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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 MEQNILNSILDKFGDGDQERSDIRHNSGDENDNHSDEHGNHGNNECCEGNEDGDKEYEVDVEDMTDEQYAQFIQEQQEPKIKSGGNTGVKGVLSDYAEHREKQKQKYLQKKYETQK
>EhPhLP1 -----MSKDIVMESDSERNMSSEENLSYDEFEQKPLKLRPYGNAGVKGVIN DYKEAREHAEQRLKERVEETKR
>CePhLP1 -----MNLESRI LDGKPAGYCSSSEGEEDDFKVVNDEDEHQANVMKRMGPSSTNGAKGVLNEFKAFREQTRLAVESKNQKLIE
>CpBDM-1 -----MSKTAAQEEFDDFLAKNSADPDDNVHPEDREDAAYERELHARDNSDDEEEQYRASKIDAAMRMPGNDRPVQLPPASFDAGRATGVKGV IADARSFEKAKKSSKWGEKMRNAR
>HsPhLP1 -----MTTLDDKLLGEKLQYYYSSSEDESDHEDKD-----RGRCAPASSSVPAEELAG--EGISVNTGPKGVINDWRRFKQLETEQREEQCREMER
>MmPhLP1 -----MTTLDDKLLGEKLQYYYSTSEDESDHEDKD-----RGRGAPASSSTPAEELAG--EGISINTGPKGVINDWRRFKQLETEQREEQCREMER
>DmPhLP1 -----MATLEDKLLGEKLEYCYSSSEGEDNGDEGGDNKGASGKSRCSGLTIDTNPDATPAGGFRQQSSTNTGPKGVVKDWQRFKQLEAERRDETERQRLA
>HsPhd -----MEEAKSQSLEEDFEG-----QATHTGPKGVINDWRKFKLESQSDSIPPSKKEI
>MmPhd -----MEEAASQSLEEDFEG-----QATHTGPKGVINDWRKFKLESESDGDSIPPSKKEI
>DdPhLP2 -----MGLGKTEWEDIQIKYGNMEAPPKQLTEDELFDL I KEAEMA
>OsPhLP2 -----MADYHFVYKDVEGASTEWDDIQRRLGNL--PPKPE--PFKPPAYAPKVDAD
>AtPhLP2 -----MADYHFVYKDIEGASTQWDDIQRKLGIL--PEKAP--AFKPPAYTPAEDES
>MmPhLP2B-----MQDPNEDTEWNEILRNFGIL--PPK---EEPKDEIEEMVLRL
>HsPhLP2B-----MQDPNEDTEWNDILRDFGIL--PPK---EESKDEIEEMVLRL
>MmPhLP2A-----MQDPNADTEWNDILRKKGIL--PPK-ESLKELEEEAEKEEQQL
>HsPhLP2A-----MQDPNADTEWNDILRKKGIL--PPK-ESLKELEEEAE--EQRI
>CaPhLP2 -----MNNDPKFQVQVDPNEDTEWNDILRQHGI--PEKPPS---PSVELETALEEA
>ScPlp2 -----MQNEPMFQVQVDESESDSEWNDILRAKGI--PERAPS---PTAKLEEALEEA
>AfPhLP2 -----MEVQVNPNEDETEWNDILRKHGI--PEKPQ--DPEPLIQE-ALVEA
>SpPhLP2 -----MNPDEDETEWNDILRSKGIL--PEKEP--DVDDVLDD-ALVDA
>DmPhLP2 -----MDDAIQRRTDLPL
>EhPhLP2 -----SVLERNTEWQDAIAKVNKAALSPEE---QKLYDEGNILYKE
>PfPhLP2 -----MSTTNPTRETTEWDDLQRKFGNL--PPLP---KEIKEEEIYLENL
>DdPhLP3 -----
>HsPhLP3 -----MEADASVDMFSKVL E H
>MmPhLP3 -----MEGNGSVDMFSEVLEN
