

C.elegans APL-1 1 -----MTVGKLMGLLIPILVATVYAEGS-----PAGSKRHEKFIEMVAFSCGYRNOYMTTEE-GSWK
Drosophila APPL 1 -----MCAALRRNLLLRSLWVYLAIGTAQV-----QAASPRWEPQIAVLCEAGIYQPYLSEGRWV
Zebrafish APPa 1 -----MRSRELFLLMAVASTLAVEVP-----SDSGTG-LLAEPQIAMFCGKLNMMHNTIQSGKWE
Xenopus APP-A 1 -----MLP-HITLLVLTAG-ALALEVP-----ADGNGG-LLAEPQIAMFCGKLNMMHNVQNGKWE
hAPP 1 -----MLP-GLALLLLAAWTAARLEVP-----TDGNAG-LLAEPQIAMFCGKLNMMHNVQNGKWD
hAPLP1 1 MGPA SPAARGLSRRPGQPPLPLLLPLLLLRAQPAIGSLAG-----GSPGAAEAPGSAQVAGLCGRLLTHRDLRTRGRWE
hAPLP2 1 MAATGTAAA-----AATGRLLLLLVLGTAPALALAGYIEALAAAGTGFAVAEPQIAMFCGKLNMMHVNITQTKWE

C.elegans APL-1 57 TDDERYAT--CFSGKLDILKYCRKAAPSMNITNIVEYSEHVSISDWCRE--EGS--PCKWTHSVRPHYCIGDFEHSSEAL
Drosophila APPL 59 TDLSSKKTGPTCLRDKMDLLDYCKKAYPNRDI TNIVESSHYQKIGGWCRGALNAACKGSHRWIKPFRCLG-PFQSDAL
Zebrafish APPa 55 PDPSSGSKS--CIGNKEGILQYQCEYYPELQITNVVEANQPVS IWDWCKK--SRK-QCRSHMHIVVYRCLVGEFVSDAL
Xenopus APP-A 53 TDVSGTKG--CIGTKEGILQYQCEYYPELQITNVVEANQPVTIQNWCKK--GRK-QCKSRTHIVVYRCLVGEFVSDAL
hAPP 54 SDPSGKT--CIDTKEGILQYQCEYYPELQITNVVEANQPVTIQNWCKR--GRK-QCKTHPHFVIVYRCLVGEFVSDAL
hAPLP1 76 PDPQRSRR--CLRDPGRVLEYCRQMYPELOIARVEGATQAIPIERWCGG--SRSGSCAHPHQVVPFRCLPGEFVSEAL
hAPLP2 72 PDPGTGK--CFETKEEVLQYQCEYYPELQITNVVEANQVSIQNWCKR--DKK-QCKSR--FVTPFKCLVGEFVSDVL

C.elegans APL-1 130 QVPHDCQFHVNSRDQNDYQHWKDEAGCKTKKSKGNKDMI VRSFAVLEPCALDMFTGVEFVCCPNDQTKNTDQVQTKK
Drosophila APPL 138 LVPFGCLFDHIIHNASRCWPFWRWNQTGAACQER-----GMQMRSFAMLLPCGIVSFGVEFVCCPKHFKTDEIHVKKT
Zebrafish APPa 129 LVPDKCKFLHQERMDQCESHLHWHTVAKESGGDR-----SMNLHDYGMLLPCGIDFRGVEFVCCP-ADAGKESESAVA
Xenopus APP-A 127 LVPDKCKFLHQERMDQCEHLLHWHTVAKESGSEK-----SMSLEYGMLLPCGIDKFRGVEFVCCP-SEESFSDADA
hAPP 128 LVPDKCKFLHQERMDQCEHLLHWHTVAKETGSEK-----STNLHDYGMLLPCGIDKFRGVEFVCCP-LEESDNVSDADA
hAPLP1 151 LVPFGCFLHQERMDQCESSTRRHQEAQEAQSSQ-----GLLIHSGMLLPCGSDRFRGVEVCCPPPGTDP--SGTA
hAPLP2 144 LVPFKCQDFHKERMEVCENHCHWHTVYKCAQLTC-----GMTLVYGMLLPCGVDDQFHGTEVYCCPQTKIIGSVSKEEE

