYQNPQGTFQTQLQAGGRLSVDSKWNLVDNGSAEYK
DmApoLTPII	309	-----
DmCG31659	100	-----
DmCvD	401	-----
DmFabp	87	-----
DmGlaz	101	-----
DmMic26-27	109	-----
DmNlaz	93	-----
DmMtp	327	-----
DmApoLppI	1366	AVEHTTLIIIVDLRDFGYPYEFELKSQNTQRGLKYQHLSFIITGNNFKYQFTANVQPTSSTIKLALPKRQILFETTQKI
DmApoLppII	266	-----NPSGTKANSPGTGSTVRSILIFQRPETYTSKN--INAKLTILSDLVDSGDY
DmApoLTPI	1816	SVDDFKFRVITALPLPVGDRHQLSASYQGNVISQQFNPDVLEASYEFQAQNKLLSRISYKNATNNLKGHVEWGKI
DmApoLTPII	309	-----GVESYSAGEFLEQNPVELVERRATLVFDHTPAVKPSHDEIKAARELLVEMCRVGFNP
DmCG31659	100	-----PEF-----
DmCvD	401	-----QIAVQLLIPMPFHIFELSAELVQKCEDFLNIGDPDRPDVRQAAILSFATLIHNVYVAKGIDKEKFEEYVQKYFNA
DmFabp	87	-----
DmGlaz	101	-----PNVNI-----
DmMic26-27	109	-----MLNEPQNSLHRS-----
DmNlaz	93	-----PSNVT-----
DmMtp	327	-----EQFEDLLTEHAEVLPQLVDLLGAVQTFDAHNATFGFLYKESETTSEQLDLLEKYLQSLAVATHPDR

DmApoLppI	1446	PADGSLFGRYEQTASFFIDK-----
DmApoLppII	315	VKKETAKKFVEFIRLLRQS-----
DmApoLTPI	1896	QNLVVEGDFELLHKQGAQREFSAKIITPKFKNEHTFALTGSYDLEKSGHHNVVGLDYPASRRITDLDVSVSSLSNMHG
DmApoLTPII	365	IQREFIDVFTNFLQTSKSL-----
DmCG31659	103	-----
DmCvD	475	YLSDRDFDQKMLYLQGL-----
DmFabp	87	-----
DmGlaz	106	-----
DmMic26-27	121	-----
DmNlaz	98	-----
DmMtp	393	KIVEHLFGLLEQESIKKHLKLRESVIQTV-----
DmApoLppI	1466	-----LQKPDDVARFSAIVDVTGTERVAFNANGKLKFEHPTIRPLSISG
DmApoLppII	334	-----
DmApoLTPI	1976	IFNSTLPTFLNVSWLKTDFNFTTNNGKSYRYCRCFWPQDTAYFKLNSNYDSOSSNFNHNLNNGVEIEVPLATRHRADIVY
DmApoLTPII	384	-----
DmCG31659	103	-----
DmCvD	492	-----
DmFabp	87	-----
DmGlaz	106	-----
DmMic26-27	121	-----
DmNlaz	98	-----
DmMtp	422	-----
DmApoLppI	1510	QLNGDVNQQIASAEVIFDIFRLPEQKVVGNSSELNRSRQNGFNIAIYITTVKSAGLQFYQINSNAAVDIEAHEYNIIGLEL
DmApoLppII	334	-----
DmApoLTPI	2056	GLQKRRNQDAGNVKVVYNEKQVLGDKYKRLEQAKAPIYKETTDISLENEVKPLGIHFVSTRDASDPAGSQDVKHIEIYEL
DmApoLTPII	384	-----
DmCG31659	103	-----
DmCvD	492	-----
DmFabp	87	-----
DmGlaz	106	-----
DmMic26-27	121	-----
DmNlaz	98	-----
DmMtp	422	-----
DmApoLppI	1590	NNGEI----DVKAISFLNKEKFEISLSESNKHIIYIVGDFSKQNHAKLNTKVQILDK-----
DmApoLppII	334	-----
DmApoLTPI	2136	RNTQNFNLTGELHSRATLKAQDFKVVAIHPNRAVVLSTKYEDVSPEVVRHHSKLELSETAWIGYNLELGNFSKVGNESQS
DmApoLTPII	384	-----
DmCG31659	103	-----
DmCvD	492	-----
DmFabp	87	-----
DmGlaz	106	-----
DmMic26-27	121	-----
DmNlaz	98	-----
DmMtp	422	-----
DmApoLppI	1644	-----NPIEITSEVQPNSAKIILKRQDFIDGTAEVKLGKEFKVDVIGSGKQLF-----NGRVALDAT
DmApoLppII	334	-----DSETLLELAAPHPNKLARKVYLDGLFRSTAESARVILKQLSKF-----DEKEKLLAI
DmApoLTPI	2216	FALEIFYPKRNLSSSGQYYMTDTNFNSDLFSQWLGGNYDQPKIIHSNLQWKAEPHHRGDREH-----RTIALTVAH
DmApoLTPII	384	-----DYKTLVLLQRSASTCEQGRNHLLLESPLFIGSTASYKVMRDQIINEKL-----TKQMAHDWM
DmCG31659	103	-----GRYVLG-----
DmCvD	492	-----NNLQLGNVANYLEPIVQDPNEHEDLKFQAAWTTLALADRRARIYEVYWPIFESRNASLELRVAA
DmFabp	87	-----GNKLTQEKGKD-----
DmGlaz	106	-----GYATPENS-----
DmMic26-27	121	-----GAIVVGGLAGFIFAARGGF-----
DmNlaz	98	-----GQAKVLGPGQ-----
DmMtp	422	-----ATLTRQSGLDVEDPLLKEVRSYLLQGLTSKEPTLYIRALQNLQDPATIEALLEHAQTGEAPNLSV
DmApoLppI	1701	NFLQTNFYFINEDHLNGFWHIVESEINKDSEYISENIKERLKKSRQVTDKIVKL-----
DmApoLppII	389	LSLNIIVKSVDKETLNQAASQLLPN-----
DmApoLTPI	2288	PLLEKDINCKATYYRGLRDLLRTHLTIDYSEYPDQLIELGAQLTDRYSELGHTNYTFHVGKHIASELDVQLNGTLAAMN
DmApoLTPII	441	TALSFITRPDEETLETFSILEY-----
DmCG31659	109	-----
DmCvD	557	VTLLNISNPTAARLISIHRIIQSETDPHMINYYRTTVTS-----
DmFabp	98	-----
DmGlaz	115	-----
DmMic26-27	140	-----
DmNlaz	108	-----
DmMtp	487	AALQALKAFPLGSFNSSHRLQFESIFYQRKRRFDSSARTLALD-----

DmApoLppI	1754	-----AKEAGPDFSKL
DmApoLppII	413	-----
DmApoLTPI	2368	SYKTESTAHYKRDIFPARYGKFLALLDVNKRELEYERQSPFHAVRLHLLPTIRYPIYGLNATIWDTPDNTNHSGYIYMDI
DmApoLTPII	464	-----
DmCG31659	109	-----
DmCvD	596	-----
DmFabp	98	-----
DmGlaz	115	-----
DmMic26-27	140	-----
DmNlaz	108	-----
DmMtp	530	-----
DmApoLppI	1765	QGKLLDYKNDIVQELEADQSIAPIIDGIRTLFKKIAGIVDD-----INKAISEILEKA
DmApoLppII	413	-----A
DmApoLTPI	2448	LERYARMDFNLTEDASQNLQMVGYIPDTRSAFLDIWRNYEEIRVIDVSSYLKMNSRLITGRFHWRSIRQEVREKIQAV
DmApoLTPII	464	-----A
DmCG31659	109	-----
DmCvD	596	-----I
DmFabp	98	-----K
DmGlaz	115	-----
DmMic26-27	140	-----I
DmNlaz	108	-----L
DmMtp	530	-----I
DmApoLppI	1818	QKSIVDIYDKL--QALWKDSLKAW--DFIITVQKLISTLKTEFIK-----
DmApoLppII	414	PKELYIAVGNL--VAKYCLKNYCQGP-----EIDAISKKFSDDLKHCKPNTKREE-----
DmApoLTPI	2528	GKSVYSSFSEG--IDFWIKSIYTETT--ESMGVVWNTAKEYNRDFIDDIGQLSVLEEDLADLRLFVNQSYEANDFYIKNV
DmApoLTPII	465	KNRLDAEYTLG--ATAVVSFCKHHEACEENLRVQIINLLETEFLNLYNLFKGERRTR--
DmCG31659	109	--TTSTAFPEG--VLMYV--LTDYV--
DmCvD	597	SETTYPCYQHLRRLLSYMRHLPQKPESRYWWTGNYIFDYRDSKFGIGAMLQVFLVGDPKSDMPVVAFFKFDTEALGKFT
DmFabp	99	PTTIVREFTDNELITLIPHLTPSQHG-----
DmGlaz	115	--SSIMDFKFTTRFPDVIARLLPGSG-----KYQVLYTDYE-----
DmMic26-27	141	KKVLYSGIGAG--AVASMCYPRQA-----
DmNlaz	109	AVAFYPTQPLT--KANYLV--LGTDY-----
DmMtp	531	ILSLRPTQEQLGNFLDYLASNDRQFEIKTYVLQKLRLAEKCPFRALFKSELVKRRHVN-----
DmApoLppI	1861	-----ICTQSFKDLLSALEKYGPALKNYGKAIGEIVKPINDAA-----
DmApoLppII	462	-----
DmApoLTPI	2604	VNFTLTILDELAIRDHIESLPKIFSELWQAMGDSGKALRNSIVWLIETIKTTYNNLLDAVARFFHGESLVYISGLLEKGI
DmApoLTPII	522	-----
DmCG31659	129	-----
DmCvD	677	GQLALYIKARGLPDTILNKMQRNGSDPFTFKSIKALLAMLQAPIINSK-----
DmFabp	125	-----
DmGlaz	149	-----
DmMic26-27	163	-----
DmNlaz	132	-----
DmMtp	591	-----
DmApoLppI	1899	-----QEVIKIVN-----
DmApoLppII	462	-----ERIVYILKGLG-----
DmApoLTPI	2684	AKYDSFIKDLHIKFIKYIENLWHKTWTLAENHWKAVLKRFEPLFKMISFIETTAWNLSKEVDFIYKRTNELAESPYFN
DmApoLTPII	522	-----ERMVILLKGLG-----
DmCG31659	129	-----NFAIRFMC-----
DmCvD	726	-----DLHLEFILQMEGKTVLSYYLNQRMFRQL-----
DmFabp	125	-----SLRLRVPC-----
DmGlaz	149	-----NFAILWSCG-----
DmMic26-27	163	-----EENCRRVLY-----
DmNlaz	132	-----SYAVVYSCT-----
DmMtp	591	-----NYNVLGQKG-----
DmApoLppI	1908	-----AAEGVTHEFK--QYVASLPSFESIRNEFNKVKVLKLFKATELTNSLFDQINILPQTPETSEFLQKLHDYLI
DmApoLppII	473	-----NAKSLSGNTV-----AALSECASTGRSNRIRVAALHAFSKV-----KCEETLQSKSL
DmApoLTPI	2764	KVSSFTADAERLYRDFKANDAITNIKKYSTIAWNFVKE-KYFKLVFPGAELNEVLTEIWQEIKELEKIDQVQIMVQKYIE
DmApoLTPII	533	-----NIGVVSSAF--QLQWIIREDEAPVDIRLHGILAFRRV-----DCARHSYFL
DmCG31659	138	-----DASKIF-----SFHWAVIQTR-----
DmCvD	754	-----TYDNILERMQQIIRTDSHINMQTVRWPFMNRYSVPTVLGTSSDVLLQTTVLTSLRGNITEQRNSPITKHTLEI
DmFabp	133	-----
DmGlaz	158	-----SIGSLGHS-----DQIWILGR-----
DmMic26-27	172	-----EGRKIF-----AVAYNFIKGV-----
DmNlaz	141	-----SVTPLANF-----KIVWILTR-----
DmMtp	600	-----LTTVLTRQLSQAPAFNETLLSTQEYVQGILKRGSVFLLHAGRSQASSFKLGIYTAGLGSLVGDGDSGDGND

DmApoLppI	1979	AKLKQEHIDNEKYIEELGQLLIKAVRSIWVSI-----RSTYPGSSDHVIDFQSWIGSLTHSF-----
DmApoLppII	520	ELLKNRNEDSELRIEAYLSAISCNAEVANQI-----SEIVNSETVNQVGGFISSNLKA-----
DmApoLTPI	2843	VMAKVDWVADELQLEHR-----LHQVYGLV-----RNKFRNYAMNALETADMYREAKTKFVFDPEVGIIDLEQKLPM
DmApoLTPII	580	DNYGNYTLNSELRIYSYLQAMRCPDYISVGV-----KSILEHEEINQVGSFVWSHLTN-----
DmCG31659	154	-----
DmCvD	827	DARYSSYASVRSRSYNPFLNLDHEINREQGLIYIPFSSELHLNESGSKCRRYSFSRPQNLTSGLSFKSRAVTKTRGLIT
DmFabp	133	-----
DmGlaz	174	-----
DmMic26-27	188	-----
DmNlaz	157	-----
DmMtp	673	IPADDEFSEDEAVTAGMEISVQGAQLRPLVFF-----SGQTELMGHVWGGSSAS-----
DmApoLppI	2036	-----DSLAVLPSILSFR-----SSILNCLLNENWDVFNKKLLYSWIFFNDFELRGHVVDGKHIFTFDGLNFAY
DmApoLppII	574	-----IRDSTDVSRDQK-----YHLANIRVTKTFPV-----
DmApoLTPI	2910	SWHAFNETPRFEEIPEYQVLAKAQ-----SFFSETNSSIVMKLYNMRTHLDPKTLWPPYSRALLIDSRHYMTFDQRYVGL
DmApoLTPII	634	-----LAKSNSPVRIEAQ-----GLLLNDELSERFKM-----
DmCG31659	154	-----KRLPSTQVIHMAQ-----
DmCvD	907	KTAAAPFEEIMVPEGRNDVVQLFS-----YPMTDLGVRLSMTTNLNELIKYRGMLLKSEFTENGFSGNMVVNALMYIFGFT
DmFabp	133	-----QVPVPTSVDGAR-----
DmGlaz	174	-----DRDFEVDIRSKVY-----
DmMic26-27	188	-----KPGEDVPVVPFPT-----
DmNlaz	157	-----QREPSAEAVDAAR-----
DmMtp	721	-----DSTPAYQATTLSDQNEHYIILTSGATLHWRVLGARSVDLNGKVGFSLWNRNAQTE-----
DmApoLppI	2101	-----PGNCKYILAQSDVDNFTIIGQLTNGKLKSITLIDREGSY-----FEVADNLALKLNGNLVEYPQH
DmApoLppII	601	-----
DmApoLTPI	2986	NLNFDELGNRSTSQCSYLLAHDFFKRNFTLLLEPASKSLAGQGLTRKLSFIANGQLIEIDLETDHISINGNPQPIPLK
DmApoLTPII	661	-----
DmCG31659	167	-----
DmCvD	983	QLSSIHLGHDRNFTMLMYNEKNTRIEGNFCAEDVLKTS-----
DmFabp	146	-----
DmGlaz	187	-----
DmMic26-27	201	-----
DmNlaz	170	-----
DmMtp	776	-----
DmApoLppI	2162	LSGLHAWRRFYTIHLYSEYGVGIVCTSDLKVCHININGFYTSKTRGL-LGNNAEPYDDFLLIDGTLAENSAALGNDYGV
DmApoLppII	601	-----DYRRYSFNNEVSYKLESLGVA-----
DmApoLTPI	3066	LGDVNIHRDLVLSITSDTEFSLHCNVQFDLCWFEEVSGWYFGRTAGL-LGTLNNEPYDEYTMSSGVISNETQLFTDSWSL
DmApoLTPII	661	-----DIRKFSRNYEHSLLFFDEYNFGT-----
DmCG31659	167	-----YFGKSAGLVIGDMSKVP-----
DmCvD	1022	-----MKGKQIGLTLTLEHTDHMNENHAADALHRWNITLDVLASTKSN
DmFabp	146	-----
DmGlaz	187	-----DVLKRLSLDP-----
DmMic26-27	201	-----SLEDLKMA-----
DmNlaz	170	-----KILEDNDVSQ-----
DmMtp	776	-----IQQNTGSAVLGHLAVGFTYAKLVQDFSITHEPKLSLNA---
DmApoLppI	2241	GKCTAIEFDNNQFKSSKRQEMC-----SELFGIESTLAFNFITLDSRPYRKACDIALAKVAEKEKEAT---A
DmApoLppII	623	-----STDYQIIYSQHGL-----PRSSRINVT-----
DmApoLTPI	3145	KQCRQNKLAAQTQEVSQEVSDAC-----TSFFRTGILATCSAVLDPTPFYEMCMDLGMKSPPIRKGPVAVKGA
DmApoLTPII	683	-----TTDANVIFGTDSYL-----PRIASVNFT-----
DmCG31659	184	-----QESC-----PYDT-----
DmCvD	1063	WFKLTGQVQRNSKDEDDWKACTKLTYEPLVFTKRPHTLNGDVVFGATEESECEKGSTVQFAARAGPSEHARAFLRSD
DmFabp	146	-----SGGC-----GQRPGGPG-----
DmGlaz	197	-----ERLIISKNKQC-----PEAL-----
DmMic26-27	210	-----SDLYDEAKDLI-----FPKKK-----
DmNlaz	180	-----AFLIDTVQKNC-----PRLDGNGTGL-----
DmMtp	814	-----DLDFYSGIKLC-----MQLQRPEQLLKQTNV-----
DmApoLppI	2305	CTFALAYGSAVKQINKWLLPPRCIKCAGPAGQHDFGDEFTVKLPNNKVDVVFVDINVTGPVLSNL-----IAPAINDI
DmApoLppII	646	-----
DmApoLTPI	3212	CAAALAYIEACTALKVPMRVPSQCVFCQLSNGSYVPEGTFMELSGPEIPKSSDVVFIVEAKECNANLKTSKNIMTVVSSI
DmApoLTPII	706	-----
DmCG31659	192	-----
DmCvD	1143	KISLTDTDFCPKEVLKFSPIPTSRYCKRSNFENFTSITQYDMDLKFDNMPAWFELWSNRLDHLVSALSADKVDSLHMSQE
DmFabp	158	-----
DmGlaz	212	-----
DmMic26-27	226	-----
DmNlaz	201	-----
DmMtp	840	-----

DmApoLppI	2380	RESLRSRGFSQVGVIVFEETKRYPALLTSDGGKINYKGNVADVLAGIKSFCDCNCVEQIITEKRILDIYNSLKEIVKG
DmApoLppII	646	-----TEFFGTNYNVFEASVRQENVEDVLEYLGPGLVNDKDFDEI-----
DmApoLTPI	3292	EEQLQAAKITNNRYAVVAFGGVSPY-----DKARSVIYEHNEFTSKPEQLADYFGHINTGNGSSNDILMAISAAAKLNFR
DmApoLTPII	706	-----ADLFGQSVNFFFTARAEGLEELAANAFGPKGPLSGQLL-----
DmCG31659	192	-----
DmCvD	1223	INISMQTPQDQFRLAVEVNGVKWRFHQIPFFYKLDKSKFDASHELTFDSGLKRSCSVINGIVNTFDDYLINLRE-----
DmFabp	158	-----
DmGlaz	212	-----
DmMic26-27	226	-----
DmNlaz	201	-----AGEDGLDVDDFVSTTVPNIEKA?EWLRRLYERLYDIFMNFLSY-----
DmMtp	840	-----RSVFLQSVDRPYAKHVRSTLSHKTAGCTFALNQKNEMCNLIFRDL-----
DmApoLppI	2460	IAPQADEKAFQLALDYPFRAGAAKSIIGVRSDSLEYKNWWKFVRAQLTGSITKFDGALIHLIAPVKGLSLEGLVSEKLIG
DmApoLppII	687	-----
DmApoLTPI	3367	-----PGVSKTFILLSCSKCAARDMRFDYTSILQYLLEEGVNLHILADTEFDFERNKKLRHFFGLDSKL
DmApoLTPII	745	-----
DmCG31659	192	-----
DmCvD	1296	-----IAVRPDCLTLLVADCSPLPQIAVFVTPSPVQGLSTNYGLRVHIGQNYFNFRARTDNSSLPTD
DmFabp	158	-----
DmGlaz	212	-----
DmMic26-27	226	-----
DmNlaz	245	-----
DmMtp	886	-----
DmApoLppI	2540	FNSRLVATVDGKDSKKRTKLQFDNDMGIDFVLNNGGWVFATQNFELKASDQKKMLNQITSSLADTLFKTEIVSDCRCLP
DmApoLppII	687	-----VKLIEVGNGVAAGGRARR-----
DmApoLTPI	3431	VYSKRFPEGDAETRNTTHIPKSNLGICTTLAVETQGSVFSARKLQPERKYPIKRFATIFAKRVALSATPIQSQTCECSAH
DmApoLTPII	745	-----RKKLSFLNRWLGNSAEEDDTLENLLSLDNLRLK-----
DmCG31659	192	-----
DmCvD	1358	EPVLIYLNQDQTPHNVRKKPYQWPIETSDYDFRVELNEQNILIVECTQLSSTIQFDLYNILNFEIYGVYKHQMCGLCCKP
DmFabp	158	-----
DmGlaz	212	-----
DmMic26-27	226	-----
DmNlaz	245	-----
DmMtp	886	-----
DmApoLppI	2620	IHGLHGQHKCVIKSSTFVANKKAKSA-----
DmApoLppII	706	-----
DmApoLTPI	3511	NTGVSVMACSPQALPEEKYDLDYDSFNNWDWGDEPESETNVM
DmApoLTPII	779	-----
DmCG31659	192	-----
DmCvD	1438	LNRMQNYTICELEANTPTPVPLQNSSDVVVVA-----
DmFabp	158	-----
DmGlaz	212	-----
DmMic26-27	226	-----
DmNlaz	245	-----
DmMtp	886	-----

Fig. S10. Alignment of 25 human and 11 fly sequences with ApoB, ApoLpp and ApoLTP separated plus both outgroups.

DmApoLppI	1	-----S
DmApoLppII	0	-----
DmApoLTPI	1	RKAQEQRASEEEVDEYDFEESLEGNKQRQKRDVSTTRKQEIDRNVDLSGYKLKYDYNPRAQFGLRVFGNDLRYFNVES
DmApoLTPII	0	-----
DmCG31659	0	-----
DmCvD	0	-----
DmFabp	0	-----
DmGlaz	0	-----
DmMic26-27	0	-----
DmNlaz	0	-----
HsApoA1	0	-----
HsApoA2	0	-----
HsApoA4	0	-----
HsApoA5	0	-----
HsApoB48	0	-----
HsApoB52	1	-----FDQYIKDSYDLHDLKIAIANI
HsApoC1	0	-----
HsApoC2	0	-----
HsApoC3	0	-----
HsApoC4	0	-----
HsApoD	0	-----
HsApoE2	0	-----
HsApoF	0	-----
HsApoH	0	-----
HsApoJ	0	-----
HsApoL1	0	-----
HsApoL2	0	-----
HsApoL3	0	-----
HsApoL4	0	-----
HsApoL5	0	-----
HsApoL6	0	-----
HsApoM	0	-----
HsApoO	0	-----
HsApoOL	0	-----
HsMTTP	0	-----
DmMtp	0	-----
DmApoLppI	2	IVDDVSKISKKYKMYGVKNVQDLNLDVSLKLFGESELAFLSLGDNIPSSLDDIINYFSTSFEEKAKQELSSFEKQFSSHHLF
DmApoLppII	1	-MARMKYNIALLIGILASVLLTIAVNAENACNLGCPKSDNGLLKYIPGNYYDYSFDSILTIGASSDVPNDSDDTSLKVS
DmApoLTPI	81	LVEVMALAAKFNPFPQAKNVLSGKEFTYTKSRVFLDASYTVPLAVGLPLAIHAFGASSIDLRVSGNLDMDPPTDWHFDV
DmApoLTPII	1	-----MGGLKPQAAIWL LLLIAHTQAVRENPLKDPRIICGRPCQDSKSAKFNYGEQLYKYQYTVAVRTEFAGSGDNSSDL
DmCG31659	0	-----
DmCvD	1	-----MRLKCSVFVYLFLIFDAGHAFSIIGLNKQMLYIEYEGNVLVGAKPQDEGHQAPPTTGWIVRG
DmFabp	1	-----MSFVG
DmGlaz	1	-----MMSGQPL
DmMic26-27	1	-----MLRKTATMGIMA
DmNlaz	0	-----
HsApoA1	0	-----
HsApoA2	0	-----
HsApoA4	1	-----MFLKAVVLTALVAVAGARAESADQV
HsApoA5	1	-----MASMAAVLTWALALLSAFSATQARKGF
HsApoB48	1	-----MDPPRPALLALLPALL LLLLAGARAEEMLENVSLVCPKDTRFKHLRKYTYNYEAESSSGVPGTADSR
HsApoB52	22	IDEIIEKLKSLDEHYHIRVNLVKTIHDLHLFIENIDFNKSGSSTASWIQNVDTKYQIRIQIQEKLQQLKRHIQNDIQHL
HsApoC1	0	-----
HsApoC2	0	-----
HsApoC3	0	-----
HsApoC4	1	-----MSL
HsApoD	1	-----MVML LLLSALAGLFGAAEGQAFHLGKCPNPPVQENFDV
HsApoE2	1	-----MKVLWAALLVTFLAGCQAKVEQAVETEPEPELRQQTEWQSGQRWELA
HsApoF	1	-----MTGLCGYSAPDMRG
HsApoH	1	-----MISPVLILFSSFLCHVAIAGRTCPKDDLPFSTVVPLKTFYEPGEEITYSCKPGYVS
HsApoJ	1	-----MMKTLLLFVGLLLTWESGQVLGDQTVSDNELQEMSNGSKYVNKEIQN
HsApoL1	1	-----MEGAALLRVSVLCIWM SALLFLGVGVRAEEAGARVQQNVPSGTDGDPQSKPLGDWAAGTMDPESSIFIEDA
HsApoL2	1	-----MNPESIFIEDY
HsApoL3	1	-----MDSEKKRFTEEA
HsApoL4	1	-----MGSWVQLITSVG VQQNHHPGWTVAGQFQEKKRFTEEV
HsApoL5	1	-----MPCGKQGNLQVPGSKVLPGLGEGCKEMWLRKVIY
HsApoL6	1	-----MDNQAERESEAG
HsApoM	0	-----
HsApoO	1	-----M
HsApoOL	1	-----MAA
HsMTTP	1	-----MILLAVLFLCFISSYSASVKGHTTGLSLNDRLYKLTYSDEVLLDRGKGKLDQSVGYRISSNVD
DmMtp	1	-----MENKNKKCLRTLL LALLFLGLLEDGKTALIPNSQIFKLQNVILQELGRDSSSAETS YTFETDLK

DmApoLppI	82	LDTDLAYP--TSIGVPLELVAQGFAA-----
DmApoLppII	80	AKIFAKGN--CGYTLQLSSVKVTNTK-----
DmApoLTPI	161	EGQFKPSV--SVDVITTMQDMFWEQSGIKVKS NLYSNSELVAKLKVRGRNLVSFSFDLPRDKNEIFSVRSELLVQKRE
DmApoLTPII	75	LLKSDLEI--FFPKPCEGYLRINDAK-----
DmCG31659	0	--MIKWKI--FVPAILYLQSSMAMRA-----
DmCvD	63	KLTLLQRQS--ELVLAALVIDDVTLN-----
DmFabp	6	KKYKLDKS--ENFDEYMKELGVGLVT-----
DmG1az	8	GSRVWLLS--GVLLVTFAGTDAYGFG-----
DmMic26-27	13	AVAVKAAP--EPQKPASSAADCSLVC-----
DmN1az	0	--MNHHS--SHLLLLISVVFAGVWV-----
HsApoA1	0	--MSKDL--EEVKAKVQPYLDDFQK-----
HsApoA2	0	MKLLAATV--LLLTIC-----
HsApoA4	28	ATVMWDYF--SQLSNAKEAVEHLQK-----
HsApoA5	28	WDYFSQTS--GDKGRVEQIHQQKMAR-----
HsApoB48	75	RINCKVEL--EVPQLCSFILKTSQCT-----
HsApoB52	102	AGKLKQHI--EADIVRVLLDQLGTTI-----
HsApoC1	0	--MRLFLSL--PVLVVVLSIVLEGPAP-----
HsApoC2	0	--MGTRL--LPALFLVLLVLFGEVQ-----
HsApoC3	0	--MQP--RVLLVVALLALLASAR-----
HsApoC4	4	LRNRLQAL--PALCLCVLVLACIGAC-----
HsApoD	40	NKYLGRWY--EIEKIPTTFENGRCIQ-----
HsApoE2	48	LGRFWDYL--RWVQTLSEQVQEELS-----
HsApoF	15	LRLIMIPV--ELLLCYLLLHPVDATS-----
HsApoH	58	RGGMRFKI--CPLTGLWPINTLKCTP-----
HsApoJ	49	AVNGVKQI--KTLIEKTNEERKTLLS-----
HsApoL1	72	IKYFKEKV--STQNLLLLLTDNEAWN-----
HsApoL2	13	LKYFQDQV--SRENLLQLLTDDEAWN-----
HsApoL3	13	TKYFRERV--SPVHLQILLTNNEAWK-----
HsApoL4	37	IEYFQKKV--SPVHLKILLTSDEAWK-----
HsApoL5	35	GGEVWGKS--PEPEFPSLVNLCQSWK-----
HsApoL6	13	VGLQRDED--DAPLCEDELVDQGDLS-----
HsApoM	0	--MFHQIW--AALLYFYGIILNSIYQ-----
HsApoO	2	FKVIQRSV--GPASLSLLTFKVYAAP-----
HsApoOL	4	IRMGKLT--MPAGLIYASVSVHAAK-----
HsMTTP	65	VALLWRNP--DGGDDQLIQITMKDVN-----
DmMtp	68	INSVWSGDEDQLLEVFISSKVDASG-----

DmApoLppI	106	-----TKVDL
DmApoLppII	104	-----ESVEK
DmApoLTPI	238	EQLPQAGIANRSANSTCTWPVLDQAIGLQMC SHYSVPDLSNATEIYPSLLLAGPLNFSILKKS DLSAKKYVFEYKWDQ
DmApoLTPII	99	-----LYDTL
DmCG31659	22	-----FHGAC
DmCvD	87	-----NSGEK
DmFabp	30	-----RKMGN
DmG1az	32	-----RCPNY
DmMic26-27	37	-----RPSEL
DmN1az	22	-----AHAQV
HsApoA1	21	-----KWQEE
HsApoA2	14	-----
HsApoA4	52	-----SELTQ
HsApoA5	52	-----EPATL
HsApoB48	99	-----LKEVY
HsApoB52	126	-----SFERI
HsApoC1	23	-----AQGTP
HsApoC2	21	-----GTQQ-
HsApoC3	19	-----ASEAE
HsApoC4	28	-----QPEAQ
HsApoD	64	-----ANYSL
HsApoE2	72	-----SQVTQ
HsApoF	39	-----YGKQT
HsApoH	82	-----RVCPF
HsApoJ	73	-----NLEEA
HsApoL1	96	-----GFVAA
HsApoL2	37	-----GFVAA
HsApoL3	37	-----RFVTA
HsApoL4	61	-----RFVRV
HsApoL5	59	-----INNLM
HsApoL6	37	-----PEEKI
HsApoM	22	-----CPEHS
HsApoO	26	-----KKDSP
HsApoOL	28	-----QESK
HsMTTP	89	-----VENVN
DmMtp	94	-----KARSI

DmApoLppI	111	AVSLDINAILEQNWQKAKYRLKFVPSVDINANVQIGFNAQVLSTGLRVVSSAHSATGSDITVAVISDGEGFNVDLELPRE
DmApoLppII	109	KILNS-----
DmApoLTPI	318	EEDNNFSLVFTTPGSKVPRVLVANVTKVPDFNASVAFVNGPNRVVSAGCSYDGNPDFRRLDIYLDTNGNRSLDLGMELRR
DmApoLTPII	104	DELND-----
DmCG31659	27	PSNMT-----
DmCvD	92	FLQNK-----
DmFabp	35	SLSPT-----
DmG1az	37	PSMPK-----
DmMic26-27	42	PIYGS-----
DmN1az	27	PFP GK-----
HsApoA1	26	MEL YR-----
HsApoA2	14	-----
HsApoA4	57	QLNAL-----
HsApoA5	57	KDSLE-----
HsApoB48	104	GFNPE--GKALLKKTKNSEEFAAAMSR YELKLA IPEGKQVFLYPEKDEPTYILNKRGIISALLVPPETEEAKQVFLD T
HsApoB52	131	NDILEHV KHFVINLIGDFEVAEKINAFRAKVHEL IERYEVDQQIQV LMDKLVELAHQYK LKETIQKLSNVLQQVKIKDYF
HsApoC1	28	DVSSA-----
HsApoC2	25	-----
HsApoC3	24	DASLL-----
HsApoC4	33	EGT LS-----
HsApoD	69	MENGK-----
HsApoE2	77	ELRAL-----
HsApoF	44	NVLMH-----
HsApoH	87	AGILE-----
HsApoJ	78	KKKKE-----
HsApoL1	101	AELPR-----
HsApoL2	42	AELPR-----
HsApoL3	42	AELPR-----
HsApoL4	66	AELPR-----
HsApoL5	64	STVHS-----
HsApoL6	42	-----
HsApoM	27	QLTTL-----
HsApoO	31	PKNSV-----
HsApoOL	33	KQLVK-----
HsMTTP	94	QQRGE-----
DmMtp	99	TRIPD-----
DmApoLppI	191	KLELINFNVDTELYVAEQDKQKAIALKGNKKNKNSQPSEICFNQLELVGLNICIKSSTSLSEVQAGNGNVAERGLSVSEK
DmApoLppII	114	-----
DmApoLTPI	398	HQDFTAWIYNPRMLLAINGVNITGLAGTVKVNEKNGIKQHVDVLSFETKKLQAVIKGNVVQSEITTSTNMTIKYRFQANK
DmApoLTPII	109	-----
DmCG31659	32	-----
DmCvD	97	-----EMYPPYKPFKIALTKDGAISHVVFKEGDPIWSMNFKRAIASVLQFQMKSSGAFVVDE
DmFabp	40	-----
DmG1az	42	-----
DmMic26-27	47	-----
DmN1az	32	-----
HsApoA1	31	-----
HsApoA2	14	-----
HsApoA4	62	-----
HsApoA5	62	-----
HsApoB48	182	VYGNCSHTFTVKTRKGNVATEISTERDLGQC DRFKPIRTGISPLALIKGMTRPLSTLISSQSCQYTLD AKRKHVAEAIC
HsApoB52	211	EKLVGFI DD AVKKLNELSFKTFIEDVNKFLDMLIKKLKSF DYHQFVDETNDKIREVTQRLNGEIQAELPQKAEALKFL
HsApoC1	33	-----
HsApoC2	25	-----
HsApoC3	29	-----
HsApoC4	38	-----
HsApoD	74	-----
HsApoE2	82	-----
HsApoF	49	-----
HsApoH	92	-----
HsApoJ	83	-----
HsApoL1	106	-----
HsApoL2	47	-----
HsApoL3	47	-----
HsApoL4	71	-----
HsApoL5	69	-----
HsApoL6	42	-----
HsApoM	32	-----
HsApoO	36	-----
HsApoOL	38	-----
HsMTTP	99	-----
DmMtp	104	-----

DmApoLppI	271	FHLSRPFNFAYVLTTERKFTFKGIHTQEAFSQKWKLDYSTPGSKVSHDTTVVYELGNKPKTFSRLSFDNSQCHFAVEGGI
DmApoLppII	114	-----
DmApoLTPI	478	IEEINFAGKLVNNGDKSKTEYRGNMKLQTSAYPKLNFASESTWLSLQGHTEGMITYNNAPDYVNPNYTSLVRLIFARSHS
DmApoLTPII	109	-----
DmCG31659	32	-----
DmCvD	154	LGIHGTCRTEYFVSNRTNYISIRKTPEVKTCKPYSEAVHTTRSNVPPNTCEFDHQKSVIIGNEAIYGMSPHNETGYLISM
DmFabp	40	-----
DmGlaz	42	-----
DmMic26-27	47	-----
DmNlaz	32	-----
HsApoA1	31	-----
HsApoA2	14	-----
HsApoA4	62	-----
HsApoA5	62	-----
HsApoB48	262	KEQHLFLPFSYKNKYGMVAQVTQTLKLEDTPKINSRFFGEGTKKMGLAFESTKSTSPPKQAEAVLKTQLKELKLTISEQN
HsApoB52	291	EETKATVAVYLESQDQTKITLIINWLQEALSSASLAHMKAKFRETLEDTRDRMYQMDIQQELQRYLSLVGQVYSTLVTYI
HsApoC1	33	-----
HsApoC2	25	-----
HsApoC3	29	-----
HsApoC4	38	-----
HsApoD	74	-----
HsApoE2	82	-----
HsApoF	49	-----
HsApoH	92	-----
HsApoJ	83	-----
HsApoL1	106	-----
HsApoL2	47	-----
HsApoL3	47	-----
HsApoL4	71	-----
HsApoL5	69	-----
HsApoL6	42	-----
HsApoM	32	-----
HsApoO	36	-----
HsApoOL	38	-----
HsMTTP	99	-----
DmMtp	104	-----
DmApoLppI	351	NNDKNELVVGQYEQDKEIKKSKIGFSKNGNEYKPLIEIQDNNGISNSINGYHADGKIVVKNS - - - NNIERYNFENFQ
DmApoLppII	114	-----
DmApoLTPI	558	EDSFLDGTQTRASLELKLPRSKIDYRILVKHKEHIKNGTEHNVIVGLKYTPEKEITGLFSVHLPRRNLFAIDAYMNVTVP
DmApoLTPII	109	-----
DmCG31659	32	-----
DmCvD	234	AHAKGTTLIHTFESTGEAQFINSELLNLFNETPIDNPIDIETSMAAEPNLELQRLDPNDPTGGRSPQQQETLIAQAGT
DmFabp	40	-----
DmGlaz	42	-----
DmMic26-27	47	-----
DmNlaz	32	-----
HsApoA1	31	-----
HsApoA2	14	-----
HsApoA4	62	-----
HsApoA5	62	-----
HsApoB48	342	IQRANLFNKLVTLELRGLSDEAVTSLLPQLIEVSSPITLQALVQCGQPQCSTHILQWLKRVHANP - - - LLIDVVTYLVAL
HsApoB52	371	SDWWTLAANKLTDFAEQYSIQDWAKRMKALVEQGFTVPEIKTILGTMPAFEVSLQALQKATFQTPDFIVPLTDLRIPSVQ
HsApoC1	33	-----
HsApoC2	25	-----
HsApoC3	29	-----
HsApoC4	38	-----
HsApoD	74	-----
HsApoE2	82	-----
HsApoF	49	-----
HsApoH	92	-----
HsApoJ	83	-----
HsApoL1	106	-----
HsApoL2	47	-----
HsApoL3	47	-----
HsApoL4	71	-----
HsApoL5	69	-----
HsApoL6	42	-----
HsApoM	32	-----
HsApoO	36	-----
HsApoOL	38	-----
HsMTTP	99	-----
DmMtp	104	-----

DmApoLppI	427	VSNSNNAHVAVNGWSDVGTNSLTSELRISLDHQTFLLIKENLKLLENGLYEAGFFINDEHSPENIYGSSIHLLTIADQSYALK
DmApoLppII	114	-----
DmApoLTPI	638	EFNSTASLKVNEKATKDYIIFINGSWFTGHSVAVKANYKDRSSRVQALHHLKMIVESPSFNITSLNIIYRRKQLLIFYD
DmApoLTPII	109	-----
DmCG31659	32	-----NESDSSEKKEYDYDNLANEESSESQNYDNMHP
DmCvD	314	LLDSLAEALETTEFKFSEPYDSTLSDVIKLLSEMDFDSLTKLYREVDIGTSYRQETIRNIFHEIIPRIGTKASVFLTHHL
DmFabp	40	-----
DmGlaz	42	-----
DmMic26-27	47	-----
DmNlaz	32	-----
HsApoA1	31	-----
HsApoA2	14	-----
HsApoA4	62	-----
HsApoA5	62	-----
HsApoB48	418	IPEPSAQQLRIFNMARDQRSRATLYALSHAVNNYHKTNPQTGTQELLDIANYLMEQIQDDCTGDEDYTYLILRVIGNMGQ
HsApoB52	451	INFKDLKNIKIPSRFSTPEFTILNTFHIPSFTIDFVEMKVKIIRTIDQMLNSELQWPVPDIYLRDLKVEDIPLARITLPD
HsApoC1	33	-----
HsApoC2	25	-----
HsApoC3	29	-----
HsApoC4	38	-----
HsApoD	74	-----
HsApoE2	82	-----
HsApoF	49	-----
HsApoH	92	-----
HsApoJ	83	-----
HsApoL1	106	-----
HsApoL2	47	-----
HsApoL3	47	-----
HsApoL4	71	-----
HsApoL5	69	-----
HsApoL6	42	-----
HsApoM	32	-----
HsApoO	36	-----
HsApoOL	38	-----
HsMTTP	99	-----KSIFKGKSPSKIMGKENLEALQRPTLLHLIHGKVKEFYSYQNEAVAIEN
DmMtp	104	-----RPFYISLVRGQPDKVIAHTSKDQSLN
DmApoLppI	507	TNGKAAAWSIGSDGSFNFQKLADSN SARAGSLVENVEIQYKNKQVGGIKIMS NFDVNKMDVDVEISREQKIGSIIVKYES
DmApoLppII	114	-----IQKPVQFTLVSGILEPQICSDSSDLDYSLNIKRAVVSLLSGIEAEHEVDVFGMCPHTHTSTSKVGNA
DmApoLTPI	718	IQAKYDQDPYGLTIQYASNAHNRNTNAEVRLKVKERDYWINAKLLSEQPKLLQLEIHMDKIRDVHIQVGLLNVDKRKELS
DmApoLTPII	142	KSSDFNVDLTKNLLRFAFHDLISEVCPQEETPWVLNIKKGILSAFQNTMMRFVDVANTTETDVSQCQVQYALEDTDS
DmCG31659	32	-----
DmCvD	394	VLNKLTKPQIAVQLLIPMPFHIFELSAELVQKCEDFLNIGPDRPDVRQAAILSFATLIHNVYVAKGIDKEKFEEYVQKYF
DmFabp	40	-----
DmGlaz	42	-----
DmMic26-27	47	-----
DmNlaz	32	-----
HsApoA1	31	-----
HsApoA2	14	-----
HsApoA4	62	-----
HsApoA5	62	-----
HsApoB48	498	TMEQLTPELKSSILKCVQSTKPSLMIQKAAIQALRKMEPKDKDQEVLLQTFLDDASPGDKRLAAYLMLMRSPSQADINKI
HsApoB52	531	FRLPEIAIPEFIIPTLNLNDFQVPDLHIPEFQLPHISHTIEVPTFGKLYSILKIQSPLFTLDANADIGNGTTSANEAGIA
HsApoC1	33	-----
HsApoC2	25	-----
HsApoC3	29	-----
HsApoC4	38	-----
HsApoD	74	-----
HsApoE2	82	-----
HsApoF	49	-----
HsApoH	92	-----
HsApoJ	83	-----
HsApoL1	106	-----
HsApoL2	47	-----
HsApoL3	47	-----
HsApoL4	71	-----
HsApoL5	69	-----
HsApoL6	42	-----
HsApoM	32	-----
HsApoO	36	-----
HsApoOL	38	-----
HsMTTP	148	IKRGLASLFQTQLSSGTTNEVDISGNCKVITYQAHQDKVIKIKALDSCKIARSGFTTPNQVLGVSSKATSVTTYKIEDSFV
DmMtp	131	LERGIASLLQLRLDASQEEELDVSGLCRVSYNVKSSTKVEKTRDCSLWDLRVNYPPEALGVTQQAQETVFYELSSGT

