>gi|226502628|ref|NP\_001150193.1| peroxin Pex14 [Zea mays]

MAEKSPSSAPQGGSGGNESFDNLVIQAPQLMREDYIQNAVKFLSHPKVKGSPVFHRRSFLEKKGLTSEEI

DEAFCRVPDPKPNGTDAVAAGRQQANNPSQSVVLQPYTEVQPQAATASATAGPIVPHTKAQLSWVNTLLG

AGLFLGLGASAAITLKKLVIPSLKSWTRRVVAEGDENAKSEHTSKLCEEIREAIKVSASAFSDIAKINQE

VLASKDEDRKVLMKLTEAFESQENVFKSLSETLNRIRENQLSQHSLLEEHVQPSSWNGPIDYQGRAFQQT

NMYATPPNNSFDTGRNSFMPLAAESSYGPFPGSYSERVQRPGGYGFQQQTSSDRLNVVGPRSSYQGGSSN

HHAGSNAMDDPAAVAAELQRRWVPPQPPGVIMPEAAAAIRQARSVPRQLPSGDGRLGADVPRQPEPAIAM

ATTEHVNVAPEAPGGELPSDGGGAMTADASNGGGSGEQQEQEAS

>gi|226507804|ref|NP\_001152579.1| peroxin Pex14 [Zea mays]

MDEIBEAFQRLQSPSSNSASSNMCTSQGVFDHSCRITEEIKVDRKCMDGLXRVEPEAGPVAPVVPRHPKS

YMEIMEMIQRGERPDDIQDINDDPPNPDQPISEPRMAPKPKPWEKQGQGSLACDLKSPPRESDVLRSEVQ

HDGTNKATESADGANQTHSLLQVGVAAGSESPAVPDDAASSLE

>gi|226499598|ref|NP\_001149369.1| peroxin Pex14 [Zea mays]

MASGTGSGQPQPAAADADPGAGDNKLVFETPLQPQPVREDYVENAVKFLSHPKVRGSPVVYRRSFLEKKG

LTTQEIDEALRRVPDPEPITTATASPQQQVGSQNQSAGAQTYAPARSMHPATAGPVVRPRFSWYQAFLAA

GLLLGFGASTAVFIKKLFLPRLKSWIRNVVAQGDGAEGNQLKHRIDEETAEAVKASASAVSAIAKTNQQL

LASKDEEKKILVTLTQALDSQAKELKSLTESINRTREPINITRDDRFSQHRPLEDHVPPVTRNGAINSSW

RSSQQTNMYGVSHGDFGSARSASFVPAPAEPTAGSFSRSCAEQTSTAAQRADRSSGGKPWEMQQYSQQRP

GYGSNSQLNDDGSYSDAQDSYAPSYYQNGKAPDFQSDEPRSLTYNTGIEERPPPPQRRWVPPQPPGVAMP

EAAAAIRQPKVPPKQPSSDASRAAGEMQVNGASSASPDAVTEVPVNSATTSDAGHSEIEEQPVAV

>gi|374607382|ref|ZP\_09680183.1| peroxisomal biogenesis protein peroxin [Mycobacterium tusciae JS617]

MRIQSTSLTTLLALAAAAVAIIAAPTAMAASTIAAKPGQVLTACDSTGPGTECITPGNAQINDSLPVDNF

YSYGSYGYPYGGYGLALGGIGGIGGMHGGMHGGGHNGGHGGR

>gi|19075601|ref|NP\_588101.1| peroxin Pex32 (predicted) [Schizosaccharomyces pombe 972h-]

MIRAHLFSEPDNSKLWAKSTGSDAFDLILKVLLWTAPWYYCLTTLFFTWLIILYPRPTLACSVAAWLFWF

TSLDTLEPDDRKNTLKASEAVSTSAKTSEETAKPSETREDGEWNTLKNTLEADAQNLMSGFQMLQRRWSQ

PKTTTLKTEVKEQQASQSPSVEGENEPAGVKSNEATKPSVTEEKEKNAEQNKRRERLSISHIVTELAKKD

EVSSESGSNEIVNAKLKNEQLDSNFTLLDAYLEPLVHLHEYSRRSNTLFFFYLPIVMSILIFCLPTQALF

IVLSSVFLAWHSPPLQAVLFCIRRISFFNLLYEKFVIGKTKEPAKPVPQPSSNEPPAPSAENKQPSVSSP

EKKESPATHLLKVIGSSPYVVHSNHTNNTLTDKESSDPTEKCLYLIEHQRYWVGVGWLNRTLPTDPPNFT

NAGSTDPVAEPTAQLLPPDGLAWIDDKWSISPWTFTDTFWAQPAKTQFRTAFTRSREWRRRYRVAPPAEN

EKPHTSRTNTASSLSSTSEDQVSTHGSISSAKVTAIPDSNGAEAL

>gi|213407732|ref|XP\_002174637.1| peroxin Pex28/29 [Schizosaccharomyces japonicus yFS275]

MKKQATSLLHTTPNSELSPFILSQSSIRFATRIAFVFIIRDEIVQAATWADPGKSICLGLTLTLFSLYPL

TIGLILFVCVITMMPNNLKRDFTSNLRDLQNSMTLYCDIYDKMVAFRENWCHYVSPKIISSIVFAGVCSV

FLLASLRITIDRYLPLLIWVSLLALHPAVRKYFGRDLRVRQSAMQGFQLRNETAIVWSHSLGSSNEPCYF

TNSPDDNERTERVTSLDLVLPPTNYNWAPNSRWKFVPPDQYCRHIRWSPTASK

>gi|157868062|ref|XP\_001682584.1| putative peroxin 13 [Leishmania major strain Friedlin]

MISLRRSSSLLVEEWKSIVAPVCYASLEFFVVSSTFSLIRPFIMFSGMYGGGLGGMGSAMYGGGLGGMGG

MYGGGLGGMSGMYGNSGLMGGSSYAMSGGLNSFVRNNPYGSNSNYSVGGFNSLGSNADGTQNNGMQSSIN

LQQQADQSNHLASPIHQHAATLPPLNESPEERSRRIQAEHKKERQLIRQQREQHRQARLQARMEIVGHLT

NVLVQGLRSAMELFGVCFGTYYSMKAVRAFSSAQERMPSMGMGMGANYPYGAAVAKTQAVATGASGVQQV

AKAASGGSSKWRAWLLCIAFFLLGEVVYGIATRQRAKLPQRRRRITGPAEDAYGNVLSQDEYEVSIRSSD

AESRLTEGDKGEEETLSEAWGQAYNANGVCGVSQAARPSGGNGTRRVYYALYDYQAPQADGSCLSFKAGD

EFVVENYAEGSWCEAMAVEGGSYSSHGRRGLVPSNFLRLAERITKL

>gi|389602810|ref|XP\_001567860.2| putative peroxin 14 [Leishmania braziliensis MHOM/BR/75/M2904]

MATAVPAQSQGALPEPLPEPEQPSASEMDADATVQSAIRFLQDPRVRRSPIESQIRFLKGKSVSDGQIKY

AFAKVGRAVTTEKIASVRASPANTAPPTATATVGATPLSPQLETARQNAPVTMGPGLQYTQTLFPYSPLP

LQVERQKRTVDWRDVVIGAGAAMLAGLSGYKLFNRYSPYEFRRKSEKKSRLYRGSCSRHRPANNASSESE

IDALSTSQRGRAPPLPPSPPVAAPAEPIVPATPPPDLTEVKKLLAELNETKEALANERKKCADLAVSAAK

IRADKQQLSRANDRLTQQIDELKKDIERLEKGTAASEATQMAGESVVAAESTSTSTYFPSVTAEGEQARK

SPAVTPVPSVSAPNPNAVPGLPVLPSTESSTVVTAAPAILDLNAEVTPVSPTSVAAVAPTPEPFPAAVAA

AASSADAAVPGASATEVVERLLPTSSADPPKAREDTPVSAS

>gi|157869194|ref|XP\_001683149.1| putative peroxin 14 [Leishmania major strain Friedlin]

MAAEVPSQPQAALEAPLPEPEQPSLSELDADTTVQSAIRFLQDPRVRCSPVESQIRFLKGKGVSDGQIKY

ALAKVGRTVTAEKIASVRAPLANAAPTGATATAYATPLSAQLKTARQNAPVAMTPGPQYTQMLFPHSPPP

PQVERQTKTVDWRDVVIGAGAAMLAGFSAYKLFNRYSPYEFRRKSDKKPRLYRGSSSRPRPANIASSGSE

TDASSTPQRGCVLPLPPPPPMAAAAEPSVSAASPAALTEEVKRLQTELDEAKEALANERKKCADLAVSAA

KIRADKQQLSRANDRLTQQIDGLKKDIESLEGKKSSAVGEATQTAAEGAVAAVPAPPSTYFPSVTTEGEQ

ARNSAEVTSVTSASAPNSDVMPVLPVVPSPEATAIAAAAPAMPDPITEAAQAAPASVAAVAPAPESPPAV

FAASTPYVDAAAPVATVTEVAAPLLSIGSAEPPKAGDGTPMSTG

>gi|339898161|ref|XP\_001465481.2| putative peroxin 14 [Leishmania infantum JPCM5]

MAAEVPAQPQAALEAPLPEPEQPSSSELDADTTVQSAIRFLQDSRVRRSPVESQIRFLKGKGVPDEQIKY

ALAKVGRTVTAEKIASVRAPPANAAPTGATATACTTPLSAQLKTARQNAPVTMTPGPQYTQTLFPHSPPP

PQVERQTKTVDWRDVVIGAGAAMLSGFSAYKLFNRYSPYEFRRKTDKKSRLYRGSSSRPRSANIASSGSE

TDASSTPQRGCVPPLPPPPPMAAAAEPSVSAASPAALTEEVKRLQTELDEAKEALANERKKCADLAVSAA

KIRADKQQLSRANDRLTQQIDGLKKDIERLEREKSSAVGEATQTTAEGAVAAAPGPPSTYFPSVTTEGEQ

ARNSPEVTSVTSASAPNSDVVPVLPVVPSLEAPATATAAPAMPDPITEAVQVAPASAAAVAPAPELPPVV

VAASTPYADAAAPVATVTEVAAPLLPIGGAEPPKAGDGTPMSIG

>gi|339897920|ref|XP\_003392410.1| putative peroxin 13 [Leishmania infantum JPCM5]

MFGGMYGGGLGGMYGGGLSGMYGSSMYGGGLGGMGSSIYGGGMYGNSGLMGGSSHGMSGGLNSFARNNPY

GSNSNYSLGGFNSLGSNADGTQNNGMQSSLTLQQQADQPNQLASPIHQHAASLPPLNESPEERSRRIQAE

HKKERQLIRQQREQHRQARLQARMEIAGHLTNVLVQGLRSAMELFGVCFGTYYSMKAVRAFSNAQERMPG

MGMGMGATYPYGAAVAKTQAVVTGASGVQQAAKAASGGPSRWRAWLLCIAFFLLGEVLYGIATRQRANPP

QRRHRITSPAEDAYGNVISQDEYEVSIRSSDAESRLTEEDKGEEETLSEAWGHTYNANGVYGASQAVRPS

GGTGARRVYYALYDYQAPQADGSRLSFKAGDEFVVENYAEGSWCEAMAVEGGSYSSHARRGLVPSNFLRL

AERITKL

>gi|321257627|ref|XP\_003193656.1| peroxisome biogenesis protein peroxin 19 (Pex19) [Cryptococcus gattii WM276]

MKTRTRTICPTLTVRSPYRCANGFADDTTTDVLESFQSSRPSASTLQREASLPSSTQPRPSTPPSEETDE

DFEASLMQGMESLLRQLAGDYPPGVMPDIEGDGSPKPTDPTMAGSRSVEPSPLSGEAEEAAWQNAVNTLL

SGEGLAALGMDESRSSRDKEKASSKPPHLNGTAPKPSYEDTLRKTLESLKSAGQNTGASSSAAKDGQNDI

ASLFASLGGDPDLLKGMNLGEEGGEEDFEGILEGMMAQLMTKEVLEEPMSELAVKYPPYLASPPPDTSPE

DIAKYHQQYTLVTRIVEMFKKPGYTDEKDGKDIARLVSEMQDLGGPPKEVMGDLPEGFDLGVLGNEDGCT

IM

>gi|317145527|ref|XP\_003189715.1| peroxin PEX11-1 [Aspergillus oryzae RIB40]

MTVKTLIQKPKPNLLRQFANFTRTTAGLEKTCRLIQSLAQLAIELDITPGSTTTAQWQTARSQIALTRRF

FRFFAFIDCFSQVYGLLGGAQGQGLFMTLIEIGRWSCLGLYLVLEDLTILHALGVHPVAWNTPVLVEAFK

FWFYSLALSVIGAVWGLLSTSSSSASSKTGSDEKKNKKKNAEKTVSNTDDSQTKAQRTALMKRIVVDGCD

LLIPGVFVGWMQVSDLMIGVTMVISTVVSGGDAWVKAQG

>gi|317143759|ref|XP\_001819683.2| peroxin Pex23-like protein [Aspergillus oryzae RIB40]

MEDRPSLNLIDNTSPTRRLSDDEGLSEVTTADDLSRNTSRRWKKPSVRRELTKRKYKKWQPHKLGITDDN

ADRRPSDARLSLTATYTNTEGESLVDTPTVPTTEQRDFGASEQENDDPESVTGHGVRGLKPGSELDILYE

NQRGWFFFGIPLYSQGSLLNFDPSAWVTYDFRDSPVNITNAQVPDPSWEWAWKTWYVDMSGDVDDQGWQY

SFSFSSSAWHGSHPWFHSFVRRRRWVRLRVKKASERSRRGRSGFEMAHMLNEDYFTIHTAKKKRAASAGR

GSQGPSTHLSRATTNVDEEGPLEEIGNIPTLMYALKNAKIDREKFDILRRFVAEGGQELYYLDEKMQDIM

ALFVFQASRWQLVTYMTDLIEELSGKEPESSGMDAEETRRQKDYLSKAVATAKHYLTGPEILAPEGRVPA

REMSEMLDLTPEAKRESLLSRSSGKFSHKPIDNGGEIKGIPQAAEIGREGHIYQYTS

>gi|317025624|ref|XP\_001389464.2| peroxin Pex22-like protein [Aspergillus niger CBS 513.88]

MSFPYSQDARRRRVGAGAGFSSTGNRTVLGYWVPLAVTVGIATVSIAAWIWSERSEDDDDNNNNNDRDAN

PPPHDGRFPAPEGYPHGEYADDYARSTATDIPGAMPDDASMMARMQGALRRTPSPQQIFDGASKKVAAGV

AAAGAFVGGALTSIREEDRGDFEDHSRWSEEVASRAQRAEQPAPTMTGALPVRDVGVGGPASATKKRTVA

IVVSSESAQVDPDDIVSQHVSILSHLPEHVNLDTARVFIMIYAPGLKHAPKQGSSSQPDLSVASSYSNIA

PEEAVASGELPEGESPSESRQVDEEDGSTPLFKTLYTQAQALVEKENTIMPFSTATGYVHLVRHLSPEVV

YVQESLTGESGEHVKLFSGWVRETVVVVGGEIGHGGLVDSDDESALADKGEKWWQKEGVTGLGKRINVVD

VHRIGDDWRRRVSGLD

>gi|169779789|ref|XP\_001824359.1| peroxin PEX11-2 [Aspergillus oryzae RIB40]

MVANTLDCHTTLAHSLRFVATTVGRDKLLRTAQYFSQFYIWHLHRRNYKRSAIDPYHALRKQLGTTRRIL

RIGNFLGNLQTVARLMSQKNSSEPVLKYLAIGGQLGFAGYLVFDNITSIKAIGIHELPSAERLDILADKC

WAAGLIFSIMACLYILVHTQPKKRAKPAERERYSDENKCAKERSDAWIQLISDLCDLTVPGKSLGCAAFN

DGLVGLAGTMSSLIGAWSQWKKTA

>gi|169769843|ref|XP\_001819391.1| peroxin PEX11-2 [Aspergillus oryzae RIB40]

MVANALAYHPTLAHYLRFVATTVGRDKILRTLQYFSRFYAWYLYRTNRPQSSIDPYNAVKKQFGTTRKIL

RIGKFAEHLKAAAVAADNKSPVDPVLRYLAVGRQLGYAGYLTLDTITVIDVIGFRKLAAAKRLQDTAYRS

WLAGLICSAIASVYSLWRLREKERTLDRTEGEGVVEAKKLEKERSAARIQLFSDLCDLTIPVSGLGLANL

DDGIVGIGGTISSLLGVVSQWRKTA

>gi|169767096|ref|XP\_001818019.1| peroxin Pex22-like protein [Aspergillus oryzae RIB40]

MSFPPDARRRRVGAGTGFSSSGRRTALGYWVPLALTVGVAAAGVAAWIWSERIEDEDNDGNYPRGDDGFP

APGRGGDELPPGYDGDYARSTATDIHDTDDVSMVARMQGALRRTPSPQQIFDGASKRVAAGMAAAGAFVG

GALTSIREEDRGDFEDHSRWSEEVESRSRRDLPDLAAPTASGTLPGPGVAAGTSSGSKKKKTVAIVVSSD

TSRLDPEEYTSDHASILSHLPEHIDPDTTRVFVMIYAPGLKHAPNQGTGSHPTMSVTSSYSNIAPEEVLS

PGEPPIGDLNASDSRQDDQTPLFKTLYTQAQAIAEKESMIMPFSTSTGFVHLVRHISPDIVYVQESLTGK

EGEPVQHITRWVRQVVVVVGERGGLVDSEDESALADSGEKWWQKEGTTGIGKRIDVVDVLRTGDDWRRRV

SGLD

>gi|145252320|ref|XP\_001397673.1| peroxin Pex23-like protein [Aspergillus niger CBS 513.88]

MDNNDQSNTSSSIALIDNTAPRRRHSETPTATTNGGSHVSRKWTKRSIRGELKKRKYAKWQPDRLGLTTD

DEDNDNYNYNNNEGEENIPSSSRRPSERPETDLFTTETATTTSNPPSQYQSQSDSQSRSPSQQPSPPSHD

ISATDFAPESTLTNTTTTHSHGPTKLTGLKPNTELDILYENQRGWFFFGIPLYSHSSLLNFDPSAWQTAD

LRDSPVDITNAQVPDPSWVWAWRSWYVDMSGDVDDQGWQYSFSFKSTAWHGSHPWFHSFVRRRRWVRVRT

KRLVDRHGRTGLEMAHRLNEDYFTIHSGKKKKRPVSEVGGGGYGATSLGRTTTATTAREEEEVPIEEIAD

VPALMHALRVAIVDREKVDALDRFVEEGGEELFYLDEKIPEIMSMFVFQASRWHFVIHLTDVVESLSQRL

SSASGNEATELQRKLNHLQKATETARRHLTGPGVLRTENRKSSMEMLDLTPVSKRGSLLARYSGRFEFKS

MDDGGEIKGIPKEAEVGREGHIFQYSS

>gi|145243466|ref|XP\_001394260.1| peroxin PEX11-2 [Aspergillus niger CBS 513.88]

MVADALVYHPALAHYLRFVATTVGRDKILRTLQYFSRFYAWYLYRTNRPQSAIEPFNAVKKQFGTTRKIL

RIGKFVEHLKAAALASDNKNPIDPVLRYLAVGRQLGYAGYLSLDTVTVIDTIGVRKLASAKRLQEHAYRS

WMAGLVCSAVAGVYTLFRLREKEKTLDRKEGEGVVEAKKLEKERSAARIQLISDLCDLSVPVSALGLASL

DDGIVGLAGTVSSLIGIWSQWRKTA

>gi|308814186|ref|XP\_003084398.1| Peroxisomal biogenesis protein (peroxin) (ISS) [Ostreococcus tauri]

MTYADVAASTPSKTARARGSGRTRGTNVNDDAIDRALVLAARIRTFLTTYDARDKCASMAQYCALFVSNG

EAGRALNASKSLAMARKPFRALKELDALAPAVERKFGSKTRARARMSAIEEGAFYGKALGMFAYFAFDHV

VWATSAGIVGSTRDAALQEKAQRASYWGWFLGSACGLFXX

>gi|308799599|ref|XP\_003074580.1| peroxin Pex14 (ISS) [Ostreococcus tauri]

MGEDAIASAVTFLRHPNVRASADARAKRGFLEGKGLREDEIDEAFRRAGEDASASGEGGGVKMPAEGVKG

SMASSALRLVALVGAGYLAYPSARRLLERARDYLEKKGDAESGKEGTTATVMSTPMVTPRTEFTSDGLTP

ELTRRLELVVESAERAEERAVELREEMKRDVRESVRDLKSDLETQIRLEMAELKRAYTESPVRTSSAKNE

TWPLKASPPESESDGESDAFTPESRMKPPRYDVSQIATTPSEQPNYFSALQTQRPPNRASDESLVDPPHP

GNFMDILQMLENGKTPPGIKDVDDTPPNPNAAIPTSSANRPGKPWEATPSFGSNGRSFMEEDVPIKRVQG

NSTSDSTWKPPPAPEFSRVMSTASSSETNERAAMSPKSPRRSVDDKSDRAKDASHYAKTLI

>gi|255931625|ref|XP\_002557369.1| peroxin Pex16-Penicillium chrysogenum [Penicillium chrysogenum Wisconsin 54-1255]

METVRNIQNPIPPVLLQPSKWLSIYEDFVTKNASSVGQVESALRSLTYIIPGRYRESEIPSECVHSGVQL

LSLYHDSLVSRVVDRLPSTVPRPPPTPHSRYTKYWASRSSLYRQVALALQMLQYTELLWEMAARRRGQKT

RWRVVIFIEFAKAVCRLLLLRLTNSRPLVSPPLPEREVDPRTTEEEEPQSDWNGMDTPVSDRSSDLSWTM

PRTGLSLPSLPDVNDVSNYLISKVLTADDIKPPKALLHRATGQGQLAEVLYILRPVVYAMAMQKWRGDKR

SWRPWLIGFGMEYGCRQLAKRDFRERVAGGLRGLTGLEREELKKRGWSMGWWMMRGAFYENITKSWLHSL

TGKMKGKPLLDLVGSVVEDYEYLWDNFYFSTATL

>gi|255934154|ref|XP\_002558358.1| peroxin Pex23-like-Penicillium chrysogenum [Penicillium chrysogenum Wisconsin 54-1255]

MENSPSISLVDNTAPQQPTGEGSTRRTSTLNQGSLTKHLSRASVQSQLKKRKYAKWQPDRLGIAPGTNDS

PSRESSQVRGDSISASSRGEGSGGRDVETADFAPSRVSTNNGNGSGSGSGSDQVNGVGDQTNGGEDTKSR

SEMDVLYENQRGWFFFGVPRYSHSSLLNFDPSPWMTQDRRASPVNITNAQLPDPSWEWTWKTWYVDMSGD

TDEQGWQYSFSFASSSWHGTQPWFHSFVRRRRWVRLRTKVHPRRNLGRSDFEKSHMLTEDYFTIHSSKVR

SREQSTTGLPRVESGFLNQASMTVDEESHVDEIGDIPTLMNALKLASIDRERIDALKKFIEEGGDELYYL

NDKIPDIMPMFLFQTSRWQFVTYLSDVIRELSKPSTDSDKDADAVQRKKDNLTRAAESCRRHITGPDVFK

GDHGESGTGLLDLTPVAKNDTLMAKRPVLEERARSMRRVFKGIPKAAEIDHEGHIY

>gi|242014658|ref|XP\_002428002.1| peroxin, putative [Pediculus humanus corporis]

MEENFFYHQNNPSILDFFAQEALDNLFYPAAQKFLFYLANRYDNLTVVKKWFNEIYYFSLLFPLQYHYLK

KYNATFFENFYGLERKNIQNPLGKLSKKNLILSLGTVVIWPYLKSKLNEFSEKLSYENDFSINDNKKLNW

KKFIIGSNSAINIIFIVINTFQHIKYLSEKSEIISPLLWISGVKLKYNERLMAENENFTLKNIIKGIFPS

NIFGIGAFLIELTNMLQTENKNNGNSFFIPPPPPPPRLNQGYSHDDNPIKCHHVGNYSKAVIPESGHMYC

LECIIKFLIENGYCPITKIPADVHNLIRIYSPV

>gi|241957443|ref|XP\_002421441.1| AAA-family ATPase, peroxisome biogenesis protein, putative; peroxin 1, putative [Candida dubliniensis CD36]

MDNHKAKVSYKTLKSNLVNLPSNLTNLLFTANIQVQDVIIEIVTTTTTTSNKSLIKRYAGWSGMSSSDIS

NLEIDPIFAQSLNLIDKTPITVNLKLGNYESTNINLEPLTSSDWELVELHAQSIEDKLLSQTRCVALNQV

LVVYPSISTSAKLLVTDLGSTDHTFAKISAYCEIAIAPKVREEKQHKDKTGSSNKSIASSKSTKKTPTSS

SEDYSDLPSVLKRGISLPHKLYDGNETVNIAGYFVYVDIKDELPQGFSSEYVAVSVIPGPNDKTSTKTLP

ITEDDDNDKNKNLKENKRIIAKLVDYKFGPSGNIGLSHNLSIALNIENQIGNIISLKPAIKNLPKRPTTF

TIHPYIIHSKKKEITISNNKKENKLAQQLTEIMYPDIASLPITNFMKIPIIANILPYGGLLKFRKNDEYN

AWIKPYNLDTKKPIKFEIGDEILRPSSFIQQEQKINNHNNGTEYEYGEKEGKEEEEEEDEELEAIGLDDT

VEEIVDSFITSENTGTLIYGNSGSGKTLLLKLVARQLNQQYGYFTKYISCDTIMNENFQNLSKNHFFKWI

QVCSWNKPSILILDNIDKLMNIEMENMDNTKSNQLTEFFIANLTKIHHQLNSNLSILLSANSKDNINKLL

LGSHLIENFHHLTPPDKSLRFEILEKYLINKLGLIIKVDLMDLVSETDGYLPNDLKILSDRIYHEVLFNS

NNTNLQEVTEEHITKALTGYTPSNLRGVKLQKSSINWSDIGGLKEAKNILLETLEWPTKYAPIFANCPLR

LRSGILLYGYPGCGKTLLASAIAGQCGLNFISIKGPEILNKYIGASEQSVRELFERAQAAKPCILFFDEF

DSIAPKRGHDSTGVTDRVVNQMLTQMDGAEGLDGVYVLAATSRPDLIDSALLRPGRLDKSVICDMPNYED

RLDILKSITLKMDLSEDVNLHEIAEKTIGFSGADMQGLGYNAYLKAVHVTLEELSQREQDEANNDDGNNI

EKKENSIEFFQVGNSEKKLNTNEKIQLLHQIQQFMTKKDNSDPKLKTGQDEVINKSKVLITHENFLASLK

ETKPSISHSEKIKLTKIYKEFVNDRDGNMPNGTPSNEIGGRTTLM

>gi|241953946|ref|XP\_002419694.1| peroxin, putative; peroxisomal targeting signal receptor, putative [Candida dubliniensis CD36]

MSFVGGGSECSVNGNAVAQFNKHAQQDRSLQQQVANQHGNLAQNQGFKKDNLMNVRDRANLDQFMNNGAP

QNSFQFQPMRHELNAIQNQPNPIHQQQNNWSQDFVAQSPSAQIATPIAKTGSPVNAQWANEFSQVSSTTQ

PQQHNQRPGQFGPRLGGYRPMMGMSMAYQSQPQQQQQHAQTQNQEQQVDWENQFKEIEELTNKAEEVEEI

QREQSPEIVVDDKYQATFQEVWDSLNSEAFENDFINQQYEDFKRTQKDGYPADMNQWEKDFAKYASTRAH

FGDYQFEDKQSNQFLDLPKDQDPYEIGLQLMENGAKLSEAALAFEAAIQRNENHVDAWLKLGEVQTQNEK

EIAGISALEKCLELHPENSEALMNLAISYINEGYDNAAFATLERWISTKYPQIVEKARQENPTITDEDRF

SLNKRVTELFLKAAQLSPNQASMDADVQMGLGVLFYANEEFDKTIDCFKAALSIRPDDAILWNRLGASLA

NSNRSEEAVDAYFKALQLKPTFVRARYNLGVSCINIGCYKEAAEHLLSGLSMHQVEGVDTVSTLNHNQST

SLTETLKRAFIAMERRDLLELVKPNMDLNQFRGEFSF

>gi|241951494|ref|XP\_002418469.1| peroxin, putative; peroxisomal biogenesis factor, putative; peroxisome biosynthesis protein, putative [Candida dubliniensis CD36]

MPSVASSSNDVSISQEAFESVTTIANVSIINDPSLNQYDTLDIGDELFSKLFPKEEINSSTQIVNNKFVL

VKLLGAPDYFNKFRIMKLHEVRYQLRESIVITNDSNLVKFNNDSLTLNKAVIKSIDYDDIPKLSQIFVSI

PHEIYQLLHEKSPQVIKQKFLTQLLVDNGNVVNEGDSLRLINGTVNLCEPLTQGRVEYNTNIVLINQNED

KPSEQDSTDNNKNIDIEYEQDLVFDQDESLDLSGYLSSSLQFDQFTKSDKLNRFKVGPLPQKFNIDDLPS

NWKKDDTELFVFINNIDFIKLGFPIFNGDLVKVKTGTETVVVRIFTFTEPQNSFKIGTVYMSPILLINLK

LQSDSYIEFDPVTQLDTLSNTIPIAESVTISRVSSQITMDKTYQQSFFSSLKTTLSTRLKCVKQGDYLPV

VIDTVLAKTMFDNLIEDGNDNEETAGSGDGIDAIPIGNPDAVAWFKITEVKGANSIDTNQFLIDPLKTML

VSSGVESIRLPQNSFVKWYQYLNLPPIFNYQEGTNFKYAQEFKKTLSTCLSSKINLKTSILLTSMSRGIG

KTTLVRNSCIELGLNLIELDCFDLLNPGQELKTIGLLTGKIDKLIANVQSTSSFHVIYLKHIENLCPKTD

ENDQNSSIFTSLSLKIIQVLHDYLKNYPNLVVVMSCNDYDKLNDNLKSIIKFTIEFTVPSENERLEIFQF

LINNEKNKNFTKDINSYPFIIRKDINYKNLALQSAGLTPRDLISIIKKSKKLAIKRLIKLSKDSKISIQN

IVNIGNGGVINWVPDDFNAAINEARNQFSDSIGAPRIPNVKWEDIGGLDLVKDEILDTIDMPLKHPELFN

NGLKKRSGILFYGPPGTGKTLLAKAIATNFSLNFFSVKGPELLNMYIGESEANVRRVFQRARDAKPCVIF

FDELDSVAPKRGNQGDSGGVMDRIVSQLLAELDGMSSEGGDGVFVVGATNRPDLLDEALLRPGRFDKMLY

LGISDTDEKQTKILEALTRKFKLGDNVNLQQVAAKCSFTFTGADFYALCSDSMLNAMTRVANEVDEKIKQ

YNLQLSQQGKEKVNTRWWFDNVATEKDTTVLVQMEDFIKAQNELIPSVSAEELQHYLRVRENFEGGKEKA

KQQQEQQIQNHEDQQDTPEIIHEEDLLNNVLKLNGNGH

>gi|241951444|ref|XP\_002418444.1| peroxin, putative; peroxisomal biogenesis factor, putative; peroxisomal protein, putative [Candida dubliniensis CD36]

MIPISYPSPRVSQLDAGILDSELFSLLKDQLSSIFQLHNTSRYSFSQHSELYSLLLNLLIFRLTIWKSGS

SYGSSLQNLKLTDSKSGKIIGNSRKTLLGAVIIGGYLYKKLESYLFSLDESSTHNSASTLDKLKNYLLIN

KTSILSGLENSLKIANLVNFTFFLVNGRYSSLVNRVLGIIETPISSDLLKFNGSNVNYEFQNRQLVWNVM

TEFLVFILPLLQLRKLGRMTRKLLGRSKTSLDVQSGNVPTLTSYTNLPVSECAICHDNNNQASQTGGRTF

PSAGPVTNPYITNCGHIYCYVCISTRFNIIKVNGEDMPCLRCGKRLEWFEEFGLADGAVDEDAIVLSIEN

DASEESEEESDEEGSITSEKEVHSYEPELGQNRIQRHLSERSTIFDNQSADEFSEDEYSEEEEFDADEMM

>gi|241950723|ref|XP\_002418084.1| peroxin 12, putative; peroxisome assembly protein 12, putative [Candida dubliniensis CD36]