C.elegans APL-1 210 EDEDD--DDEDDAYEDDSEDEKDE-----
Drosophila APPL 212 DLPVMPAAQINSANDELVMNDEDSNDSNYSKDANEDDLDEDDLMGDDEEDMVADEAATAGGSPNTGSSGDSNSGSLD
Zebrafish APPa 202 EEDSDVVMGGADADYDENSMTDRDAEAAPVLEDEDADEEEDDQDGGDRDEKIEEEE-----EPE
Xenopus APP-A 201 E-DDSDVVMGGADADYDRSDDKAVEAQPDEEEVEVEEETDDEDD--GDEAEEPE-----EY
hAPP 202 EEDSDVVMGGADADYADGSEDKVVEVA--EEEEVAVEEEDDDEDEDEGVEEAA-----EY
hAPLP1 223 VGDPSSTRSWPPGSR-----VEGADEEEEFSPQVDDYFVPEPQ-----A
hAPLP2 218 EDEEEEEEDEEDYDVYKSEFPTTEAD--LDFTEAAVDEDEDEEE--GEVVEEDRY--YDTFKGD

C.elegans APL-1 235 -----EESPQDPYFKIANWNTNEHDDFKKAEARMDEKHKRKKVDMKMEWGTLETNYNE
Drosophila APPL 372 AFVAAANSNGSGTG-----AGAPPSTAQPTSDPYTFHDFPHYEQSYKVSQRLEESHREKVTRVMKDWSDLEEKYOD
Zebrafish APPa 345 GVL-----PTSSPPDAVDRYLETFADENEHAHFLQAKESLETKHREMSQVMREWEAERQAKS
Xenopus APP-A 341 SVI-----PATAASTPDADVKYLENPNDENEHDRLKAKERLEKHKREMSQVMREWEAERQAKN
hAPP 343 SANSSQLLKTTOEPLARDPVKLPPTTAASTPDADVKYLENPNDENEHAHFLQAKERLEKHKREMSQVMREWEAERQAKN
hAPLP1 283 KVT-----PTPRPTDGDVIFYGMPGEISEHEGFLRAKMDLEEARMRQINEMVREWAMAQNSKN
hAPLP2 362 AMIP-----PTPLPTNDVDFYFETSADNEHARFKAKEQLEIRHRNRMDRVKKEWEEAELQAKN

C.elegans APL-1 289 QKADPKGAEFKLSQMNARFOKTVSLEEEHKMRKEIEAVHEERVQAMLNEKKRDATHDYRQALATHVNKFNKHSVLQS
Drosophila APPL 444 MRLADPKAAQSFKQRMARFQTSVDALEEGNAEKHQLAAMHQORVLAHINQRKREMTCTYQALTEQ--PNAHHVEKC
Zebrafish APPa 406 LPND-----KKAVIQHFQEKVEALEQESASERQQLVETHMARVEALNDRRLALESYISALQADP--PRPRHVFSL
Xenopus APP-A 402 LPKAD-----KKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQADP--PRPRHVFM
hAPP 423 LPKAD-----KKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQADP--PRPRHVFM
hAPLP1 342 LPKAD-----RQALNEHFQSLQTLLEEQVSGERORLVETHATRVIALINDORRALEGFALALQADP--PQAEVLLA
hAPLP2 422 LPKAE-----RQTLIQHFQAMVKALEKEAASEKQQLVETHLARVEAMLNDRRLMALENYLALQADP--PRPHRLQA

C.elegans APL-1 369 LKAYIRAEKDRMHTLNRYRHLLKADS----KEAAYKPTVIHRLRYIDLRINGTLAMLRDFDLEKYVRIAVTYWKDY
Drosophila APPL 522 LQKLLRALHKDRAHALAHYRHLLNSGGPGLKAAASERPTLERLIDIDRAVNSQMTMLKRYPELSAKIAQLMNDYILAL
Zebrafish APPa 477 LKKYVRAEQKDRQHTLKHFEHVRMVDP----KKAQIRPQVTLHLRVIERMNQSLGLLYKVPVAVDIDQDV-ELQRE
Xenopus APP-A 473 LKKYVRAEQKDRQHTLKHFEHVRMVDP----KKAQIRSQVMTHLVRINERMNQSFLLYKVPVAVAEIQDEVDELQKE
hAPP 494 LKKYVRAEQKDRQHTLKHFEHVRMVDP----KKAQIRSQVMTHLVRINERMNQSFLLYNVPVAVAEIQDEVDELQKE
hAPLP1 413 LRRYLRAEQKDRQHTLRHYQHVAVDP----EKAQMRFOVHTLQVIERVNSQSLGLLNDONPHLAQLRPIQELLHSE
hAPLP2 493 LRRYVRAENKDRLHTLRHYQHVAVDP----EKAQMKSQVMTHLHVIERRNQSLSLLYKVPVAVAEIQEDELLEQED