DmApoLppI	587	NQRHAQDYSLEASAKINKHSIDVISKCDFNGNVYVVDNSLVTSWGTL LSAKGEIGQRYSAQDININIQGNVQISGKDKVT
DmApoLppII	181	NII-----
DmApoLTPI	798	LELKWDANRDPSQRLGLLAEYNTPGTHYDGNLMITYPERTIHFNFNSFTGGPKYFGKVHASWSINEVIEFEYEAGILPG
DmApoLTPII	222	SYVTIRKTKDINSCRQRYATHSVLQTTPYTF-----
DmCG31659	32	-----
DmCvD	474	NAYLSDRDFDQKMLYLQGLNNLQLGNVANYLEPIVQDPNEHEDLKFQAAWTTLALADRRRAERIYEVYWPFI FESRNASLEL
DmFabp	40	-----
DmGlaz	42	-----
DmMic26-27	47	-----
DmNlaz	32	-----
HsApoA1	31	-----
HsApoA2	14	-----
HsApoA4	62	-----
HsApoA5	62	-----
HsApoB48	578	VQILPWEQNEQVKNFVASHIANILNSEELDIQDLKKLVKEALKESQLPTVMDFRKFSRNYQLYKSVSLPSLDPASAKIEG
HsApoB52	611	ASITAKGESKLEVLNFDQANAQLSNPKINPLALKESVKFSSKYLRTHEGSEMLFFGNAIEGKSNTVASLHTEKNTLELS
HsApoC1	33	-----
HsApoC2	25	-----
HsApoC3	29	-----
HsApoC4	38	-----
HsApoD	74	-----
HsApoE2	82	-----
HsApoF	49	-----
HsApoH	92	-----
HsApoJ	83	-----
HsApoL1	106	-----
HsApoL2	47	-----
HsApoL3	47	-----
HsApoL4	71	-----
HsApoL5	69	-----
HsApoL6	42	-----
HsApoM	32	-----
HsApoO	36	-----
HsApoOL	38	-----
HsMTTP	228	I AVLAEETHNFGNLFLTQTIKGIKIVSKQKLELKTTEAGPRLMSGKQAAAAIKAVDSKYTAIPIVGQVFQSHCKGCPSLSEL
DmMtp	211	LLHAESQENHRLNLAAPKPDVGSFVKSSLILQHVSQGSEEVKQLQLGSLDKAIQSLLEWYRVFELESVDVGMISAIKEQ--
DmApoLppI	667	QWILKVI GTPDKTNSDFRISRDTS ELIKLTSESQHPQDKISFAKLN LIVKNQLTAKGEFRVAKNGKGDFTASIDTLKTEP
DmApoLppII	184	-----
DmApoLTPI	878	HTLHNWVKAELRTPFDGWRVNSLDAGIYSLKNLILVNSTLFWADDQKLQVGKYSYDVNDQLMSFDVRFGINSTIRDIPT
DmApoLTPII	253	-----
DmCG31659	32	-----
DmCvD	554	RVAAVTLLLISNPTAARLISIHRIIQSETDPHMINYYRTTVT-----
DmFabp	40	-----
DmGlaz	42	-----
DmMic26-27	47	-----
DmNlaz	32	-----
HsApoA1	31	-----
HsApoA2	14	-----
HsApoA4	62	-----
HsApoA5	62	-----
HsApoB48	658	NLIFDPNNYLPKESMLKTTLTAFGFASADLIEIGLEGKGFEPTLEALFGKQGFFPD SVNKALYWVNGQVPDGVSKVLVDH
HsApoB52	691	NGVIVKINNQLTLDSENTKYFHKLNI PKLDFSSQADLRNEIKTLLKAGHIAWTSSGKGSWKWACPRFSDEGTHESQISFTI
HsApoC1	33	-----
HsApoC2	25	-----
HsApoC3	29	-----
HsApoC4	38	-----
HsApoD	74	-----
HsApoE2	82	-----
HsApoF	49	-----
HsApoH	92	-----
HsApoJ	83	-----
HsApoL1	106	-----
HsApoL2	47	-----
HsApoL3	47	-----
HsApoL4	71	-----
HsApoL5	69	-----
HsApoL6	42	-----
HsApoM	32	-----
HsApoO	36	-----
HsApoOL	38	-----
HsMTTP	308	WRSTRKYLQPDNLSKAEAVRNFLAFIQHLRTAKKEEILQILK MENKEVLPQLVDAVTS AQTS-----
DmMtp	289	-----

DmApoLppI	747	KHKLEIESKFHIQSPKYDIDASLTLDGKRKVHLKSENTIEKLKFSTKNIGEANDKIIAFEANGSLKGELRGNGEIQGTFI
DmApoLppII	184	-----
DmApoLTPI	958	INVKVKHWMVDVKKVDTELYLGYSGQNDTFNTYSMDSSWEIEKNQRYNNYSGLVHLVSPFKGYEKGGGLVAHFSLSDQRRVS
DmApoLTPII	253	-----
DmCG31659	32	-----
DmCvD	596	-----
DmFabp	40	-----
DmGlaZ	42	-----
DmMic26-27	47	-----
DmNlaZ	32	-----
HsApoA1	31	-----
HsApoA2	14	-----
HsApoA4	62	-----
HsApoA5	62	-----
HsApoB48	738	FGYTKDDKHEQDMVNGIMLSVEKLIKDLKSKEV-----
HsApoB52	771	EGPLTSFGLSNKINSKHLRVNQNLYESGSLNFSKLEIQSQVDSQHVGHSVLTAKGMALFGEKAEFTGRHDAHLNGKVI
HsApoC1	33	-----
HsApoC2	25	-----
HsApoC3	29	-----
HsApoC4	38	-----
HsApoD	74	-----
HsApoE2	82	-----
HsApoF	49	-----
HsApoH	92	-----
HsApoJ	83	-----
HsApoL1	106	-----
HsApoL2	47	-----
HsApoL3	47	-----
HsApoL4	71	-----
HsApoL5	69	-----
HsApoL6	42	-----
HsApoM	32	-----
HsApoO	36	-----
HsApoOL	38	-----
HsMTTP	370	-----
DmMtp	289	-----
DmApoLppI	827	FNAPDGRVIDGSINRKISTNAKSGLSQGNIDAQL-----
DmApoLppII	184	-----TKARNLNSCSHREQINSGLVSGKV-----
DmApoLTPI	1038	GAASLNFDLREFTLTMNGYVKKFTDNMLTVNITTPLEKFGTINARFGLNEKKRHAVA-EVRAPTAALGVEVLADIKNLLNF
DmApoLTPII	253	-----RDDKTIWPIILKSQSHCNLTIDNNV-----
DmCG31659	32	-----AVGD-----
DmCvD	596	-----SISSETTYPCYQHLRRLLSYMRHL-----
DmFabp	40	-----
DmGlaZ	42	-----
DmMic26-27	47	-----LRKTEPKPERH-----
DmNlaZ	32	-----CPDVKLLDT-----
HsApoA1	31	-----
HsApoA2	14	-----
HsApoA4	62	-----FQDKLGEVNTYAGDLQKKL-----
HsApoA5	62	-----QDLNMMNKFLKLRPLSGSEAPRL-----
HsApoB48	771	-----PEARAYLRILGEELGFASLHDLQL-----
HsApoB52	851	GTLKNSLFFSAQPFEITASTNNEGNLKVRFPLRL-----
HsApoC1	33	-----
HsApoC2	25	-----
HsApoC3	29	-----
HsApoC4	38	-----P-----
HsApoD	74	-----IKVLNQELRADGTVNQIEGEATPVNLTE-----
HsApoE2	82	-----MDETMKELKAYKSELEEQL-----
HsApoF	49	-----FPLSLESQTPSSDPLSCQFLHPKSL-----
HsApoH	92	-----NGAVRYTTFEYPNT-----
HsApoJ	83	-----DALNETRESETKLKEPGVCNETM-----
HsApoL1	106	-----NEADELRKALDNLARQMIMKDKNW-----
HsApoL2	47	-----DEADELRKALNKLASHMVMKDKNR-----
HsApoL3	47	-----DEADALYEALKKLRTYAAIEDEYV-----
HsApoL4	71	-----EEADALYEALKNLTPYVAIEDKDM-----
HsApoL5	69	-----DEAGMSYFLFEELMRCDKDSMP-----
HsApoL6	42	-----
HsApoM	32	-----GVDGKE-----
HsApoO	36	-----KVDELSL-----
HsApoOL	38	-----PEQLPI-----
HsMTTP	370	-----DSLEAILDFLDFKSDSSIILQERF-----
DmMtp	289	-----TLEDQLKASLTQLQADVGKSSLA-----

DmApoLppI	861	-----SDTPFGSNKK-----
DmApoLppII	208	-----NEKAGITSSL-----
DmApoLTPI	1118	DVKLSVATPIESFQQAIFALFNPERVDMRGLWNNVTLGFTGVVHMQNITDFEYSYHVFTPLAGFEENGFIQVLLKRKEF
DmApoLTPII	277	-----YKEIKCLETH-----
DmCG31659	36	-----LMDRFKGGK-----
DmCvD	620	-----PQKPESRYWVT-----
DmFabp	40	-----
DmG1az	42	-----FNMSRVLGHW-----
DmMic26-27	58	-----PPQDSVLHKN-----
DmN1az	41	-----FDAEAYMGVW-----
HsApoA1	31	-----
HsApoA2	14	-----
HsApoA4	81	-----VPFATELHER-----
HsApoA5	86	-----PQDPVGMRRQ-----
HsApoB48	795	-----LGKLLLMGAR-----
HsApoB52	885	-----TGKIDFLNNYA-----
HsApoC1	33	-----LDKLKEFGNT-----
HsApoC2	25	-----
HsApoC3	29	-----
HsApoC4	39	-----PPKLKMSRWS-----
HsApoD	102	-----PAKLEVKFSW-----
HsApoE2	101	-----TPVAEETRAR-----
HsApoF	74	-----PGFSHMAPLP-----
HsApoH	106	-----ISFSCNTGFY-----
HsApoJ	107	-----MALWEEKPC-----
HsApoL1	130	-----HDKGQQYRNW-----
HsApoL2	71	-----HDKDQQHRQW-----
HsApoL3	71	-----QQKDEQFREW-----
HsApoL4	95	-----QQKEQQFREW-----
HsApoL5	92	-----DGNLSEEEKL-----
HsApoL6	42	-----
HsApoM	38	-----FPEVHLGQWY-----
HsApoO	43	-----YSVPEGQSKY-----
HsApoOL	44	-----YTAPPLQSKY-----
HsMTTP	394	-----LYACGFASHP-----
DmMtp	313	-----LAYVKLIPLAR-----
DmApoLppI	871	-----RSISLIGKLDL-----
DmApoLppII	218	-----LLQANYIKESR-----
DmApoLTPI	1198	VFQLHGKMSNYKLGVKINGEPKSDLVNQLGSNKMEMLYDADFKPLNAETDYKPDADDEEYFSYFTNFQVDTLWPTIVG
DmApoLTPII	287	-----LLVPFSNASSG-----
DmCG31659	46	-----YTHSIYPHLSLR-----
DmCvD	631	-----GNYIFDYRDSKFG-----
DmFabp	40	-----VEVT-----
DmG1az	52	-----YEVERSFYLPE-----
DmMic26-27	68	-----LEAGVRYVREE-----
DmN1az	51	-----YEYAAYPFAFE-----
HsApoA1	31	-----
HsApoA2	14	-----
HsApoA4	91	-----LAKDSEKLKEE-----
HsApoA5	96	-----LQEELEEVKAR-----
HsApoB48	805	-----TLQGIPQMIGE-----
HsApoB52	896	-----LFLSPSAQQASWQ-----
HsApoC1	43	-----LEDKARELISR-----
HsApoC2	25	-----
HsApoC3	29	-----
HsApoC4	49	-----
HsApoD	112	-----FMPSAPYWILA-----
HsApoE2	111	-----LSKELQAAQAR-----
HsApoF	84	-----KFLVSLALRNA-----
HsApoH	116	-----LNGADSAKCTE-----
HsApoJ	117	-----LKQTCMKFYAR-----
HsApoL1	140	-----FLKEFPRLKSE-----
HsApoL2	81	-----FLKEFPRLKRE-----
HsApoL3	81	-----FLKEFPQVKRK-----
HsApoL4	105	-----FLKEFPQIRWK-----
HsApoL5	102	-----FLSYFPLHKFE-----
HsApoL6	42	-----FLREFPRLKED-----
HsApoM	48	-----FIAGAAPTKEE-----
HsApoO	53	-----VEEARSQ-----
HsApoOL	54	-----VEEQPGHLQMG-----
HsMTTP	404	-----NEELLRALISK-----
DmMtp	324	-----ITRQEQFEDLLTE-----

DmApoLppI	882	-----
DmApoLppII	229	-----
DmApoLTPI	1278	NVDIQEIIDFYLVVGHVELPQGKVEFKDRLHYPDYINVHNLTVTTPFAVAKNIKSIVEYHVDLNFNAFYERVKFIVNDD
DmApoLTPII	298	-----
DmCG31659	58	-----
DmCvD	644	-----
DmFabp	44	-----
DmGlaz	63	-----
DmMic26-27	79	-----
DmNlaz	62	-----
HsApoA1	31	-----
HsApoA2	14	-----
HsApoA4	102	-----
HsApoA5	107	-----
HsApoB48	816	-----
HsApoB52	909	-----
HsApoC1	54	-----
HsApoC2	25	-----
HsApoC3	29	-----
HsApoC4	49	-----
HsApoD	123	-----
HsApoE2	122	-----
HsApoF	95	-----
HsApoH	127	-----
HsApoJ	128	-----
HsApoL1	151	-----
HsApoL2	92	-----
HsApoL3	92	-----
HsApoL4	116	-----
HsApoL5	113	-----
HsApoL6	53	-----
HsApoM	59	-----
HsApoO	60	-----
HsApoOL	65	-----
HsMTTP	415	-----
DmMtp	337	-----

DmApoLppI	882	-----	LNT--KTKEFSANSNLVYTAFNGEKS-----
DmApoLppII	229	-----	IVN--HLIENVQLTETYKFIGNTRNSDI-----
DmApoLTPI	1358	KDNTQELGFVFNYTALQDNVKKPAHDVQVTLLTPYEMLHEIYVHGHIELDDNAYKGNISAVTAHTHLSMAASIENEDNFL	
DmApoLTPII	298	-----	ALT--TSTSRLKLDGVESYSAGEFLEQNPELV-----
DmCG31659	58	-----	VEK-----
DmCvD	644	-----	IGA--MLQVFLVGDPKSDMPVVAFFKFDTEALG-----
DmFabp	44	-----	LEG--D-----
DmGlaz	63	-----	
DmMic26-27	79	-----	VQS--GYKAVA-----
DmNlaz	62	-----	IGK-----
HsApoA1	31	-----	
HsApoA2	14	-----	
HsApoA4	102	-----	IGK--ELE-----
HsApoA5	107	-----	LQP--YMAEAHELVGWNLE-----
HsApoB48	816	-----	VIR--KGSKNDFFLHYIFMENAFELPTGAGLQLQI---
HsApoB52	909	-----	VSA--RFNQYKYNQNFSAAGNNENIMEAHVGINGEANLD
HsApoC1	54	-----	IKQ--S-----
HsApoC2	25	-----	
HsApoC3	29	-----	
HsApoC4	49	-----	
HsApoD	123	-----	T---DYENYALV-----
HsApoE2	122	-----	LGA--DME-----
HsApoF	95	-----	LEE--AGCQAD-----
HsApoH	127	-----	EGK--WSPEL-----
HsApoJ	128	-----	VCR--SGSGLVGRQLEEF-----
HsApoL1	151	-----	LED--NIRRLRALADGVQK-----
HsApoL2	92	-----	LED--HIRKLALAEVEEQ-----
HsApoL3	92	-----	IQE--SIEKLRALANGIEE-----
HsApoL4	116	-----	IQE--SIERLRVIANEIEK-----
HsApoL5	113	-----	LEQ--NIKELNTLADQVDT-----
HsApoL6	53	-----	LKG--NIDKLALADDIDK-----
HsApoM	59	-----	LAT--F-----
HsApoO	60	-----	LEE--SISQLR-----
HsApoOL	65	-----	FASIR-----
HsMTTP	415	-----	FKG--SIGSSDIRETVMITGTLVRKLC-----
DmMtp	337	-----	HAE--VLPQLVDLLGAVQTFD-----

DmApoLppI	906	-----EISYQIKQQPN--GDAKNIDFSLKAYGNPLPQP-----FEIAFALG
DmApoLppII	256	-----SAKVVTILKLKNPSGTKANSPTGSTVRSLIFQRPETYTSKNI-----NALKTILS
DmApoLTPI	1438	ETSVGIQLETDAlPHYGCQVYFKK--DFSADVKAIDIRFEVTDNGTLNQLHISTDWHOTDPSYIVNANGRIKTTMLPLQMA
DmApoLTPII	328	-----ERRATLVFDHT--PAVKPSHDEIKAARELLV-----EMCRVGFP
DmCG31659	61	-----CQSTDFIEKEE-----NKFSVVAR
DmCvD	675	-----KFTGQLALYIKARGLPDTILNKMQRNGSDPFTFKSIK-----ALLAMLQA
DmFabp	48	-----TYTLTTTSTFK--TSAISFKLGVE-----
DmGlaZ	63	-----IASGCTTFQFE--PYNKGEQSKFS-----
DmMic26-27	88	-----DQAGIVGHYVE--TAKAHTQSTI-----DMLNEPQN
DmNlaZ	65	-----KCIYANYSLIDNSTV-----SVVNAAIN
HsApoA1	31	-----QKVEPLRAELQ--EGARQKLHEL-----
HsApoA2	14	-----SLEGALVR-----
HsApoA4	108	-----ELRARLLPHAN--EVSQKIGDNL-----RELQQRLE
HsApoA5	124	-----GLRQQLKPYTM--DLMEQVALRV-----QELQEQLR
HsApoB48	849	-----SSSGVIAPGAK--AGVKLEVANMQAELVAKPSVSVEFV-----TNMGIIIP
HsApoB52	945	FLNIPLTIPEMRLPYTIITTPPLK--DFSLWEKTGLKEFLKTTKQSFDSLVAQYKKKNKHSITNPLAVLCEFISQSIK
HsApoC1	58	-----ELSAKMRLEPF--PG-----
HsApoC2	25	-----
HsApoC3	29	-----SFMQGYMKHAT--KTAKDALSSVQ-----
HsApoC4	49	-----LVRGRM-----
HsApoD	132	-----YSCTCIIQLFH--VDFAWILARNP-----NLPPETVD
HsApoE2	128	-----DVCGRLVQYRG--EVQAMLGQST-----EELRVRLA
HsApoF	104	-----VWALQLQLYRQ--GGVNATQVLIQ-----HLRGLQKG
HsApoH	135	-----PVCAPIIICPPP--SIPTFATLRV-----YKPSAGNN
HsApoJ	145	-----NQSSPFYFWMNGDRIDSLLENDRQQT-----HMLDVMQD
HsApoL1	168	-----VHKGTTIANVV--SGSLSISSGIL-----TLVGMGLA
HsApoL2	109	-----VHRGTTIANVV--SNSVGTTSGIL-----TLLGLGLA
HsApoL3	109	-----VHRGCTISNVV--SSSTGAASGIM-----SLAGLVLA
HsApoL4	133	-----VHRGCVIANVV--SGSTGIL-----SVIGVMLA
HsApoL5	130	-----THELLTKTSLV--ASSSGAVSGVM-----NILGLALA
HsApoL6	70	-----THKKFTKANMV--ATSTAVISGVM-----SLLGLALA
HsApoM	63	-----DPVDNIVFNMA--AGSAPMQLHLRATI-----
HsApoO	69	-----HYCEPYTTWCQ--ETYSQTKPKMQ-----SLVQWGLD
HsApoOL	70	-----TATGCYIGWCK--GVYVFVKNGIM-----DTVQFGKD
HsMTTP	441	-----QNEGCKLKAVV--EAKKLILGGLEKAEKKEDTRMYLLALKN-----ALLPEGIP
DmMtp	356	-----AHNATFGFLYKESETTSEQLDLLEKYLQSLAVATHPDRKIVE-----HLFGLLEQ
DmApoLppI	945	-----
DmApoLppII	307	-----
DmApoLTPI	1516	STSVLVIQGQNPHLNFIDLNLLSQNGQSIAYGARANKKKDVFNIEVWTPMKNFRNISMHGTAIRSPRDPGRYDVSGFLYRN
DmApoLTPII	365	-----
DmCG31659	80	-----
DmCvD	721	-----
DmFabp	70	-----
DmGlaZ	85	-----
DmMic26-27	117	-----
DmNlaZ	88	-----
HsApoA1	52	-----
HsApoA2	22	-----
HsApoA4	137	-----
HsApoA5	153	-----
HsApoB48	893	-----
HsApoB52	1023	-----
HsApoC1	71	-----
HsApoC2	25	-----
HsApoC3	51	-----
HsApoC4	55	-----
HsApoD	162	-----
HsApoE2	157	-----
HsApoF	134	-----
HsApoH	164	-----
HsApoJ	179	-----
HsApoL1	198	-----
HsApoL2	139	-----
HsApoL3	139	-----
HsApoL4	159	-----
HsApoL5	160	-----
HsApoL6	100	-----
HsApoM	88	-----
HsApoO	99	-----
HsApoOL	100	-----
HsMTTP	488	-----
DmMtp	406	-----

DmApoLppI	945	-----DYSA-QHAVVSITSKYGEIFSVSANGNYYNNQALEYGLQANIEIPKSTLKSLEINSHGKVLKSL
DmApoLppII	307	-----DLVD-----STGDYVKKETAKKFVEFIRLLRQSDSETLLELAAPHPNKV
DmApoLTPI	1596	MATYEVGTGAVRMTNSLPIDVVLRVQPKAGGRDGVIELNIHEAGPKKIRFSFSAIEDGKMCQMSGGYSVSKTNGAMDFSVL
DmApoLTPII	365	-----NIQR-----EFIDVFTNFLTQTSKSLDYKTLVLLQRSASTCE
DmCG31659	80	-----
DmCvD	721	-----PIIN-----SKDLHLEFILQMEGKTVLSYYLNQRMFRQL
DmFabp	70	-----
DmGlaz	85	-----
DmMic26-27	117	-----SLHR-----
DmNlaz	88	-----RFTG-----
HsApoA1	52	-----
HsApoA2	22	-----
HsApoA4	137	-----PYAD-----QLRTQVSTQAEQLRRQLTPYAQRMERV
HsApoA5	153	-----VVGE-----DTKAQLLGGVDEAWALLQGLQSRV
HsApoB48	893	-----DFAR-----SGVQMNTNFFHESGLEAHVALKAGKLFIPSPKRPVKLLS
HsApoB52	1023	-----SFDRHFEKRNNDLDFVTKSYNETKIKFDKYKAEKSHDELPRTFQIPGYTPVVNNEVSPFTIE
HsApoC1	71	-----
HsApoC2	25	-----
HsApoC3	51	-----
HsApoC4	55	-----
HsApoD	162	-----SLKN-----
HsApoE2	157	-----SHLR-----KLRKRL
HsApoF	134	-----RSTE-----
HsApoH	164	-----SLYR-----
HsApoJ	179	-----HFSR-----ASSIIDELFQDRFFTREPQDTYHYLPFSLP
HsApoL1	198	-----PFTE-----
HsApoL2	139	-----PFTE-----
HsApoL3	139	-----PFTA-----
HsApoL4	159	-----PFTA-----
HsApoL5	160	-----PVTa-----
HsApoL6	100	-----PATG-----
HsApoM	88	-----
HsApoO	99	-----SYDY-----
HsApoOL	100	-----AYVY-----
HsMTTP	488	-----SLLK-----YAEAGEGPISHLATTALQRYDLPFITDEVKKTNLN
DmMtp	406	-----ESIK-----KHLKLRESVIQTVATLTRQSGLDVEDPLLKEVRSYL
DmApoLppI	1008	IGNENAAYNVEFFLDSKTSLGQYARVNTVWNGTANDGSYDFEAQTNM---ESPLKFNGKY-----
DmApoLppII	352	LARKVYLDGLFRTSTAESARVILKQLSKFDEKEKLLAILSLNIVKSVDKETLNQAAQSLLPN----APKELYIAVGNLV
DmApoLTPI	1676	VESTEPEIARINFYGNLSPNSEGLVGDLSLETPWKALGIDTVHLHSDVGFLNKGGHIVGEYKIGQYIGRGSCLSWILA
DmApoLTPII	402	QGRNHLLESPLFIGSTASYKVMRDQII----NEKLTQKMAHDMWTALSFITRPDEETLETF-----
DmCG31659	80	-----ELNTQTGTVMRKADILNVEPEFGRYVLGT-----
DmCvD	755	TYDNILERMQQIIRTDSHINMQTVRWPFMNRITYPTVLGT---SSDVLLQTTVLVTSLRGNI--TEQRNSPITKHTLEID
DmFabp	70	-----FDEETLDG-----RNVKSIITLD-----
DmGlaz	85	-----NFKLAVAI-----KNINRITGNP-----
DmMic26-27	121	-----SGAIVVGG-----LAGF-----IFAARGGF-----
DmNlaz	92	-----QPSNVTGQ-----AKVL-----GPGQLAVAF-----
HsApoA1	52	-----QEKLSPLG-----EEMR-----DRARAHVDAL-----
HsApoA2	22	-----RQAKEPCV-----ESLV-----SQYFQTVTDY-----
HsApoA4	169	RENADSLQASLRPHADELKAKIDQNVEEL---KGRLTPYA---DEFK---VKIDQTVVEEL-----
HsApoA5	181	VHHTGRFKELFHPYAESLSVSGIRHVQEL---HRSVAPHA---PASP---ARLSRCVQVL-----
HsApoB48	938	GGNTLHLVSTTKTEVIPPLIENRQSWSVCKQVFPGLNYCTSGAYSNASSTDSASYPLTGDTRLELELRPTGEIEQYSVS
HsApoB52	1087	MSAFGYVFPKAVSMPSFSILGSDVRVPSYTLILPSLELPV---LHVP---RNLKLSLPDFKELCTISHIFIPAMGNIT
HsApoC1	71	-----HGRAGVCF-----
HsApoC2	25	-----PQQDEMPS-----PTFL-----TQVKESLSSY-----
HsApoC3	51	-----ESQVAQQA-----RGWV-----TDGFSSLKDY-----
HsApoC4	55	-----KELLETVVNR-----
HsApoD	166	-----ILTSNNIDVKKMTVTDQVNCPL---SQAKEPCV---ESLV---SQYFQTVTDY-----
HsApoE2	167	LRDADDLQKRLAVYQAGAREGAERGLSAI---RERLGPLV---EQGR---VRAATVGLA-----
HsApoF	138	-----RNVSVREALASALQLLAREQQSTGRVG---RSLPTEDCENEKEQAVHN-----
HsApoH	168	-----DTAVFECL---PQHAFMGNDITCTTHGN-----
HsApoJ	213	HRRPHFFFPKSRIVRSLMPFSPIEPLNFHAMFQPFLEMIHEAQQAMDIHFHSPAFQHPPTF-----IREGD
HsApoL1	202	-----GGSLVLL---EPGMELGI---TAAL---TGITSSTMDY-----
HsApoL2	143	-----GISFVLL---DTGMGLGA---AAAV---AGITCSVVEL-----
HsApoL3	143	-----GTSLALT---AAGVGLGA---ASAV---TGITTSIVEH-----
HsApoL4	163	-----GLSLSIT---AAGVGLGI---ASAT---AGIASSIVEN-----
HsApoL5	164	-----GGSLMLS---ATGTGLGA---AAAI---TNIVTNVLEN-----
HsApoL6	104	-----GGSLLLS---TAGQGLAT---AAGV---TSIVSGTLER-----
HsApoM	88	-----RMKDGLCV---PRKWI---YHLTEGSTDL-----
HsApoO	103	-----LQNAPPGF---FPLRGVIGF-----AGLIGLLAR-----
HsApoOL	104	-----LKNPPRDF---LPKMGVIT---VSGL---AGLVSARKGS-----
HsMTTP	527	IYHQNRKVHEKTVRTAAAIILNNNPSYM---DVKNILLSIGELPQEMNKYMLAIVQDILRF-----
DmMtp	446	LQGLTSKEPTLYIRALQNLQDPATIEALLEHAQTGEAPNLSVAALQALKAFPLGSFNSSHRL-----

DmApoLppI	1066	-HRKQ-----TGNIKDGDLTGKQTYVLNAQYGAQYVKMDASLGYGAEKVDIAAYVIDSSFDSVKDIKVNIR-----TFK
DmApoLppII	427	AKYCL-----KNYCQGPE-----
DmApoLTPI	1756	EDMQLVLENYLERPNAKPRIVHASAKYQNPQGTFQTLQAGGRLSVDSKWNLDVNGSAEYKSVDDFKFRVITALPLPVGDR
DmApoLTPII	459	--HSI-----LEYAKNRL-----DA-----EYT
DmCG31659	110	-----TSTAFPEG-----
DmCvD	829	ARYSS-----YASVRSRSYNPFLNLDHEINREQGFLIYIPFSSELHLNESGSKCRRYSFSRPQNLTSGLS-----FKS
DmFabp	88	-GNKL-----TQEKGDK-----
DmGlaz	103	-NVNI-----GYATPEN-----
DmMic26-27	141	-IKKV-----LYSGIGAG-----
DmNlaz	113	--YPT-----QPLTKANY-----
HsApoA1	74	-RTHL-----APYSDELRL-----
HsApoA2	44	-GKDL-----MEKVKSP-----
HsApoA4	220	-RRSL-----APYAQDTQ-----EK
HsApoA5	232	-SRKL-----TLKAKALH-----
HsApoB48	1018	ATYEL-----QREDRALVDTLKFVTQAEGAKQTEATMTFKYNRQSMTLSSSEVQIPDFVDVLGTILRVNDE-----STE
HsApoB52	1159	YDFSF-----KSSVITLNTNAELFNQSDIVAHLLSSSSVIDALQYKLEGTTRLTRKRGKLKLTALSLSNKFVEGSHN
HsApoC1	79	-WVEP-----WQMVQDEQ-----
HsApoC2	47	-----WESAKTAA-----
HsApoC3	73	-----WSTVKDKF-----
HsApoC4	65	-TRDG-----WQWFWSPS-----
HsApoD	202	-GKDL-----MEKVKSP-----
HsApoE2	218	-GQPL-----QERAQAWG-----
HsApoF	182	-VVQL-----LPGVGTFY-----
HsApoH	194	-WTKLPECREVKCPFPSRPD-----
HsApoJ	280	DDRTV-----CREIRHNS-----
HsApoL1	231	-GKKW-----WTQAQAH-----
HsApoL2	172	-VNKL-----RARAQARN-----
HsApoL3	172	-SYTS-----SAEAEASR-----
HsApoL4	192	-TYTR-----SAELTASR-----
HsApoL5	193	-RSNS-----AARDKASR-----
HsApoL6	133	-SKNK-----EAQARAED-----
HsApoM	111	-----RTEGRPDM-----
HsApoO	130	-GSKI-----KKLVYPPG-----
HsApoOL	134	-KFKK-----ITYPLGLA-----
HsMTTP	586	-EMPA-----SKIVRRVL-----
DmMtp	508	-QFES-----IFYQRKRRFDSSARTLALDIILSLRPTQEQLGNFLDYLASNDRQFEIKTYVLQKLRLAEKCPFRAL
DmApoLppI	1133	PLDDSTYVVLTALFKQTDKSYGLDTTFYHSAHKKGVDIRLDLLKEKPIIISSIAELLGDRKGKVLFEILNLADLDIKINSE
DmApoLppII	440	-----IDAISKKFSDDLKH-----
DmApoLTPI	1836	HQLSASYQGNVISQQFNPDFVLEASYESFEA-----QNKLLSRISYKNATNNLKGGLHVEWGKIQLNSVVEG
DmApoLTPII	475	LGATAVVHSFCKHHEACEENLRVQIINLLET-----
DmCG31659	118	-----VLMYVLDTDYVNFAL-----
DmCvD	897	RAVTKTRGLITKTAAPFEEIMVPEGRNDVVQ-----
DmFabp	100	-----PTTIVREFTD-----
DmGlaz	114	-----SRSSIMDFKF-----
DmMic26-27	153	-----AVASMCYPRQA-----
DmNlaz	124	-----LVLGTDYESYAV-----
HsApoA1	86	-----QRLAARLEALKE-----
HsApoA2	56	-----LQAEAKSYFEKSKE-----
HsApoA4	234	LNHQLEGLTFQMKNNAEELKARISASAEELRQ-----
HsApoA5	244	-----ARIQQNLQDLRE-----
HsApoB48	1086	GKTSYRLTLDIQNKKITEVALMGHLSCDTKEE-----
HsApoB52	1232	STVSLTTKNMEVSVATTTKAQIPILRMNFKQE-----
HsApoC1	91	-----IEKKTS-----
HsApoC2	55	-----QNLYEKTY-----
HsApoC3	81	-----
HsApoC4	77	-----TFRGFMQTYDDH-----
HsApoD	223	-----LQAEAKSYFEKSKE-----
HsApoE2	230	-----ERLRARMEEMGS-----
HsApoF	194	-----NLGTALYYATQN-----
HsApoH	213	-----NGFVNYPAPKPTLYYKDKAT-----
HsApoJ	293	-----TGCLRMKDQCCKCRE-----
HsApoL1	243	-----LVIKSLDKLKE-----
HsApoL2	184	-----LDQSGTNVAKV-----
HsApoL3	184	-----LTATSIDRLKV-----
HsApoL4	204	-----LTATSTDQLEA-----
HsApoL5	205	-----LGPLTTSHEAFGGINWSEIEA-----
HsApoL6	145	-----ILPTYDQEDRE-----
HsApoM	119	-----KTELFSSSCPPGGIM-----
HsApoO	142	-----FMGLAASLYYPQQA-----
HsApoOL	146	-----TLGATVCYPVQS-----
HsMTTP	598	-----KEMVAHNYDRFSR-----
DmMtp	580	FKSELVKRRHVNNYNVLGQKGLTTVLTRQLSQ-----

DmApoLppI	1213	ASYVVSIDEFYIIVNWSSKKLKDGYELEARAQSKNIKIQLKNENGIIFSGTATYALKKELNKTIIDGGQKVQYQGKALSG
DmApoLppII	454	-----
DmApoLTPI	1904	DFELLHKQGAQREFSAKIITPKFKNEHTFALTGSYDLEKSGHHNVGSLDYPASRRITDLDVSVSSLSNMHGIFNSTLPT
DmApoLTPII	507	-----
DmCG31659	133	-----
DmCvD	929	-----
DmFabp	110	-----
DmGlaz	124	-----
DmMic26-27	164	-----
DmNlaz	136	-----
HsApoA1	98	-----
HsApoA2	70	-----
HsApoA4	266	-----
HsApoA5	256	-----
HsApoB48	1118	-----RKIKGVISIPRLQAEARSEILAHWSPAKLLLQMDS
HsApoB52	1264	-----LNGNTSKSPTVSSSMFEKYDFNSSMLYSTAKGAVDHLKLSLESLTSYFSIESSTKGDVKGSVLSREYSGTAS
HsApoC1	97	-----
HsApoC2	63	-----
HsApoC3	81	-----
HsApoC4	90	-----
HsApoD	237	-----
HsApoE2	242	-----
HsApoF	206	-----
HsApoH	232	-----
HsApoJ	308	-----
HsApoL1	254	-----
HsApoL2	195	-----
HsApoL3	195	-----
HsApoL4	215	-----
HsApoL5	226	-----
HsApoL6	156	-----
HsApoM	133	-----
HsApoO	156	-----
HsApoOL	158	-----
HsMTTP	611	-----
DmMtp	612	-----
DmApoLppI	1293	NFKLTRQHFDGTDREVGFSYTFMGNLGSKNGLGTLKITNKEFNTKFSVCEEKRQCTNLIVQSIVSIDEQKLDAVEHTTL
DmApoLppII	454	-----
DmApoLTPI	1984	FLNVSWLKTDFNFTTNNGKSYRYCRCFWPQDTAYFKLNSNYDSDSSNFNHNLNGNVEIEVPLATRHRADIVYGLQKRRNQ
DmApoLTPII	507	-----
DmCG31659	133	-----
DmCvD	929	-----
DmFabp	110	-----
DmGlaz	124	-----
DmMic26-27	164	-----
DmNlaz	136	-----
HsApoA1	98	-----
HsApoA2	70	-----
HsApoA4	266	-----
HsApoA5	256	-----
HsApoB48	1153	SATAYGSTVSKRVAWHYDEEKIEFEWNTGTNVDTKKMTSNFPVDLSDYPKSLHMYANRLLDHRVPQDTMTFRHVGSKLIV
HsApoB52	1336	EANTYLNKSTRSSVKLQGTSKIDDIWNLEVKENFAGEATLQRIYSLWEHSTKNHLQLEGLFFTNGEHTSKATLELSPWQ
HsApoC1	97	-----
HsApoC2	63	-----
HsApoC3	81	-----
HsApoC4	90	-----
HsApoD	237	-----
HsApoE2	242	-----
HsApoF	206	-----
HsApoH	232	-----
HsApoJ	308	-----
HsApoL1	254	-----
HsApoL2	195	-----
HsApoL3	195	-----
HsApoL4	215	-----
HsApoL5	226	-----
HsApoL6	156	-----
HsApoM	133	-----
HsApoO	156	-----
HsApoOL	158	-----
HsMTTP	611	-----
DmMtp	612	-----

DmApoLppI	1373	IIVDLRDFGYPIYEFELKSQNTRQGLKYQYHLDSFIITGNNFKYQFTANVQPTSSTIKLALPKRQILFETTQKIPADGSLF
DmApoLppII	454	-----
DmApoLTPI	2064	DAGNVKVVYNEKQVLDGKYKRLEQAKAPIYKETTDISLENEVKPLGIHFVSTRDASDPAGSQDVVKHIEIYELRNTQNFNL
DmApoLTPII	507	-----
DmCG31659	133	-----
DmCvD	929	-----
DmFabp	110	-----
DmGlaz	124	-----
DmMic26-27	164	-----
DmNlaz	136	-----
HsApoA1	98	-----
HsApoA2	70	-----
HsApoA4	266	-----
HsApoA5	256	-----
HsApoB48	1233	AMSSWLQKASGSLPYTQTLQDHLNSLKEFNLQNMGLPDFHIPENLFLKSDGRVKYTLNKNLSLKIEIPLPFGGKSSRDLM
HsApoB52	1416	MSALVQVHASQPSSFHDFDLGQEVNANTKNQKIRWKNEVRIHSGSFQSQVELSNDQEKAHLDIAGSLEGLRFLKNI
HsApoC1	97	-----
HsApoC2	63	-----
HsApoC3	81	-----
HsApoC4	90	-----
HsApoD	237	-----
HsApoE2	242	-----
HsApoF	206	-----
HsApoH	232	-----
HsApoJ	308	-----
HsApoL1	254	-----
HsApoL2	195	-----
HsApoL3	195	-----
HsApoL4	215	-----
HsApoL5	226	-----
HsApoL6	156	-----
HsApoM	133	-----
HsApoO	156	-----
HsApoOL	158	-----
HsMTTP	611	-----
DmMtp	612	-----
DmApoLppI	1453	GRYEQTASFFIDKLQKPDDVARFSAIVDVT-----
DmApoLppII	454	-----
DmApoLTPI	2144	TGELHSRATLKAQDFKVVAIHPPNRAVVLSTKYEDVSPEVVRHHSKLELSETAWIGYNLELGNFSKVGNESQSFALEIFYP
DmApoLTPII	507	-----
DmCG31659	133	-----
DmCvD	929	-----
DmFabp	110	-----
DmGlaz	124	-----
DmMic26-27	164	-----
DmNlaz	136	-----
HsApoA1	98	-----
HsApoA2	70	-----
HsApoA4	266	-----
HsApoA5	256	-----
HsApoB48	1313	LETVRTPALHFKSVGFHLPSREFQVPTFTI-----
HsApoB52	1496	ILPVYDKSLWDFLKLDTVTSIGRRQHLRVS-----
HsApoC1	97	-----
HsApoC2	63	-----
HsApoC3	81	-----
HsApoC4	90	-----
HsApoD	237	-----
HsApoE2	242	-----
HsApoF	206	-----
HsApoH	232	-----
HsApoJ	308	-----
HsApoL1	254	-----
HsApoL2	195	-----
HsApoL3	195	-----
HsApoL4	215	-----
HsApoL5	226	-----
HsApoL6	156	-----
HsApoM	133	-----
HsApoO	156	-----
HsApoOL	158	-----
HsMTTP	611	-----
DmMtp	612	-----

DmApoLppI	1483	-----GTERVA
DmApoLppII	454	-----
DmApoLTPI	2224	KRNLSSSGQYYMTDTNFNSDLFSQWLGGNVDQPKIIHSNLQWKAEP LHRGDREHRTIALTVAHPLLEKDINCKATYYRG
DmApoLTPII	507	-----
DmCG31659	133	-----
DmCvD	929	-----
DmFabp	110	-----
DmGlaz	124	-----
DmMic26-27	164	-----
DmNlaz	136	-----
HsApoA1	98	-----
HsApoA2	70	-----
HsApoA4	266	-----
HsApoA5	256	-----
HsApoB48	1343	-----PKLYQL
HsApoB52	1526	-----TAFVYT
HsApoC1	97	-----
HsApoC2	63	-----
HsApoC3	81	-----
HsApoC4	90	-----
HsApoD	237	-----
HsApoE2	242	-----
HsApoF	206	-----
HsApoH	232	-----
HsApoJ	308	-----
HsApoL1	254	-----
HsApoL2	195	-----
HsApoL3	195	-----
HsApoL4	215	-----
HsApoL5	226	-----
HsApoL6	156	-----
HsApoM	133	-----
HsApoO	156	-----
HsApoOL	158	-----
HsMTTP	611	-----
DmMtp	612	-----
DmApoLppI	1489	FNANGKLKFEHPTIRPLSISGQLNGDVNQQIASAEVIFDIFRLPEQKVVGNSELRNSRSQNGFNIAIYITTVKSAGLQFQY
DmApoLppII	454	-----
DmApoLTPI	2304	LRDLLRTHLTIDYSEYPDQLIELGAQLTDRYSELGHTNYTFHVYGGKHIASELVDVQLNGTLAAMNSYKTESTAHYKRDIF
DmApoLTPII	507	-----
DmCG31659	133	-----
DmCvD	929	-----
DmFabp	110	-----
DmGlaz	124	-----
DmMic26-27	164	-----
DmNlaz	136	-----
HsApoA1	98	-----
HsApoA2	70	-----
HsApoA4	266	-----
HsApoA5	256	-----
HsApoB48	1349	QVPLLGVLDLSTNVYSNLYNWSASYSGGNTSTDHFSLRARYHMKADSVVDLLSYNVQGSGETTYDHKNTFTLSCDGSRLH
HsApoB52	1532	KNPNGYSFSIPVKVLADKFIIPGLKLNLDLNSVLVMPFTFHVPTDLQVPSCKLDFREIQIYKKLRTSSFALNLP LPEVKF
HsApoC1	97	-----
HsApoC2	63	-----
HsApoC3	81	-----
HsApoC4	90	-----
HsApoD	237	-----
HsApoE2	242	-----
HsApoF	206	-----
HsApoH	232	-----
HsApoJ	308	-----
HsApoL1	254	-----
HsApoL2	195	-----
HsApoL3	195	-----
HsApoL4	215	-----
HsApoL5	226	-----
HsApoL6	156	-----
HsApoM	133	-----
HsApoO	156	-----
HsApoOL	158	-----
HsMTTP	611	-----
DmMtp	612	-----

DmApoLppI	1569	QINSNAAVDIEAHEYNIGLELNNGEIDVKAISFLNKEKFEISLSESNKHIIYIVGDFSKQNHYAKLNTKVQILDKNPIEI
DmApoLppII	454	-----
DmApoLTPI	2384	PARYGKFLALLDVNKRELEYERQSPFHAVRLHLLPTIRYPIYGLNATIWDTPDTHSGYIYMDILERYARMDFNLTEDAS
DmApoLTPII	507	-----
DmCG31659	133	-----
DmCvD	929	-----
DmFabp	110	-----
DmGlaz	124	-----
DmMic26-27	164	-----
DmNlaz	136	-----
HsApoA1	98	-----
HsApoA2	70	-----
HsApoA4	266	-----
HsApoA5	256	-----
HsApoB48	1429	KFLDSNIKFSSHVEKLGNNPVSKGLLIFDASSSWGPMASVHLDSSKKKQHLFVKEVKIDGQFRVSSFYAKGTYGLSCQRD
HsApoB52	1612	PEVDVLTKYSQPEDSLIPFFEITVPESQLTVSQFTLPKSVSDGIAALDLNAVANKIADFELPTIIVPEQTIEIPSIKFSV
HsApoC1	97	-----
HsApoC2	63	-----
HsApoC3	81	-----
HsApoC4	90	-----
HsApoD	237	-----
HsApoE2	242	-----
HsApoF	206	-----
HsApoH	232	-----
HsApoJ	308	-----
HsApoL1	254	-----
HsApoL2	195	-----
HsApoL3	195	-----
HsApoL4	215	-----
HsApoL5	226	-----
HsApoL6	156	-----
HsApoM	133	-----
HsApoO	156	-----
HsApoOL	158	-----
HsMTTP	611	-----
DmMtp	612	-----
DmApoLppI	1649	TSEVQPNsAKIIILKRQDFIDGTAEVKLGKEFKVDVIGSGKQLFNGRVALDATNFLQTNYFINEDHNLGFWHIVeseinkD
DmApoLppII	454	-----
DmApoLTPI	2464	QNLQMGVGYIPDTRSAFLDIWRNYEEIRVIDVSSYLKMNHSLITGRFHWRPsiRQEVREKIqAVGKsvYSSfSEGIDFWI
DmApoLTPII	507	-----
DmCG31659	133	-----
DmCvD	929	-----LFSYPMTDLGVRL
DmFabp	110	-----
DmGlaz	124	-----
DmMic26-27	164	-----
DmNlaz	136	-----
HsApoA1	98	-----
HsApoA2	70	-----
HsApoA4	266	-----
HsApoA5	256	-----
HsApoB48	1509	PNTGRLNGESNLRFNssYLqGTnQITGRYEDGTLsLTSTSDlQSGIIKNTASLKYENYELtLKSDtNGKYKNF-----
HsApoB52	1692	PAGIVIPsFQALtARFEVDSPVYNATWSASLKNKADYVETVLDSTCSSTVQfLEYELNVLGTHKIEDGTlASKTKGTFaH
HsApoC1	97	-----
HsApoC2	63	-----
HsApoC3	81	-----
HsApoC4	90	-----
HsApoD	237	-----
HsApoE2	242	-----
HsApoF	206	-----
HsApoH	232	-----
HsApoJ	308	-----
HsApoL1	254	-----
HsApoL2	195	-----
HsApoL3	195	-----
HsApoL4	215	-----
HsApoL5	226	-----
HsApoL6	156	-----
HsApoM	133	-----
HsApoO	156	-----
HsApoOL	158	-----
HsMTTP	611	-----
DmMtp	612	-----