MEYYSSLDASQLDSERPTLFELISANQLESLLSPSLRYILVHYASKYPRYLLQVNNNFDELNLLLRSFIE

WYFLTYWQGTFTENFYGLKRVSQTPLSQGDYNSSRLTQLVPSMIEERRKLSKLQKLVSLFEVTGVSFVSE

KLNYCYEVWYTKYITNQLNTSDTLTTEENVKIKIKRKFVEIYPYLQSAYRAANFITTLLYLSGSSKSPTL

LTYLFRINFSRLNQYDYSKNEPKQPLSDSKRPNRIHPPTAIEYILRLLSNNITKPSWKVIKFVLGTFFPV

AIFTLKFLEWWNNSDFSSKLSKNLGNVLDFTLPPPSSLTLALRSYKKNEDKKNTETEVKQQKKKQYKSGK

VCPLCKKELTNPAIIETGYVFDYKCIYNYLEKSHIIVSKKVQTRQEEEDEDIYSEDESEDENIGHEKEEQ

KENIVIDINKGGRCPVTGRRLLGCKWNPIKEEWDIEGIRRLIF

>gi|241956322|ref|XP\_002420881.1| peroxin, putative; peroxisomal import protein, putative; peroxisomal targeting signal receptor, putative [Candida dubliniensis CD36]

MLSFRTKGYNGYGIQYSPFFDNKLAVATAANYGLVGNGRLFILNIEPNGTVSNQVSWETQDGLFDLAWSE

VHENQAVVASGDGTLKLFDLTVPNFPVMNWKEHSREVFCVNWNLVDKTNFVSGSWDGNIKLWSPNRPQSL

LTLNSHVIDYSTRVAPNTSSASVPLSHQPAHQPQSQQQQVNTANCIYSAQFSPHSPSMIVSCNGGSQVQV

WDIRSPNPLQLKFTAHGGLEALSVDWNKYKSTVIASGGTDKSVRIWDLRSITKIDQPIAQSPMASGHIRG

PTPLNELIGHEFAVRRVQWSPHNPKELMSTSYDMTARIWSDESDERARFLNSRVGGLKGVFGKHKEFVIG

SDYSLWGEPGWAATTGWDEMVYIWDSKRL

>gi|241956151|ref|XP\_002420796.1| peroxin, putative; peroxisomal ubiquitin-conjugating enzyme, putative; ubiquitin protein ligase, putative [Candida dubliniensis CD36]

MAEKRLFKEYNQYQKQLPQLNNDQIVSLSPVSPDKNILLWEATIAKPGKPDSPYYYGGQWKLSISVPTSY

PIDPPVIKFITPIVHPNINLTTGEICLDILKKESWSPAWNLEHLVVAILMLLDQPEPDSPLNIDAANLYR

QDKVAYESIVQFNMWKHHCFKSAVRNIRGVRDCV

>gi|241957443|ref|XP\_002421441.1| AAA-family ATPase, peroxisome biogenesis protein, putative; peroxin 1, putative [Candida dubliniensis CD36]

MDNHKAKVSYKTLKSNLVNLPSNLTNLLFTANIQVQDVIIEIVTTTTTTSNKSLIKRYAGWSGMSSSDIS

NLEIDPIFAQSLNLIDKTPITVNLKLGNYESTNINLEPLTSSDWELVELHAQSIEDKLLSQTRCVALNQV

LVVYPSISTSAKLLVTDLGSTDHTFAKISAYCEIAIAPKVREEKQHKDKTGSSNKSIASSKSTKKTPTSS

SEDYSDLPSVLKRGISLPHKLYDGNETVNIAGYFVYVDIKDELPQGFSSEYVAVSVIPGPNDKTSTKTLP

ITEDDDNDKNKNLKENKRIIAKLVDYKFGPSGNIGLSHNLSIALNIENQIGNIISLKPAIKNLPKRPTTF

TIHPYIIHSKKKEITISNNKKENKLAQQLTEIMYPDIASLPITNFMKIPIIANILPYGGLLKFRKNDEYN

AWIKPYNLDTKKPIKFEIGDEILRPSSFIQQEQKINNHNNGTEYEYGEKEGKEEEEEEDEELEAIGLDDT

VEEIVDSFITSENTGTLIYGNSGSGKTLLLKLVARQLNQQYGYFTKYISCDTIMNENFQNLSKNHFFKWI

QVCSWNKPSILILDNIDKLMNIEMENMDNTKSNQLTEFFIANLTKIHHQLNSNLSILLSANSKDNINKLL

LGSHLIENFHHLTPPDKSLRFEILEKYLINKLGLIIKVDLMDLVSETDGYLPNDLKILSDRIYHEVLFNS

NNTNLQEVTEEHITKALTGYTPSNLRGVKLQKSSINWSDIGGLKEAKNILLETLEWPTKYAPIFANCPLR

LRSGILLYGYPGCGKTLLASAIAGQCGLNFISIKGPEILNKYIGASEQSVRELFERAQAAKPCILFFDEF

DSIAPKRGHDSTGVTDRVVNQMLTQMDGAEGLDGVYVLAATSRPDLIDSALLRPGRLDKSVICDMPNYED

RLDILKSITLKMDLSEDVNLHEIAEKTIGFSGADMQGLGYNAYLKAVHVTLEELSQREQDEANNDDGNNI

EKKENSIEFFQVGNSEKKLNTNEKIQLLHQIQQFMTKKDNSDPKLKTGQDEVINKSKVLITHENFLASLK

ETKPSISHSEKIKLTKIYKEFVNDRDGNMPNGTPSNEIGGRTTLM

>gi|241953946|ref|XP\_002419694.1| peroxin, putative; peroxisomal targeting signal receptor, putative [Candida dubliniensis CD36]

MSFVGGGSECSVNGNAVAQFNKHAQQDRSLQQQVANQHGNLAQNQGFKKDNLMNVRDRANLDQFMNNGAP

QNSFQFQPMRHELNAIQNQPNPIHQQQNNWSQDFVAQSPSAQIATPIAKTGSPVNAQWANEFSQVSSTTQ

PQQHNQRPGQFGPRLGGYRPMMGMSMAYQSQPQQQQQHAQTQNQEQQVDWENQFKEIEELTNKAEEVEEI

QREQSPEIVVDDKYQATFQEVWDSLNSEAFENDFINQQYEDFKRTQKDGYPADMNQWEKDFAKYASTRAH

FGDYQFEDKQSNQFLDLPKDQDPYEIGLQLMENGAKLSEAALAFEAAIQRNENHVDAWLKLGEVQTQNEK

EIAGISALEKCLELHPENSEALMNLAISYINEGYDNAAFATLERWISTKYPQIVEKARQENPTITDEDRF

SLNKRVTELFLKAAQLSPNQASMDADVQMGLGVLFYANEEFDKTIDCFKAALSIRPDDAILWNRLGASLA

NSNRSEEAVDAYFKALQLKPTFVRARYNLGVSCINIGCYKEAAEHLLSGLSMHQVEGVDTVSTLNHNQST

SLTETLKRAFIAMERRDLLELVKPNMDLNQFRGEFSF

>gi|241951494|ref|XP\_002418469.1| peroxin, putative; peroxisomal biogenesis factor, putative; peroxisome biosynthesis protein, putative [Candida dubliniensis CD36]

MPSVASSSNDVSISQEAFESVTTIANVSIINDPSLNQYDTLDIGDELFSKLFPKEEINSSTQIVNNKFVL

VKLLGAPDYFNKFRIMKLHEVRYQLRESIVITNDSNLVKFNNDSLTLNKAVIKSIDYDDIPKLSQIFVSI

PHEIYQLLHEKSPQVIKQKFLTQLLVDNGNVVNEGDSLRLINGTVNLCEPLTQGRVEYNTNIVLINQNED

KPSEQDSTDNNKNIDIEYEQDLVFDQDESLDLSGYLSSSLQFDQFTKSDKLNRFKVGPLPQKFNIDDLPS

NWKKDDTELFVFINNIDFIKLGFPIFNGDLVKVKTGTETVVVRIFTFTEPQNSFKIGTVYMSPILLINLK

LQSDSYIEFDPVTQLDTLSNTIPIAESVTISRVSSQITMDKTYQQSFFSSLKTTLSTRLKCVKQGDYLPV

VIDTVLAKTMFDNLIEDGNDNEETAGSGDGIDAIPIGNPDAVAWFKITEVKGANSIDTNQFLIDPLKTML

VSSGVESIRLPQNSFVKWYQYLNLPPIFNYQEGTNFKYAQEFKKTLSTCLSSKINLKTSILLTSMSRGIG

KTTLVRNSCIELGLNLIELDCFDLLNPGQELKTIGLLTGKIDKLIANVQSTSSFHVIYLKHIENLCPKTD

ENDQNSSIFTSLSLKIIQVLHDYLKNYPNLVVVMSCNDYDKLNDNLKSIIKFTIEFTVPSENERLEIFQF

LINNEKNKNFTKDINSYPFIIRKDINYKNLALQSAGLTPRDLISIIKKSKKLAIKRLIKLSKDSKISIQN

IVNIGNGGVINWVPDDFNAAINEARNQFSDSIGAPRIPNVKWEDIGGLDLVKDEILDTIDMPLKHPELFN

NGLKKRSGILFYGPPGTGKTLLAKAIATNFSLNFFSVKGPELLNMYIGESEANVRRVFQRARDAKPCVIF

FDELDSVAPKRGNQGDSGGVMDRIVSQLLAELDGMSSEGGDGVFVVGATNRPDLLDEALLRPGRFDKMLY

LGISDTDEKQTKILEALTRKFKLGDNVNLQQVAAKCSFTFTGADFYALCSDSMLNAMTRVANEVDEKIKQ

YNLQLSQQGKEKVNTRWWFDNVATEKDTTVLVQMEDFIKAQNELIPSVSAEELQHYLRVRENFEGGKEKA

KQQQEQQIQNHEDQQDTPEIIHEEDLLNNVLKLNGNGH

>gi|241951444|ref|XP\_002418444.1| peroxin, putative; peroxisomal biogenesis factor, putative; peroxisomal protein, putative [Candida dubliniensis CD36]

MIPISYPSPRVSQLDAGILDSELFSLLKDQLSSIFQLHNTSRYSFSQHSELYSLLLNLLIFRLTIWKSGS

SYGSSLQNLKLTDSKSGKIIGNSRKTLLGAVIIGGYLYKKLESYLFSLDESSTHNSASTLDKLKNYLLIN

KTSILSGLENSLKIANLVNFTFFLVNGRYSSLVNRVLGIIETPISSDLLKFNGSNVNYEFQNRQLVWNVM

TEFLVFILPLLQLRKLGRMTRKLLGRSKTSLDVQSGNVPTLTSYTNLPVSECAICHDNNNQASQTGGRTF

PSAGPVTNPYITNCGHIYCYVCISTRFNIIKVNGEDMPCLRCGKRLEWFEEFGLADGAVDEDAIVLSIEN

DASEESEEESDEEGSITSEKEVHSYEPELGQNRIQRHLSERSTIFDNQSADEFSEDEYSEEEEFDADEMM

>gi|241950723|ref|XP\_002418084.1| peroxin 12, putative; peroxisome assembly protein 12, putative [Candida dubliniensis CD36]

MEYYSSLDASQLDSERPTLFELISANQLESLLSPSLRYILVHYASKYPRYLLQVNNNFDELNLLLRSFIE

WYFLTYWQGTFTENFYGLKRVSQTPLSQGDYNSSRLTQLVPSMIEERRKLSKLQKLVSLFEVTGVSFVSE

KLNYCYEVWYTKYITNQLNTSDTLTTEENVKIKIKRKFVEIYPYLQSAYRAANFITTLLYLSGSSKSPTL

LTYLFRINFSRLNQYDYSKNEPKQPLSDSKRPNRIHPPTAIEYILRLLSNNITKPSWKVIKFVLGTFFPV

AIFTLKFLEWWNNSDFSSKLSKNLGNVLDFTLPPPSSLTLALRSYKKNEDKKNTETEVKQQKKKQYKSGK

VCPLCKKELTNPAIIETGYVFDYKCIYNYLEKSHIIVSKKVQTRQEEEDEDIYSEDESEDENIGHEKEEQ

KENIVIDINKGGRCPVTGRRLLGCKWNPIKEEWDIEGIRRLIF

>gi|241956322|ref|XP\_002420881.1| peroxin, putative; peroxisomal import protein, putative; peroxisomal targeting signal receptor, putative [Candida dubliniensis CD36]

MLSFRTKGYNGYGIQYSPFFDNKLAVATAANYGLVGNGRLFILNIEPNGTVSNQVSWETQDGLFDLAWSE

VHENQAVVASGDGTLKLFDLTVPNFPVMNWKEHSREVFCVNWNLVDKTNFVSGSWDGNIKLWSPNRPQSL

LTLNSHVIDYSTRVAPNTSSASVPLSHQPAHQPQSQQQQVNTANCIYSAQFSPHSPSMIVSCNGGSQVQV

WDIRSPNPLQLKFTAHGGLEALSVDWNKYKSTVIASGGTDKSVRIWDLRSITKIDQPIAQSPMASGHIRG

PTPLNELIGHEFAVRRVQWSPHNPKELMSTSYDMTARIWSDESDERARFLNSRVGGLKGVFGKHKEFVIG

SDYSLWGEPGWAATTGWDEMVYIWDSKRL

>gi|241956151|ref|XP\_002420796.1| peroxin, putative; peroxisomal ubiquitin-conjugating enzyme, putative; ubiquitin protein ligase, putative [Candida dubliniensis CD36]

MAEKRLFKEYNQYQKQLPQLNNDQIVSLSPVSPDKNILLWEATIAKPGKPDSPYYYGGQWKLSISVPTSY

PIDPPVIKFITPIVHPNINLTTGEICLDILKKESWSPAWNLEHLVVAILMLLDQPEPDSPLNIDAANLYR

QDKVAYESIVQFNMWKHHCFKSAVRNIRGVRDCV

>gi|198419568|ref|XP\_002127420.1| PREDICTED: similar to peroxin 2 [Ciona intestinalis]

MEKPEQNEILPPALRVAQLDMQSLDDFLMQQFSNQLHQCFKYTMFEGVVVKLEPCIRTGLFALLLHQTLI

RSNQTIGQKLLGLKYDTKSRKILKIWVAVTILKYGYENLVKAGFSVFAQSNLFEFIQKVFSFATMLNFLW

FLRKGDYHSVLLRVCGLRTVYNQPNPQERDVTFPTISRELLWHGYAETAVRFLSFLNAEKVKTYVKKMLF

DQTNPKVSKDADKTCYDKCSYCNKVPIMPHTSNCEIHAHCYYCVASSLVKNSKCECPSCHTPIVKIIPLK

LQYTKLN

>gi|68490731|ref|XP\_710833.1| potential peroxin Pex20 fragment [Candida albicans SC5314]

MDSASCGPSTALQNLNKHAQRDNSLQHQRHQHPQHPQQQGASIHQFRQGQQVDSRLNADFPQFNSGNDFA

NSFMNQMRIKPSMHQHEHQQHQHQQTAWVNDFSNLS

>gi|68490702|ref|XP\_710847.1| potential peroxin Pex20 fragment [Candida albicans SC5314]

MDSASCGPSTALQNLNKHAQRDNSLQHQRHQHPQHPQQQGASIHQFRQGQQVDSRLNADFPQFNSGNDFA

NSFMNQMRIKPSMHQHEHQQHQHQQTAWVNDFSNLS

>gi|68484588|ref|XP\_713825.1| potential peroxin Pex20 fragment [Candida albicans SC5314]

MKTIDSHDSEMNEKFQNSQFLKLMSSIGNRQVELEGDKLVTSDSKEDIREKGIPETITATNPTITTAPRD

TQEGQFTSQGPSNPDFAREMYDQIPRPKPANTAFPHPLSGDSEHEQQQEPNDPHQNTLPDPLAHIQDGQL

SDINDPLTAARIISGGQVQMSDWVEDYDTISDTPSKLETDSNNNPNVRPFRKGQIVDHHWDEMYRDYRHD

DDYF

>gi|68484513|ref|XP\_713867.1| potential peroxin Pex20 fragment [Candida albicans SC5314]

MKTIDSHDSEMNEKFQNSQFLKLMSSIGNRQVELEGDKLVTSDSKEDIREKGIPETITATNPTITTAPRD

TQEGQFTSQGPSNPDFAREMYDQIPRPKPANTAFPHPLSGDSEHEQQQEPNDPHQNTLPDPLAHIQDGQL

SDINDPLTAARIISGGQVQMSDWVEDYDTISDTPSKLETDSNNNPNVRPFRKGQIVDHHWDEMYRDYRHD

DDYF

>gi|58265190|ref|XP\_569751.1| Pex3p [Cryptococcus neoformans var. neoformans JEC21]

MPQSQSSWQRRFRRLFFFVGTASTFYLLSSYLLDRLKENRLRAIKEKRHKDLLKNHFTSLISSISFTLYA

LLPTLQPQVFEAYPVEKTSQAMQGTATTSASSTTTGSTSSIGTSEPLNSLHLYGQGSQELEPPKEAVDNQ

SPQFSPSVPLVLTVDESWASEFQKKDNAGAEAETESGIMVGGSVGIPEIDDGLSSTVSQPISLPATDTTS

GSLSPPSDMSSSAQLGPSPPLLRDPTPSPPVLTKSKKELWKELKLQSIARTITTAYLLPMLYLLTSSQLS

ILARNTYLNDLASENSHAKGTSNLRGVQSHDNENEYDEDDDYQTPRRNVSEATLTGLSAERPLKKDNKKA

TGWFSSFSVESMGLTEFVENHASFLPNPVDYLPGTITSYLPSFLSIRQGDDQKNQAQRIGEVQAAEMARQ

RRIEEEEAERLFLSYSWWLLNEGWKGVAERVDRAVAKVFGSMLLKKELSLHDWEKAIKEVRAQVEMDEAA

ESGPKLFDFTPFLLPLKPPTSLRAPFPHNPSDHSSHLVSLFDETLTHICSADGRYLLEKGIATLTKSLIN

SLKEECYALEATSQSQSGFELEGRKKRLVECLPVVSRWGKNIWESVPDSGVEEMLAVSEFEGFAAIIFGD

WAGK

>gi|321254607|ref|XP\_003193133.1| pex3p [Cryptococcus gattii WM276]

MPQTQSSWQRRFRRLFFFVGTASTFYLLSSYFLDRLKENRLRAIKEKRHKDLLKNHFTSLISSISFTLYA

LLPTLQPQVFEAYPVEKTSQAIQGTATTAISSVRTDSTSSIETSEPLNSLHLYEQGPQESKPPKEAVDNR

SPQFGPSVSLVPTVDESWASEFQRKDSEGTTAETESGIIVGGSVGVPETDDGLSSIVSQSISLPASDTSS

AFPSPPSEMSSSAQLGPSPPMLRDPTPSPPVSTKSKKGLWKELKIQSIARTITTAYLLPMLYLLTSSQLS

ILARNTYLNDLASENSRAKGISDLRGGQSHDNEDEYDEDDDYQTPRRNASEATLTGLSAERPSKKDSKKT

TGWFSSFTIESMGLTEFVESHTSFLANPVDYLPGTMASYLPSFLSSHRGDGQKNQAQRIGEVQASEMARQ

RRIEEEEAERLFLSYSWWLLNEGWKGVAERVDQAVGKVFGSMLLKKELSLQDWEKAIREVRAQVEMDEAT

ESGPKLFDFTPFLLPLNPQTSLRAPFPHNTTDHSSHLVSLFDETLSHLRSADGRYLLEKGIATLTKSLCN

SLREECYAAETNSQSQNAFELEGRKKRLAECLPVVSRWGKNIWESVPDSGVEEMLAVPEFEGFAAIIFGD

WAGK

>gi|193209553|ref|NP\_001123111.1| Protein PRX-3, isoform a [Caenorhabditis elegans]

MLASAWEFAKRNKGKIIAGGVLVGSAIAYVQSSSRPKTLEKVSTSSELPNQARRHYIFDSTHRSCDQSIT

DLIPSIVTQIQARFDVESIQEKLQNTPDLTAEQKMQLWEQLKKNAFCRIVSVAFGFSILTLTLKAQISIL

AADTCSQFEQRNKKPTWQNYIPESMNSMWNSRTGSNGLSPTDNPMDVGNRRIFLQCVQYFTLRGIPELME

YVAEAIPNELQNWKLTDIKSKTEMRDFFDRVSYRISFNGLLTKLVAPLDGDGQDNSSSVMKLLQKLTTNL

ESSKSIHVLNSLLDFYFSAALKMVENDEQPLVKYVPAFSNSFPILTSTAFDSPLFNSLYSSDIHQFAVYV

FNS

>gi|17550472|ref|NP\_509024.1| Protein PRX-3, isoform b [Caenorhabditis elegans]

MILTLEAFRQNYIPESMNSMWNSRTGSNGLSPTDNPMDVGNRRIFLQCVQYFTLRGIPELMEYVAEAIPN

ELQNWKLTDIKSKTEMRDFFDRVSYRISFNGLLTKLVAPLDGDGQDNSSSVMKLLQKLTTNLESSKSIHV

LNSLLDFYFSAALKMVENDEQPLVKYVPAFSNSFPILTSTAFDSPLFNSLYSSDIHQFAVYVFNS

>gi|17533615|ref|NP\_495513.1| Protein PRX-13 [Caenorhabditis elegans]

MSAPPTNQPPPLPPRSFDNQMSNPMINTGFGYGGGYGMNTFPGSGMYGGGGMYGGGMGYGGFGGGFNHMG

YGQGPDSNFARLAEEQSRGAFQSIESVVNAVSSVANMLNSTHNAVYSSFRAVIGVVEQFGRLKTQLSSVV

VSLAVFRWVYRFWRWLLVMLKLKPASYASAAEMAWGTSQPYATDVLGATRTPASVNWPAALFWVVAIGGP

WLIYRCVSQMVQAAEEKRKWATGAAPHYTAQALFDFQASNEQELSFMNGETLRVAPKEEQPRVRGWLLAS

VADGSRIGLVPINYVRIVGKQSQSPPLTQQSNLDTFVNAFPARDLNSNIQ

>gi|4505727|ref|NP\_003621.1| peroxisomal biogenesis factor 3 [Homo sapiens]

MLRSVWNFLKRHKKKCIFLGTVLGGVYILGKYGQKKIREIQEREAAEYIAQARRQYHFESNQRTCNMTVL

SMLPTLREALMQQLNSESLTALLKNRPSNKLEIWEDLKIISFTRSTVAVYSTCMLVVLLRVQLNIIGGYI

YLDNAAVGKNGTTILAPPDVQQQYLSSIQHLLGDGLTELITVIKQAVQKVLGSVSLKHSLSLLDLEQKLK

EIRNLVEQHKSSSWINKDGSKPLLCHYMMPDEETPLAVQACGLSPRDITTIKLLNETRDMLESPDFSTVL

NTCLNRGFSRLLDNMAEFFRPTEQDLQHGNSMNSLSSVSLPLAKIIPIVNGQIHSVCSETPSHFVQDLLT

MEQVKDFAANVYEAFSTPQQLEK

>gi|357521563|ref|XP\_003631070.1| Peroxisomal biogenesis factor [Medicago truncatula]

MFSVRDFWRRHRRKIFLSVGIVGGGYCLYKLYGAHRQRLDALEMELDVQRQSDELIKSQMQAHFENIQRI

SDTITLPHSMHNLSCRIAQDLDLSHLLERLIQGKGQPNTLTQSEKLDLWGRLKILSFTRMALSVWATVML

SLYTKVQVNILGRHLYIDTARSLESSNLLMCVFVLSPMYVSSNLPRDSLKNQDVLSENCLPKELRHVLFR

KASLDSNSKFQRQQTAYYRELSHSSTRKKNSVLDQQYAALSPPQKHKYIFENNALLGAWVFTIVMFVSIS

LVEYSYPSRRLEFGVFWISKGVSYEKINICLFSRMSKKWKKEITIKHLITIFSHNFEQIWLLTLSGFKLL

DTTHRSNIKESEDVVDGEDKQKFLGSVDFLSQHGMPALISDMEEATKEVLKGKQLTSLFNNTTFDETITD

ILNTFMSRGSPHFWVKYIIPEDAKLHSTASGSNDTVPLDMTEFDQLVMEARGVLSSAEFGSVVEISLKAV

VDTLRELMGTTSVPLARALPQVAQMCPLLLEEPSKNQFIQILKNIPEVELFLTFLYANMPSA

>gi|308503052|ref|XP\_003113710.1| CRE-PRX-13 protein [Caenorhabditis remanei]

MSTPSMNQPPPLPPRPIDNQQLSNPMMSSGFGYGGYSMNGFPGSGMYGTGGMYGGMGYGGYGGGFNHMGY

GQSPDSNFARLAEEQSRGAFQSIESVVNAVSSVANMLNSTHNAVYSSFRAVIGVVEQFGRLKTQLSSVVV

SLALFRWVYRFWRWLLVMLKLKPANYASAAEMAWGASQPYATDVLGSTRTPASVNWPAALFWVVAIGGPW

LIYKCVSQMVQAAEEKRKWATGSAAHYTAQALFDFQASNDQELSFMNGETLRVAPKEEQPRVRGWLLASA

ADGSRIGLVPINYVRIVGKQSQSPPLTQQSNLDSFVDAFPSKDLNSNFQ

>gi|308511247|ref|XP\_003117806.1| CRE-PRX-3 protein [Caenorhabditis remanei]

MLASAWEFAKRHKGKIIAGGVLVGSAIAYIQSSSKNEALQKVNTSSELPNQARRHYIFDSTHRSCDQSIT

DLIPSIVSQIQARFDVEAIQEKLKNTPDLTADQKIQLWDQLKKNVFCRIVSVAFGFSILTLTLKAQISIL

AADTCAQFEQRNKQPTWQNYLPESMNSILSSKMGSNSSNPTDNPMDVGNRRIFLQCVQYFTLRGIPELME

YVAESVSAELQNWKLTDVKTKHEMRDLFDKVSYKISFTGLLTKLVAPLDGDVDSSSSVMKLLQKLTNNLE

SSKSIHVLNSLLDFYFSAALRMVENDEQSLVKYVPSFSNSFPVLTSTSFDSPLFNSLYSSDIHQFAVYVF

NS

>gi|170107498|ref|XP\_001884959.1| predicted protein [Laccaria bicolor S238N-H82]

MITFLHQARDGALVFTNFAKNYVYNHRKGLSTTAGFVGGLYLTKTYITERLEEVRHKIEEERSSRDCLKR

RFRQTQEDVSYTVLAMLPTLAEQVLEEMDVEYLTKELQNRSKARNSRQLQQRPPSSLASSIEMVHEHETR

SEGGPAAQRGENSSSSWVESSSAVSSPPRDGSPAGMRSPLSASVTTNGSSVNGEAASVDGSALSESFISP

SVVSDSGDSRTKAELWNETKILTITRTLTTLYSTTLLCLFTTIQLTLLARSKYIHSVYQQEHDERLREQL

ASEFTMSNILLGGSKGLEDLISGVNVREEEVDEYQINEELENKYLTLSWWLLHVGWKDVGERVRRGVEEV

FDGVSLKTKLSLLDLHHLIRDVRRRIEHEITFEGNERRTTFLSTLLPPTPETTHHVLIQGGFPLHASYTS

STSSQITHHFTASPAVIPSLTTTHPSDFLLPPTHIQDQDPGFTALIEETRGIISSPDFASVLETCLDRAT

QVLFVGLEKNVFVDTATATVEDGTIPGEEEEGEVRIRLAGLLPGLARWSSLALNGLPNELADTLLDVSQV

VALSAILFGRFEERFR

>gi|170095431|ref|XP\_001878936.1| predicted protein [Laccaria bicolor S238N-H82]

MLESVRTYIYDRRKGLSITAFCVGGLYIAKRYFNDRLEEVKDGMEQERSARETLKRRFAQTQEDVSYMIL

ALIPDLAEQIIEGMDIEALTRELQARSRVRQGRLIERPPSSVASSIDVVHNVDQELQETRSDAGSVVVVD

EGQRDMATSMTSWIEASSSSIVVTESSSSPPGHHLLAASSESIIEVQSSLGVLTNDSGDNSSVADSGLSD

SMISASDFSGPRTKTELWNEVKMLTFTRTLTTLYSTTLLTLLTTIQLTILAHTKYVHSVLQQERSERLRE

RLAAELTMSNILLGGGRALEDLMAGTEMEGEGEEGGISEEVESKYLTLSWWLLHVGWKDVGERVRRGVEE

VFDGVSLKSKLAAKDLHRLLSDVRKKVERVDGTDRRTSFASVLFPPTPETIQHVLIQGGFQQTRIDYEES

AFTALLEETRSVFASSDFSLVLQTCLDQAAQTLLAHLESKVFVDSATSIGSQEDVRIRLAGLLPGLAGWS

MEAMRGVPNELVDGLLNLREVKALSAIVFSRFEEKYR

>gi|189083737|ref|NP\_001121121.1| peroxisome assembly protein 26 isoform a [Homo sapiens]

MKSDSSTSAAPLRGLGGPLRSSEPVRAVPARAPAVDLLEEAADLLVVHLDFRAALETCERAWQSLANHAV

AEEPAGTSLEVKCSLCVVGIQALAEMDRWQEVLSWVLQYYQVPEKLPPKVLELCILLYSKMQEPGAVLDV

VGAWLQDPANQNLPEYGALAEFHVQRVLLPLGCLSEAEELVVGSAAFGEERRLDVLQAIHTARQQQKQEH

SGSEEAQKPNLEGSVSHKFLSLPMLVRQLWDSAVSHFFSLPFKKSLLAALILCLLVVRFDPASPSSLHFL

YKLAQLFRWIRKAAFSRLYQLRIRD

>gi|8923625|ref|NP\_060399.1| peroxisome assembly protein 26 isoform a [Homo sapiens]

MKSDSSTSAAPLRGLGGPLRSSEPVRAVPARAPAVDLLEEAADLLVVHLDFRAALETCERAWQSLANHAV

AEEPAGTSLEVKCSLCVVGIQALAEMDRWQEVLSWVLQYYQVPEKLPPKVLELCILLYSKMQEPGAVLDV

VGAWLQDPANQNLPEYGALAEFHVQRVLLPLGCLSEAEELVVGSAAFGEERRLDVLQAIHTARQQQKQEH

SGSEEAQKPNLEGSVSHKFLSLPMLVRQLWDSAVSHFFSLPFKKSLLAALILCLLVVRFDPASPSSLHFL

YKLAQLFRWIRKAAFSRLYQLRIRD

>gi|4758898|ref|NP\_004804.1| peroxisomal biogenesis factor 16 isoform 1 [Homo sapiens]

MEKLRLLGLRYQEYVTRHPAATAQLETAVRGFSYLLAGRFADSHELSELVYSASNLLVLLNDGILRKELR

KKLPVSLSQQKLLTWLSVLECVEVFMEMGAAKVWGEVGRWLVIALIQLAKAVLRMLLLLWFKAGLQTSPP

IVPLDRETQAQPPDGDHSPGNHEQSYVGKRSNRVVRTLQNTPSLHSRHWGAPQQREGRQQQHHEELSATP

TPLGLQETIAEFLYIARPLLHLLSLGLWGQRSWKPWLLAGVVDVTSLSLLSDRKGLTRRERRELRRRTIL

LLYYLLRSPFYDRFSEARILFLLQLLADHVPGVGLVTRPLMDYLPTWQKIYFYSWG

>gi|17136080|ref|NP\_476515.1| peroxisomal biogenesis factor 16 isoform 2 [Homo sapiens]