C.elegans APL-1 445 RDEVSPDLSVEDSELTPII-----HDDEFKNAKLDVKAPTTAKPVKE
Drosophila APPL 602 RSKDDIPGSSLGMSEEAAGILDKYRVEIERKVAEKERLRLAEKORKEQRAAEREKLRREKLRLEAKKVDMLKQSAVEQ
Zebrafish APPa 552 QEMSACLANLQS-----DARVSYGNDALMP--DS
Xenopus APP-A 549 QNYSDDMYSNMYS-----DHRVSYGNDALMPSLET
hAPP 570 QNYSDDVLANMIS-----EPRIYSGNDALMPSLET
hAPLP1 489 HLGPSLEAPAPG-----GSEDKGLQPP--DS
hAPLP2 569 RADMDDQFTASISETPV-----DVRVSESEEEIPP-FHP

C.elegans APL-1 489 TDNAKVLPTASDSEEADEYYEDEDEEQVKKTPDKMKK-VKVVDIKPKIKEKVTIEEEKKAPKLVETSVQTDDEDDDEDS
Drosophila APPL 682 QSQPTQSSTQSQAQQKESLPGKELGPDALVTAANPLETTKSEKDLSDTEYGEATVSSTKVQTVLPTVDDDDVQRA
Zebrafish APPa 580 TAGLELLPAED--TQGFIFHP-ESFNQP-----NTHNQ-VEPVDARP-----VPDLDL
Xenopus APP-A 580 KTTVELLPVVG--EFNIEDLQVWHSFGVDSVPAANTENE-VEPVDARP-----AADRGL
hAPP 601 KTTVELLRVNG--EFLDLDLPWHSFGVDSVPAANTENE-VEPVDARP-----AADRGL
hAPLP1 516 KDDTPMLTPKG--STQDAASP-----EKEKMP-LEQYERKV-----NASVP
hAPLP2 602 FHPFPALENE--DTQPELYHP--MKKSGVGVGEQDGG-LIGAEKV-----INSK--

C.elegans APL-1 568 SSTSSEDEDEDKNIKELRVDIEPIIDEPASFYRHDKLIQSPVEERSASVYFQPYLASAMFITAICIFAFITNARRR
Drosophila APPL 762 VEDVAAAHQEAEPQVGHFMTHDLGHRSSFLRREFAQHAHAKEGRNVYFTLSFAGJALMAAVFVGAFAKWRSTRS
Zebrafish APPa 625 ATRPVSGUK--PDDIPELRMAEERHS-----EVYHOKLVFAEDVSSNKGAIIGLMVGGVVIAITVIVITLVMRL-KKQYT
Xenopus APP-A 630 TTRPGSGLTNIKTEEISEVKMDESEYRHDATYEVHOKLVFAEDVSSNKGAIIGLMVGGVVIAITVIVITLVMRL-KKQYT
hAPP 651 TTRPGSGLTNIKTEEISEVKMDEAFRHDSSTYEVHOKLVFAEDVSSNKGAIIGLMVGGVVIAITVIVITLVMRL-KKQYT
hAPLP1 555 -----RGFPFHS-----EIQDELAPAGTGM--REAVSGLLIMGAGGSLIYLSMILLRKKKPYG
hAPLP2 646 -NKVDENVIDETLDYKEMIFNAERVGG--LEERESVGPLREDFLSALIGLLVIAVAIATVIVISLVMRL-KRQYG

C.elegans APL-1 648 RAMRGFEVD-----VYTPPEERHVMGMQVNGYENPTYSFFDSKA-
Drosophila APPL 842 PHAOGFEVDQNVTTTHPIVREEXIIPMNOQINGYENPTYKYFVEKE-
Zebrafish APPa 698 SHHGIEVDA-----AVTPEERHLSKMQQNGYENPTYKFFEQMHN
Xenopus APP-A 709 THHGVEVDA-----AVTPEERHLSKMQQNGYENPTYKFFEQMHN
hAPP 730 SHHGVEVDA-----AVTPEERHLSKMQQNGYENPTYKFFEQMHN
hAPLP1 611 AISHGVVEVDP-----MLTLEEQQLRELQRHGYENPTYRFLEERP-
hAPLP2 723 TISHGIVEVDP-----MLTPEERHLNKMQNHGYENPTYKYLEQMI