DmApoLppI	1729	SEYISENIKERLKKSRQVTDKIVKLAKEAGPDFSKLQGKLLDYKNDIVQELEADQSIAPIIDGIRTLFKKIAGIVDDINK
DmApoLppII	454	-----
DmApoLTPI	2544	KSIYTETTESMGVVWNTAKEYNRDFIDDIGQLSVLEEDLADLRLFVNQSYEANDFYIKNVVNFTLTILDELAIRDHIESL
DmApoLTPII	507	-----
DmCG31659	133	-----
DmCvD	942	SMTTNLNELIKYRGMLLKSEFTENGFSGNMVVNALMYIFGFTQLSSIHLGHDRNFTMLMYNEKNTRIEGNFCAEDVLKTS
DmFabp	110	-----
DmGlaZ	124	-----
DmMic26-27	164	-----
DmNlaZ	136	-----
HsApoA1	98	-----
HsApoA2	70	-----
HsApoA4	266	-----
HsApoA5	256	-----
HsApoB48	1582	-----ATSNKMDMTFSKQNALLRSEYQADYESLRFFSLLSGSLNSHGLELNADILGTDKINSQA
HsApoB52	1772	RDFSAEYEEEDGKYEGLQEWEGKAHLNIKSPAFTDLHLRYQKDKKGISTSAASPAVGTVGMDMEDDDFSKWNFYSPQSS
HsApoC1	97	-----
HsApoC2	63	-----
HsApoC3	81	-----
HsApoC4	90	-----
HsApoD	237	-----RFMCFDA
HsApoE2	242	-----
HsApoF	206	-----
HsApoH	232	-----
HsApoJ	308	-----
HsApoL1	254	-----
HsApoL2	195	-----
HsApoL3	195	-----
HsApoL4	215	-----
HsApoL5	226	-----
HsApoL6	156	-----
HsApoM	133	-----
HsApoO	156	-----
HsApoOL	158	-----
HsMTTP	611	-----
DmMtp	612	-----APAFNETLLSTQEVYQGILKRGSVEFLLHAGRSQASSFKL
DmApoLppI	1809	AISEILEKAQKSIVDIYDKLQALWKDSLLKAWEDFIITVQKLISTLKTEFIKICTQSFKDLLSALEKYGPALKNYGKAIG
DmApoLppII	454	-----CKPNTKREEERIVYILKGLGNAKSLSGNTVAA
DmApoLTPI	2624	PKIFSELWQAMGDSGKALRNSIVWLIETIKTTYNNLLDAVARFFHGESLVYISGLLEKGIKYDSFIKDLHIKFIKYIEN
DmApoLTPII	507	-----EFLNLYNLFKGERRTRERMVILLKGLGNIGVV
DmCG31659	133	-----RFMCFDA
DmCvD	1022	DMKGKQIGLTLEHTDHMMENHAADALHRWNITLDVLASTKSNWFKLTGQVQRN
DmFabp	110	-----NELITLIPH
DmGlaZ	124	-----TTRFPDVIARLLPG
DmMic26-27	164	-----EENCRVLYEG
DmNlaZ	136	-----VYSCTSV
HsApoA1	98	-----NGGARLAEY
HsApoA2	70	-----QLTPL
HsApoA4	266	-----RLAPLAEDVRGNLRNTEGLQKSLAEL
HsApoA5	256	-----ELSRFAAGTGTEEGAGPDPQML
HsApoB48	1641	HKATLRIGQDGISTATTNLKCSLLVLENELNAELGLSGASMKLTNGRFREH
HsApoB52	1852	PDKKLTIFKTELVRVRESDEETQIKVNWEEEAASGLLTSLKDNVPKATGVLYDYVNKYH
HsApoC1	97	-----PGEADNIPL
HsApoC2	63	-----
HsApoC3	81	-----
HsApoC4	90	-----
HsApoD	237	-----QLTPL
HsApoE2	242	-----RTRDRLDEVKEQVAEV
HsApoF	206	-----CLGKARERGRDGAIDLGYDLLMT
HsApoH	232	-----FGCHDGYSLDGPEEIECTKLGNWSA
HsApoJ	308	-----ILSVDCSTNNPSQAKLRRELDLQV
HsApoL1	254	-----VREFLGENISNFLSLAGNTYQL
HsApoL2	195	-----MKEFVGGNTPNVLTLDVNWYQV
HsApoL3	195	-----FKEVMRDITPNLLSLNNYYEA
HsApoL4	215	-----LRDILHDITPNVLSFALDFDEA
HsApoL5	226	-----AGFCVNKCVKAIQGIKDLHAYQMAKS
HsApoL6	156	-----DEEEKADYVTAAGKIIYNLNT
HsApoM	133	-----
HsApoO	156	-----IVF
HsApoOL	158	-----VIIAKVTAKKVYAT
HsMTTP	611	-----SGSSSAYTGYIERSPRASTYSLDILYSGSGILRRSNLIFQY
DmMtp	652	GIYTAGLGLSVGDGSDGNDIAPADDEFSEDEAVTAGMEISVQGAQLRPLVFF

DmApoLppI	1889	EIVKPINDAAQEVIKIVVNAAE-----
DmApoLppII	486	-----LSECASTGRSNRIRVAA-----
DmApoLTPI	2704	LWHKTWTLAENHWKAVLKRFEPLFKMISFIETTAWNLSKEVDFDIYKRTNELAESPYFNKVSSFTADAERLYRDFKAND
DmApoLTPII	539	-----SSAFAEQLQWIIREDEA-----
DmCG31659	140	-----SKIFSFWAVIQTTRKRL-----
DmCvD	1075	-----SKDDEDDWKACTKLTYE-----
DmFabp	119	-----LTPSQHGSRLRLRVPQCP-----
DmGlaz	138	-----SGKYQVLYTDYEN-----
DmMic26-27	175	-----RKIFAVAYNFIKGVKPG-----
DmNlaz	143	-----TPLANFKIWIWILTRQRE-----
HsApoA1	107	-----HAKATEHLSTLSEKAKP-----
HsApoA2	75	-----IKKAGTELVNFLSYFVE-----
HsApoA4	293	-----GGHLDQQVEEFRRRVEP-----
HsApoA5	278	-----SEEVQRQLQAFRQDTYL-----
HsApoB48	1694	-----NAKFSLDGKAALTELSL-----
HsApoB52	1910	-----WEHTGLTLREVSSKLRR-----
HsApoC1	106	-----VTQLDLKGVVFRDISES-----
HsApoC2	63	-----LPAVDEKLRDLYSKSTA-----
HsApoC3	81	-----SEFWDLDPVPRPTSAVA-----
HsApoC4	90	-----LRDLGPLTKAWFLESKD-----
HsApoD	242	-----IKKAGTELVNFLSYFVE-----
HsApoE2	258	-----RAKLEEQAQIRLQAEA-----
HsApoF	229	-----MAGMSGGPMGLAISAA-----
HsApoH	257	-----MPSCKASCKVPVKKATV-----
HsApoJ	334	-----AERLTRKYNELLKSYQW-----
HsApoL1	276	-----TRGIGKDIRALRRARAN-----
HsApoL2	217	-----TQGIGRNIRAIRRRARAN-----
HsApoL3	217	-----TQTIGSEIRAIRQARAR-----
HsApoL4	237	-----TKMIANDVHTLRRSKAT-----
HsApoL5	252	-----NSGFMAMVKNFVAKRHI-----
HsApoL6	178	-----LKYAKKNVRAFVKLRAN-----
HsApoM	133	-----LNETGQGYQRFLLYNRS-----
HsApoO	159	-----AQVSGERLYDWGLRGYI-----
HsApoOL	172	-----SQQIFGAVKSLWTKSSK-----
HsMTTP	654	-----IGKAGLHGSQVVIEAQG-----
DmMtp	706	-----SGQTELMGHVWGGSASD-----
DmApoLppI	1911	-----GVTHEFKQYVASLPSFESIRNEFNKVKVLKLFEKATELTNSLFDQINILPQTPETSEFLQKL
DmApoLppII	503	-----L-----
DmApoLTPI	2784	AITNIKKYSTIAWNFVKEKYFKLVFPGAELNEVLTEIWQEIKELEKIDQVQIMVQKYYEVMKVDWVADELQLEHRLHQV
DmApoLTPII	556	-----P-----
DmCG31659	157	-----P-----
DmCvD	1092	-----PLVFTKRPHTLNGDVVFGATEESECPEKGSTVQFAARAGPSEHARAFLRSDKISLTDTFCP
DmFabp	136	-----V-----
DmGlaz	151	-----F-----
DmMic26-27	192	-----E-----
DmNlaz	160	-----P-----
HsApoA1	124	-----A-----
HsApoA2	92	-----L-----
HsApoA4	310	-----Y-----
HsApoA5	295	-----Q-----
HsApoB48	1711	-----GSAYQAMILGVDSKNIFNFKVSQEGKLKLSNDMMGSAEMKFDHTNSLNIAGLSLDFSSKLDNI
HsApoB52	1927	-----N-----LQN
HsApoC1	123	-----E-----
HsApoC2	80	-----A-----
HsApoC3	98	-----A-----
HsApoC4	107	-----S-----
HsApoD	259	-----L-----
HsApoE2	275	-----F-----
HsApoF	246	-----K-----
HsApoH	274	-----V-----
HsApoJ	351	-----K-----
HsApoL1	293	-----L-----
HsApoL2	234	-----P-----
HsApoL3	234	-----A-----
HsApoL4	254	-----V-----
HsApoL5	269	-----P-----
HsApoL6	195	-----P-----
HsApoM	150	-----P-----
HsApoO	176	-----V-----
HsApoOL	189	-----E-----
HsMTTP	671	-----L-----
DmMtp	723	-----S-----

DmApoLppI	1974	HDYLIAKLKQEHIDNEKYIEELGQLLIKAVRSIWVSIRSTYPGSSDHVIDFQSWIGSLTHSFDSL A-----
DmApoLppII	504	-----
DmApoLTPI	2864	YGLVRNKFRNYAMNALETADMYREAKTKFVFDPEVGIIDLEQKLPMSWHAFNETPRFEEIPEYQVLAKAQSFSETNSSI
DmApoLTPII	557	-----VDIRLHG
DmCG31659	158	-----
DmCvD	1155	KEVLKFSPIPTSRYCKRSNFENFTSITQYDMDLKFDMMPAWFELWSNRLDHLVSALSADKVDSLHMSQEINISMQTPQDQ
DmFabp	137	-----
DmGlaz	152	-----
DmMic26-27	193	-----
DmNlaz	161	-----
HsApoA1	125	-----
HsApoA2	93	-----
HsApoA4	311	-----
HsApoA5	296	-----
HsApoB48	1774	YSSDKFYKQTVNLQLQPYSLVTTLNSDLKYNALDLTNNGKLRLEPLKLHVAGNLKGAYQNNEIKHI-----
HsApoB52	1931	NAEWVYQGAIRQIDDIDVRFQKAASGTTGTQYQEWKDKAQNLQYELLTQEGQASFGQLKDNVFDGLVRVTQEFHMKVKHLI
HsApoC1	124	-----
HsApoC2	81	-----
HsApoC3	99	-----
HsApoC4	108	-----
HsApoD	260	-----
HsApoE2	276	-----
HsApoF	247	-----
HsApoH	275	-----
HsApoJ	352	-----
HsApoL1	294	-----
HsApoL2	235	-----
HsApoL3	235	-----
HsApoL4	255	-----
HsApoL5	270	-----
HsApoL6	196	-----
HsApoM	151	-----
HsApoO	177	-----
HsApoOL	190	-----
HsMTTP	672	-----EALIAATPDEGEENLDSYAGMSAILFDVQLRPVTFNFNGYSDLMSKMLSASGD-----
DmMtp	724	-----
DmApoLppI	2040	VLPSILSFRSSILNCLLNENWDVVFNNKLLYSWIFFNDFELRGHVVDGKHIFTDGLNFAYPGNCKYILAQDSVDNNFTI
DmApoLppII	504	HAFSKVKCEETLQSKSLELLKRNEDSELRIEAYLSAISCNPAEVANQISEIVNS-----
DmApoLTPI	2944	VMKLYNMRTHLDPKTLWLPYYSRALLIDSRHYMTFDQRYVGLNLNFDDELGNRSTSQCSYLLAHDFFKRNFTLLLEPASK
DmApoLTPII	564	ILAFRRVDCARHSYFLDNYGNYTLNSELRIYSYLQAMRCPDYISVGVIKSILEH-----
DmCG31659	158	-----
DmCvD	1235	FRLAVEVNGVKWRFHQIPFFYKLDKFDASHELTFDSGLKRSCSVINGIVNTFDD-----
DmFabp	137	-----
DmGlaz	152	-----
DmMic26-27	193	-----
DmNlaz	161	-----
HsApoA1	125	-----
HsApoA2	93	-----
HsApoA4	311	-----
HsApoA5	296	-----
HsApoB48	1840	YAISSAALSASYKADTVAKVQGVFESHRLNTDIAGLASAIDMSTNYNSDSLHFSN-VFRSVMAPFTMTIDAHTNGNGKLA
HsApoB52	2011	DSLIDFLNFRPFQFPGKPGIYTREELCTMFIREVGTVLVSQVYSKVHNGSEILFSYFQDLVITLPFELRKHKLIDVISMYR
HsApoC1	124	-----
HsApoC2	81	-----
HsApoC3	99	-----
HsApoC4	108	-----
HsApoD	260	-----
HsApoE2	276	-----
HsApoF	247	-----
HsApoH	275	-----YQGERVKIQE-----
HsApoJ	352	-----
HsApoL1	294	-----QSVPHASASRPVTEPISAESGEQVERVNEPSILEMSR-----
HsApoL2	235	-----QLGAYAPPPHVIGRISAEGGEQVERVVEGPAQAMSR-----
HsApoL3	235	-----RLPVTTWRISAGSGGQAERTIAGTTTRAVSR-----
HsApoL4	255	-----GRPLIAWRYVPINNVETLRTRGAPTRIVRK-----
HsApoL5	270	-----FWTARGVQRAFEGTTLAMTN-----
HsApoL6	196	-----RLANATKRLLTTGQVSSRSRVQVQKAFAGTTLAMTK-----
HsApoM	151	-----
HsApoO	177	-----
HsApoOL	190	-----
HsMTTP	724	-----PISVVKGLILLIDHSQELQLQSGLKANIEVQGGLAIDISG-----
DmMtp	724	-----TPAYQATTLSQDNEHYIILTSGATLHWRVLGARSVDLNG-----

DmApoLppI	2120	IGQLTNGKLKSITLIDREGSYFEVADNLALKLNGNLVEYPQHLSGLHAWRRFYTIHLYSEYGVGIVCTSDLKVCHINIG
DmApoLppII	559	-----ETVNQVGGFISSNLKAIRDSTDVSRDQQKYHLANIRVTK
DmApoLTPI	3024	SLAGQGLTRKLSFIANGQLIEIDLETDHISINGNPQPILPLKLGDVNIHRDLVLSITSDTEFSLHCNVQFDLCWFEVSG
DmApoLTPII	619	-----EEINQVGSFVWSHLTNLAKSNSPVRIEAQGLLLNDELSE
DmCG31659	158	-----STQVIHMA
DmCvD	1290	-----YLINLREIAVRPDCLTLLVADCSPLPQIAVFVT
DmFabp	137	-----P
DmGlaZ	152	-----AILWSCSGSIGSLGHSQDI
DmMic26-27	193	-----DVPVVPFPTSLEDLKYMAS
DmNlaZ	161	-----SAEAVDAARKILEDNDVVSQAFLID
HsApoA1	125	-----
HsApoA2	93	-----
HsApoA4	311	-----GENFNKALVQQMEQLRQKLGPAG
HsApoA5	296	-----IAAFTRAIQETEEVQQQLAP
HsApoB48	1919	LWGEHTGQLYSKFLKAEPLAFTFSHDYKGSTSHHLVSRKSISAALEHKVSALLTPAEQTGTWKLKTQFNNNEYSQDLDA
HsApoB52	2091	ELLKDLKSKEAQEVFKAIQSLKTTEVLRLNQLDLLQFIFQLIEDNIKQLKEMKFTYLINYIQDEINTIFSDYIPYVFKLLKE
HsApoC1	124	-----
HsApoC2	81	-----MSTYTG
HsApoC3	99	-----
HsApoC4	108	-----LLK
HsApoD	260	-----
HsApoE2	276	-----QARLKSWEPLVE
HsApoF	247	-----PALRSGVQQLIQYYQDQKD
HsApoH	285	-----KFKNGMLHGDKVSFFCKNKEKK
HsApoJ	352	-----MLNTSSLLLEQLNEQFNWVSRAN
HsApoL1	332	-----GVKLTDVAPVSFFLVLDVV
HsApoL2	271	-----GTMIVGAATGGILLLLDVV
HsApoL3	265	-----GARILSATTSGIFLALDVV
HsApoL4	285	-----VARNLGKATSGVLVVLVV
HsApoL5	290	-----GAWVMGAAGAGFLLMKDMS
HsApoL6	232	-----NARVLGGVMSAFSLGYDLA
HsApoM	151	-----HPPEKCVVEEFKSL
HsApoO	177	-----IE
HsApoOL	190	-----ESLPKPKEKTKLGSSEI
HsMTTP	764	-----AMEFSLWYRESKTRVKNRVTVVIT
DmMtp	763	-----KVGFSLWNRNAQTEIQNTGSAVLGHLAVGFTYAKLVQ
DmApoLppI	2200	FYTSKTR---GLLGNGNAEYPDDFLLIDG-----TLAENSAALGNDYGVGKCTAIEFDNNQFK
DmApoLppII	598	TFPVDYR---RYSFNNEVSYLESLGVA-----STDYQIIYSQHGLFRSSRINVTTEFFGT
DmApoLTPI	3104	WYFGRTA---GLLGLTLNNEPYDEYTMSSG-----VISNETQLFTDSWSLKQCRQNKLAQTQEVSQEVS DACT
DmApoLTPII	658	RFKMDIR---KFSRNYEHSLEFFDEYNFGT-----TTDANVIFGTDSYLPRIASVNFATDLFGQ
DmCG31659	166	QYFGKSA---GLVIGDMSKVPQESCPYDT-----
DmCvD	1323	PSPVQGL---STNYGLRVHIGQNYFNRA-----RTDNSSLPTDEPVLIIYNLQDQTPHNVRKK
DmFabp	138	PTSVDG---ARSGGCGQRPGGPG-----
DmGlaZ	170	WILGRDR---DFEVDIRSKVYDVLKRLSL-----DPERLIISKKNQCPEAL-----
DmMic26-27	212	DLYDEAK---DLIFPKKK-----
DmNlaZ	185	TVQKNCP---RLDGNGTGLAGEDGLDVDD-----FVSTTVPNIEKA?EWLRLRYERLYDIFM
HsApoA1	125	-----LE---DLRQGLLPVLESFKVSFLS-----ALEEYTKKLNTQ-----
HsApoA2	93	-----GTQPATQ-----
HsApoA4	335	DVEGHLS---FLEKDLRDKVNSFFSTFKE-----KESQDKTSLSPLELEQQEQEQEQEQEQVQ
HsApoA5	317	PPPGHSA---FAPEFQQTDSGKVLKLAQ-----RLDDLWEDITHSLHDQGHSHLGD-----
HsApoB48	1999	YNTKDKI---GVELTGRTLADLTLLDSPI-----KVPLLLSEPNIIDALEMRDAVEKPEFT
HsApoB52	2171	NLCLNLHKFNEFIQNELQEASQELQIHYQYIMALREEYFDPSIVGWTVKYEELEEKIVSLIKNLLVALKDFHSEYIVSAS
HsApoC1	124	-----GETQD-----
HsApoC2	87	IFTDQVL---SVLKGE-----
HsApoC3	99	-----
HsApoC4	111	KTHSLCP---RLVCGDKDQG-----
HsApoD	260	-----GTQPATQ-----
HsApoE2	289	DMQRQWA---GLVEKVQAAVGTSAAPVPS-----DNH-----
HsApoF	266	ANISQPE---TTKEGLRAISDVSDLEETT-----TLASFISEVVSSAPYWGWAIIKSYDLDPG
HsApoH	307	CSYTEDA---QCIDGTIEVPKCFKEHSSL-----AFWKTDASDVKPC-----
HsApoJ	375	LTQGEDQ---YYLRVTTVASHTSDSDVPS-----GVTEVVVKLFSDPITVTVPVEVSRKNPK
HsApoL1	351	YLVYESK---HLEGAKESETAEELKKVAQ-----ELEEKLNILNNNYKILQADQEL-----
HsApoL2	290	SLAYESK---HLEGAKSESAAELKKRAQ-----ELEGKLNFLTKIHEMLQPGQDQ-----
HsApoL3	284	NLVYESK---HLEGAKSASAEELRRQAQ-----ELEENLMELTQIYQRLNPCHTH-----
HsApoL4	304	NLVQDSL---DLHKGEKSESALLRQWAQ-----ELEENLNEALTHIHSKAG-----
HsApoL5	309	SFLQSWK---HLEDGARTETAELRALAK-----KLEQELDRLTQHRRHLPQKASQTCSSSRG
HsApoL6	251	TLSKEWK---HLKEGARTKFAELRAKAL-----ELERKLTQLYKSLQQKVRSRARGVGK
HsApoM	164	TSCLDSK---AFLLTPRNQEACELSN-----
HsApoO	179	DLWKENF---QKPGNVKNSPGTK-----
HsApoOL	208	EVPAKTT---HVLKHSVPLPTLSSEAKT-----KSESTSGATQFMPDPKLMDHGQSHPEDID
HsMTTP	788	TDITVDS---SFVKAGLETSTETEAGLEF-----ISTVQFSQYPFLVCMQMDKDEAPFRQFEK
DmMtp	801	DFSITHEPKLSLNADLDFYSGIKLCMQQLQ-----RPEQLLKQTNVRSVFLQSVDRPYAKHVR

DmApoLppI	2255	SSKRQEMCSELFGIESTLAFNFITLDSRPYRKACDIALAKVAEKEKEATACTFALAYGSAVKQINKWLLPPRCIKCAGP
DmApoLppII	653	NYNVFEASVRQENVEDVLEYLGPVKGLVNDKDFEIVKLIIEVGNNNGVAAGGRARR-----
DmApoLTPI	3168	SFFRTGILATCSAVLDPTPFYEMCMDLGMKSPPIRKGHPAVKGACAAALAYIEACTALKVPMRVPSQCVCQLSNGSYVP
DmApoLTPII	713	SVNFFFEFTARAEGLEELAANAFGPKGPLSGQLLRKKLSFLNRWLGNEAEEDDTLENLLSLDNLRLK-----
DmCG31659	192	-----
DmCvD	1378	PYQWPIETSDYDFRVELNEQNILIVECTQLSSTIQFDLYNILNFEIYGVYKHQMCGLCSKPLNRMQNYTICELEANTPTP
DmFabp	159	-----
DmGlaz	213	-----
DmMic26-27	227	-----
DmNlaz	240	NFLSY-----
HsApoA1	158	-----
HsApoA2	100	-----
HsApoA4	390	MLAPLES-----
HsApoA5	367	-----
HsApoB48	2054	IVAFVKYDKNQDVHSINLPFFETLQEYFERNRQTIIVVLENVQRNLKHINIDQFVRKYRAALGKLPQQANDYLNSEFNWER
HsApoB52	2251	NFTSQLSSQVEQFLHRNIQEYLSILTDPDGKGKEKIAELSATAQEIIKSQAIATKKIISDYHQQFRYKQLQDFSDQLSDYY
HsApoC1	129	-----
HsApoC2	101	-----
HsApoC3	99	-----
HsApoC4	128	-----
HsApoD	266	-----
HsApoE2	318	-----
HsApoF	321	AGSLEI-----
HsApoH	346	-----
HsApoJ	430	FMETVAEKALQEYRKKHREE-----
HsApoL1	399	-----
HsApoL2	338	-----
HsApoL3	332	-----
HsApoL4	349	-----
HsApoL5	364	RAVRGSRVVKPEGSRSPLPWVVEHQPRLGPGVALRTPKRTVSAPRMLGHQPAPPAPARKGRQAPGRHRQ-----
HsApoL6	306	DLTGTCEATEAYWKELREHVWMLWLCVCLCVCVYVQFT-----
HsApoM	188	-----
HsApoO	199	-----
HsApoOL	263	MYSTRS-----
HsMTTP	843	KYERLSTGRGYVSQKRKESVLAGEFPLHQENSEMCKVVFAPQPDSTSSGW-----
DmMtp	859	TLSHKTAGCTFALNQKNNECMNLIFRDL-----
DmApoLppI	2335	AGQHDFGDEFTVKLPNNKVDVVFVVDINVTPGVLSNLIAPAINDIRESLRSRGFSDVQVGIVFEETKRYPALLTSDGGK
DmApoLppII	707	-----
DmApoLTPI	3248	EGTFMELSGPEIPKSSDVVFIVEAKECNANLKTSKNIMTVVSSIEEQLQAAKITNNRYAVVAFGGVSPYDKARSVIYEHN
DmApoLTPII	780	-----
DmCG31659	192	-----
DmCvD	1458	VPLQNSSDVVVVA-----
DmFabp	159	-----
DmGlaz	213	-----
DmMic26-27	227	-----
DmNlaz	245	-----
HsApoA1	158	-----
HsApoA2	100	-----
HsApoA4	397	-----
HsApoA5	367	-----
HsApoB48	2134	QVSHAKEKLTALTKKYRITENDIQIALDDAKINFNEKLSQLQTYMIQ-----
HsApoB52	2331	EKFIAESKRLIDLISIQNYHTFLIYITELLKKLQSTTVMNPYMKLAPGELTIIL-----
HsApoC1	129	-----
HsApoC2	101	-----
HsApoC3	99	-----
HsApoC4	128	-----
HsApoD	266	-----
HsApoE2	318	-----
HsApoF	327	-----
HsApoH	346	-----
HsApoJ	450	-----
HsApoL1	399	-----
HsApoL2	338	-----
HsApoL3	332	-----
HsApoL4	349	-----
HsApoL5	434	-----
HsApoL6	344	-----
HsApoM	188	-----
HsApoO	199	-----
HsApoOL	269	-----
HsMTTP	895	-----
DmMtp	887	-----

DmApoLppI	2415	INYKGNVADV KLAGIKSFCDCNCVEQIITEKRILDIYNSLKEIVKGIAPQADEKAFQLALDYPFRAGAAKSIIGVRSDSLE
DmApoLppII	707	-----
DmApoLTPI	3328	EFTSKPEQLADYFGHINTGNGSSNDILMAISAAKLNFRPGVSKTFILLSCSKCAARDMRFDYTSILQYLLEEGVNLHIL
DmApoLTPII	780	-----
DmCG31659	192	-----
DmCvD	1471	-----
DmFabp	159	-----
DmGlaz	213	-----
DmMic26-27	227	-----
DmNlaz	245	-----
HsApoA1	158	-----
HsApoA2	100	-----
HsApoA4	397	-----
HsApoA5	367	-----
HsApoB48	2181	-----
HsApoB52	2384	-----
HsApoC1	129	-----
HsApoC2	101	-----
HsApoC3	99	-----
HsApoC4	128	-----
HsApoD	266	-----
HsApoE2	318	-----
HsApoF	327	-----
HsApoH	346	-----
HsApoJ	450	-----
HsApoL1	399	-----
HsApoL2	338	-----
HsApoL3	332	-----
HsApoL4	349	-----
HsApoL5	434	-----
HsApoL6	344	-----
HsApoM	188	-----
HsApoO	199	-----
HsApoOL	269	-----
HsMTTP	895	-----
DmMtp	887	-----
DmApoLppI	2495	YKNWWKFVRAQLTGSITKFDGALIH LIAPVKGLSLEGVLSEKLIGFNSRLVATVDGKDSKKRTKLQFDNDMGIDFVLNNG
DmApoLppII	707	-----
DmApoLTPI	3408	ADTEFDFERNKKLRHFFGLDSKLVYSKRFPEGDAETRNTTHIPKSNLGICTTLAVETQGSVFSARKLQPERKYPIKRFAT
DmApoLTPII	780	-----
DmCG31659	192	-----
DmCvD	1471	-----
DmFabp	159	-----
DmGlaz	213	-----
DmMic26-27	227	-----
DmNlaz	245	-----
HsApoA1	158	-----
HsApoA2	100	-----
HsApoA4	397	-----
HsApoA5	367	-----
HsApoB48	2181	-----
HsApoB52	2384	-----
HsApoC1	129	-----
HsApoC2	101	-----
HsApoC3	99	-----
HsApoC4	128	-----
HsApoD	266	-----
HsApoE2	318	-----
HsApoF	327	-----
HsApoH	346	-----
HsApoJ	450	-----
HsApoL1	399	-----
HsApoL2	338	-----
HsApoL3	332	-----
HsApoL4	349	-----
HsApoL5	434	-----
HsApoL6	344	-----
HsApoM	188	-----
HsApoO	199	-----
HsApoOL	269	-----
HsMTTP	895	-----
DmMtp	887	-----

DmApoLppI	2575	GWVFATQNFELKASDQKKMLNQITSSSLADTLFKTEIVSDCRCLPIHGLHGQHKCVIKSSTFVANKKAKSA
DmApoLppII	707	-----
DmApoLTPI	3488	IFAKRVALSATPIQSQTCECSAHNTGVSVMACSPQALPEEKYDLDDYDSFNNWDWGDEPESETNVMS----
DmApoLTPII	780	-----
DmCG31659	192	-----
DmCvD	1471	-----
DmFabp	159	-----
DmG1az	213	-----
DmMic26-27	227	-----
DmN1az	245	-----
HsApoA1	158	-----
HsApoA2	100	-----
HsApoA4	397	-----
HsApoA5	367	-----
HsApoB48	2181	-----
HsApoB52	2384	-----
HsApoC1	129	-----
HsApoC2	101	-----
HsApoC3	99	-----
HsApoC4	128	-----
HsApoD	266	-----
HsApoE2	318	-----
HsApoF	327	-----
HsApoH	346	-----
HsApoJ	450	-----
HsApoL1	399	-----
HsApoL2	338	-----
HsApoL3	332	-----
HsApoL4	349	-----
HsApoL5	434	-----
HsApoL6	344	-----
HsApoM	188	-----
HsApoO	199	-----
HsApoOL	269	-----
HsMTTP	895	-----
DmMtp	887	-----

Fig. S11. Alignment of 14 nematode and 11 fly sequences with Vit1-6, ApoLpp and ApoLTP separated plus both outgroups.

CeApoL1	0				
CeApoL3-Like	0				
CeMoma1	0				
CeVit1I	0				
CeVit1II	0				
CeVit2I	0				
CeVit2II	0				
CeVit3I	0				
CeVit3II	0				
CeVit4I	0				
CeVit4II	0				
CeVit5I	0				
CeVit5II	0				
CeVit6I	0				
CeVit6II	0				
DmApoLppI	1	SIVDDVSKISKKYKMYGVKNVQDLNLDVSLKLFGESELAFLSLGDNIPSSLDDIINYFSTSFEKAKQELSSFEKQFSSHHL			
DmApoLppII	0				
DmApoLTPI	1	-----RKA-----			
DmApoLTPII	0				
DmCG31659	0				
DmCvD	0				
DmFabp	0				
DmGlaz	0				
DmMic26-27	0				
DmNlaz	0				
DmMtp	0				
CeDSc4	0				
CeApoL1	0				
CeApoL3-Like	0				
CeMoma1	0				
CeVit1I	1	-----RIQTGITL-----		LKEL-----	
CeVit1II	1	-----MRSI-----		LIGI-----	
CeVit2I	1	-----RIQTGIKL-----		LKEL-----	
CeVit2II	1	-----MRSI-----		LIGI-----	
CeVit3I	1	-----RVQSGIQM-----		LQEI-----	
CeVit3II	1	-----MKSI-----		LQEI-----	
CeVit4I	1	-----RVQSGIQM-----		LQEI-----	
CeVit4II	1	-----MKSI-----		LQEI-----	
CeVit5I	1	-----RVQSGIQM-----		LQEI-----	
CeVit5II	1	-----MKSI-----		LQEI-----	
CeVit6I	1	-----RASGSFQ-----		PTEF-----	
CeVit6II	1	-----MKFF-----		LQEI-----	
DmApoLppI	81	FLDTDLAYPTSIGVPLELVAQGF AATKVDLAVSLDINAILEQNWQKAKYRLKFVPSVDINANVQIGFNAQVLSTGLRVVS			
DmApoLppII	1	-----MARMKYNIA-----		LIGI-----	
DmApoLTPI	4	QEQRASEEEVDEDYDFEESLEGNKRQKRDVSTTRKQEIDRNVDSLGYKLYDYNNPRAQFGLRVFGNDLRYFN-VESL			
DmApoLTPII	1	-----MGGLKPQAAIWL-----		LL-----	
DmCG31659	0				
DmCvD	1	-----MRLLKCSVFVYLFILFDAGHAFSII-----			
DmFabp	0				
DmGlaz	0				
DmMic26-27	0				
DmNlaz	0				
DmMtp	1	-----MFSSRIWL-----MENKN-----			
CeDSc4	1	-----MFSSRIWL-----			
CeApoL1	0				
CeApoL3-Like	0				
CeMoma1	0				
CeVit1I	13	-----ALK-----	MNIRAR- PANYNEKDA-		
CeVit1II	5	-----IIA-----	SIVALA- IA- - - -F-		
CeVit2I	13	-----AQK-----	MNIRAR- PATYTEKDA-		
CeVit2II	5	-----IIA-----	SLVALA- LA- - - -S-		
CeVit3I	13	-----VKK-----	MNIRPR- VQQTDSQNA-		
CeVit3II	5	-----IIA-----	SLVALA- IA- - - -A-		
CeVit4I	13	-----VKK-----	MNIRPR- VQQTDSQNA-		
CeVit4II	5	-----IIA-----	SLVALA- IA- - - -A-		
CeVit5I	13	-----VKK-----	MNIRPR- VQQTDSQNA-		
CeVit5II	5	-----IIA-----	SLVALA- IA- - - -A-		
CeVit6I	12	-----LSN-----	LLEKLRIITRRQSSEQDP-		
CeVit6II	5	-----IAL-----	ALLGAALASTHLDRYNSI-		
DmApoLppI	161	SAHSATGSDITVAVISDGE GFNVDELPREKLELIN- - - - -FNVDTELYVAEQDKQKATAALKGNKKNKNSQPSEI			
DmApoLppII	14	-----LAS-----VLLTIAVNAENACNLGCP-			
DmApoLTPI	82	-----VEV-----MALAAKFNPFPQQAKNVL-			
DmApoLTPII	15	-----LIA-----HTQAVRENPLKDPRICG-			
DmCG31659	0	-----MIK-----			
DmCvD	26	GLNKQMLYIEGPNVLVGAKPQDEGHQAPPTTGWIVRGKLT LQRQSELVLAALVIDDVTLNNS-			
DmFabp	0				
DmGlaz	0				
DmMic26-27	0				
DmNlaz	0				
DmMtp	6	KK-----CLR-----	TLLLLALFLGLLEDGKT-		
CeDSc4	9	-----LLA-----	VTGVCLAVPDLDEIKK-		

CeApoL1	0	-----	
CeApoL3-Like	0	-----	
CeMoma1	0	-----	
CeVit1I	31	-----	
CeVit1II	17	-----	
CeVit2I	31	-----	
CeVit2II	17	-----	
CeVit3I	31	-----	
CeVit3II	17	-----	
CeVit4I	31	-----	
CeVit4II	17	-----	
CeVit5I	31	-----	
CeVit5II	17	-----	
CeVit6I	32	-----	
CeVit6II	26	-----	
DmApoLppI	231	CFNQLELVGLNICIKSSTSLSEVQAGNGNVAERGLSVSEKFHLSRPFNFAVYLTTERKFTFKGIHTQEAFSQKWKLDYST	
DmApoLppII	35	-----	
DmApoLTPI	102	-----	
DmApoLTPII	35	-----	
DmCG31659	3	-----	
DmCvD	89	-----	-GEKFLQNKEMYPPYKPFKIALTKDGA
DmFabp	0	-----	
DmGlaz	0	-----	
DmMic26-27	0	-----	
DmNlaz	0	-----	
DmMtp	28	-----	
CeDSc4	29	-----	
CeApoL1	0	-----	
CeApoL3-Like	0	-----	MQIKDD
CeMoma1	0	-----	MTQD
CeVit1I	31	-----	FAMVYLRYKDMDY --- AILPVD
CeVit1II	17	-----	SPAFERTFEPKID --- YHYKFD
CeVit2I	31	-----	FAMVYLRYKDMDY --- AFLPID
CeVit2II	17	-----	SPAFERTFEPKID --- YHYKFD
CeVit3I	31	-----	HAVFYLYRYKEMDY --- IVLPID
CeVit3II	17	-----	SPALDRTFSPKSE --- YVYKFD
CeVit4I	31	-----	HAVFYLYRYKEMDY --- IVLPID
CeVit4II	17	-----	SPALDRTFSPKSE --- YVYKFD
CeVit5I	31	-----	HAVFYLYRYKEMDY --- IVLPID
CeVit5II	17	-----	SPALDRTFSPKSE --- YVYKFD
CeVit6I	32	-----	HAFVYIRHRDMDY --- AFLPID
CeVit6II	26	-----	ERNIQESSFRAGRE --- YRYLFN
DmApoLppI	311	PGSKVSHDTTVVYELGNPKTF --- SRLSFDNSQCHFAVEGGINNDKNELVVYGGQYEQDKEIKKSKIGFSKNGNEYKPL	
DmApoLppII	35	-----	KSDNGLLKYIPGNY --- YDYSFD
DmApoLTPI	102	-----	SGKEFTYTKSRVF --- LDASYT
DmApoLTPII	35	-----	RPQCDSKSAKFNYGEQLYKYQYT
DmCG31659	3	-----	WKIFVPA --- ILYLQS
DmCvD	115	ISHVVFKEGDPIWSMNFKRAIA --- SVLQFQ	
DmFabp	0	-----	MSFVGKKY
DmGlaz	0	-----	MMSGQPLGS --- RVWLLS
DmMic26-27	0	-----	
DmNlaz	0	-----	MNHHSS
DmMtp	28	-----	ALIAPNSQ --- QIFKLQ
CeDSc4	29	-----	NLRKHGPDYYKNQPKMNENTVRLKVD
CeApoL1	0	-----	
CeApoL3-Like	6	-----	
CeMoma1	4	-----	
CeVit1I	50	-----	
CeVit1II	36	-----	
CeVit2I	50	-----	
CeVit2II	36	-----	
CeVit3I	50	-----	
CeVit3II	36	-----	
CeVit4I	50	-----	
CeVit4II	36	-----	
CeVit5I	50	-----	
CeVit5II	36	-----	
CeVit6I	51	-----	
CeVit6II	46	-----	
DmApoLppI	387	IEIQDNNGISNSINGYHADGKIVVKKSNNIERYNFENFQVSNNSNAHVAVNGWSDVGTNSLTSELRIQLDHQTFLLIKEN	
DmApoLppII	55	-----	
DmApoLTPI	121	-----	
DmApoLTPII	58	-----	
DmCG31659	16	-----	
DmCvD	143	-----	
DmFabp	8	-----	
DmGlaz	15	-----	
DmMic26-27	0	-----	
DmNlaz	6	-----	
DmMtp	42	-----	
CeDSc4	56	-----	

CeApoL1	0	-----MSIYESLKSTLMNGEE-----	
CeApoL3-Like	6	-----HDDAG.QSEDNGVPIYDSLESLLFIP-----	
CeMoma1	4	-----KP.V.TI-----	
CeVit1I	50	-----TQLI.K.IEKYISNGKVQFSEIRRLNQE-----	HEFETHHAAYFYEA
CeVit1II	36	-----GLVLSG.PTASSELQSQRFSARVRIQAVD-----	DRHIHLQLVNIHMAA
CeVit2I	50	-----RQLV.N.IEKFTSNGKVQFSEIRRLNQE-----	LEFETHHAAYFYEA
CeVit2II	36	-----GLVLSG.P.ASSELQSQRISARARIQAVD-----	DRYIHLQLVNIRMAA
CeVit3I	50	-----ETIDNVVEKYVRNG.FDIKSLLTFLTND-----	SKFELHRLFFYEAE
CeVit3II	36	-----GLLLSG.PT.FSDASQTLISCRTRLQAVD-----	DRYIHLQLIDIQYSA
CeVit4I	50	-----ETIDNVVEKYVRNG.FDIKSLLTFLTND-----	SKFELHRLFFYEAE
CeVit4II	36	-----GLLLSG.PT.FSDASQTLISCRTRLQAVD-----	DRYIHLQLIDIQYSA
CeVit5I	50	-----ETIDT.VEKYVRNG.FDIKSLLTFLTND-----	SKFELHRLFFYEAE
CeVit5II	36	-----GLLLSG.PTASSDASQTLISCRTRLQAVD-----	DRYIHLQLTDIQYSA
CeVit6I	51	-----ADSIPEVVRSMIQ.GRLEIGDIERVLAQG-----	IHFSASNAAFLYETV
CeVit6II	46	-----GQLSAG.PVPSTPQGISRLQSQVTLQWTD-----	GNTVRMQLQKTRFATSQ
DmApoLppI	467	LKLENGLYEAGFFINDEHSP.NIYGSSIHITIADQSYALKTNKGAAAWSIGSDGSFNFQKLADSN SARAGSLVENVEIQY	
DmApoLppII	55	-----SILTIGAS.DVP.DSD-----	DTSLKVSQSAKIFAK
DmApoLTPI	121	-----VPLAVG.PLAIHAFGASSIDL RVSGNLD EMDPPTDWHFDVEGQFKPSVSVDVITTMQTD MFWEQSGIKVKS NLYS	
DmApoLTPII	58	-----VAVRTEFAGSGD.SSDLLKSDLEIFFPKPC-----	EGYLRINDAKLYDTL
DmCG31659	16	-----SMAMRAF-----	
DmCvD	143	MKSSGAFVUDE.GIHGTCRT.YFVSNRTNYISIR-----	KTPEVKTCCKPYSEAVHTTRS
DmFabp	8		
DmGlaz	15	-----GVLLVTFAG.DAY-----	
DmMic26-27	0		
DmNlaz	6		
DmMtp	42	-----NQVILQELGRDSSSA.TSYTFETDLKINSV-----	WSGDEQQLLEVFISG
CeDSc4	56	YWFRT.E.MIYDDIDNKEKDPSTVIAGNFSFETLH-----	HDVEGMLGRFTLT
CeApoL1	16	-----	
CeApoL3-Like	32	-----	
CeMoma1	11	-----	
CeVit1I	94	-----	
CeVit1II	80	-----	
CeVit2I	94	-----	
CeVit2II	80	-----	
CeVit3I	94	-----	
CeVit3II	80	-----	
CeVit4I	94	-----	
CeVit4II	80	-----	
CeVit5I	94	-----	
CeVit5II	80	-----	
CeVit6I	95	-----	
CeVit6II	92	-----	
DmApoLppI	547	KNKQVGGIKIMSNFDVNKMDVDVEISREQIGSIIVKYESNQRHAQDYSLEASAKINKHSIDVISKCDFNNGVYVVDNSL	
DmApoLppII	86		
DmApoLTPI	196	NSELVAKLKVRGRNLVSFSFDLPRDKNEIFSRSSELLVQKREEQLPQAGIANRSANSTCTWPVLDAQIGLQMCSHYSVDP	
DmApoLTPII	104	-----	
DmCG31659	23	-----	
DmCvD	197	-----	
DmFabp	8	-----	
DmGlaz	29	-----	
DmMic26-27	0	-----	
DmNlaz	6	-----	
DmMtp	87	-----	
CeDSc4	104	-----	
CeApoL1	16	-----	
CeApoL3-Like	32	-----	
CeMoma1	11	-----	
CeVit1I	94	-----	RKFPTTLGLPLIV
CeVit1II	80	-----	SHLPESEQIPSLN
CeVit2I	94	-----	RKFPTTLGLPLTI
CeVit2II	80	-----	SHLPESEQMPSLN
CeVit3I	94	-----	RRIPTTIGMPLTI
CeVit3II	80	-----	SHIPQSEQWPKIK
CeVit4I	94	-----	RRIPTTIGMPLTI
CeVit4II	80	-----	SHIPQSEQWPKIE
CeVit5I	94	-----	RRIPTTIGMPLTI
CeVit5II	80	-----	SHIPQSEQWPKIE
CeVit6I	95	-----	RRVPTPMGLPVQF
CeVit6II	92	-----	QESNSMKMLPFER
DmApoLppI	627	VTSWGTL LSAKGEIGQRYSAQDININIQGNVQISGDKVTQWILKVIGTPDKTNSDFRISRDTSELIKLTSESQHPQDKI	
DmApoLppII	86		GNCGYTLQLSSVK
DmApoLTPI	276	LSNATEIYPSLLLAGPLNFSLLILKSDLSAKKYVFEYKWDQOEEDNNFSLVFTTPGSKVPRVLVANVTKVPAFNASVAF	
DmApoLTPII	104	-----	DELNDNESDSSEKTEKYDDYDNLANEESSESQNY
DmCG31659	23	-----	
DmCvD	197	-----	NVPNTCEFDHQK
DmFabp	8	-----	
DmGlaz	29	-----	
DmMic26-27	0	-----	
DmNlaz	6	-----	
DmMtp	87	-----	SKVDA
CeDSc4	104	-----	QCNTDNCGNPSPI