MEKLRLLGLRYQEYVTRHPAATAQLETAVRGFSYLLAGRFADSHELSELVYSASNLLVLLNDGILRKELR

KKLPVSLSQQKLLTWLSVLECVEVFMEMGAAKVWGEVGRWLVIALIQLAKAVLRMLLLLWFKAGLQTSPP

IVPLDRETQAQPPDGDHSPGNHEQSYVGKRSNRVVRTLQNTPSLHSRHWGAPQQREGRQQQHHEELSATP

TPLGLQETIAEFLYIARPLLHLLSLGLWGQRSWKPWLLAGVVDVTSLSLLSDRKGLTRRERRELRRRTIL

LLYYLLRSPFYDRFSEARILFLLQLLADHVPGVGLVTTSQRAASPCLPARPHTQPWSPPAFLPGHP

>gi|281604198|ref|NP\_001164055.1| peroxisomal targeting signal 1 receptor [Rattus norvegicus]

MAMRELVESECGGANPLMKLATHFTQDKALRQEGLRPGPWPPGASAAETVSKPLGVGTEDELVAEFLQDQ

NATLVSRAPQTFKMDDLLAEMQEIEQSNFRQAPQRAPGVADLALSENWAQEFLAAGDAVDVAQDYNETDW

SQEFIAEVTDPLSVSPARWAEEYLEQSEEKLWLGDPEGTSTTDRWYDEYHPEEDLQHTASDFVSKVDDPK

LANSEGTSEAWVDQFTRPGNKLAALQVEFERAKSAIESDVDFWDKLQAELEEMAKRDAEAHPWLSDYDDL

TSASYDKGYQFEEENPLRDHPQPFEEGLRRLEEGDLPNAVLLFEAAVQQDPKHMEAWQYLGTTQAENEQE

LLAISALRRCLELKPDNRTALMALAVSFTNESLQRQACETLRDWLRYSPAYAHLVAPGEEGASGAGLGPS

KRVLGSLLSDSLFLEVKELFLAAVRLDPTSIDPDVQCGLGVLFNLSGEYDKAVDCFTAALSVRPNDYLLW

NKLGATLANGNQSEEAVAAYRRALELQPGYIRSRYNLGISCINLGAHREAVEHFLEALNMQRKSRGPRGE

GGAMSENIWSTLRLALSMLGQSDAYGAADARDLPALLTMFGLPQ

>gi|13786194|ref|NP\_112640.1| peroxisomal biogenesis factor 3 [Rattus norvegicus]

MLRSMWNFLKRHKKKCIFLGTVLGGVYILGKYGQKKLREIQEREAAEYIAQARRQYHFESNQRTCNMTVL

SMLPTLREALMQQLNSESLTALLKNRPSNKLEIWEDLKIISFTRSIVAVYSTCMLVVLLRVQLNIIGGYI

YLDNATVGKNGTSILAPPDVQQQYLSSIQHLLGDGLTELVTVIKQAVQRILGSISLKHSLSLLDLEQKLK

EIRTLVEQHRSCWNDKDASKSSLCHYMMPDEETPLAAQAYGLSPRDITTIKLLNETRDMLESPDFSTVLN

TCLNRGFSRLLDNMAEFFRPTEQDLQHGNSINSLSSVSLPLAKIIPIVNGQIHSVCSETPSHFVQDLLMM

EQVKDFAANVYEAFSTPQQLEK

>gi|313482834|ref|NP\_001186248.1| peroxisome assembly protein 26 isoform b [Homo sapiens]

MKSDSSTSAAPLRGLGGPLRSSEPVRAVPARAPAVDLLEEAADLLVVHLDFRAALETCERAWQSLANHAV

AEEPAGTSLEVKCSLCVVGIQALAEMDRWQEVLSWVLQYYQVPEKLPPKVLELCILLYSKMQEPGAVLDV

VGAWLQDPANQNLPEYGALAEFHVQRVLLPLGCLSEAEELVVGSAAFGEERRLDVLQAIHTARQQQKQEH

SGSEEAQKPNLEASPSSLHFLYKLAQLFRWIRKAAFSRLYQLRIRD

>gi|150866213|ref|XP\_001385728.2| Peroxisomal biogenesis factor 3 (Peroxin-3) [Scheffersomyces stipitis CBS 6054]

MAIFSSLASFFNRHKRKIFITSTLTVSIYFLFNHFVIKKFRDYQNALRQELIFKQQIKQRFIQTQQDCYY

TLLALLPVLTTPVIDYLPVELITHVLRLKKNNPNGQTAAGSVTGGSNSELTTDNLNLLDTNNNPQSKMTV

YMNKSKVELWALLKIKTITRTLTLIYSISGLLLITRLQLNILARRSYLESAISMAGVKSTNNDINPHDNY

LIEQSYLSLSWWLLNKGWVNLNSIIEPLVIKKFESITPKSELSIEQFDLILHDIVNDISINHKQTILANL

FPLNYDDLVETLFSTNPDLLVQLEISDSNLNKLINETNSIMLDSQSGFFDLFNSVVSNMLNTLANNLSLS

MNNGNDIAAESFLSNANKTFKLASFLAQLSVQNFILSDNDNLKLEDQVNEEDDIEGNNDLTGNVYINNLY

LEELDDFSAGIYSNFE

>gi|115478488|ref|NP\_001062839.1| Os09g0314300 [Oryza sativa Japonica Group]

MLASARGFWGRHRRKILVSLGVAGAGYAAYRYLDSHRRQLVRVEQRALEERAAEEIIKNQLQTHFENVQK

ISDTTTLPFAMHYLRSRIMEELDISHLTEKLMHGKGESSAPALTPKEKYDTWEKIKILSFTRTVSSIWAM

TLLSLYVRVQVTILGRHLYLDFARVTDGAQLQEGSDTFSKSGHKDFLATADYLATYGINALITKMQHAAT

EILKEKQLKDPMGIDEVLETILQILKQFMGLCEDNSWINYLVPENANVYAQLMAVSSSGFDDSSLLKDVR

KLDQLMSETRIVLSSDDFRNIMDRSLKKIASVVVEDLAVQIGAPIPPPGLPLAKLLAKVAQLSLPLLEEP

DKNKHIQIIRSMPEVELFYTFLYANMPPET

>gi|50548037|ref|XP\_501488.1| YALI0C05775p [Yarrowia lipolytica]

MSVPRPKPWEGASGSSAATATPAATATPASTDAVSSSAGSATGAPELPSRPSAMGSTSNALSSPMGSSMN

SGYGGMNSGYGGMGSSYGSGYGSSYGMGSSYGSGYGSGLGGYGSYGGMGGMGGMYGSRYGGYGSYGGMGG

YGGYGGMGGGPMGQNGLAGGTQATFQLIESIVGAVGGFAQMLESTYMATQSSFFAMVSVAEQFGNLKNTL

GSLLGIYAIMRWARRLVAKLSGQPVTGANGITPAGFAKFEATGGAAGPGRGPRPSYKPLLFFLTAVFGLP

YLLGRLIKALAAKQEGMYDEHGNLLPGAQMGMGGPGMEGGAEIDPSKLEFCRANFDFVPENPQLELELRK

GDLVAVLAKTDPMGNPSQWWRVRTRDGRSGYVPANYLEVIPRPAVEAPKKVEEIGASAVPVN

>gi|254588036|ref|NP\_067458.2| PEX5-related protein isoform 1 [Mus musculus]

MSDSEMDGRTHIPSLLNALLSRNRVMQMSYLKSKEQGYGKLSSDEDLEIIVDQKQLVNEQQESRPLLSPS

IDDFLCETKSEAIAKPVTSNTAVLTTGLDLLDLSEPVSQTQTKAKKSEPSSKSSSLKKKADGSDLISADA

EQRAQALRGPETSSLDLDIQTQLEKWDDVKFHGDRTSKGHLMAERKSCSSRTGSKELLWSAEHRSQPELS

TGKSALNSESASELELVAPAQARLTKEHRWGSALLSRNHSLEEEFERAKAAVESDTEFWDKMQAEWEEMA

RRNWISENQEAQNQVTVSASEKGYYFHTENPFKDWPGAFEEGLKRLKEGDLPVTILFMEAAILQDPGDAE

AWQFLGITQAENENEQAAIVALQRCLELQPNNLKALMALAVSYTNTSHQQDACEALKNWIKQNPKYKYLV

KNKKGSPGLTRRMSKSPVDSSVLEGVKELYLEAAHQNGDMIDPDLQTGLGVLFHLSGEFNRAIDAFNAAL

TVRPEDYSLWNRLGATLANGDRSEEAVEAYTRALEIQPGFIRSRYNLGISCINLGAYREAVSNFLTALSL

QRKSRNQQQVPHPAISGNIWAALRIALSLMDQPELFQAANLGDLDVLLRAFNLDP

>gi|254553496|ref|NP\_001156988.1| PEX5-related protein isoform 2 [Mus musculus]

MYQGHMQLVNEQQESRPLLSPSIDDFLCETKSEAIAKPVTSNTAVLTTGLDLLDLSEPVSQTQTKAKKSE

PSSKSSSLKKKADGSDLISADAEQRAQALRGPETSSLDLDIQTQLEKWDDVKFHGDRTSKGHLMAERKSC

SSRTGSKELLWSAEHRSQPELSTGKSALNSESASELELVAPAQARLTKEHRWGSALLSRNHSLEEEFERA

KAAVESDTEFWDKMQAEWEEMARRNWISENQEAQNQVTVSASEKGYYFHTENPFKDWPGAFEEGLKRLKE

GDLPVTILFMEAAILQDPGDAEAWQFLGITQAENENEQAAIVALQRCLELQPNNLKALMALAVSYTNTSH

QQDACEALKNWIKQNPKYKYLVKNKKGSPGLTRRMSKSPVDSSVLEGVKELYLEAAHQNGDMIDPDLQTG

LGVLFHLSGEFNRAIDAFNAALTVRPEDYSLWNRLGATLANGDRSEEAVEAYTRALEIQPGFIRSRYNLG

ISCINLGAYREAVSNFLTALSLQRKSRNQQQVPHPAISGNIWAALRIALSLMDQPELFQAANLGDLDVLL

RAFNLDP

>gi|254553500|ref|NP\_001156989.1| PEX5-related protein isoform 3 [Mus musculus]

MQAEWEEMARRNWISENQEAQNQVTVSASEKGYYFHTENPFKDWPGAFEEGLKRLKEGDLPVTILFMEAA

ILQDPGDAEAWQFLGITQAENENEQAAIVALQRCLELQPNNLKALMALAVSYTNTSHQQDACEALKNWIK

QNPKYKYLVKNKKGSPGLTRRMSKSPVDSSVLEGVKELYLEAAHQNGDMIDPDLQTGLGVLFHLSGEFNR

AIDAFNAALTVRPEDYSLWNRLGATLANGDRSEEAVEAYTRALEIQPGFIRSRYNLGISCINLGAYREAV

SNFLTALSLQRKSRNQQQVPHPAISGNIWAALRIALSLMDQPELFQAANLGDLDVLLRAFNLDP

>gi|48477968|ref|YP\_023674.1| geranylgeranyl hydrogenase [Picrophilus torridus DSM 9790]

MEVNYDVLVIGAGPAGSSAARFAARKGLKTLLIEKRPDIGSPVRCGEGVSKSWMPEVELKPEDHWISDEV

KGARIYGPSEKKPIMLTAENAGNEVGYVVERDKFDKHIAALAASEGADVWVKSPALSVIKDGNRIVGAKV

RHNSEIVDVRAKMVIAADGFESEFGRWAGLKSLILAKNDIISCVEYRMINVDSDEDYTDFYLGSCAPAGY

IWVFPKGKHEANVGIGVTISKMRDRFDVKNYLDAFIKSHPGYSKGKTIQLITGGVSVSKVRDKFTLPGLL

TVGDAARLIDPITGGGIANGMISGKYAAEVSKKAIDNEDYSQEMMNNYERMVKDKFERKHLRNWFAKEKL

GTLSDETLDKLVDVIADVKINEISVEEILKAVQLKYPELVEELESLI

>gi|114321030|ref|YP\_742713.1| cytochrome c oxidase, cbb3-type, subunit III [Alkalilimnicola ehrlichii MLHE-1]

MSSFWHWWVIVLVLANILGMVWLIKWAEKKKPGEAAEHETTGHSWDEGTLAEYNRPMPRWWLWLFYITIV

FGLVYLILYPGLGNFGGVLGWSSAAQYDREVERIEERLEPIFAQYTELSIPELAQNDEAMQTGRRLFGYE

CAVCHGVDGGGARGFPNIANDKWQWGGTPEKIVETLTQGRSAVMPPHAGRPALEGDGLDNLVAYVQHLGG

REGISEDTITAGRSAYEQAGCIACHGADGTGNQAAGWPNLTLGEYTYGGDAETMKETILNGRSGEMPAFL

ERLGEDRIHVLAAYVYSLNN

>gi|4505723|ref|NP\_002609.1| peroxisome biogenesis factor 13 [Homo sapiens]

MASQPPPPPKPWETRRIPGAGPGPGPGPTFQSADLGPTLMTRPGQPALTRVPPPILPRPSQQTGSSSVNT

FRPAYSSFSSGYGAYGNSFYGGYSPYSYGYNGLGYNRLRVDDLPPSRFVQQAEESSRGAFQSIESIVHAF

ASVSMMMDATFSAVYNSFRAVLDVANHFSRLKIHFTKVFSAFALVRTIRYLYRRLQRMLGLRRGSENEDL

WAESEGTVACLGAEDRAATSAKSWPIFLFFAVILGGPYLIWKLLSTHSDEVTDSINWASGEDDHVVARAE

YDFAAVSEEEISFRAGDMLNLALKEQQPKVRGWLLASLDGQTTGLIPANYVKILGKRKGRKTVESSKVSK

QQQSFTNPTLTKGATVADSLDEQEAAFESVFVETNKVPVAPDSIGKDGEKQDL

>gi|403269819|ref|XP\_003926909.1| PREDICTED: peroxisomal biogenesis factor 3 [Saimiri boliviensis boliviensis]

MLRSVWNFLKRHKKKCIFLGTVLGGVYILGKYGQKKIREIQEREAAEYIAQARRQYHFESNQRTCNMTVL

SMLPTLREALMQQLNSESLTALLKNRPSNKLEIWEDLKIISFTRSIVAVYSTCMLVVLLRVQLNIIGGYI

YLDNAAVGKNGTTILAPPDVQQQYLSSIQHLLGDGLTELVTVIKQAVQKILGSVSLKHSLSLLDLEQKLK

EIRNLVEQHKSSSWINKDGSKSLLCHYMMPDEETPLAVQACGLSPRDITTIKLLNETRDMLESPDFSTVL

NTCLNRGFSRLLDNMAEFFRPTEQDLQHGNSMNSLSSVSLPLAKIIPIVNGQIHSVCSETPSHFVQDLLT

MEQVKDFAANVYEAFSTPLQLEK

>gi|403260632|ref|XP\_003922766.1| PREDICTED: peroxisomal membrane protein PEX13 [Saimiri boliviensis boliviensis]

MASQPPPPPKPWETRRIPGTGPGPGPGPTFQSADLGPTLMTRPGQPALTRVPPPILPRPSQQTGSSSVNT

FRPAYSSFSSGYGAYGNSFYGSYSPYSYGYNGLGYNRLRIDDLPPSRFVQQAEESSRGAFQSIESIVHAF

ASVSMMMDATFSAVYNSFRAVLDVANHFSRLKIHFTKVFSAFALVRTIRYLYRRLQWMLGLRRGSENEDL

WAESEGTVACLGAEDRAANSAKSWPIFLFFAVTLGGPYLIWKLLSTHSDEITDSSNWASGEDDHVVARAE

YDFTAVSEEEISFRAGDMLNLALKEQQPKVRGWLLASLDGQTTGLIPANYVKILGKRRGRKTVESSKISK

QQQSFNNPTLTKGATVAYSLDEQEAAFESVFVETNKVPVASDSTGKGGEKQDL

>gi|403159293|ref|XP\_003319928.2| hypothetical protein PGTG\_00840 [Puccinia graminis f. sp. tritici CRL 75-36-700-3]

MDYLSSLIQRSKRPMTIVASVFGGGYLAVSYLRSKLDEMQDSLTRTRACTENLRRRFEQNQDDCSFTVLA

LIPTLGKQVIQAMNVERLVEVLSQTKSRSTTQIGRSPSNQEKEPSIKSTPPPEPESIPNEDHSSEPHPSL

ENSITTSSSSEIINPLDPTPTERAPSDEPPASKPTTAPFPQDLAELLVRPDGTVLQKRSEIWREMMVVSF

TRLFTCLYGVSLLTLQTHVQLGLLGRDAYLSSILSVEKRDESEDELRDDEQVELWPEPVDSLDSPTERRY

LTFSYWYLHQGWLVLARRTRIAVVDALASRNLKDFVSASDLLEIFDLVRKKVELEADGSQFNFAPILLPT

NESDEIRTLEQGGMSSAECQIDERLRKLLDETQDFIDCPDFRLVLSNVMTRILDLCLSNLFRHAQLDPPQ

LLPSLPRFSELQGEEACPPSSSTRFVDILPIISKESLEILNVIPNEYIQTIGDTSELKEFSSVIYTTFDR

LTELMMTSSKPIHSEVKSPNDQTQKKPKNQNQPTTSHSQDRIRMTAIKLTELPPAVIKTIFELEPSLIHL

FLVRLANRALHQLTRDIVYQSITIQDNNQQQQQLNSILNGPQSYSLAVRTIQFINQLTEEEQEQEQEQQE

TNNHPTNWDILIRLLSKLPNLKTFIWSSNRIPDQQLISLIGIHSTNLESFTLDIPNPNQLNDHHHQHSPP

RPNNNGRQRSHTTGGWIEDSDSETELLTIRPIRWDAYPIEALPPTLTQLSISSLSVIGARNLSRAFHSLT

WTALTDLTLSKSLFIDDELMASIAIGSKKIKRISIQGMSGTKLTERGIEQLFSGLDGLEEIELFDVEGRF

SKVGWLKLDDLPPSLKSIKFGYHETGSYHSWTLDHLQNIVSLLALYPQKLEHFSVTRFVPLPTMLPGRHA

IFPELSCNNRTTPQRISKEQILSIVAQGKSLKELNLDWWLISVEGLEVIVKGLPNLRKLTALVDAPFHRI

ITSTVFVHSKIQTLKVSIPPEHTPLVQELSQVPMTPTMTSAGSPIMTQQSGSCGVVSPGGMWGSQSSTSP

IPTRDLKKFIKRAGHLKEIIWTGRGGLGAWKFVRNGPSALNVRVEFTPVAACLPPEAFAYQHSLPSSAPS

SKSSHIRAGSSPRQFFGHPTSFVRNGTPIAHRTSRRTSSTVTTEDGSTTTTTYDGYSRRSSSTSLATSWA

SSSCAHLPPLPPPSSSSSSSCSAPSTGFHHQSILKHGILDDIPGTPPVALSDQVVGSNLVPPTSDSPDLL

LNDRLDHHPHYLLNHHQHQLGLDLKDHPSSTPKHIALDNALNLDTLSLLPSSDTHQQIPSADLNSSSFKS

SSSDSSESVKVLPLST

>gi|402868072|ref|XP\_003898144.1| PREDICTED: peroxisomal biogenesis factor 3 [Papio anubis]

MLRSVWNFLKRHKKKCIFLGTVLGGVYILGKYGQKKIREIQEREAAEYIAQARRQYHFESNQRTCNMTVL

SMLPTLREALMQQLNSESLTALLKNRPSNKLEIWEDLKIISFTRSIVAVYSTCMLVVLLRVQLNIIGGYI

YLDNAAVGKNGTTILAPPDVQQQYLSSIQHLLGDGLTELITVIKQAVQKILGSVSLKHSLSLLDLEQKLK

EIRNLVEQHKSSSWINKDGSKSLLCHYMMPDEETPLAVQACGLSPRDITTIKLLNETRDMLESPDFSTVL

NTCLNRGFSRLLDNMAEFFRPTEQDLQHGNSMNSLSSVSLPLAKIIPIVNGQIHSVCSETPSHFVQDLLT

MEQVKDFAANVYEAFSTPQQLEK

>gi|346716373|ref|NP\_001231114.1| peroxisomal biogenesis factor 3 [Sus scrofa]

MLRSTWNFLKRHKKKCIFLGTVLGGIYILGKYGQKKIREIQEREAAEYIAQARRQYHFESNQRTCNMTVL

SMLPTLREALMQQLNSESLTVLLKNRPSNKLEIWEDLKIISFTRSIVAVYSTCMLVVLLRVQLNIIGGYI

YLDNAAVGKNGTTVLAPPDVQQQYLSSIQHLLGDGLTELITVIKQSVQKILGSVSLKHSLSLLDLEQKLK

EIRDLVEQHKSSSWINKDGSRSLLCHYMMPDEETPLAVQACGLSPRDVTTIKLLNETRDMLESPDFSTVL

NICLNRGFSRLLDNMAEFFRPTEQDLQHGNSRNSLSSVSLPLAKIIPIINGQIHSVCSETPSHFVQDLLM

MEQVKDFAANVYEAFSTPQQLEK

>gi|318901370|ref|NP\_001188055.1| peroxisomal biogenesis factor 3 [Ictalurus punctatus]

MLSSTWNFIKRHKRKFIIAGAFAGGVYLLGKYAQRKLQEMQERETAEYIAQARRQFHFESNQRTCNMTVL

SLLPTLREAIIHHLNSESLTELLKSRPANKIEIWEDLKTISFTRSIVAVYSTCMLVVLLRVQLNIIGGYL

YLDNSVTKNGTMPLAPPEVQQKYLSSIQHLLGDGLVELVTVVKKAVQEILGPISLKQSLSLQELEQHIIQ

IRQLVEENSVSSKFRTLTCYMMADEEDPLADQACGLTENDVTTIKLLNETRDMLENPDFSTILGACLNRG

FSRFLDNMAEFFCPPQGDSTPSSTSDSLLHVSLPLAKIIPIANGQIHSICSEVPSQFVQDLLMTEQVKEF

AANVYEAFSNPHELQK

>gi|297632422|ref|NP\_001172095.1| HAUS augmin-like complex subunit 1 [Sus scrofa]

MEAPEEKEAQVAAWLKKIFGDHSIPQYEVNPRTTEILHHLAECNRVRDRDVCLVIEDLKQKAREYESEAK

HLQDLLMESVNFSPANLSSAGSKYLNALVDSAVALETKDTSLASFIPAVNDLTSDLFRTKSKNEEIQLEL

GKLEKNLTAALVLEKCLREDLKKAELHLSMERAKVDNRLQNMDFLKAKAEEFRSGIRAAEKQLSARGMDA

SLSHQSLVALSEKLAELKQQTMPLKKKLESYLDLMPNPSLAQVKIEEAKRELDTIEAELTKKVNMMEL

>gi|283046720|ref|NP\_001164306.1| peroxisome biogenesis factor 1 [Danio rerio]

MLGSQGIQPVTLVFNNSKNCFLHLSSNFATHLCLHENQILELSWGVSAPVFLSWIRSRSSGPEDRVEISR

QLGEKLGLRDGEQGYLRPCLQVQSVQQVSVEPLSPDDWEILELHSLALEQRILDQIRVVFSDGVFPVWVD

QHTVIYIRIASLTPSVPYGRLEQFTELIVSPKLHPGSELLHKPQSEEPRQHQNVNITSSSISNASQDSQN

DHPESLNEGHWGGIADLKGLVRYLFTRGREPAKEKIAVPTIPAILKDCILRTCGSPPRSVSHHGSCHGDV

HILPWNLQEQENWNPGQSALTYGRLSKILSPKELREKVKQAMEKKKIRDASHKEKDTEEHMENSAVVRML

CHNINRLQEDQKLNKCEEIYSGKIWIPKMLQRRLKIDLHSAVRIQPLKSMPRLAETVMVQPLQPLAESEK

EEDIQMAFLNWFDAQSHQPLTCLTGRSNIILLPCAEGKEEFALTVLKPEQQQEDELFFLSNSLLRKTDIQ

IAREPHNSDHRGSDNDTEDQCLGFPSLSSLGGVEDISRSAFQHISHALLGGSLSRELISTGRGLRGGALL

ITGAKGSGKSSLSRALCRKASEDLDAHIQLLDCKTLKGKRTDTIRQRLEDVFEQAVWRQPSVVLLDDLDH

VAGAATSPEHEHGPEAVLRQHISQSLKDLVDEIVLRSSLIALIVTAQTEHALHPTLTVVQGSHFFQSFCK

IPTPDQAQRVEILKSLIVKKSFQVCQTTLDLDSVAKETEGFMARDLNLLLERAIHANTLHNSEDLSCKDF

RQALQGFTPPSLWDAQLQAPSGAGMERIGGLHEARQLLMDIILLPAKYPLLFSSLPLRQCSGVLLYGAPG

TGKTLLAGAVAKESGMNFISIKGPELLSKYIGASEQAVRDVFQRAQQAKPCILFFDEFDSLAPRRGHDNT

GVTDRVVNQLLTQLDGVEGLTGVYVLAASSRPDLIDPALLRPGRLDKSLYCPPPDREARLEILRALTHSV

PLAADVDLDQIAGATELFTGADLKALLYNAQLEAIHSSLGPNLLHDLGSGSDSDVSLSSLIFLNHSSGSD

DSAGEGDAGLEHSMVLLEPSELPPEDPRHNIWRLYFGSSFESELDNQSLNSQCLSGPNSTAPDLTGASVR

DPSSCHAPVFMSCVQQGFQELSHEQSERLRAEVSTVKNSYRKTTDESSSSLVQTSPSKPGSLICQTHLTT

ALANTRASVSREDWKRYTELYESFGAPKERKSQSNVLFKAGQRVTLA

>gi|115496179|ref|NP\_001069680.1| peroxisome biogenesis factor 13 [Bos taurus]

MASQPPPPPKPWETRRIPGTGPGPGPGPTFQSAELGPTLLTRPGQPTLTRVPPPILPRPSQQTGSGNLNT

FRPAYSSFSSGYGAYGNSFYGSYSPYSYGYNGLGYNRLRIDDLPPSRFVQQAEESSRGAFQSIESIVHAF

ASVSMMMDATFSAVYNSFRAVLDVANHFSRLKIHFTKVFSAFALVRTIRYLYRRLQWMIGLRRGLENEDL

WAESEGTVACLGAEDRAANSAKSWPIFLFFAVILGGPYLIWKLLSTHSDEVTDSTNWASGEDDHVVARAE

YDFVAVSEEEISFRAGDMLNLALKEQQPRVRGWLLASLDGQTTGLIPANYVKILGKRRGRKTVESSRISK

QQQSFTNTTLIKGATAADSLDDQEAAFESVFVETNKVPVASDSTGKNGDKQDL

>gi|226501402|ref|NP\_001150013.1| LOC100283640 [Zea mays]

MASGIGSGQQQPPAPAADADPGAVGDKLVFEAPPQPVREDYVQNAVKFLSHPKVRGSPVVYRRSFLEKKG

LSTEEIDEAFRRVPDPQPSTTATTSPQQQVNSQNQSVGVQAYAPAQPVHPANAGPVVLPTQPRFSWYQAF

LAAGLLLGFGASAAVFIKKLFLPRLKSWIRNVVAEGNGTEGNQLKPRIDDETADAVKASASAVSAIAKTN

QQLLASKDEEKKILVTLTQALDSQAKELKSLTDSIGHTREPINITRDDRFSQYRPLEDHAPTVIRNGAIN

SSWRASQQTNMYGVSNGDFGSVRSSFAPAPVEPTAGSFSRSYGEQPMSTAQRSDRSSGSKPWEMQQYSQQ

RPGYGSNSQLSEEGSYSDAQDSYAPSYHQNGKAPDFQADEPRPLTYNTGVEERPPPQRRWVPPQPPGVAM

PEAAAAIRQPKALPKQPSSDASEAAGEMQVNGSSASDAVTEVPVNGATASDAGRSEIQEQSVAA

>gi|114052659|ref|NP\_001040264.1| peroxisomal biogenesis factor 3 [Bombyx mori]

MFSNIKNFLNRHRRKFLVTGAVVGGLYVLTSYAQKKLRDGQEKEAKKFFEMTRKKQHFEGTERTCNQTIL

SLSKMVSESIWSWLNTEEIVQKLQENPEDKWALWEQLKITIFTRIGVLVYGLCMLQVALRVQLNVMGGYL

YKDSVQEGDPMVDSNLQTKYLSLCHYFVGQGIEDLIKRIEKIVKRVVEPVWLKKKITLQEVEQMFWSIQT

IWCTDTVEGDPLKNMVYYLIGHNEINDSKWDTIVKETMDILESDEVISVTMSSVSRSFSCVIDEVANLLV

TKSIPPSKNQLEVEDHVITSGVLKLKSEPFVDVNKVEIYFVKLLPVINDLITKNMCKGDNNIPDLLTQQL

TLNEKLKLLGANIYEVFSNS

>gi|56605902|ref|NP\_001008454.1| peroxisomal biogenesis factor 2 [Gallus gallus]

MASSIGNEKSVNPVLRISQLDALELNKALEQLVWSQFTSCFHGFKPGVLAHIEPEVKAFLWLLLWRFTIY

SKNATVGQAILNIQYKNNLSQTEKYQPLSKHQKLWYLIFTVGGRWLEERCYDLFSNRQLQSVSKIKHYIN

FGAGLLKLCGLVNFLIFLQKGTFATLTERILGIRSVFCKPQSVRQVGFEYMNRELLWHGFAEFLIYLLPL

INVQKLKLKICSWCFPIANLPNSDKTLATHYKVCSLCGEWPTMPHTIGCSHVFCYYCIKSNYLFDMYFTC

PKCGSEVHSLQPLKYKIEMTELHV

>gi|41055494|ref|NP\_956522.1| peroxisomal biogenesis factor 3 [Danio rerio]

MLSSTWNFIKRHKRKFIFTGVFVGGVYLLGKYAQRKIQEMQEREAAEYIAQARRQFHFESNQRTCNMTVL

SMLPTLREAIIHHLNSESLTTLLKTKPANKLEIWEDLKIISFTRSIVAVYSTCMLVVLLRVQLNIIGGYL

YLDNSVTKNGMTPLAPPDVQQQYLSSIQHLLGEGLMELITVVKKAVQEVFGLVSLKQSLSLQELEQQLTQ

IRQLVEDDSSKYKGLSWYMMPDEENTLASQACGLTENDVTTIKLLNETRDMLESPDFNIVLHTCLNRGFV

RFLDNMAEFFRPPQRDSTPSSTPDQLSHVSLPLAKIIPIINGQIHSICSEIPSHFVQDLLLIDQVKEFAA

NVYETFSTPQELQK

>gi|154152035|ref|NP\_001093818.1| peroxisome biogenesis factor 2 [Bos taurus]

MASGDENAERTNRVLRISQLDALELNKALEQLVWSQFTQCFHGFKPGLLARFEPEVKAFLWLFLWRFTIY

SKNATVGQSVLNIQYQNDLSPNLSYQPPSRNQKLWYAVCTIGGKWLEERCYDLFRNRHIASFRKAKQCMN

LVVGLLKLGGLINFLIFLQRGKFATLTERLLGIHSVFHKPQSVREVGFEYMNRELLWHGFAEFLIFLLPL

INVQKLRAKLSSWCVPLTGAPGSNSTLATSGRQCSLCGEWPTMPHTVGCEHVFCYYCVKSSFLFDMSFTC

PKCGTEVHSLQPLKSGIEMAEVSVP

>gi|148236992|ref|NP\_001085641.1| peroxisomal biogenesis factor 3 [Xenopus laevis]

MLSMWNFLKRHKKKFIFVGAFAGSVYLLGKYAQRKIREIQEREAAEYIAQARRQYHFESNQRTCNMTVLS

MLPALREALMQQLNSESLTSLLKNKPSNKLDIWEDLKIISFSRSIVAIYSTCMLVVLLRVQLNIIGGYIY

LDNSSVTKNGTALQASPEVQQQYLSSIQHLLGDGLTELITVVKQAVQEVLGSFSLKHSFSLIELEQKIKE

IRSLVEKKRGSLNGEESDGKVRLCQYLMSDEENPLTTQAYGLTEKDVKTIRLLNETRDMLESEDFNTVLN

SCLSRGFGRLLDSTAEFFRPADQELKQHNTMHSLSSISLPLAKIIPIINGQIHSICSELPNHFVQDLLLM

EQVKDFAANVYEAFSTPQQLEK

>gi|45188170|ref|NP\_984393.1| ADR296Cp [Ashbya gossypii ATCC 10895]

