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## Phosducin-like proteins in *Dictyostelium discoideum*

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## Sequence alignment of 33 phosducin family proteins

33 438

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>DdPhLP1 MEQNILNSILDKFGDGQERSDIRHNDSGDENDNHSDEHGNHGNNCECEGNEDGDKEYEVDVEDMTDEQYAQFIQEQQEPKIKSGGNTGVKGVLSDYAEHREKQKQKYLQKKYETQK
>EhPhLP1 -----MSKDIVMESDSERNMSSEENLSYDFEFQKPLKLRPYGNAGVKGVIN DYKEAREHAEQRLKERVEETKR
>CePhLP1 -----MNLESRI LDGKPAYC SSSSEGEEDDFKVVNDEDEHQANVMKRMGPSNTGAKGVLNEFKAFREQTRLAVESKNQKLI E
>CpBDM-1 -----MSKTAAQEEFDDFLAKNSADPDDNVHPEDREDAAYERELHARDNSDDEEEQYRASKIDAAMRMPGNDRPVQLPPASFDAGRATGVKGV IADARSFEKAKKSSKWGEKMRNAR
>HsPhLP1 -----MTTLDDKLLGEKLYYYYSSSEDESDHEDKD-----RGRCAPASSSVPAEELAG---EGISVNTGPKGVINDWRRFKQLETEQREEQCREMER
>MmPhLP1 -----MTTLDDKLLGEKLYYYYSTSEDESDHEDKD-----RGRGAPASSSTPAEELAG---EGISINTGPKGVINDWRRFKQLETEQREEQCREMER
>DmPhLP1 -----MATLEDKLLGEKLEYCYSSSEGEDNGDEGGDNKGASGKSRCSGLTIDTNPDATPAGGFRQQSSSTNTGPKGVVKDQWRFKQLEAERRDETERQRLA
>HsPhd -----MEEAKSQSLEEDFEG-----QATHTGPKGVINDWRKFKLESQSDSIPPSKKEI
>MmPhd -----MEEAASQSLEEDFEG-----QATHTGPKGVINDWRKFKLESQSDSIPPSKKEI
>DdPhLP2 -----MGLGKTEWEDIQIKYGNMEAPPKQLTEDELFDL I KEAEMA
>OsPhLP2 -----MADYHFVYKDVEGASTEWD DIQRRLGNL--PPKPE--PFKPPAYAPKVDAD
>AtPhLP2 -----MADYHFVYKDI EGASTQWDDIQRKLGNL--PEKAP--AFKPPAYTPAEDES
>MmPhLP2B-----MQDPNEDTEWNEILRNF GIL--PPK---E EPKDEIEEMVLRL
>HsPhLP2B-----MQDPNEDTEWNDILRDFGIL--PPK---EESKDEIEEMVLRL
>MmPhLP2A-----MQDPNADTEWNDILRKKGIL--PPK--ESLKELEEEEA EKEEQ L
>HsPhLP2A-----MQDPNADTEWNDILRKKGIL--PPK--ESLKELEEEEA E-EQRI
>CaPhLP2 -----MNNDPKFQVQVDPNEDTEWNDILRQHGI I--PEKPPS---PSVELETALEEA
>ScPlp2 -----MQNEPMPFQVQVDESESDSEWNDILRAKGI I--PERAPS---PTAKLEEAL EEA
>AfPhLP2 -----MEVQVNPNEDETEWNDILRKHGI I--PEK PQ--DPEPLIQE-ALVEA
>SpPhLP2 -----MNPDEDETEWNDILRSKGIL--PEKEP--D VDDVLDD-ALVDA
>DmPhLP2 -----MDDAIQRRTDLPL
>EhPhLP2 -----SVLERNTEWQDAIAKVNKAALSPEE---QKLYDEGNILYKE
>PfPhLP2 -----MSTTNP TRETTEWDDLQRKFGNL--PPLP---KEIKEEEIYLENL
>DdPhLP3 -----MEADASVDMF SKVLEH
>HsPhLP3 -----MEGNGSVDMFSEVLEN
>MmPhLP3 -----MANILEN
>CePhLP3 -----MAANIQQQFGE
>CspPhLP3-----MDSNSIN