CeApoL1	47	-----EIAKD-----	-----LDGLEKA-----
CeApoL3-Like	62	-----QMEGI-----	-----,EKLDNW
CeMoma1	33	---TTNNGDSK-P.KIE---	-----QLPIYAEDNA-----PLKQKFL-----
CeVit1I	194	QKSIIISLTTR-PVVFL---	-----RFPGFSKFY-----IEAE.RTVVVPQW
CeVit1II	171	NTSFFT-NEK-TLEG---	-----CQVAYTVIR-----EQKKTIIITKSIN
CeVit2I	194	QKSIVSLTTR-PVVFL---	-----RFPGFSKFY-----IEAE.RTVVVPQW
CeVit2II	171	NTSFFT-NEK-TLEG---	-----CQVAYTVIR-----EQKKTIIITKSIN
CeVit3I	195	KKTTVSVHTR-PV.FI---	-----RVPKNQDSEY-----VETE..TISHSQY
CeVit3II	167	DSLFFNVHEK-TMEG---	-----CEVAYTIVQ-----E.EKTIYTKSVN
CeVit4I	195	KKTTVSVHTR-PV.FI---	-----RVPKNQDSEY-----VEAE..TISHSQY
CeVit4II	167	DSLFFNVHEK-TMEG---	-----CEVAYTIVQ-----E.GKTIYTKSVN
CeVit5I	195	KKTTVSVHTR-PV.FI---	-----RVPKNQDSEY-----VEAE..TISHSQY
CeVit5II	167	DSLFFNVHEK-TMEG---	-----CEVAYTIVQ-----E.EKTIYTKSVN
CeVit6I	201	EKRIAMIQSR-PVTFT---	-----RTVAPDARQY-----PEPI.MTYMLPAH
CeVit6II	178	TFSFTNV-ER-TLEGE---	-----CEVLYTVEEI-----KKED.QRWAKSIN
DmApoLppI	905	SEISYQIKQQ-PNGDA---	-----KNIDFSLKAYGNLPQPF.I.FALGDY
DmApoLppII	153	QSGIAEAEHV-DVFGM---	-----CPTHSTSK-----V.NANIITKARN
DmApoLTPI	590	EHKNGTEHN-V.VGLKYTPEKEITGLFSVHLPRRNLFAIDAYMNVTVPEFNSCTASLKVNEK---	-----ATKDYIIFINGSW
DmApoLTPII	199	---ANTTET-DVSGQ---	-----CQVQYALD-----T.SSYVTIRKTKD
DmCG31659	37	-----DMDRF-----	-----KGGK
DmCvD	335	STLSDVIKLLS.MDF---	-----SLTKLYREVDI-----GTSYRQETIRNIF
DmFabp	38	-----TVEVT-----	-----E.DTYTLTTTST
DmGlaz	37	-----SMPKFNMRSRV-----	-----LGHW
DmMic26-27	14	-----AVKAA-----	-----PEPQKP.SSAADC
DmNlaz	22	-----AHAQVPFPGK-----	-----CPDVKL-----TFDAEAYMGVW
DmMtp	163	VKSSTKVEKT---KR---	-----CSLWDLRVNYPNEEAL.VTQQAQETVF
CeDSc4	212	QDVWYTQNTKVDADII---	-----MVDAIEMLAFKSPLEHYGFTLESRTH
CeApoL1	59	-----SAIATTVGSSVDIASGLAVFGGLF	
CeApoL3-Like	74	EKGCA-----	-----S.A...T.G...I...I
CeMoma1	63	-----PEEPLQREFATIRIACEQE---	
CeVit1I	232	QQKTQEI-----	-----EKVFNFL.LE.STRGNILNQHT.E
CeVit1II	206	FDKCT-----	-----ERSEIAY.LRYSSECEPECEKDTVL
CeVit2I	232	QQKTQEI-----	-----EKVFNFL.LE.STRGNILNQHT.E
CeVit2II	206	FDKCT-----	-----ERSEIAY.LRYSSECEPECEKDTVL
CeVit3I	233	QMSTEEI-----	-----DRQYE.F.LRINAQGNVLSQWT.P
CeVit3II	203	FDKCI-----	-----TRPE.AY.LRFGSECKEKE.Q.
CeVit4I	233	QMSTEEI-----	-----DRQYE.F.LRINAQGNVLSQWT.P
CeVit4II	203	FDKCI-----	-----TRPE.AY.LRFGSECKEKE.Q.
CeVit5I	233	QMSTEEI-----	-----DRQYE.F.LRINAQGNVLSQWT.P
CeVit5II	203	FDKCI-----	-----TRPE.AY.LRFGSECKEKE.Q.
CeVit6I	239	KQLSQSL-----	-----DREYPQIRVQGTILNRPTS.RIPQW
CeVit6II	215	FDKCT-----	-----RRPYIHHVQT--PVCKDCQQTLEQ
DmApoLppI	947	SAQHAVVSITSKYGEIFSVSANGNYN---	-----NNQ.LEY.LQAN.EIPKSTLKS.E
DmApoLppII	189	LNSCS-----	-----HREQINS.L--VSGKVNEKA.IT
DmApoLTPI	665	FTGHSVAVKANYKDRSSRVQALHHLKMIVESPSFNITSLNIIYRRKQLLIFYDIQAKYDQDPY.LTIQY..NAHNRTNTA	
DmApoLTPII	232	INSC-----	-----RQRYA.HSVLQTTPTYFRDDKTIW
DmCG31659	46	YT-----	-----HS.YPHLSLR.---EKCQSTDFI
DmCvD	375	HEIIPRIGTK-----	-----ASVFL.HHLVLNKLTKP-QIAVQL
DmFabp	56	FKT-----	-----SFKL.VEF.EETLDGRNVKSI
DmGlaz	51	Y-----	-----EVERSFYLPEIASGCTT---
DmMic26-27	32	SLVCR-----	-----PSELPIY..LRKTEPKPERHPPQD
DmNlaz	51	Y-----	-----EYA.YPFAFEIGKKCIY.NYSLID
DmMtp	203	YELSSSEGTLLH-----	-----AESQENHRLNLAAPDVGS.VKSS
CeDSc4	255	VEITNR-----	-----TRVFV.SYCNDDTVP.AKCAEQAFG
CeApoL1	83	FMPP-----	
CeApoL3-Like	101	L...-----	
CeMoma1	84	-----	
CeVit1I	263	NWLL-----	-----AEQDFEVSVENKYRPAE---
CeVit1II	235	IR.Q-----	-----TVYTYILENEELKESEVRSL-----
CeVit2I	263	NWLL-----	-----AEQDFEVSVENKNRPAE---
CeVit2II	235	IR.Q-----	-----TVYTYVLENEELKESEVRSL-----
CeVit3I	264	MVLM-----	-----TEQDFEFTLENKNRPVE-----
CeVit3II	232	VK.Q-----	-----TVYTYTFKNEKLQSEVHSI-----
CeVit4I	264	MVLM-----	-----TEQDFEFTLENKNRPVE-----
CeVit4II	232	VQ.Q-----	-----TVYTYTFKNEKLQSEVNSI-----
CeVit5I	264	MVLM-----	-----TEQDFEFTLENKNRPVE-----
CeVit5II	232	VK.Q-----	-----TVYTYTFKNEKLQSEVHSV-----
CeVit6I	270	IVDS-----	-----NVEVYKPNVEQYEAI-----
CeVit6II	242	DKMS-----	-----STVLNYNITGTSSSFLINSVELRSQHL-----
DmApoLppI	997	INSHGKVLKSLIGNENAAYNVEFFLDSKTSLGQYARVNTVWNGTANDGSYDFAQTNNMESPLKFNGKYHRKQTGNIKDG	
DmApoLppII	215	SSLL-----	-----LQANYI-----
DmApoLTPI	745	EVRL-----	-----KVKERDYWNAKLLSEQPKLLQLEIHMDKIRDV
DmApoLTPII	260	PILK-----	-----SQSHCNLTIDNNVYKEI-----
DmCG31659	68	EKEE-----	
DmCvD	408	LI.M-----	-----PFHIFELSAELVQKCEDF-----
DmFabp	83	ITLD-----	
DmGlaz	69	-----	
DmMic26-27	61	SVLH-----	
DmNlaz	76	NSTV-----	
DmMtp	238	LILQ-----	-----HVSQGSSEVKQLQLGSLDKAIQSLLEWYRV-----
CeDSc4	285	AVRV-----	-----GGKLYEHVKIAQEQSNKLTCLI-----

CeApoL1	87	-----
CeApoL3-Like	105	-----
CeMoma1	84	-----
CeVit1I	284	-----
CeVit1II	259	-----
CeVit2I	284	-----
CeVit2II	259	-----
CeVit3I	285	-----
CeVit3II	256	-----
CeVit4I	285	-----
CeVit4II	256	-----
CeVit5I	285	-----
CeVit5II	256	-----
CeVit6I	290	-----
CeVit6II	273	-----
DmApoLppI	1077	DLTGKQTYVLNAQYGAQYVKMDASLG- - - - -
DmApoLppII	225	-----
DmApoLTPI	782	HIQVGLLNVDKRKELSLELKW DANRDP SQRLGLLAEYN SPG TKHYDGNLMITYPERTIHF GFNSFTGGPKYFGK VHASWS
DmApoLTPII	281	-----
DmCG31659	72	-----
DmCvD	430	-----
DmFabp	87	-----
DmGlaz	69	-----
DmMic26-27	65	-----
DmNlaz	80	-----
DmMtp	272	-----
CeDSc4	311	-----
CeApoL1	87	-----
CeApoL3-Like	105	-----
CeMoma1	84	-----
CeVit1I	284	-----
CeVit1II	259	-----
CeVit2I	284	-----
CeVit2II	259	-----
CeVit3I	285	-----
CeVit3II	256	-----
CeVit4I	285	-----
CeVit4II	256	-----
CeVit5I	285	-----
CeVit5II	256	-----
CeVit6I	290	-----
CeVit6II	273	-----
DmApoLppI	1104	-----
DmApoLppII	225	-----
DmApoLTPI	862	INEVIEFEYEAGILPGHTLHNWVKAELRTPFDGWRVNSLDAGIYSLKNLILVNSTLFWADDQKLQVGYSYDVNDQLMS
DmApoLTPII	281	-----
DmCG31659	72	-----
DmCvD	430	-----
DmFabp	87	-----
DmGlaz	69	-----
DmMic26-27	65	-----
DmNlaz	80	-----
DmMtp	272	-----
CeDSc4	311	-----
CeApoL1	87	-----VAIAGLIVGAASGVSNVA-----TG VNKKLAT---
CeApoL3-Like	105	-----.....T.....L-----..IT.FFH.---
CeMoma1	84	-----YDRVAERFKVVDC.MTQTKKA.-----..KC.AY.TE---
CeVit1I	284	----FTARLTVGQLEKTELSQIKYNKIFEKEFELEQENTESRREY-FTK--MVKSIQKEQGYK---SV.SLR.EA-PR
CeVit1II	259	----YTVNVNGQEV MKTETR SKLVLEENHSIKSHIEKVN.EKESI-IYS--SRWEQLVEDFFK---N.DKAEF.P-FE
CeVit2I	284	----FTARLTVGQLEKTELSQIKYNKIFEKEFELEQENTESRREY-FNK--MVKNIQKEQGYK---SVISL.EA-PR
CeVit2II	259	----YTVNVNGQEV MKTETR SKLVLEENHSIKSHIKKVN.EKESI-IYS--SRWEQLVEDFFK---N.DKAEF.P-FE
CeVit3I	285	----FTARVTIGNLEKTDLSEIKFDKIFEKEFDLENNE.ENRRQY-FHK--MIREIQSEQGFK---NLITL.EA-PQ
CeVit3II	256	----YTLNVNGQEVVKSETRSKVT FVEESKINREIKKV..PKEEI-VYS--MENEKLIEQFYQ---Q.DKAEVNP-FK
CeVit4I	285	----FTARVTIGNLEKTDLSEIKFDKIFEKEFDLENNE.ENRRQY-FHK--MIREIQSEQGFK---NLITL.EA-PQ
CeVit4II	256	----YTLNVNGQEVVKSETRAKVT FVEESKINREIKKV..PKEEI-VYS--MENEKLIEQFYQ---Q.DKAEVNP-FK
CeVit5I	285	----FTARVTIGNLEKTDLSEIKFDKIFEKEFDLENNE.ENRRQY-FHK--MIREIQSEQGFK---NLITL.EA-PQ
CeVit5II	256	----YTLNVNGQEVVKSETRAKVT FVEESKINREIKKV..PKEEI-VYS--MENEKLIEQFYQ---Q.DKAEVNP-FK
CeVit6I	290	----FELNLNYYNKM EKNYEVYKKHNGRRYLEAEPEYDEEEHREQITK--KFEWLQNEKVVYQ---HVAKFEIKP--E
CeVit6II	273	----FAPISEKHQLVSAFTLNTMELIYAGEKKTEIKQVRNEKTSELVYN--QESWAEQQAQ----..EE.Y.RQ-LP
DmApoLppI	1104	----GAEKVDIAYVIDSSFSVDKIKVNIRTFKPLDDSTY.VTALFKQT--DKSYGLDTTFYHSAHKK..DIR.DL-LK
DmApoLppII	225	----KESRIVNHLIENVQLTET YKFIGNTKRNSDIS.KVVTILKL-KNP--SGTKANSPGTGS---.VRSLIFQR-PE
DmApoLTPI	942	FDVRFGINSTIRDIP TINVKV KHWMDVKKVDT ELYLGY..QNDTFNTYS--MDSSWEIEKNQRYNNYS.LVHLVSP-FK
DmApoLTPII	281	-----KCLETHLLVPFSNASSGALTTSRLKLDGVES-YSA--GEFLEQNPELVE---RRATLVFDHTPA
DmCG31659	72	-----NKFSVVARELNTQT.TVKMR-----KADILNVEPEFG
DmCvD	430	----LNIGPDRPDVRQAAILSFATLIHNVYVAKGIDKEKFEEY.QKYFNAYLSDRDFDQKMLYLQLGLNNLQLGNV.NYLE
DmFabp	87	-----GNKLTQEOK.DKP-----TIVREFTD---
DmGlaz	69	-----FQFEPYNK.EQSKF-----SNFKLAV.I---
DmMic26-27	65	-----KNLEAGVRY.REEVQ-----S.YKAVADQ---
DmNlaz	80	-----SVVNAAINRFT.QPSNV-----QA.V.GP---
DmMtp	272	----FELESVDVGMISAIKEQTLEDQLK.SLTELS.DV.K.SL.LAYVKLIPLARITRQEQFE---DLLTEHAEVLPQ
CeDSc4	311	----GTYRRHLQDMGDSHICEKHSLLYSQ..QEARL.KRQDWEA.-IQY---PENDHVLSLIASALGGV.TAESIT.-AR

CeApoL1	114	-----	
CeApoL3-Like	132	-----	
CeMoma1	115	-----	
CeVit1I	351	DYTMN-----	
CeVit1II	326	KFPLD-----	
CeVit2I	351	DYTMN-----	
CeVit2II	326	KFPLD-----	
CeVit3I	352	QMYWN-----	
CeVit3II	323	AIEME-----	
CeVit4I	352	QMYWN-----	
CeVit4II	323	AIEIE-----	
CeVit5I	352	QMYWN-----	
CeVit5II	323	AIEME-----	
CeVit6I	357	VVKME-----	
CeVit6II	341	QWTEN-----	
DmApoLppI	1176	EKP II-----	
DmApoLppII	292	TYTSK-----	
DmApoLTPI	1018	GYEKGGLVAHFSLSDQRVVSGAASLNFDLREFTLTMNGYVKKFTDNMLTVNITTPLEKFGTINARFGLNEKKRHAVA EVR	
DmApoLTPII	341	VKPSH-----	
DmCG31659	104	RYVLG-----	
DmCvD	506	PIVQD-----	
DmFabp	109	-----	
DmGlaz	92	-----	
DmMic26-27	89	-----	
DmNlaz	106	-----	
DmMtp	344	LVDLL-----	
CeDSc4	382	EVLLT-----	
CeApoL1	114	-----	-----DHKIREINR
CeApoL3-Like	132	-----	-----KGQHK.VAA
CeMoma1	115	-----	-----
CeVit1I	356	-----	-----TEVTTVCDKQV
CeVit1II	331	-----	-----KKM.L.KT.TE
CeVit2I	356	-----	-----TELTTVCDKQV
CeVit2II	331	-----	-----KKM.L.KT.TE
CeVit3I	357	-----	-----TELRTVCDKWI
CeVit3II	328	-----	-----QKVEQLD..F.
CeVit4I	357	-----	-----TELRTVCDKWI
CeVit4II	328	-----	-----QKVEQLE..F.
CeVit5I	357	-----	-----TELRTVCDKWI
CeVit5II	328	-----	-----QKVEQLQ..F.
CeVit6I	362	-----	-----VEAVCNNDP
CeVit6II	346	-----	-----KVEM.KKMFS
DmApoLppI	1181	-----	-----ISSIAELLGDRKGKVLFEILNLADLDI
DmApoLppII	297	-----	-----NINALKT.LS
DmApoLTPI	1098	APTAALGVEVLADIKNLLNFDVKLSVATPIESFQQAIFALFNPERVDMRGLWNNVTLGFTGVVHMQNITD FEYSYHVFT	
DmApoLTPII	346	-----	-----DEIKAA..LLV
DmCG31659	109	-----	-----
DmCvD	511	-----	-----PNEHE.L.FQAAWT
DmFabp	109	-----	-----
DmGlaz	92	-----	-----KNINR.-----
DmMic26-27	89	-----	-----
DmNlaz	106	-----	-----
DmMtp	349	-----	-----GAVQTFDAHNATFG
CeDSc4	387	-----	-----ASPDYLDLDDL
CeApoL1	123	MLAED-----	
CeApoL3-Like	141	.I.-----	
CeMoma1	115	-----	
CeVit1I	367	RMQWEVEIRRSPILEETK-----	
CeVit1II	342	QIQ.VENNIPETSHFL-----	
CeVit2I	367	RMQWEVEIRRSPILEETK-----	
CeVit2II	342	QIQ.VENNMPETSHFL-----	
CeVit3I	368	RMCKVEMDARRSPMEHENK-----	
CeVit3II	339	QIQ.HEQNTPETVHLI-----	
CeVit4I	368	RMCKVEMDARRSPMEHENK-----	
CeVit4II	339	QIQ.HEQNTPETVHLI-----	
CeVit5I	368	RMCKVEMDARRSPMEHENK-----	
CeVit5II	339	QIQ.HEQNTPETVHLI-----	
CeVit6I	371	HFCKTQIR-----	
CeVit6II	356	LM.KQIEQGAELEAAHTV-----	
DmApoLppI	1208	KINSEASYVSIDEFYIIV-----	
DmApoLppII	307	D.VDSTGDYVKKET-----	
DmApoLTPI	1178	P..GFEENGFIQQLKRKEVFVQLHGKMSNYKLGVKINGEPKSDLVNQLGSNKMELEMLYDADF KPLNAETDYKPDAD EE	
DmApoLTPII	357	EMCRVGFPNIQREFIDVF-----	
DmCG31659	109	-----	
DmCvD	525	T..LADRRARIYEV-----	
DmFabp	109	-----	
DmGlaz	98	-----	
DmMic26-27	89	-----	
DmNlaz	106	-----	
DmMtp	363	F.YKESETTSEQLDLL-----	
CeDSc4	398	GISQSSSNNE-----	

CeApoL1	128	-----AKFFEEELLHSRND-----	
CeApoL3-Like	145	-----DGVLF.E.LKSRE-----	
CeMoma1	115	-----EWTA-----	
CeVit1I	386	-----EWTLSQ.LVVRP-----	
CeVit1II	358	-----RLVRIFRTTSTS-----	
CeVit2I	386	-----EWTLSQ.LVVRP-----	
CeVit2II	358	-----RLVRIFRTTSTS-----	
CeVit3I	387	-----EWTLRTE.LAARP-----	
CeVit3II	355	-----RAVRMFRMCTIE-----	
CeVit4I	387	-----EWTLRTE.LAARP-----	
CeVit4II	355	-----RAVRMFRMCTIE-----	
CeVit5I	387	-----EWTLRTE.LAARP-----	
CeVit5II	355	-----RAVRMFRMCTIE-----	
CeVit6I	379	-----GEELKATIQYVYP-----	
CeVit6II	375	-----RIVKV.RECNEE-----	
DmApoLppI	1226	-----NWSSKK.KLDGYELEARAQSKNIKIQLKNENGIIFS	TATYALKKELNKTIIDGQG
DmApoLppII	321	-----K.V.FIRLLRQ-----	
DmApoLTPI	1258	YFSYFTNFQVDTLVWPTIVGNVDIQEIIDFY.VVGHV	
DmApoLTPII	375	-----TN.LQTSKSLDYK-----	
DmCG31659	109	-----	
DmCvD	540	-----YWPIF.SRNASLELRVAAVTLLISNPTAA-----	
DmFabp	109	-----	
DmGlaz	98	-----	
DmMic26-27	89	-----GIVGHYVETAKA-----	
DmNlaz	106	-----	
DmMtp	379	-----E.YLQS.AVATHPDRKIVE-----	
CeDSc4	408	-----KWHKQLMYWLG-----	
CeApoL1	141	-----LLNEVRRFVEDKQSSKIF-----	-----KNFDDVQSHLKTFLF--
CeApoL3-Like	158	-----E.M.AV.KIVEDEEFFKHF-----	-----DG.IENK...V--
CeMoma1	119	-----	
CeVit1I	399	-----EMPSSL.QLH.QPHREVQLSLTSTWGSQK-----	-----SEVT.NAQ.QQSK--
CeVit1II	371	-----Q.K.IHETLYV.ADK..QSLMEHALAI-----	-----AGTKNTIQ.ILVHI--
CeVit2I	399	-----EMPSSL.QLR.QPHREVQLSLTSTWGSQK-----	-----SEVT.NAQ.QQSK--
CeVit2II	371	-----Q.K.IHETLYV.ADK..QSLMEHALAI-----	-----AGTKNTIQ.ILVHM--
CeVit3I	400	-----QMPSSL.QLREQPHREVQLALNAKWGSSK-----	-----SEITFNAQ.EQST--
CeVit3II	368	-----E.KK.HTTIYT.AEK.VQLVIETTLAV-----	-----AGTKNTIQ..IHH.--
CeVit4I	400	-----QMPSSL.QLREQPHREVQLALNAKWGSSK-----	-----SEITFNAQ.EQST--
CeVit4II	368	-----E.KK.HTTIYT.AEK.VQLVIETTLAV-----	-----AGTKNTIQ..IHH.--
CeVit5I	400	-----QMPSSL.QLREQPHREVQLAFNAKWGSSK-----	-----SEIT.NAQ.EQST--
CeVit5II	368	-----E.KK.HTTIYT.AEK.VQLVIETTLAV-----	-----AGTKNTIQ..IHH.--
CeVit6I	392	-----QTPRTVEELKEQKYRQLVVMGMENY-----	-----E.TIHININGQSQS--
CeVit6II	388	-----Q.EQIY.H.AEHKDE..AEQLRSIYFNTLAL-----	-----AGTRVTIQQFVVDK--
DmApoLppI	1282	KVQYQKALSGNFK.TRQHDFGTDREVGFSYTFMGNLGSKNGLGTLKITNKEFNTKFSVCEEKRGCTNLIVQSIVSIDE	
DmApoLppII	334	-----SDS.TLLELAAPFHPNPKVLARKVYLDGLF-----	-----RTSTAESARVILKQ--
DmApoLTPI	1295	-----E.PQGGKVEFK.RLHYPDYINVHNLTTVTPF-----	-----AVAKNIK.IVEYHVDL--
DmApoLTPII	388	-----T.SVLLQRSASTCEQGRNHLLESLPF-----	-----IGSTASYKVMRDQI--
DmCG31659	109	-----	-----TTSTAFPEGVLMYV--
DmCvD	570	-----R.ISIH.IIQSETDPHMINYRTVTTSIS-----	-----ETTPCYQ..RR.LSY--
DmFabp	109	-----	-----NELITLIP..TPSQ--
DmGlaz	98	-----	-----TGPNP.NIGYA.PE--
DmMic26-27	102	-----HTQSTIDMLNEP.N.L-----	-----HRSGAIVVGGLAG.--
DmNlaz	106	-----	-----GQLA.AFYPTQPL--
DmMtp	398	-----H.FGLLEQESI.KHL.LRESVIQTVATLTRQSGLDVEDPLL-----	-----EVRSYLLQGL.SK--
CeDSc4	419	-----S.DKKSEEYKWKVANTIATVLNKRCEAS-----	-----TSSLNSCNKG.ETI--
CeApoL1	173	-----GVSLAGI-TGFGIKMAASSMGHLTNA-----	
CeApoL3-Like	191	-----G.VT...I.TRF.IT...R.SSS-----	
CeMoma1	119	-----	
CeVit1I	442	-----EQKKYERNMMDRHF.N.M-PEYELLIK.ARLNQINAV-----	-----AEYKL TRE--
CeVit1II	412	-----E-NEDIVPLEAAQLLK-SIQETPFPSQTIAEALIK-----	-----FAESRVSK--
CeVit2I	442	-----EQKKYERNMMDRQFN.M-PEYELLIK.ARLNQINAV-----	-----AEYKL TRE--
CeVit2II	412	-----E-NEDILPL--GQILK-.IQETPFPSQ.IAEALIK-----	-----FAESRVAK--
CeVit3I	443	-----EQKKFLRNIEREYK..-PEYELLIK.ARLNQVNVV-----	-----SEYKL TPE--
CeVit3II	409	-----E-KKSITPLRAAELLK-SVQETLYPSEHIAD.LIQ-----	-----LAQSPLSE--
CeVit4I	443	-----EQKKFLRNIEREYK..-PEYELLIK.ARLNQVNVV-----	-----SEYKL TPE--
CeVit4II	409	-----E-KKSITPLRAAELLK-SVQETLYPSEHIAD.LIQ-----	-----LAQSPLSE--
CeVit5I	443	-----EQKKFIRNIEREYK..-PEYELLIK.ARLNQVNVV-----	-----SEYKL TPQ--
CeVit5II	409	-----E-KKSITPLRAAELLK-SVQETLYPSEHIAD.LIQ-----	-----LAQSPLSE--
CeVit6I	432	-----EQKKFVKIEQA-----PEHETLLE..RLDQYQTV-----	-----VEYEFEPK--
CeVit6II	433	-----QSRKNIAPLKA.V.IK-.LVDMPYPSLAIAEDIAR-----	-----LCESDVSS--
DmApoLppI	1362	QKLDAVEHTTLIIVDLRDFGYPEFE.KSQ-NTRQGLKYQYHLDSFIITGNFKYQFTAN	
DmApoLppII	377	-----LSKFDEKEKLL-AILSLNIVK.VDKETL.Q-----	-----AASQLLPN--
DmApoLTPI	1342	NFNAFYERVKFIVNDDKDNTQEL.FVFNYT-ALQDNVKKPAHDVQV.LL---	TPYEMLHEIYVHGHIELDNAYKGNISA
DmApoLTPII	428	-----INEKLTKQMAHDWMTA-LS.ITRPDEETLETFHSI-----	-----LEY--
DmCG31659	123	-----LDTDYVNF-AIRFMCFD..KIFSFWH-----	
DmCvD	615	MHRHLPQKPESRYWVTGNIFYDYRD.KF..GAMLQVFLVGDPKSDMPVV---	AFFKFDTE--
DmFabp	123	-----	
DmGlaz	112	-----NSRSSIMDFKFTTRFP-DVIARLLPG.GKYQVLYT-----	
DmMic26-27	132	-----IFAARGGFIKKVLY.GI.AGAVASMCYPROAEENCRVV-----	
DmNlaz	119	-----KANYLVLTGDYESYAVV-----	-----YSCTSVTP--
DmMtp	453	-----EPTLYIRALQNLQDPA-.I-EALLEHAQT.EAP.LSVAALQALKAF-----	
CeDSc4	460	-----VNKFITDLTAGGVEV-RVLEVLNIPIF.SY.F.---	KKFICETE--

CeApoL1	198	-----	
CeApoL3-Like	216	-----	
CeMoma1	119	-----	
CeVit1I	484	-----	
CeVit1II	453	-----	
CeVit2I	484	-----	
CeVit2II	451	-----	
CeVit3I	485	-----	
CeVit3II	450	-----	
CeVit4I	485	-----	
CeVit4II	450	-----	
CeVit5I	485	-----	
CeVit5II	450	-----	
CeVit6I	470	-----	
CeVit6II	475	-----	
DmApoLppI	1421	-----	
DmApoLppII	414	-----	
DmApoLTPI	1418	VTATHLSMAASIENEDNFLETSGVIGLETDIAIPHYGCQVYFKKDFSAVDKAIDIRFEVTDNGTLNQLHISTDWHTDPSY	
DmApoLTPII	465	-----	
DmCG31659	149	-----	
DmCvD	672	-----	
DmFabp	123	-----	
DmGlaz	146	-----	
DmMic26-27	170	-----	
DmNlaz	145	-----	
DmMtp	497	-----	
CeDSc4	501	-----	
CeApoL1	198	-----	
CeApoL3-Like	216	-----	
CeMoma1	119	-----	
CeVit1I	484	-----	TEQVLARYFD
CeVit1II	453	-----	NNQVVRQSAW
CeVit2I	484	-----	TEQVLARYFD
CeVit2II	451	-----	NNLVVRQAAW
CeVit3I	485	-----	SEYTFSRIFD
CeVit3II	450	-----	KYEPLRQSAW
CeVit4I	485	-----	SEYTFSRIFD
CeVit4II	450	-----	KYEPLRQSAW
CeVit5I	485	-----	SEYTFSRIFD
CeVit5II	450	-----	KYEPLRQSAW
CeVit6I	470	-----	PAQYFARYWN
CeVit6II	475	-----	SFPALRQSCW
DmApoLppI	1421	-----	VQPTSSTIKLALPKRQILFETTQKIPADGS
DmApoLppII	414	-----	APKELYIAVGN
DmApoLTPI	1498	IVNANGRIKTTMLPLQMASTSVLVIQGNPHLNFDLNLSSQNGQSIAYGARANKKKDVFNIEVWTPMKNFRNISMHGTAI	
DmApoLTPII	465	-----	AKNRLDAEYT
DmCG31659	149	-----	
DmCvD	672	-----	ALGKFTGQLALYIKARGLPDITILNKMQRNGSDPFTFKSIKALLA
DmFabp	123	-----	
DmGlaz	146	-----	DYENF
DmMic26-27	170	-----	
DmNlaz	145	-----	
DmMtp	497	-----	PLGSFNSSHR
CeDSc4	501	-----	SEDVQKAALNVI
CeApoL1	198	-----	
CeApoL3-Like	216	-----	
CeMoma1	119	-----	
CeVit1I	494	-----	
CeVit1II	463	-----	
CeVit2I	494	-----	
CeVit2II	461	-----	
CeVit3I	495	-----	
CeVit3II	460	-----	
CeVit4I	495	-----	
CeVit4II	460	-----	
CeVit5I	495	-----	
CeVit5II	460	-----	
CeVit6I	480	-----	
CeVit6II	485	-----	
DmApoLppI	1451	-----	
DmApoLppII	425	-----	
DmApoLTPI	1578	RSPRDPGRYDVSGFLYRNMATYEVTVAVRMTNSLPIDVVLRVQPKAGGRDGVIELNIHEAGPKKIRFSFSAIEDGKMCQM	
DmApoLTPII	475	-----	
DmCG31659	149	-----	
DmCvD	717	-----	
DmFabp	123	-----	
DmGlaz	151	-----	
DmMic26-27	170	-----	
DmNlaz	145	-----	
DmMtp	507	-----	
CeDSc4	513	-----	

CeApoL1	198	-----
CeApoL3-Like	216	-----
CeMoma1	119	-----
CeVit1I	494	-----
CeVit1II	463	-----
CeVit2I	494	-----
CeVit2II	461	-----
CeVit3I	495	-----
CeVit3II	460	-----
CeVit4I	495	-----
CeVit4II	460	-----
CeVit5I	495	-----
CeVit5II	460	-----
CeVit6I	480	-----
CeVit6II	485	-----
DmApoLppI	1451	-----
DmApoLppII	425	-----
DmApoLTPI	1658	SGGYSVSKTNGAMDFSVLVESTPEIARINFYGNLSPNSEGLVGDLSTETPWKALGIDTVHLHSDVGFLNKGGHIVGEY
DmApoLTPII	475	-----
DmCG31659	149	-----
DmCvD	717	-----
DmFabp	123	-----
DmGlaz	151	-----
DmMic26-27	170	-----
DmNlaz	145	-----
DmMtp	507	-----
CeDSc4	513	-----
CeApoL1	198	-----LMKG-----
CeApoL3-Like	216	-----V-----
CeMoma1	119	-----P.AAAITV-----
CeVit1I	494	-----V.AYNYWT-----
CeVit1II	463	-----AA.SVVRG-----
CeVit2I	494	-----V.TYNYWT-----
CeVit2II	461	-----AA.SVVRG-----
CeVit3I	495	-----I.AYNFWT-----
CeVit3II	460	-----AA.SVVRG-----
CeVit4I	495	-----I.AYNFWT-----
CeVit4II	460	-----AA.SVVRG-----
CeVit5I	495	-----I.AYNFWT-----
CeVit5II	460	-----AA.SVVRG-----
CeVit6I	480	-----MVQAYLRTQ-----
CeVit6II	485	-----TY.AIVNG-----
DmApoLppI	1451	-----FGRYEQTA-----
DmApoLppII	425	-----VAKYCLKN-----
DmApoLTPI	1738	KIGQYIGR.SCLWSWILAEDMQLVLENYLERPNAKPRIVHASAKYQNPQGTFQTLQAGGRLSVDSKWNLDVNGSAEYKSV
DmApoLTPII	475	-----GATAVVHS-----
DmCG31659	149	-----
DmCvD	717	-----MLQAPIINS-----
DmFabp	123	-----
DmGlaz	151	-----AILWS-----
DmMic26-27	170	-----YE.RKIFA-----
DmNlaz	145	-----ANFKIVWI-----
DmMtp	507	-----QFESIFYQ-----
CeDSc4	513	-----AASKNLYE-----
CeApoL1	202	-----
CeApoL3-Like	220	-----
CeMoma1	128	-----
CeVit1I	503	-----
CeVit1II	472	-----
CeVit2I	503	-----
CeVit2II	470	-----
CeVit3I	504	-----
CeVit3II	469	-----
CeVit4I	504	-----
CeVit4II	469	-----
CeVit5I	504	-----
CeVit5II	469	-----
CeVit6I	489	-----
CeVit6II	494	-----
DmApoLppI	1460	-----
DmApoLppII	434	-----
DmApoLTPI	1818	DDFKFRVITALPLPVGDRHQLSASYQGNVISQQFNNPDFVLEASYESFEAQNKLLSRISYKNATNNLKGLGHVEWGKIQN
DmApoLTPII	484	-----
DmCG31659	149	-----
DmCvD	726	-----
DmFabp	123	-----
DmGlaz	156	-----
DmMic26-27	179	-----
DmNlaz	154	-----
DmMtp	516	-----
CeDSc4	522	-----

CeApoL1	202	-----			
CeApoL3-Like	220	-----			
CeMoma1	128	-----			
CeVit1I	503	-----	V	SSRPENNE	
CeVit1II	472	-----	I	VDYKNIRPL	VR
CeVit2I	503	-----	V	SSRPENNE	
CeVit2II	470	-----	I	VDYKNIRPL	VR
CeVit3I	504	-----	V	SEKRVQNE	
CeVit3II	469	-----	F	ASKTQDLPL	IR
CeVit4I	504	-----	V	SEKRVQNE	
CeVit4II	469	-----	F	ASKTQDLPL	IR
CeVit5I	504	-----	V	SEKRVQNE	
CeVit5II	469	-----	F	ASKTQDLPL	IR
CeVit6I	489	-----	YPWTSRIETREEPSR		
CeVit6II	494	-----	V	CGQTPRVFV	
DmApoLppI	1460	-----	SFFIDKLQKPPDDVARFSAIVDVTGTERVAFNA		
DmApoLppII	434	-----	Y	CQGPEID	
DmApoLTPI	1898	LSVVEGDFELLHKQGAQREFSAKIITPKFKNEHTFALTGSYDLEKSGHHNVVGSGLDYPASRRITDLDVSVSSLSNMHGIF			
DmApoLTPII	484	-----	F	CKHHEACE	
DmCG31659	149	-----			
DmCvD	726	-----	KDLHLEFILQMEGKTVLSYYLNQRMFRQLTYDNILERMQQIIRTDSDSHINMQTVRWPFM		
DmFabp	123	-----			
DmGlaz	156	-----	CG		
DmMic26-27	179	-----			
DmNlaz	154	-----			
DmMtp	516	-----	RKRRFD		
CeDSc4	522	-----	T		
CeApoL1	202	-----			
CeApoL3-Like	220	-----			
CeMoma1	128	-----			
CeVit1I	512	-----			
CeVit1II	484	-----			
CeVit2I	512	-----			
CeVit2II	482	-----			
CeVit3I	513	-----			
CeVit3II	481	-----			
CeVit4I	513	-----			
CeVit4II	481	-----			
CeVit5I	513	-----			
CeVit5II	481	-----			
CeVit6I	504	-----			
CeVit6II	504	-----			
DmApoLppI	1492	-----			
DmApoLppII	442	-----			
DmApoLTPI	1978	NSTLPTFLNVSWLKTDFNFTTNGKSYRYRCRCFWPQDTAYFKLNSNYDSDSSNFNHNNGNVEIEVPLATRRHADIVYGL			
DmApoLTPII	493	-----			
DmCG31659	149	-----			
DmCvD	784	NRYTV			
DmFabp	123	-----			
DmGlaz	158	-----			
DmMic26-27	179	-----			
DmNlaz	154	-----			
DmMtp	522	-----			
CeDSc4	523	-----			
CeApoL1	202	-----		MLQ	SVA
CeApoL3-Like	220	-----		V.H	
CeMoma1	128	-----		GGMAGFVL	G.K
CeVit1I	512	-----	NDRV	VVQLTVEPMSRQYVNITMQSPIERV	E.K
CeVit1II	484	-----	EDKR	ELKEKFLRVFMQQYKDAETTYEKIL	A.K
CeVit2I	512	-----	NDRV	VVQLTVEPMSRQYVNITMQSPMERI	E.K
CeVit2II	482	-----	EDKR	ELKEKFLRVFMQQYKDAETTYEKIL	A.K
CeVit3I	513	-----	DRRV	VLQLSVEPLSRQYMNMTIQTPEQEV	E.K
CeVit3II	481	-----	PASR	QTKEYVVRVFMQHFRNADSTYEKVL	A.K
CeVit4I	513	-----	DRRV	VLQLSVEPLSRQYMNMTIQTPEQEV	E.K
CeVit4II	481	-----	PASR	QTKEYVVRVFMQHFRNADSTYEKVL	A.K
CeVit5I	513	-----	NRRV	VLQLSVEPLSRQYMNMTIQTPEQEV	E.K
CeVit5II	481	-----	PASR	QTKEYVVRVFMQHFRNADSTYEKVL	A.K
CeVit6I	504	-----	KNMI	RATINVEPRQLTVNMTIETPMETT	V.E
CeVit6II	504	-----	QKNGVKMCPRDAKQIRVDKLVQQFESASTRYEKVL	A.K	TL
DmApoLppI	1492	-----	NGKLKFEHPTIRPLSISGQLNGDVNQIIASAEVIF	DIF	RLPEQKVVGNSSELRNS
DmApoLppII	442	-----	AISKFSDDLKHKCPNTKREEERIVYI	K	GLG
DmApoLTPI	2058	QKRRNQDAGNVKVYNEKQVLDGKYKRLEQAKAPIYKETTDISLENEVKPL	GIH		F.STRDASDPAGSQDV
DmApoLTPII	493	-----	ENLRVQIINLLETEFLNLYNLFKGERRTRERMI	L.K	GLG
DmCG31659	149	-----	VI		
DmCvD	789	-----	PTVLGTSSDVLLQTTVLTSLRGNITEQRNSPITKH	T.EIDARYSSYA	R
DmFabp	123	-----			HGS
DmGlaz	158	-----		SIG	LG
DmMic26-27	179	-----		VAYNFIK	G.VK
DmNlaz	154	-----		LTQREPSAEAVDAARKIL	EDN
DmMtp	522	-----	SSARTLALDIILSRPTQEQLGNFLDYLASNDRQF	EIK	TYV
CeDSc4	523	-----	QLTHKLIKLFRTNCQSETPTSHSQL	AID	ILLKCVPDHQN

CeApoL1	208	-----A
CeApoL3-Like	226	-----V
CeMoma1	142	-----V
CeVit1I	547	-----V
CeVit1II	519	-----N
CeVit2I	547	-----V
CeVit2II	517	-----N
CeVit3I	548	-----I
CeVit3II	516	-----N
CeVit4I	548	-----I
CeVit4II	516	-----N
CeVit5I	548	-----I
CeVit5II	516	-----N
CeVit6I	539	-----
CeVit6II	545	-----N
DmApoLppI	1546	RSQNGFNIAIYITTVKSAGLQFQYQINSNAAVDIEAHEYN
DmApoLppII	474	-----
DmApoLTPI	2128	KHIEIYELRNTQNFNLTGELHSRATLKAQDFKVVAIHPNRAVVLSTKYEDVSPEVVRHHSKLELSETAWIGYNLELGNFS
DmApoLTPII	534	-----N
DmCG31659	152	-----
DmCvD	839	-----
DmFabp	126	-----
DmGlaz	164	-----
DmMic26-27	189	-----
DmNlaz	179	-----
DmMtp	563	-----L
CeDSc4	562	-----V
CeApoL1	209	-----
CeApoL3-Like	227	-----
CeMoma1	143	-----
CeVit1I	548	-----
CeVit1II	520	-----
CeVit2I	548	-----
CeVit2II	518	-----
CeVit3I	549	-----
CeVit3II	517	-----
CeVit4I	549	-----
CeVit4II	517	-----
CeVit5I	549	-----
CeVit5II	517	-----
CeVit6I	539	-----
CeVit6II	546	-----
DmApoLppI	1585	-----
DmApoLppII	474	-----
DmApoLTPI	2208	KVGNESQSFALEIFYPKRNLSSSGQYYMTDTNFNSDLFQWLGGNYDQQPKIIHSNLQWKAEP LHRGDREHRTIALTVAH
DmApoLTPII	535	-----
DmCG31659	152	-----
DmCvD	839	-----
DmFabp	126	-----
DmGlaz	164	-----
DmMic26-27	189	-----
DmNlaz	179	-----
DmMtp	564	-----
CeDSc4	563	-----
CeApoL1	209	-----
CeApoL3-Like	227	-----
CeMoma1	143	-----
CeVit1I	548	-----
CeVit1II	520	-----
CeVit2I	548	-----
CeVit2II	518	-----
CeVit3I	549	-----
CeVit3II	517	-----
CeVit4I	549	-----
CeVit4II	517	-----
CeVit5I	549	-----
CeVit5II	517	-----
CeVit6I	539	-----
CeVit6II	546	-----
DmApoLppI	1585	-----
DmApoLppII	474	-----
DmApoLTPI	2288	PLLEKDINCKATYYRGLRDLLRTHLTIDYSEYPDQLIELGAQLTD RYSELGHTNYTFHVGKHIASELDVQLNGTLAAMN
DmApoLTPII	535	-----
DmCG31659	152	-----
DmCvD	839	-----
DmFabp	126	-----
DmGlaz	164	-----
DmMic26-27	189	-----
DmNlaz	179	-----
DmMtp	564	-----
CeDSc4	563	-----

CeApoL1	209	-----IGIVLDGVTLA-----
CeApoL3-Like	227	-----.....S.....
CeMoma1	143	-----GRLTTTIG.....
CeVit1I	548	-----PRVY.PSIAQR-----
CeVit1II	520	-----A.LDISVNQ.N-----
CeVit2I	548	-----PRVY.PSIAQR-----
CeVit2II	518	-----A.LDISVNQ.N-----
CeVit3I	549	-----PRV..PTIARR-----
CeVit3II	517	-----A..D.SVYE.V-----
CeVit4I	549	-----PRV..PTIARR-----
CeVit4II	517	-----A..D.SVYE.V-----
CeVit5I	549	-----PRV..PTIARS-----
CeVit5II	517	-----A..D.SVYE.V-----
CeVit6I	539	-----LPFR.PTAQIH-----
CeVit6II	546	-----A.LD.SVYP.E-----
DmApoLppI	1585	-----..LE.NNGEID-----V
DmApoLppII	474	-----NAKS.S.N.V-----
DmApoLTPI	2368	SYKTESTAHYKRDIFPARYGKFLALLDVNKRELEYERQSPFHAVRLHLLPT.RYPIYG.NATIWDTPDTNHSGYIYMDI
DmApoLTPII	535	-----..V.SSAFAEQ-----
DmCG31659	152	-----TRKR.PSTQVI-----
DmCvD	839	-----SRSYNPFLN.D-----
DmFabp	126	-----LRLRVPCQPVP-----
DmGlaz	164	-----HSDQIWILGRD-----
DmMic26-27	189	-----P.EDVPV.PFP-----
DmNlaz	179	-----QAFLI.T.Q-----
DmMtp	564	-----QKLRMLAEKCP-----
CeDSc4	563	-----ATLI.RTE..N-----
CeApoL1	220	-----
CeApoL3-Like	238	-----
CeMoma1	154	-----
CeVit1I	559	-----
CeVit1II	531	-----
CeVit2I	559	-----
CeVit2II	529	-----
CeVit3I	560	-----
CeVit3II	528	-----
CeVit4I	560	-----
CeVit4II	528	-----
CeVit5I	560	-----
CeVit5II	528	-----
CeVit6I	550	-----
CeVit6II	557	-----
DmApoLppI	1597	KAISFLNKEKFEISLSES NKHIYIVGDFSKQNHYAKLNTKVQILDKNPIEITSEVQPN SAKIILKRQDFIDGTAEVKLG
DmApoLppII	485	-----
DmApoLTPI	2448	LERYARMDFNLTEDASQNLQMVGYIPDTRSAFLDIWRNYEEIRVIDVSSYLKMNH SRLITGRFHW RPSIRQEVREKIQAV
DmApoLTPII	546	-----
DmCG31659	163	-----
DmCvD	850	-----
DmFabp	137	-----
DmGlaz	175	-----
DmMic26-27	200	-----
DmNlaz	188	-----
DmMtp	575	-----
CeDSc4	574	-----
CeApoL1	220	-----
CeApoL3-Like	238	-----
CeMoma1	154	-----
CeVit1I	559	-----
CeVit1II	531	-----
CeVit2I	559	-----
CeVit2II	529	-----
CeVit3I	560	-----
CeVit3II	528	-----
CeVit4I	560	-----
CeVit4II	528	-----
CeVit5I	560	-----
CeVit5II	528	-----
CeVit6I	550	-----
CeVit6II	557	-----
DmApoLppI	1677	KEFKVDVIGSGKQLFNGRVALDATNFLQTN YFINEDHLNGFWHIVESEINKDSEYISENIKERLKKSRQVTDKIVKLAKE
DmApoLppII	485	-----
DmApoLTPI	2528	GKSVYSSFSEGIDFWIKSIYTETTESMGVVWNTAKEYNRDFIDDIGQLSVLEEDLADLRLFVNQSYEANDFYIKNVVNFT
DmApoLTPII	546	-----
DmCG31659	163	-----
DmCvD	850	-----HEINREQGFLIYIPFS
DmFabp	137	-----
DmGlaz	175	-----
DmMic26-27	200	-----
DmNlaz	188	-----
DmMtp	575	-----
CeDSc4	574	-----