>DmPhLP3 -----MANILEN
>CePhLP3 -----MAANIQQQFGE
>CspPhLP3-----MDSNSIN
>AtPhLP3 -----MDPDTVKSTLSNLAFGNVLA A AARDYK
>ScPlp1 -----MEDKLD RY YTNVLSNAEKDKHTT
>KlPhLP3 -----
>AfPhLP3 -----MN

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>DdPhLP1 MLEKMCFTTRDQPPPTTEENQ-----LDSDDDDLERIRKARMEQWKSQQITSQVKKPEK-----KVFGYFKQID-SSQYI-HEIDNEPPN-----
>EhPhLP1 IMRGESSNSIVQEKCEE-----EDLDEIEKELFGEVVSAQVFKERQKPEVLKKIVK-----RRYGDVLELD-EEEYA-NTITTTLEDD-----
>CePhLP1 QAKKGMMIGSKEEREKA-----QREDDDED FEMTLEGLKAKRLREMRKI-----AANRVIEMTD-KKQYS-DAVDGSSS-----
>CpBDM-1 RSVIGLTSMKMTSDSKS-----SDSEEHSGDEDEEQFLRQWRESRRRELEAEDRSRVNRRTSPSS---RNYGRFEKVD-AMGYL-DAIEKVS RD-----
>HsPhLP1 LIKKLSMTCRSHLDEEEEQKQKDLQEKISGKMTLKEFAIMNEDQDDEEFLQQYRKQRMEE MRQQFLHKG-----PQFKQVFEISSGEGFL-DMIDKEQKS-----
>MmPhLP1 LIKKLSMSCRSHLDEEEEQKQKDLQEKISGKMTLKEFGTKDKNLDEEFLQQYRKQRMEE MRQQFLHKG-----PQFKQVFEIPSGEGFL-DMIDKEQKS-----
>DmPhLP1 LAKKLTITATTSAEDEE---RKRQE-----ELDAELDELMSDFLQQYQKQRM AEMLRQTGHH-----QQFGQVQQLTSHEEFL-ACVEQENKH-----
>HsPhd LRQMSSPQSRNGKDSKERVSRKMSIQ-----EYELIHKEKEDENCLRYRRQCMQDMHQKLSFG-----PRYGFVYELETGKQFL-ETIEKELKI-----
>MmPhd LRQMSSPQSRD--DSKERMSRKMSIQ-----EYELIHQDKEDESCLRYRRQCMQDMHQKLSFG-----PRYGFVYELETGEQFL-ETIEKEQKV-----
>DdPhLP2 TEAEKNEKLENASL-----KDLKDMEDDED-VLEQLRKKRIQQMKVEAEL-----NKFGELKEISEPS-YKSEVTE-CKGV-----
>OsPhLP2 EQPKSKEWLDEREP-----DELEDLEDDLDDDRFLEQYRRMRLAELREAAKA-----AKFGSIVPITGSD-FVREVSQAPSDV-----
>AtPhLP2 SAPKDQAWFDKKTEEE-----LEDLEDDKDLDDDRFLEEYRKKRLSELREAAKV-----KRYGTVTPISGSD-FVREVTQASAED-----
>MmPhLP2B QQEAMVKPYEKMTLAQL-----KEAEDEFDEEDIKAIEIYREKRLQEWKALKKK-----QKFGELREISGNQ-YVNEVTNAEKDL-----
>HsPhLP2B QKEAMVKPFEKMTLAQL-----KEAEDEFDEEDMQAVETYRKKRLQEWKALKKK-----QKFGELREISGNQ-YVNEVTNAEEDV-----
>MmPhLP2A LQQS VVKTYEDMTLEEL-----ENEDEFSEEDERAIEMYRQRLAEWKATQLK-----NKFGEVLEISGKD-YVQEVTKAGEGL-----
>HsPhLP2A LQQS VVKTYEDMTLEEL-----EDHEDEFNEEDERAIEMYRRRLAEWKATKLK-----NKFGEVLEISGKD-YVQEVTKAGEGL-----
