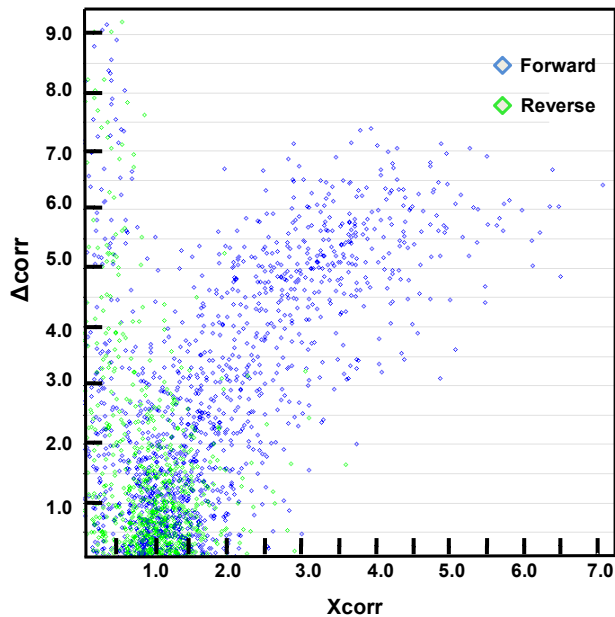
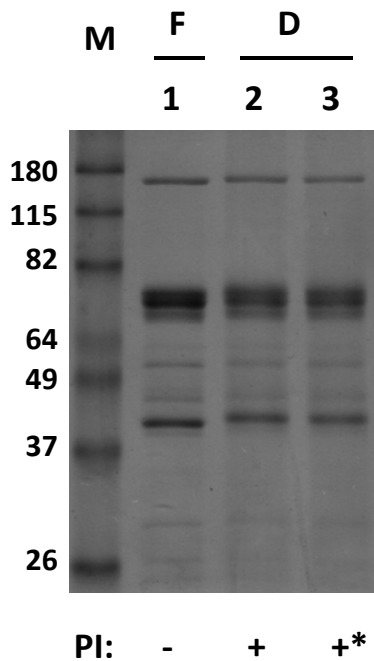


Roskens et al. Supporting Information Figure 1



Scatter plot of SEQUEST Xcorr scores vs. ΔCn values for each top peptide assignment matching to the forward (blue), or reverse (green) human IPI protein database. Scatter plot is for only one of the six regions analyzed and represents visually (along with Figure 1B) the establishment of criteria to filter the data to a less than 0.01% false discovery rate.

Roskens et al. Supporting Information Figure 2



SDS-PAGE analysis of *V. vulgaris* larval trophallactic fluid preserved for three weeks by freezing, or desiccation in the presence of protease inhibitors (P.I.) as indicated. “*” indicated the protease inhibitors were desiccated and stored for three weeks at 37°C prior to sample addition. Molecular weight markers in lane “M” are in kilodaltons. The gel was stained with Coomassie.