>AtPhLP3 -----MDPDTVKSTLSNLAFGNVLA A AARDYK
>ScPlp1 -----MEDKLD RY YTNVLSNAEKDKHTT
>KlPhLP3 -----
>AfPhLP3 -----MN

```

>DdPhLP1 MLEKMCFTTRDQPPTEENQ-----LSDDDDLERIRKARMEQWKSQQITSDVKKPEK-----KVFGYFKQID-SSQYI-HEIDNEPPN-----  
 >EhPhLP1 IMRGESSNSIVQEKCEE-----EDLDEIEKELFGEVVSQAQVFKERQKPEVLKIVK-----RRYGDVLELD-EEEYA-NTITTTLEDD-----  
 >CePhLP1 QAKKMMIGSKEEREKA-----QREDDDED FEMTLEGLKAKRLREMRKI-----AANRVIEMTD-KKQYS-DAVDGSSS-----  
 >CpBDM-1 RSVIGLTSMKMTSDSKS-----SDSEEHS GDEDEEQFLRQWRESRRRELEAEDRSRVNRRTSPSS-----RNYGRFEKVD-AMGYL-DAIEKVS RD-----  
 >HsPhLP1 LIKKLSMTCRSHLDEEEEQKQKDLQEKISGKMTLKEFAIMNEDQDDEEFLQYRQRMEE MRQQFLHKG-----PQFKQVFEISSGEGFL-DMIDKEQKS-----  
 >MmPhLP1 LIKKLSMTCRSHLDEEEEQKQKDLQEKISGKMTLKEFGTKDKNLDDEEFLQYRQRMEE MRQQFLHKG-----PQFKQVFEISSGEGFL-DMIDKEQKS-----  
 >DmPhLP1 LAKKLTITATTSAEDEE--RKRQE-----ELDAELDELMSDFLQQYQQRMAEMLRQTGHH-----QQFGVQQLTSHEEFL-ACVEQENKH-----  
 >HsPhd LRQMSSPQSRNGKSKERVSRKMSIQ-----EYELIHKEKEDENCLRKYRRCMQDMHQLSFG-----PRYGFVYELETGKQFL-ETIEKELKI-----  
 >MmPhd LRQMSSPQSRD--DSKERMSRKMSIQ-----EYELIHQDKEDESCLRKYRRCMQDMHQLSFG-----PRYGFVYELETGQFL-ETIEKEQKV-----  
 >DdPhLP2 TEAEKNEKLENASL-----KDLKDMEDDED-VLEQLRKKRIQQMKVEAEL-----NKFGELKEISEPS-YKSEVTE-CKGV-----  
 >OsPhLP2 EQPKSKEWLDEREP-----DELEDLEDDLDDDRFLEQYRRMLAELREAAKA-----AKFGSIVPITGSD-FVREVSQAPSDV-----  
 >AtPhLP2 SAPKDQAWFDKKTTEE-----LEDLEDDKLDLDDDRFLEERYKRLSELREAAKV-----KRYGTVTPISGSD-FVREVTQASAE-----  
 >MmPhLP2B QKEAMVKPYEKMTLAQL-----KEAEDEFDEEDIKAIETIYREKRLQEWKALKKK-----QKFGELREISGNQ-YVNEVTNAEKDL-----  
 >HsPhLP2B QKEAMVKPFKMTLAQL-----KEAEDEFDEEDMQAVETYRKKRLQEWKALKKK-----QKFGELREISGNQ-YVNEVTNAEEDV-----  
 >MmPhLP2A LQQSVVKTYEDMTLEEL-----ENEDEFSEEDERAIEMYRQRLAEWKATQLK-----NKFGEVLEISGD-YVQEVTKAGEGL-----  
 >HsPhLP2A LQQSVVKTYEDMTLEEL-----EDHEDEFNEEDERAIEMYRRRLAEWKATKLL-----NKFGEVLEISGD-YVQEVTKAGEGL-----  
 >CaPhLP2 IVKQYDNRLVKNKDL-----DELDELEDEDEDFLNHQKQRMAEIKKLSK-----KKFGHVLPI SKNE-YENEVTKASKES-----  
 >ScPlp2 IAKQHENRLEDKDL-----SDLEELEDDED FLEAYKIKRLNEIRKLQER-----SKFGEVFHINKPE-YNKEVTLASQGK--KYEGA  
 >AfPhLP2 ERKAHENRLEDKDL-----DELHDLEDEDEEFLEQYSKKRLAELSTLQKT-----SIYNQVYPLQKVD-YAREVTEASSKS-----  