MARTGLQRHRGKLLGTGAVLGGLVVAGVVAAVAAKRWVRRQQQRLSEQHYVREQIKRRFTQTQQDALYTM

YELVPVLALVLGKELDVEELVETLKGKKLKRAGEDDEQGSGGHASAGEGSVSSTVARSKAELWQELKMRS

AVKLLAVVYTTCMLLLLTRLQLNILARREYLETAIRVAKGEEATRRDAAGWLGAVWEYGAAALGALGPRP

AVTAVEPVDQHEETRYVNEQAFLSLSWWLLNRGWLQFKPLIERQVEQQFGTLSPRDTLSMEQFSARLSNT

IHAVNRELFDSDSRALLLRALLPDATEELHVLQQTLDEGSLRVIERDDSMLRELLQETCRCAESTASLIV

LESLVNESFQFVMQQLETKVTKKLRKPATDAPEADGAADAPSQKFQVALYSVALKDCCQEMLKNGLVSMN

NEYLQDLDAVPELDDLSASVYSNFGV

>gi|45185916|ref|NP\_983632.1| ACR230Cp [Ashbya gossypii ATCC 10895]

MSASKPRPKPWETANMSSATSSSGTMDESNTVIPTSVTAASSLGGGSGDYGHTPDLPTKPAGLGDESGYK

SMNSQFGMNSTPYGGSMYGSGGLYGNSMYGGGGFGSMYGGGFGNGYGGYGSMYGGGYGGMYGMGANGMNN

NGGIAESTQATFHLIENLIGAVAGFAQMLEATYMATHNSFLTMVSVAEQFQYVKEMLGSFFGIFAMIKFL

KRVLFKLTGGRMGVAPKKQLPPASGDKGKMLQEFDQFRSGKNSAGSTGERKRARIAWKPLFLFFAAVFGF

PWLLNKFIMKLQEMQNRGRIATPHQPQSLDLNSLEFARAIYDFTPENPRIECALKKGDLMAIISRQDPTG

KESQWWKVRTKKGDVGYVPCNYIELIRRKKEIELSAGSGTGPSEVVSA

>gi|398366493|ref|NP\_010616.3| Pex3p [Saccharomyces cerevisiae S288c]

MAPNQRSRSLLQRHRGKVLISLTGIAALFTTGSVVVFFVKRWLYKQQLRITEQHFIKEQIKRRFEQTQED

SLYTIYELLPVWRMVLNENDLNLDSIVTQLKDQKNQLTRAKSSESRESSPLKSKAELWNELELKSLIKLV

TVTYTVSSLILLTRLQLNILTRNEYLDSAIKLTMQQENCNKLQNRFYNWVTSWWSDPEDKADDAMVMAAK

KSKKEGQEVYINEQAFLSLSWWILNKGWLSYNEIITNQIEIEFDGIHPRDTLTLEEFSSRLTNIFRNTNS

QIFQQNNNNLTSILLPKDSSGQEFLLSQTLDADALTSFHSNTLVFNQLVNELTQCIESTATSIVLESLIN

ESFHFIMNKVGIKTIAKKKPGQEDQQQYQMAVFAMSMKDCCQEMLQTTAGSSHSGSVNEYLATLDSVQPL

DDLSASVYSNFGVSSSFSFKP

>gi|6324000|ref|NP\_014070.1| Pex6p [Saccharomyces cerevisiae S288c]

MKASLTFSLSGIYAPCSISRDIYLEYGDKKAECLYGTIRLPQYGPGCTPGKIVHCVLDDSLPFCSIVVPS

KLFGFMPTQPTMDFCYFEPILDNVVPVLDSVTFLINEQLYSKLMDLPQEMQQIQFLHYKYNINSMETVVH

SRDILTSGLCQILNCSPFPQGLVDFTETQLILVNDTEQKLSALKYANEDEEYALPKIGTNSALSIDLESL

PCTISRDLLRPAPHINDDNSIYAFTDAETLLRLDVTSGSFITVSNMGCVRLVKLFVLLLPNGFKKRTIYA

PPKIIASFPDCSVVTISKSNIGHTDIPIANQVFISRVGGWLQSQKCFQNIILTTLKKFFSESKRILCQND

LIPIAFDSSMADLNIAEENDESDDEDELGQYYKNDSLVWFFVTSAELDCFSKDNSHFIIDPNRTKLITTN

ITNRRPLPLSRSNLQRYYGFAETFYYDLHIFPYVRQLVNILETSFNCSQRGITLNASVLLHSTTNNVGKA

TMVRFASKYLGIHLLEIDCLSLTSNSRQLDSTSKIIGYIRAKCENVLPYASPAVIFLAHLDSILLDVNAN

QDPEAIKLQKSINFEMSKLLDDFTFKFPGTTFVGSVNNIDNVPSSFRSHMRFEILVPVPSEAQRLRIFQW

YLSSHELNRDVQQKVPVSYMDNISFSSLSSYSAGLTPLDIKSIVETARMTATARFYQESKKCGWLPQSIL

ITQEDLSKATSKARNEFSVSIGAPQIPNVTWDDIGGIDFVKGEILDTIDMPLKHPELFTSGMKKRSGILF

YGPPGTGKTLMAKAIATNFSLNFFSVKGPELLNMYIGESEANVRRVFQKAREAKPCVIFFDEIDSVAPKR

GNQGDSGGVMDRIVSQLLAELDGMSTDADGVFVIGATNRPDLLDEALLRPGRFDKLLYLGIPDTDTKQLN

ILEALTRKFVLDNDVKLIELAKLCPFNYTGADFYALCSDAMLNAMSRIARMVEKKVSQHNELTGENISTR

RWFDKIATKEDTKVVVKMEDFLKAQEQLTPSVSRAELNHYEAVRANFEGA

>gi|6323220|ref|NP\_013292.1| Pex13p [Saccharomyces cerevisiae S288c]

MSSTAVPRPKPWETSASLEEPQRNAQSLSAMMTSNQQDSRPTEESNNSNSASESAPEVLPRPAALNSSGT

YGESNTIPGIYGNSNYGIPYDNNPYSMNSIYGNSIGRYGYGGSYYGNNYGSFYGGGYGAGAGYGMNNGSG

LGESTKATFQLIESLIGAVTGFAQMLESTYMATHNSFFTMISVAEQFGNLKEMLGSFFGIFAIMKFLKKI

LYRATKGRLGIPPKNFAESEGSKNKLIEDFQKFNDSGTINSNEKATRRKISWKPLLFFLMAVFGFPYLLN

KFITKLQTSGTIRASQGNGSEPIDPSKLEFARALYDFVPENPEMEVALKKGDLMAILSKKDPLGRDSDWW

KVRTKNGNIGYIPYNYIEIIKRRKKIEHVDDETRTH

>gi|6322651|ref|NP\_012724.1| Pex1p [Saccharomyces cerevisiae S288c]

MTTTKRLKFENLRIQFSNAIVGNFLRLPHSIINVLESTNYAIQEFGIAVHSHNSDIPIVHLGWDGHDSGS

SENVVLINPVLATVYDLNQKSPLVDLYIQRYDHTHLATEVYVTPETSDDWEIIDANAMRFQNGEILHQTR

IVTPGETLICYLEGIVTKFKIDRVEPSMKSARITDGSLVVVAPKVNKTRLVKAEYGHSNKTILKNGAIQL

LKKVILRSTVCKMDFPKDNLFVVYISDGAQLPSQKGYASIVKCSLRQSKKSDSDNKSVGIPSKKIGVFIK

CDSQIPENHIALSSHLWDAFFTHPMNGAKIKLEFLQMNQANIISGRNATVNIKYFGKDVPTKSGDQYSKL

LGGSLLTNNLILPTEQIIIEIKKGESEQQLCNLNEISNESVQWKVTQMGKEEVKDIIERHLPKHYHVKET

GEVSRTSKDEDDFITVNSIKKEMVNYLTSPIIATPAIILDGKQGIGKTRLLKELINEVEKDHHIFVKYAD

CETLHETSNLDKTQKLIMEWCSFCYWYGPSLIVLDNVEALFGKPQANDGDPSNNGQWDNASKLLNFFINQ

VTKIFNKDNKRIRVLFSGKQKTQINPLLFDKHFVSETWSLRAPDKHARAKLLEYFFSKNQIMKLNRDLQF

SDLSLETEGFSPLDLEIFTEKIFYDLQLERDCDNVVTRELFSKSLSAFTPSALRGVKLTKETNIKWGDIG

ALANAKDVLLETLEWPTKYEPIFVNCPLRLRSGILLYGYPGCGKTLLASAVAQQCGLNFISVKGPEILNK

FIGASEQNIRELFERAQSVKPCILFFDEFDSIAPKRGHDSTGVTDRVVNQLLTQMDGAEGLDGVYILAAT

SRPDLIDSALLRPGRLDKSVICNIPTESERLDILQAIVNSKDKDTGQKKFALEKNADLKLIAEKTAGFSG

ADLQGLCYNAYLKSVHRWLSAADQSEVVPGNDNIEYFSINEHGRREENRLRLKTLLQQDVVHETKTSTSA

ASELTAVVTINDLLEACQETKPSISTSELVKLRGIYDRFQKDRNGEMPNGENSIDIGSRLSLM

>gi|6321944|ref|NP\_012020.1| Pex28p [Saccharomyces cerevisiae S288c]

MSETSSSRRSASKDAVKSYFAGKYNKVLDSILEAEAAISKSPTVAEDLSGSSSSGNSEMSHPSLTASSAT

SQGISKKELLQQIAGSLFSTSIERLKTAHSSEVSSTPEYSVNDSYGEQECRECDGVFKCSAHFEGAPEYY

DDETESGPALEPMTSNSEKDPFIDVFLDKLISRLVPEKLPEREHFSSKTTIEHDLDTGRVPVFSATTLGS

NFKKLSKKMGSIFELQDSIVRLLTWRNPTGTVTSLILFTLICFNPMYLVILPIFRFVYGIVVPGYVRKHP

LQRSIYPLKRNHGSSLLYDVCYEGKNEYSYGQQFFSKSFMDTLESRNQEIDEISELDKRTENTGELKQGM

KVLINLRDMQNMTSGTLHVIEAINSFLRKSSSFQNEECSTKRFFTGFLLIVFLKILSPFVNWSYVCSIFA

WCLLIYMHPRAHPKIISFFKTGTMGKEYKNLKKREHQALNMIFDEQPETKFIEIFEIYKKALLPNDWKFF

RYSNRIFDPQDPYRRAQQFPPGVDSLADVIPPTGWSFDPNFEWKIDNDVDRWVVERGLNLPITGEFLFDP

MFKRRRLIHRVIKNATPVA

>gi|6320687|ref|NP\_010767.1| Pex29p [Saccharomyces cerevisiae S288c]

MDSVTNFFWNDTYNAGTPTRSTLKGKKVQNGIDGKSQAKKESISSGSRTSDPTRGSLPSSSGQPTSGGGF

PSTSNIQKMMADTLVEKIIKMALPPSSKTAVDTIHHRMVAGKERPKLSVQITSRNFIQMNSRLGVPFMIM

DELIKILNWTNPAYTVSIMFLYTLIILKPFQMLSSLPIFYLLFCVMVPQYLYIHKPNPTSYLDNNQTPAQ

GPPLRRPEVPKPVPELSQEFVLNLTDLQNHMLLYVKFYDFTLLILQKFAFFTNEAISSFYFIVLLIIATL

NFLYMDKFIKLIPMRPVLILLGWGFFIASHPSNREYLLTKLNSEETRLKTLTISTNLESKILQHLKLIEA

REHRLVMIFEIQKYLPEYKEWRPVGFSDDDYSLFSSLRIYQRRIEENSVKSLEEIEPPKDWEWEANSHWV

LDLDPKEWVEDEFIQYVEIDSETKWVYDLNLDGQRGSYRRRMWTNSCVRKKLDSGISSNLGEEEVVNPLR

EETYRQGVHGVTKGSMSGGLTHSSDDDRADEESINGTIPNLNNIDADASYPSIEELTDTLNSTI

>gi|397480668|ref|XP\_003811599.1| PREDICTED: peroxisomal biogenesis factor 3 [Pan paniscus]

MLRSVWNFLKRHKKKCIFLGTVLGGVYILGKYGQKKIREIQEREAAEYIAQARRQYHFESNQRTCNMTVL

SMLPTLREALMQQLNSESLTALLKNRPSNKLEIWEDLKIISFTRSIVAVYSTCMLVVLLRVQLNIIGGYI

YLDNAAVGKNGTTILAPPDVQQQYLSSIQHLLGDGLTELITVIKQAVQKILGSVSLKHSLSLLDLEQKLK

EIRNLVEQHKSSSWINKDGSKPLLCHYMMPDEETPLAVQACGLSPRDITTIKLLNETRDMLESPDFSTVL

NTCLNRGFSRLLDNMAEFFRPTEQDLQHGNSMNSLSSVSLPLAKIIPIVNGQIHSVCSETPSHFVQDLLT

MEQVKDFAANVYEAFSTPQQLEK

>gi|395855297|ref|XP\_003800102.1| PREDICTED: peroxisomal biogenesis factor 3-like [Otolemur garnettii]

MLRSMWNFLKRHKKKCIFLGTVLGGVYILGKYGQKKIREIQEREAAEYIAQARRQYHFESNQRTCNMTVL

SMLPTLREALMQQLNSESLTALLKNRPPNKLEIWEDLKIISFTRSIVAVYSTCMLVVLLRVQLNIIGGYI

YLDNAAVGKNGTTVLAPPDVQQQYLSSIQHLLGDGLTELITVIKQSAQKILGSVSLKHSLSLLDLEQKLK

EIRNLVEEHKSSSWINKDGSKSLLCHYMMPDEETPLAVQACGLSPRAIITIKLLNETRNMLESPDFSTVL

NTCLNRGFSRLLDNMAEFFRPTEQDLQHSNSMNSLSSVSLPLAKIIPIVNGQIHSACSETPSHFVQDLLM

MEQVKDFAANVYEAFSTPQQLEK

>gi|395834680|ref|XP\_003790322.1| PREDICTED: peroxisomal biogenesis factor 3 [Otolemur garnettii]

MLRSMWNFLKRHKKKCIFLGTVLGGVYILGKYGQKKIREIQEREATEYIAQARRQYHFESNQRTCNMTVL

SMLPTLREALMQQLNSESLTALLKNRPPNKLEIWEDLKIISFTRSIVAVYSTCMLVVLLRVQLNIIGGYI

YLDNAAVGKNGTTVLAPPDVQQQYLSSIQHLLGDGLTELITVIKQSVQKILGSVSLKHSLSLLDLEQKLK

EIRNLVEEHKSSSWINKDGSKSLLCHYMMPDEETPLAVQACGLSPRDIITIKLLNETRDMLESPDFSTVL

NTCLNRGFSRLLDNMAEFFRPTEQDLQHSNSMNSLSSVSLPLAKIIPIVNGQIHSVCSETPSHFVQDLLM

MEQVKDFAANVYEAFSTPQQLEK

>gi|395821491|ref|XP\_003784072.1| PREDICTED: LOW QUALITY PROTEIN: peroxisomal membrane protein PEX13-like [Otolemur garnettii]

MSSQTCQTSMIALMPIPGKEFQNCFESRGNHNPAKSGGRGWSIEVTVPEKESDSAALLQQRPQVVEGGSD

LQILKFALQLEISLTEVLEDLKVCASENDETEETHKILGAGPGLGSSPTFQSAALDPTLVTRPRQPTLTR

VPPPIPPRPSQQTGSSNVNTXRHAYSSFSSGFGAYGNSFYGNYSSYGCRYSGLDYNCLPVDDLLPCRFVQ

QAEKSSRGHFSPXQSTVHAFASVSVMMDATFSATYIRFRVVLDVANALYKGLPGFRLVRIIRSLYRWLQX

MVSLRRGFENENLWAESERTVACLSAEDRADNSAKSXAVFLFLGGPYLTRKLLSIHSDEVTRNINXVSGE

DDHVVATQEYDFAAVSEEKISFQTSDMLNLALKVQXPRIHGWLLASLYGQTTKLIPANYIKILGKRRDRK

MMEYSKISKQQQSFTNPTLIKRTITADSLEVQKAAFESIFVETSKFPFAPDSTRKGGDKQNL

>gi|297679307|ref|XP\_002817479.1| PREDICTED: peroxisomal biogenesis factor 3 [Pongo abelii]

MLRSVWNFLKRHKKKCIFLGTVLGGVYILGKYGQKKIREIQEREAAEYIAQARRQYHFESNQRTCNMTVL

SMLPTLREALMQQLNSESLTALLKNRPSNKLEIWEDLKIISFTRSIVAVYSTCMLVVLLRVQLNIIGGYI

YLDNAAVGKNGTTILAPPDVQQQYLSSIQHLLGDGLTELITVIKQAVQKILGSVSLKHSLSLLDLEQKLK

EIRNLVEQHKSSSWINKDGSKPLLCHYMMPDEETPLAVQACGLSPRDITTIKLLNETRDMLESPDFSTVL

NTCLNRGFSRLLDNMAEFFRPTEQDLQHGNSMNSLSSVSLPLAKIIPIVNGQIHSVCSETPSHFVQDLLT

MEQVKDFAANVYEAFSTPQQLEK

>gi|395535076|ref|XP\_003769558.1| PREDICTED: peroxisomal biogenesis factor 3 [Sarcophilus harrisii]

MLKSVWNFLKRHKKKCLFLGTVLGGVYILGKYGQKKIREIQEREAAEYIAQARRQYHFESNQRTCNMTVL

SMLPTLRDALMQQLNSENLTALLKNRPSNKLEIWEDLKIISFTRSIVAVYSTCMLVVLLRVQLNIIGGYI

YLDNAAVGKNGTTLLAPPEVQQQYLSSIQHLLGDGLTELITVVKQAVQKILGSVSLKHSLSLLELEQKLK

EIRKITEQHASSSWTDKTGSKSLLCQYMMPDEETPLAIQACGLTAGDITTIKLLNETRDMLESPDFSTVL

NTCLDRGFSRLLDNMAEFFRPTEQDLNHSDSMNSLSSVSLPLAKIIPIINGQIHSVCSETPSHFVQDLLM

MEQVKDFAANVYEAFSTPQQLEK

>gi|27465633|ref|NP\_775175.1| PEX5-related protein [Rattus norvegicus]

MYQGHMQGKGSRAADKAVAMVMKEIPREESAEEKPLLTMTSQLVNEQQESRPLLSPSIDDFLCETKSEAI

AKPVTSNTAVLTTGLDLLDLSEPVSQTQTKAKKSESSSKSSSLKKKADGSDLISADAEQRAQALRGPETS

SLDLDIQTQLEKWDDVKFHGDRTSKGHLMAERKSCSSRAGSKELLWSSEHRSQPELSTGKSALNSESASE

LELVAPAQARLTKEHRWGSALLSRNHSLEEEFERAKAAVESDTEFWDKMQAEWEEMARRNWISENQEAQN

QVTVSASEKGYYFHTENPFKDWPGAFEEGLKRLKEGDLPVTILFMEAAILQDPGNAEAWQFLGITQAENE

NEQAAIVALQRCLELQPNNLKALMALAVSYTNTSHQQDACEALKNWIKQNPKYKYLVKNKKGSPGLTRRM

SKSPVDSSVLEGVKDLYLEAAHQNGDMIDPDLQTGLGVLFHLSGEFNRAIDAFNAALTVRPEDYSLWNRL

GATLANGDRSEEAVEAYTRALEIQPGFIRSRYNLGISCINLGAYREAVSNFLTALSLQRKSRNQQQVPHP

AISGNIWAALRIALSLMDQPELFQAANLGDLDVLLRAFNLDP

>gi|255958309|ref|NP\_001157667.1| peroxisomal biogenesis factor 3 isoform 2 [Mus musculus]

MLRSMWNFLKRHKKKCIFLGTVLGGVYILGKYGQKKIREIQEREAAEYIAQARRQYHFESNQRTCNMTVL

SMLPTLREALMQQLNSESLTALLKSRPSNKLEIWEDLKIISFTRSIVAVYSTCMLVVLLRVQLNIIGGYI

YLDNATVGKNGTTVLAPPDVQQQYLSSIQHLLGDGLTELVTVIKQAVQRILGSVSLKHSLSLLDLEQKLK

EIRILVEQHQSSWNDKDVSRSSLCQYMMPDEETPLAAQAYGLSHRDITTIKLLNETRDMLESPDFSTVLN

TCLNRGFSRLLDNMAEFFRPTEQDLQHGNSINSLSSVSLPLAKIIPIVNGQIHSVCSETPSHFVQLTCGS

SLRRALEQK

>gi|9910484|ref|NP\_064345.1| peroxisomal biogenesis factor 3 isoform 1 [Mus musculus]

MLRSMWNFLKRHKKKCIFLGTVLGGVYILGKYGQKKIREIQEREAAEYIAQARRQYHFESNQRTCNMTVL

SMLPTLREALMQQLNSESLTALLKSRPSNKLEIWEDLKIISFTRSIVAVYSTCMLVVLLRVQLNIIGGYI

YLDNATVGKNGTTVLAPPDVQQQYLSSIQHLLGDGLTELVTVIKQAVQRILGSVSLKHSLSLLDLEQKLK

EIRILVEQHQSSWNDKDVSRSSLCQYMMPDEETPLAAQAYGLSHRDITTIKLLNETRDMLESPDFSTVLN

TCLNRGFSRLLDNMAEFFRPTEQDLQHGNSINSLSSVSLPLAKIIPIVNGQIHSVCSETPSHFVQDLLMM

EQVKDFAANVYEAFSTPQQLEK

>gi|113930737|ref|NP\_033021.2| peroxisomal biogenesis factor 5 isoform 1 [Mus musculus]

MAMRELVEGECGGANPLMKLATHFTQDKALRQEGLRPGPWPPGASAAETVSKPLGVGTEDELVSEFLQDQ

NATLVSRAPQTFKMDDLLAEMQEIEQSNFRQAPQRAPGVADLALSENWAQEFLAAGDAVDVAQDYNETDW

SQEFIAEVTDPLSVSPARWAEEYLEQSEEKLWLGDQEGSSTADRWYDEYHPEEDLQHTASDFVSKVDDPK

LANSEFLKFVRQIGEGQVSLESAAGSGGAQAEQWAAEFIQQQGTSEAWVDQFTRPGNKIAALQVEFERAK

SAIESDVDFWDKLQAELEEMAKRDAEAHPWLSDYDDLTSASYDKGYQFEEENPLRDHPQPFEEGLHRLEE

GDLPNAVLLFEAAVQQDPKHMEAWQYLGTTQAENEQELLAISALRRCLELKPDNRTALMALAVSFTNESL

QRQACETLRDWLRYSPAYAHLVAPGEEGATGAGPSKRILGSLLSDSLFLEVKDLFLAAVRLDPTSIDPDV

QCGLGVLFNLSGEYDKAVDCFTAALSVRPNDYLMWNKLGATLANGNQSEEAVAAYRRALELQPGYIRSRY

NLGISCINLGAHREAVEHFLEALNMQRKSRGPRGEGGAMSENIWSTLRLALSMLGQSDAYGAADARDLSA

LLAMFGLPQ

>gi|28565271|ref|NP\_787947.1| peroxisomal biogenesis factor 5 isoform 2 [Mus musculus]

MAMRELVEGECGGANPLMKLATHFTQDKALRQEGLRPGPWPPGASAAETVSKPLGVGTEDELVSEFLQDQ

NATLVSRAPQTFKMDDLLAEMQEIEQSNFRQAPQRAPGVADLALSENWAQEFLAAGDAVDVAQDYNETDW

SQEFIAEVTDPLSVSPARWAEEYLEQSEEKLWLGDQEGSSTADRWYDEYHPEEDLQHTASDFVSKVDDPK

LANSEGTSEAWVDQFTRPGNKIAALQVEFERAKSAIESDVDFWDKLQAELEEMAKRDAEAHPWLSDYDDL

TSASYDKGYQFEEENPLRDHPQPFEEGLHRLEEGDLPNAVLLFEAAVQQDPKHMEAWQYLGTTQAENEQE

LLAISALRRCLELKPDNRTALMALAVSFTNESLQRQACETLRDWLRYSPAYAHLVAPGEEGATGAGPSKR

ILGSLLSDSLFLEVKDLFLAAVRLDPTSIDPDVQCGLGVLFNLSGEYDKAVDCFTAALSVRPNDYLMWNK

LGATLANGNQSEEAVAAYRRALELQPGYIRSRYNLGISCINLGAHREAVEHFLEALNMQRKSRGPRGEGG

AMSENIWSTLRLALSMLGQSDAYGAADARDLSALLAMFGLPQ

>gi|24797089|ref|NP\_722540.1| peroxisome biogenesis factor 10 isoform 1 [Homo sapiens]

MAPAAASPPEVIRAAQKDEYYRGGLRSAAGGALHSLAGARKWLEWRKEVELLSDVAYFGLTTLAGYQTLG

EEYVSIIQVDPSRIHVPSSLRRGVLVTLHAVLPYLLDKALLPLEQELQADPDSGRPLQGSLGPGGRGCSG

ARRWMRHHTATLTEQQRRALLRAVFVLRQGLACLQRLHVAWFYIHGVFYHLAKRLTGITYQALRPDPLRV

LMSVAPSALQLRVRSLPGEDLRARVSYRLLGVISLLHLVLSMGLQLYGFRQRQRARKEWRLHRGLSHRRA

SLEERAVSRNPLCTLCLEERRHPTATPCGHLFCWECITAWCSSKAECPLCREKFPPQKLIYLRHYR

>gi|4505721|ref|NP\_000277.1| peroxisome assembly protein 12 [Homo sapiens]

MAEHGAHFTAASVADDQPSIFEVVAQDSLMTAVRPALQHVVKVLAESNPTHYGFLWRWFDEIFTLLDLLL

QQHYLSRTSASFSENFYGLKRIVMGDTHKSQRLASAGLPKQQLWKSIMFLVLLPYLKVKLEKLVSSLREE

DEYSIHPPSSRWKRFYRAFLAAYPFVNMAWEGWFLVQQLRYILGKAQHHSPLLRLAGVQLGRLTVQDIQA

LEHKPAKASMMQQPARSVSEKINSALKKAVGGVALSLSTGLSVGVFFLQFLDWWYSSENQETIKSLTALP

TPPPPVHLDYNSDSPLLPKMKTVCPLCRKTRVNDTVLATSGYVFCYRCVFHYVRSHQACPITGYPTEVQH

LIKLYSPEN

>gi|4505715|ref|NP\_002608.1| peroxisome biogenesis factor 10 isoform 2 [Homo sapiens]

MAPAAASPPEVIRAAQKDEYYRGGLRSAAGGALHSLAGARKWLEWRKEVELLSDVAYFGLTTLAGYQTLG

EEYVSIIQVDPSRIHVPSSLRRGVLVTLHAVLPYLLDKALLPLEQELQADPDSGRPLQGSLGPGGRGCSG

ARRWMRHHTATLTEQQRRALLRAVFVLRQGLACLQRLHVAWFYIHGVFYHLAKRLTGITYLRVRSLPGED

LRARVSYRLLGVISLLHLVLSMGLQLYGFRQRQRARKEWRLHRGLSHRRASLEERAVSRNPLCTLCLEER

RHPTATPCGHLFCWECITAWCSSKAECPLCREKFPPQKLIYLRHYR

>gi|224047462|ref|XP\_002199395.1| PREDICTED: peroxisome biogenesis factor 13 [Taeniopygia guttata]

MAAKPPPKPWESRRLPGTATAFQSADLGDNLLTRPGQPTVARIPPPILPRPSQQTASSSLSAFRPAYSSF

SPGYGSYGTSFYGSYSPYSYGYGGLGYNRFCADGIPPSRFVQQAEESSRGAFQSIESIVHAFASVSMMMD

ATFSAVYNSFRAVLDVANHFSRLKIHFTKVFSAFALVRTIRYLYQRLQRLLGLRQSCENEDLWSESEGKV

ARAGLEDKVANSAKSWPIFLFFAVILGGPYLIWKLLSTYSEEETVSSNWASGEDDHVVGRAEYDFNALSE

EEISFRAGDMLRLAPKEQQPKIRGWLLASYDGQTTGLVPANYIKILGKRRGRKTVVLERIPEQQPAFPST

AVRGAPAAVTLEEQEAAFETVFAKSSKVPIALDSSVAGGEKQEL

>gi|226500812|ref|NP\_001141850.1| uncharacterized protein LOC100273992 [Zea mays]

MLASARGFWARHRRKILVSLGVAGVGYAAYHFYDARRAQVVRVEQLRAMEEQAADDFVKNQLQAHFEKVK

RICDTTTLPLAMHHLSDKITSQLDISKLTDKLRQAKVDSSALTPKEKYETWEEIKIKSFAKIVSSMWAMT

LLSLYVRVQVTILGRHLYLDFAQGTNGPQLQAESDTFSENGHRSFLAMADYLVTDKITGFLTQMQRAATE

VLKEKQLKDRMNMDQVLQTVLQILDMFMGLSEDNSWINYLVPENPPVYAQLMAVSSSGFDDSSLLNDFRK

LDQLMSETRIVLASDDFRNIMERSLRKIAGVVVEDLGVQIVTPGSGLPLATLLPKVDHLSSPLLEEPNKN

KHIQIIRSMPEVELFYTLLYTNMPPET

>gi|224047990|ref|XP\_002195948.1| PREDICTED: peroxisomal biogenesis factor 3 [Taeniopygia guttata]

MEIHNESDEGGSDPQEKRVYLLGKYGQKKIREIQEREAAEYIAQARRQYHFESNQRTCNMTVLSMLPTLR

DALMHQLNSESLTSLLKNRPANKLEIWEDLKIISFTRSIVAVYSTCMLVVLLRVQLNIIGGYIYLDNATL

GKNGTTPLAPPEVQQQYLSSIQHLLGDGLTELITIVKQAVQKVFGSISLKQTLSLLELEQKLKDIREVVE

HKDSDQIASYSPLCHYLMPDEENPLASQACGLTERDIATIKLLNETRDMLESPDFSTVLSTCLNRGFSRL

LDNMAEFFRPTEKDLSQNSSVNSLSSVSLPLAKIIPIINGQIHSVCSETPSHFVQDLLMMEQVKDFAANV

YEAFSTPQQLEK

>gi|391345983|ref|XP\_003747260.1| PREDICTED: uncharacterized protein LOC100904484 [Metaseiulus occidentalis]

MFSKVADFARRHPKKLIFGGLVAGGMYAAHRYQSSFEENRQQIRKKIVDEMKRAEHFDAILKTSDQSVLN

LLETLRRKLNAELGVEEILEEVRAKPENRIFLWDEIKIRVLTYGVASVYTESLLICALRTMMGIIGGYML

ANSRRKSNQANEVHSAYLNMLQNFLDKGVHEVIRVVKIHVLAAFGPIELKQVVTADDFLLGFNFVRTNVK

IIENAPAYLMMDHWTPACTSQENPLSNSEILNQLTSETRDILQCHDCQAVLERLIGSGFRGLNAIATKAF

GYVGDGKCHLITLLPSLKTEIYKRDNGFVKESLNSSCSKDFSANVYEAFCNNPRD

>gi|391335984|ref|XP\_003742364.1| PREDICTED: uncharacterized protein LOC100899324 [Metaseiulus occidentalis]