>CaPhLP2 IVKQYDNRLVNKDL-----DELDELEDEDED FLNHYKQKRMAEIKKLSEK-----KKFGHVLPI SKNE-YENEVTKASKES-----
>ScPlp2 IAKQHENRLEDKDL-----SDLEELEDEDED FLEAYKIKRLNEIRKLQER-----SKFGEVFHINKPE-YNKEVTLASQ GK---KYEGA
>AfPhLP2 ERKAHENRLEDKDL-----DELHDLEDEDEEFLEQYSKKRLAELSTLQKT-----SIYNQVYPLQKVD-YAREVTEASSKS-----
>SpPhLP2 KQLAHENRLENKDL-----DELAELEDEDEDFLQMYRNKRMQEWKQMSK-----AKFGSVYPISKPE-YTAEVTDASKEV-----
>DmPhLP2 NEGQRDKKIDMSL-----DELDELEDS EDAVLEQYRQRRIAEMRATAEK-----ARFGSVREISGQD-YVNEVTKAGEGI-----
>EhPhLP2 APVVEHNAKEDKSL-----KEIDELLEDDSD EELQRIKEKRLAEMRAIAE-----KNKYKEVVELTAGEYKQEVTEASKEC-----
>PfPhLP2 EKLEENILDKKNL-----NELNDIEEKCIDDEYLKII-EKYKNDRINEIN-----RMKAEDI-----YG-EVFEISKENFLTDINEA
>DdPhLP3 -----MSENNTNN-----GLDED FDDDELAKIREQRMKQLKEESKL-KQSFLS-----THGELKEIDEQD-FLKEVTGTDNV-----
>HsPhLP3 QLLQTTKLVEEHL DSE-----IQKLDQMDEDELERLKEKRLQALRKAQQQ-KQEWLS-----KGHG EYREIPSERDFFQEVKESENV-----
>MmPhLP3 QFLQA AKLVENHLDSE-----IQKLDQIGEDELELLKEKRLAALRKAQQQ-KQEWLS-----KGHG EYREIGSERDFFQEVKESEKV-----
>DmPhLP3 QLFTA AKTIEQQLDQQ-----LDRLDNLDSDDLKVLREQRLREMKDLNNK-KQEWLR-----NGHGTYTELADEKEFFEMSKKSPNI-----
>CePhLP3 QLLRAAQVV EEQIDQE-----MNKLENLEEDDLEVIRQRMEQMKAQKD-RIEMLS-----HGHGKYEEVADEKEFFEATKKSDKV-----
>CspPhLP3 VIKKVL EES ENIIDEE-----IRAFDNIQNDENELNRLREKRIEELRQEF-KQKNKFIQ-----FGHGKYDFISDEKEFFDVIKKS ENV-----
>AtPhLP3 KEVLANEKAQGS RPVN-----EEVDLDELMD DPELEKLHADRIAALRREVEKREAFKRQ-----GHGEYREVS-EGD FLGEVTRSEKV-----
>ScPlp1 VSDDKSSGEENLDEL-----LNELDRELDEDEHFLSAYR SERLQQISDHLKQVKKNVEDD-----GYGRLQCIDNEADAIQICTKTTMV-----
>KlPhLP3 -----SGD-----YGSVQTF LDEQRLIQVTASAER-----
>AfPhLP3 QDSEQKHQPARELDDD-----NDDDSLFEAL ENEDDSAYRAHRIEQLNAEFSAAKNNRSSLHDLATTVIEEGIYPTLKDDQAVLDFTTQTHR-----

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>DdPhLP1 -----VFVIIHLFQNY-IPECVLLNQQLGQLAVKYRYIKFLKILSKEAKEN---YHDEALPSLLVYIGGKLLVSFVPLTEELG-----RNFDQEDLELLLSSYDIIP