 >SpPhLP2 KQLAHENRLENKDL-----DELALEDEDEDFLQMYRNKRMQEWKQMSK-----AKFGSVYPI SKPE-YTAEVT DASKEV-----  
 >DmPhLP2 NEGQRDKKIDMSL-----DELDELEDESEDAVLEQYRQRRIAEMRATAEK-----ARFGSVREISGQD-YVNEVT KAGEGI-----  
 >EhPhLP2 APVVEHNAKEDKSL-----KEIDELLEDDSDDEELQRIKEKRLAEMRAIAE-----KNKYKEVVELTAGEYKQEVTEASKEC-----  
 >PfPhLP2 EKLEENILDKKNL-----NELNDIEEKCIDDEYLKII-EKYKNDRINEIN-----RMKAEDI-----YG-EVFEISKENFLTDINEA  
 >DdPhLP3 -----MSENNTNN-----GLDED FDDDELAKIREQRMKQLKEESKL-KQSFLS-----THGELKEIDEQD-FLKEVTGTDNV-----  
 >HsPhLP3 QLLQTTKLVEEHL DSE-----IQKLDQMD EDELERLKEKRLQALRKAQQQ-KQEWLS-----KGHG EYREIPSERDFFQEVKESENV-----  
 >MmPhLP3 QFLQA AKLVENHLDSE-----IQKLDQIG EDELELLKEKRLAALRKAQQQ-KQEWLS-----KGHG EYREIGSERDFFQEVKESEKV-----  
 >DmPhLP3 QLFTA AKTIEQQLDQQ-----LDRLDNLSDDDLKVLREQRLREMKDLNKN-KQEWLR-----NGHGTYTELADEKEFFEMSKSPNI-----  
 >CePhLP3 QLLRAAQVVEEQIDQE-----MNKLENLEEDDLEVI RRQRMEQMKKAQKD-RIEMLS-----HGHGKYEEVADEKEFFEATKKS DKV-----  
 >CspPhLP3 VIKKVL EES ENI IDEE-----IRAFDNI QNDENELNRLREKRIEELRQEF-KQKNKFIQ-----FGHGKYDFISDEKEFFDVIKKSENV-----  
 >AtPhLP3 KEVLANEKAQGSRPVN-----EEVDLDELMDPELEKLHADRIAALRREVEKREAFKRQ-----GHG EYREVS-EGDFLGEVTRSEKV-----  
 >ScPlp1 VSDDKSSGEENLDEL-----LNELDRELD EHEFLSAYRSERLQQISDHLKQVKNVEDD-----GYGRLQCIDNEADAIQICTKTTMV-----  
 >KlPhLP3 -----SGD-----YGSVQTF LDEQRLIQVTASAER-----  
 >AfPhLP3 QDSEQKHQPARELDDD-----NDDDSLFEAL ENEDDSAYRAHRIEQLNAEFSAAKNRSSLHDLATTVIEEGIYPTLKDDQAVLDFTTQTHR-----

>DdPhLP1 -----VFVI IHLFQNY - IPECVLLNQQLGQLAVKYRYIKFLKILSKEAKEN---YHDEALPSLLVYIGGKLLVSFVPLTEELG-----RNFDQEDLELLLSSYDIIP  
 >EhPhLP1 -----VFAVIHIYTTTF - VKDCTLINRMMEEYAQKYPFVCFAKITWEDSNKP---FPEKS-----  
 >CePhLP1 -----YLLCVLIYEPE - SDECEYLTRIVKILAADC PKTKFVRATSTLLEMSRA - FRTNGVPCLOFYNSGNLIGNFVKISAILG-----QDYDCKKLTkFLRGQHIDL  
 >CpBDM-1 -----TTVVVFVYDPE - SEVCSLIESALGPLVSNPNTRFVKVHYEEIE-----FDSAGVPAVLAYRNQGDLFANLTALIDMIPED---DDFDTSLSLKKLFLRHGII-  
 >HsPhLP1 -----IVIMVHIYEDG - IPGTEAMNGCMICLAAEYPVKFKCKVKS SVIGASSQ - FTRNALPALLIYKGGELIGNFVRVTDQLG-----DDFFAVDLEAFLQEFGLLP  
 >MmPhLP1 -----TLIMVHIYEDG - VPMCLVNVNQHLSVLARKFPETKFKVKAIVNSCIEH---YHDNCLPTIFVYKNGQIEGKFIGIECGG-----EDFFAVDLEAFLQEFGLLP  