MFSKVADFARRHRKKLIFGGLVAGGMYAAHRYLSSLEENRQKIRKEIMDEMKRAEHFNSILKTSDQSVLN

LLETLRKKLDAELGVEEILEKVRAKPENRIFLWDEIKIRVLTYGLASVYAESLLICALRTMMGIIGGYML

ANSRRKSNQANEVHSAYLNMLQNFLDKGVLEVIRVVKIHVLAAFGPIELKQVVTADDFLLGFNFVRTNVK

IIENAPAYLMMDHWTPACTSQENPLSNSEILNQLTSDTRDILQCNDCQAVLERLIGSGFRDLNAIVTKAF

GYVGDGKCHLVTLLPSLKTEIYKRDSGFVKESLNSACSKDFLANVYEAFCNNPRDSCSQPKNS

>gi|296199379|ref|XP\_002747142.1| PREDICTED: peroxisomal biogenesis factor 3 [Callithrix jacchus]

MLRSVWNFLKRHKKKCIFLGTVLGGVYILGKYGQKKIREIQEREAAEYIAQARRQYHFESNQRTCNMTVL

SMLPTLREALMQQLNSESLTALLKNRPSNKLEIWEDLKIISFTRSIVAVYSTCMLVVLLRVQLNIIGGYI

YLDNAAVGKNGTTILAPPDVQQQYLSSIQHLLGDGLTELITVIKQAVQKILGSVSLKHSLSLLDLEQKLK

EIRNLVEQHKSSSWINKDGSKSLLCHYMMPDEETPLAVQACGLSPRDITTIKLLNETRDMLESPDFSTVL

NTCLNRGFSRLLDNMAEFFRPTEQDLQHGNSMNSLSSVNLPLAKIIPIVNGQIHSVCSETPSHFVQDLLT

MEQVKDFAANVYEAFSTPLQLEK

>gi|390345788|ref|XP\_780894.3| PREDICTED: LOW QUALITY PROTEIN: peroxisomal biogenesis factor 3-like [Strongylocentrotus purpuratus]

MLGSIWNFVKRHRRKFLVLGAVAGGASLLYKYAEWKLKEWRETEEAECLAMARRAHHFESNQRTCNMTVL

SMIPKLRELLLYHLNSEELIQKLKSGTENKVVVWNELKVVSFTRMVVSVYSTVLLTAFLRVQLNILGGYM

YLDTLAGKNGLTYYQVHATQDVQKEYLAMVQYLLTDGLTELINHVQEVVQNVVGSISLQQLLSLSDMEEI

IAKVRGQVETTQYGGEVVVPDCSIHPLGRYLLKPEGLDGEESACRLSDDQLVLSQMQIETRDLVESHDFS

CVMNSCLDIGFSRLLDNMAEFFRPSQLEMEKAHVDSN

>gi|390369832|ref|XP\_001200198.2| PREDICTED: peroxisomal biogenesis factor 3-like [Strongylocentrotus purpuratus]

MLNTCLSFLFPPTVVVPDCSIHPLGRYLLKPEGLDGEESACRLSDDQLVLSQMQIETRDLVESHDFSCVM

NSCLDIGFSRLLDNMAEFFRPVTTRNGESPCGLKLAMAKAIPIVNGQVNALCCDTPNHFIQELLLMQCVK

DFASNVYEGFSQPPAHEERNGDVRSPNDNGSVERI

>gi|125978273|ref|XP\_001353169.1| GA19910 [Drosophila pseudoobscura pseudoobscura]

MLSRLQDFLSRHRRKFIVTGVLVGGAYCAARYAQRKLVEIHEKQAREMFERTRRTHHFESTEKTCNQVIL

GLGEEMCDAVLRECSTDELLEQLRQNPKNKVELWEEMKVVAFTRLATFVYASSMLVIALRVQLNLLGGYI

YRDITTEQTRITDELKQQYLSLIRHFITEDGIRDLVRYIRTQVIAVVKSSMPLSRQLSLNDLEQLFWSLQ

MAINADTRRDPNSKMTKYLLPSQSSSFSPLLQQMYNETLDLLESEDAISVCTHNVTRGFVLACDVIAESL

GETLHHLPTAEVQKQAETQQSQQFNQGSSSTSLPSSQAVDNNNLLNINTVLMAMAKLIPIISGITSGGYD

SSARSTNLPTQLLSFYLVAEKSKTLGANVYETFSSA

>gi|125808500|ref|XP\_001360774.1| GA18339 [Drosophila pseudoobscura pseudoobscura]

MADNNNLRSAVINEAPLVPPTSIVGPGFSSGPPPDAVLRTPFAGNVRALPNLAPPLPLSPFQQTQYGYGG

AYGNNSYAGGYGGYNTGGGFGGGYGGMGQFGSGWGGPYRSYGGDFGGGYNRFGGMGGIDPEQRFIQMAEA

SSRPAFQSIESLVSAIGNIASMLDSTFFALTSSFRAILGVAANFGRLRSVFAQFWTTFAIFRGLKWIYRK

ILFWLRLSNLDPSSEAFKKAFAEALNENHSQVGGGPQPPRKRNSPWPVLAFISFIFTAPYLIMKLLGSVT

NTAQEEARNPSKWVAPIHTQAVYDFAGRNQSELSLSAGQSLQVAPREIQQTLNLLNTGWALATTNGQTSG

IIPISYVKSPQQLRQDHQEQVKPTQPRPELMNLSTDAFPAPPLDQQMNYDFNLAAQQQAPLGPPSTATAA

FEEGFA

>gi|389639020|ref|XP\_003717143.1| peroxisomal biogenesis factor 3 [Magnaporthe oryzae 70-15]

MYSATRRWLRRNRTPIAVGAGVIGAGYLVSRYVMGKINDARERMSSDRIAKENLRRRFEQNQEDCTFTVL

ALLPTATQNVLEAMDTEKITYEIQQLKARPAGPPSIADTTLTEDDGRSVSASGPASSALATESDPQPQAA

EAAAPANASRKTKRQLWDDLAISSIARAFTLLYVLALLTMLTRIQLNLLGRRSYLSSVITLATGSAQASI

GLENNDDDSPDVVYGSDFDVNRRYLTFSWWLLNKGWAELRDRVEVAVRGAFGHLSPRDELSLDMFGRLTK

QVRDEVEADVKWLAFLLPPRDQEDSVLAESGILGESETAAGADGSMIVVQSQSPVVPPPLRRLLDETSDI

IDSPAFSHVLAKILDAGFSTLMEGELAQSVFGSGGVPKPTVQLPKVLSCLTRQAHAVGNGMPNKYLQAME

TVRELEGFAAVVYSSNWQNEMRDDEGDAMAGSAAVIVPPTASFEAAWNRAVEGRQAS

>gi|21357431|ref|NP\_648753.1| CG6859 [Drosophila melanogaster]

MLSRLQDFLSRHRRKFIVTGVLVGGTIFAARYAQRRFVEFQEKQAREFFERTRRTTHFESTEKTCNQVIL

GMGEEMCQAVLRECSTDELLEQLRQNPKNKLELWEDMKIVAFTRLATYVYASSMLVIALRVQLNLLGGYI

YRDIMTEQKQVTDELKQQYLSLIRHFITDSGIRDLARYIRTQVIAVTKTIPLSEQLSLSDLEQLFWSLQM

AINADTRRDPNSRMSKYLLPSQNPSHSPLLQKMVNETLDLLESEDAVGVCSHNVSRGFVLACDAIAESMG

ETLQHLPQAKVQTQQEQSVKFNQAGSLGASTSKSQNGLENNNLLNINRVLLALAKLIPIISGLTSRGFDT

TSRPHNLPTQLLTFYVVAEKTKTLGANVYESFSSA

>gi|149642693|ref|NP\_001092457.1| peroxisomal biogenesis factor 3 [Bos taurus]

MFRSTWNFLKRHKKKCIFLGTVLGGVYILGKYGQKKIREIQEREAAEYIAQARRQYHFESNQRTCNMTVL

SMLPTLREALMQQLNSESLTALLKTRPSNKLEIWEDLKIISFTRSIVAVYSTCMLVVLLRVQLNIIGGYI

YLDNAAVGKNGTTVLAPPDVQQQYLSSIQHLLGDGLTELITVIKQAVQKILGSVSLKHSLSLLDLEQKLK

EIRDLVEQHKSSSWINNDGSKSLLCHYMMPDEETPLAVQACGLSPRDVTTIKLLNETRDMLESPDFSTVL

NTCLSRGFSRLLDNMAEFFRPTEQDLQHGNSINSLSSVSLPLAKIIPIINGQIHSVCSETPSHFVQDLLM

MEQVKDFAANVYEAFSTPQQLEK

>gi|383872699|ref|NP\_001244856.1| peroxisomal biogenesis factor 3 [Macaca mulatta]

MLRSVWNFLKRHKKKCIFLGTVLGGVYILGKYGQKKIREIQEREAAEYIAQARRQYHFESNQRTCNMTVL

SMLPTLREALMQQLNSESLTALLKNRPSNKLEIWEDLKIISFTRSIVAVYSTCMLVVLLRVQLNIIGGYI

YLDNAAVGKNGTTILAPPDVQQQYLSSIQHLLGDGLTELITVIKQAVQKILGSVSLKHSLSLLDLEQKLK

EIRNLVEQHKSSSWINKDGSKSLLCHYMMPDEETPLAVQACGLSPRDITTIKLLNETRDMLESPDFSTVL

NTCLNRGFSRLLDNMAEFFRPTEQDLQHGNSMNSLSSVSLPLAKIIPIVNGQIHSVCSETPSHFVQDLLT

MEQVKDFAANVYEAFSTPQQLEK

>gi|383861681|ref|XP\_003706313.1| PREDICTED: peroxisomal biogenesis factor 3-like [Megachile rotundata]

MFSRIRGFVSRHRRKFIFGGIVFGSIVIIRYTTRKLREWQEKEIKEMLDKTKRRHYFECTERTCSQMIMS

LTATLRDSIIQVLDTETIVNKLRSGCPDKVACWNELKVLAIARSAVVIYSYAMLATLIRIQFNVMGGHVY

KDIQNSNGITTENIVRTKYLSLSRHFIYDGIKKLSMLIKDKVAEITASISLKDELTLRDIEEIYWAITSS

ISADNSKDPIKNLAEYMLLLNCEDDQEPMLSKLITETLDLLESEEVQNLTQSNIRSGFSLLVDHISAFFV

GTPTVENGKTVQNGFSVPGTSSQNHNSWTEKNSISANYDSSTFVNINKISMPMAKLIPIVNGQVPDKPTS

KDFQTDLLQRLVTNNELKTLGANIYEAFSF

>gi|380011479|ref|XP\_003689830.1| PREDICTED: LOW QUALITY PROTEIN: DDB1- and CUL4-associated factor-like 1-like [Apis florea]

MAPERMNDNNGNQLKNVPNIITSLPSALSPFPVSNIQSGNPPPVPPRQPVQNYYGFSDHRLFGSNYYNGY

GLSYNNQYRGFNGNSYNPIYSNYNNYGIFGGHNSDAENRFFHYVEESTRPTFHLIETILHTFSSMTMLLE

STYFALTNSFRAILNVAENIGKLRSTLNQLFSTFALIKFLKWLYKKIIYTIGSKNQDLINEELWNKSLTK

IEGENVHNSSFWSGFIIFSIFFVVPYIIHKISYNIRNMQMKGKDPKEWHQIEEPAYIATVLHDFIAINND

ELNVKAGQKIYLAPRNLQPKNLPGWCKVSDSVNIGLIPYNYIKVIGQLKKVVIIIKRINCQILKRIIGTK

MSSAESLAEVTDVVQILRQWEEEHSSSTYDPVPTLRRLAEIIELETENYLKMDPDPFDERHPSRTDPECN

FGHILKVLFRKDNFMTKLINDYLRDTYWSRAGITGRDVRKLNIAACRLMLDILPGLETSAVFQPDMEGLI

HRLFSWAEKSVEPLQSYATGLVAAAMEVQEIATGFREQNAKMVPLMLQRLHKLQEEAQEERQLAVNNRPF

AHFGQDRNSGGDGENKGVPGKRKVREKRKENEILKNSNHSNYFSEEEEDCARSSEDSAPLPKKKKSDAEC

ETPVKNNIYPEIMSPPLSVPKKXSNFNNQITPSKAQNAHNRSLNTSSVRCNLQKNSSSSMQSSTTLSTLL

EGNSNSSWAEMESYVIGNVQMHPPTLATRQMLILRYLTPMGEYQEFLGHVFEQNALELILKYINVRETKD

SRLAFEALKYLASLLCHKKFSIEFLNVGGLQKLLDVPRPSVAATGVSICLYYLAYCEDAMERVCLLPKHV

ISDLVTYALWLLERSHDSGRCHATMFFGFSFPFKVILEEFDAQDGLRKLFNVVSITLNNFNIEEEPALND

DEECASRQIVRHVAVALKRYMEAHLHLKTEQLQRAENVRAERDTWQPSLPPYKAVKLSSEEVQAKVEILQ

ELMSVRAVWPPVEELYRLGGITLLLQIIAFAREWNYSGRVHTTSSAETVRSCLDVIAICSVVPKVMLLLC

ERVDMPDMSMTMAINLLLAAAECEIIADPDVQRAALRAVINCVCAPINRIGGNVARYSVTGSAKKKSKXN

NSEELIQKIWGSVRSNNGIMVLLQLMMVKTPITDADSIRALACRALAGLARSEKVRQIISKLPMFTDGQI

QALMKDPILQEKRQEHVMFQKYALELMGRVSGEAKPTGAEYEISLASLHRANVVAQTRIQYNEQQLNQLI

YQHLMSKGLTETASTLHKEANLDFSAIMKPVCTYQPFTYRSPATTGTRNGFSPGATVNLYNTNRCNQREV

TSRNNTTPTSSFRYISHSNNSSSSSSLSSGNNIRMKHSDCLNQNVVSNSTNQLIKLQINQKKNQVDKQPL

VNQINCHSINQPTVCRSLQKQISRDPAGGGGPGVATSNPSTITLDSIITEYLTNQHALCKNPMVTCPQFN

LFEPHKCPDPCTKNSIPTNVTVRLAKRALGMDGRRLDRRLIYSRFCPVKTFRPTDVATFTYCIFSPCQQY

LMLGTYAGDVKMYNIHTGLEEATYSCHESYVYHMECNQRGNLLLTSTPWRSPMSVLWSIGTFFDLKLSLE

NVEYVEFGKLQDRIIGTDSDIATIYDIATGQLLTSFAPTISNRYTMNRATFSMNDELVLHDGILWDANSG

KQIHKFDKLNQTLNGVFHPNGIEVVSNTEVWDLRTFHLLKTVPTLDQMEVIFSPVNDIIYAVSLEKENID

EANYITSFKTLDALDYSNIATYDVRRGVYGLACNKFDTQIAVVEILNEFDDNHESSVRLYDVGRRKCDKD

ETDEDDDEEDLDASDDDGSNSSSDDNNADDADNPDAAAEENGDENERNNRENNDDDDDDDEDDSGDGDDS

GDDMTHYSGSPDSPDIFLSDIDLESLSSSS

>gi|380014159|ref|XP\_003691107.1| PREDICTED: peroxisomal biogenesis factor 3-like [Apis florea]

MFSRLRGFVNRHRRKFIVGGIVVGSVIFIRYTARRLREWQEKEIKDMLDRSKRRQYFECNERTCSQMIVS

LTSTLKDSIVKVLDTNTIINKLRNGCPDKIACWNELKVLAIARSAVVVYSYAMLATFIRIQFNVMGGHVY

KDIQNSNGTTTENIIQTKYMSLSRHFIYDEIKKLSLLIKDKVAEITASISLKDELTLRDIEEIYWALTSS

ISADSSKDPIKNLAEYMLLSNCEEEQSPVLLKLFNETLDLLETEEVQNLTQSNIRNGFSLLVDHISAFFV

GSPIIENNKTAQNGISVPGTSNQNSISMKYDSSIFTNINKVSMPMAKLIPIINGQVPDKSTSRDFQNDLL

QRLITNNELKTLGANIYEAFSI

>gi|50742652|ref|XP\_419708.1| PREDICTED: peroxisomal biogenesis factor 3 [Gallus gallus]

MLRSLWSFLKRHKKKCLVLGTFLGGVYLLGKYGQKKIREIQEREAAEYIAQARRQYHFESNQRTCNMTVL

SMLPTLRDALMHQLNSESLTSLLKNRPANKLEIWEDLKIISFTRSIVAVYSTCMLVVLLRVQLNIIGGYI

YLDNAAVCKNGTTPLAPPEVQQQYLSSIQHLLGDGLTELITIVKQAVHKVFGSISLKHALSLLELEQKLK

EIRDVVEHRDSDQVAPYSPLCHYLMPDEENPLATQACGLTERDTATIKLLNETRDMLESPDFSTVLSTCL

NRGFSQLLDNMAEFFRPTEQDFSQNGSVNSLSSVSLPLAKIIPIINGQIHSICSETPSHFVQDLLMMEQM

KDFAANVYEAFSTPQQLEK

>gi|225456094|ref|XP\_002281306.1| PREDICTED: peroxisome biogenesis protein 3-2 [Vitis vinifera]

MFSVRDFWRRHRRKIFVSVGVFGSGYLLYKLYDAHRRRLDDLERELAVQRENEELIKAQMQAHFESIQRI

ADTTTLPHSMLYLSGRIAEELDLSHLTERLMKGKGQPNTLTPSEKLELWDRLKILSFTRMVLSLWAMTML

SLYIRVQVNILGRHLYIDTARGGGSSHLLEEADPIDRHDQQKFLASADFLSNYSIPALISNMHAAAAEVL

KGKQLRDVFNSMVLHGTIMQILDLFISTGKPHNLVDYLMPDDTKSYKPASPSNGDSSTPADVTKFDQLMV

ETRAVLSSAEFINVIDVSLRTVVDAVVEDMMGVQLGGGSPSSGMVLAKLLPRVAQMGPLLLEEPSKNRFI

QIIQKAPEVEFFFTLLYANMPTL

>gi|345784633|ref|XP\_541132.3| PREDICTED: peroxisomal biogenesis factor 3 [Canis lupus familiaris]

MLRSTWNFLKRHKKKCIFLGTVLGGVYILGKYGQKKIREIQEREAAEYIAQARRQYHFESNQRTCNMTVL

SMLPTLREALMQQLNSESLTALLKNRPSNKLEIWEDLKIISFTRSIVAVYSTCMLVVLLRVQLNIIGGYI

YLDNAAVGKNGTTVLAPPDVQQQYLSSIQHLLGDGLTELITVIKQAVQKILGSVSLKHSLSLLDLEQKLK

EIRNLVEQHKSSSWINKDESKSLLCHYMMPDEETPLAVQACGLSPRDVTTIKLLNETRDMLESPDFSTVL

NTCLNRGFSRLLDNMAEFFRPTEQDLQHSNSMSSLSSVSLPLAKIIPIVNGQIHSVCSETPSHFVQDLLM

MEQVKDFAANVYEAFSTPQQLEK

>gi|357495743|ref|XP\_003618160.1| hypothetical protein MTR\_6g005280 [Medicago truncatula]

MVDGSKLKSLTYFLTLIYDGPTLMSHSCLLVPKHIELNLLGREMPTSEVAKRKGRKNNA

>gi|357114410|ref|XP\_003558993.1| PREDICTED: peroxisome biogenesis protein 3-2-like isoform 1 [Brachypodium distachyon]

MLISSARFWARHRWKVLLSLGVAGAGYAAYRLYDAHRSQLVRVEQRQLEERAADELVKNQLQAHFENVQR

ISDTTTLPFAMHYLRSRIVEELDISHLTEKLLQGKGESGVLTTKEKYDTWEKIKIMSFTRTVSSMWAMTL

LSLYVRVQVTILGRHLYLDFARGTDGSQLQAESDTLGRNGHKDFLATADYLATYGINTLIMQMEHAATEI

LKEKQLKDLMSMDQVLQTVLQIFDQFMSLCEDKSWINYLVPENANRYAQLLAVSGSGFDDSSLLMDVRKL

DQLMTETRIVLASDDFRNVMDMSLRKIADVVIEDLGAQLGAAVPPSGLPLAKLLARVAQLSSPLLEEPSK

NKHIQIIRSMPEVELFYTFLYANMPPQT

>gi|357114412|ref|XP\_003558994.1| PREDICTED: peroxisome biogenesis protein 3-2-like isoform 2 [Brachypodium distachyon]

MFQLGPAPGKRFWARHRWKVLLSLGVAGAGYAAYRLYDAHRSQLVRVEQRQLEERAADELVKNQLQAHFE

NVQRISDTTTLPFAMHYLRSRIVEELDISHLTEKLLQGKGESGVLTTKEKYDTWEKIKIMSFTRTVSSMW

AMTLLSLYVRVQVTILGRHLYLDFARGTDGSQLQAESDTLGRNGHKDFLATADYLATYGINTLIMQMEHA

ATEILKEKQLKDLMSMDQVLQTVLQIFDQFMSLCEDKSWINYLVPENANRYAQLLAVSGSGFDDSSLLMD

VRKLDQLMTETRIVLASDDFRNVMDMSLRKIADVVIEDLGAQLGAAVPPSGLPLAKLLARVAQLSSPLLE

EPSKNKHIQIIRSMPEVELFYTFLYANMPPQT

>gi|356524660|ref|XP\_003530946.1| PREDICTED: peroxisome biogenesis protein 3-2-like [Glycine max]

MLSVRDFWRRHRRKVFVTVGVLGSGYLLYKLYGAQRHGVQELERELAVQRETEDLMKAQMQAHFENIQKM

SDVTLPHAMHELSCRITEELDLSHLLERLIQGKGQPNTLTQSEKLDLWSRLKILSFTRMTLSVWATTMLS

LYTKVQVNILGRHLYIDTARSLGISDSVESGDVVDREDQKKFLDNIDFLSQHGMPALISDMEAATKEVLK

GKQLSTFFNSTTLHETIMQILNSFMSMGTPNSWIKYMIPEDVRPYSTTYGSDDPVPFDMTEFEQLMMEAW

AVLSSAEFGSIVEISLKAVVDTLVELMGTKFSGGSVAGGLPLARVLPQVAQMCPLLLEEPRKNQFIQIIK

NIQEVELFFTLLYANMPHA

>gi|356512996|ref|XP\_003525200.1| PREDICTED: peroxisome biogenesis protein 3-2-like [Glycine max]

MLSVRDFWRRHRRKVFVTVGVLGSGYLLYKLYGAHRHGVQELERELAVQRETEELMKAQMQAHFENIQRM

SDVTLPHAMHELSCRITEELDLSHLLERLIQGKGQPNTLTQSEKLDLWSRLKILSFTRMTLSVWATTMLS

LYTKVQVNILGRHLYIDTARSLGISDSVESGDVVDREDQKKFLDSVDFLSQHGMPALISDMEAATKEVLK

GKQLSTFFNSTTLHETIMQILNTFMSMGTPNSWIKYMIPEDVRPYSTTSGSDDPVPFDVTEFEQLMIEAR

AVLSSAEFGSIVEISLKAVVDTLVELMRTKFSGGSVAEGMPLARVLPQVAQMCPLLLGEPSKNQFIQIIK

NIQEVELFFTLLYANMPHE

>gi|354475551|ref|XP\_003499991.1| PREDICTED: peroxisomal biogenesis factor 3-like isoform 2 [Cricetulus griseus]

MLRSMWNFLKRHKKKCIFLGTVLGGVYILGKYGQKKIREIQEREAAEYIAQARRQYHFESNQRTCNMTVL

SMLPTLREALMQQLNSESLTALLKNRPSNKLEIWEDLKIISFTRSIVAVYSTCMLVVLLRVQLNIIGGYI

YLDNATVGKNGTTVLAPPDVQQQYLSSIQHLLGDGLTELVTVIKQAVQRILGSVSLKHSLSLLDLEQKLK

EIRILVEQHRSPSWIDKDVSKSSLCQYMMPDEETPLAAQAYGLSPRDITTIKLLNETRDMLESPDFSTVL

NTCLNRGFSRLLDNMAEFFRPTEQDLQHGNSINSLSSVSLPLAKIIPIVNGQIHSVCSDTPSHFVQFICG

SSFRGALRQN

>gi|354475549|ref|XP\_003499990.1| PREDICTED: peroxisomal biogenesis factor 3-like isoform 1 [Cricetulus griseus]

MLRSMWNFLKRHKKKCIFLGTVLGGVYILGKYGQKKIREIQEREAAEYIAQARRQYHFESNQRTCNMTVL

SMLPTLREALMQQLNSESLTALLKNRPSNKLEIWEDLKIISFTRSIVAVYSTCMLVVLLRVQLNIIGGYI

YLDNATVGKNGTTVLAPPDVQQQYLSSIQHLLGDGLTELVTVIKQAVQRILGSVSLKHSLSLLDLEQKLK

EIRILVEQHRSPSWIDKDVSKSSLCQYMMPDEETPLAAQAYGLSPRDITTIKLLNETRDMLESPDFSTVL

NTCLNRGFSRLLDNMAEFFRPTEQDLQHGNSINSLSSVSLPLAKIIPIVNGQIHSVCSDTPSHFVQDLLM

MEQVKDFAANVYEAFSTPQQLEK

>gi|350399287|ref|XP\_003485479.1| PREDICTED: peroxisomal biogenesis factor 3-like [Bombus impatiens]

MFSSLRGFVNRHRRKFILGGIVVGGVIFVRYTARRLREWQEKEIKDMLDRSKRRQYFECNERTCSQMIMS

LTLTLKDSIIKVLDTNAVVDKLRNGCPDKVTCWNELKVLAIARSALVVYSYAMLATLIRIQFNVMGGHVY

KDIQNSNGTTTENVVQTKYMSLSSHFIYKGIKKLGLLIKDKVAEITASICLKEELNLRDIEEIYWALTSS

LSADSSKDPVKNLAEYMLLSNCEEEQTPILLKLFNETLDLLESEEVQNLTQSSIRSGFSLLVDHISAFFI

ASPIVENGKTIQNGVSVPGTSSQTSINTKYDSNAFININKVSMPMAKIIPIINGQVPDKPTLKDFQSDLL

QRLITNNELKTLGANIYEAFSF

>gi|348518503|ref|XP\_003446771.1| PREDICTED: peroxisomal biogenesis factor 3-like [Oreochromis niloticus]

MFSSAWNFIKRHKKKFIFTGALIGGVYLLGKYAQIKFREIQEREATEYIAQARRQFHFESNQRTCNMTVL

SMLPALKEAIVTQLNSESLTTLLKSKPANKLEIWEDLKIISFTRTIVAVYSTCMLVVLLRVQLNIIGGYL

YLDNSVGKSTTTLLAPPDVQQQYLSSIQHLLGDGLTELITVVKKAVQSSLGSVSLKETWSLLELEQQLNW

IRAEVEASSRRSLSWYLLADDENVLADQACGLTDNDIMTIKLLNETRDMLDSPDFTTVLKACLNRGFSRL

CDNLAEFFRPPPGDSAPSCGPDSLSAVSLPLAKIIPIINGQINTICSETPSHFVQELLMNDQVKEFAANV

YETFSTPQELQK

>gi|348559780|ref|XP\_003465693.1| PREDICTED: peroxisomal biogenesis factor 3-like [Cavia porcellus]

MLRSMWNFLKRHKKKCIFLGTVLGGVYILGKYGQKKIREIQEREAAEYIAQARRQYHFESNQRTCNMTVL

SMLPTLREALMQQLNSESLTALLKNRPSNKVEIWEDLKIISFTRSIVAVYSTCMLVVLLRVQLNIIGGYI

YLDNAAVGKNGTTVLAPPDVQQQYLSSIQHLLGDGLTELITVIKQAVQKVLGSVSLKHSLSLLDLEQKLK

EIRTLVEEHIPSSSANKDGSRSFLCHYMMPDEETPLAVQACGLSARDITTIKLLNETRDMLESPDFSTVL

NTCLNRGFSRLLDNMATFFRPTEQDLQPSNSMTSYSSVSLPLAKIIPIINGQIHSICSETPSHLVQDLLM

MEQVKDFAANVYEAFSTPQQLEK

>gi|118782681|ref|XP\_312432.3| AGAP002507-PA [Anopheles gambiae str. PEST]

MWSSIKDFIYRHRRKFITTGVVIGGSVFLLKWLQYKLRELQERQAKEIGEKLKRMQHYECTDRTCNQTIL

GLSPALSEKVFQSLSTDDILAKLRTNPDNKLELWEELRIVAFTRLITLVYGASMLAVTLRVQINILGGYL

YKATVEDSQQQAISLEVQTAYLSLIQHFMRDGIDRLIEIVRKNVTTVMQRYSLKQQLTLADTETLLWSIE

MALNNEKGNPIDGIATYTLPNPGASLTGVDGAFSTMFQETLDVLESVESTEVSLANVSIGLAKVMDKLAD

YYMSSSSGASKQNSKSNLNVESIANINGITISLAKLIPIVNGLASKVAPVPAGANGTVSNGLVPALPEET

DLMSSMIVHFLHSEKLRTLGANVYETFCH

>gi|158299123|ref|XP\_319231.4| AGAP010074-PA [Anopheles gambiae str. PEST]

MATNFRNTTLNEERIFGNTNGLNTSAGVIPTNHPPPLPPRPQFSGGGGDMMFGNRYGFPGQSGYHSYSPY

GGYSSMDYYGHRSYGGYGGYGQGYGGGYGNPGGGFNYPEHRFIQLAEESSRPAFQILESLVGAVGNVATM

LDSTFFAVTSSFRAVLSVAANLAHLKGTFAQFWSSLAVVRAAVWLYKKMLYKLRITKTDPTLEAFKEAFN

VSTGSDVNGNNNGRKHSSSLLAALFMGFMLSVPYMLIKLFAPKVSEDTGKSDPAMWNNPVEVQALHNFDA

SNAQEMSIRAGQSVLLAPKQIQTDRHLLNSGWVLAATADRRTSGIIPLNYVQALKQSVESQ

>gi|345479837|ref|XP\_003424038.1| PREDICTED: peroxisomal biogenesis factor 3-like isoform 1 [Nasonia vitripennis]

MFTRIRNFFYNHRRKFLFSGVFFGTLIILARYARSKLREWQEKEVNELLERSRRRQHFESTERTCDQTVL

MLSKNLRTATTKCLDCMKIVNDLRNGSTDKISAWNRLKILAISRTATIIYSYTMLVITLRIQLNVLGGSM

LKDSKIGDSSPQSSEKVDDRMKEKYLSLCENLMEHGVEKLSLLIQEKVEEITASYSLGDKLHLRDVQHIY

WAITSTVSAVEKSEPVKNISSYLIADDFIKNNQSDKPLAKLLDQTLDLLESQEVQDLMQTNLRSGFALLI

DRISEYFNENAKSDGETSNGDNFVNLNAVTMPMAKIIPILNGQVPENPTPGDLPSDWLQRLLLSEELKAL

GANIYEAFCY

>gi|345479839|ref|XP\_003424039.1| PREDICTED: peroxisomal biogenesis factor 3-like isoform 2 [Nasonia vitripennis]

MFTRIRNFFYNHRRKFLFSGVFFGTLIILARYARSKLREWQEKEVNELLERSRRRQHFESTERTCDQTVL

MLSKNLRTATTKCLDCMKIVNDLRNGSTDKISAWNRLKILAISRTATIIYSYTMLVITLRIQLNVLGGSM

LKDSKIGDSSPQSSEKVDDRMKEKYLSLCENLMEHGVEKLSLLIQEKVEEITASYSLGDKLHLRDVQHIY

WAITSTVSAVEKSEPVKNISSYLIADDFIKNNQSDKPLAKLLDQTLDLLESQEVQDLMQTNLRSGFALLI

DRISEYFNENAKSDGETSNGDNFVNLNAVTMPMAKIIPILNGQVPENPTPGDLPSDWLQRLLLSEELKAL

GANIYEAFCY

>gi|345305174|ref|XP\_001507262.2| PREDICTED: peroxisomal biogenesis factor 3-like [Ornithorhynchus anatinus]