CeApoL1	220	-----
CeApoL3-Like	238	-----
CeMoma1	154	-----
CeVit1I	559	-----SVKHLLNEASGSVCKVQ-----
CeVit1II	531	-----EIIIVDKRQLLPVRKEAI-----
CeVit2I	559	-----SVKHQLTEASGSVCKVQ-----
CeVit2II	529	-----EIIIVDKRQPLPVRKEAI-----
CeVit3I	560	-----AMFQQTWEKTGATCKVG-----
CeVit3II	528	-----QLIQDPRQPLSIRTEAV-----
CeVit4I	560	-----AMFQQTWEKTGATCKVD-----
CeVit4II	528	-----QLIQDPRQPLSIRTEAV-----
CeVit5I	560	-----AMFQQTWEKTGATCKVD-----
CeVit5II	528	-----QLIQDPRQPLSIRTEAV-----
CeVit6I	550	-----YQPRNSRYEQKPVMEKIAHHASKQANCV-----
CeVit6II	557	-----KIILNEQHETTIRTQAI-----
DmApoLppI	1757	AGPDFSKLQGKLLDYKNDIVQELEADQSIAPIID-----
DmApoLppII	485	-----ALSECASTGRSNRIRVA-----
DmApoLTPI	2608	LTILDELAIRDHIESLPKIFSELWQAMGDSGKALRNSIVWLITETIKTTYNNLLDAVARFFHGESLVYISGLLEKGIKYD
DmApoLTPII	546	-----LQWIIREDEAPVDIRLHGI-----
DmCG31659	163	-----
DmCvD	866	SELHLNESGSKCRRYSFSRPQNLTSGLSFKSRAV-----
DmFabp	137	-----
DmGlaz	175	-----
DmMic26-27	200	-----
DmNlaz	188	-----
DmMtp	575	-----RFRALFKSELV-----
CeDSc4	574	-----PDDQEKWHYLYKAIEAS-----
CeApoL1	220	-----
CeApoL3-Like	238	-----
CeMoma1	154	-----
CeVit1I	576	-----
CeVit1II	548	-----
CeVit2I	576	-----
CeVit2II	546	-----
CeVit3I	577	-----
CeVit3II	545	-----
CeVit4I	577	-----
CeVit4II	545	-----
CeVit5I	577	-----
CeVit5II	545	-----
CeVit6I	578	-----
CeVit6II	574	-----
DmApoLppI	1791	-----
DmApoLppII	502	-----
DmApoLTPI	2688	SFIKDLHIKFIKYIENLWHKTWTLAENHWKAVLKRFEPLFKMISFIETTAWNLSKEVFDFIYKRTNELAESPYFNKVSS
DmApoLTPII	565	-----
DmCG31659	163	-----
DmCvD	900	-----
DmFabp	137	-----
DmGlaz	175	-----
DmMic26-27	200	-----
DmNlaz	188	-----
DmMtp	586	-----
CeDSc4	591	-----
CeApoL1	220	-----MSANTLKN-----
CeApoL3-Like	238	-----L..K..GE-----
CeMoma1	154	-----
CeVit1I	576	-----KNQIR.FDDVL---YNTPLTTCYSLIA---KDC---SEEPTFAVLSSKTEKNSEE-----
CeVit1II	548	-----DALRL..DTMPRKIQKVLLPIYK---N---RQY---EPEIRMLALWRMMHTRPEE-----
CeVit2I	576	-----KNQIR.FDDVL---YNTPLTTCYSLIA---KDC---SEEPTFAVLSSKTEKNSEE-----
CeVit2II	546	-----DALRL..DTMPRKIQKVLLPIYK---N---RQY---EPEIRMLALWRMMHTRPEE-----
CeVit3I	577	-----QSEVS.FD.VI---YRAPLTTCYSLVA---KDC---SEQPRFAVLAKKINKNSEE-----
CeVit3II	545	-----DALRL..DVMPRKIQKVLLPVYK---N---RQN---KPELRMAALWRMMHTIPEE-----
CeVit4I	577	-----QSEVS.FD.VI---YRAPLTTCYSLVA---KDC---SEQPRFAVLAKKINKNSEE-----
CeVit4II	545	-----DALRL..DVMPRKIQKVLLPVYK---N---RQN---KPELRMAALWRMMHTIPEE-----
CeVit5I	577	-----QSEVS.FD.VI---YRAPLTTCYSLVA---KDC---SEQPRFAVLAKKINKNSEE-----
CeVit5II	545	-----DALRL..DVMPRKIQKVLLPVYK---N---RQN---KPELRMAALWRMMHTIPEE-----
CeVit6I	578	-----VKSTKI..FDQVA---YRNQFTPCYSVLA---KDCGSEKSEPRFVVLKMKINEKKEW-----
CeVit6II	574	-----E.FRR.RTQMPTKIQRVLMVYLL---N---RQQ---POHIRMSALHQIIYTQPEW-----
DmApoLppI	1791	-----GIRTLFKKIAGIVDDI.KAISEILEKAQKSIVDIYDKLQALWKDSLKAWEDFIITVQKLISLTKEFIKICTQSFKD
DmApoLppII	502	-----ALHAFS.VKCEETLQSKSLELLK---N---RNE---DSELRIEAYLSAI-SCPNA-----
DmApoLTPI	2768	FTADAERLYRDFKANDAITNI.KYSTIAWNFVKEKYFKLVP---FGA---ELNEVLTEIWQEIKELEKI-----
DmApoLTPII	565	-----LAFRRVDCARHRSYFLDNYGNYTL-----NSELRIYSYLQAM-RCPDY-----
DmCG31659	163	-----HMAQYFG-----
DmCvD	900	-----TKTRGLITKTA.APFEEIMVPEGRNDVVQLFSYPMTDLGVRLSMTTNLNELIKYRGMLLKSEFTENGFSGNMVV
DmFabp	137	-----
DmGlaz	175	-----RDF---EVDIR-----
DmMic26-27	200	-----T.L-----
DmNlaz	188	-----KNC-----
DmMtp	586	-----KRRHV..NYNVLGQKGLTTVLTRQLS-----QAPAFNETLLSTQEYVQGIKRGSV-----
CeDSc4	591	-----GNKDE..AEFWSMRK---FKVFR-----PNFLHRALQADSHVHWQEIADASN-----

CeApoL1	228	-----GSSSELAGKIREASGK-----MERMHR-----NVV
CeApoL3-Like	246	..V...GSS.L...S.-----..M..Q-----K..
CeMoma1	154	-----T.AAFCY-----PIE
CeVit1I	622	-----MIIKVIR.EQEIVAQL-----QN.EI.V-----K.D
CeVit1II	594	-----SLLVQVVSQMEKETNQ-----QVAALT-----QMI
CeVit2I	622	-----MIIKVIR.EQEIVAQL-----QN.EI.V-----K.D
CeVit2II	592	-----SLLVQVVSQMEKETNQ-----QVAALT-----QMI
CeVit3I	623	-----LLVKVVRREEEIVVK-----SDDKFLV-----K.D
CeVit3II	591	-----PVLAHIVSQMENE.NQ-----HVAAFY-----..L
CeVit4I	623	-----LLVKVVRREEEIVVK-----SDDKFLV-----K.D
CeVit4II	591	-----PVLAHIVSQMENE.NQ-----HVAAFY-----..L
CeVit5I	623	-----LLVKVVRREEEIVVK-----SDDKFLV-----K.D
CeVit5II	591	-----PVLAHIVSQMENE.NQ-----HVAAFY-----..L
CeVit6I	629	-----KNVKVYV.ENEIEMY-----TE.GLIC-----R.N
CeVit6II	620	-----SVL.QIGNQL.QERNQ-----QVRAFTL-----SLL
DmApoLppI	1869	LLSALEKYGPALKKNYGKAIGEIVKPIINDAAQEVIKIVVNAAEGVTHEFKQYVASLPSFESIRNEFNKDV-----K.L
DmApoLppII	547	-----EVANQISEIVNSETVN-----QVGGFIS-----SNL
DmApoLTPI	2831	-----DQVQIMVQ.YY.VMA.VDWVADELQLEHRLHQVYGLVR-----..KF
DmApoLTPII	607	-----I.VGVIKSILEHEEIN-----QVGSFVW-----SHL
DmCG31659	170	-----K.AGLVI.DMSKVPQE-----
DmCvD	974	-----NALMYIF.FTQLS.IH-----LGHDRNFTMLMYNEKNTRIE
DmFabp	137	-----
DmGlaz	183	-----SKVYDVLKRLSLDPER-----
DmMic26-27	203	-----EDLYYM.SDLYDEAKD-----
DmNlaz	191	-----PRLDNGTGLAGED..L-----DVDDFVS-----
DmMtp	636	-----EFLHAGRSQASSFKL-----GIYTAGLGSVLGDDSGD
CeDSc4	637	-----QLF.TANTEFLQK.F.RSIFELSMKKGRKEHNLFSLSI-----DTE
CeApoL1	253	TNFLNYD-----
CeApoL3-Like	271	KH...E.V-----WKDDDDVLSDVGS-----IEMVQPESP-----
CeMoma1	164	AVDVAKTG-----
CeVit1I	648	GKKILSED-----YSAHQIERLGESD-----IVIELPEGE-----
CeVit1II	620	RH.AKSTNPC-----YQ RVAIVCSKVL-----FTRYQPQEQ-----
CeVit2I	648	GKKIQSED-----YSAYQIERLGESA-----IVIELPEGE-----
CeVit2II	618	RH.AMSTNPC-----YQ RVAIVCSKVL-----FTRYQPQEQ-----
CeVit3I	649	EKKV.PTE-----LEQYNIIEILGDN-----IVIRLPHE-----
CeVit3II	617	RQ.SKSTNPC-----YQQLAVRCSKVL-----FTRYQPQEQ-----
CeVit4I	649	GKKV.PTE-----LEQYNIIEILGDN-----IVIRLPHE-----
CeVit4II	617	RQ.SKSTNPC-----YQQLAVRCSKVL-----FTRYQPQEQ-----
CeVit5I	649	GKKV.PTE-----LEQYNIIEILGDN-----IVIRLPHE-----
CeVit5II	617	RQ.YKSTNPC-----YQQLAVRCSKILL-----FTRYQPQEQ-----
CeVit6I	655	GEEIE.QPESEIE-----KKQYNIILWLNKNT-----LKFDSDVT-----
CeVit6II	646	RSYA.NESPC-----EQTFSSRVQSLN-----NIPFSSQEI-----
DmApoLppI	1941	KL.EKATELTNSL----FDQINILPQTPETSEFLQKLHDYLIAKLKQEHIDNEKYIEELGQLLIKAVRSIWSIRSTYPG
DmApoLppII	573	KAIRDSTDVSRDQKQYHLANIRVTKTFPVD-----YRRYSFNNE-----
DmApoLTPI	2872	R.YAMNALETADM----YREAKTKFVFDPE-----VGIIIDLEQKLPMWSHAFNETPRFEEIPEYQVLAKAQSFSS
DmApoLTPII	633	..LAKSNSPVRIEAQGLLLNDELSERFKMD-----IRKFSRNYE-----
DmCG31659	186	-----
DmCvD	1010	G..CAE.VLKTSDMKGKQIGLTLEHTDHMMENHAADALHRWNITLDVLA STKSNWFKLTGQVQRNSKDDDEDDWKACTKLT
DmFabp	137	-----
DmGlaz	199	-----
DmMic26-27	219	-----
DmNlaz	214	-----
DmMtp	670	G.DAIPADDEFSEDEAVTAGMEISVQGAQL-----RPLVFFSGQ-----
CeDSc4	678	HLEQFVTGSASSRS GAPQGSVRIGVAGHKL-----PTHHIFKGS-----
CeApoL1	260	-----
CeApoL3-Like	301	-----NQ-----
CeMoma1	172	-----
CeVit1I	678	----VRFDGYTIKTQL-----PSYSRKNQLCG-----LCGNNDDESTNEFYTSNDTETK
CeVit1II	652	----MIASSYAQ-----LPLFLQNSFSG-----AQFDFAAIFEKN
CeVit2I	678	----VRFDGYTIKTQL-----PSYSRKNQLCG-----LCGNNDDESTNEFYTSNDTETE
CeVit2II	650	----MIASSYAQ-----LPLFLQNSFSG-----AQFDFAAIFEKN
CeVit3I	679	----VRFDGYTVKTNM-----PSVASQNQLCG-----LCGNNDGERDNEFMTADNYETE
CeVit3II	649	----ML-STYSQ-----LPLFNSEWLSG-----VQFDFATIFEKN
CeVit4I	679	----VRFDGYTVKTNM-----PSVASQNQLCG-----LCGNNDGERDNEFMTADNYETE
CeVit4II	649	----ML-STYSQ-----LPLFNSEWLSG-----VQFDFATIFEKN
CeVit5I	679	----VRFDGYTVKTNM-----PSVASQNQLCG-----LCGNNDGERDNEFMTADNYETE
CeVit5II	649	----ML-STYSQ-----LPLFNSEWLSG-----VQFDFATIFEKN
CeVit6I	690	----VQFDGVNARIH-----LSALYRNQCCG-----LCGHYDNEKETEFYDAENQENT
CeVit6II	678	----DRFESVYGK-----WSTYSRRHQSG-----FEANFASLFTTE
DmApoLppI	2017	SSDHVIDFQSWIGSLTHSFDSLAVLPSILSFRSSILNCL--LNENWDVVFNKLLYSWIFFNDFELRGHVVDGKHIFTFD
DmApoLppII	612	-----VSYKLESLGVG-----ASTDYQIIYSQH
DmApoLTPI	2938	ETNSSIVMKLYNMNRTHLDPKTLW----PPYYSRALLIDSRHYMTFDQRYVGLNLFDELGNRSTSQCSYLLAHDFFKR
DmApoLTPII	672	-----HSLFFDEYNFG-----TTTDANVIFGTD
DmCG31659	186	-----
DmCvD	1090	YEPLVFTKRPHTLNGDVVFGFLATEESECEPKGSTVQFAA-----RAGPSEHARAFLRSDKISLT
DmFabp	137	-----PTSVDGARGSG-----
DmGlaz	199	-----
DmMic26-27	219	-----
DmNlaz	214	-----
DmMtp	709	-----TELMGHVWGGG-----ASDSTPAYQATTLSDQN
CeDSc4	717	-----TDLLSTVWEAD-----GRTHKAFEGHVPVRD

CeApoL1	260	-----	SLIMDPHQQESSVQH-----
CeApoL3-Like	303	-----	RAHAEQ-----
CeMoma1	172	-----	-----
CeVit1I	723	DIEEFHR-----	SYLLKNE--ECEAEERLSEKK-----
CeVit1II	683	-----	SFLKDL--HASLDAVFGG-----
CeVit2I	723	DIEEFHR-----	SYLLKNE--ECEAEERLSEKKNYR-----
CeVit2II	681	-----	SFLPKDL--HASLDAVFGG-----
CeVit3I	724	DVEEFHR-----	SYLLKNE--ECEVENDRISEKKNYRN-----
CeVit3II	679	-----	AFLPKEV--QASFETVFGG-----
CeVit4I	724	DVEEFHR-----	SYLLKNE--ECEVEKDRISEKKNYKN-----
CeVit4II	679	-----	AFLPKEV--QASFETVFGG-----
CeVit5I	724	DVEEFHR-----	SYLLKNE--ECEVENDRISEKKNYRN-----
CeVit5II	679	-----	AFLPKEV--QASFETVFGG-----
CeVit6I	734	IPKFAK-----	SYLYKDS--KCNYEREMFEKEE-----
CeVit6II	710	-----	SVLPTEM--MASIEGVLSG-----
DmApoLppI	2095	GLNFAYPGNC-----	KYILAQD--SVDNFTIIGQLTNGKLKSITLIDREGSYFEVADNLALKLNGNLVEYPQ
DmApoLppII	635	-----	GFLPRSS--RINVTEFFGT-----
DmApoLTPI	3013	NFTLLLEPASKSLAGQGLTRKL	SFIANGQLIEIDLETDHISINGNPQPILPLKLGDVNIHRDLVDLSITSDTEFSLHCNV
DmApoLTPII	695	-----	SYLPRIA--SVNFTADLFGQSV-----
DmCG31659	186	-----	SCPYDT-----
DmCvD	1149	DT-----	DFCPKEVLKFSPIPTSRYCKRSNFENFTSITQYDMDLKFDMMPAWFE-----
DmFabp	148	-----	GCGQRPGGPS-----
DmGlaz	199	-----	LIISKNK--QCPEAL-----
DmMic26-27	219	-----	LIFPKK-----
DmNlaz	214	-----	TTVPNAI--EKA?EWLRR-----
DmMtp	737	E-----	HYIILTS--GATLHWRVLGARSVDLNGKVGFS-----
CeDSc4	743	-----	VRLSVPLLSGLTLDVDSVGAISMRVLASAEVS-----
CeApoL1	260	-----	AWNSDI-----
CeApoL3-Like	318	-----	-----
CeMoma1	178	-----	T.Y.FQESP-----
CeVit1I	750	-----	NYRKYDERK-----
CeVit1II	700	-----	N..KYFAQI-----
CeVit2I	753	-----	KYER.EEQS-----
CeVit2II	698	-----	N..KYFAQI-----
CeVit3I	755	-----	K..REEKKS-----
CeVit3II	696	-----	N..KYFAQV-----
CeVit4I	755	-----	K..REEKKS-----
CeVit4II	696	-----	N..KYFAQV-----
CeVit5I	755	-----	K..REEKKS-----
CeVit5II	696	-----	N..KYFAQV-----
CeVit6I	760	-----	NFQRIEKNQ-----
CeVit6II	727	-----	E..QYFAQI-----
DmApoLppI	2161	HLSGLH..RRFYTIH-----	LYSEYGVGIVCTSD-----
DmApoLppII	653	-----	NY.VFEASV-----
DmApoLTPI	3093	QFDL--C.FEVSGWYFGRTAGLLGLTNNEPYDEYTMSSGVISNETQLFTDSWSLKQCRQNKLAQTQEVSQEVSDACTSFF	
DmApoLTPII	715	-----	NFFEFTARA-----
DmCG31659	192	-----	-----
DmCvD	1198	-----	L.SNRLDHL-----
DmFabp	159	-----	VSALSADKV-----
DmGlaz	212	-----	-----
DmMic26-27	225	-----	-----
DmNlaz	230	-----	LYERLYDIF-----
DmMtp	768	-----	L..RNAQTE-----
CeDSc4	775	-----	L..QRSNAK-----
CeApoL1	266	-----	-----
CeApoL3-Like	318	-----	-----
CeMoma1	187	-----	-----
CeVit1I	759	-----	-----
CeVit1II	709	-----	-----
CeVit2I	762	-----	-----
CeVit2II	707	-----	-----
CeVit3I	764	-----	-----
CeVit3II	705	-----	-----
CeVit4I	764	-----	-----
CeVit4II	705	-----	-----
CeVit5I	764	-----	-----
CeVit5II	705	-----	-----
CeVit6I	769	-----	-----
CeVit6II	736	-----	-----
DmApoLppI	2190	LKVCHININGFYTSKTRGLLGNGNAEPYDDFLLIDGTLAENSAALGNDYGVGKCTAIEFDNNQFKSSKRQEMCSELFIE	
DmApoLppII	662	-----	-----
DmApoLTPI	3171	RTGILATCSAVLDPTPFYEMCDLGMKSPPIRKGPAPVKGACAAALAYIEACTALKVPMRVPSPQCVCQLSNGSYVPEGT	
DmApoLTPII	724	-----	-----
DmCG31659	192	-----	-----
DmCvD	1216	DSLHMSQEINISMQTPQDQFRLAVEVNGVKWRFHQIPFFYKLDKSKFDASHELTFDGSLKRSCSVINGIVNTFDDYLINLR	
DmFabp	159	-----	-----
DmGlaz	212	-----	-----
DmMic26-27	225	-----	-----
DmNlaz	239	-----	-----
DmMtp	777	-----	-----
CeDSc4	784	-----	-----

CeApoL1	266	-----
CeApoL3-Like	318	-----
CeMoma1	187	-----
CeVit1I	759	-----YESEEYSFEETYDYEQENTNKKQKNQRS
CeVit1II	709	-----
CeVit2I	762	-----DEYSSEETYDYEQENTKKSQKNQRS
CeVit2II	707	-----
CeVit3I	764	-----DYVSSSDYENNYDEKETENQ--
CeVit3II	705	-----
CeVit4I	764	-----DYESSSDYESNYDEKETEKE--
CeVit4II	705	-----
CeVit5I	764	-----DYESSSDYESNYDEKETEKE--
CeVit5II	705	-----
CeVit6I	769	-----EEEKDQEMNYEESRR
CeVit6II	736	-----
DmApoLppI	2270	STLAFNFITLDSRPYRKACDIALAKVAEKEKEATACTFALAYGSVAVKQINKWVLLPPRCIKCAGPAGQHDFGDEFTVKLP
DmApoLppII	662	-----
DmApoLTPI	3251	FMELSGPEIPKSSDVVFIVEAKECNANLKTSKNIMTVSSIEEQQAQKITNNRYAVVAFGGVSPYDKARSVIYEHNEFT
DmApoLTPII	724	-----
DmCG31659	192	-----
DmCvD	1296	EIAVRPDCLTLLVADCSPLPQIAVFVTPSPVQGLSTNYGLRVHIGQNYFNFRARTDNSSLPTDEPVLIIYNQDQTPHNVR
DmFabp	159	-----
DmGlaz	212	-----
DmMic26-27	225	-----
DmNlaz	239	-----
DmMtp	777	-----IQQNTGSAVLGHLAVGFTYAKL
CeDSc4	784	-----AEAYTSGSLHLTASLYHHSEPV
CeApoL1	266	-----
CeApoL3-Like	318	-----
CeMoma1	187	-----
CeVit1I	787	QKKSDDLVEKTQIKEFSHRICFSVEPVAECRRRGYEAVEQQQRKVRFTCLPRHSSEARRLV--
CeVit1II	709	-----
CeVit2I	787	QKKSDDLVEKTQIKEFSHRICFSVEPVAEC--RRGYEVEQQQRKIRFTCLQRHNRDASRL-----L
CeVit2II	707	-----
CeVit3I	784	-----LFFKTLIKEFSNRVCFSEIEPVSEC--RRGLESEKTSNEKIRFTCMPRHSKNARRF-----L
CeVit3II	705	-----
CeVit4I	784	-----LVKKTLIKEFSNRVCFSEIEPVSEC--RRGLESEKTSNKKIRFTCMPRHSKNARRF-----L
CeVit4II	705	-----
CeVit5I	784	-----LVKKTLIKEFSNRVCFSEIEPVSEC--RRGLESEKTSNKKIRFTCMPRHSKNARRF-----L
CeVit5II	705	-----
CeVit6I	784	EQDDEPTEQVAIVERQHEICFTQKPVLR--QNGKSQESKKQKTSVYCLPSSNSWARRQ-----M
CeVit6II	736	-----
DmApoLppI	2350	NNKVDVVFVVDINVTPGVLSNLIAPAINDIRESLRSGFSDVQVGVIVFEETKRYPALLTSDGGKINYKGNVADVLAGI
DmApoLppII	662	-----
DmApoLTPI	3331	SKPEQLADYFGHINTGNGSSNDILMAISAAAKLNFRPGVSKTFILLSCSKCAARDMRFD-----Y
DmApoLTPII	724	-----EGLEELAANAFGPKGPLSGQLLRKKLSFLNRWLGNE-----
DmCG31659	192	-----
DmCvD	1376	KKPYQWPIETSDYDFRVELNEQNILIVECTQLSSTIQFDLYNILNFEIYGVIYKHQ-----M
DmFabp	159	-----
DmGlaz	212	-----
DmMic26-27	225	-----
DmNlaz	239	-----
DmMtp	799	VQDFSITHEPKLSLNADLDFYSGIKLCMQLQRPEQLLKQTNVRSVFL-----
CeDSc4	806	RHVESTISALSTFTTDTRAIFETLPYDFCLRTSNSNVNDINQKTVVQDQIGKHKKK-----
CeApoL1	266	-----
CeApoL3-Like	318	-----
CeMoma1	187	-----TPSAIVK-----TN-----
CeVit1I	847	-KEARQGTVQLDD-----HK-----
CeVit1II	709	-GFSQQHMDKYVQ-----MA-----
CeVit2I	846	KESRQQPL-QLDD-----YP-----
CeVit2II	707	-GFSQQHMDKYVQ-----MA-----
CeVit3I	838	KEAREQTVADLVD-----FP-----
CeVit3II	705	-GFSQQNFEQVIL-----KT-----
CeVit4I	838	KEAREQTVADLVD-----FP-----
CeVit4II	705	-GFSQQNFEQVIL-----KT-----
CeVit5I	838	KEAREQTVAEVLVD-----FP-----
CeVit5II	705	-GFSQQNFEQVIL-----KT-----
CeVit6I	842	REIRREPLAQWPE-----HK-----
CeVit6II	736	-GFTQKNMEKIIK-----KL-----
DmApoLppI	2430	KSFCDCNVEQIITEKRILDIYNSLKEIVKGIAPQADEKAFQLALDYPFRAGAAKSIIGVRSDSLEYKNWWKFVRAQLTGS
DmApoLppII	662	---RQENVEDVLE-----YY-----
DmApoLTPI	3391	TSILQYLLEEGVNLHILADTEFDFERNKKLRHFFGLDSKLVYSKRFP-----
DmApoLTPII	760	SAEEDDTLENLLS-----
DmCG31659	192	-----
DmCvD	1432	CGLCSKPLNRMQN-----YT-----
DmFabp	159	-----
DmGlaz	212	-----
DmMic26-27	225	-----KP-----
DmNlaz	239	-----
DmMtp	846	-QSVDRPYAKHVR-----ST-----
CeDSc4	861	-TLNRKRVHPGVT-----YR-----

CeApoL1	266	-----	
CeApoL3-Like	318	-----	
CeMoma1	196	-----	-LSPPKS-
CeVit1I	861	-----	-ISFVHS- -VQVPVACVAY-
CeVit1II	723	-----	-LEKLES- -IEKESTTVVRGR-
CeVit2I	860	-----	-VSFVES- -VKVPTACVAYI-
CeVit2II	721	-----	-LEKLES- -LEKESTTVVRGRI-
CeVit3I	853	-----	-VSFVES- -VKIPTACVAY-
CeVit3II	719	-----	-LEKLSL- -YGKQSDE-LRSR-
CeVit4I	853	-----	-VSFVES- -VKIPTACVAYP-
CeVit4II	719	-----	-LEKLSL- -YGKQSDE-LRSRE-
CeVit5I	853	-----	-VSFVES- -VKIPTACVAYP-
CeVit5II	719	-----	-LEKLSL- -YGKQSDE-LRSRN-
CeVit6I	857	-----	-LRNLRDQPQMEERTVRVAVDQKCKFDYS-
CeVit6II	750	-----	-LSNVQ- -EKGLEQIVVRGKV-
DmApoLppI	2510	ITKFDGALIHLIAPVKGLS	LEGVLSEKLIGFNSRLVATVDGKDSKKRTKLQFDNDMGIDFVLNNGGWVFATQNFEKLGAS
DmApoLppII	674	-----	-LGPKGL- -VNKDFDEIVKLIIEVGNGVAAGGRARR-
DmApoLTPI	3438	-----	-EGDAETRNTTHIPKSNLGICTTLAVETQGSVFSARKLQPERKYPIKRFATIFAKRVALSAT
DmApoLTPII	773	-----	-LDNLRK-
DmCG31659	192	-----	
DmCvD	1447	-----	-ICELEANTPTPVP- -LQNSSDVVVVA-
DmFabp	159	-----	
DmGlaz	212	-----	
DmMic26-27	227	-----	
DmNlaz	239	-----	-MNFLSY-
DmMtp	860	-----	-LSHKTAGCTFALN- -QKNNEMCNLIFRDL-
CeDSc4	875	-----	-LDDST- -IRQCNSYLEQFRL-
CeApoL1	266	-----	
CeApoL3-Like	318	-----	
CeMoma1	202	-----	
CeVit1I	877	-----	
CeVit1II	741	-----	
CeVit2I	877	-----	
CeVit2II	740	-----	
CeVit3I	869	-----	
CeVit3II	736	-----	
CeVit4I	870	-----	
CeVit4II	737	-----	
CeVit5I	870	-----	
CeVit5II	737	-----	
CeVit6I	886	-----	
CeVit6II	768	-----	
DmApoLppI	2590	DQKKMLNQITSSLADTLFKTEIVSDCRCLPIHGLHGQHKCVIKSSTFVANKKAKSA	
DmApoLppII	707	-----	
DmApoLTPI	3499	PIQSQTCESAHNTGVSVMACSPQALPEEKYDLDDYDSFNNWDWGDPESETNVMS	
DmApoLTPII	780	-----	
DmCG31659	192	-----	
DmCvD	1471	-----	
DmFabp	159	-----	
DmGlaz	212	-----	
DmMic26-27	227	-----	
DmNlaz	245	-----	
DmMtp	887	-----	
CeDSc4	893	-----	

Fig. S12. Alignment of 25 human, 11 fly and 14 nematode sequences with ApoB, ApoLpp and ApoLTP separated plus all outgroups.

HsApoA1	0	-----
HsApoA2	0	-----
HsApoA4	0	-----
HsApoA5	0	-----
HsApoB48	0	-----
HsApoB52	0	-----
HsApoC1	0	-----
HsApoC2	0	-----
HsApoC3	0	-----
HsApoC4	0	-----
HsApoD	0	-----
HsApoE2	0	-----
HsApoF	0	-----
HsApoH	0	-----
HsApoJ	0	-----
HsApoL1	0	-----
HsApoL2	0	-----
HsApoL3	0	-----
HsApoL4	0	-----
HsApoOL(2)	0	-----
HsApoL6	0	-----
HsApoM	0	-----
HsApoO	0	-----
HsApoOL	0	-----
HsMTTP	0	-----
DmCG31659	0	-----
DmMtp	0	-----
DmCvd	0	-----
DmGlaz	0	-----
DmFabp	0	-----
DmApoLTPII	0	-----
DmApoLTPI	1	RKAQEQARASEEEVDDEDYDFEESLEGNKRQKRDVSTTRKQEIFDRNVDSLGYKLYDYNNPRAQFGLRVFG
DmNlaz	0	-----
DmApoLII	0	-----
DmApoLI	0	-----
DmMICOS_A	0	-----
Cel_MICOS	0	-----
Cel_Vit_2	0	-----
Cel_Vit_4	0	-----
Cel_Vit_5	0	-----
Cel_ApoL_1	0	-----
Cel_MTTP	0	-----
Cel_Vit_6	0	-----
Cel_Vit_3	0	-----
Cel_Vit-1	0	-----
Cel_Apo_L3_Like	0	-----
HsApoA1	0	-----
HsApoA2	0	-----
HsApoA4	1	-----MFLKAVVLTALVAVAGARAEVSA
HsApoA5	1	-----MASMAAVLTWALALLSAFSA
HsApoB48	1	-----MDPFRPALLALLPALLLLLAGARAEEMLENVS
HsApoB52	1	-----FDQYIKDSYDLHDLKIAIANIIDEITIEKLKS
HsApoC1	0	-----
HsApoC2	0	-----
HsApoC3	0	-----
HsApoC4	0	-----
HsApoD	0	-----
HsApoE2	1	-----MKVLWAALLVTFLAGCQA
HsApoF	1	-----MTGLCGYSA
HsApoH	0	-----
HsApoJ	1	-----MMKTLLLFVGLLLTWE SGQVLGDQT
HsApoL1	1	-----MEGAALLRVSVLCIWMSALFLGVGVRAEEAG
HsApoL2	0	-----
HsApoL3	0	-----
HsApoL4	1	-----MGSWVQLITSVG
HsApoOL(2)	1	-----MPCGKQGNLQVPGSKVLPGLGEGC
HsApoL6	0	-----
HsApoM	0	-----
HsApoO	0	-----
HsApoOL	0	-----
HsMTTP	1	-----MILLAVLFLCFISSYSASVKGHTTGLSL
DmCG31659	0	-----
DmMtp	1	-----MENKNKKCLRTLALLFLGLLEDGK
DmCvd	1	-----MRLKCSVFVYLFIFDAGHAFSIIGL
DmGlaz	0	-----
DmFabp	0	-----
DmApoLTPII	1	-----MGGLKPQAAIWLLLLIAHTQAVRENPL
DmApoLTPI	71	NDLRYFNVESLVEVMALAAKFNPFOQAKNVLSGKEFTYTKSRVFLDASYTVPLAVGLPLAIHAFGASSID
DmNlaz	0	-----
DmApoLII	1	-----MARMKYNIALIGILASVLLTIAVNAENACNLGC
DmApoLI	1	-----SIVDDVSKISKKKYKMYGVKNVQDNLNDVS
DmMICOS_A	0	-----
Cel_MICOS	0	-----
Cel_Vit_2	1	-----MRSIIIASLVALALASSP-----A
Cel_Vit_4	1	-----MKSIIIASLVALAIAASP-----A
Cel_Vit_5	1	-----MKSIIIASLVALAIAASP-----A
Cel_ApoL_1	0	-----
Cel_MTTP	1	-----MFSSRIWLLLAVTVGVCLAV
Cel_Vit_6	1	-----MKFFIALALLGAALASTHLDYNS
Cel_Vit_3	1	-----MKSIIIASLVALAIAASP-----A
Cel_Vit-1	1	-----MRSIIIASIVALAIAFSP-----A
Cel_Apo_L3_Like	0	-----

HsApoA1	0	-----
HsApoA2	0	-----
HsApoA4	25	DQVATVMWDYFSQLSNNAK-----
HsApoA5	21	TQARKGFWDYFSQTSQDKGRVEQIH-----
HsApoB48	37	LVCPKDATRFKHLRKYTYNYEAESSSGVPGTADSRSATRINCK-----
HsApoB52	32	LDEHYHIRVNLVKTIHDLHLFIENIDFNKSGSSTASWIQNVDTKYQIRIQIQEKLQQLKRHIQNIDI---
HsApoC1	0	-----
HsApoC2	0	-----
HsApoC3	0	-----
HsApoC4	0	-----
HsApoD	0	-----
HsApoE2	19	KVEQAVETEPEPELRQQTEWQS-----
HsApoF	10	PDMRGLRLIMIP-----
HsApoH	0	-----
HsApoJ	26	VSDNELQEMSNOGSKYVNKEIQNAVNGV-----
HsApoL1	32	ARVQQNVPSGTDGDPQSKPLGDWAAGT-----
HsApoL2	0	-----
HsApoL3	0	-----
HsApoL4	13	VQQNHPGWTVAGQFQEKKRFTTEEVI-----
HsApoOL(2)	25	KEMWLRKVIYGGEVWGKSPEPE-----
HsApoL6	0	-----
HsApoM	0	-----
HsApoO	0	-----
HsApoOL	0	-----
HsMTTP	29	NNDRLYKLTYSTEVLLDRGKGLQDSVGYRISSNVVDVALLW-----
DmCG31659	0	-----
DmMtp	27	TALIAPNSQQIFKLQNQVILQELGRD-----
DmCvD	28	NKQMLYEEYEGNVLVGAKPQDEGHQ-----
DmGlaz	0	-----
DmFabp	0	-----
DmApoLTPII	28	KDPRICGRPCQDCKSAKFNYGEQLYKYQYTVAVRTEFAGSGDNSSDLLKSDLEIFFPKPCBEGYLRLINDA
DmApoLTPi	141	LRVSGNLDEMPPPTDWHFDVEGQFKPSVSDVITTMQTDMFWEQSGIKVKSNNLYSNSSELVAKLKVRGRNL
DmNlaz	0	-----
DmApoLII	34	PKSDNGLLKYIPGNYDYDSFDSILTIGASSD-----
DmApoLI	30	LKLFSGELAFLSLGDNI PSSLDIIN YFSTSFEKAKQELSSFEKQFSSHHFLDITDLYPTSIGVPLELV
DmMICOS_A	0	-----
Cel_MICOS	0	-----
Cel_Vit_2	20	FER-----TFEPKTDYHYKFDGLVLSGLPSASSELSQSRISARAR-----
Cel_Vit_4	20	LDR-----TFSPKSEYVYKFDGLLLSGLPTTFSDASQTLISCRTR-----
Cel_Vit_5	20	LDR-----TFSPKSEYVYKFDGLLLSGLPTASSDASQTLISCRTR-----
Cel_ApoL_1	0	-----
Cel_MTTP	21	PDLDEIKKNLRKHGPDYKYNQPKMNENTVRLKVDYWFRTESM-----
Cel_Vit_6	25	IERNIQESSFRAGREYRYLFNGQLSAGLPVPSTPQGISRLQSQVT-----
Cel_Vit_3	20	LDR-----TFSPKSEYVYKFDGLLLSGLPTTFSDASQTLISCRTR-----
Cel_Vit-1	20	FER-----TFEPKIDYHYKFDGLVLSGLPTASSELSQSRFSARVR-----
Cel_Apo_L3_Like	0	-----
HsApoA1	0	-----
HsApoA2	0	-----
HsApoA4	43	-----
HsApoA5	45	-----
HsApoB48	79	-----VELEVPLCSFILKTSQCTLKEVYGFNPEGKALLKTKNSEEFAAAMSRVELKLAIP EG
HsApoB52	98	-----QHLAGLKLQHIEAIDVRVLLDQLGTTISFERINDILEHVKHFINIGDFEVAEKINAFRAK
HsApoC1	0	-----
HsApoC2	0	-----
HsApoC3	0	-----
HsApoC4	0	-----
HsApoD	0	-----
HsApoE2	40	-----GQR
HsApoF	21	-----
HsApoH	1	-----MISPVILFSSFLCHVA
HsApoJ	53	-----KQIKTLIEKTNEERKTLNLEEAKKK
HsApoL1	59	-----MDPESSIFIEDAIKYFKEKVSTQNLL
HsApoL2	1	-----MNPESSIFIEDYLYFQDQVSRNLL
HsApoL3	1	-----MDSEKKRFTTEATKYFRERVSPVHLQ
HsApoL4	38	-----YFQKKVSPVHLK
HsApoOL(2)	46	-----FPS
HsApoL6	0	-----
HsApoM	0	-----
HsApoO	0	-----
HsApoOL	0	-----
HsMTTP	69	-----RNPDGDDQLIQITMKDVNVENVNQQRGEKSIFKGKSPSKIMGKENLEALQRPTLLHLIHGK
DmCG31659	0	-----
DmMtp	52	-----SSSAETSYTFETDLKINSVWVGDEDEQLLEVFISGSKVDASGKARSITRIPDRPFYISLVRGQ
DmCvD	51	-----APPTTGWIVRGKLTQRQSELVLAALVIDDVTLNNSGEKFLQNKEMYPKYKPKIALTKDG
DmGlaz	0	-----
DmFabp	0	-----
DmApoLTPII	98	KLY-----DTLDELNDNESDSSEKTEKEYDYDNLANEESQNYDNMHPKSSDFNVDLTKNLLRFAFHG
DmApoLTPi	211	VSFPSFDLPRDKNEIFSVRSELIVQKREEQLPQAGIANRANSANSTCTWPVLDAQIAGLQMC SHYSVPDLSNAT
DmNlaz	0	-----
DmApoLII	64	-----VPNDSDDTSLKVSGSAKIFAKGNCGYTLQLSSVKVTNTKESVEKKILNSIQKPVQFTLVSGI
DmApoLI	100	AQGFAATKVDLAVSLDINAILEQNWQKAKYRLKFVPSVDINANVQIGFNAQVLSTGLRVVSSAHSATGSD
DmMICOS_A	0	-----
Cel_MICOS	0	-----
Cel_Vit_2	59	-----IQAVDDRYIHLQLVNIIRMAASHL-PESEQMPSLNSMEQRE-LSEEEKQMLELPLRAQLRNGL
Cel_Vit_4	59	-----LQAVDDRYIHLQLIDIQYSASHI-PQSEQWPKIESLEQRE-LSDELKELLELPFRAQIRNGL
Cel_Vit_5	59	-----LQAVDDRYIHLQLTDIQYSASHI-PQSEQWPKIESLEQRE-LSDEFKELLELPFRAQIRNGL
Cel_ApoL_1	0	-----
Cel_MTTP	63	-----IYDDIDNKEKDPSTVIAGNFSFETLHHDVEGGMGRFTLTQCNTDNCGNPSPYIAFRQGGN
Cel_Vit_6	69	-----LQWTDGNTVRMQLQKTRFATSQSESNSMKMLPFRFEEVERMNRHEQELLSMPVEFDYEHGL
Cel_Vit_3	59	-----LQAVDDRYIHLQLIDIQYSASHI-PQSEQWPKIESLEQRE-LSDELKELLELPFRAQIRNGL
Cel_Vit-1	59	-----IQAVDDRHIHLQLVNIIRMAASHL-PESEQIPSLNSMEQRE-LSEEEKQMLELPLRAQLRNGL
Cel_Apo_L3_Like	0	-----

HsApoA2	1	-----MKLLA-----
HsApoA4	43	---EAVEHLQKSELTQQLNALFQDKLGEVNTYAGDL---
HsApoA5	45	---QQKMAREPATLKDSLEQDLNNMKNF---
HsApoB48	139	KQVFLYPEKDEPTYILNKRGIISALLVPPETEEAKQVLFLLD---
HsApoB52	161	VHELIEREYEDQQIQVLMMDKLVELAHQYKLETIQKLSNVLQ---
HsApoC1	1	-----MRLFLSLPVLVVLVLSIV-----
HsApoC2	1	-----MGTRLLPALFLVL-----
HsApoC3	1	-----MQPRVLL-----
HsApoC4	1	-----MSLLRNRLQALPALCLCVLVL-----
HsApoD	0	-----
HsApoE2	44	WELALGRFWDYLRWVQTLSEQVQEELLSSQV-----
HsApoF	22	VELLLCYLLLHPVDATSYGKQTNVLMHFPLS-----
HsApoH	18	IAGRTCPKPDLLPFSTVVPLKTFYE-----
HsApoJ	81	KEDALNETRESETKLKELPGVCNETMMALWEECKPCLKQT-----
HsApoL1	86	LLLTDNNEAWNGFVAAAELPRNEADELRKA-----
HsApoL2	27	QLLTDDEAWNGFVAAAELPRDEADELRKA-----
HsApoL3	27	ILLTNNEAWKRFVTAELPRDEADALYEA-----
HsApoL4	51	ILLTSDEAWKRFVRVAELPREEADALYEA-----
HsApoOL(2)	50	LV-NLCQSWKINNLMSTVHSDEAGMLSY-----
HsApoL6	1	-----MDNQAERESEAGVGLQ-----
HsApoM	1	-----MFHQIWAALLYFYG-----
HsApoO	1	-----MFKVIQRSVGPASLS-----
HsApoOL	1	-----MAAIRMGLTTMPAGLIYAS-----
HsMTTP	132	VK-EFYSYQNEAVAIAENIKRGLASLFQTQLSSGTTNEVDISG-----
DmCG31659	1	-----MIKWKIFVPAILYLQSSM-----
DmMtp	115	PD-KVIAHTSKDQSLNLERGIASLLQLRLDASQEEELDVSG-----
DmCvD	114	ATSHVVFKEGDPIWSMNFKRATASVLQFMKSSGAFVVDELG-----
DmGlaz	1	-----MMSGQPLGSRVWLLSGVLLVTFAG-----
DmFabp	0	-----
DmApoLTPII	163	LISEVCPQEQTTPWVLNIIKKGILSAFQNTMMRFDVDANT-----
DmApoLTPI	281	EIYPSLLLAGPLNFSLLILKKSLSAKKYVFYKWDQQEEDNNFSLVFTTPGSKVPRVLVANVTKVPDAFN-----
DmNlaz	1	-----MNHSSSHLLLLISVVFVAVVVAH-----
DmApoLII	127	LEPQICSDSSDLDYSLNKRRAVVSLLQSGIEAE-----
DmApoLI	170	ITVAVISDGEFGFNVDELPREKLELINFNVDTELYVAEQDKQ-----
DmMICOS_A	1	-----MLRKTAT-----
Cel_MICOS	0	-----
Cel_Vit_2	120	IS-ELQFDKEDAWEWSKNMKRAVVNMISFNPIAPRNEIEKIES-----
Cel_Vit_4	120	VS-EIQFSSEDAEWSKNAKRSILNLFSLRKSAPVDEMSQDQ-----
Cel_Vit_5	120	IS-EIQFSSEDAEWSKNAKRSILNLFSLRKSAPVDEMNQDQ-----
Cel_ApoL_1	1	-----MSI-----
Cel_MTTP	126	NAEHILKASDES DATWNFLYAI VNTIYTPAEYGEQDEQTVDT-----
Cel_Vit_6	132	VR-EIRFAENDQPWSENKRAVINMLQ-----VNILKKEY-----
Cel_Vit_3	120	VS-EIQFSSEDAEWSKNAKRSILNLFSLRKSAPVDEMSQDQ-----
Cel_Vit-1	120	IA-ELQFDKEDAWEWSKNMKRAVVNMISFNPIAPRNEIEKIES-----
Cel_Apo_L3_Like	1	---MQIKDDHDDAGSQSEDNGVPI-----
HsApoA1	8	-----
HsApoA2	5	-----
HsApoA4	76	-----
HsApoA5	70	-----
HsApoB48	180	-----
HsApoB52	202	-----
HsApoC1	17	-----
HsApoC2	13	-----
HsApoC3	7	-----
HsApoC4	21	-----
HsApoD	0	-----
HsApoE2	74	-----
HsApoF	52	-----
HsApoH	42	-----
HsApoJ	120	-----
HsApoL1	114	-----
HsApoL2	55	-----
HsApoL3	55	-----
HsApoL4	79	-----
HsApoOL(2)	76	-----
HsApoL6	16	-----
HsApoM	14	-----
HsApoO	15	-----
HsApoOL	20	-----
HsMTTP	172	-----
DmCG31659	18	-----
DmMtp	155	-----
DmCvD	155	-----
DmGlaz	24	-----
DmFabp	0	-----
DmApoLTPII	201	-----
DmApoLTPI	351	ASVAFVNGPNRVSAGCSYDGNPDFRRLDIYLDTNGNRSLLDGMELRRHQDFTAWIYNPRMLLAINGVNIIT-----
DmNlaz	24	-----
DmApoLII	159	-----
DmApoLI	211	-----
DmMICOS_A	7	-----
Cel_MICOS	0	-----
Cel_Vit_2	160	-----
Cel_Vit_4	159	-----
Cel_Vit_5	159	-----
Cel_ApoL_1	3	-----
Cel_MTTP	167	-----
Cel_Vit_6	166	-----
Cel_Vit_3	159	-----
Cel_Vit-1	160	-----
Cel_Apo_L3_Like	21	-----