>EhPhLP1 -----VFAVIHIYTTF-VKDCTLINRMEEYAQKYPFVCFAKITWEDSNKP---FPEKS-----
>CePhLP1 -----YLLCVLIYEPE-SDECEYLTRIVKILAADCPKTKFVRATSTLLEMSRA-FRTNGVPCLQFYSNGNLIGNFVKISAILG-----QDYDCKKLTkFLRGQHIDL
>CpBDM-1 -----TTVVVFVYDPE-SEVCSLIESALGPLVSNPNTRFVKVHYEEIE----FDSAGVPAVLAYRNQGDLFANLTALIDMIPED---DDFDTSLSLKKLFLRHGII-
>HsPhLP1 -----IVIMVHIYEDG-IPGTEAMNGCMICLAAEYPVKFCKVKSSVIGASSQ-FTRNALPALLIYKGGELIGNFVRVTDQLG-----DDFFAVDLEAFLQEFGLLP
>MmPhLP1 -----TLIMVHIYEDG-VPGTEAMNGCMICLATEYPVKFCKVRSSVIGASSR-FTRNALPALLIYKAGELIGNFVRVTDQLG-----EDFFAVDLEAFLQEFGLLP
>DmPhLP1 -----TTIIHIIYERQ-LAACATLNKCLDSLADSYPSIKFAKICSSVAGMSRD-FRTKGLPALLVYKAQAVIGNFVRLTDDLS-----DDFFASDVESFLIEHGIII
>HsPhd -----TTIVVHIYEDG-IKGCDALNSSLTCLAAEYPIVKFKIKASNTGAGDR-FSLDVLPTLLIYKGGELISNFISVAEQFA-----EEFFAGDVESFLNEYGLLP
>MmPhd -----TTIVVNIYEDG-VRGCDALNSSLACLAVEYPMVKFKIKASNTGAGDR-FSTDVLPTLLVYKGGELISNFISVAEQFA-----EEFFAVDVESFLNEYGLLP
>DdPhLP2 -----MVVVHLFKNG-IPQCQLVNQHLTILAKKFKATKFKVIRSEEAHN---YDPKNLPPILVYFNGDIVGQIITLRATGG-----DATTVNDIEWQLKQAHAIK
>OsPhLP2 -----WVVVFLYKDG-IPEGCLLQTCDELATRYPATKFKVKIISTDCIPN---YDRNVPTILVYNNSAVKGTYYVGLQKFGG-----KRCTPESVALALCQSEPVL
>AtPhLP2 -----WVVVCLYKDG-VAECSLLLGCDELGSRYPATKFKVKIISTDCIPN---YPCNLPPTLLVYHHGAIKGTHVGLKSFG-----RRCTPESVALLLCQSEPVL
>MmPhLP2B -----WVVIHLYRSS-VPMLVNVHLSVLARKFPETKFKVKAIVNSCIEH---YHDNCLPTIFVYKNGQIEAKFIGIIECGG-----INLKLELEWKLAEVGAIQ
>HsPhLP2B -----WVIHLYRSS-IPMCLLVNQHLSLLARKFPETKFKVKAIVNSCIEH---YHDNCLPTIFVYKNGQIEAKFIGIIECGG-----INLKLELEWKLAEVGAIQ
>MmPhLP2A -----WVILHLYKQG-IPLCSLINHHLSGLARKFPDVKFKAISTTCIPN---YDRNLPTVYVYREGDIKAQFIGPLVFGG-----MNLTIDELEWKLSESGAIK
>HsPhLP2A -----WVILHLYKQG-IPLCALINQHLSGLARKFPDVKFKAISTTCIPN---YDRNLPTIFVYLEGDIKAQFIGPLVFGG-----MNLTRDELEWKLSESGAIM
>CaPhLP2 -----YVLVHLSLQS-SLQSRLLSSILIDLASKFPELKICDIPAQCIEH---YPSNCPTLIYHDTNVVKQFITLTQLGG-----NATTLKDVETALADLNIVIG
>ScPlp2 QTNNDNGEEDDGGVYVFVHLSLQS-KLQSRILSHLFQSAACKFREIKFVEIPANRAIEN---YPSNCPTLIVYYRGEVIKMNITLLELGG-----NNSKMEDFEDFMVKVGAVA