MLLKRLQSLLVVVAGVYLLGKYGQKKIKEIQEREAAEYIAQARRQYHFESNQRTCNMTVLSMLPALRDAL

MQQLNSESLTALLKSRPSNKLEIWDDLKIISFTRSIVAVYSTCMLVVLLRVQLNIIGGYIYLDNAAVGKN

GTMLLAPPDVQQQYLSSIHHLLGDGLTELITVVKQAVQKILGSVSLKHSMSLLDLEQKVKEIRKITEEQK

PPSWVDTTGPRSLLCHYMMPDEETPLATQACGLTAGDVTTIKLLNETRDMLESPDFSTVLNTCLNRGFSR

LLDNMAEFFRPTEQDLQRKDSMNSLSSVSLPLAKIIPIINGQVHAVCSETPSHFVQDLLMMEQVKDFAAN

VYEAFSTPQQLEK

>gi|344263832|ref|XP\_003403999.1| PREDICTED: peroxisomal biogenesis factor 3-like [Loxodonta africana]

MLRSMWNFLKRHKKKCIFLGTVLGGVYILGKYGQKKIREIQEREAAEYIAQARRQYHFESNQRTCNMTVL

SMLPTLREALMQQLNSESLTALLKNRPSNKLEIWEDLKIISFTRSIVAVYSTCMLVVLLRVQLNIIGGYI

YLDNAAVGRNGTTVLAPPDVQQQYLSSIQHLLGDGLTELITVIKQAVQKILGSVSLKHSLSLLDLEQKLK

KIRNLVEQHKSSSSVNKDGSKSLLRHYMMPDEETPLAAQACGLSPRDVTTIKLLNETRDMLESPDFSTVL

NTCLNRGFSRLLDNMAEFFRPTEQDLQHGNSINSLSSVSLPLAKIIPIINGQIHSVCSETPSHFVQDLLM

MEQVKDFAANVYEAFSTPQQLEK

>gi|340713534|ref|XP\_003395297.1| PREDICTED: peroxisomal membrane protein PEX13-like isoform 2 [Bombus terrestris]

MAPERTNGINGNHLKNVPNIINSIPNPASPFPSSNLQPGNPPPVPPRQPVQNYSGSSDHRPYGSNYYGGY

GFGGYGNQYRGFNGYGGYSSYSSYGPYSSYNNYGMFGGHSGDAENRFSLYVEENTRSTFQLIETVLHTFS

SITMLLESTYFALTNSFRAILNVAENVGKLRSTVNQLLNTFALIRFFKWLYRKIVRSTGYQNQDSINEEL

WNKSLAKVRSVNVHNSSYWSGFLIFSVFFVVPYIIHKISNNIKNMQIKGKDPKEWQDIEEPAYIATVLYD

FVATHNDELSIKAGQKVYLAPKSLQPKNLPGWCKATDNVNVGLIPYNYIKVIGQLKKLKRDNETNPVNEE

KSSTDESSNHSNRKDSQPTRNDRTVENEA

>gi|340727839|ref|XP\_003402242.1| PREDICTED: peroxisomal biogenesis factor 3-like [Bombus terrestris]

MFSSLRGFVNRHRRKFILGGIIVGGVIFVRYTARRLREWQEKEIKDMLDRSKRRQYFECNERTCSQMIMS

LTLTLKDSIIKVLDTNAVVDKLRNGCPDKVSCWNELKVLAIARSALVVYSYAMLATLIRIQFNVMGGHVY

KDIQNSNGTTTENVVQTKYMSLSSHFIYKGIKKLGLLIKDKVAEITASICLKEELTLRDIEEIYWALTSS

LSADSSKDPVKNLAEYMLLSNCEEEQTPILLKLFNETLDLLESEEVQNLTQSSIRSGFSLLVDHISAFFV

ASPIVENGKTIQNGVSVPGTSSQTSINTKYDSNAFININKVSMPMAKIIPIINGQVPDKPTLKDFQSDLL

QRLITNNELKTLGANIYEAFSF

>gi|194227620|ref|XP\_001497293.2| PREDICTED: peroxisomal biogenesis factor 3-like [Equus caballus]

MHLLARTRRWVAAVRGGAAFRTEDRRPESWGGRSTVGGERAANPGPAPVAPNRAARLSPPTPPPPGPGAS

PRAPNLASGRPGAARAARSQPPRGVQSVGSREHSAGVLKGWENPDRSPSAASARSACKLSWKSRREKALA

GCCAGALRIVGIGTAPARVYILGKYGQKKIREMQEREAAEYIAQARRQYHFESNQRTCNMTVLSMLPTLR

EALMQQLNSESLTALLKNRPSNKLEIWEDLKIISFTRSIVAVYSTCMLVVLLRVQLNIIGGYIYLDNAAV

GKNGTTVLAPPDVQQQYLSSIQHLLGDGLTELITVIKQAVQKILGSISLKHSLSLLDLEQKLKEIRNLVE

QHKSSSWINKDGSKSLLCHYMMPDEETPLAVQAYGLSPRDVTTIKLLNETRDMLESPDFSTVLSTCLNRG

FSRLLDNMAEFFRPTDQDLQQGSSMDSLSSVSLPLAKIIPIVNGQIHSVCSETPSHFVQVG

>gi|126310649|ref|XP\_001370565.1| PREDICTED: peroxisomal biogenesis factor 3-like [Monodelphis domestica]

MLKSVWNFLKRHKKKCLFLGTFLGGVYILGKYGQKKIREIQEKEAAEYIAQARRQYHFESNQRTCNMTVL

SMLPTLRDALMQQLNSENLTALLKNRPSNKLEIWEDLKIISFTRSIVAVYSTCMLVVLLRVQLNIIGGYI

YLDNAAVGKNGTTLLAPPEVQQRYLSSIQHLLGDGLTELITVVKQAVQKILGSVSLKHSLSLLELEQKLK

EIRKISEQHTSSSWIDKTGPKSLLCQYMMPDEETPLAIQACGLTEGDITTIKLLNETRDMLESPDFSTVL

NTCLNRGFSRLLDNMAEFFRPTEQDLNHSDSMNSLSSVSLPLAKIIPIINGQIHSVCSETPSHFVQDLLM

MEQVKDFAANVYEAFSTPQQLEK

>gi|55627480|ref|XP\_518776.1| PREDICTED: peroxisomal biogenesis factor 3 isoform 2 [Pan troglodytes]

MLRSVWNFLKRHKKKCIFLGTVLGGVYILGKYGQKKIREIQEREAAEYIAQARRQYHFESNQRTCNMTVL

SMLPTLREALMQQLNSESLTALLKNRPSNKLEIWEDLKIISFTRSIVAVYSTCMLVVLLRVQLNIIGGYI

YLDNAAVGKNGTTILAPPDVQQQYLSSIQHLLGDGLTELITVIKQAVQKILGSVSLKHSLSLLDLEQKLK

EIRNLVEQHKSSSWINKDGSKPLLCHYMMPDEETPLAVQACGLSPRDITTIKLLNETRDMLESPDFSTVL

NTCLNRGFSRLLDNMAEFFRPTEQDLQHGNSMNSLSSVSLPLAKIIPIVNGQIHSVCSETPSHFVQDLLT

MEQVKDFAANVYEAFSTPQQLEK

>gi|332226592|ref|XP\_003262474.1| PREDICTED: LOW QUALITY PROTEIN: peroxisomal membrane protein PEX13-like [Nomascus leucogenys]

MASQPPPPPKPWETRRILGAGPGPGPGPTFQSADLGPTLMTRPGQPALTRVPPPILPRPSQQTGSSNVNT

FRPAYSSFSSGYGAYGNSFYGGYSPYTYGYNGLGYNRLRVDDLPPSRFVQQAEESSRGAFQSIESIVHAF

ASVSMMMDATFSAVYNSFRAVLDVANHFSRLKIHFTKVFSAFALVRTIRYLYRRLQRMLGLRRGSENEDL

WAESEGTVACLGAEDRAATSAKSWPIFLFFAVILGGPYLIWKLLSTHSDEVTDSINWASGEDDHVVARAE

YDFAAVSEEEISFRAGDMLNLALKEQQPKVRGWLLASLDGQTTGLIPANYVKILGKRKGRKTVESSKISK

QQQSFTNPTLTKGATVADSLDEQEAAFESVFVETNKVPVAPDSTGXDGEKQDL

>gi|332213489|ref|XP\_003255856.1| PREDICTED: peroxisomal biogenesis factor 3 [Nomascus leucogenys]

MLRSVWNFLKRHKKKCIFLGTVLGGVYILGKYGQKKIREIQEREAAEYIAQARRQYHFESNQRTCNMTVL

SMLPTLREALMQQLNSESLTALLKNRPSNKLEIWEDLKIISFTRSIVAVYSTCMLVVLLRVQLNIIGGYI

YLDNAAVGKNGTTILAPPDVQQQYLSSIQHLLGDGLTELITVIKQAVQKILGSVSLKHSLSLLDLEQKLK

EIRNLVEQHKSSSWINKDGSKPLLCHYMMPDEETPLAVQACGLSPRDITTIKLLNETRDMLESPDFSTVL

NTCLNRGFSRLLDNMAEFFRPTEQDLQHGNSMNSLSSVSLPLAKIIPIVNGQIHSVCSETPSHFVQDLLT

MEQVKDFAANVYEAFSTPQQLEK

>gi|328778061|ref|XP\_003249441.1| PREDICTED: peroxisomal biogenesis factor 3-like [Apis mellifera]

MFSRLRGFVNRHRRKFIVGGIVVGSIIFIRYTARRLREWQEKEIKDMLDRSKRRQYFECNERTCSQMIVS

LTSTLRDSIIKVLDTNTIVNKLRNGCPDKIACWNELKILAIARSAVVVYSYAMLATLIRIQFNIMGGHVY

KDIQNSNGTTTENIIQTKYMSLSRHFIYDEIKKLSLLIKDKVAEITASISLKDELTLRDIEEIYWALTSS

ISADSSKNPIKNLAEYMLLSNCEEEQSPILLKLFNETLDLLETEEVQNLTQSNIRNGFSLLVDHISAFFV

GSPIIENSKTAQNGISVPGTSNQNSISMKYDSSIFTNINKVSIPMAKLIPIINGQVPDKSTSRDFQNDLL

QRLITNNELKTLGANIYEAFSI

>gi|193641012|ref|XP\_001949951.1| PREDICTED: peroxisomal biogenesis factor 3-like [Acyrthosiphon pisum]

MYDSVKKFVSRHKHKLIISGALFCSTAYVVYTIKNKLAEKKDKESREYLERSRRQQHYEATENTSNRMIT

EFVKQLHVKYFAKNLRIENIIDKLKKQNDLALWEEMRICVFTRACLLVYAETMLVITLKIQLNLLGGLVY

KSLSQDSPPICSKTQEDYLLHFSYFIEDGIQRLEEYLHSKVIKYVQQVPIQEQYNLQELEKLFFLIQTEI

ASDTDSPFRCIDSYMLHQMPQVREALLQDMVNETRELLKNDEIISVARYCTSHSFNKLMDAITVNTPNRS

ANLPTTVKMPFAKWLPIVDRSTKVTESGDCSLKQNVHLDGKVKVLSANVYEAFCSA

>gi|327305257|ref|XP\_003237320.1| peroxisomal docking factor component Pex13 [Trichophyton rubrum CBS 118892]

MASVSPPKPWERAAVAASGSSVAQRVVTASAAPPSSTTAVAPSSSSTTSSSSAPELPSRPSALNAVVNQT

ASTYSPYGASRLGTSPYTGGYNNYSSPYSRFGAMGGMGSMYGGYGGMGGMYGSYGGMGGMYGGIQNGDPN

SLTHSFNQSTQATFQMIESIVGAFGGFAQMLESTYMATHSSFFAMVSVAEQFGTLKNTLGSVLGIFTLLR

WLRTLLAKLTGRPPPADATALTPSAFSAFTGNNGGVPDGSGRPKPSKKPFFFFLAAVFGLPYLMSKLIRV

LARSQEQEAKRQQELLNEAQQQGSIDPSKLDFCRVLYDYSPDTQATGGIDLAVKKGDLVAVLSKSDPMGN

PSEWWRCRSRDGSVGYLPSPYLEAIQRRPQQQAITAGAASSTSSAPATRTSTLVGNAAESRTKSLTALKQ

APEPVKGKPTDISLENFQKSNFYS

>gi|327300695|ref|XP\_003235040.1| peroxisomal matrix protein importer Pex3 [Trichophyton rubrum CBS 118892]

MFNSTKQWLRRHRSGIAIGAGVIGVGYLAGQYVLGKISEARERMSSERIARENLRRRFEQNQTDCTFTVL

ALLPTATENILGALPVEELTNELQQKRAERLAKQLNGGEAAGSEISSDPLSTVDDDGKSLSSLRSQGYVH

TSQMGDSVAGDGTPRKKSRTQLWNELKVNSLTRSFTLLYTLSLLTLLTRIQLNLLGRRNYLSSVISLASP

QADPAIISLEENDGDNAFGNDFETNRRYLTFSWWLLHRGWKDLMEKVEEAVVEVFGPLNPREDITQERLS

ELTLQVRKKVEGATSEERRAKQWLPYLLPAVEQEDYVLQESGVLLSSEEVSPQTASNLRHLLDETADLIE

SPQFTHILSLLNNEAFSYLIDHKCAIDAFKKPPTVPATQAPEASPANLFSSSATVVPSDSQQPPPNPRVK

LATILAVVSRQAHTIGQGSNPPNEYLSAMEEGVRELEAFAAVVYSSNFGLEGTMSPGGSVGGSFVVVPQS

EKTEKVSKIEMRDVEADDEAGAGAGAGADVEESNFESAWGKATTDEK

>gi|327261877|ref|XP\_003215753.1| PREDICTED: peroxisomal biogenesis factor 3-like [Anolis carolinensis]

MLLAVWGFLRRHKKKCFFLGAFLGGVYVLGKYGQKKMKEIQEREAAEYIAQARRQYHFESNQRTCNITVL

SMLPTLRDALMYQLNTESLTSLLKNKPANKLEIWGDLKIISFTRSIVAVYSTCMLVVLLRVQLNIIGGYI

YLDNAAVCKNETTLLAPPDVQQQYLSSIQHLLGDGLIELITVVKKAVQKVFMSVSLKHALSLLDLDEKLR

EIRRAVEEPEDNFTSEETGSHSLLCHYMMPDEENPLASQANGLTEKDITTIKLLNETRDMLESPDFNRVL

TSCLNRGFSRLLDNMAEFFKPTEQDICHTASMNSLSSVSLPLAKIIPIINGQIHLICSETPSHFVQDLLM

MEQVKNFAANVYEAFSTPQQLQK

>gi|326915808|ref|XP\_003204204.1| PREDICTED: peroxisomal biogenesis factor 3-like [Meleagris gallopavo]

MVTSECRVYLLGKYGQKKIREIQEREAAEYIAQARRQYHFESNQRTCNMTVLSMLPTLRDALMHQLNSES

LTSLLKNRPANKLEIWEDLKIISFTRSIVAVYSTCMLVVLLRVQLNIIGGYIYLDNAAVCKNGTTPLAPP

EVQQQYLSSIQHLLGDGLTELITIVKQAVHKVFGSISLKHALSLLELEQKLKEIRKVVEHKDSDQVAPYS

PLCHYLMPDEENPLATQACGLTERDTATIKLLNETRDMLESPDFSTVLSTCLNRGFSQLLDNMAEFFRPT

EQDFSQNGSVNSLSSISLPLAKIIPIINGQIHSVCSETPSHFVQDLLMMEQMKDFAANVYEAFSTPQQLE

K

>gi|260773446|ref|ZP\_05882362.1| chromate transport protein ChrA [Vibrio metschnikovii CIP 69.14]

MWEIFIRFFTLGWISFGGPAAHIGYFRHTFVEKLKWMSDQQYGQIVALSQFLPGPGSSQVGFAIGYQRGG

LLGASLAFIGFTLPSIILMVLLATFSRYWLDTSQYALLIHGLKLLAVVVVAEATWGMYQNFCRTKTTASL

GLFSAVILLCIPGILAQILVIVLAAIIGIIWLKNPHPTTTLTPFRPTWWPLVLFVAILFGLPWLVSSSAS

VMLFKQFFHAGSLVFGGGHVVMPLLQNLLADQISSDIFLTGYAAAQAVPGPMFTLATYLGYYLLPASPVT

GAIIATIGVFLPGFLLLLGVLKHWQNLANLPFVSGALAGVNASVVGLLLAALYQPVFISAVFNAWDVALL

LIGLWLLKIMKWPILGLVMFYLLTALIRGVL

>gi|308812191|ref|XP\_003083403.1| unnamed protein product [Ostreococcus tauri]

MTTRARWRRRASTLATVAAIGLGWSYLASERARAWRARLRAVLNDFGFESAPDAREGTLATNAGGMTDDD

SRENESSADDKLSREMARVNGITKTVAAPGRMAALRRGLNEALGRESETPEEKLGKACVALAAASAMELL

TRTTVNLIARRGFLDRESGVTRETLDDTSRAAFLQATSVYFFASGVRELTSIARAIVERELEDFGRESWT

REDTIDFMRRCRETMSRALLVPSDVFSDPKALPFERKNRLHVMAPRAFPSWESMLLPPKNPDFNEILGPA

PKDDADGHELQVRNLRDVMNETRLVVRSPHFVVAMNDAMHAAWRAHADALPRELFGGTRSSTIDVVDAAH

VVDATTERIASDATLLAAIANESGVVFFGDAIW

>gi|302927490|ref|XP\_003054509.1| hypothetical protein NECHADRAFT\_98944 [Nectria haematococca mpVI 77-13-4]

MASPPKPWEQPGAATTAAAATVSPSTATSTTDSSAPPLPNRPSSLTSTVNQNAANYSRMATSPYNSMGGA

YSSPYSSPYSRLGMGGYGGGMYGGYGGYGGGMYGGMGGGMYGGMGGGMGMPGDPNSLTNSFNNSTQATFQ

MLEGIVTAFGGFAQMLESTYMATHSSFFAMISVAEQFGNLRDTLGSVLGIFTLLRWIRTLIAKITGRPPP

ADAMALTPAAFARFEGRSMGPDGKPLPPKASKKPLLFFVLAAFGIPYLMSKMIKSLAASQEEEQRRLQAQ

AMESQQPMDPSKLEFCRLTFDFLPQPNTGMELEARKGDLVAVLSKNDPSGNPSEWWQCRSRDGRQGYLPS

TYLEVLKRPTQEPKKLKAAPSESSRTNSLTSSIERPEEGKKEYATVDGMQRSHFYS

>gi|302410991|ref|XP\_003003329.1| peroxisomal biogenesis factor 3 [Verticillium albo-atrum VaMs.102]

MDGVLVGGAPLGTKLPTEEDGLRSTRVVQLPRILSVLTRQAHLIGNGMPNEYLREMERVRDLEGFAAVVY

SSNWENEVMRDQNLAAGVAEAKDGGDKPAAGSGEESIVLVDRQPSLEDAWSRAQQK

>gi|301753664|ref|XP\_002912676.1| PREDICTED: peroxisomal biogenesis factor 3-like [Ailuropoda melanoleuca]

MLRSMWNFLKRHKKKCIFLGTVLGGVYILGKYGQKKIREIQEREAAEYIAQARRQYHFESNQRTCNMTVL

SMLPTLREALMQQLNSESLTALLKSRPSNKLEIWEDLKIISFTRSIVAVYSTCMLVVLLRVQLNIIGGYI

YLDNAAVGKNGTTVLAPPDVQQQYLSSIQHLLGDGLTELITVIKQAVQKILGSISLKHSLSLLDLEQKLK

EIRNLVEQHKSSSWINKDGSKSLLCHYMMPDEETPLAVQACGLSPRDVITIKLLNETRDMLESPDFSTVL

NTCLNRGFSRLLDNMAEFFRPTEQDLQRSNSMSSLSSVSLPLAKIIPIVNGQIHSVCSETPSHFVQDLLM

MEQVKDFAANVYEAFSTPQQLEK

>gi|294655232|ref|XP\_457335.2| DEHA2B08734p [Debaryomyces hansenii CBS767]

MSEKTGKDNFKYRERASKVLSKMYDKTSDIAGNNSGKNKGIAAGTAASLISLGIDRINQGQSVDETDGLP

YTEDELNQLKELESEMDDSKSSHFVDRFMEKLLKHAIPTDGPEKEMLERRVADPERLKKPNLSIRILTSN

FKRLSSKMSSFFVLQYGLIHIITWRKPTKTLSFLVFYTSICLWPHLILAYPMIFLIFGVMLPAYIHRHPM

RTPELIKVKKRGQSILDFFNSSSDTSVIEDLIGKDYHNDSGSESDSLQPVISKSSDTSSMFSKKPVSASK

LKDGDVNERIQKKDKTRHVKSQMTLFINMRDLQNLTTDVLNGINGAEKFWYETAGFKDERLSTFIFYGVI

AATSIVLVFGRFIPWRLIFIQSGWAGLIVCHPNSKKYIMSIKKSKKAKKVKDVKESKEKEGRFERHDIII

DDSAEIRIVEVFELQNKNMSNNQWSFHRYTSNMFDIKNHARAAGKRPLGVDDLSKVLPPPDWKFDMGYAN

KWEIDIDPQKFFKERNINNPYLQVHEDEKEGWIYDKLDGVDNSDSSYEFRRRRLSRECYRYSRPPVIPKN

T

>gi|50425749|ref|XP\_461471.1| DEHA2F26026p [Debaryomyces hansenii CBS767]

MPIFSSLNSFLRRHKKKLIVTATLTFSAYFLVNQFIIKKLKNFQNSLRQELFVKEQIKRRFVQTQNDCYL

TILALLPVLTQPIINHLPIELITQALKLKKTNSNPTPQEISDSLLTTDNLTMHQNTNDSSDLSHYMSLSK

TELWKLLKIKTLTRTLTLMYSISGLLLLTRLQLNILARRSYLESAIILAGGKVNDTETSQDYFIEQSYLS

LSWWLLNKGWLKISDLVEKVVTEKFNTINARTELSINKFDDLLCEMVNELSTNHNQEILNAVFPISYDNL

IESLLNTNPELIKELDIEDSIMLKLINETTYLVSNEAFGDILINMVDSCKSTLIENLLLSLDPENAYTNQ

EKVIDISNIKQFKLANLLAQLSIQCGVLCDNNNLMNDTFSNELSGNIYMNNLNEIESLDEFSASIYSNFE

>gi|294656026|ref|XP\_458260.2| DEHA2C13376p [Debaryomyces hansenii CBS767]

MSAPRTKPWEVSSGTSTATATGDNMNSINGGATTNPIGDNSSTQAQVPDRPTSLTSDLSSMSNTSPYGST

GYGSTTGSRYGGGYGSSMYGGGLGSSMYGDGYGSSMYGSGGLGSSMYGGGYGSSMYGMGSMGSMGGMGGM

GGYGMGGMGGYGGGMYGQQRPGMGGGLAEGTQATFQLIESIIGAVGGFAQMLEATYMATHSSFFTMISVA

EQFGNLKNALGSLLGIFAVIKFAKKIFYKITGRTYNHGISVNEFAKFEKGQKKLEENMRKQQSGKAPRIS

FKPLLLFLAASIGFPYLLSKAIQKIAEQQQRKQQMLGAQGDVPGAVNPTNLQFAKALYEFNPENPNIEIE

LKPNELVAILSKLDPMGNESKWWKVRSRQGKVGYVPSNYLGVIERKVQQIEPSNQLPHQNPNLTQVPVPE

QPATNQQHDKQFNKKISVDEFKSFQS

>gi|291397094|ref|XP\_002714902.1| PREDICTED: peroxisomal biogenesis factor 3 [Oryctolagus cuniculus]

MLRSTWNFLKRHKKKCIFLGTVLGGVYILGKYGQRKIREIQEREAAEYIAQARRQYHFESNQRTCNMTVL

SMLPTLREALMQQLNSESLTALLKNRPSNKVEIWEDLKIISFTRSIVAVYSTCMLVVLLRVQLNIIGGYI

YLDNAAVGKNGTTVLAPPDVQQQYLSSIQHLLGDGLTELITVIKQAVQKILGSVSLKQSLSLLDLEQKLE

EIRNLVEQHKSSSWINKDESKSLLCHYMMPDEETPLAVQACGLSPRDVTTIKLLNETRDMLESPDFSTVL

NTCLNRGFSRLLDNMAEFFRPTEQDLQHDNSMNSLSSVSLPLAKIIPIINGQIHSVCSETRSHFVQDLLM

MEQVKDFAANVYEAFSTPQQLEK

>gi|291386744|ref|XP\_002709900.1| PREDICTED: peroxisomal biogenesis factor 13 [Oryctolagus cuniculus]

MASQPPPPPKPWETRRIPGAGPGPGPGPTFQSADLGPSLLTRPGQPTLTRVPPPILPRPSQQTGSSNVNT

FRPAYSSFSSAYGAYGNSFYGSYSPYSYGYGGLGYNRLRVDDLPPSRFVQQAEESSRGAFQSIESIVHAF

ASVSMMMDATFSAVYNSFRAVLDVANHFSRLKIHFTKVFSAFALVRTIRYLYRRLQWMIGLRRGSENEDL

WAESEGTVACLGAEDQAANSAKSWPIFLFFAVILGGPYLIWKLLSTHSDEVTDNHNWASGEDDHVVARAE

YDFAAVSEEEISFRAGDMLNLALKEQQPRIRGWLLASLDGQTTGLIPANYVKILGKRRGRKTVESSKISK

QQQSFTNPTLIKGATANDSLDEQEAAFESVFVETNKAPVAPDSTGKSGDKQDL

>gi|291220699|ref|XP\_002730362.1| PREDICTED: peroxisomal biogenesis factor 13-like [Saccoglossus kowalevskii]

MAAPLKPWERASGANVGQNQQNVDGISAGLTPGLSGMTNARSTTLPSTYQTPGLAPPLPTRPGLTSGVGV

NSYSPYSSSLYGGGYGGGYGGGMYGGGMYGGGYSPYSSSYGSSMGYGGIGGYGGGMYGMNRYGMDAQGGS

RFVQQAEESSRAAFQSIESIVQAFGSVSMMLESTFNAVYSSFRAVLGVADHFSRLKHHMVSVISAFALFR

TLKYLYRRLLVLLRLREPNLPNDVWNDVQAEVHQQAEQKLSENGPKSWPIIMFFGVVIGAPWLIWKLLSS

LNNGTSEDPNGWATGEDDHIVARAEYDFDSERSEEISFRAGSLINVAPKELQPRVRGWLLGSVNGQKPGL

LPANYVKILGKRRGKKHVNAQQQQLPPQQQQQSRPIPGDVSGIHQTPSSLDLSSMASGNYFEGRQPSNDN

RTDFDNLQEFEENFQNKQTVPNTSEQSPPAAVVANTADNSATENP

>gi|291237316|ref|XP\_002738581.1| PREDICTED: peroxisomal biogenesis factor 3-like [Saccoglossus kowalevskii]

MHWQNTTLDESWIDHQRDDTVTLAADGGGIGIFGRENAYFKNTYYMTPIVIVIVTIFIICGNSLVLAVVF

FGKSLSNASGRFTASLACADLGIGVIVTPFSIYTAVLNDWPYGHTVCIMASFFTELFSCISVCSLALIGV

DRYIAVVKPLRYHALMPPETARNIVIMTWIAGICLCSATPLQLVKTIYYADLMVCNVSWETELVYSFVMI

SIVAIPAFVTIAFTYYHIFRISYKAARQIESEEQRFLGPNSTLGTNRRKNAMKSFLIVLGFFVCWSPWLA

LQIQESAVFAANDGAIGVTVCPTINDNIGDVVATTPLGDKCYWFQAEGSHNRQWNEAVDWCISQNGYLVK

FETLQEESDVIEHINIQNYTKTEDFWTAGECTGDVTKGDCDNNDNWYWAIESRPGKTGDIMEHKNWAPQE

PNPLKGGNGKGYNMVLKRVSDIWQWYDENYDKKTNYICEFDAIDVTTNTQRTISTSTHHTTTYTTPTEQL

GCSSVTDNNGDISPTVHIKDRCYSFQLYGNQLSWNEAVDWCYIRNGSLVRFETPTEWDSVYEYINMNISE

HDSPIWTGGGCYGNISAGEYDCDYNWYWIEDDGSQGDVISFTVWDHGEPNPSEANAGQYVAMVMDETNSV

DTWAWYDWNYLDHHSFICEFAYGNQLSWNEAVDWCYIRNGSLVRFETPTEWDSVYEYINMNISEHDSPIW

TGGCCYGNISAGECDYDCNWYWIEDDGSQGDVISFTVWDHGEPNPSEADAGQYVAMVMDETNSVDTWAWY

DWNYLDHHSFICEFSAVLLGKYASWKLNELREQEAVEYLSLTRRQHHFDSNQRTCNMTVLSMIPNLKEIL

MQLLDSENLTAQLKNKPTNRVEIWEELKIISFTRTIVAVYSSCMLVVLLRIQLNIIGGYMYLDGMSSQDM

FQSTDQKLPPEIQQRYLATIQYLLEQGLKDFITSVRSAVEAVLTCVSLKHCISTHEVTAMINKVRSLIET

EKTEQFDSAHSLCKYMLPSEATVMQENGIIHQLMIETKDMLESDDCSNIINLCLKTGFNRLEDNIQQFYN

PVDVTNENNLQYLNIPLAKIIPVMNGQIHSICSDTPNHFVQELLLLQPVKDFAANIYEAFSQSASASIAP

>gi|166240426|ref|XP\_640208.2| RING zinc finger-containing protein [Dictyostelium discoideum AX4]

MSNVQSQSNSHHPVHNIVNRSPTSRSEQQIRSIPPTNNNNNNNNNSINNINNNTQRQPLNNNNNNNNNIN

RNNSNLYPSYADQPDILRSSQKDEYYKKLFEDQCFEMLTRITGPRFIMNRQSESKLLANTIYYLLTTMIG

SQTLGEEYCNLRKIKDKTFSIPSIPDRIKLYFFHLLAPYLIKKSLPKLFQRHPKLYILKEIFPKFERLHL

ALFYFNGSYFEFSKRLSDIRYIFNRKIDQKRPKYDILGLLIIIQILLSTFMYLKENSFFLKQQQKDGGCN

GDGEEDNQDLNKDIKIEQVDSVINNNNQDQNNNQEEEEEQKCTLCLEVRTHTTATICGHLFCWHCITEWC

NNKEQCPVCRCPISIRTCVPLYNY

>gi|111226782|ref|XP\_642972.2| peroxisomal biogenesis factor 16 [Dictyostelium discoideum AX4]

MIPKQPKSNILIFLLENSDHLGLLKSLITFLPGRYGDSELFSEGLYSVANILQSYLDYRSSGILLSNNID

KISNGEKVPPPYYLTTLRWITTVQSLELFFEMLATKKGEQHDDSNSNNNNSNNNIKKMIIFIIELLKAIL

RLKLLIKTNGDMLVHHSFYVPSKDVKTILENNRNQQKQFQNKRPAVTMSINNNNNINNNDNNNINNNNNT

NDDNFNNNNNNNNNRRTLSDQIFEQQRIVNQENNLLYQQQRELQQNESTLIKLLPPPPPKDYNTKTIGEI

LFIFRPVIYWVSYCIFGKKSWKPWFLSLVTELLSKSFSEYGNFKQKIRLTLLEAKELNRRKKLLFFYLIR

SPFYEKFIGDGLLNKFLNFLKKIHIFKTLIDILINYLNVYRTRYFYTSAS

>gi|66823899|ref|XP\_645304.1| RING zinc finger-containing protein [Dictyostelium discoideum AX4]

MVDNYNNNNILPTNTSTTTTTNTTITPTPPLPPPPPISNILDNNNNNNLIKNDIKNDKVAVSNSNVRPSS

SSVSYENSDWNKVYNSEREKLHEVNKQILNIKRPSTSIVRVSQLDSARLDEEILDLLRSQFMKIFTFFKP

NFIHNFQPEINLVLKSVIYKLSIFNLGTTYGNQLQNLTYRNEKAFDPIRGSDQLNKLTMRQKWLSGLINI

GGEWLWTRINRYLINNNWSEHPPNDIRKKFWNFLNFAESAYKALALLNFLTFLFNGKYVTLVNRILHMRL

VYAHPTLSRNISFEYMNRLLVWHGFTEFILFIMPLINIDRIKSFLYRLLVKTSFGNSSGNNNNTASNPLQ

QLQKQQLLIQQQQMALAKCPICMNDPISMPYSADCGHLFCYYCIKTSCMIDSSFTCPRCNSLISNIKRFS

IQD

>gi|66814620|ref|XP\_641489.1| WD40 repeat-containing protein [Dictyostelium discoideum AX4]