HsApoA2	5	-----
HsApoA4	76	-----
HsApoA5	70	-----
HsApoB48	181	TVYGNCSHTFTVKTRKGNVATEISTERDLGQCDRFKPIRTGISPLALIKGMRPLSTLISSSQSCQYTL
HsApoB52	202	-----QVKIKDYFEKLVGFIDDAVKKLNELSFKTFIEDVNKFLDMLIKKLSFDYHQFVDETNDKIREV
HsApoC1	17	-----
HsApoC2	13	-----
HsApoC3	7	-----
HsApoC4	21	-----
HsApoD	0	-----
HsApoE2	74	-----
HsApoF	52	-----
HsApoH	42	-----
HsApoJ	120	-----
HsApoL1	114	-----
HsApoL2	55	-----
HsApoL3	55	-----
HsApoL4	79	-----
HsApoOL(2)	76	-----
HsApoL6	16	-----
HsApoM	14	-----
HsApoO	15	-----
HsApoOL	20	-----
HsMTTP	172	-----NCKVTYQAHQDKV-----
DmCG31659	18	-----
DmMtp	155	-----LCRVSYNVKSSTKVEKTKRDCSLWD-----
DmCvD	155	-----IHGTCRTEYFVSNRTNYISIRKTPEVKTKCKPYSEAVHTT-----
DmGlaz	24	-----
DmFabp	0	-----
DmApoLTPII	201	-----
DmApoLTPI	421	GLAGTVKVNKNGIKQHDVDLSFETKKLQAVIKGNVVQSEITTTSTNMTIKYRFQANKIEEINFAGKLVNN
DmNlaz	24	-----
DmApoLII	159	-----
DmApoLI	211	-----KAIALKGNNKKNKNSQPSEICFNQLELVGLNICIKSSTSLSEVQAGNGNVAERGLSVSEKFHL
DmMICOS_A	7	-----
Cel MICOS	0	-----
Cel_Vit_2	160	-----SYDKEEQSEENTSFFT-NEKTLEGDCQVAYTV--IREQKKTIIITKSINFDKCTERSEIAYGL--
Cel_Vit_4	159	-----KDMESDKDSLFFNVHEKTMEGDCEVAYTI--VQEGGKTIYTKSVNFDKCITRPETAYGL--
Cel_Vit_5	159	-----KDMESDKDSLFFNVHEKTMEGDCEVAYTI--VQEGEKTIYTKSVNFDKCITRPETAYGL--
Cel_ApoL_1	3	-----
Cel MTTP	167	-----IYGRCFVNFGRPEDKRFRIIEKCD-----
Cel_Vit_6	166	-----EGAESDNDQEPFSTFNTVERTLEGECEVLYTVEEIKKEDEQRWAKSINFDKCTRRPYIHH-----
Cel_Vit_3	159	-----KDMESDKDSLFFNVHEKTMEGDCEVAYTI--VQEGEKTIYTKSVNFDKCITRPETAYGL--
Cel_Vit-1	160	-----SYDKEEQSEENTSFFT-NEKTLEGDCQVAYTV--IREQKKTIIITKSINFDKCTERSEIAYGL--
Cel_Apo_L3_Like	21	-----
HsApoA1	8	-----
HsApoA2	5	-----
HsApoA4	76	-----
HsApoA5	70	-----
HsApoB48	251	AK-----
HsApoB52	267	TQRLNGEIQALELPQKAEALKLFLEETKATVAVYLESLODQTKITLIINWLQEALS-----
HsApoC1	17	-----
HsApoC2	13	-----
HsApoC3	7	-----
HsApoC4	21	-----
HsApoD	0	-----
HsApoE2	74	-----
HsApoF	52	-----
HsApoH	42	-----
HsApoJ	120	-----
HsApoL1	114	-----
HsApoL2	55	-----
HsApoL3	55	-----
HsApoL4	79	-----
HsApoOL(2)	76	-----
HsApoL6	16	-----
HsApoM	14	-----
HsApoO	15	-----
HsApoOL	20	-----
HsMTTP	185	-----
DmCG31659	18	-----
DmMtp	180	-----
DmCvD	194	-----
DmGlaz	24	-----
DmFabp	1	-----M
DmApoLTPII	201	-----
DmApoLTPI	491	GDKSKTEYRGNMKLQTSAYPKLNFASESTWLSLQGHTEGMITYNNAVDYVNPNTSLVRLIFARSHSEDS
DmNlaz	24	-----
DmApoLII	159	-----
DmApoLI	276	PFNFAYVLTTERKFTFKGIHTQEAFSQKWLDYSTPGSKVSHDTTVVYELGNKPKTFSRLS-----
DmMICOS_A	7	-----
Cel MICOS	0	-----
Cel_Vit_2	219	-----
Cel_Vit_4	216	-----
Cel_Vit_5	216	-----
Cel_ApoL_1	3	-----
Cel MTTP	192	-----
Cel_Vit_6	226	-----
Cel_Vit_3	216	-----
Cel_Vit-1	219	-----
Cel_Apo_L3_Like	21	-----

HsApoA2	6	ATVLLLTICSLEGALVR-----
HsApoA4	77	QKKLVFPATELHERLAK-DSEKLKE-----
HsApoA5	71	LEKLRPLSGSEAPRLPQDPVGMRRQ-----
HsApoB48	253	RKHVAEAIICQEHLFLP-FSYKNKY-----G
HsApoB52	322	SASLAHMKAKFRETLEDTRDRMYQM-----
HsApoC1	18	LEGPAPAQGTDPDVSSALDKLKEFGN-----
HsApoC2	14	LVLGFVEVQGTQQPQQDEMPSPFTFLT-----
HsApoC3	8	VVALLALLASARASEAE-DASLLSF-----
HsApoC4	22	ACIGACQPEAQEGTSLPPPKLKMSR-----
HsApoD	1	-QAFHLGKCPNPPVQEN-FDVNKKYL-----
HsApoE2	75	TQELRALMDETMKELKA-YKSELEE-----
HsApoF	53	LESQTPSSDPLSCQFLH-PKSLPGF-----
HsApoH	43	PGEEITYSCKPGYVSRG-GMRKFIC-----
HsApoJ	121	CMKFYARVCRSGSLVGRQLEEFNL-----
HsApoL1	115	LDNLARQMIMKDKNWDH-KGQQYRN-----
HsApoL2	56	LNKLASHMVMKDKNRHD-KDQQRHQ-----
HsApoL3	56	LKKLRTYAAIEDEYVQQ-KDEQFRE-----
HsApoL4	80	LKNLTPYVAIEDKDMQQ-KEQQFRE-----
HsApoOL(2)	77	FLFEELMRCDKDSMPDG-NLSEEEK-----
HsApoL6	17	RDEDDAPLCEDELQDQG-DLSPEEK-----
HsApoM	15	IILNSIYQCPEHSQLT-T-LGVDGKE-----
HsApoO	16	LLTFKVYAAPKKDSPPK-NSVKVDE-----
HsApoOL	21	VSVHAAKQEESSKKQLVK-PEQLPIY-----
HsMTTP	186	IKIKALDSCKIARSGFTTPNQVLGV-----
DmCG31659	19	AMRAFHGACPSNMTAVG-DLDMDRF-----
DmMtp	181	LRVNYNPEEALGVTQQA-QETVFYE-----
DmCvD	195	RSNVPPNTCEFDHQKSVIIGNEAIY-----
DmGlaz	25	TDAYGFGRCPNYPSMPK-FNMSRVL-----
DmFabp	2	SFVGKKYKLDKSENFDE-YMKELGV-----
DmApoLTPII	202	TETDVSGQCQVQYALED-TDSSYVT-----
DmApoLTPi	561	FLDGTQTRASLELKLPR-SKIDYRILVKHKEHIKNGTEHNVIVGLKYTPEKEITGLFSVHLPRRNLFAID
DmNlaz	25	AQVPFPGKCPDVKLLDT-FDAEAYM-----
DmApoLII	160	HEVDVFGMCPHTHTSTSKVGNANIIT-----
DmApoLI	337	FDNSQCHFAVEGGINND-KNELVVYQYEQDKEIKKSKIGFSKNGNEYKPLIEIQDNNGISNSINGYHAD
DmMICOS_A	8	MGIMAAVAVKAAPEPQK-PASSAAD-----
Cel MICOS	1	MTQDKPIVETISNAGEQ-VTNVFGQ-----
Cel_Vit_2	220	RYSSECECEKDTLIR-PQTVITY-----
Cel_Vit_4	217	RFGSECKEKEGQFVQ-PQTVITY-----
Cel_Vit_5	217	RFGSECKEKEGQFVK-PQTVITY-----
Cel_ApoL_1	4	YESLKSTLMNGEEMPKE-LQVKAWG-----
Cel MTTP	193	LGYGNTFTKFEGIESVQ-YDQDVWY-----
Cel_Vit_6	227	VQTPVCKDCQQTLEQDKMSSTVLNY-----
Cel_Vit_3	217	RFGSECKEKEGQFVK-PQTVITY-----
Cel_Vit-1	220	RYSSECECEKDTVLIR-PQTVITY-----
Cel_Apo_L3_Like	22	YDSLESLLFIPRSMSELSETALRT-----
-----KVEPLRAE-----		
HsApoA1	32	-----
HsApoA2	22	-----
HsApoA4	100	-----EIGKELEELRAR-----
HsApoA5	95	-----LQEELEEVKAR-----
HsApoB48	278	MVAQVQTTLKLEDTPKINSRFFGEGTKKMGLAFESTKSTSPKQAE-----
HsApoB52	346	-----DIQQELQRYLSLVGQVYSTLVITYISDWWTAAKNLTDFA-----
HsApoC1	42	-----
HsApoC2	38	-----
HsApoC3	31	-----
HsApoC4	46	-----WSL-----
HsApoD	23	-----GRWYIEIKIPTTFE-----
HsApoE2	98	-----QLTPVAEETRAR-----
HsApoF	76	-----SHMAPLPKFLVS-----
HsApoH	66	-----PLTGLWPINTLK-----
HsApoJ	145	-----QSSPFYFWMNGDRIDSL-----
HsApoL1	138	-----WFLKEFPRLKSE-----
HsApoL2	79	-----WFLKEFPRLKRE-----
HsApoL3	79	-----WFLKEFPQVKKR-----
HsApoL4	103	-----WFLKEFPQIRWK-----
HsApoOL(2)	100	-----LFLSYFPLHKFE-----
HsApoL6	40	-----IFLREFPRLKED-----
HsApoM	38	-----FPEVHLG-----
HsApoO	39	-----LSLYSVPEGQSK-----
HsApoOL	44	-----TAPPLQSK-----
HsMTTP	210	-----SSKATSVTTYKIEDSFVIAVLAEEETHNFGNLFQTIKGKIVSKQK-----
DmCG31659	42	-----KGKWTYSIYPHLSL-----
DmMtp	204	-----LSSEGTLHAESQENHRLNLAAPDVGSFVKSSLI-----
DmCvD	219	-----GMSPHNETGYLLSMAHAKGTTLIHTFESTGEAQFINSE-----
DmGlaz	48	-----GHWYEVERSFY-----
DmFabp	25	-----
DmApoLTPII	225	-----IRKTKDINSCRQRYATHSVLQTTPTPTFRDDKTIWPIILKSQ-----
DmApoLTPi	630	AYMNVTVPEFNSTASLKVNEKATKDYIIFINGSWFTGHSAVKANYKDRSSRVQALHHLKMIVESPSFN
DmNlaz	48	-----GVWYEAAYPFAGE-----
DmApoLII	184	-----KARNLNSCSHREQINSGLVSGKVNKAGITSSLLQANYIKESR-----
DmApoLI	406	GKIVVKNSNNIERYNFENFQVSNNSNAHAVNGWSDVGTNSLTSE-----
DmMICOS_A	31	-----
Cel MICOS	24	-----FWQLVTSK-----
Cel_Vit_2	243	-----VLENEE-----LKESEVRS-----LYTVNVNGQEVVMTETRSKLV-----
Cel_Vit_4	240	-----TFKNEK-----LQSEVNS-----IYTLNVNGQEVVVKSETRAKVT-----
Cel_Vit_5	240	-----TFKNEK-----LQSEVHS-----VYTLNVNGQEVVVKSETRAKVT-----
Cel_ApoL_1	27	-----AQWHLDRWSSNRQE-----
Cel MTTP	216	-----TQNTKVDADIIMVDAIEMLAFAKSPHLEK-----
Cel_Vit_6	251	-----NITGTSSSFLINSVELRSQHLFAPISEKHQLVSAFTLNTME-----
Cel_Vit_3	240	-----TFKNEK-----LQSEVHS-----IYTLNVNGQEVVVKSETRSKVT-----
Cel_Vit-1	243	-----ILENEE-----LKESEVRS-----LYTVNVNGQEVVMTETRSKLV-----
Cel_Apo_L3_Like	46	-----QFLLDKWSNNRRK-----

HsApoA2	22	-----
HsApoA4	112	-----
HsApoA5	106	-----
HsApoB48	323	-----
HsApoB52	385	-----
HsApoC1	42	-----
HsApoC2	38	-----
HsApoC3	31	-----
HsApoC4	49	-----
HsApoD	37	-----
HsApoE2	110	-----
HsApoF	88	-----
HsApoH	78	-----
HsApoJ	162	-----
HsApoL1	150	-----
HsApoL2	91	-----
HsApoL3	91	-----
HsApoL4	115	-----
HsApoOL(2)	112	-----
HsApoL6	52	-----
HsApoM	45	-----
HsApoO	51	-----
HsApoOL	52	-----
HsMTTP	255	-----
DmCG31659	57	-----
DmMtp	239	-----
DmCvD	257	-----
DmGlaz	59	-----
DmFabp	25	-----
DmApoLTPII	265	-----
DmApoLTPI	700	ITSLNIYYRRKQLLIIFYDIQAKYDQDPYGLTIQYASNAHNRNTNAEVRLKVKERDYWINAKLLSEQPKLL
DmNlaz	62	-----
DmApoLII	228	-----
DmApoLI	451	-----
DmMICOS_A	31	-----
Cel_MICOS	32	-----
Cel_Vit_2	278	-----
Cel_Vit_4	275	-----
Cel_Vit_5	275	-----
Cel_ApoL_1	41	-----
Cel_MTTP	244	-----
Cel_Vit_6	292	-----
Cel_Vit_3	275	-----
Cel_Vit-1	278	-----
Cel_Apo_L3_Like	59	-----
HsApoA1	40	-----
HsApoA2	22	-----
HsApoA4	112	-----
HsApoA5	106	-----
HsApoB48	323	-----
HsApoB52	385	-----
HsApoC1	42	-----
HsApoC2	38	-----
HsApoC3	31	-----
HsApoC4	49	-----
HsApoD	37	-----
HsApoE2	110	-----
HsApoF	88	-----
HsApoH	78	-----
HsApoJ	162	-----
HsApoL1	150	-----
HsApoL2	91	-----
HsApoL3	91	-----
HsApoL4	115	-----
HsApoOL(2)	112	-----
HsApoL6	52	-----
HsApoM	45	-----
HsApoO	51	-----
HsApoOL	52	-----
HsMTTP	255	-----
DmCG31659	57	-----
DmMtp	239	-----
DmCvD	257	-----
DmGlaz	59	-----
DmFabp	25	-----
DmApoLTPII	265	-----
DmApoLTPI	770	QLEIHMDKIRDVHIQVGLLNVDKRKELSLELKWDANRDPSQRLGLLAEYNSPGTKHYDGNLMITYPERTI
DmNlaz	62	-----
DmApoLII	228	-----
DmApoLI	451	-----
DmMICOS_A	31	-----
Cel_MICOS	32	-----
Cel_Vit_2	278	-----
Cel_Vit_4	275	-----
Cel_Vit_5	275	-----
Cel_ApoL_1	41	-----
Cel_MTTP	244	-----
Cel_Vit_6	292	-----
Cel_Vit_3	275	-----
Cel_Vit-1	278	-----
Cel_Apo_L3_Like	59	-----

HsApoA2	22	-----
HsApoA4	112	-----
HsApoA5	106	-----
HsApoB48	323	-----
HsApoB52	385	-----
HsApoC1	42	-----
HsApoC2	38	-----
HsApoC3	31	-----
HsApoC4	49	-----
HsApoD	37	-----
HsApoE2	110	-----
HsApoF	88	-----
HsApoH	78	-----
HsApoJ	162	-----
HsApoL1	150	-----
HsApoL2	91	-----
HsApoL3	91	-----
HsApoL4	115	-----
HsApoOL(2)	112	-----
HsApoL6	52	-----
HsApoM	45	-----
HsApoO	51	-----
HsApoOL	52	-----
HsMTTP	255	-----
DmCG31659	57	-----
DmMtp	239	-----
DmCvD	257	-----
DmGlaz	59	-----
DmFabp	25	-----
DmApoLTPII	265	-----
DmApoLTPI	840	HFGFNSFTGGPKYFGKVHASWSINEVIEFEYEAGILPGHTLHNWVKAELRTPFDGWRVNSLDAGIYSLKN
DmNlaz	62	-----
DmApoLII	228	-----
DmApoLI	451	-----
DmMICOS_A	31	-----
Cel_MICOS	32	-----
Cel_Vit_2	278	-----
Cel_Vit_4	275	-----
Cel_Vit_5	275	-----
Cel_ApoL_1	41	-----
Cel_MTTP	244	-----
Cel_Vit_6	292	-----
Cel_Vit_3	275	-----
Cel_Vit-1	278	-----
Cel_Apo_L3_Like	59	-----
HsApoA1	40	-----
HsApoA2	22	-----
HsApoA4	112	-----
HsApoA5	106	-----
HsApoB48	323	-----
HsApoB52	385	-----
HsApoC1	42	-----
HsApoC2	38	-----
HsApoC3	31	-----
HsApoC4	49	-----
HsApoD	37	-----
HsApoE2	110	-----
HsApoF	88	-----
HsApoH	78	-----
HsApoJ	162	-----
HsApoL1	150	-----
HsApoL2	91	-----
HsApoL3	91	-----
HsApoL4	115	-----
HsApoOL(2)	112	-----
HsApoL6	52	-----
HsApoM	45	-----
HsApoO	51	-----
HsApoOL	52	-----
HsMTTP	255	-----
DmCG31659	57	-----
DmMtp	239	-----
DmCvD	257	-----
DmGlaz	59	-----
DmFabp	25	-----
DmApoLTPII	265	-----
DmApoLTPI	910	LILVNSTLFWADDQKLQVGYSYDVNDQLMSFDVRFGINSTIRDIPITINVKKVHWMVDVKKVDTELYLGY
DmNlaz	62	-----
DmApoLII	228	-----
DmApoLI	451	-----
DmMICOS_A	31	-----
Cel_MICOS	32	-----
Cel_Vit_2	278	-----
Cel_Vit_4	275	-----
Cel_Vit_5	275	-----
Cel_ApoL_1	41	-----
Cel_MTTP	244	-----
Cel_Vit_6	292	-----
Cel_Vit_3	275	-----
Cel_Vit-1	278	-----
Cel_Apo_L3_Like	59	-----

HsApoA2	22	-----
HsApoA4	112	-----
HsApoA5	106	-----
HsApoB48	323	-----AVLKTLQELKKLT
HsApoB52	385	-----
HsApoC1	42	-----
HsApoC2	38	-----
HsApoC3	31	-----
HsApoC4	49	-----
HsApoD	37	-----
HsApoE2	110	-----
HsApoF	88	-----
HsApoH	78	-----
HsApoJ	162	-----
HsApoL1	150	-----
HsApoL2	91	-----
HsApoL3	91	-----
HsApoL4	115	-----
HsApoOL(2)	112	-----
HsApoL6	52	-----
HsApoM	45	-----
HsApoO	51	-----
HsApoOL	52	-----
HsMTTP	255	-----
DmCG31659	57	-----
DmMtp	239	-----
DmCvd	257	-----
DmGlaz	59	-----
DmFabp	25	-----
DmApoLTPII	265	-----
DmApoLTPI	980	SGQNDTFNTYSMDSSWEIEKNQRYNNYSGLVHLVSPFKGYEKGGLVAHFSLSDQRVVSGAASLNFDLREF
DmNlaz	62	-----
DmApoLII	228	-----
DmApoLI	451	-----
DmMICOS_A	31	-----
Cel_MICOS	32	-----
Cel_Vit_2	278	-----
Cel_Vit_4	275	-----
Cel_Vit_5	275	-----
Cel_ApoL_1	41	-----
Cel_MTTP	244	-----
Cel_Vit_6	292	-----
Cel_Vit_3	275	-----
Cel_Vit-1	278	-----
Cel_Apo_L3_Like	59	-----
HsApoA1	40	-----IQEGARQKLHE-----
HsApoA2	22	-----RQAKEPCVESL-----
HsApoA4	112	-----LLPHANEVSQKIG-----
HsApoA5	106	-----LPYMAEAHELIV-----
HsApoB48	337	ISEQNIQRANLFNKLVTETLRLGLSDEAVTSLLPQLIEVSSPITLQALVQCGQPQCSTHILQWLKRVHANPL
HsApoB52	385	-----EQYSIQDWAKRMKALVEQGFVPEIKTILGTMPAFEVSLQA-----
HsApoC1	42	-----TLEDKARELIS-----
HsApoC2	38	-----
HsApoC3	31	-----
HsApoC4	49	-----
HsApoD	37	-----NGRCIQANYSLMENGK-----
HsApoE2	110	-----LSKELQAAQARLGADM-----
HsApoF	88	LALRNALEEAGCQADVWA-----
HsApoH	78	-----CTPRVCPFAGILENGA-----
HsApoJ	162	-----LENDRQOTHMLD-----
HsApoL1	150	-----LEDNIRRLRALA-----
HsApoL2	91	-----LEDHIRKLRLALA-----
HsApoL3	91	-----IQESIEKLRLALA-----
HsApoL4	115	-----IQESIERLRVIA-----
HsApoOL(2)	112	-----LEQNIKELNTLA-----
HsApoL6	52	-----LKGNIIDKLRLALA-----
HsApoM	45	-----QWYFIAGAAAPTKEELATFD-----
HsApoO	51	-----YVEEARSQLEES-----
HsApoOL	52	-----YVEEQPGHLQMG-----
HsMTTP	255	-----LELKTTEAGPRLMSGK-----
DmCG31659	57	-----RVEKQSTDFIEKEEN-----
DmMtp	239	-----LQHVSGQSEEVKQLQLGSLDKAIQSL-----
DmCvd	257	-----LLLNLNETPIDNPIDIETSMAAEPSNLLEQLRDPNDPTG-----
DmGlaz	59	-----
DmFabp	25	-----
DmApoLTPII	265	-----SHCNLTIDNNVYKEIK-----
DmApoLTPI	1050	TLTMNGYVKKFTDNMLTVNITTPLEKFGTINARFGLNEKKRHAVAIEVRAPTAALGVEVLADIKNLLNFDV
DmNlaz	62	-----IGKKCIYANYSLIDNS-----
DmApoLII	228	-----IVNHLEIENVQLTETIK-----
DmApoLI	451	-----LRISLDHQTFLIKENKLENGLYEAGFFINDEHSPENIYGS-----
DmMICOS_A	31	-----CSLVCRPSELP-----
Cel_MICOS	32	-----NTTNNGDSKPIK-----
Cel_Vit_2	278	-----LEENHSIKSHIKKVNGEK-ESIIYSSRWELVEDF-----
Cel_Vit_4	275	-----FVEESKINREIKKVSGPK-EEIVYSMENEKLEIQF-----
Cel_Vit_5	275	-----FVEESKINREIKKVSGPK-EEIVYSMENEKLEIQF-----
Cel_ApoL_1	41	-----IMNRMEEIAKDLDGLE-----
Cel_MTTP	244	-----YGFTLESRTHVEITNRTRVFTSYCNDTVPSAKCAE-----
Cel_Vit_6	292	-----LIYAGEKKTEIKQVRNEKTSELVYNQESAEQW-----
Cel_Vit_3	275	-----FVEESKINREIKKVSGPK-EEIVYSMENEKLEIQF-----
Cel_Vit-1	278	-----LEENHSIKSHIEKVNGEK-ESIIYSSRWELVEDF-----
Cel_Apo_L3_Like	59	-----IVRQMEGIAEKLDNWE-----

HsApoA2	33	-----
HsApoA4	125	-----
HsApoA5	118	-----
HsApoB48	407	LIDVVTYLVALIPEPSAQQLRIFNMARDQRSRATLYALSHAVNNYHKTNPTGTQELLDIANYLMEQIQD
HsApoB52	427	LQKATFQTPDFIVPLTDLRIPSVQINFKDLKNIKIPSRFSTPEFTILNTFHIPSFTIDFVEMKVKIIRTI
HsApoC1	53	-----
HsApoC2	38	-----
HsApoC3	31	-----
HsApoC4	49	-----
HsApoD	53	-----
HsApoE2	126	-----
HsApoF	106	-----
HsApoH	94	-----
HsApoJ	174	-----
HsApoL1	162	-----
HsApoL2	103	-----
HsApoL3	103	-----
HsApoL4	127	-----
HsApoOL(2)	124	-----
HsApoL6	64	-----
HsApoM	64	-----
HsApoO	63	-----
HsApoOL	64	-----
HsMTTP	271	-----QAAAIKAVDSK
DmCG31659	73	-----
DmMtp	265	-----LEWYRVFELESVDGMSIAIKEQTLEDQL
DmCvD	297	-----GRSPQQQETLIAQAGTLLDSLAEALET
DmGlaz	59	-----
DmFabp	25	-----
DmApoLTPII	281	-----
DmApoLTPI	1120	KLSVATPIESFQQAIFALFNPERVDMRGLWNNVTLGFTGVWHMQNITDFEYSYHVFTPLAGFEENGFI
DmNlaz	78	-----
DmApoLII	244	-----
DmApoLI	493	SIHLTIADQSYALKTNGKAAAWSIGSDGSFNFQKLADSN SARAGSLVENVEIQYKNKQVGGIKIMS
DmMICOS_A	42	-----
Cel MICOS	44	-----
Cel_Vit_2	312	-----FKNGDKAEFAPFEKFPLDKKMHLIKTI
Cel_Vit_4	309	-----YKQGDKAENVNPFKAIEIEQKVEQLEEI
Cel_Vit_5	309	-----YQQGDKAENVNPFKAIEMEQKVEQLQEI
Cel_ApoL_1	57	-----
Cel MTTP	280	-----
Cel_Vit_6	327	-----AQTGEEKYLRLPQWT-ENKVEIMKKM
Cel_Vit_3	309	-----YQQGDQAEVNPFKAIEMEQKVEQLDEI
Cel_Vit-1	312	-----FKNGDKAEFAPFEKFPLDKKMHLIKTI
Cel_Apo_L3_Like	75	-----
HsApoA1	51	-----
HsApoA2	33	-----
HsApoA4	125	-----
HsApoA5	118	-----
HsApoB48	477	DCTGDEDYTYLILRVIGNMGQTEQLTPELKSSILKCVQSTKPSLMIQKAAIQALRKMEPKDKDQEVLLQ
HsApoB52	497	DQMLNSELQWPVPDIYLRDLKVEDIPLARITLPDFRLPEIAIPEFI IPTNLNDFQVPDLHIPEFQLPHI
HsApoC1	53	-----
HsApoC2	38	-----
HsApoC3	31	-----
HsApoC4	49	-----
HsApoD	53	-----
HsApoE2	126	-----
HsApoF	106	-----
HsApoH	94	-----
HsApoJ	174	-----
HsApoL1	162	-----
HsApoL2	103	-----
HsApoL3	103	-----
HsApoL4	127	-----
HsApoOL(2)	124	-----
HsApoL6	64	-----
HsApoM	64	-----
HsApoO	63	-----
HsApoOL	64	-----
HsMTTP	284	YTAIPIVQVFQSHCKGCPSELWLRSTRK-----YLQPDNLSKAEAVRNFLAFIQHLRT
DmCG31659	73	-----
DmMtp	295	K-----ASLTELQSDVGVKSSALAYVKLIP-----LARITRQEFEDLLTEHAEVLPQLV
DmCvD	325	TEFKFSEPYDSTLSDVIKLLSEMDFDSLTK-----LYREVDIGTSYRQETIRNIFHEIIP
DmGlaz	59	-----
DmFabp	25	-----
DmApoLTPII	281	-----
DmApoLTPI	1190	QLLKRKEFVFQLHGKMSNYKLGVKINGEPKSDLVNQLGSNKMELEMLYDADFKPLNAETDYKPDADDEEYF
DmNlaz	78	-----
DmApoLII	244	-----
DmApoLI	563	NKMDVDVEISREQIGSIIVKYESNQRAHQ-----DYSLEASAKINKHSIDVISKCDFNG
DmMICOS_A	42	-----
Cel MICOS	44	-----
Cel_Vit_2	340	T-----EQIQEVENNMPETSHFLARLVRIFR-----TTSTSQLKEIHETLYVKADKKI---
Cel_Vit_4	337	F-----RQIQEHEQNTPETVHLIARAVRMFR-----MCTIEELKKVHTTIYTAEKKV---
Cel_Vit_5	337	F-----RQIQEHEQNTPETVHLIARAVRMFR-----MCTIEELKKVHTTIYTAEKKV---
Cel_ApoL_1	57	-----
Cel MTTP	280	-----QAFGAVRVGGKLYEHVKIAEQSNK-----LTKLIGTYRRHLQDMGDSHICEKHS
Cel_Vit_6	354	FSLMAKQIEQGEAEL-EAAHTVARIVKVL-----ECNEEQLEQIYRHVAEHKDEKIAEQ
Cel_Vit_3	337	F-----RQIQEHEQNTPETVHLIARAVRMFR-----MCTIEELKKVHTTIYTAEKKV---
Cel_Vit-1	340	T-----EQIQEVENNIPETSHFLARLVRIFR-----TTSTSQLKEIHETLYVKADKKI---
Cel_Apo_L3_Like	75	-----

HsApoA2	33	-----
HsApoA4	125	-----DNLRELQQRLEPYADQLRTQVSTQAEQLR
HsApoA5	118	-----GWNLEGLRQQLKPYTMDLMEQVA
HsApoB48	547	TFLDDASPGDKRLAAYLMLMRSPSQADINKIVQILPWEQNEQVKNFVASHIANILNSEELDQDLKLVK
HsApoB52	567	SHTIEVPTFGKLYSILKIQSPLFTLDANADIGNGTTSANEAGIAASITAKGESKLEVNFDQANAQLSN
HsApoC1	53	-----
HsApoC2	38	-----
HsApoC3	31	-----
HsApoC4	49	-----
HsApoD	53	-----IKVLNQELRADGTVNQIE
HsApoE2	126	-----EDVCGRLV
HsApoF	106	-----LQLQLYRQGGVNATQVLIQHRLGLQKGRST
HsApoH	94	-----VRYTTFEYPNTISFSCNTGFYLNAGDSAKCT
HsApoJ	174	-----VMQDHFSRASSIIDELFQDRFFTR
HsApoL1	162	-----DGVQKVHKGTTIANVVS
HsApoL2	103	-----EEVEQVHRGTTIANVVS
HsApoL3	103	-----NGIEEVHRGCTISNVVS
HsApoL4	127	-----NEIEKVHRGCVIANVVS
HsApoOL(2)	124	-----DQVDTTHELLTKTSLVA
HsApoL6	64	-----DDIDKTHKKFTKANMVA
HsApoM	64	-----
HsApoO	63	-----ISQLRHYCE
HsApoOL	64	-----FASIRTATG
HsMTTP	339	AKKEEILQILKM-----ENKEVLPQLVDAVTSAQTSDSLEAILDFDK
DmCG31659	73	-----KFSVVA
DmMtp	346	DLGAVQTFDAH-----NATFGFLYKESETTSEQLDLEKYLQSLAVAT
DmCvD	380	RIGTKASVFLTH-----HLVLNKLTKPQIAVQLLIPMPFHIFELSAELV
DmGlaz	59	-----
DmFabp	25	-----
DmApoLTPII	281	-----CLETHLLVPFSSNASSGAL
DmApoLTPI	1260	SYFTNFQVDTLVWPTIVGNVDIQEIIDFYLVVGHVELPQGVKVEFKDRLHYPDYINVHLLTVTTPFAVAK
DmNlaz	78	-----TVSVVNAAINRFTGQPSNVT
DmApoLII	244	-----FIGNTKRNSDISAKVVITILKLNPSGTGA
DmApoLI	618	NVYVVDNSLVTSWGTLSSAKGEIGQRYSAQDININIQGNVQISGKDKVTQWILKVIGTPDKTNSDFRIS
DmMICOS_A	42	-----IYGSL
Cel MICOS	44	-----IEQLPIYA
Cel_Vit_2	387	-QSLMEHALAIA-----GTKNTIQHILVHME-NEDILPL--GQILKTIQ
Cel_Vit_4	384	-QLVIETTLAVA-----GTKNTIQHLIHFFE-KKSITPLRAAELLKSQV
Cel_Vit_5	384	-QLVIETTLAVA-----GTKNTIQHLIHFFE-KKSITPLRAAELLKSQV
Cel_ApoL_1	57	-----KASAIATTV
Cel MTTP	331	LLYSQIAQEARL-----AKRQDWEAAIQVPENDHVLSLIASALGGVGTA
Cel_Vit_6	408	LRSIYFNTLALA-----GTRVTIQQFVDKVQSRKNIAPLKASVAIKTLV
Cel_Vit_3	384	-QLVIETTLAVA-----GTKNTIQHLIHFFE-KKSITPLRAAELLKSQV
Cel_Vit-1	387	-QSLMEHALAIA-----GTKNTIQHILVHIE-NEDIVPLEAAQLKSIQ
Cel_Apo_L3_Like	75	-----KGCAISTAVG
HsApoA1	51	-----
HsApoA2	33	-----
HsApoA4	154	-----
HsApoA5	141	-----
HsApoB48	617	EALKESQLPTVMDFRKFSRNYQLYKSVSL-----
HsApoB52	636	-----
HsApoC1	53	-----
HsApoC2	38	-----
HsApoC3	31	-----
HsApoC4	49	-----
HsApoD	71	-----
HsApoE2	134	-----
HsApoF	136	-----
HsApoH	125	-----
HsApoJ	198	-----
HsApoL1	179	-----
HsApoL2	120	-----
HsApoL3	120	-----
HsApoL4	144	-----
HsApoOL(2)	141	-----
HsApoL6	81	-----
HsApoM	64	-----
HsApoO	72	-----
HsApoOL	73	-----
HsMTTP	382	-----
DmCG31659	79	-----
DmMtp	389	-----
DmCvD	423	-----
DmGlaz	59	-----
DmFabp	25	-----
DmApoLTPII	299	-----
DmApoLTPI	1330	NIKSIVEYHVDLNFNAFYERVKFI VDDDKDNTQELGFVFNYTALQDNVKKPAHDVQVTLTTPYEMLHEIY
DmNlaz	98	-----
DmApoLII	273	-----
DmApoLI	687	-----
DmMICOS_A	47	-----
Cel MICOS	52	-----
Cel_Vit_2	427	-----
Cel_Vit_4	426	-----
Cel_Vit_5	426	-----
Cel_ApoL_1	66	-----
Cel MTTP	374	-----
Cel_Vit_6	451	-----
Cel_Vit_3	426	-----
Cel_Vit-1	429	-----
Cel_Apo_L3_Like	85	-----

HsApoA2	33	-----VSQYFQTVTDYGKDLMEKVKSP-----
HsApoA4	154	-----RQLTP-----YAQRMERVLRENADSLQASLRP-----
HsApoA5	141	-----LRVQE-----LQEQLRVVGEDTKAQLLGGVDE-----
HsApoB48	645	-----PSLDPASAKIEGNLIFDPNNYLPKESMLKT-----
HsApoB52	636	-----PKINPLALKESSVKFSSKYLRTHEGSEMLFFGNAIEGKSNTVASLHTEKNTLELS-----
HsApoC1	53	-----RIKQSELSAKMRLEFPFGHGHA-----
HsApoC2	38	-----QVKESLSSYWESAKTAAQNLYEK-----
HsApoC3	31	-----MQGYMKHATKTAKDALSSVQES-----
HsApoC4	49	-----VRGRMKELLETVVNRTRDGWQW-----
HsApoD	71	-----GEATP-----VNLTEPAKLEVKFSWFMPSPAPY-----
HsApoE2	134	-----QYRGE-----VQAMLGQSTEELRVRLASHLRK-----
HsApoF	136	-----ERNVSVEALASALQLLAREQQSTGRVGRSL-----
HsApoH	125	-----EEGKWSPELPVCAPICPPPSIPTFATLRV-----
HsApoJ	198	-----EPQDTYHYLPFSLPHRRPHFFPKSRIVRS-----
HsApoL1	179	-----GSLG-----ISSGILTLVGMGLAPFTEGGSL-----
HsApoL2	120	-----NSVG-----TTSGLITLLGLGLAPFTEGIF-----
HsApoL3	120	-----SSTG-----AASGIMSLAGLVLPFTAGTSL-----
HsApoL4	144	-----GSTGILSVIGVMLAPFTAGLSL-----
HsApoL(2)	141	-----SSSGA-----VSGVMNLLGLALAPVTAGGSL-----
HsApoL6	81	-----TSTAV-----ISGVMSLLGLALAPATGGGSL-----
HsApoM	64	-----PVDNIVFNMAAGSAPMQLHLRA-----
HsApoO	72	-----PYTTW-----CQETYSQTKPKMQSLVQWGLDS-----
HsApoOL	73	-----CYIGW-----CKGVYVFVKNGIMDTVQFGKDA-----
HsMTTP	382	-----SDSSII-----LQERFLYACGFASHPNEELLRA-----
DmCG31659	79	-----RELNT-----QTGTVMKMKADILNVEPEFGRY-----
DmMtp	389	-----HPDRK-----IVEHLFGLLEQESIKKHLKRE-----
DmCvD	423	-----QKCEDFLNIGPDRPDVRQAAILSFATLIHN-----
DmGlaz	59	-----LPEIASGCTTFQFEPYNKGEQS-----
DmFabp	25	-----GLVTRKMGNSLSPTVEVTLE-----
DmApoLTPII	299	-----TTSTSRCLKLDGVESYSAGEFLEQNPELVER-----
DmApoLTPI	1400	VHGHIELDDNAYKGNISAVTAHTLSMAASIENEDNFLETSGVIGLETDAIPHGYCQVYFKKDFSASVDKA
DmNlaz	98	-----GQAKV-----LGPQGLAVAFYPTQPLTKANYL-----
DmApoLII	273	-----NSPGTGSTVRSLIFQRPETYTSKNINAKKT-----
DmApoLI	687	-----DTSELIKLTSESQHPQDKISFAKLNLIKVN-----
DmMICOS_A	47	-----RKTEP-----KPERHPPQDSVLHKNLEAGVRY-----
Cel_MICOS	52	-----EDNAP-----LKQKFLPEEPLPLQREFATIRI-----
Cel_Vit_2	427	-----ETPFPSQSIAEALIKFAESRVAKNNLVVRQ-----
Cel_Vit_4	426	-----ETLYPSEHIADLLIQLAQSPLESEKYEPLRQ-----
Cel_Vit_5	426	-----ETLYPSEHIADLLIQLAQSPLESEKYEPLRQ-----
Cel_ApoL_1	66	-----GSSVD-----IASGLAVFGGLFFMPPVAIAGL-----
Cel_MTTTP	374	-----ESITT-----AREVLLTASPDYLDLDFGISQ-----
Cel_Vit_6	451	-----DMRYPSLAIAEDIARLCESDVSSSFPALRQ-----
Cel_Vit_3	426	-----ETLYPSEHIADLLIQLAQSPLESEKYEPLRQ-----
Cel_Vit-1	429	-----ETPFPSQTIAEALIKFAESRVSKNNQVVRQ-----
Cel_Apo_L3_Like	85	-----STVG-----IASGIAVIGLILMPPVAIAGL-----
HsApoA1	72	-----
HsApoA2	55	-----
HsApoA4	181	-----
HsApoA5	168	-----
HsApoB48	675	-----TLTAFGFASADLIEIGLEGKGFEPTEALFGKQGFPPDSVNKALYWVNGQVPDGVSKVL
HsApoB52	691	NGVIVKINNQLTLDSENTKYFHKLNIPKLDSSQADLRNEIKTLKAGHIAWTSSGKGSWKWACPRFSDEG
HsApoC1	75	-----
HsApoC2	61	-----
HsApoC3	53	-----
HsApoC4	71	-----
HsApoD	98	-----
HsApoE2	161	-----
HsApoF	166	-----
HsApoH	155	-----
HsApoJ	228	-----
HsApoL1	205	-----
HsApoL2	146	-----
HsApoL3	146	-----
HsApoL4	166	-----
HsApoOL(2)	167	-----
HsApoL6	107	-----
HsApoM	86	-----
HsApoO	99	-----
HsApoOL	100	-----
HsMTTP	410	-----L
DmCG31659	106	-----S
DmMtp	416	-----
DmCvD	453	-----
DmGlaz	81	-----
DmFabp	45	-----
DmApoLTPII	329	-----RATLVFDHTPAVKPSHDEIKA
DmApoLTPI	1470	IDIRFEVTDNGTLNQLHISTDWHOTPSYIVNANGRIKTMPLQMASTSVLVIQGNPHLNFNLLSQN
DmNlaz	125	-----
DmApoLII	303	-----
DmApoLI	717	-----QLTAKGEFRVAKNGKGDFTASIDTLKTEPKHKEIESKFHIQSPKYDIDASLTLDGKRKV
DmMICOS_A	74	-----
Cel_MICOS	79	-----
Cel_Vit_2	457	-----AAWLAAGSVVRGIVDYKN
Cel_Vit_4	456	-----SAWLAAGSVVRGFASKTQ
Cel_Vit_5	456	-----SAWLAAGSVVRGFASKTQ
Cel_ApoL_1	93	-----
Cel_MTTTP	401	-----
Cel_Vit_6	481	-----SCWLTYGAIVNGVCQTP
Cel_Vit_3	456	-----SAWLAAGSVVRGFASKTQ
Cel_Vit-1	459	-----SAWLAAGSVVRGIVDYKN
Cel_Apo_L3_Like	111	-----