 >DmPhLP1 -----TTII IHIYERQ - LAACATLNKCLDSLADYPSIKFAKICSSVAGMSRD - FRTKGLPALLVYKAQAVIGNFVRLTDDLS-----DDFFASDVESFLIEHGII I  
 >HsPhd -----TTIVVHIYEDG - IKGCDALNSSLTCLAAEYPIVKFKIKASNTGAGDR - FSLDVLPTLLIYKGGELISNFI SVAEQFA-----EEFFAGDVESFLNEYGLLP  
 >MmPhd -----TTIVVNIYEDG - VRGCDALNSSLACLAVEYPMVKFKIKASNTGAGDR - FSTDVLP TLLVYKGGELISNFI SVAEQFA-----EEFFAVDVESFLNEYGLLP  
 >DdPhLP2 -----MVVVHLFKNG - IPQCQLVNHILTILAKKFKATKFKIRSEEAHN---YDPKNLPPILVYFNGDIVGQIITLRATGG-----DATTVNDIEWQLKQAHAIK  
 >OsPhLP2 -----WVVVFLYKDG - IPECGLLQTCLELATRYPATKFKVIISTDCIPN---YDRNVPTILVYNNSAVKGT YVGLQKFGG-----KRCTPESVALALCQSEPVL  
 >AtPhLP2 -----WVVVCLYKDG - VAEC SLLLGCLEDELGSRYPATKFKVIISTDCIPN---YPCNLP TLLVYHHGAIKGT HVLKSFSG-----RRCTPESVALLLCQSEPVL  
 >MmPhLP2B -----WVVIHLYRSS - VPMCLVNVNQHLSVLARKFPETKFKVKAIVNSCIEH---YHDNCLPTIFVYKNGQIEGKFIGIECGG-----INLKLEBELEWKLAEVGAIQ  
 >HsPhLP2B -----WVI IHLYRSS - IPMCLLVNQHLSLARKFPETKFKVKAIVNSCIEH---YHDNCLPTIFVYKNGQIEGKFIGIECGG-----INLKLEBELEWKLAEVGAIQ  
 >MmPhLP2A -----WVILHLYKQG - IPLCSLINHHLSGLARKFPDVKFKIKAI STTCIPN---YDRNLPTV FVYREGDIKAQFIGPLVFGG-----MNL TIDELEWKLSESGAIK  
 >HsPhLP2A -----WVILHLYKQG - IPLCALINQHLSGLARKFPDVKFKIKAI STTCIPN---YDRNLPTIFVYLEGDIKAQFIGPLVFGG-----MNLTRDELEWKLSESGAIM  
 >CaPhLP2 -----YVLVHLSLQS - SLQSRLSSILIDLASKFPELKI CDIPAQRCIEN---Y PESCNCPTLI IYHDTNVVKQFILTTLQLGG-----NATTLKDVETALADLNVIG  
 >ScPlp2 QTNDNGEEDDGGVYV FVHLSLQS - KLSRILSHL FQSAACKFREIKFVEIPANRAIEN---Y PESCNCPTLI VYRGEVIK NMITLLELGG-----NNSKMEDFEDFMVKGAVA  
 >AfPhLP2 -----FVLVHLTSTSGNVESRVLSDLWRQLAMKYGDIKFCEIRGDMCIEG---YPERNTPTILVYKDG EIRRQLVTLRELNG-----PKTKLES AFTNDXCCINVG  
 >SpPhLP2 -----FVVVHMFQDS - LPACKLLAAILERLAPMPQIKFVKIPGKQAVEN---YPEAMMPTLLIYGHGDLQQQILTLATLGG-----MNTSVVDVAEALVRAGALK  
 >DmPhLP2 -----WVVLHLYANG - VPLCALIHHMQQLAVRFPQTKFVRSVATTCIPN---FPEKNLPTIF IYHEGALRKQYIGPLELRG-----DKLTAEELFMLGQAGAVP  
 >EhPhLP2 -----YVVVLLYKNG - IEGCDILSARLNELARKKRSTKFKV KILSHLAIPD---YDPKLLPTLIVYRNTNHVKQFIGLAEFGG-----NNMTCDDLEWALSRVGAVE  
 >PfPhLP2 SKKNPLKRKPKGTHVLLHLYSEN - VISCKVLNNILKELAQKHKYIKFTKGIYNR I IEN---Y PENKLP TILIYYNGTCI HQICNVLDHIKGG---NNLNMPTEFEK FINKYHIFR  