MKRFHSHFNGYSVEFSPFEEQRLACVTSQHFGIIGNGRQYILDVLDRDIGAFKTFDTRDGLYDCTWSEEN

ECHVASSSGDGSIKIWDTQAPSGGRPIKSFEEHTKEVYSVDWNLVTKDTFITGSWDQSIKIWNPRMDRSL

KTFREHRYCIYSAIWSPRNAHLFASVSGDRTLKIWDSRDNRSLNTIKAHDHEILTCDWNKYNDKEVVTGS

VDKTIRIWDIRYPDRPTTILRGHTYAVRRIKCSPHSESMLASCSYDMSVIVWDRAREQDPIIARMDHHTE

FVVGLDWNMFIDGQMASCSWDEQVCVWNLGRPGQFR

>gi|66800955|ref|XP\_629403.1| SH3 domain-containing protein [Dictyostelium discoideum AX4]

MRRSPPKPWENNSGGGGSTSMTGSGGISRPMSGPQRTTSPGGGSSTTTQTSTLNNTGSPSTSVGGPLVTR

PRTPMRPWESGGAGSSSIDSFGGGVGGSSGYRSSYGGGYRDSYSSGGYGSSGYGSSYGSGGSGGYGSSLY

GGGGYSSGGYGGSGYGSSYGGGYGSSYGSGYGSSYGGSGYGSSYGGGYGSSYGGGYGGGYGGGYGQRGYD

NMDGKGGALQSVVSSGHSWMEALHSIVDTFSRFSRLLDANFDAVHGSFSSIIRLCQSMSHFSYEIMAIIK

TYSLFRMFQSVASRFLRVFRYLLGKKSKSNSSNNNTSSKFGSNAITESLRQANMDVSDFRNFQNEKKQSV

GTLILIIAATFIGVPMVIGQLLNLRRRGQASRLDKGWEEQQGGGYGQVKAIYEFNPETTRDLPLRVGDIV

NVIDKPHDNWWVGECNGLSGFFPVDFTEKISPNDINNNNNNNNNNNNNINTSVQIYDNNNGFNRNNSNNN

LNNSEYSDYSSSNNNNNNNNNNNNNSNYQLQSNFSSNNDGISKNIIYNNNNDNQRPISPSKTSQQLSRSE

LMDKPYVEES

>gi|66800571|ref|XP\_629211.1| transmembrane protein [Dictyostelium discoideum AX4]

MDNDDINNNNNNNNNNNNNNNSQELDQQEQTQEEITKQRIQKRKEEAKRIMEERKKREQQPPSQRQYEDV

EDDQQQQPIRPIKQLPQRQQQYDDNDEPPQQQQYEPKISQRKVPLPPMKQPTTSSTASAATGSILSPSSN

FREDMVKKAVLFLNNPNVKNTALARKVAYLEKKGLTSDEVKEALKRVETGNINGSSTNNSNITQSNSISR

TRNDNYGNNNNNSSNNNNNIQQQQYYQQQQQQHQQQQQMALTQIQSYQKRLEADDQRIAQLMMNNNRFSW

NSFLFSVTAIVGAASGLAYLTSNYIIPFLNGGKTNKDASANMDKKITSLQEEIIKLQSTIIQQGNDFRES

TKSLKTLIEQQQQQILQQQQINSVSTTTNSATSASNSSEIVEIKKELKNLINLIGNKENSNNSNNNSNNS

NNNNGYSKYNGFNGVYNKSSYDDVSTNNNNKTNSPPSPNKPTTTTTTTATSTPGSNISNTNKTLPPIIKT

NPYSHLSWKLPTDQPPVIPSWQQKSSNPPSDLSNANDKSSPSNSNPSTPTKPYQSSFNYGDVNSFVGGSN

TLNFDEKPTTTTTTSTTPSNERPSSPSVNNNNNNNNNNNNNNNNNNNNNNNTTIASTSNESNNSKVETTS

NDSDKSTSPSSSSNNTTSTTATTTTITSASTEDNKQQSDETPYSSDFLDVINQLKQGKTPPGIRTDIDDK

PLENSTVTKSAKERPKKPWERDTLTSVTNNLSVEETQTINNTDSSVEK

>gi|66801075|ref|XP\_629463.1| AAA ATPase domain-containing protein [Dictyostelium discoideum AX4]

MIGLFKDEWFNISILNDNLFLKRYCYESNNNNNNNNTLYTIIVPFDKSINPSQFDPSTINDYFIFLYKNT

KKINLNSINKLQYKSNKKEILVSFDITYIHNSNNNNNNNNNKLKSVLISNSCSKKLNLFNNDIVHLKPIK

KKLTVLQRVVLLANDNESFIESSNPSESSSSTTTINSKYLVNEEFRNYLVENSILFQSPNNIVIENHQKH

KSFSYKVLECFPLLQGTVSNSTTIIIISPDDKILNTLPSNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN

NKEEEVEEEEVEVEEEEKDNKLKLNNNLRLSNFIIHPIINISNNTTTKNEDIGDSNNLFHFTPSSKGILS

NNKKFINISQLKSIPTEIDFEFDISKEYDYLVDCLVSLNTLKSLNLFNGSWIKIKNITNNNNNNNNKEYE

IAIRIFSITSSLKLKDQVLYLPPISIFNLNIDYKNFLKLSNYEIISNQFELILLKSNKPNINNNNNNDSF

PINYPTANRIKISRIKNQNSSGYKSYSHQLEKYFQKKRLLKQNDIIVISTKVNNEEELINSNNSNNNNNY

NNNNNNNNNNNLVYFKVEIILCNQFENINGNQIYLIDKNTTSIIQEGSSNSMVPSKIESFYWRGGDQEES

KDNSMVPLELIYENEFKTIVDLISPFLMGDKFSFDFNCTLLLNGPQGVGKRTLLNRVAKQMGIHVYEVDC

YKLYDFVESKKDWNIRNVLEQASNSTPTLLILKNFEVLEQTAQSMQQEKKESNLSQTLINILKDINDSNT

SNINSNKYPLIITVTVNSMDELSNKVRNWFKHEITLNSPDENQRFKILKYLTKNLPIDIGNTVSIKNLSI

RTASFLNSNLRALIQRSSINALKRVLSIQQMMNDEIKPIEIYNCGFLVMGDDIQKSLSEMQEYQSSSIGA

PKIPNVSWDDVGGLANVKSEIMDTIQLPLEHPHLFASGIGKRSGILLFGPPGTGKTLLAKAIATECSLNF

LSVKGPELINMYIGESEKNIREIFNKARQAKPCVIFFDELDSLAPSRGNGADSGGVMDRVVSQLLAELDG

MQKSSDVFIIGATNRPDLLDSSLMRPGRLDRLLYLGISSEKENQFKILQALTRKFNLADDVDLRKVVENC

PMNLTGADFYALASDAMSNAFHERITASINGEINEEEQNQKLIVYQNHFIKAVNSLVPSVSLDELEYYHK

VQKQFSGNNKS

>gi|66808361|ref|XP\_637903.1| tetratricopeptide-like helical domain-containing protein [Dictyostelium discoideum AX4]

MSVFRDLVEGECSEPNALGNFVQHFTNERSYHDKFEDHGKNEFYDSLYRHEEEYNEQRHLDSIFDGEGQE

DDIHLMMDRHLNLRDGPREHKELPLSNVESDLQFLFQDFINSTRAGQLFHPSSLNHLPLTFEDKSKIKNR

SSIMLKHFSNGESEQFEEDQLNRMLDSLGIEVGDDFDQVWDSQPHHTTTTTTTTTTTTTGQYDQYQKYVN

DLPEEYEDYEQHQQELFDDGDLEDYELDEEWDKGDDFHPYDSAWTESDRSVEAAWDETARRTISDITRPI

TQINDPKLKKSNFMKFMNQLNSGEASIVGSDVVHNPDFKRQEEYQQQADQWTEDYNDFHEHIPQHRIQEY

QFSIQEARDSDTLERGMGLFNEGHLSDSIIALESEVKRNPENAMAWMYLGIAHAENDQDSQATTCLIKSL

QIDPTNSKARLALAVSHTNDYQKERALDTLEEWLQRTPEYTALYKQFKGSVDPNSFLDTWSRHEFTTNLF

IEAARSRPSNPDPEVQTALGLLYNMSYDYDKAVDCFKAALQNSPTDYQLWNKLGATLANSNRSQEALGAY

FKALEHKPSYVRARSNLGISYLSLNMFQESATTFLGAIAIHPAPNIWDNLKMVFRLMNREDLVQKADLRD

VNAFLDEFQFM

>gi|66808761|ref|XP\_638103.1| RING zinc finger-containing protein [Dictyostelium discoideum AX4]

MFMFNFDNGHDPNRPSFFEMLNQHQMMPSFKPALKYIFTVLSQRNPKFRYIVNYYDECFYSLLLLLEYHY

LKYYEGSFSENFYNLKRIKPRNNNANGDGDTLFSLLKRLVVTPSNAGQGPETYTKSQILKKSFAMIRRNR

AAASSSQQAKDDLNTMIQDSDRKESLIYLVLIPYFKGKLDEYYKKESDPLAELGLVSSDNNNNNNDNIND

QIQQLEEQIQQQQTIVNGNNNSNNNNKKLKIKFLILIRFLKGSKTLKKLKTIFLKVYPFISAIYEALFFI

YQLLYLYEYTNYYTPFFHFQNIQLKRLNHKDIESHRVVISNRRRDRINFVRDWPGSSFFVRLVSILDSIL

DYSKYILPLSVFIFKSLEWWYSENRISAPTLPIPTPPTPSKRAPGGLEIPRDKRLCPLCLKERTNPTICG

SGFVFCYPCIFGYVNEHSKCPITFLPTNTEQLRKIYETV

>gi|66804811|ref|XP\_636138.1| transmembrane protein [Dictyostelium discoideum AX4]

MAGILSKPNYNQFLESLIKLLAQTSGKDKIAKILQYGAKLLGYIFLKRSKHWVDVMKKLETTSGSARKVW

RLGNTLAEQQKILALFKVKNPFAFLNILALIRQSGMYFYWVFDHLILGTNIGLCKFDTVKLGWYSSVSWF

FGLLCSIIIDLNTLAIMLKKEKSLRLTITQNKINANNNNIDTHTITSEVENKAIIDQFNEVIKKKNEIYL

NCAKNGSDLIIASTLLKIYPFSQGTIGISGIISALIGAYQMWPK

>gi|66804599|ref|XP\_636032.1| peroxisomal biogenesis factor 1 [Dictyostelium discoideum AX4]

MELHVQLKHSTDCFVSLPPKIVHSLLLLSEKQSKSLGTLGLEITWYDKINKKENKGYVGWAGGSTDPRFT

DSIEMSQEMAQCLGGIKNEQKLKLKALNNIELAHSVQVEPLTSDDWEIMEVHQQYLEEQLLNQVNILYSG

QIVPIWIHHKTIIKLKVTETLPTPVVKLSSNSEIIVAPKPRNLPTTTTSSQQQQISKETLKPRFLQIKDF

KIDYNNNNTFINEIYINKELLNQFQWNIGDIIEISKVSKNNNKNNKKEKNNNGGDEEEDDDDNEEFDDDD

DDDNNNNEDDTSKLQKQLDNKNNNNKKNKKNNKTIYARVFINDKSNNQQVLIHRNIRTIGNFYINTIVRL

KYTTSHSLPICPIGSILVKQVIWKQNSLSNLIKQQSSQKIYSVEQIKEQIKVWSNNNLSNNQRYPLLNGS

IVSINSNLDLSFNFNNLTSSIIPPTSSSSSSPSNNLDSQRSNNNNNNINNDQLNDITNNMNNPYLSSIQQ

IGDIMSNLNTNNNQNNQNNNSNKLMNQFQMNNGIFMLSLEILSNDKLLKIESGGNNSIEKKKSLEDYNEI

GDRLFQRIGGMEKQIKQAKEFLSLYMYKDLSVIREQLNTPGVNGMIIAGSHGSGKSLLATSLGGYYSTDS

RSNAFIIKLDCNQLKELKVENIRKQFNKLFYKSCKESGNTLSATTSTNTTPPPIIIILESLDLILGTPND

QDPGSKIRCEQLVSHIKSLCFKYQNRSSPIVMIATVISSQSLCQSIQIPELFGLTIELQAPTREERVEIL

ERYLKYQGKQLKDQQSLNLMKFSASMEGYLGCDVEQIVDRSIHLSSIKEIENNNNNNDDNDDDNIIEFSI

IEKAKEGYTPITLKGIKLHSSEIKWQDIGGLDSVRAMLKETIEWPTKYPKLFQSSPLRLRSGILLYGPTG

CGKTLLASAIAGECGLNFISVKGPELLNKYIGSSEQGVRDVFSRASSAKPCVLFFDEFDSIAPRRGHDNS

GVTDRVVNQFLTQLDGVEGLTGVYVLAATSRPDLIDPALLRPGRLDKSLYCNIPEFNERLDILTCLKSKM

NLSPSISLEQLSTNTQYYTGADLRALMYNAQLKSIHEWMNHLEEEKKRKRKEKEDQSNKNSSQQQDDFII

FQPKNNDNSISKSNLTFEEKTNLQKQIDTIKSQFINSNTSTLNKSNLSNEQPPLITQSHIDLALKESSPS

ISESERKKYERIYNNFLKERGSVTGNKKEGVPKQTLA

>gi|224118704|ref|XP\_002317886.1| predicted protein [Populus trichocarpa]

MLSLRNFWRRHRSKILITAGVLGSGYFLYRLYNAHEQRLADLERELARQRANDELIKAQLQAHFENVQLI

ADTTTLPHAMQYLRSRIAEELDLSQLTERLQKGKGKPYTLTSSEKLELWDRLKILSFTQMVVSLWAVTIL

SLYIKVQVNILGRHLYIDTARGLGSSLLLENVDLIDRDDQQNFLAGADFLANNGLLALISNIQAVVTEVI

EGKKLIDLFNTTSFHETVMQILDKFMSVGSLHQWIDYLMPEDSGHYKLGTSSSIDDTVLPNSTNFDQLMV

EARTVLSSAEFGKIMGISLKVAVDALVEDMEAQCQSTGASLTSGMPLAKLLSRVMQMVPSLLREASQNQF

IKIIRTVPEVELFFTLLYANNLVD

>gi|238503536|ref|XP\_002383001.1| MFS transporter, putative [Aspergillus flavus NRRL3357]

MIGATRRWFRRNRKGLAIGAGMIGAGYLAGQYVLSKISEARERMSSDRIARENLRRRFEQNQTDCTYTVL

ALLPTAAEDILDALPVEELTKELQRKRAERLARLNAGEGTGSDLSSVSPSLPEDDRRSLSSFQSDGFVRT

SQPGEPFVEGDGEARPKRNKTQLWNEVKITSITRSFTLVYTLSLLTIFTRIQLNLLGRRNYLSSVISMAT

PPANESTIRLEDHDDDDLTQTLGNDFETNRRYLAFSWWLLHRGWKQLMNEVQTAVTEVFGPLNPREDISL

ARLSELFLEVRKRVEGYTEEERKYVSSYPHSQPNFLLTSGVLGVTELANSQTAATLRHLLDETADLIESP

TFTRVLMLLNNECFQTLIHQCTADAFKSTSQTPRSVPQSFTSVATVVPGADSSEPKAKLANILAVLARQA

HVIGNGTNPPNLYLTAMDQGVRELEGHVDSQSTDLPQLRNTTERKLMAKIDWHIMPCLCVMYLLAFLDRV

NISNAAVLGLQEDLNIVDGTNYNTALTIFFVPYIIFEIPSNILLKKLRPHVWLTGCMFLFGLVTICQGLV

SNWGGLMTTRWFLGMFETGMFPGCTFCFYLLGMWYKRSEAQKRFSFFFSSTTLAGAFGGLLASGLGKMDG

TRGYRGWRWVFIIEGLITCVVSLAWFFIIPDFPEDVKWLTDEERQFIRAKLARDSGSAGHDAKIGWRDVL

EVFKDCEQNIHRWFDVLRSGCHSIWICLLRADHYQELWLRWYVSIKTQLYSIPPWAAAWGFSMLVAILSD

RTRHRFAFTIGPMLIAMAGFGILLNVHGQARRNIQYGALFMVTCGCYSAMPVIVCWFAMNLAGHRRRSVG

TAWQVGFGNIGGIISTYAFLKKDAPEYRPGYIISVSFLSFSAACCIGYFAAVWYDNRRRDQAIADGMAIP

SDEEQELRGDMALNYRYSY

>gi|224135481|ref|XP\_002322084.1| predicted protein [Populus trichocarpa]

MGFWVNFWRRHKRKILITSGVLGSGYFLCKLYNAHQQKLADLERELARQRANDELIKAQLQDHFENVQLI

ADTTTLPHAMQYLRTRIAEELDLSQLTERLQKGKGQPTTLTSSEKLELWDRLKILSFTQMLVSLWAVTML

SLYIKVQVNILGRHLYIDTARGLGSSLLLENVDLVDRDDQQKFLASADFLANNGLLALISNIQAVVTEVL

EGKKLTDLFNTTSLHETVMQILNKFMSMGSPHQWIDYLMPEDCGHCKLGPSSSIDDMILPDSMNFDQLMV

EARAVLSSAEFGKIMEISLKVAVDALVDDMEAQSQSTGASLTLGMPLAKLLSRVLQIVPSLLGEASQNQI

IQIIRNVPEVELFFTLLYANNLLD

>gi|170054875|ref|XP\_001863328.1| peroxisomal biogenesis factor 3 [Culex quinquefasciatus]

MLAAVKNFFTRHRRKFVVTGIVLGSGVFLIKIIQYKLREFQERQAKEIAERFKRMQHYESTERTCNQTIV

GLAPTVSEKALKNLGTAEILEKLRSNPDNKLELWEELKILAFARIVTLVYASSMLAVTLKTQINLLGGYL

YKDTVEQDDKQVTVDIQTTYLSMIQHFMGDGLDELMDTIRKNVTTVMQRYSLKQQLTLADAETLFWSIQV

ALSSEDNSPTKCIASYTLPKEINRSDLLSKMYDETLDVLESAEVSDVCLSNISNGFSLIVDKLAEYYAEA

EPAATQQNGASTKAALNVVAADCGVSNINNIKISLAKLIPIVNGLSSKALGSSAGGAPGTNGLTNGFDQH

RNGDMMASLVARFMQTEKLKTLGVNVYETFCQ

>gi|268562663|ref|XP\_002646729.1| C. briggsae CBR-PRX-13 protein [Caenorhabditis briggsae]

MSVPPTNQPPPLPPRPIDSQQLANPMMNSGFGYGGYGMNGFPGSGMYGTSGMYGGMGYGGYGGFNHMGYG

QPAESNFARLAEEQSRGAFQSIESVVNAVSSVANMLNSTHNAVYSSFRAVIGVVEQFGRLKTQLSSVVVS

LALFRWVYKFWRWLLVMLKLKPANYASVAEMAWGSSQLYATDVLGSTRTPATVNWPAALFWVVAIGGPWL

IYKCVSQMVQAAEEKRKWATGSAAHYTAQALFDFQASNDQELSFMNGETLRVAPKEEQPRVRGWLLASAA

DGTRIGLVPINYVRIVGKQSQSPPLTQQSNLDTFVNSFPSKDLNSNLQ

>gi|156384232|ref|XP\_001633235.1| predicted protein [Nematostella vectensis]

YGGYGGGYGGYSSYGMMNRGYGQEGTSTFVRRAEESSQAAFQSVESIVQAFGSIAMMLESTHFAMFNSFR

AVIGAADHFSRLKNHLLSAFGAVAIFRTLKYLYQKLLYMLGLIKTSGLDEEVWTDAATSAASAAAEGDAK

RASRSWPIIMFFAVVMGVPWLIWKFLQSVSSEEDSSKDWMTGEGDHVLAKAEFDFNAQGEDELSFAAGTV

LRLAPKGKQPRMRGWLLATVDGVKDGIVPGNYVKVWNTLTSQLTNL

>gi|156390523|ref|XP\_001635320.1| predicted protein [Nematostella vectensis]

MWESIKGFFRRHKRKFVVGGIVITGIYIVSRYARWRLDEWRANQELEYIAQARKQHHFESNQRTCSVTLY

SLIPSLRDSLLDKLNTEEITAKLREKPANKLELWESLKTLSFARTVTAVYSSCMLFVFLRVQLNVIGGYM

YLDSLVTPVEGGSNGKRKHVAEGMQKKYLALVKYLLSEGLDKMTDTIKRSTEDILSDISLKDKLTHAELQ

RLINHIRQTFEFSQQTSSSMRSSQTGSTPLSSTRPFCQFMVPEDMAALDGRGETAVGGVEGEEFMRLVEE

TLDVLESEDCSAVLQGCLDVAFAHILGNIAPFFQAEELGMSFKYLLAVSLPLAKIIPIVNGQIYHMFSDS

DNSYLQDLFKVRFAGEFAANVYEAFSTEVD

>gi|255952869|ref|XP\_002567187.1| peroxisomal matrix protein importer Pex3-Penicillium chrysogenum [Penicillium chrysogenum Wisconsin 54-1255]

MIGATRRWFQRNRKGLAIGAGVIGAGYLAGQYVLSKISEARERMSSDRIARENLRRRFEQNQTDCTYTVL

ALLPTAAENIIDALPVEELTKELQQKRAERLARLNAGEATGSDLSSVPPSLPDDDRRSLSSFQSEGYVHA

SQVGDSSVNSDGQPRPKRNKTQLWNEVKITSVTRSFTMIYTLSLLTIFTHIQLNLLGRRNYLSSVISLAT

PPANASTIRLEDHDDELTQTLGDDFETNRRYLAFSWWLLHRGWKDLMGRVQVAVEEVFGPLNPREDISLA

KLSELTLQIRKKVEGSTEDERRSQKWLSCLLPPAEEEEHVLQESGVEGVADPSSSQTASKLRHLLDETAD

LIDSPSFSLVLTLLNNEGFSTLIDQRCAADAFKAPTSNPEAPLQSFDSVATVVPLAANSERKTKLANLLA

VMTRQAHVIGNGAHPPNEYLVAMDQNVRELEAFSAVVYSSNFDLELLGANNKAVPSRETDLADTEAASSS

FSQVLVEKEVDADLKEEEEEEEIIEPQSHSAVPSAVPEESVFSAPGPEALADSAFEEAWGKATDDGNASS

TEEKQPTQ

>gi|255945623|ref|XP\_002563579.1| peroxisomal docking factor component Pex13-Penicillium chrysogenum [Penicillium chrysogenum Wisconsin 54-1255]

MATPSPPKPWERAGAAGNALSTAPITGSPAASTAMTTTTNPAASTSTAPDLPSRPSALNSVVNNTASSYS

PYGASRLGTGAYGSTYGGMGAMGSPYSRFGTMGGMGSMYGGGYGGYGGGMYGGMGGMGGMGGMGGMYGGM

PGQDPNDPNSLTNSFGQSTQATFHMIESIVGAFGGFAQMLESTYMATHSSFFAMVSVAEQFGNLRNTLGS

ALGIFTLIRWFRTLIAKITGRPPPADATALTPAAFAAFMGGRAAATLPDGSPAPAKPSKKPFFMFLIALF

GLPYLMGKLIKTMARSQEEEAKRRQLVGPNGEPGSASLDPAKLDFCRVLYDYTPETQESNGIDLAVKKGD

IVAVLSKSDPMGNASEWWRCRARDGRVGYLPGPYLETIQRRPNQQAITAGSEPATRTSTMKGDSVAEGRT

QSLSSVGKPELNSKIGDISPESFQKSTFYS

>gi|195495124|ref|XP\_002095134.1| GE22224 [Drosophila yakuba]

MLSRLQDFLSRHRRKFIVTGVLVGGTIFAARYAQRRFVEFQEKQAREFFERTRRTTHFESTEKTCNQVIL

GMGEEMCQAVLRECSTEELLEQLRQNPKNKLELWEDMKIVAFTRLATYVYASSMLVIALRVQLNLLGGYI

YRDIMTEQKQVTDELKQQYLSLIRHFITESGIRDLARYIRTQVIAVTKTMPLSQQLSLGDLEQLFWSLQM

AINADTRRDPNSRMSKYLLPSQNPSHSPLLQKMFNETLDLLESEDAIGVCSHNVSRGFVLACDAIAESMG

ETLQHLPQAEVQTQQEQNLKFNQAGSSGAKNTKSLNGLENNNLLNINRVLLALAKLIPIISGLTSRGFDT

TSRPHNLPTQLLTFYVVAEKTKTLGANVYESFSSA

>gi|195485061|ref|XP\_002090933.1| GE13380 [Drosophila yakuba]

MVDNNNLRSAVISEAPLLPPSSSIGVGVSSGGGSPPEAVLRTPYGNVRALPGPAQPPPLPQSPFQQTQQF

GGFGSGYGGNNYGLGGYGGFNSGAFGYGGLSGFGSGFGSGYGYGGGYGGGYGGGFGGGYNRFGALGDNDP

EQRFIHMAEASSRPAFQSIESLVSAIGNIASMLDSTFFALTSSFRAILGVATNFVRLRSVFAQFWTTFAI

FRGLNWIYRKILFWLRISNLDPSSAAFKKAFAEALNEGNAQAGGAPKVPRKGNSPWAVLAFISFIFTAPY

LIMKLLGTVTNTAQEEARNPAKWTAPIQTQAVYDFVGRSPSELSLRAGQTLHVAPRDIQQTLNLLNTGWA

LATTNGQTSGIIPISYVKSPQQMRQEMQDQIKPAQPQPELMNLSAAAFASPPLEQQMNYDFNLAAQQQAP

LGPPSTTSAVLGEGFA

>gi|255729886|ref|XP\_002549868.1| conserved hypothetical protein [Candida tropicalis MYA-3404]

MAIFSSLSGFFNRNKRRILITSAVSVSVYLLINEFVIKKFRNYQQSLRQELLFKQQIKQRFIQTQQDCYY

TILALLPVLATPIIDALPVELITQALRLKKSGGSKSSTTNENNELTTDNLNLLDNNNDPESKLSIYMNKS

KIELWNLLKIKSITRILTLMYTMSGLLLITRLQLNILARRSYLESAIQMAGVKSINHEIDPHENYIIEQS

YLSLSWWLLNKGWMNLNSIIEALVIAKFEKITPKSELSVESFEQSLLDIINEINTNNKEYILANLFPINY

SDLLETLLNTNPDLVNQLDSADSNLIKLINETNSIMLNNDLYFFDLLNSLILTNLNTLTTNLSFSLSGGN

LGNSLMSTTGNLQESRVTELPNKAFKLASFLAQLSVQTNIMIDNDNIKNEATSPRYDTDLEEILNSLNAG

EDLSSNQPQQESGGNIYINNMNELEELDDFSAGIYSNFE

>gi|255723104|ref|XP\_002546486.1| predicted protein [Candida tropicalis MYA-3404]

MTSQIRTKPWEVSQGKSAASTVPVPESTVPSMSSSTTTAPANSATPSTTSAAAAAATSSSIAPNIPERPT

NLISDFNTASDSPYGGYSANRGGYGYGGGYGSSMLGGGYGSSMYGGYGSSMYGGGYGSSMYGGGYGGYGG

YGSSFGGMYPSIGAGLYQVIDAINMIDQTFFALSNVAEQFRHMGNVVTSLLGIYALKDFLKKILRKILGI

KTKFSLQEFQKFQSLDNKNTNKSRFRIWPILVFVGLPLLISKLISGLQKQHQEQQLAQQTQQQQQLTQSP

ASVQFAKALYEFTPENTQIEIPLEVGEIVAILEDKSGWSRIRKRKGEMGWVPTNYLELIKRNANV

>gi|255714727|ref|XP\_002553645.1| KLTH0E03762p [Lachancea thermotolerans]

MSGRRSIWQRHRSKLYFSSAILATLLTTGAVSLYLIKKWLLRQQLKISEQQFVKEQIKRRFTQTQQDALY

TIYELMPVLSLVLAKDLDVDEIVGELKGKKLSRHLSQRSASVKEDGEQDGLSSGMSTSLTDAQAPRASFA

GQDPTAKTKAELWNELKLKSLTKLCTVIYSTSSLLLLTRLQLNILARREYIETAVKVAVDKESSQSSIAG

WLANWWHAETWAAVQEDEKEPEGPELSEKAQQARRSSYINEQAFLSFSWWLLNRGWLQFKSLAENLVERH

FGDLNPRDMLTVEEFGGRLSSVLHAINQELLVKTDAEQALQMILLPDPNLEQFVLQQTLDSEALKLLYED

NTVLRQLLNETTKCIESTASLIVLESLVNDAYQFAMSLIADNVSKKSKQKIDQDNSEASEPKFQMALFSI

TSKHCCDEMLKSGIVSMNNLFLQRLDSITELDDLSASVYSNFGF

>gi|255711428|ref|XP\_002551997.1| KLTH0B04818p [Lachancea thermotolerans]

MSTSVKQPRPKPWEAQGGQNTPMDDGAMITAGEAQGTRGEGAKADGNAAPEPPQKPAALGPENGVGARSG

LGNAGTFLGSGGPYSSGYGGSLYGGGMGSMYSGGYNSMYGGGYGSMYGGGYGSMMGGGYGAGGMYGMNNN

GAQTLAESTQATFQLIEGLIGAVAGFAQMLEATYMATHNSFFTMVSMAEQISSLKEMVGSFFGIFAAMKM

LKRLLYKVTNGRAGLAPARAAAGSKSPLVQEFAKFGDASAQAKRRRRMSWKPLLVFVAAVVGFPLLLRKF

IAKLSEIQQRRLGAGAVGAGAGGTLDPRNLEFARAVYDFTPENPQVEAALRKGDLMAVISKQDPLGNASE

WWQVRTKKGDVGYVPSNYVELIRRTRSESS

>gi|255577364|ref|XP\_002529562.1| amino acid transporter, putative [Ricinus communis]

MLSLRDFWRRHRRKIIIASGVLGSGYFLYKLYNAHKCRLAELERELASNREHDELINAQVLAHFENIQRI

ADTTTLPHAMHYLSSRIAEELDLSQLTERLMKGKGQPNALTPSEKLELWDRLKILSFTRLVVSLWAMTML

SLYIRTQVNILGRHLYLATARVLGSSDLIEDIDLIERDGQQKFLASSDFFANSGILALSSDVQLAAAEVL

KGKQLRDFFNTATLHETIMQILDLLMSRGSPHHWVEYLMPADARFDKRPIDSSSDDIIMTDGTKFEQLMA

EARAVISSAEFLGVVEKSLEVSVDALVADMGAESSGGSLMAGMPLARLVPRVAQMGPLLLEEPSRNRFLQ

IIWSIPQVEGFFSALYANQWIKR

>gi|242012849|ref|XP\_002427139.1| Peroxisomal biogenesis factor, putative [Pediculus humanus corporis]

MFTRFKNFFSRHRNKFITGGILVGGVVLFSKYAQKVKEWQEKEAKEFLERARKQQHYDSIEKTCNLTAMT

LASTLKEVIIKLIKSEELIQKLQSGVKNRVELWEELKILAFSKLVILLYAQAILTVTLRIQLNLIGGYMF

RYTTDDSEENKITSNMQEKYLGLCQFFIEEGIHKLCDVIKEKVKVVLEKKSLKEKLSLKDIEQIFWAVQT

SISNDDRDPCKSLPDYVLPNDLRRILYVPDLSVFDNIIVETHDILESEEIIHLIKSCISHGFCYVTDKIS

QYYKENDSLKQKTDFANPVPTTSSSLDANYVLNLNAVTIPMAKIIPLVNGFVQNQTKKDDVPHAWIQQLI

LMDSLKVMGANIYETFSSKK

>gi|254581800|ref|XP\_002496885.1| ZYRO0D10362p [Zygosaccharomyces rouxii]