HsApoA2	55	-----	-----
HsApoA4	181	-----HADELKAKIDQ-----	NVEELKGR
HsApoA5	168	-----AWALLQGLQSRVHH-----	HTGRFKEL
HsApoB48	735	VDHFGYTKDDKHEQDMVNGIMLSVEKLKIDLSKEVP	EARYLRI
HsApoB52	761	THESQISFTIEGPLTSFGLSNKINSKHLRVNQNLVYESGSLNFSKLEIQSQVDSQHVGHSVLTAKGMALF	
HsApoC1	75	-----	-----
HsApoC2	61	-----TYL-----	P-----
HsApoC3	53	-----	-----
HsApoC4	71	-----FW-----	SPSTFRGF
HsApoD	98	-----WILATDYENYA-----	LVYSTCI
HsApoE2	161	-----LRKRLLRDAD--DLQ-----	KRLAVYQA
HsApoF	166	-----PTEDCENEKEQ-----	AVHNVVQL
HsApoH	155	-----YKPSAGNNS-LYR-----	DTAVFECL
HsApoJ	228	-----LMPFSPYEPLNFHAMFQPFLEMIHEAQQ--AMD-----	IHFHSPAF
HsApoL1	205	-----VLLEPGM--ELG-----	ITAALTGI
HsApoL2	146	-----VLLDTGM--GLG-----	AAAAVAGI
HsApoL3	146	-----ALTAAGV--GLG-----	AASAVTGI
HsApoL4	166	-----SITAAGV--GLG-----	IASATAGI
HsApoL(2)	167	-----MLSATGT--GLG-----	AAAAITNI
HsApoL6	107	-----LLSTAGQ--GLA-----	TAAGVTSI
HsApoM	86	-----TIRMKDG--LCV-----	PRKWIYHL
HsApoO	99	-----YDYLQNAAPP--GFF-----	PRLGVIGF
HsApoOL	100	-----YVYLKNPPR--DFL-----	PKMGVITV
HsMTTP	412	ISKFKGSIGSSDIRETVMIITITLVRKLCQNEGCKLK	AVVEAKKL
DmCG31659	106	-----VLGTST--AFP-----	EGVLMYVL
DmMtp	418	VIQTVATLTRQSGLDVEDPLLKEVRSYLLQGLT--SKE-----	PTLYIRAL
DmCvD	453	-----VYVAKGIDKEKFEEYVQKYFNAYLSDRD--FDQ-----	KMLYLQGL
DmGlaz	81	-----KFS--NFK-----	LAVAIKNI
DmFabb	45	-----	GDTYTL
DmApoLTPII	351	ARELLVEMCRVGFNPNIQREFIDVFTNFLQTSKSLDYK-----	TLSVLLQR
DmApoLTPI	1540	GQSIAYGARANKKKDVFNIEVWTPMKNFRNISMHGTA-----	IRSPRDPGRYDVSGFLYRNMATYEVTVG
DmNlaz	125	-----VLGTDYE--SYA-----	VVYSTSV
DmApoLII	303	-----ILSDLVDSTGDYVKKETAKKFVEFIRLLRQSDSE-----	TLLELAFA
DmApoLI	778	HLKSENTIEKLKFSTKNIGEANDKIIAFAEANGS--LKG-----	ELRGNGEI
DmMICOS_A	74	-----VREEVQS--GYK-----	AVADQAGI
Cel MICOS	79	-----ACEQ--EYD-----	RVAERFKV
Cel_Vit_2	476	IRPL----VREDKRELKEKFLRVFMQQYKDAET--TYE-----	KILALKTI
Cel_Vit_4	475	DLPL----IRPASRQTKEKYVRVFMQHFRNADS--TYE-----	KVLALKTL
Cel_Vit_5	475	DLPL----IRPASRQTKEKYVRVFMQHFRNADS--TYE-----	KVLALKTL
Cel_ApoL_1	93	-----IVGAASG--VSN-----	VATGVNKK
Cel MTTP	401	-----SSSNNEKWHKQLMYWLGSLDKKSE--EYW-----	KVANTIAT
Cel_Vit_6	500	RVFVQKNGVKMCPRDAKQRIVDKLVQQFESAST--RYE-----	KVLALKTL
Cel_Vit_3	475	DLPL----IRPASRQTKEKYVRVFMQHFRNADS--TYE-----	KVLALKTL
Cel_Vit-1	478	IRPL----VREDKRELKEKFLRVFMQQYKDAET--TYE-----	KILALKSI
Cel_Apo_L3_Like	111	-----IVGTASG--VSN-----	LATGITKF
HsApoA1	72	-----	-----
HsApoA2	55	-----	-----
HsApoA4	201	LTPYADEFKVKIDQTVVEELRR-----	
HsApoA5	191	FHPYAESLVSGI-----	
HsApoB48	780	LGEELGFASLHDLQLLGKLLLMGARTLQGIQMIQEVIRKSGSKNDFFLHYIFMENAFELPTGAGLQLOIS	
HsApoB52	831	GEGKAEFTGRHDAHLNGKIVIGTLKNSLFFSAQPFITASTNNEGNLKVRFPLRLTGKIDFLNLYALFLSP	
HsApoC1	75	-----	-----
HsApoC2	65	-----	-----
HsApoC3	53	-----	-----
HsApoC4	82	MQTTYDDHLR-----	
HsApoD	118	IQLFHVDFAWILAR-----	
HsApoE2	183	GAREGAERGLS-----	
HsApoF	186	LPGVGTFYNLGT-----	
HsApoH	176	PQHAMFGNDTITCTHGNWTK-----	
HsApoJ	268	QHPPTFEIREGDDDRTVCREIRHNS-----	
HsApoL1	224	TSSTMDYGKKWWTQ-----	
HsApoL2	165	TCSVVELVN-----	
HsApoL3	165	TTSIVEHSYTSSAE-----	
HsApoL4	185	ASSIVENTYTRSAE-----	
HsApoL(2)	186	VTNVLENRS-----	
HsApoL6	126	VSGTLERSKNK-----	
HsApoM	105	TEGSTDLRT-----	
HsApoO	120	AGLIGLLAR-----	
HsApoOL	121	SGLAGLVSARK-----	
HsMTTP	457	ILGGLKAEKKEDTRMYLLALKNALLPEGIPS-----	
DmCG31659	125	DTDYVNFAR-----	
DmMtp	462	QNLQDPATIEALLEHAQTGEAPNL-----	
DmCvD	493	NNLQLGNVANYLEPIVQDPNEHEDLKFAAWT-----	
DmGlaz	96	NRITGNPNVN-----	
DmFabb	52	TTTSTFKTS-----	
DmApoLTPII	396	SASTCEQGRNHLESPLFIGS-----	
DmApoLTPI	1605	VRMTNSLPIDVVLRVQPKAGGRDGVIELNIHEAGPKKIRFSFSAIEDGKMCMSGGYSVSKTNGAMDFSV	
DmNlaz	144	TPLANFKIIVILTRQREP-----	
DmApoLII	346	PHPNKVLARKVYLDGLFR-----	
DmApoLI	822	QGTFFIFNAPDGRVIDGSINRKISTNAKSGLSQGNIDAQLSDTFPGSNKKRSISLIGKLDRLNKTKEFSA	
DmMICOS_A	93	VGHYVETAK-----	
Cel MICOS	95	VDCAMTQTK-----	
Cel_Vit_2	516	GNAGLDSVNLNEIIVDKRQPLPVRKEAIDA-----	
Cel_Vit_4	515	GNAGIDLSVYELVQLIQDPRQPLSIRTEAVDA-----	
Cel_Vit_5	515	GNAGIDLSVYELVQIIQDPRQPLSIRTEAVDA-----	
Cel_ApoL_1	112	LATDHKIRE-----	
Cel MTTP	437	VLNKRCEASTSSLSNCKGKETIVNKFITDLT-----	AGGVEV
Cel_Vit_6	544	ANAGLDLSVYPLEKIIILNEQHETTIRTQAIES-----	
Cel_Vit_3	515	GNAGIDLSVYELVQLIQDPRQPLSIRTEAVDA-----	
Cel_Vit-1	518	GNAGLDSVNLNEIIVDKRQPLPVRKEAIDA-----	
Cel_Apo_L3_Like	130	FHTKGQHKEVAAMI-----	

HsApoA2	55	-----
HsApoA4	221	-----
HsApoA5	202	-----
HsApoB48	850	SSGVIAPGAKAGVKLEVANMQAELVAKPSVSVEFVTNMGIIIPDFARSGVQMNTNFFHESGLEAHVALKA
HsApoB52	901	SAQQASWQVSARFNQYKYNQNFSAAGNNENIMEAHVGINGEANLDFLNIPLTIPEMRLPYTIITTPPLKDF
HsApoC1	75	-----
HsApoC2	65	-----
HsApoC3	53	-----
HsApoC4	91	-----
HsApoD	131	-----
HsApoE2	193	-----
HsApoF	197	-----
HsApoH	196	-----
HsApoJ	292	-----
HsApoL1	237	-----
HsApoL2	173	-----
HsApoL3	178	-----
HsApoL4	198	-----
HsApoOL(2)	194	-----
HsApoL6	136	-----
HsApoM	113	-----
HsApoO	129	-----
HsApoOL	131	-----
HsMTTP	488	-----
DmCG31659	134	-----
DmMtp	485	-----
DmCvD	524	-TLALADRRARIYEVYWP IFESRNASLELRVAAVTLLLSISNPTAA-----
DmGlaz	105	-----
DmFabp	60	-----
DmApoLTPII	416	-----
DmApoLTPI	1675	LVESTPEIARINFYGNLSPNSEGSLVGDLSETPWKALGIDTVHLHSDVGFLNKGGHIVGEYKIGQYIG
DmNlaz	161	-----
DmApoLII	363	-----
DmApoLI	892	NSNLVYTA FNGEKSEISYQIKQQPNGDAKNIDFSLKAYGNPLPQPFEIAFALGDYSAQHAVVSITSKYGE
DmMICOS_A	101	-----
Cel MICOS	103	-----
Cel Vit_2	547	-LRLLKDTMPRKIQKVLLPIYKNRQYEPEIRMLALWRMMHTRPEES-----
Cel Vit_4	546	-LRLLKDVMPRKIQKVLLPVYKNRQNKPELRMAALWRMMHTIPEEP-----
Cel Vit_5	546	-LRLLKDVMPRKIQKVLLPVYKNRQNKPELRMAALWRMMHTIPEEP-----
Cel ApoL_1	120	-----
Cel MTTP	475	RVLEVLNIPIFGSYTFAKKFICETESQKAAALNVILAASKNLYETQ-----
Cel Vit_6	575	-FRRLRTQMPTKIQRVLMPVYLNRRQOPQHIRMALHQQIYTQPEWS-----
Cel Vit_3	546	-LRLLKDVMPRKIQKVLLPVYKNRQNKPELRMAALWRMMHTIPEEP-----
Cel Vit-1	549	-LRLLKDTMPRKIQKVLLPIYKNRQYEPEIRMLALWRMMHTRPEES-----
Cel_Apo_L3_Like	143	-----
HsApoA1	72	-----ALRTHLAPYSDELQRRLAARLEALKENGARLAE
HsApoA2	55	-----ELQAEAKSYFEKSKEQLTPLIKKAGTELVNFLSY
HsApoA4	221	-----SLAPYAQDTQEKLNHOLE-----GLTFQMKKNAEELKARISASAEELQRRLAPLAED
HsApoA5	202	-----GRHVQ-----ELHRSVAPHAPASPARLSRCVQLSRKLTAKA
HsApoB48	920	GKLKFIIPSPKRPVKLLSGGNTL-----HLVSTTKTEVIPPLIENRQSWSVCKQVFPGLNYC
HsApoB52	971	SLWEKTGLKEFLKTTKQSFDSLVS-----KAQYKKNKHRHSITNPLAVLCEFIQSQIKSFDHR
HsApoC1	75	-----GVCFWVEPWQMVQDEQIEKKTSPGEADNIPLVTO
HsApoC2	65	-----AVDEKLRLDLYSKSTAMSTYTGTFTDQVLSVLKG
HsApoC3	53	-----QVAQQARGWVTDGFSLSKDYWSTVK-----
HsApoC4	91	-----DLGPLTKAWFLESKDSLLKKTTHSLCPRLVCGDKD
HsApoD	131	-----NPNLP-----PETVDSLKNILTSNNIDVKKMTVTDQVNCPKLSQ
HsApoE2	193	-----AIRERLGPLVEQGRVRAATVGSLAGOPLQERAQA
HsApoF	197	-----ALYYATQNCGLGARERGRDGAIDLGYDLLMTMAG
HsApoH	196	-----LPECR-----EVKCPFPSPRDNGFVNYPAPKPTLYYKDKATFGCH
HsApoJ	292	-----TGCLRMDQCDKCREILSVDCSTNNPSQAKLRE
HsApoL1	237	-----AQAHDLVIKSLDKLKEVREFLGGENISNFLSLAGN
HsApoL2	173	-----KLRR-----AQARNLDQSGTNVAKVMKEFVGNGTNPVLTVDN
HsApoL3	178	-----AEASRLTATSIDRLKVFKEVMRDITPNLLSLNN
HsApoL4	198	-----LTASRLTATSTDQLEALRDILHDITPNVLSFALD
HsApoOL(2)	194	-----NSAAR-----DKASRLGPLTTSHEAFGGINWSEIEAAGFCVNKC
HsApoL6	136	-----EAQ-----ARAEDILPTYDQEDREDEEEKADYVTAAGKIYN
HsApoM	113	-----EGRPDMKTELFSSSCPGGIMLNETGGQYQRFLLY
HsApoO	129	-----GSKIK-----KLVPYPPGFMGLAASLYYPQQAIVFAQVSGERLYD
HsApoOL	131	-----GSKFK-----KITYPGLATLGATVCYPVQSVIIAKVTAKKVYA
HsMTTP	488	-----LLKYAEAGEGPISHLATTALQRYDLPFITDEVKKTLNRIYHQNKRKVEKTVRTAAAIILNNNP
DmCG31659	134	-----FMCDFASKIFSFHWAIVQTRKRLPSTQVHMAQY
DmMtp	485	-----SVAALQALKAFPLGFSFNS-----SHRLQFESIFYQRRRFDSSARTLALDILSLRP
DmCvD	569	-----RLSIHRIIQSETDPHMI-----NYYRTTVTSISETTYPCYQHLRRLLSYMRHLPO
DmGlaz	105	-----IGYAT-----PENSRSSIMDFKFTTRFPDVIARLLPGSGKY-----
DmFabp	60	-----AISFKLGVEFDEETLDGRNVKSIITLDGNKLTQE
DmApoLTPII	416	-----TASYKVMRDQIINEKLTQMAHDMWTALSFITRP
DmApoLTPI	1745	RGSCLSWSWILAEDMQLVLENYLERP-----NAKPRIVHASAKYQNPQTFTTQLQAGGRSLVDSK
DmNlaz	161	-----SAEAV-----DAARKILEDNDVSAQLIDTVQKNCPRLDNGTG
DmApoLII	363	-----TSTAESARVILKQLSKPFDEKEKLLATLSLNIKVS
DmApoLI	962	IFSVSANGNYYNNQALEYGLQANIEIPKSTLKSLEINSHGKVLKSLIGNENAAYNVEFLDSTSLGQYA
DmMICOS_A	101	-----AHTQSTIDMLNEPQNSLHRSAGIIVGGLAGFIFA
Cel MICOS	103	-----KAATKCNAYLTEEWTALPKAAAITVGGMAGFVLG
Cel Vit_2	592	-----LLVQVVSQMEKETNQQA-----ALTHQMIHRHAMSTNPQYQRAIVCSKVLSTTRY
Cel Vit_4	591	-----VLAHIVSQMENESNQHVA-----AFTYNVLRQFSKSTNPQYQQLAVRCSKVLSTTRY
Cel Vit_5	591	-----VLAHIVSQMENESNQHVA-----AFTYNVLRQFYKSTNPQYQQLAVRCSKVLSTTRY
Cel ApoL_1	120	-----INRML-----AEDAKFFEEELHRSNDLLNEVRRFVBDKQSSKIF
Cel MTTP	523	-----LTHKLIKLFRTCSQETP-----TSHSQLAIDILLKCPVDPHQNVATLILRTETLNP
Cel Vit_6	620	-----VLSQIGNQLRQERNQQVR-----AFTLSLLRSYANNESPCQTFSRRVQSLNNIPF
Cel Vit_3	591	-----VLAHIVSQMENESNQHVA-----AFTYNVLRQFSKSTNPQYQQLAVRCSKVLSTTRY
Cel Vit-1	594	-----LLVQVVSQMEKETNQQA-----ALTHQMIHRFAKSTNPQYQRAIVCSKVLSTTRY
Cel_Apo_L3_Like	143	-----AEDGVLFEEELKSREELMEAVRKIVEDEEFFKHF

HsApoA2	90	FVE-----
HsApoA4	274	VRGNLRGNTTEGLQKSL-----
HsApoA5	242	LHARIQQNL-----
HsApoB48	977	TSGAYSNASSTDSASYPLTGDTRLELELRPTGEIEQYSVSATYELQREDRALVDTLKFVTQAEQAKQTE
HsApoB52	1028	FEKNRNNALDFVTKSYNETKIKFDKYKAEKSHDELPRTFQIPGYTVPVVNVVEV-----
HsApoC1	109	-----
HsApoC2	100	EED-----
HsApoC3	78	-----
HsApoC4	126	QQQ-----
HsApoD	171	AKE-----
HsApoE2	228	WGERLRARM-----
HsApoF	232	MSG-----
HsApoH	236	DGYSLD-----
HsApoJ	327	LDESQVA-----
HsApoL1	272	TYQLT-----
HsApoL2	213	WYQVT-----
HsApoL3	213	YYEAT-----
HsApoL4	233	FDEAT-----
HsApoOL(2)	234	VKA-----
HsApoL6	174	LRNTL-----
HsApoM	148	NRSP-----
HsApoO	169	WGLRGY-----
HsApoOL	171	TSQQIF-----
HsMTTP	553	SYMDVKNILLSI-----
DmCG31659	169	FGKSA-----
DmMtp	538	TQEQLGNFLDYLASNDRQ-----
DmCvD	622	KPESRYWVTGNYIFDYRDSK-----
DmGlaz	141	-----
DmFabp	95	QKG-----
DmApoLTPII	451	DEETLETFHSILEYAKNRLDAEYT-----
DmApoLTPI	1804	WNLDVNGSAEYKSVDDFKFRVITALPLPVGDRHQLSASYQGNVISQQFNNPDFVLEASYESFEAQNKLLS
DmNlaz	201	LA-----
DmApoLII	398	VDKETLNQAASQLLPNAPKELY-----
DmApoLI	1032	RVNTVWNGTANDGSYDFAEQTNNMESPLKFNGKYHRKQTGNIKDGDLTGKQTYVLNAQYGAQYVKMDASL
DmMICOS_A	136	ARG-----
Cel_MICOS	138	LKR-----
Cel_Vit_2	645	QPQE-QMIASSYAQLPLFLQNSFSGAQDFAAIFEKNSFLPKDLHASLD-----
Cel_Vit_4	644	QPQE-QML-STYSQLPLFNSEWLSGVQDFATIFEKNAFLPKQEVQASFE-----
Cel_Vit_5	644	QPQE-QML-STYSQLPLFNSEWLSGVQDFATIFEKNAFLPKQEVQASFE-----
Cel_ApoL_1	160	KNF-----
Cel_MTTP	576	DQEKWHYLYKAIEA-----
Cel_Vit_6	673	SSQEIDRFESVYGKSTYSRRHQSGFEANFASLFTTESVLPTEMMASIE-----
Cel_Vit_3	644	QPQE-QML-STYSQLPLFNSEWLSGVQDFATIFEKNAFLPKQEVQASFE-----
Cel_Vit-1	647	QPQE-QMIASSYAQLPLFLQNSFSGAQDFAAIFEKNSFLPKDLHASLD-----
Cel_Apo_L3_Like	178	KND-----
HsApoA1	108	-----
HsApoA2	92	-----
HsApoA4	289	-----
HsApoA5	250	-----
HsApoB48	1047	ATMTFKYNRQSMTLSSSEVQIPDFDVLGTLIRVNDESTEGKTSYRLTLDIQNKKITEVALMGHLSCDTKE
HsApoB52	1080	-----
HsApoC1	109	-----
HsApoC2	102	-----
HsApoC3	78	-----
HsApoC4	128	-----
HsApoD	173	-----
HsApoE2	236	-----
HsApoF	234	-----
HsApoH	241	-----
HsApoJ	334	-----
HsApoL1	276	-----
HsApoL2	217	-----
HsApoL3	217	-----
HsApoL4	237	-----
HsApoOL(2)	236	-----
HsApoL6	178	-----
HsApoM	151	-----
HsApoO	174	-----
HsApoOL	176	-----
HsMTTP	564	-----
DmCG31659	173	-----
DmMtp	555	-----
DmCvD	641	-----
DmGlaz	141	-----
DmFabp	97	-----
DmApoLTPII	474	-----
DmApoLTPI	1874	RISYKNATNNLK-----
DmNlaz	202	-----
DmApoLII	419	-----
DmApoLI	1102	GYGAEKVDAIYVIDSSFDSVKDIKVNIRTFKPLDDSTYVVVTLFKQTDKSYGLDITTFYHSAHKKGVDIRL
DmMICOS_A	138	-----
Cel_MICOS	140	-----
Cel_Vit_2	692	-----
Cel_Vit_4	690	-----
Cel_Vit_5	690	-----
Cel_ApoL_1	162	-----
Cel_MTTP	589	-----
Cel_Vit_6	721	-----
Cel_Vit_3	690	-----
Cel_Vit-1	694	-----
Cel_Apo_L3_Like	180	-----

HsApoA2	92	-----
HsApoA4	289	-----AELGGHLDQQVE-----
HsApoA5	250	-----DQLREELSRFA-----
HsApoB48	1117	ERKIKGVISIPRLQAEARSEILAHWSPAKLLL
HsApoB52	1080	-----SPFTIEMSAF-----
HsApoC1	109	-----
HsApoC2	102	-----
HsApoC3	78	-----DKFSEFWDL-----
HsApoC4	128	-----
HsApoD	173	-----PCVESLVSQY-----
HsApoE2	236	-----EEMGSRTDRDL-----
HsApoF	234	-----GPMGLAISAA-----
HsApoH	241	-----GPEIECTKL-----
HsApoJ	334	-----ERLTRKYNELLK-----
HsApoL1	276	-----RGIGKDIRAL-----
HsApoL2	217	-----QGIGRNIRAI-----
HsApoL3	217	-----QTIGSEIRAI-----
HsApoL4	237	-----KMIANDVHTL-----
HsApoOL(2)	236	-----IQGIKDLHAY-----
HsApoL6	178	-----KYAKKNVRAFVK-----
HsApoM	151	-----HPPEKCVVEF-----
HsApoO	174	-----IVIEDLWKEN-----
HsApoOL	176	-----GAVKSLWTKSSK-----
HsMTTP	564	-----GELPQEMNKYML-----
DmCG31659	173	-----GLVIGDMSKV-----
DmMtp	555	-----FEIKTYVLQKLR-----
DmCvD	641	-----FGIGAMLQVF-----
DmGlaz	141	-----QVLYTDYENF-----
DmFabp	97	-----DKPTTIVREF-----
DmApoLTPII	474	-----LGATAVVSFSCK-----
DmApoLTPI	1885	-----GLGHVWGKIQNL SVVEGDFELLHKQGAQREFSAKIITPKFKNEHTFALTGS
DmNlaz	202	-----GEDGLDVDDF-----
DmApoLII	419	-----IAVGNLVAKY-----
DmApoLI	1172	DLLKEKP I I S S I A E L L G D R K G K V L F E I L N L A D L D I K I N S E A S Y V S I D E F Y I I V N W S S K K L K L D G Y E L E A
DmMICOS_A	138	-----GFIKKVLYSGIG-----
Cel MICOS	140	-----GPVGRLLTTTIG-----
Cel_Vit_2	692	-----AVFGGNWNKYFA-----
Cel_Vit_4	690	-----TVFGGNWNKYFA-----
Cel_Vit_5	690	-----TVFGGNWNKYFA-----
Cel_ApoL_1	162	-----DDVQSHLKTFLG-----
Cel MTTP	589	-----SGNKDELKAEFW-----
Cel_Vit_6	721	-----GVLSGEWNQYFA-----
Cel_Vit_3	690	-----TVFGGNWNKYFA-----
Cel_Vit-1	694	-----AVFGGNWNKYFA-----
Cel_Apo_L3_Like	180	-----GDIENKLT VFG-----
HsApoA1	118	-----
HsApoA2	92	-----
HsApoA4	301	-----
HsApoA5	262	-----
HsApoB48	1148	-----
HsApoB52	1090	-----GYVFPKAVSMPSFSILGSDVRVPSYT
HsApoC1	109	-----
HsApoC2	102	-----
HsApoC3	88	-----
HsApoC4	128	-----
HsApoD	183	-----
HsApoE2	248	-----
HsApoF	244	-----
HsApoH	251	-----
HsApoJ	346	-----
HsApoL1	286	-----
HsApoL2	227	-----
HsApoL3	227	-----
HsApoL4	247	-----
HsApoOL(2)	246	-----
HsApoL6	190	-----
HsApoM	161	-----
HsApoO	184	-----
HsApoOL	188	-----
HsMTTP	576	-----
DmCG31659	183	-----
DmMtp	567	-----
DmCvD	651	-----
DmGlaz	151	-----
DmFabp	107	-----
DmApoLTPII	486	-----
DmApoLTPI	1938	YDLEKSGHHNVVGS LDYPASRRITDLDVSVSSLSNMHGIFNSTLPTFLNVSWLKTDFNFTTNNKGSYRYC
DmNlaz	212	-----
DmApoLII	429	-----
DmApoLI	1242	RAQSKNIKIQLKNENGIIFSGTATYALKKELNKTIIDGQGVQYQKALSGNFKLTRQHFDFTDREVGF
DmMICOS_A	150	-----
Cel MICOS	152	-----
Cel_Vit_2	704	-----
Cel_Vit_4	702	-----
Cel_Vit_5	702	-----
Cel_ApoL_1	174	-----
Cel MTTP	601	-----
Cel_Vit_6	733	-----
Cel_Vit_3	702	-----
Cel_Vit-1	706	-----
Cel_Apo_L3_Like	192	-----

HsApoA2	92	-----
HsApoA4	301	-----EFRRRVEPYGENF-----
HsApoA5	262	-----GTGTEEGAGPDPQ-----
HsApoB48	1148	-----QMDSSATAYGSTV-----SK
HsApoB52	1117	LILPSLELPVLHVPRNLKLSLPDFKELCTTISHIFIPAMGNITYDFSFKSSVITLNTNAELFNQSDIVAH
HsApoC1	109	-----
HsApoC2	102	-----
HsApoC3	88	-----
HsApoC4	128	-----
HsApoD	183	-----FQTVTDYGKDL-----
HsApoE2	248	-----EVKEQVAEVRACL-----
HsApoF	244	-----LKPALRSQVQQLI-----
HsApoH	251	-----GNWSAMPSCKASC-----
HsApoJ	346	-----SYQWKMLNTSSLL-----
HsApoL1	286	-----RRARANLQSV-----
HsApoL2	227	-----RRARANPQLGAYA-----
HsApoL3	227	-----RQARARARLPVTT-----
HsApoL4	247	-----RRSKATVGRPL-----
HsApoL(2)	246	-----QMAKSNSGFMAMV-----
HsApoL6	190	-----LRANPRLANAT-----
HsApoM	161	-----
HsApoO	184	-----FQKPG-----
HsApoOL	188	-----EESLPKPKEKTKL-----
HsMTTP	576	-----AIVQDILRFEMPA-----
DmCG31659	183	-----
DmMtp	567	-----MLAEKCPFRFALF-----
DmCvD	651	-----LVGDPKSDMPVVA-----
DmGlaz	151	-----AILWSCGSIGSLG-----
DmFabp	107	-----TDNELITLI-----
DmApoLTPII	486	-----HHEACEENLRVQQ-----
DmApoLTPI	2008	RCFWPQDTAYFKLNSNYSDSDSNFNHNL
DmNlaz	212	-----VSTTV-----
DmApoLII	429	-----CLKNYCQGPEIDA-----
DmApoLI	1312	SYTFMGNLGSKNGLTLKITNKEFNTKF-----SVCEE
DmMICOS_A	150	-----AGAVASMCYPRQA-----
Cel MICOS	152	-----LATMAAFICYPIEA-----
Cel_Vit_2	704	-----QIGFSQQHMDKYV-----
Cel_Vit_4	702	-----QVGFSQQNFEQVI-----
Cel_Vit_5	702	-----QVGFSQQNFEQVI-----
Cel_ApoL_1	174	-----VSLAGITGFGIKM-----
Cel MTTP	601	-----SRMRKFKVFRPNF-----
Cel_Vit_6	733	-----QIGFTQKNMEKII-----
Cel_Vit_3	702	-----QVGFSQQNFEQVI-----
Cel_Vit-1	706	-----QIGFSQQHMDKYV-----
Cel_Apo_L3_Like	192	-----GSVTGITGIGTRF-----
HsApoA1	130	-----
HsApoA2	92	-----
HsApoA4	314	-----
HsApoA5	275	-----
HsApoB48	1164	RVAWHYDEEKIEFEWNTGTNVDTKKMTSNFPVDLSDYPKSLHMYANRLLDHRVPQDTMTFRHVGSKLIVA
HsApoB52	1187	LSSSSSVIDALQYKLEGTTRLTRKRLGLKATALSLSNKFVEGSHNSTVSLTTKNMEVSVATTTKAQIPIL
HsApoC1	109	-----
HsApoC2	102	-----
HsApoC3	88	-----
HsApoC4	128	-----
HsApoD	194	-----
HsApoE2	261	-----
HsApoF	257	-----
HsApoH	264	-----
HsApoJ	359	-----
HsApoL1	297	-----
HsApoL2	240	-----
HsApoL3	240	-----
HsApoL4	258	-----
HsApoOL(2)	259	-----
HsApoL6	201	-----
HsApoM	161	-----
HsApoO	189	-----
HsApoOL	201	-----
HsMTTP	589	-----SKIVRRVLKEMVAHNYDRFSRSGSSSAYTGYIERSPRASASTYSL
DmCG31659	183	-----
DmMtp	580	-----KSELVKKRRHVNNYNVLGQKGLTTLVLRQLSQAPAFNETLLS
DmCvD	664	-----FFKFDTEALGKFTGLALYIKARGLPDTILNKMQRNGSDP
DmGlaz	164	-----
DmFabp	116	-----
DmApoLTPII	499	-----
DmApoLTPI	2035	-----NGNVEIEVPLATRHRADIVYGLQKRRNQDAGNVKVYVNEKQVLDGKYKRLEQAKAPIYKETT
DmNlaz	217	-----
DmApoLII	442	-----
DmApoLI	1345	KRQCTNLIVQSIVSIDEQKLDAVEHTTLIIVDLRDFGYPYEFELKSQNTROGLKYQYHLDSTIITGNNF
DmMICOS_A	163	-----
Cel MICOS	165	-----
Cel_Vit_2	717	-----QMALEKLESLEKESTTVVRGRRITGTGK-----LLKELAQKMNIRA
Cel_Vit_4	715	-----LKTLEKLSLYGKQSD-LSRRRVQSGIQ-----MLQEIVKKMNIRP
Cel_Vit_5	715	-----LKTLEKLSLYGKQSD-LSRRRVQSGIQ-----MLQEIVKKMNIRP
Cel_ApoL_1	187	-----
Cel MTTP	614	-----LHRALQADSHVHWQEIADASNFLQFSTANTFEFLQSFKRSIF
Cel_Vit_6	746	-----KLLSNVQEKGLEQIV-VRGKRASGSFQPTFELSNLLEKLRI
Cel_Vit_3	715	-----LKTLEKLSLYGKQSD-LSRRRVQSGIQ-----MLQEIVKKMNIRP
Cel_Vit-1	719	-----QMALEKLESIEKESTTVVRGRRITGTG-----LLKELALKMNIRA
Cel_Apo_L3_Like	205	-----

HsApoA2	92	-----
HsApoA4	314	-----
HsApoA5	275	-----
HsApoB48	1234	MSSWLQKASGSLPYTQTLDHLNSLKEFNLQNMGLPDFHIPENLFLKSDGRVKYTLNKNLSLKIEIPLPFG
HsApoB52	1257	RMNFKQELNGNTKSKPTVSSSMEFKYDFNSSMLYSTAKGAVDHKLSLESITSYFSIESSTKGDVKGSVLS
HsApoC1	109	-----
HsApoC2	102	-----
HsApoC3	88	-----
HsApoC4	128	-----
HsApoD	194	-----
HsApoE2	261	-----
HsApoF	257	-----
HsApoH	264	-----
HsApoJ	359	-----
HsApoL1	297	-----H
HsApoL2	240	-----
HsApoL3	240	-----
HsApoL4	258	-----
HsApoOL(2)	259	-----
HsApoL6	201	-----
HsApoM	161	-----
HsApoO	189	-----
HsApoOL	201	-----
HsMTTP	634	DILYSGS-----GILRRSNLNIQYIGKAGLHGSQVVI
DmCG31659	183	-----
DmMtp	622	TQEVYQG-----ILKRGSVFLLHAGRSQASSFKLGIY
DmCvD	706	FTFKSIKALLAMLQAPIINSKDLHLEFILQMEGKTVLSYYLNQRMFRQLTYDNILERMQQIIRTD SHINM
DmGlaz	164	-----
DmFabp	116	-----
DmApoLTPII	499	-----IINLLETEFLNLYNLF
DmApoLTPI	2098	DISLENEVKPLGIHFVSTRDASDPAGSQDVKHIEIYELRNTQNFNLTGELHSRATLKAQDFKVAIHPNR
DmNlaz	217	-----
DmApoLII	442	-----ISKKFSGLKHCKPNTKREE
DmApoLI	1415	YQFTANVQPTSSTIKLALPKRQILFETTQKIPADGSLFGRYEQTASFFIDKLQKPDVARFSAIVDVTGT
DmMICOS_A	163	-----
Cel MICOS	165	-----
Cel Vit_2	759	RPATYTEKDAFAMVYLRYKDMDYAFLPIDRQLVENLIEKFTSNGKVQFSEIRRLNQELEFETHHAAIFY
Cel Vit_4	756	RVQQTDSQNAHAVFYLRKEMDYIVLPIDMETIDNVVEKYVRNGEFDIKSLLTFLTNDSKFELHRAFFY
Cel Vit_5	756	RVQQTDSQNAHAVFYLRKEMDYIVLPIDMETIDTLVEKYVRNGEFDIKSLLTFLTNDSKFELHRAFFY
Cel ApoL_1	187	-----
Cel MTTP	657	ELSMKKG-----RKEHNLFSLSIDTEHLEQFVTGSA
Cel Vit_6	790	R--QSSEQDPHAFVYIRHRDMDYAFLPIDADSIPEVVRSMIQQGRLEIGDIERVLAQGIHFSASNAAFLY
Cel Vit_3	756	RVQQTDSQNAHAVFYLRKEMDYIVLPIDMETIDNVVEKYVRNGEFDIKSLLTFLTNDSKFELHRAFFY
Cel Vit-1	761	RPANYNEKDAFAMVYLRYKDMDYAILPVDTLIEKLEIKYISNGKVQFSEIRRLNQEHEFETHHAAIFY
Cel Apo_L3_Like	205	-----
HsApoA1	130	-----
HsApoA2	92	-----
HsApoA4	314	-----
HsApoA5	275	-----
HsApoB48	1304	GKSSRDLKMLETVRTPALHFKSVGFHLPSPREFQVPTFTIPKLYQLQVPLLGVLDSLSTNVYSNLYNWSASY
HsApoB52	1327	REYSGTIASEANTYLNKSKSTRSSVKLQGTSKIDDIWNLEVKENFAGEATLQRIYSLWEHSTKNHLQLEGL
HsApoC1	109	-----
HsApoC2	102	-----
HsApoC3	88	-----
HsApoC4	128	-----
HsApoD	194	-----
HsApoE2	261	-----
HsApoF	257	-----
HsApoH	264	-----
HsApoJ	359	-----
HsApoL1	299	ASASRPRVTEPISAESGEQVE-----
HsApoL2	240	-----PPPHVIGRISAE-----
HsApoL3	240	-----WRISAGSGGQAE-----
HsApoL4	258	-----IAWRYVPIINVVETL-----
HsApoOL(2)	259	-----KNFVAKRHIPFW-----
HsApoL6	201	-----KRLLTGQVSSR-----
HsApoM	161	-----
HsApoO	189	-----
HsApoOL	201	-----
HsMTTP	667	EAQGLEALIAATPDEGEENLDSYAGMSA-----
DmCG31659	183	-----
DmMtp	655	TAGLGSVLVDGSDGSDGND AIPAD-----
DmCvD	776	QTVRWPFMNRYTVP TVLTSSDVL LQT TVLTSLRGNITEQRNSPITKHTLEIDARYSSYASVRSRSYNPF
DmGlaz	164	-----
DmFabp	116	-----
DmApoLTPII	516	KGERRTRERMVILLKGLGNIGVVS-----
DmApoLTPI	2168	AVVLSTKYEDVSPVVRHHSKLELSETAWIGYNLELGNFSKVGNESQSFALEIFYPKRNLSSSGQYYMTD
DmNlaz	217	-----
DmApoLII	463	ERIVYILKGLGNAKSLSGNTVAALSECA-----
DmApoLI	1485	ERVAFNANGKLKFEHPTIRPLSISGQLNGDVNQIASEVIFDIFRLPEQKVVGNSSELNRSRQNGFNIA
DmMICOS_A	163	-----
Cel MICOS	165	-----
Cel Vit_2	829	EAIRKFPTTLGLPLTISGKIPTVISAEQGSLELEGT-----ELRLTVEARPSVAATHVYEMRMFTPLF
Cel Vit_4	826	EAERRIPTTIGMPLTISGKMPTILSINGKVSIELEKL-----GARLVLDIVPTVATTHVTEMRFWYPVI
Cel Vit_5	826	EAERRIPTTIGMPLTISGKMPTILSINGKVSIELEKL-----GARLVLDIVPTVATTHVTEMRFWYPVI
Cel ApoL_1	187	-----
Cel MTTP	688	SSRSGAPQGSVRIGVAGHKLPTHHIFKG-----
Cel Vit_6	858	ETVRRVPTPMGLPVQFTSKMPTISSIRGQVTFELEPKNGKSF DGLRLRVQAGPRVASTHVLSLRVICPIA
Cel Vit_3	826	EAERRIPTTIGMPLTISGKMPTILSINGKVSIELEKL-----GARLVLDIVPTVATTHVTEMRFWYPVI
Cel Vit-1	831	EAIRKFPTTLGLPLIVSGKIPTVFSAEQGSGLLEET-----ELRLTVEARPSVAATHVYEMRMFTPLF
Cel Apo_L3_Like	205	-----

HsApoA2	92	-----
HsApoA4	314	-----
HsApoA5	275	-----
HsApoB48	1374	SGGNTSTDHFSLRARYHMKADSVVDLLSYNVQGSGETTYDHKNTFTLSCDGLRHKFLDSNIKFSHVEKL
HsApoB52	1397	FTTNGEHTSKATLELSPWQMSALVQVHASQPSSFHDFPDLGQEVNANTKNQKIRWKNEVRIHSGSFQS
HsApoC1	109	-----
HsApoC2	102	-----
HsApoC3	88	-----
HsApoC4	128	-----
HsApoD	194	-----
HsApoE2	261	-----
HsApoF	257	-----
HsApoH	264	-----
HsApoJ	359	-----
HsApoL1	319	-----
HsApoL2	252	-----
HsApoL3	252	-----
HsApoL4	272	-----
HsApoOL(2)	271	-----
HsApoL6	213	-----
HsApoM	161	-----
HsApoO	189	-----
HsApoOL	201	-----
HsMTTP	694	-----
DmCG31659	183	-----
DmMtp	677	-----
DmCvD	846	LNLDHEINREQGFLIYIPFSSELHLNESGSKRRYSFSRPQNLTSGLSFKSRAVTK-----
DmGlaz	164	-----
DmFabp	116	-----
DmApoLTPII	539	-----
DmApoLTPI	2238	TNFNSDLSPQWLGGNYDQQPKIIHSNLQWKAEPHHRGDREHRTIALTVAHPLLEKDINCKATYYRGLRDL
DmNlaz	217	-----
DmApoLII	490	-----
DmApoLI	1555	YITTVKSAGLQFYQINSNAAVDIEAHEYNI GLELNNGEIDVKAISFLNKEKFEISLSES NKHIIYIVGD
DmMICOS_A	163	-----
Cel MICOS	165	-----
Cel Vit_2	893	EQGVKSVQSVRAYTPIKIQA VAGMKRN-FEIVYKVVVPENQKSIVSLTTRPVVFLR-----
Cel Vit_4	890	EQGVKSLQSARLHTPLRFESTVELKKNTLEITHKFVVVPENKKT TVSVHTRPVAFIR-----
Cel Vit_5	890	EQGVKSLQSARLHTPLRFESTVELKKNTLEITHKFVVVPENKKT TVSVHTRPVAFIR-----
Cel ApoL_1	187	-----
Cel MTTP	715	-----
Cel Vit_6	928	EVGTFKLHQAVLNTFVDTEIRMNWEDK-VVIRAIYNTPSEEKRIAMIQSRPVTFTTR-----
Cel Vit_3	890	EQGVKSLQSARLHTPLRFESTVELKKNTLEITHKFVVVPENKKT TVSVHTRPVAFIR-----
Cel Vit-1	895	EQGVKSVQSVRAYTPIKIQA VAGMKRN-FEIVYKVVVPENQKSIIISLTTRPVVFLR-----
Cel_Apo_L3_Like	205	-----
HsApoA1	130	-----
HsApoA2	92	-----
HsApoA4	314	-----
HsApoA5	275	-----
HsApoB48	1444	GNNPVSKGLLIFDASSSWGPMQMSASVHLD SKKKQH L FVKEVKIDGQFRVSSFYAKGT YGLSCQRDPNTGR
HsApoB52	1467	QVELSNDQEKALHD IAGSLEGLHRLFKNI ILPVYDKSLWDFLKL DVTTSIGRRQHLRVSTAFVYTKPNPG
HsApoC1	109	-----
HsApoC2	102	-----
HsApoC3	88	-----
HsApoC4	128	-----
HsApoD	194	-----
HsApoE2	261	-----
HsApoF	257	-----
HsApoH	264	-----
HsApoJ	359	-----
HsApoL1	319	-----
HsApoL2	252	-----
HsApoL3	252	-----
HsApoL4	272	-----
HsApoOL(2)	271	-----
HsApoL6	213	-----
HsApoM	161	-----
HsApoO	189	-----
HsApoOL	201	-----
HsMTTP	694	-----
DmCG31659	183	-----
DmMtp	677	-----
DmCvD	902	TRGLITKTAAPFEEIMVPEGRNDVVQLFSYPM TDLGVRLSMTTNLNELIKYRGMLLKSEFTENGFSGNM
DmGlaz	164	-----
DmFabp	116	-----
DmApoLTPII	539	-----
DmApoLTPI	2308	LRTHLTIDYSEYPDQLIELGAQLTD RYSELGHTNYTFHVYKGH IASELDVQLNGTLAAMNSYKTESTAH
DmNlaz	217	-----
DmApoLII	490	-----
DmApoLI	1625	FSKQNHYAKLNTKVQILDKNPIEITSEVQPN SAKIILKRQDFIDGTAEVKLGKEFKVDVIGSGKQLFNGR
DmMICOS_A	163	-----
Cel MICOS	165	-----
Cel Vit_2	948	FPGFSKFEYIEAERTVVVPQWQQKTQEIEKVFNF LGLLEVSTRGNILNQHTLENWLLAEQDFEVSVENKN
Cel Vit_4	946	VPKNQDSEYVEAEKTI SHSQYQMSTEEIDRQYETFGLRINAQGNVLSQWTLPMVLMTEQDFEFTLENKN
Cel Vit_5	946	VPKNQDSEYVEAEKTI SHSQYQMSTEEIDRQYETFGLRINAQGNVLSQWTLPMVLMTEQDFEFTLENKN
Cel ApoL_1	187	-----
Cel MTTP	715	-----
Cel Vit_6	983	TVAPDARQYPEPIEMTYMLPAHKQLSQSLDREY PQ--IRVQGT LNRPTSVRIPQWIV---DSNVEVYYPK
Cel Vit_3	946	VPKNQDSEYVETEKTISHSQYQMSTEEIDRQYETFGLRINAQGNVLSQWTLPMVLMTEQDFEFTLENKN
Cel Vit-1	950	FPGFSKFEYIEAERTVVVPQWQQKTQEIEKVFNF LGLLEVSTRGNILNQHTLENWLLAEQDFEVSVENKY
Cel_Apo_L3_Like	205	-----

HsApoA2	92	-----
HsApoA4	314	-----
HsApoA5	275	-----
HsApoB48	1514	LNGESNLRFNSSYLQGTNQITGRYEDGTLSTSTSDLSQGIKNTASLKYENYELTLKSDTNGKYKNFAT
HsApoB52	1537	YSFSIPVKVLADKFIIPGLKLNDLSNVLVMPFTFHVPTDLQVPSCKLDFREIQIYKKLRTSSFALNLP
HsApoC1	109	-----
HsApoC2	102	-----
HsApoC3	88	-----
HsApoC4	128	-----
HsApoD	194	-----MEKVKS-----
HsApoE2	261	-----EEQAQQ-----
HsApoF	257	-----
HsApoH	264	-----KVPVKK-----
HsApoJ	359	-----
HsApoL1	319	-----
HsApoL2	252	-----GGEQVE-----
HsApoL3	252	-----
HsApoL4	272	-----
HsApoOL(2)	271	-----TARGVQ-----
HsApoL6	213	-----SRVQVQ-----
HsApoM	161	-----
HsApoO	189	-----
HsApoOL	201	-----
HsMTTP	694	-----
DmCG31659	183	-----
DmMtp	677	-----DEFSED-----
DmCvd	972	VVNALMYIFGFTQLSSIHGLHDRNFTMLMYNEKNTRIEGNFCAEDVLKT-----
DmGlaz	164	-----
DmFabb	116	-----
DmApoLTPII	539	-----
DmApoLTPI	2378	YKRDIFPARYGKFLALLDVNKRELEVERQSPFHAVRLHLLPTIRYPIYGLNATIWDTPDNTNHSGYIYMDI
DmNlaz	217	-----
DmApoLII	490	-----STGRSN-----
DmApoLI	1695	VALDATNFLQTNFYINEDHLNGFWHIVSEINKDSEYISENIKERLKKSRQVTDKIVKLAKAEPDFSKL
DmMICOS_A	163	-----EENCRV-----
Cel MICOS	165	-----
Cel Vit_2	1018	RPAEFTARLTGVQLEKTELSQIKYNKIFEKE-----FELEQE-NTESRR-----
Cel Vit_4	1016	RPVEFTARVTIGNLEKTDLSEIKFDKIFEKE-----FDLENN-ESENRR-----
Cel Vit_5	1016	RPVEFTARVTIGNLEKTDLSEIKFDKIFEKE-----FDLENN-ESENRR-----
Cel ApoL_1	187	-----AASSMG-----
Cel MTTP	715	-----STDLLS-----
Cel Vit_6	1048	NVEQYEAIFELNLYNNYKMEK-NYEKVKKHNGRRYLEAEPEYDEEEHR-----
Cel Vit_3	1016	RPVEFTARVTIGNLEKTDLSEIKFDKIFEKE-----FDLENN-ESENRR-----
Cel Vit-1	1020	RPAEFTARLTGVQLEKTELSQIKYNKIFEKE-----FELEQE-NTESRR-----
Cel_Apo_L3_Like	205	-----AITSMG-----
HsApoA1	130	-----
HsApoA2	92	-----
HsApoA4	314	-----NKALVQOMEQLRQKLGPAGDVEGHLSFLE-----
HsApoA5	275	-----MLSEEVQRQLQAFRQDTYLQIAAFTRAID-----
HsApoB48	1584	SNKMDMTFSKQNALLRSEYQADYESLRFFSLLSGSLNSHGLELNADILGTDKINSKAHKATLRIGQDGIS
HsApoB52	1607	PEVKFPEVDVLTYSQPEDSLIPFFFEITVPESQLTVSQFTLPKSVSDGIAALDLNAVANKIADFELPTII
HsApoC1	109	-----
HsApoC2	102	-----
HsApoC3	88	-----
HsApoC4	128	-----
HsApoD	200	-----
HsApoE2	267	-----IRLQAEAFQARLKSWE-----
HsApoF	257	-----QYYQDQKDANISQPETTK EGLRAI-----
HsApoH	270	-----ATVVYQGERVKIQEKFKNGMLHGDKVS-----
HsApoJ	359	-----EQLNEQFNWVSRLANLTQGEDQYYLRVTTVASHTSDSDVP-----
HsApoL1	319	-----RVNEPSILEMSRGVKLTDVAPVSFFLV-----
HsApoL2	258	-----RVVEGPAQAMSRGTMIVGAAATGGILL-----
HsApoL3	252	-----RTIAGTTRAVSRGARILSATTSIGIFLA-----
HsApoL4	272	-----RTRGAPTRIVRKVARNLGKATSGVLVV-----
HsApoOL(2)	277	-----RAFEGTTLAMTNGAWMGAAGAGFLLM-----
HsApoL6	219	-----KAFAGTTLAMTKNARVLGGVMSAFSLG-----
HsApoM	161	-----
HsApoO	189	-----
HsApoOL	201	-----GSSSEIEVPAKTTTHVLKHSVLP-----
HsMTTP	694	-----ILFDVQLRPVTFPFGYSDLMSKMLSASGDPI-----
DmCG31659	183	-----
DmMtp	683	-----EAVTAGMEISVQGAQLRPLVFFSGQTELMGHVWGGASDST-----
DmCvd	1020	-----SDMKGKQIGLTLEHTDHMNENHAADALHRWNIITLDVLASTKSNWFKLGTGVQRNSKDEDDW-----
DmGlaz	164	-----HSDQIWIILGRD-----
DmFabb	116	-----
DmApoLTPII	539	-----SAFAEQLQWIIREDEAPVDIRLHGILAFRRVDCARHRSYFLDNYGNYTLNSELRIYSYLQAMRC-
DmApoLTPI	2448	LERYARMDFNLTEDASQNLQMGVYIPDTRSAFLDIWRNYEEIRVIDVSSYLKMNHSRLITGRFHWRPISIR
DmNlaz	217	-----
DmApoLII	496	-----RIRVAALHAFSKVKCEETLQSKSLELLKNRNDESELRIEAYLSAISC-----
DmApoLI	1765	QGKLLDYKNDIVQLEADQSIAPIIDGIRTLFKKIAGIVDDINKAISEILEKAQKSIVDIYDKLQALWKD
DmMICOS_A	169	-----VLYEGRKIFAVAYNFIKGVKPGEDVPV-----
Cel MICOS	165	-----
Cel Vit_2	1060	-----EYFNKMVKNIQKEQGQYKSVISLKLEAPRDYTMNTELTVCQVQVRCQWEVEIRRSPILEETKEW
Cel Vit_4	1058	-----QYFHKMIREIQSEQGFKNLITLKLAPQQMYWNTLRTVCDKWIRMCQVEMDARRSPIEHENKEW
Cel Vit_5	1058	-----QYFHKMIREIQSEQGFKNLITLKLAPQQMYWNTLRTVCDKWIRMCQVEMDARRSPMEHENKEW
Cel ApoL_1	193	-----HLTNALMKGMLQSVAAIGIV-----
Cel MTTP	721	-----TVWEADGRTHKAFEGHVPVRDRLSVPLL-----
Cel Vit_6	1095	-----EQITKKFEWLQNEKVYQHVAKFEIKPE-----VVKMEVEAVCNNDHFHCKTQI-----RGE
Cel Vit_3	1058	-----QYFHKMIREIQSEQGFKNLITLKLAPQQMYWNTLRTVCDKWIRMCQVEMDARRSPMEHENKEW
Cel Vit-1	1062	-----EYFTKMVKSIQKEQGQYKSVLSRLAPRDYTMNTEVTVTCQVQVRCQWEVEIRRSPILEETKEW
Cel_Apo_L3_Like	211	-----RLSSSLVKGLHSAVIGIV-----