 >DdPhLP3 -----VVHFYHSD - FQRCKILDKSEILAKTHLGT KFLKVNAEKAQFFTGLGIRILPTLVFFSNGIAVDR CVGFEEFGGI-----DSFKIEQLAIRISKAGVLD  
 >HsPhLP3 -----VCHFYRDS - TFRCKILDRHLA ILSKKHLET KFLKLNVEKAPFLCERLHIKVIPTLALLKDGKTDYVVGFTDLGNT-----DDFTTETLEWRLGSSDILN  
 >MmPhLP3 -----VCHFYRDT - TFRCKILDRHLA I LAKKHLET KFLKLNVEKAPFLCERLRIKVIPTLALLRDKGKTDYVVGFTDLGNT-----DDFTTETLEWRLGCSVDIN  
 >DmPhLP3 -----VCHFYRDS - TERCKIVDMHLKILA AKHVEAKFCKVNAEKT PFLTQRLRIKVIPTIALVKDSKTKDFIVGF TDLGNC-----DDFATEMLEWRIAHS GAID  
 >CePhLP3 -----VCLFYLPG - NFRCKIVDKHFEILARKHVGTFR I HVNAEKVHFLTTRLNIRVIPSIAI VVKQQTVDYIRGFDELGGK-----DEFTTETMENRLARSEVLT  
 >CspPhLP3 -----VCHFFRPS - TLRCEIFDRHLEI I SKKHLEAKFIKINA EKSHFVCSNLNINILPTIALIKNSKLIHKIIGFEELSSR-----DNFTTTQLEELLVRRNMIQ  
 >AtPhLP3 -----ICHFYHKE - FYRCKIMDKHLKTLAPRHVDTKFKIKMDAENAPFFVTKLAIKTLPCVILFSGKIAMDRLVGFQDLGAK-----DDFSTTKLENLLVKKGFFT  
 >ScPlp1 -----VIHFELET - FGKCYMNEKLENLAKRYL TTRFIKVNVTQCPFLVNKLN I KVLFPVVG YKNGLEKVRVYGF SKLGNDP-----NGFDIRREQLS LAHSGVIE  
 >KlPhLP3 -----CVVHFFVDS - FRKCQVMSKLVMAESHLSTRFFRISVADCPFLVEKLSLKVLPVVIAYQNGKEQDR LIGFAKLG NNA-----NDFSIDHLEKWLQ RSGVVP  
 >AfPhLP3 -----CVIHFAHPD - FARCGFMDEHIRALATRHHEVR FARVDVRNTPFVVNKNLNRVLP CVIGFKDGI VVERVVGFEGLGAGGRDGADSFDIATLEKRL LWKGIILT

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>DdPhLP1 NPMKAKNSNWETS-----LSRKR-----ESDDND-----
>EhPhLP1 -----
>CePhLP1 MAGGYASD-----SDNESEDD-----
>CpBDM-1 -----
>HsPhLP1 EKEVLVLTSVR-----NSATCHSESDLEID-----
>MmPhLP1 EKEVLVLTSVR-----NSATCHSESDLEID-----
>DmPhLP1 SI-----
>HsPhd EREHVLEHTK-----IEEDVE-----
>MmPhd EREIHDLEQTN-----MEDEDIE-----
>DdPhLP2 SDLQEDPRITL-----ARKKSQKSRY-----SKADSESDNSDSD-----
>OsPhLP2 NDGQSGGD-SSRDNVIEG-----VRRKFIEKVV-----AQHEEREEDDDSD-----
>AtPhLP2 NDGKGGDDSSREAVMAG-----VRRQFIERVV-----KDHEKDNDDGGYNSD-----
>MmPhLP2B SDLEENP-----KGIADMMVSSI-----RNISIYD--SDSSGDTEAK-----
>HsPhLP2B TDLEENP-----RKDMVDMVSSI-----RNTSIHDD-SDSNSDNDTK-----
>MmPhLP2A TALEENP-----KKPIQDLLLSSV-----RGPVPMRRDSDSEDD-----
>HsPhLP2A TDLEENP-----KKPIEDVLLSSV-----RRSVLMKRDSSEGD-----
>CaPhLP2 FHKRLIINNDEDELE-----QARKLRFAKKSIRDGNR-----NNEKDKEDDDDDDDDFYD-----
>ScPlp2 EGDNR LIMNRDDEESRE-----ERKLHYGEKKSIRSGIRGKF-NVGIGGNDDGNINDDDDGFFD-----