>AfPhLP2 -----FVLVHLTSTSGNVESRVLSDLWRQLAMKYGDIKFCEIRGDMCIEG---YPERNTPTILVYKDGEIRRQLVTLRELNG-----PKTKLESAFTNDXCCINVG
>SpPhLP2 -----FVVVHMFQDS-LPACKLLAAILERLAPMPQIKFVKIPGKQAVEN---YPEAMMPTLLIYGHGDLQQQILTLATLGG-----MNTSVVDVAEALVRAGALK
>DmPhLP2 -----WVVLHLYANG-VPLCALIHHMQQLAVRFPQTKFVRSVATTCIPN---FPEKNLPTIFIYHEGALRKQYIGPLELRG-----DKLTAELEFMLGQAGAVP
>EhPhLP2 -----YVVVLLYKNG-IEGCDILSARLNELARKKRSTKFKVILSHLAIPD---YDPKLLPTLIVYRNTNHVKQFIGLAEFGG-----NNMTCDDLEWALSRVGAVE
>PfPhLP2 SKKNPLKRKPKGTHVLLHLYSEN-VISCKVLNNILKELAQKHKYIKFTKGIYNRIIEN---YPENKLPITLIYYNGTCIHQICNVLDHIKGG---NNLNMPTFEKFINKYHIFR
>DdPhLP3 -----VVHFYHSD-FQRCKILDKSEILAKTHLGTkFLKVNAEKAQFFTGLGIRILPTLVFFSNGIAVDRCVGFEEFGGI-----DSFKIEQLAIRISKAGVLD
>HsPhLP3 -----VCHFYRDS-TFRCKILDRHLAILSKKHLETkFLKLNVEKAPFLCERLHKI KVIPTLALLKDGKTQDYVVGFTDLGNT-----DDFTTETLEWRLGSSDILN
>MmPhLP3 -----VCHFYRDT-TFRCKILDRHLAILAKKHLETkFLKLNVEKAPFLCERLRI KVIPTLALLRDGKTQDYVVGFTDLGNT-----DDFTTETLEWRLGCSDVIN
>DmPhLP3 -----VCHFYRDS-TERCKIVDMHLKILAACHVEAKFCKVNAEKT PFLTQRLRIKVIPTIALVKDSKTKDFIVGFTDLGNC-----DDFATEMLEWRIAHS GAID
>CePhLP3 -----VCLFYLPG-NFRCKIVDKHFEILARKHVGTFRFIHVNAEKVHFLTTRLNIRVIPSIAIVVKQQTVDYIRGFDELGGK-----DEFTTETMENRLARSEVLT
>CspPhLP3 -----VCHFFRPS-TLRCEIFDRHLEIISKKHLEAKFIKINAESHFVCSNLNINILPTIALIKNSKLIHKIIGFEELSSR-----DNFTTTQLEELLVRRNMIQ
>AtPhLP3 -----ICHFYHKE-FYRCKIMDKHLKTAPRHVDTKFIKMDAENAPFFVTKLAIKTLPCVILFSKGIAMDRLVGFQDLGAK-----DDFSTTKLENLLVKKGFFT
>ScPlp1 -----VIHFELET-FGKCQYMNKLENLAKRYLTTRFIKVNVTQCPFLVNKLNIKVLFPVVGKNGLEKVRVYVGFSGKLGNDP-----NGFDIRRLQSLAHSGVIE
>KlPhLP3 -----CVVHFFVDS-FRKCQVMSKQLQVMAESHLSTRFFRISVADCPFLVEKLSLKVLPVVIAYQNGKEQDRLIGFAKLGNNA-----NDFSIDHLEKWLQRSVGPV
>AfPhLP3 -----CVIHFAHPD-FARCGFMDEHIRALATRHHEVRFARVDVRNTPFVVNKLNI RVLPCVIGFKDGIVVERVVGFEGLGAGGRDGADSFDIATLEKRLWLKGIILT

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>DdPhLP1  NPMKAKNSNWETS-----LSRKRP-----ESDDDNDD-----