HsApoA2	92	-----	-----
HsApoA4	344	-----	-----KDLRDKVNSFFSTFKEKESQD
HsApoA5	304	-----	-----QETEEVQQQLAPPPPGHSAFA
HsApoB48	1654	TSATTNLKCSLLVLENELNAELGLSG	-----ASMKLTTNGRFREHNAKFSLD
HsApoB52	1677	VPEQTIEIPSIKFSVPAGIVIPSFQALTARFEVDSPVYNATWSASLKNKADYVETVLDSTCSSTVQFLEY	-----
HsApoC1	109	-----	-----LDLKGVVFRDISESEGETQD-
HsApoC2	102	-----	-----
HsApoC3	88	-----	-----PEVRPTS AVAAE-----
HsApoC4	128	-----	-----
HsApoD	200	-----	-----PELQAEAKSYFEKSKEQLTPL
HsApoE2	284	-----	-----PLVEDMQRWAGLVEKVQAAV
HsApoF	281	-----	-----SDVSDLEETTTLASFISEVVS
HsApoH	297	-----	-----FFCKNKEKKCSYTEDAQCIDG
HsApoJ	399	-----	-----SGVTEVVVKLFDSDPITVTVP
HsApoL1	346	-----	-----LDVVYLVEYESKHLHEGAKSET
HsApoL2	285	-----	-----LDVVSLAYESKHLLEGAKSES
HsApoL3	279	-----	-----LDVVNLVYESKHLHEGAKSAS
HsApoL4	299	-----	-----LDVVNLVQDSLDLHKGEKSES
HsApoL(2)	304	-----	-----KDMSSFLQSWKHLEDGARTET
HsApoL6	246	-----	-----YDLATLSKEWKHLKEGARTKF
HsApoM	161	-----	-----KSLTSCLDKSAFLLTTPRNQEA
HsApoO	189	-----	-----
HsApoOL	224	-----	-----TELSSEAKTKSESTSGATQFM
HsMTTP	725	-----	-----SVVKGLILLIDHSQELQLQSG
DmCG31659	183	-----	-----
DmMtp	724	-----	-----PAYQATTLSQDNEHYIILTSG
DmCvD	1082	-----	-----KACTKLTYEPLVFTKRHTLN
DmGlaz	175	-----	-----RDFEVDIRSKVYDVLRKRLSLD
DmFabp	116	-----	-----PHLTPSQHGSLRLRVPCQPVP
DmApoLTPII	603	-----	-----PDYISVGVIKSILEHEEINQV
DmApoLTPI	2518	QEVREKIQAVGKSVY	-----SSFSEGIDFWIKSIYTTETTES
DmNlaz	217	-----	-----PNAIEKA-EWLR-
DmApoLII	543	-----	-----PNAEVANQISEIVNSETVNVQV
DmApoLI	1835	SLLKAWEDFIITVQKLSTLKTETFIKICTQSFKDLL	-----SALEKYGPAKKNYGAIGEIV
DmMICOS_A	196	-----	-----VFPPTSLEDLKYMASD
Cel MICOS	165	-----	-----VDVAKTGRAHAETWYSFQES
Cel_Vit_2	1126	TLRSQLLVVR	-----PEMPSSLRQLRDQPHREVQLS
Cel_Vit_4	1124	TLRTELLAAR	-----PQMPSSLRQLREQPHREVQLA
Cel_Vit_5	1124	TLRTELLAAR	-----PQMPSSLRQLREQPHREVQLA
Cel_ApoL_1	213	-----	-----LDGVTLAMSANTLKNSSSEL
Cel MTTP	750	-----	-----SGLTLDVDSVGAISMRVLASA
Cel_Vit_6	1147	ELKATIQYVY	-----PQTPRTVEELKEQKYRQLVVM
Cel_Vit_3	1124	TLRTELLAAR	-----PQMPSSLRQLREQPHREVQLA
Cel_Vit-1	1128	TLRSQLLVVR	-----PEMPSSLRQLHDQPHREVQLS
Cel_Apo_L3_Like	231	-----	-----LDSVTLALSAKTLGEGSVSEL
HsApoA1	150	-----	-----
HsApoA2	92	-----	-----
HsApoA4	366	KTLSLPELEQQEQEQEQEQEQEQE	-----
HsApoA5	326	PEFQQTDSGKVLKQLARLDD	-----
HsApoB48	1701	GKAALTELSLGSAYQAMILGVDSKNIFNFKVSQEBGLKLSNDMMGSYAEMKFDHTNSLNIAGLSLDFSSKL	-----
HsApoB52	1747	ELNVLGTHKIEDGTLASKTKGTFAHRDFS AEYEEDGKYEGLQEWEGKAHLNIKSPAFTDLHLRYQRDKKG	-----
HsApoC1	129	-----	-----
HsApoC2	102	-----	-----
HsApoC3	100	-----	-----
HsApoC4	128	-----	-----
HsApoD	222	IKKAGTELVNFLSYF	-----
HsApoE2	306	GT	-----
HsApoF	303	SAPYWGWAIIKSYD	-----
HsApoH	319	TIEVPKCFKEHSSLA	-----
HsApoJ	421	VEVSRKNPKFMETVAEKAL	-----
HsApoL1	368	AEELKKVAQE	-----
HsApoL2	307	AEELKKRAQE	-----
HsApoL3	301	AEELRRQAQE	-----
HsApoL4	321	AELLRQWAQE	-----
HsApoL(2)	326	AEELRALAKK	-----
HsApoL6	268	AEELRAKA	-----
HsApoM	183	CELSNNW	-----
HsApoO	189	-----	-----
HsApoOL	246	PDPKLMHDHGQSHPE	-----
HsMTTP	747	LKANIEVQGGLAIDISGA	-----
DmCG31659	183	-----	-----
DmMtp	746	ATLHWRVLGARSVDLNGKVGFS	-----
DmCvD	1104	GDVVFGGLATEESECEKGSTVQFAARAGPSEHARAFLRSDKISLTDTFDPCKEVLKFSPIPTSRYCKRSN	-----
DmGlaz	197	PERLIIS	-----
DmFabp	138	PTSVDGARS	-----
DmApoLTPII	625	GSFVWSHLTNLAKSNSPVRIEAQGLL	-----
DmApoLTPI	2554	MGVVWNTAKEYNRDFIDDIGQLSVLEEDLADLRLFVNQSYEANDFYIKNVVNFTLTILDELAIRDHIESL	-----
DmNlaz	229	-----	-----
DmApoLII	565	GGFISSNLKAIRDSTDVS	-----
DmApoLI	1892	KPINDAAQEVIKIVVNAEAGVTHEFKQYVASLPSFESIRNEFNNDKVKVLKLFKATELTNSLFDQINILP	-----
DmMICOS_A	212	-----	-----
Cel MICOS	187	PTPSAI	-----
Cel_Vit_2	1157	LTSTWGSQKKSEVTVNAQLQSQKEQKKYERNMDRQFNGMPEYELLIKAARLNQINAVA EYKLTRETEQVL	-----
Cel_Vit_4	1155	LNKKGSSKKSEITFNAQLEQSTEQKKFLRNIEREYKGIPEYELLIKAARLNQVNVVSEYKLTPESEYTF	-----
Cel_Vit_5	1155	FNAKWGSSKKSEITVNAQLEQSTEQKKFIRNIEREYKGIPEYELLIKAARLNQVNVVSEYKLTPESEYTF	-----
Cel_ApoL_1	235	AGKIREASGKMERMRHNVVTFN	-----
Cel MTTP	772	EVS LWNQRSNAKAEAYTSGLH	-----
Cel_Vit_6	1178	GEMNYG---ENTI HININGQQSQEQKKFVKQIEQA---PEHETLLEASRLDQYQTVVVEYEFEPKPAQYF	-----
Cel_Vit_3	1155	LNKKGSSKKSEITFNAQLEQSTEQKKFLRNIEREYKGIPEYELLIKAARLNQVNVVSEYKLTPESEYTF	-----
Cel_Vit-1	1159	LTSTWGSQKKSEVTVNAQLQSQKEQKKYERNMDRHFNGMPEYELLIKAARLNQINAVA EYKLTRETEQVL	-----
Cel_Apo_L3_Like	253	GSSILEASSKMEMMRQKVVKHF	-----

HsApoA2	92	-----
HsApoA4	386	-----
HsApoA5	346	-----
HsApoB48	1771	DNIYSSDKFYKQTVNLQLQPYSLVTTLNNSDLKYNALDLTNNGLRLEPLKLHVAGNLKGAYQNNKIKHIY
HsApoB52	1817	ISTSAASPAVGTVGMDMEDDDDFSKWNFYYSPOSSPDKKLTIFKTELVRVRESDEETQIKVNWEEEAASGL
HsApoC1	129	-----
HsApoC2	102	-----
HsApoC3	100	-----
HsApoC4	128	-----
HsApoD	236	-----
HsApoE2	307	-----
HsApoF	316	-----
HsApoH	333	-----
HsApoJ	439	-----
HsApoL1	377	-----
HsApoL2	316	-----
HsApoL3	310	-----
HsApoL4	330	-----
HsApoOL(2)	335	-----
HsApoL6	275	-----
HsApoM	189	-----
HsApoO	189	-----
HsApoOL	259	-----
HsMTTP	764	-----
DmCG31659	183	-----
DmMtp	767	-----
DmCvD	1174	FENFTSITQYDMDLKFDNMPAWFELWSNRDLHLSALSADKVDLSLHMSQEBINISMQTPQDQFRLAVEVNG
DmGlaz	203	-----
DmFabp	149	-----
DmApoLTPII	650	-----
DmApoLTPI	2624	PKIFSELWQAMGDSGKALRNSIVWLIETIKTTYNNLLDAVARFFHGESLVYISGLEKGIKAYDSFIKDL
DmNlaz	229	-----
DmApoLII	582	-----
DmApoLI	1962	QTPETSEFLQKLHDYLIAKLKQEHIDNEKYIEELGQLLIKAVRSIWVSIRSTYPGSSDHVIDFQSWIGSL
DmMICOS_A	212	-----
Cel MICOS	192	-----
Cel_Vit_2	1227	ARYFDLVKTY---NY-WT--VSSRPENNENDRVVVQLTVEPMSRQYVNIITMQSPMERIELKNVQVPRVYL
Cel_Vit_4	1225	SRIFDLIKAY---NF-WT--VSEKRVQNEEDRRVVLQLSVEPLSRQYMNMTIQTPQEVEVELKNVRIIPRVVL
Cel_Vit_5	1225	SRIFDLIKAY---NF-WT--VSEKRVQNEEDRRVVLQLSVEPLSRQYMNMTIQTPQEVEVELKNVRIIPRVVL
Cel_ApoL_1	256	-----
Cel MTTP	793	-----
Cel_Vit_6	1241	ARYWNMVQAYLRTQYPWTSRIETREEPSRKNMIRATINVEPRQLTVNMTIETPMETTTLERVELP-FRL
Cel_Vit_3	1225	SRIFDLIKAY---NF-WT--VSEKRVQNEEDRRVVLQLSVEPLSRQYMNMTIQTPQEVEVELKNVRIIPRVVL
Cel_Vit-1	1229	ARYFDLVKAY---NY-WT--VSSRPENNENDRVVVQLTVEPMSRQYVNIITMQSPIERVELKNVQVPRVYL
Cel_Apo_L3_Like	274	-----
HsApoA1	150	-----YTKKLNTQ-----
HsApoA2	92	-----LGTPATQG-----
HsApoA4	386	-----QVQMLAPLES-----
HsApoA5	346	-----LWEDITHSLH-----
HsApoB48	1841	AISSAALSASYKADTVAKVQGVFESHRLNTDIA-----
HsApoB52	1887	LTSKLDNVPKATGVLYDY-----VNKYHWEHTG-----
HsApoC1	129	-----
HsApoC2	102	-----
HsApoC3	100	-----
HsApoC4	128	-----
HsApoD	236	-----VELGTQPATQ-----
HsApoE2	307	-----SAAPVPSDNH-----
HsApoF	316	-----LDPGAGSLEI-----
HsApoH	333	-----FWKTDASDVK-----
HsApoJ	439	-----QEYRKKHREE-----
HsApoL1	377	-----LEEKLNLINN-----
HsApoL2	316	-----LEGKLNFLTQ-----
HsApoL3	310	-----LEENLMELTQ-----
HsApoL4	330	-----LEENLNELTH-----
HsApoOL(2)	335	-----LEQELDRLTQ-----
HsApoL6	275	-----LE-----LERKLTTELQ-----
HsApoM	189	-----
HsApoO	189	-----NVKNSPGTKN-----
HsApoOL	259	-----DIDMYSTRSE-----
HsMTTP	764	-----MEFSLWYRES-----
DmCG31659	183	-----PQESCPYDTS-----
DmMtp	767	-----LWNRNAQTEI-----
DmCvD	1244	VKWRFHQIPFFYKLDKFD-----ASHELTFDSG-----
DmGlaz	203	-----KNKQCPEALI-----
DmFabp	149	-----CGQRPGGPGS-----
DmApoLTPII	650	-----LNDELSERFK-----
DmApoLTPI	2694	HIKFIKIYEN-----LWHKTTWTLAENHKKAVLKRFEPLFKMISFIETTAWNLSKEVFDFIY
DmNlaz	229	-----LYERLYDIFM-----
DmApoLII	582	-----RDQKYHLAN-----
DmApoLI	2032	THSFDSLAVLPSILSFRSSILNCLLNENWVVFNNKKLLYSWIFFNDFELRGHVVDGKHIFTFDGLNFAYP
DmMICOS_A	212	-----LYDEAKDLIF-----
Cel MICOS	192	-----VKTNLSPPKS-----
Cel_Vit_2	1291	PSI-----AQRS-----VKHQLTEASG-----
Cel_Vit_4	1289	PTI-----ARRA-----MFQQTWEKTG-----
Cel_Vit_5	1289	PTI-----ARSA-----MFQQTWEKTG-----
Cel_ApoL_1	256	-----LNYDAWNSDV-----
Cel MTTP	793	-----LTASLYHHSE-----
Cel_Vit_6	1310	PTAQIHYQPRNSRYEQKP-----VMEKIAHHAS-----
Cel_Vit_3	1289	PTI-----ARRA-----MFQQTWEKTG-----
Cel_Vit-1	1293	PSI-----AQRS-----VKHLLNEASG-----
Cel_Apo_L3_Like	274	-----LNEDVWKDDD-----

HsApoA2	101	-----
HsApoA4	396	-----
HsApoA5	356	-----
HsApoB48	1873	-----
HsApoB52	1914	-----
HsApoC1	129	-----
HsApoC2	102	-----
HsApoC3	100	-----
HsApoC4	128	-----
HsApoD	246	-----
HsApoE2	317	-----
HsApoF	326	-----
HsApoH	343	-----
HsApoJ	449	-----
HsApoL1	387	-----
HsApoL2	326	-----
HsApoL3	320	-----
HsApoL4	340	-----
HsApoOL(2)	345	-----
HsApoL6	287	-----
HsApoM	189	-----
HsApoO	199	-----
HsApoOL	269	-----
HsMTTP	774	-----
DmCG31659	193	-----
DmMtp	777	-----
DmCvD	1272	-----
DmGlaz	213	-----
DmFabp	159	-----
DmApoLTPII	660	-----
DmApoLTPI	2751	KRTNELAESPYFNKVSSFTADAERLYRDFKANDAITNIKKYSTIAWNFVKEKYFKLVPFGAELNEVLTEI
DmNlaz	239	-----
DmApoLII	592	-----
DmApoLI	2102	GNCKYILAQDSVDNNFTIIGQ----
DmMICOS_A	222	-----
Cel_MICOS	202	-----
Cel_Vit_2	1307	-----
Cel_Vit_4	1305	-----
Cel_Vit_5	1305	-----
Cel_ApoL_1	266	-----
Cel_MTTP	803	-----
Cel_Vit_6	1337	-----
Cel_Vit_3	1305	-----
Cel_Vit-1	1309	-----
Cel_Apo_L3_Like	284	-----
HsApoA1	158	-----
HsApoA2	101	-----
HsApoA4	396	-----
HsApoA5	356	-----
HsApoB48	1873	-----
HsApoB52	1914	-----
HsApoC1	129	-----
HsApoC2	102	-----
HsApoC3	100	-----
HsApoC4	128	-----
HsApoD	246	-----
HsApoE2	317	-----
HsApoF	326	-----
HsApoH	343	-----
HsApoJ	449	-----
HsApoL1	387	-----
HsApoL2	326	-----
HsApoL3	320	-----
HsApoL4	340	-----
HsApoOL(2)	345	-----
HsApoL6	287	-----
HsApoM	189	-----
HsApoO	199	-----
HsApoOL	269	-----
HsMTTP	774	-----
DmCG31659	193	-----
DmMtp	777	-----
DmCvD	1272	-----
DmGlaz	213	-----
DmFabp	159	-----
DmApoLTPII	660	-----
DmApoLTPI	2821	WQEIKELEKIDQVQIMVQKYYEVMKVDWVADELQLEHRLHQVYGLVRNKFERNYAMNALETADMYREAKT
DmNlaz	239	-----
DmApoLII	592	-----
DmApoLI	2122	-----
DmMICOS_A	222	-----
Cel_MICOS	202	-----
Cel_Vit_2	1307	-----
Cel_Vit_4	1305	-----
Cel_Vit_5	1305	-----
Cel_ApoL_1	266	-----
Cel_MTTP	803	-----
Cel_Vit_6	1337	-----
Cel_Vit_3	1305	-----
Cel_Vit-1	1309	-----
Cel_Apo_L3_Like	284	-----

HsApoA2	101	-----
HsApoA4	396	-----
HsApoA5	356	-----
HsApoB48	1873	-----
HsApoB52	1914	-----
HsApoC1	129	-----
HsApoC2	102	-----
HsApoC3	100	-----
HsApoC4	128	-----
HsApoD	246	-----
HsApoE2	317	-----
HsApoF	326	-----
HsApoH	343	-----
HsApoJ	449	-----
HsApoL1	387	-----
HsApoL2	326	-----
HsApoL3	320	-----
HsApoL4	340	-----
HsApoOL(2)	345	-----
HsApoL6	287	-----
HsApoM	189	-----
HsApoO	199	-----
HsApoOL	269	-----
HsMTTP	774	-----
DmCG31659	193	-----
DmMtp	777	-----
DmCvD	1272	-----
DmGlaz	213	-----
DmFabp	159	-----
DmApoLTPII	660	-----
DmApoLTPI	2891	KFVFDPEVGIIIDLEQKLPMSSHAFNETPRFEEIPEYQVLAKAQSFFSETNSSIVMKLYNMRTHLDPKTL
DmNlaz	239	-----
DmApoLII	592	-----
DmApoLI	2122	-----
DmMICOS_A	222	-----
Cel_MICOS	202	-----
Cel_Vit_2	1307	-----
Cel_Vit_4	1305	-----
Cel_Vit_5	1305	-----
Cel_ApoL_1	266	-----
Cel_MTTP	803	-----
Cel_Vit_6	1337	-----
Cel_Vit_3	1305	-----
Cel_Vit-1	1309	-----
Cel_Apo_L3_Like	284	-----
HsApoA1	158	-----
HsApoA2	101	-----
HsApoA4	396	-----
HsApoA5	356	-----
HsApoB48	1873	-----
HsApoB52	1914	-----LT
HsApoC1	129	-----
HsApoC2	102	-----
HsApoC3	100	-----
HsApoC4	128	-----
HsApoD	246	-----
HsApoE2	317	-----
HsApoF	326	-----
HsApoH	343	-----
HsApoJ	449	-----
HsApoL1	387	-----
HsApoL2	326	-----
HsApoL3	320	-----
HsApoL4	340	-----
HsApoOL(2)	345	-----
HsApoL6	287	-----
HsApoM	189	-----
HsApoO	199	-----
HsApoOL	269	-----
HsMTTP	774	-----
DmCG31659	193	-----
DmMtp	777	-----
DmCvD	1272	-----
DmGlaz	213	-----
DmFabp	159	-----
DmApoLTPII	660	-----
DmApoLTPI	2961	PPYYSRALLIDSRHYMTFDQRYVGLNLFDELGNRSTSQCSYLLAHDFFKRNFTLLLEPASKSLAGQGL
DmNlaz	239	-----
DmApoLII	592	-----
DmApoLI	2122	-----LTNGKLKSITLIDREGSYFEVADNLALKLNGNLVEYPQHLSGLHAW
DmMICOS_A	222	-----
Cel_MICOS	202	-----
Cel_Vit_2	1307	-----
Cel_Vit_4	1305	-----
Cel_Vit_5	1305	-----
Cel_ApoL_1	266	-----
Cel_MTTP	803	-----
Cel_Vit_6	1337	-----
Cel_Vit_3	1305	-----
Cel_Vit-1	1309	-----
Cel_Apo_L3_Like	284	-----

HsApoA2	101	-----
HsApoA4	396	-----
HsApoA5	356	-----
HsApoB48	1873	-----
HsApoB52	1917	LREVSSKLRRNLQNNAEWVYQGAIRQIDDDVRFQKAASGTTGTQYQEWKDKAQNLYQELLTQEGQASFG
HsApoC1	129	-----
HsApoC2	102	-----
HsApoC3	100	-----
HsApoC4	128	-----
HsApoD	246	-----
HsApoE2	317	-----
HsApoF	326	-----
HsApoH	343	-----PC-----
HsApoJ	449	-----
HsApoL1	387	-----
HsApoL2	326	-----IHEMLQ-----
HsApoL3	320	-----
HsApoL4	340	-----
HsApoOL(2)	345	-----HHRHLP-----
HsApoL6	287	-----LYKSLQ-----
HsApoM	189	-----
HsApoO	199	-----
HsApoOL	269	-----
HsMTTP	774	-----
DmCG31659	193	-----
DmMtp	777	-----QQNTGS-----
DmCvD	1272	-----LKRSCS-----
DmGlaz	213	-----
DmFabp	159	-----
DmApoLTPII	660	-----
DmApoLTPI	3031	TRKLSFIANGQLIEIDLETDHISINGNPQPIPLKLGDVNIHRDLVLSITSDTEFSLHCNVQFDLCWFE
DmNlaz	239	-----NFLSY-----
DmApoLII	592	-----
DmApoLI	2169	RRFYTIHLYSEYGVGIVCTSDLKVCHININGFYTSKTRGLLGNGNAEPYDDFLIDGTLAENSAALGNDY
DmMICOS_A	222	-----PKKKP-----
Cel MICOS	202	-----
Cel_Vit_2	1307	-----SVCK-----
Cel_Vit_4	1305	-----ATCK-----
Cel_Vit_5	1305	-----ATCK-----
Cel_ApoL_1	266	-----
Cel MTTP	803	-----PVRHVE-----
Cel_Vit_6	1337	-----KQANCV-----
Cel_Vit_3	1305	-----ATCK-----
Cel_Vit-1	1309	-----SVCK-----
Cel_Apo_L3_Like	284	-----
HsApoA1	158	-----
HsApoA2	101	-----
HsApoA4	396	-----
HsApoA5	356	-----DQGHSHLGDPT-----
HsApoB48	1873	GLASAIMSTNYSNDSLHFSNVFRSVMAPFTMTIDAHTN
HsApoB52	1987	LKDNVFDGLVRVTQEFHMKVKHLIDSLIDFLNFPFQFPQKPGIYTREELCTMFIREVGTVLSQLVSKVH
HsApoC1	129	-----
HsApoC2	102	-----
HsApoC3	100	-----
HsApoC4	128	-----
HsApoD	246	-----
HsApoE2	317	-----
HsApoF	326	-----
HsApoH	345	-----
HsApoJ	449	-----
HsApoL1	387	-----NYKILQADQELP-----
HsApoL2	332	-----PGQDQV-----
HsApoL3	320	-----IYQRLNPCHTHQ-----
HsApoL4	340	-----IHQSLKAG-----
HsApoOL(2)	351	QKASQTCSSSRGRAVRGSRVVKPEGSRSPLPWPVVEHQ
HsApoL6	293	QKVRSRARGVGKDLTGTCETEAYWKELREHVMMW
HsApoM	189	-----
HsApoO	199	-----
HsApoOL	269	-----
HsMTTP	774	-----KTRVKNRVTVVITTDITVDSSFV
DmCG31659	193	-----
DmMtp	783	-----AVLGHLAVGFTYAKLVQDFSITHEP
DmCvD	1278	-----VINGIVNTFDDYLINLREIAVRPDCLTLIVADCSPLPQIAVFTVP
DmGlaz	213	-----
DmFabp	159	-----
DmApoLTPII	660	-----MDIRKFSRNYEHSLLFFDEYNFGTTTDANVIFG
DmApoLTPI	3101	VSGWYFGRTAGLLGTLNNEPYDEYTMSSGVISNETQLFTDSWSLKQCRQNKLAQTQEVSEVSDACTSFF
DmNlaz	244	-----
DmApoLII	592	-----IRVTKTFPVYRRYSFNNEVSYKLE
DmApoLI	2239	GVGKCTAIEFDNNQFKSSKRQEMCSELFGIESTLAFNFTILDSRPYRKACDIALAKVAEKEKEATACTFA
DmMICOS_A	227	-----
Cel MICOS	202	-----
Cel_Vit_2	1311	-----VQKNQIRTFDDVLYNTPLTTCYSLI
Cel_Vit_4	1309	-----VDQSEVSTFDNVIYRAPLTTTCYSLV
Cel_Vit_5	1309	-----VDQSEVSTFDNVIYRAPLTTTCYSLV
Cel_ApoL_1	266	-----
Cel MTTP	809	-----STISALSTFTTDTRAISETLPYDFC
Cel_Vit_6	1343	-----VKSTKINTFDQVAYRNQFTPCYSVL
Cel_Vit_3	1309	-----VGQSEVSTFDNVIYRAPLTTTCYSLV
Cel_Vit-1	1313	-----VQKNQIRTFDDVLYNTPLTTCYSLI
Cel_Apo_L3_Like	284	-----DVLSDVGSITEMVQPESPNQSLIMDP

HsApoA2	101	-----
HsApoA4	396	-----
HsApoA5	367	-----
HsApoB48	1913	GNGKLALW-----
HsApoB52	2057	NGSEILFS-----
HsApoC1	129	-----
HsApoC2	102	-----
HsApoC3	100	-----
HsApoC4	128	-----
HsApoD	246	-----
HsApoE2	317	-----
HsApoF	326	-----
HsApoH	345	-----
HsApoJ	449	-----
HsApoL1	399	-----
HsApoL2	338	-----
HsApoL3	332	-----
HsApoL4	348	-----
HsApoOL(2)	391	RLGPGVAL-----
HsApoL6	328	LWLCVCLC-----
HsApoM	189	-----
HsApoO	199	-----
HsApoOL	269	-----
HsMTTP	798	KAGLETST-----
DmCG31659	193	-----
DmMtp	809	KLSLNADL-----
DmCvD	1324	SPVQGLST-----
DmGlaz	213	-----
DmFabp	159	-----
DmApoLTPII	693	TDSYL-----
DmApoLTPI	3171	RTGILATCSAVLDPTPFYEMCMDLGMSPPIRKGHPAVKGACAAALAYIEACTALKVPMRVPSQCVCQQL
DmNlaz	244	-----
DmApoLII	618	SLGVGAST-----
DmApoLI	2309	LAYGSAVK-----
DmMICOS_A	227	-----
Cel_MICOS	202	-----
Cel_Vit_2	1337	AKDCS-----
Cel_Vit_4	1335	AKDCS-----
Cel_Vit_5	1335	AKDCS-----
Cel_ApoL_1	266	-----
Cel_MTTP	835	LRTSNSNV-----
Cel_Vit_6	1369	AKDCGSEK-----
Cel_Vit_3	1335	AKDCS-----
Cel_Vit-1	1339	AKDCS-----
Cel_Apo_L3_Like	310	HQQESSVQH-----
HsApoA1	158	-----
HsApoA2	101	-----
HsApoA4	396	-----
HsApoA5	367	-----
HsApoB48	1920	-----GEHTGQLYSKFLKAEPLAFTFSDYKGSTSHHLVSRKSISAALEHKVVSALLT
HsApoB52	2064	-----YFQDLVITLPFELRKHKLIDVISMYRELLKDLKSKEAQEVFKAIQSLKTTEVLR
HsApoC1	129	-----
HsApoC2	102	-----
HsApoC3	100	-----
HsApoC4	128	-----
HsApoD	246	-----
HsApoE2	317	-----
HsApoF	326	-----
HsApoH	345	-----
HsApoJ	449	-----
HsApoL1	399	-----
HsApoL2	338	-----
HsApoL3	332	-----
HsApoL4	348	-----
HsApoOL(2)	398	-----RTPKRTVSAPRMLGHQPAPPAPARKGRQAPGRHRQ-----
HsApoL6	335	-----VCVYVQFTT-----
HsApoM	189	-----
HsApoO	199	-----
HsApoOL	269	-----
HsMTTP	805	-----ETEAGLEFISTVQFSQYPFLVCMQMDKDEAPFRQFEKKYERLSTGRGYVSQKR
DmCG31659	193	-----
DmMtp	816	-----DFYSGIKLKMQLQRPEQLLKQTNVRSVFLQSVDRPYAKHVRSTLSHKTAGCTF
DmCvD	1331	-----NYGLRVHIGQNYFNFRARTDNSSLPTDEPVLIYLNQDQTPHNVRKKPYQWPIE
DmGlaz	213	-----
DmFabp	159	-----
DmApoLTPII	697	-----PRIASVNFTADLFGQSVNFFETARAEGLEELAANAFGPKGPLSGQLLRKKLS
DmApoLTPI	3241	SNGSYVPEGTFMELSGPEIPKSSDVVFIVEAKECNANLKTSKNIMTVVSSIEEQLQAAKITNNRYAVVAF
DmNlaz	244	-----
DmApoLII	625	-----DYQIIYSQHGFLLPRSSRINVTTEFFGTNYNVFEASVRQENVEDVLEYLGPKG
DmApoLI	2316	-----QINKWVLLPPRCIKCAGPAGQHDFGDEFVVKLPNNKVDVVFVDINVTGPVLS
DmMICOS_A	227	-----
Cel_MICOS	202	-----
Cel_Vit_2	1341	-----EEPTFAVLSSKTEKNSEEMIIKVIRGEQEIVAQLQNEEIRVKVDGKKIQSE--
Cel_Vit_4	1339	-----EQPRFAVLAKKINKNSEELLVKVVRREEEIVVKSDDKFLVKVDGKKVNPT--
Cel_Vit_5	1339	-----EQPRFAVLAKKINKNSEELLVKVVRREEEIVVKSDDKFLVKVDGKKVNPT--
Cel_ApoL_1	266	-----
Cel_MTTP	842	-----DINQKTVVQDQIGKHKKTLNRKRVHPGVTYRLDDSTIRQCNSYLEQFRLV--
Cel_Vit_6	1376	-----SEPRFVVLMMKINKKEWKNVQVYGENEIEYKTEEGLICRVNGEEIEYQPE
Cel_Vit_3	1339	-----EQPRFAVLAKKINKNSEELLVKVVRREEEIVVKSDDKFLVKVDGKKVNPT--
Cel_Vit-1	1343	-----EEPTFAVLSSKTEKNSEEMIIKVIRGEQEIVAQLQNEEIRVKVDGKKILSE--
Cel_Apo_L3_Like	318	-----

HsApoA2	101	-----
HsApoA4	396	-----
HsApoA5	367	-----
HsApoB48	1974	PAEQGTGWLKLTQFNNNEYSQDLDAYNTKDKIGVELTGRTLADLTLLDSPIKVPLLLSEPINIIDALEMR
HsApoB52	2118	NLQDLLQFIFQLIEDNIKQLKEMKFTYLINYIQDEINTIFSDYIPYVFKLLKENLCLNLHKFNEFTQNEL
HsApoC1	129	-----
HsApoC2	102	-----
HsApoC3	100	-----
HsApoC4	128	-----
HsApoD	246	-----
HsApoE2	317	-----
HsApoF	326	-----
HsApoH	345	-----
HsApoJ	449	-----
HsApoL1	399	-----
HsApoL2	338	-----
HsApoL3	332	-----
HsApoL4	348	-----
HsApoOL(2)	433	-----
HsApoL6	344	-----
HsApoM	189	-----
HsApoO	199	-----
HsApoOL	269	-----
HsMTTP	859	KESVLAGCEFPPLHQENSEMCKVVFAPQPDSTSSGWF-----
DmCG31659	193	-----
DmMtp	870	ALNQKNNECMNLIFRDLD-----
DmCvD	1385	TSDDYDFRVELNEQNILIVECTQLSSTIQFDLYNILNFEIYGvyKHQMCGLCGSKPLNRMQNYTICELEANT
DmGlaz	213	-----
DmFabb	159	-----
DmApoLTPII	751	FLNRWLGNESAEDDTLENLLSLDNLRLKW-----
DmApoLTPI	3311	GGVSPYDKARSVIYEHNEFTSKPEQLADYFGHINTGNGSSNDILMAISAAAKLNFRPGVSKTFILLSCSK
DmNlaz	244	-----
DmApoLII	679	LVNKDFDEIVKLIIEVGNNGVAAGGRARR-----
DmApoLI	2370	NLIAPAINDIRESLSRGSFSDVQGVIVFEETKRYPALLTSDGGKINYKGNVADVKLAKIKSFCDCNCVEQ
DmMICOS_A	227	-----
Cel MICOS	202	-----
Cel_Vit_2	1392	---DYSAYQIERLGESAIIVIELPEGEVRFDDGYTIKTQLPSYSRKNQLCGLCGNNDDESTNEFYTSDNDET
Cel_Vit_4	1390	---ELEQYNIIEILGDNLIVIRLPHGEVRFDDGYTVKTNMPSVASQNLCLCGNNDGERDNEFMTADNYET
Cel_Vit_5	1390	---ELEQYNIIEILGDNLIVIRLPQGEVRFDDGYTVKTNMPSVASQNLCLCGNNDGERDNEFMTADNYET
Cel_ApoL_1	266	-----
Cel MTTP	893	-----
Cel_Vit_6	1430	SEIEKKQYNI IWLKNKTLKFDSDDVTQFDGVNARIHLSALYR-NQQCGLCGHYDNEKETEFYDAENQE-
Cel_Vit_3	1390	---ELEQYNIIEILGDNLIVIRLPHGEVRFDDGYTVKTNMPSVASQNLCLCGNNDGERDNEFMTADNYET
Cel_Vit-1	1394	---DYSAHQIERLGESDIVIELPEGEVRFDDGYTIKTQLPSYSRKNQLCGLCGNNDDESTNEFYTSDNDET
Cel_Apo_L3_Like	318	-----
HsApoA1	158	-----
HsApoA2	101	-----
HsApoA4	396	-----
HsApoA5	367	-----
HsApoB48	2044	DAVEKPQEFTIVAFVKYDKNQDVHSINLPFFETLQEYFERNRQTIIVVLENVQRNLKHINIDQFVRKYRA
HsApoB52	2188	QEASQELQQIHQYIMALREEYFDPISVIGWTVKYEELEEKIVSLIKNLLVALKDHFSEYIVSASNFTSOLS
HsApoC1	129	-----
HsApoC2	102	-----
HsApoC3	100	-----
HsApoC4	128	-----
HsApoD	246	-----
HsApoE2	317	-----
HsApoF	326	-----
HsApoH	345	-----
HsApoJ	449	-----
HsApoL1	399	-----
HsApoL2	338	-----
HsApoL3	332	-----
HsApoL4	348	-----
HsApoOL(2)	433	-----
HsApoL6	344	-----
HsApoM	189	-----
HsApoO	199	-----
HsApoOL	269	-----
HsMTTP	894	-----
DmCG31659	193	-----
DmMtp	887	-----
DmCvD	1455	PTPVPLQNSSDVVVVA-----
DmGlaz	213	-----
DmFabb	159	-----
DmApoLTPII	780	-----
DmApoLTPI	3381	CAARDMRFDYTSILQYLLEEGVNLHILADTEFDFERNKKLRHFFGLDSKLVYSKRFPEGDAETRNTTHIP
DmNlaz	244	-----
DmApoLII	706	-----
DmApoLI	2440	IITEKRILDIYNSLKEIVKGIAPQADEKAFQLALDYPFRAGAAKSIIGVRSDSLEYKNWWKFVRAQLTGS
DmMICOS_A	227	-----
Cel MICOS	202	-----
Cel_Vit_2	1460	EDIEEFHRSYLLKNEECEAEERLSEKKNYR-KYERDEEQSDEYSSEETYDYEQENTKKSQKNQRSQKKS
Cel_Vit_4	1458	EDVEEFHRSYLLKNEECEVEKDRISEKKNYKNKWNREEKKS---YESSSDYESNYDEKETEKE-----
Cel_Vit_5	1458	EDVEEFHRSYLLKNEECEVENDRISEKKNYRNKWNREEKKS---YESSSDYESNYDEKETEKE-----
Cel_ApoL_1	266	-----
Cel MTTP	893	-----
Cel_Vit_6	1498	NTIPKFAKSYLYKDSKCNAYEREMFEKEENFQ-RIEKNQEEEEK---DQEMNYEESRREQDDEPT-----
Cel_Vit_3	1458	EDVEEFHRSYLLKNEECEVENDRISEKKNYRNKWNREEKKS---YVSSSDYENNYDEKETENQ-----
Cel_Vit-1	1462	KDIEEFHRSYLLKNEECEAEERLSEKKNYR-KYDERKYESEBYSFEETYDYEQENTNKKQKNQRSQKKS
Cel_Apo_L3_Like	318	-----

HsApoA2	101	-----
HsApoA4	396	-----
HsApoA5	367	-----
HsApoB48	2114	ALGKLPQQANDYLNFSFNWERQVSHAKEKLTALTKKYRITENDIQIALDDAKINFNEKLSQLQTYMIQ----
HsApoB52	2258	SQVEQFLHRNIQEYLSILTPDPGKGKEKIAELSATAQEIIKSQAIATKKIISDYHQQFRYKQLQDFSDQLS
HsApoC1	129	-----
HsApoC2	102	-----
HsApoC3	100	-----
HsApoC4	128	-----
HsApoD	246	-----
HsApoE2	317	-----
HsApoF	326	-----
HsApoH	345	-----
HsApoJ	449	-----
HsApoL1	399	-----
HsApoL2	338	-----
HsApoL3	332	-----
HsApoL4	348	-----
HsApoOL(2)	433	-----
HsApoL6	344	-----
HsApoM	189	-----
HsApoO	199	-----
HsApoOL	269	-----
HsMTTP	894	-----
DmCG31659	193	-----
DmMtp	887	-----
DmCvD	1470	-----
DmGlaz	213	-----
DmFabp	159	-----
DmApoLTPII	780	-----
DmApoLTPI	3451	KSNLGICTTLAVETQGSVFSARKLQPERKYPKIRFATIFAKRVALSATPIQSQTCECSAHNTGVSYMACE
DmNlaz	244	-----
DmApoLII	706	-----
DmApoLI	2510	ITKFDGALIHLIAPVKGLSLEGLVSEKLIGFNSRLVATVDGKDSKKRTKLQFDNDMGIDFVLNNGGWVFA
DmMICOS_A	227	-----
Cel MICOS	202	-----
Cel_Vit_2	1529	DLVEKTQIKEFSHRICFSVEPVAEAC--RRGYEVEQQQQRKIRFTCLQRHNRDASRLKESRQQPL--QLDDY
Cel_Vit_4	1518	--LVKKTLIKEFSNRVCFSIEPVSEC--RRGLESEKTSNKKIRFTCMPRHSKNARRFLKEAREQTVADLVDF
Cel_Vit_5	1518	--LVKKTLIKEFSNRVCFSIEPVSEC--RRGLESEKTSNKKIRFTCMPRHSKNARRFLKEAREQTVADLVDF
Cel_ApoL_1	266	-----
Cel MTTP	893	-----
Cel_Vit_6	1556	---EQVAIVERQHEICFTQKPVLC--QNG--KSQESKKQKTSVYCLPSSNSWARRQMRIRREPLAQWPEH
Cel_Vit_3	1518	--LFKKTLIKEFSNRVCFSIEPVSEC--RRGLESEKTSNEKIRFTCMPRHSKNARRFLKEAREQTVADLVDF
Cel_Vit-1	1531	DLVEKTQIKEFSHRICFSVEPVAEACRRRGYEAVEQQQRKVRFTCLPRHSSEARRLVKEARQGTV--QLDDH
Cel_Apo_L3_Like	318	-----
HsApoA1	158	-----
HsApoA2	101	-----
HsApoA4	396	-----
HsApoA5	367	-----
HsApoB48	2180	-----
HsApoB52	2328	DYYEKFIAESKRLIDLSIQNYHTFLIYITELLKKLQSTTVMNPYMKLAPGELTIIL-----
HsApoC1	129	-----
HsApoC2	102	-----
HsApoC3	100	-----
HsApoC4	128	-----
HsApoD	246	-----
HsApoE2	317	-----
HsApoF	326	-----
HsApoH	345	-----
HsApoJ	449	-----
HsApoL1	399	-----
HsApoL2	338	-----
HsApoL3	332	-----
HsApoL4	348	-----
HsApoOL(2)	433	-----
HsApoL6	344	-----
HsApoM	189	-----
HsApoO	199	-----
HsApoOL	269	-----
HsMTTP	894	-----
DmCG31659	193	-----
DmMtp	887	-----
DmCvD	1470	-----
DmGlaz	213	-----
DmFabp	159	-----
DmApoLTPII	780	-----
DmApoLTPI	3521	PQALPEEKYDLDDYDSFNNWDWGDEPESETNVMS-----
DmNlaz	244	-----
DmApoLII	706	-----
DmApoLI	2580	TQNFELKASDQKKMLNQITSSLADTLFKTEIVSDCRCLPIHGLHGQHKCVIKSSTFVANKKAKSA
DmMICOS_A	227	-----
Cel MICOS	202	-----
Cel_Vit_2	1597	PVSFVES-----VKIPTAC--VAYS-----
Cel_Vit_4	1587	PVSFVES-----VKIPTAC--VAYV-----
Cel_Vit_5	1587	PVSFVES-----VKIPTAC--VAYV-----
Cel_ApoL_1	266	-----
Cel MTTP	893	-----
Cel_Vit_6	1622	KLRNLRDQPQMEERTVVRVAVDQKCDKFDY-----
Cel_Vit_3	1587	PVSFVES-----VKIPTAC--VAYR-----
Cel_Vit-1	1600	KISFVHS-----VQVPVAC--VAY-----
Cel_Apo_L3_Like	318	-----