>AfPhLP2 XSCLADLERMLVDL GAL-----KESDVRLKRSYSFDEERQS-----NIRSANVEDYDDD-WD-----
>SpPhLP2 DSDIAALKDPQNAEDEL-----GKRD-----SSV-----NDDLDDD-FD-----
>DmPhLP2 TEITEDPRPQIR-----DKMLADLEDKSSD-FY-----
>EhPhLP2 TTMKSDPKE-----KRHPKFSGGMF-----SRERDSYDDDDSD-----
>PfPhLP2 TCHNMYNSKDNNSDNYDDEDELN-----KKNIRTQKQYTSFNMFYKNKGNQHYDNSDNSSVEDKEIHSRGYASSYLDSKLR LNKF
>DdPhLP3 FKHTTGL-----KII-----KQDVKNKFKEDD-----
>HsPhLP3 YSGNLM EPPFQNQ-----KKFGTNFTKLEKKTIRGKKY-----DSDSDD-----
>MmPhLP3 YSGNLM EPPFQSQ-----KKFGTNFTKLEKKTIRGKKY-----DSDSDD-----
>DmPhLP3 YKGDLMQPPDV-----KR--KPFINRPQKTIRGG-Y-----DSDSDIDLDD-----
>CePhLP3 VEKKHTAPAK-----KKIIRSGVEEYDN-----EEDW-----
>CspPhLP3 EQ-----
>AtPhLP3 GMLSE-----KRKEEDEEYEQESIRRSVRSSANV-----DSDSD-----
>ScPlp1 DTFEI-----RKHSSVNTERF-----ASTNHRSESDSLDI-----
>KlPhLP3 MRDTKLTIIISNR-----SKQIRSK-----NKTNSDQEDSGSDWD-----
>AfPhLP3 QTKFKNNEDSDI SEGGSGDEGSNRRRPGTGRRTIRS-----GNRHHGGDDDDDDWDG-----

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## Species list:

Dd Dictyostelium discoideum  
Hs Homo sapiens  
Dm Drosophila melanogaster  
Mm Mus musculus  
Cp Cryphonectria parasitica  
Eh Entamoeba histolytica  
Sp Schizosaccharomyces pombe  
Os Oryza sativa  
At Arabidopsis thaliana  
Sc Saccharomyces cerevisiae  
Ca Candida albicans  
Af Aspergillus fumigatus  
Pf Plasmodium falciparum  
Csp Cryptosporidium parvum

## GenBank list:

DdPhLP1 gi|33331889|  
HsPhLP1 gi|13642199|  
DmPhLP1 gi|7294257|

MmPhLP1 gi|13879222|  
MmPhd gi|13632815|  
CpBDM-1 gi|6714950|  
HsPhd gi|187517|  
CePhLP1 gi|17543862|  
EhPhLP1 gnl|TIGR\_5759|

DdPhLP2 gi|33331891|  
MmPhLP2B gi|13937367|  
SpPhLP2 gi|6723900|  
MmPhLP2A gi|12835481|  
DmPhLP2 gi|7294636|  
OsPhLP2 gi|9558421|  
AtPhLP2 gi|7573449|  
ScPlp2 gi|6324856|  
HsPhLP2A gi|13129044|  
HsPhLP2B gi|18599461|  
CaPhLP2 gnl|SDSTC\_5476|  
EhPhLP2 gnl|TIGR\_5759|  
AfPhLP2 gnl|TIGR\_5085|  
PfPhLP2 gnl|Sanger\_36329|

DdPhLP3 gi|33331893|  
HsPhLP3 gi|13543639|  
ScPlp1 gi|6320389|  
KlPhLP3 gi|5531280|  
AtPhLP3 gi|10177522|  
DmPhLP3 gi|7299373|  
CePhLP3 gi|17552020|  
MmPhLP3 gi|12833213|  
CspPhLP3 gnl|CVMUMN\_5807|unfinished, fragment  
AfPhLP3 gnl|TIGR\_5085|