>EhPhLP1  -----
>CePhLP1  MAGGYASD-----SDNESEDD-----
>CpBDM-1  -----
>HsPhLP1  EKEVLVLTSVR-----NSATCHSESDLEID-----
>MmPhLP1  EKEVLVLTSVR-----NSATCHSESDLEID-----
>DmPhLP1  SI-----
>HsPhd    EREVHVLEHTK-----IEEEDVE-----
>MmPhd    EREIHDLEQTN-----MEDEDIE-----
>DdPhLP2  SDLQEDPRITL-----ARKKSQKSRY-----SKADSDSDNSDSDD-----
>OsPhLP2  NDGQSGGD-SSRDNVIEG-----VRRKFIEKV-----AQHEEREEDDDSD-----
>AtPhLP2  NDGKGDDDDSSREAVMAG-----VRRQFIERV-----KDHEKDNDGGSNSD-----
>MmPhLP2B SDLEENP-----KKGADMMVSSI-----RNISIYD-SDSSGSDTEAK-----
>HsPhLP2B TDLEENP-----RKDMVDMMVSSI-----RNTSIHDD-SDSSNSDNDTK-----
>MmPhLP2A TALEENP-----KKPIQDLLLSSV-----RGPVPMRRSDSEDD-----
>HsPhLP2A TDLEENP-----KKPIEDVLLSSV-----RRSVLMKRSDSEGD-----
>CaPhLP2  FHDKRLIINNDEDELE-----QARKLRFAKKSIRDGNR-----NNEKDKDEDDDDDDDFYD-----
>ScPlp2   EGDNRILIMNRDDEESRE-----ERKLHYGEKKSIRSGIRGKF-NVGIGGNDDGNINDDDDGFFD-----
>AfPhLP2  XSCLADLERMLVDLGAL-----KESDVRLKKRSYSFDEERQS-----NIRSANVEDYDDD-WD-----
>SpPhLP2  DSDIAALKDPQNAEDEL-----GKRD-----SSV-----NDDLDDD-FD-----
>DmPhLP2  TEITEDPRPQIR-----DKMLADLEDKSSD-FY-----
>EhPhLP2  TTMKSDPKE-----KRHPKFSGGMF-----SRERDSYDDDDSD-----
>PfPhLP2  TCHNNMYNSKDNNSDNYDDEDELN-----KKNIRTQKQYTSFNMFYNNKGNQHYDSDNSSVEDKEIHSRGYASSYLDSKLRLNKF
>DdPhLP3  FKHTTGL-----KIIS-----KQDVKNKFKEDD-----
>HsPhLP3  YSGNLMEPPFQNQ-----KKFGTNFTKLEKKTIRGKKY-----DSDSDDD-----
>MmPhLP3  YSGNLMEPPFQSQ-----KKFGTNFTKLEKKTIRGKKY-----DSDSDDD-----
>DmPhLP3  YKGDLMQPPDV-----KR--KPFINRPQKTIRGG-Y-----DSDSDIDLDD-----
>CePhLP3  VEKKHTAPAK-----KKIIRSGVEEYDN-----EEDW-----
>CspPhLP3 EQ-----
>AtPhLP3  GMLSE-----KRKEEDEEDYEYQESIRRSVRSSANV-----DSDSD-----
>ScPlp1   DTFEI-----RKHSSVNTERF-----ASTNHDRSESDSLDI-----
>KlPhLP3  MRDTKLTIISNR-----SKQIRSK-----NKTNSDQEDSGSDWD-----
>AfPhLP3  QTKFKNNEDDSDISEGGSGDEGSNRRRPGTGRRRTIRS-----GNGRHHGGDDDDDDDWG-----

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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|