Roskens et al. Supporting Information Figure 3

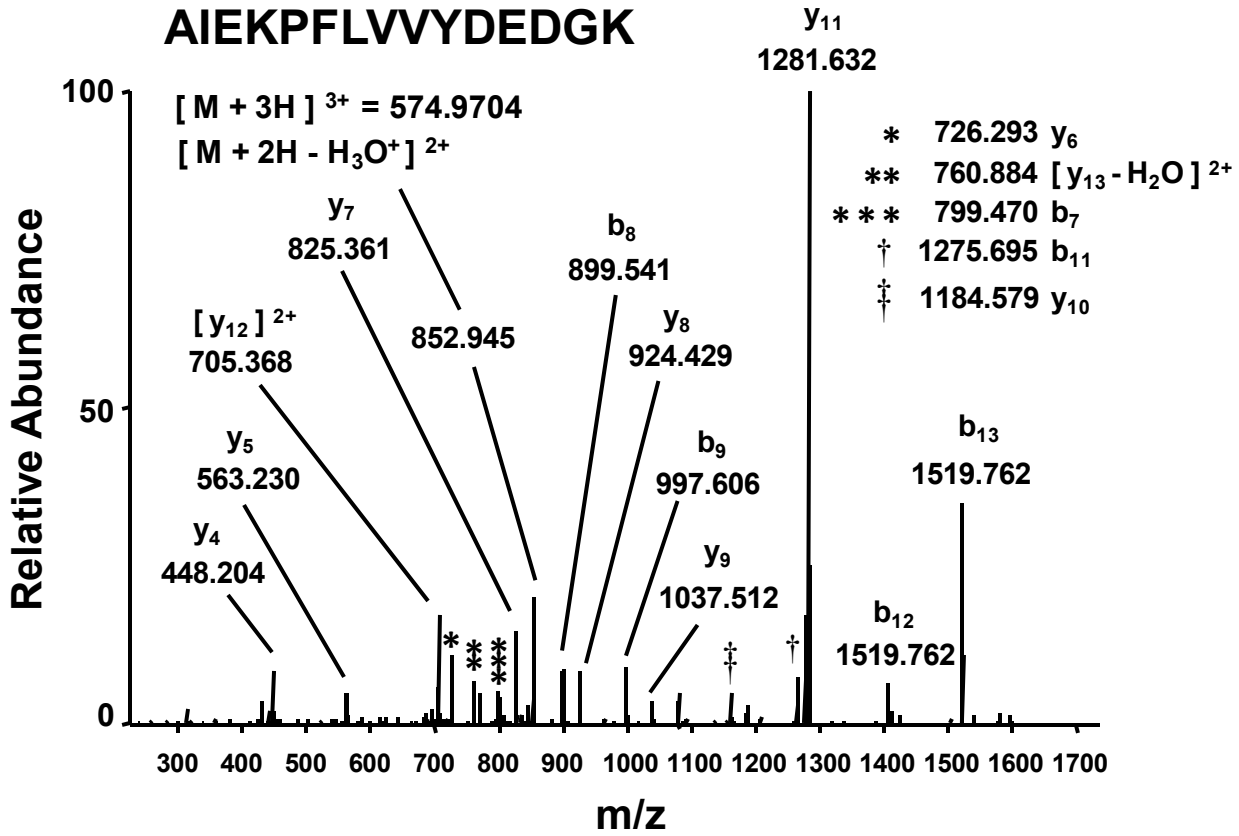
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1   MSQIVLQIFRHIKGECSAAFS SLLNKGYTIMNTLIVLLGILTTVI AVPAFPFHGKLVTY
61  KYIADV KAGVDP SLSASNYGIECLLN VQHVTDTNSKN TYVNL TNVKYRLYNGFSKHYES
      ALEK PFLV VYDE DGK
121  L SVMES I PDVAD AILN PFLV VYDEN GH LKGVK FVENEAGWSRNMKKGI V SMLQLDMT NIR
      DQQNPQSNNVFVVK
181  VQTPM KSHS F ITHEETVHGTCQVA YNVH PLDHVGSNKEFV VTK IQESKNCTRFSYHETNH
      VESENAMTTASR
241  FDSEKCHVDEWDDMTTASR RIFV VESQDNEVLIKKLIGHGMINYLPWTAESEAHLLTNQ
301  TLHLKDVSVSESRLSDVARLNPSI IENVIYDEPTTSYVPQADVDVTHGRHIVKLDLIL
361  KLRRMLDEVAGYLKESQTEKKQSDWKHDQTINRILHVMGYMDVASLERVYSEIQNGK DAN
421  EIAKRNIFLGILSSVGT PAACLFTRNVVRTK SVPKWNATMLGNL AMHVKVP SKKLLVQM
481  EELLNLD DSVSVEVKEAS IFCFATLIRKTFEHEETGAID PLLDKYLH HFMEHIRNEP THH
      MVYLMAMR      GDEVLSEK
541  MKMVYMMAMKNVRLTQILKFLEPIIRGDEVVSDKPHNIRAQAIWIMRNVVFEHPRYCYNL
      NLYWFMVYEK DQHLNYNHVTTLK
601  LWPVLT DVILPTAVRIA AFDVLMNETPQSERFI NVYWL MVYEKNEHLYNYVD TIKGLAT
      VDYVDPK
661  SVDPCLMQARELAKKLLKIVRVRNVTG PLSRKFY VDYVDNKY EYNERVKGSLIVDHASGL
721  PYIGSIEHVASVKARKPVTKLGIHWNIDGLSEIVKDI DENVFGNVVQAIKNDNVKNVLIS
781  AAKIMPKIKDVNVNVI LTMNDNVVS IFHCTKNNWQK I LNELKQWKRLI TEYMDVVNWQTV
      HGEYA
841  LYHDYHEMHVTTDLGVPAILSTKIPSLFSLVGSFEVSEDKNLLILKPKIKYQQW MHGEHT
      MSIYNPLVDVWHS LR
901  MSIYNP VADVWHS VHKTSSFDIVAPCEMTIGWNWKTSLKVTWPRLPVTDFSVAGIS IGH
      HYE VVTLG
961  KNYITVLNDQHDL LKKS CFTCH HYE VVTNNVNLRTYENTFDSKDIGTRFKMQYHCDNDFI
      PSLVYPTS
1021 PVSLVDEWLI GLSESKTIENSMMQAVIAFRHKIMNDI ILGQ GKSCSLVYKVEPS I IYPTS
      SVVVNLR
1081 VIDLIGKVS IQDFHETQKMDLLRSKRIDIRGNLNAKAASTNESIRQWDMNLNIVLSQGHV
      KEETNTK
1141 NNSMRIMITRTIPEEKNLKNEYPEITD DLLTVNGK KEETNTKMTITMGQTKEDKCVRDEMD
      GEMSEEQKK
1201 VTIIMK GEMLEEQKNQMSYDSMYIECYNQSQNPLFHTKS SKVPKTKECIEEDILHSTLRK
1261 YTLDMT VRKVPQQIMS VVNIVHDKLRAVFFDHMKHTWNHVQP GNAKIVLEFPYLTSVLNA
      HSYDLTEVPFGNK
1321 AVTTP T HSYELVQLPFGN FVWNMWMNNIHYSTSILNDYFNEKIRLCTIYPRLLNPTINDA
1381 ITINWNGVIQFIRSDEWILMSGDHIIHTYSIFVKLVQNKKLALRVYIGEHEMEIMPLEAK
1441 VSVKIDNKIIDDYQKGITVSENESSHYPMLRTTAYNYVVIDSQ TIPVHIFYKVDSVTVSL
1501 HTDLQSRVTGICGNMDVMHKDEVPDDNME

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Full amino acid sequence of larval-specific very high density lipoprotein (*A. mellifera*). *V. vulgaris* peptides from Figure 2C appear above the sequence in the boxed regions. Sequence identities are highlighted in yellow, and sequences resulting from hand interpretation of mass spectra are in blue.

Roskens et al. Supporting Information Figure 4



Low energy, high resolution MS/MS spectrum acquired in the orbitrap for the indicated peptide as a triply-charged precursor. See Supporting Information Table 2 for theoretical and observed m/z values for b- and y-type ions and Figure 2C for alignment of this peptide with its orthologous sequence in *A. mellifera*.