MATPGNGRSIVRRHRGKIVFSLAIFGSLVTAGSVFLWLVKRWLYRQQLRLTEQHFIKEQIRRRFAQTQED

SLYALYELIPVFSLVVGRKLDLEELVIALRDKKLNKMGNRASDDGISSGISTSVTSNGAPGSLQGGGETR

SKAELWNELKTKSIVKLVTVAYTVSSLLLLTRLQLNILTRREYLETAVKMAVEKEGKDEGLSNWFKSIWT

DAHANSSNSSSTTSSSSSGNSKASYINEQAFLSLSWWLLNRGWLEYEAVAQESVESEFGSLSPRDTLSLE

EFGNRLTNVFVNVNERILKSSKLQQALLPSRQMELFVLQQTLDPEALGVVQRDSTILSQLLNETTQCIES

TASAVVLESLINESFQYIMTQVESNTSTKKRSGQGYQIAVFSIACKDCCTSVLKSGVVSMDNELLSRLDT

CPQLEDLSASVYSNFG

>gi|254578174|ref|XP\_002495073.1| ZYRO0B02706p [Zygosaccharomyces rouxii]

MSANSKPRPKPWETHPPLDSQESGLDNSSLAKMNSETGNNDMHNGENSQEPPPRPAELASDPYTSSNPLY

NNGSPYGVSNGIGGGMYGNSMYGGGGGYGSMYGGGLGSMYGGGLGSMHGGGYGGYGSMYGGGYGGYGGGY

MNNGPGGPGGLGESTQATFQLIESLIGTVTGFAQMLESTYMATHSSFFSMVSVAEQFSYLKEVLGSFFGI

FALMKFVRRILFYVTKGRMGTPAPSRAIKNGTNSEMVNEFHNFKKDENSKKIKKISWKPLIFFLAAVFGF

PYALNKFITRVQSMQRGKIGTKQMGAEVDPSKLEFARALYDFTPENPQIEAPLKKGELMAIITKQHPSGN

NSEWWKVRTKTGNMGYVPFNYVEIIKRQKRIEDIPEKDMGSLQKQI

>gi|219130901|ref|XP\_002185591.1| predicted protein [Phaeodactylum tricornutum CCAP 1055/1]

MSSKTKMRRKKQSISLGSVISAAAVAYGTYKVADWAWNRYVTKRKKNDYQVNAAIATSFMNFLCSQTSVG

AHAEDGVASHIDHIPGPNRRLRMRRQRMTRCRQEAAQALRGFSPALRSIVELHTNTAQATRLLKQLRANR

TTEKHATSRRSEEQALWKEIQRKTMTRMLTTAYAHTILFLVLTTQVNLLGGRLFEESLQNTSLSSNVSMS

NDSVASDRMVSYQESHRFVLQHTYDYFLNKGVHSLLSTVEQAVDSVLGGWNVFDKACLHISREQFDCALV

KIRGLIEGGLRTDVSRTSGRSSRRESILRFLMPSSILEHSIQDDLARSILDETWDLVESPVFSDAQQECL

NATFASMRDRFWGKIFDDNGLSGTKPWAHFFR

>gi|241949255|ref|XP\_002417350.1| peroxisomal biogenesis factor 3, putative [Candida dubliniensis CD36]

MAIFSSLAGFFNRNKRKIFITSAVTVSIYLLINEFVIKKFRNYQNALRQELLFKQQIKQRFIQTQQDCYY

TILALLPVLAAPIIDSLPVELITQALRLKKNNSSQQVTSGNNSELTADNLNLLDNNNNPESKLSIYMSKS

KTELWNLLKIKTITRTLTLLYTVSGLFLITRLQLNILARRSYLESAIQMAGVKSTNNDIDPHENYIIEQS

YLSLSWWLLNKGWSNLSSIIEALVIKKFEKITPKTELSINEFEFDLIEIINEINSNNKEYILANLFPINY

SDLLETILNTNSDLIHHLDSPDSNLIKLINETNAIMLDNNLYFFDLLNALIMNTVSTLTTNLSFSLGANG

SLNNSLLMASSGNLPAHGENSKIIDITNNDQSFKLASFLAQLSVQNNIMIDNDNLKTEDISPKHESDLEE

ILNSLNGGTTELPTESYGNVYINNLNQLEELDDFSAGIYSNFE

>gi|241840590|ref|XP\_002415303.1| perixosomal biogenesis factor, putative [Ixodes scapularis]

MFSKLYNFVRQHKKKIFFSVGLTGGAYLLNRYVQRKLHEWESRTTQNYLDQIKHQHHFESILQTSDSTVL

SLLPKIREPLLTILETDSLLEKLKTRPPNRLELWEEMKARILTFAVCSVYAESLLAALLRVQLGVVGGYV

YVNSQRSQQTSGGVLPALTSQEIHQRYLSLIQHFFEGGIEELVHVVKAAVVAAFGHVSLKERVSVNDFVV

AFDYIKGYVSRGSKPLPGFMRFLLPPLNVESDSQEATVLNTMILETRDILETDDFSKVLATCIDIGFGNL

RGEVEESFHIMQMAEGSGDQVATSFALAKLLPVLKNGLVAGRADSFLKQILQVELLRSMLANVYEAFCQT

EDVDRLNHNLAPFT

>gi|168033870|ref|XP\_001769437.1| predicted protein [Physcomitrella patens subsp. patens]

MTTPLHITCYYDFKAWVKKHQRSLLVAAGLVGGGSAVYYGLHYLGLTSQARKERDAARAALLHREAEERA

EAQLQSHFESIQRISDTTTLPSVLPQLKASLFSKVDLSGLTEKLILGKDDPQALSQRDKMQLWQELKTLS

FTRTVCAMSALSLLDLFIRIQLNILGRRVYFDTARDFMNPEDLHAPLSMSVQHKFIAFAGYLHHKGLAAL

VGDIYKAAEIELRGKQLKESFTLYDLKNVFVRILATLDSKRPAWVQYVLPPDNVLPEDLAGASSAADASN

QFADVATSDNEVLDQLMNETRAVLASNEFHEVQAVCLEVMLDGVMEELYTIYRGSSDSGIPLAKLLPPVA

GAGSTLLEHPDENRFIRILASLPQVHAFCALVYTNSSEEAAA

>gi|168004808|ref|XP\_001755103.1| predicted protein [Physcomitrella patens subsp. patens]

MTTPLHLTCYYDLKAWAKKHRRSLLVAAGLVGGGAAVYYGFRYLGLASQARKERDVARAALLQREAEERA

EAQLQSHFESIQRISDTTTLPSMLPQLKDRLFSKVDLSGLTEKLILGKEDPQSLSQREKMQLWQELKTLS

FVRTVCAMSALSLLDLFIRIQLNILGRHVYFDTARDFMNPEDSHVPLSMSVQHKFIAYAGYLHHKGLDAL

VGDVNQAAEIVLRSKPLKEPYTLDDLRDVFMRIRATLDSKRSAWVQYVLPPDNVLPDDLSVASSADASNP

VAEMALNDNEVLDQLMNETRAVLVSNEFHEVMAVCVDSMLDGVMEELYAIYRGSSDNGIPLAKLLPPVAG

AGSALLESLDDNRFIRILADLPQVHAFCALVYTNSSEETLA

>gi|168001339|ref|XP\_001753372.1| predicted protein [Physcomitrella patens subsp. patens]

MTTPLHITCHYDLKAWVKKYRRSLLIAAGLVGGGTAIYYGVQYLGLDSQSRKERDAARVALVQKEAEERA

EVQLQSHFEGIQRISDSTTLPSVLPHLKASLYSKVDLEGLTDKLMLCKVDPQLLSHRDKMQLWQELKTRS

FARTVCAMTAVSLLDLFIRIQLNILGRRVYFDTARNMMNSEDSHVPLSMSVQHKFIAFAGYLHHKGLATL

VADTYKVVEIVLRGKQLKEPYTIDELRDVFMKIRASLDSRRSPWVQYVLPPENVLPDEFVATSSAADAAA

SVSDMTHEDDVLAQLMNETRAVVSSDEFNEVLAVCLDAILDGVMEELYTIYRGSPDNSIPLARMLPPVAG

AGSTLLEHPDENRFISILANLPQVHAFCALVYTNSSEEVVASASTVEVV

>gi|195334014|ref|XP\_002033681.1| GM20296 [Drosophila sechellia]

MVDNNNLRSAVISEAPLLPPSSSIGVGVSSAGGSPPEAVLRTPYGNVRALPGPAQPPPLPQSPFQQTQQF

GGFGSGYGGNNYGLGGYGGFNSGAFGYGGLGGFGSGLGSGFGSGYGYGGGYGGGYGGGFGGGYNRFGSLG

ENDAEQRFIHMAESSSRPAFQSIESLVSAIGNIASMLDSTFFALTSSFRAILGVATNFVRLRSVFAQFWT

TFAIFRGLNWVYRKILYWLRLSNLDPSSAAFKKAFAEALNENNGQARGAPNVPRKGNSPWPVLAFISFIF

TAPYLIMKLLGTVTNTAQEEARNPAKWTAPIQTQAVYDFVGRSPSELSLRAGQTLHVAPRDIQQTLNLLN

TGWALATTNGQTSGIIPISYVKSPQQMRQEMQDQTKPAQPQPQLMNLSAGAFASPPLEQQMNYDFNLAAQ

QQVPLGPPSTTSAVLGEGFA

>gi|195327723|ref|XP\_002030567.1| GM25512 [Drosophila sechellia]

MLSRLQDFLSRHRRKFIVTGVLVGGTIFAARYAQRRFVEFQEKQAREFFERTRRTTHFESTEKTCNQVIL

GMGEEMCQAVLRECSTDELLEQLRQNPKNKLELWEDMKIVAFTRLATYVYASSMLVIALRVQLNLLGGYI

YRDIMTEQKQVTDELKQQYLSLIRHFITESGIRDLARYIRTQVIAVTKTMPLSQQLSLSDLEQLFWSLQM

AINADTRRDPNSRMSKYLLPSQNPSHSPLLQKMFNETLDLLESEDAVGVCSHNVSRGFVLACDAIAESMG

ETLQHLPHAQVQTQQEQNVKFNQAGSSAAGTSKSQSGLENNNLLNINRVLLALAKLIPIISGLTSRGFDT

TSRPHNLPTQLLTFYVVAEKTKTLGANVYESFSSA

>gi|195123095|ref|XP\_002006045.1| GI18763 [Drosophila mojavensis]

MGDNNNLRSAVINETPMLTTPYGNVRALSVPPPLPQSPLQQTSYGYGGGYGNMGGYGMGLGGYSAGGYGT

GGYGYGSMGYGMGGFGGYGGNYGGYNRFGGMNSNDPEQRFIQMAENSSRPAFESIESLVSAIGNIASMLD

STFFALTSSFRAILGVAANFGRLRTVFAQFWTTFAIFRGLKWIYRKILYWLRISNLDPSSEAFKKAFAEA

LNDNSNQPGNAPRLPRKGTSPWPVLAFLSFIFTAPYLIMKLLGTVTNTAQEEARNPAKWTAPIQTQAIYN

FQARNEGELSLRAGQNVQVAPREIQQTLHLLNTGWALASTNGQNSGLIPISYVKSPQQLRLERQEPVKPL

PPQPELMNLSASAFPNPPVDQQMNYEFNLAAQQQQPLGPPSTTVTAFDEGFA

>gi|157105986|ref|XP\_001649113.1| hypothetical protein AaeL\_AAEL004417 [Aedes aegypti]

MTMQPTNFRNPVLSEPRVFGGQYSLNTPAGVVTTSSQPPPLPPRPLQQQSGVGFGGTYGGGFGSRFGMPS

YGYSGFGGGYGSYGGGFGYGGGYGGGMYGGSGYGMGANVYPEHRFIQLAEESSRPAFQNIESLVGAIGNI

AAMLDSTFFALTSSFRAVLGVAANFAHLRGVFAQFWTSFALFRWIIWAYRKILYWFRITRTDPSTASFKE

AFKAAEADKLAPAQKKGSSMPVVLFLGFIMSAPYLLMKLFGGNSETQVAAKNPRNWNGALEAVAIYNFDA

SSANELTIRAGQPVLIAPKSVQVEQNLLNTGWVLASVDNTVSGLIPVNYVQGSKQQPQQQVTNDVKLHSN

ETGQSETEA

>gi|195126503|ref|XP\_002007710.1| GI13098 [Drosophila mojavensis]

MLSRLQDFLSRHRRKFIVTGALVGGTIYAARYAQRKLVEYQEKQAREFFERTRRMHHFESTERTCNQVIL

GMGEEMCQAVLHECSTDELLEQLRQNPPNKLELWEQMKIVAFTRLATFVYASSMLVIALRVQLNLLGGYI

YRDIMTEQRQITDELKQQYLSLIRHFITHDGIRDLARFIRSQVVEVLKSMPLSRQLTLADTEQLFWSLQM

AINGDTRHDPNSKMSKYLLPDLTRLQERFNCSPLLQQMYNETLDLLESEDCIGVCAHNVSRGFVLSCDAI

AESMGETLQHLAPGELQQQESLNGQSKQSNNNNLFDVNKVLLALAKLIPIISGLTSHGYDSAARPHNLPT

QLLSFYVVSEKSKMVGANVYESFSSG

>gi|157130508|ref|XP\_001661904.1| perixosomal biogenesis factor [Aedes aegypti]

MLAAIKDFFYRHRRKFITTGVVLGSGLFLIKIIQYKLREFQERQAKEIAEKFKRMQHFESTERTCNQTIV

GLSPTVSEKALKDLSTSEVLEKLRSNPDNKLDLWDELKILAFSRIVTLVYASSMLAVTLKTQINLLGGYL

YKDTMGQDDKQITVDIQTTYLSMIQYFMGEGLDRLMAVVRKNVTVVMQRYNLKQQLTLADAETLFWSIQM

ALNNDEQSLTKNIAKYTLPQEVNRSDILSQMYDETLDVLENAEVADVCLSNVTNGFSLIVDKLAEYYAEA

EPTPPSTSKSSLNVDALSNINTIKISLAKLIPIVNGLTSKTLGGLIGSASNGSNGLNGLELRNSDMMSSL

VSRFMQSEKLKTLGVNVYETFCQ

>gi|221129345|ref|XP\_002161645.1| PREDICTED: similar to peroxisome biogenesis factor 13, partial [Hydra magnipapillata]

VGYRLLDDPQSFPPQIPPRHNNYSSTIGMQSPYALGYNSGMYNGYGGMYNPMTAYSYRGNIAGDGSVLNG

VENVTRNAFQSVESVVQAFSSVSMMLESTLFAAQNSIRAIASVADQISGLREHLFNSAYSFIRTINTLLR

KLLVTVRLQKGLTPEEIWDQNAAISSSETIGTKHWPLLIFFGIMLGGPWLLWKFLQNLSSCDNVDDWQKG

VGEHFLAEAKYNFQAGNRDELSFRKGDIIRIAPKACQPHVRGWLLASIDKKKGLIPANYVQIKGKLPSQP

KTFTECDAIKTTK

>gi|213410146|ref|XP\_002175843.1| predicted protein [Schizosaccharomyces japonicus yFS275]

MLSIVKEKTLSALSFVGNTSLFATIPTLSLKNFAESFRLAWTGYSVQQQFQAQNLRFFEQMLSDADASTA

VMLETQCQQLLEGFSTEDAIQRLRQNKLQKGSAEDKIELWNELKVTCLARVLCQFGILVRTFLINTIAFS

ILARKKQQLTLLEMESQKPLAPFGVDESTSNSSFHDENEKLFIGYLLTVLDETFPGDMQHAIECVKTSFE

STHPTDIVTKQHIASLLQTAFQNWIEATRLSFHELRKLFFADVQADVVLTGSLVACMDEFEDVWELAELE

VCMSHCFNQLIPIFLEQLSIPKEGQRLAKTLAATTKVFRDFDETSVKEFVQRLACMSERAKLAAVLYTNY

DDDEDSVL

>gi|212541088|ref|XP\_002150699.1| peroxisomal membrane protein (Pex13), putative [Penicillium marneffei ATCC 18224]

MASVSPPKPWERAAAGAGTALPTSAPSTSTMTSTPTAAPAAATITGSSPSTSTNSTTPSLPSRPDTLNAV

VNRTASTYSPYGANRFGASPYSTYGGYGAYSSPYSRFGSMYGGMGGYGGMYGGMGGMYPGMPGDPNDPNS

LTNSFSQSTAATFQMIESIVGAFGGFAQMLESTYMATHSSFFAMVSVAEQFGNLRNTLGSVLGIFTLIRW

FRTLMAKLTGRPLPADATALTPSAFSAFLNGRSAPATLPDGGPAPARPSRKPFFMFILAVFGLPYLMGKL

IRSLARSQEEEARRQQAVMGANGELQNAPLDPSKLDFCRVLYDYTPDAQNTAGIDLAVKKGDIVAVISKS

DPMGNPSEWWRCRARDGGVGYLPSPYLETIQRRPAQAAITAGPAASAPGSRTSTMTKGDSGLAQDTKPVL

SGKMGDIAAESFQKSAFNSS

>gi|50550491|ref|XP\_502718.1| YALI0D11858p [Yarrowia lipolytica]

MFRRLTGSQSESSIYGLVNDSQTSMGTMDYANELASQLDMLLKKDKPLSTDDSASVASSSAASRTSWLGP

SIPRHSRHFVDALYDKVILPKLKKSIIGDVDSDLGSAVATPTGSGSRRGSFSTIRALDISEEPFSESDIS

VFDDSVSVASTASSEPFRISQHNPPKPVFDPEAHEAGPELSIPLLLRNIAELSKRAGGVMKTQTVVLKAI

QWQNPCLSISCIFIYTAMCLYPGIVFVLPGLLFMYGIMAPAYAEKHPLPKEYRPSPWTVKNEFDMAADDD

TSIRAAQIKRIKAAEKKPVDVKKSMKNFQNATTNLIKALDKLESFLSGPAGFANESLSALIFLLIGFAMI

GTFFLSAFIPWKALQIGAGWGVIIAGHPTLLKRIVAILDELEKSDDEEKPKESPVIAILQKVQKKEFIND

EPPQGETVEIFELQRQGLTPRQWDSWVFTSLVYDLGSSWRQAKKRPPGAPFLGDVEAPEGWLFSKMHDWE

VDMNPNEWVGERGLGRCTEMDNDEWVYDVEKGVRGEWRRRRFIRTAFKESTVPKELLGLV

>gi|50547911|ref|XP\_501425.1| YALI0C04092p [Yarrowia lipolytica]

MSVCLAQNPTVTRVVKLLETHVGRDKILRSIQYFSRFLTYYLFRKGYTKDTIDIFRKIQNQFSMARKLFR

VGKPIGHLKTAAVSFENKTLDPCLRYTTIGRNLGYAIYLVFDSIIYINGSGIKKIDNIKTIKKVGSYFWA

FGIFCNILNSIHKINICKKKRAALAAEKEKDTTSAKKNDKDAAAAQKQLVWDLLDFSIPLTSLGYLHLDD

GLVGLAGFATGIMGVQKAWAATA

>gi|50556692|ref|XP\_505754.1| YALI0F22539p [Yarrowia lipolytica]

MDFFRRHQKKVLALVGVALSSYLFIDYVKKKFFEIQGRLSSERTAKQNLRRRFEQNQQDADFTIMALLSS

LTTPVMERYPVDQIKAELQSKRRPTDRVLALESSTSSSATAQTVPTMTSGATEEGEKSKTQLWQDLKRTT

ISRAFSLVYADALLIFFTRLQLNILGRRNYVNSVVALAQQGREGNAEGRVAPSFGDLADMGYFGDLSGSS

SFGETIVDPDLDEQYLTFSWWLLNEGWVSLSERVEEAVRRVWDPVSPKAELGFDELSELIGRTQMLIDRP

LNPSSPLNFLSQLLPPREQEEYVLAQNPSDTAAPIVGPTLRRLLDETADFIESPNAAEVIERLVHSGLSV

FMDKLAVTFGATPADSGSPYPVVLPTAKVKLPSILANMARQAGGMAQGSPGVENEYIDVMNQVQELTSFS

AVVYSSFDWAL

>gi|50547267|ref|XP\_501103.1| YALI0B19624p [Yarrowia lipolytica]

MLQSLNRNKKRLAVSTGLIAVAYVVISYTTKRLIEKQEQKLEEERAKERLKQLFAQTQNEAAFHTASVLP

QLCEQIMEFVAVEKIAEQLQNMRAEKRKKQNMDDDKHSVLSLGTETTASMADGQKMSKIQLWDELKIESL

TRIVTLIYCVSLLNYLIRLQTNIVGRKRYQNEAGPAGATYDMSLEQCYTWLLTRGWKSVVDNVRRSVQQV

FTGVNPRQNLSLDEFATLLKRVQTLVNSPPYSTTPNTFLTSLLPPRELEQLRLEKEKQSLSPNYTYGSPL

KDLVFESAQHIQSPQGMSSFRAIIDQSFKVFLEKVNESQYVNPPSTGGKRIAVGALQPPIISGGPKKVKL

ASLLSVATRQSSVISHAQPNPYVDAINSVAEYNGLCAVIYSSFEQ

>gi|195441346|ref|XP\_002068473.1| GK20400 [Drosophila willistoni]

MLSRLQDFLSRHRRKFVVTGLLVGGSIFAARYAQRKLVEYQERQAREFFERTRRMHHFESTERTCNQVIL

GMGEEMCQAVLKECSTVELLEQLRQNPKNKVELWEKVKIISFTRLATFVYASSMLVIALRVQLNVLGGYI

YRDIMSGEVQITDELKQQYLSLIRHFIAEDGLRELVRYIRSQVLVVIKSMPLTRQLTLNDLEQIFWSLQM

AINADTRRDPNSRMSKYLLPTTHSNFSPLLQQMYNETLDLLESEDAMAVCSHNVSRGFVLACDAIAESMG

ETLQHLAPGEVKQQPSSAQTEQTLKFNQSSSSKSNSIANTNPNQQGSPAAENNNLLNINTVLMALAKLIP

IISGLTSKGYDSKARPHNLPTQLLSFYVVAEKCKTLGANVYETFSSA

>gi|198433404|ref|XP\_002123483.1| PREDICTED: similar to PEX13 [Ciona intestinalis]

MAANGAPPKPWEINRGQSPSNNLRSSSLTRPESGEFPTPPPIPARPNQQSTSATMYRPTYGNLGSYGGGY

NFGGYGGYGSGMYGSSGLYGTGGGMYGSSYRNYGTPPNGVGSFTQQAEDSTRQAFQSVESIVRAFTSVSA

MLESTFGAVYSSFRAVLDVADHFSRVRSTFSEILSSIAIFRLFRYLYRRVLAIFGSRECEDAWSNAAVDG

ALMRPNSSSQKKSWPIMLFAAVVMGGPYLIWRLMRGANSQKPANISWMNGDGDHVVAKAEFDFSSESEEE

ISFLAGDTIILAPRAQQPHIRGWLLGTIDGKNPGYLPANYVKILGLRRGRAKPTTPPTPAANISTTTTTT

PPAGLSTEGTVSNEEWQNIHSGSERLGPPEEPPTQQS

>gi|198425778|ref|XP\_002120778.1| PREDICTED: similar to peroxisomal biogenesis factor 3 [Ciona intestinalis]

MPFLFHQKICSFLKRHKNKFIFTGVFLGGVIGSLKYAEYKLNSFVAEDQKKIMERKKQEKAFDQVQLHAC

SLVEVMLDSVLKKVLMLNDTEVILRRLKDKEYGKKLELWNQLKVGVFSRLVAGIYCLNLVTITVQVQLHQ

LAARGDVQTYNENMAVQVFLSLCHKHMLSEGIAQVSELCHKITSDIIGSMPLQHHVGGENIETALRSVFS

CLMREMKIKSRNTELEGAFHPALPSYNTDDEFSQNEKLPQNWLELTFDILESSDCSDVFFECFRESVTFI

AEAFTANVENMAISSKSSYIKDEDILPLSIPLAKALPLLNTKLKSVYSADFLQRLMINPIMGKFAFNVYK

SCFDLPS

>gi|195582999|ref|XP\_002081313.1| GD25777 [Drosophila simulans]

MVDNNNLRSAVISEAPLLPPSSSIGVGVSSAGGSPPEAVLRTPYGNVRALPGPAQPPPLPQSPFQQTQQF

GGFGSGYGGNNYGLGGYGGFNSGAFGYGGLGGFASGLGSGFGSGYGYGGGYGGGYGGGFGGGYNRFGSMG

ENDAEQRFIHMAESSSRPAFQSIESLVSAIGNIASMLDSTFFALTSSFRAILGVATNFVRLRSVFAQFWT

TFAIFRGLNWMYRKILYWLRLSNLDPSSAAFKKAFAEALNENNGQARGAPNVPRKGNSPWPVLAFISFIF

TAPYLIMKLLGTVTNTAQEEARNPAKWTAPIQTQAVYDFVGRSPSELSLRAGQTLHVAPRDIQQTLNLLN

TGWALATTNGQTSGIIPISYVKSPQQMRQEMQDQTKPAQPQPQLMNLSAGAFASPPLEQQMNYDFNLAAQ

QQAPLGPPSTTSAVLGEGFA

>gi|195590401|ref|XP\_002084934.1| GD14527 [Drosophila simulans]

MLSRLQDFLSRHRRKFIVTGVLVGGTIFAARYAQRRFVEFQEKQAREFFERTRRTTHFESTEKTCNQVIL

GMGEEMCQAVLRECSTDELLEQLRQNPKNKLELWEDMKIVAFTRLATYVYASSMLVIALRVQLNLLGGYI

YRDIMTEQKQITDELKQQYLSLIRHFITESGIRDLARYIRTQVIAVTKTMPLSQQLSLSDLEQLFWSLQM

AINADTRRDPNSRMSKYLLPSQNPSHSPLLQKMFNETLDLLESEDAVGVCSHNVSRGFVLACDAIAESMG

ETLQHLPQAQVQTQQEQNVKFNQAGSSGAGTSKSQNGLENNNLLNINRVLLALAKLIPIISGLTSRGFDT

TSRPHNLPTQLLTFYVVAEKTKTLGANVYESFSSA

>gi|195431158|ref|XP\_002063615.1| GK21322 [Drosophila willistoni]

MADNNNLRTAVINDAPLLPPSSSAPGGGFSSGPPPDAVLRTPYAGNVRALPPPLPQSPYQQTQSLYGGYG

GGYNSGGFGLGGGGYGGYQTGGFGYGLGLGMGGFGSGYGGGYGGGYNRFGMGMGANDPEQRFIQMAEASS

RPAFQSIESLVSAIGNIASMLDSTFFALTSSFRAILGVAANFGRLRTVFAQFWTTFAIFRGLNWVYRKIL

YWLRISNLDPSSVAFKKAFAEALNDNQGQTGGAGGPKLPRKGTSPWPVLAFISFIFTAPYLIMKLLGTVT

NTAQEEARDPAKWTAPIQTQAMFDFQARNQNELSLRVGQSIQVAPREIQQTLNLLNTGWALATINGQTSG

IIPINYVKSPQQIRQEQQALKVPSPPSDQPQPSLMNLSADAFPGPPLEQQLNYDFNLAAQQQQPLGPPST

MATVLEEGFP

>gi|195382161|ref|XP\_002049799.1| GJ21787 [Drosophila virilis]

MGDNNNLRSAVINESPMLATPYGNVRSLAAPPPIPQSPLQQSSYGYGGGYGNVGGYGLGLGGYNTGGYNA

GGFGYGGFGMGGMGSYGGGYGAYNRFGGLNANDPEQRFIQMAEASSRPAFQSIESLVSAIGNIASMLDST

FFALTSSFRAILGVAANFGRLRSVFAQFWTSFAIFRGLKWIYRKIIFWLRLSDLDPSSTAFKKAFAEALN

DKNVQNGSAPNIPRKGTSPWPVLAFISFIFTAPYLIMKLLGTVTNTAQEEARNPSKWTAPIQTQAVYDFQ

ARNESELTLRAGQSVQVAPREIQQTLQLLNTGWALATTNGQSSGLIPINYVKSPQQMRQERQEPVKPLQP

QPELMNLSANAFPTLPIDQQMNYEFNLAAQQQQPLGPPSTTGAAFDEGFA

>gi|195378898|ref|XP\_002048218.1| GJ13845 [Drosophila virilis]

MLSRLQDFLTRHRRKFVVTGVLVGGTIYAARYAQRKLVEYQERQAREFFERSRRMHHFESTERTCNQVIL

GMGEEMCQAVLHECSTDELLEQLRQNPTNKLELWEQMKIVSFTRLATFVYASSMLVIALRVQLNLLGGYI

YRDIMTEQRQITDELKQQYLSLIRHFITHDGIRDLARFIRSQVVEVLKSMPLTRQLTLADTEQIFWSLQM

AINGDTRHDPNSKMSKYLLPDLTRLQERFNCSPLLQQMYNETLDLLESEDCVGVCAHNVSRGFVLSCDAI

AESMGDTLQHLAPGELQQQQPMNGQSKQSNNNNLLDVNRVLVALAKLIPIISGLTSHGYDSSARPHNLPT

QLLSFYVVSEKSKMLGANVYETFSSG

>gi|195150939|ref|XP\_002016407.1| GL10505 [Drosophila persimilis]

MADNNNLRSAVINEAPLVPPTSIVGPGFSSGPPPDAVLRTPFAGNVRALPNLAPPLPLSPFQQTQYGYGG

AYGNNSYAGGYGGYNTGGGFGGGYGGMGQFGSGWGAPYRSYGGDFGGGYNRFGGMGGIDPEQRFIQMAEA

SSRPAFQSIESLVSAIGNIASMLDSTFFALTSSFRAILGVAANFGRLRSVFAQFWTTFAIFRGLKWIYRK

ILFWLRLSNLDPSSEAFKKAFAEALNENHSQVGGGPQPPRKRNSPWPVLAFISFIFTAPYLIMKLLGSVT

NTAQEEARNPSKWVAPIHTQAVYDFAGRNQSELSLSAGQSLQVAPREIQQTLNLLNTGWALATTNGQTSG

IIPISYVKSPQQLRQDHQEQVKPTQPRPELMNLSTDAFPAPPLDQQMNYDFNLAAQQQAPLGPPSTATAA

FEEGFA

>gi|195162758|ref|XP\_002022221.1| GL24760 [Drosophila persimilis]

MLSRLQDFLSRHRRKFIVTGVLVGGAYCAARYAQRKLVEIHEKQAREMFERTRRTHHFESTEKTCNQVIL

GLGEEMCDAVLRECSTDELLEQLRQNPKNKVELWEEMKVVAFTRLATFVYASSMLVIALRVQLNLLGGYI

YRDITTEQTRITDELKQQYLSLIRHFITEDGIRDLVRYIRTQVIAVVKSSMPLSRQLSLNDLEQLFWSLQ

MAINADTRRDPNSKMTKYLLPSQSSSFSPLLQQMYNETLDLLESEDAISVCTHNVTRGFVLACDVIAESL

GETLHHLPTAEVQKQAETQQSQQFNQSSSSTSLPSSQAVDNNNLLNINTVLMAMAKLIPIISGITSGGYD

SSARSTNLPTQLLSFYLVAEKSKTLGANVYETFSSA

>gi|194883404|ref|XP\_001975791.1| GG22510 [Drosophila erecta]

MVDNNNLRSAVISEAPLLPPSSSIGAGVSSGGGSPPEAVLRTPYGNVRALPGPAQPPPLPQSPFQQTQQF

GGFGSGYGGNNYGLGGYGGFNSGAFGYGGLAGLGSGFGSGYGYGGGYGGGYGGGYGGGFGGGYNRFGALG

DNDPEQRFIHIAEASSRPAFQSIESLVSAIGNIASMLDSTFFALTSSFRAILGVATNFVRLRSVFAQFWT

TFAIFRGLNWIYRKILYWLRISNLDPSSAAFKKAFAEALNENNAQTRGAPNVPRKGNSPWPVLAFISFIF

TAPYLIMKLLGTVTNTAQEEARNPAKWTAPIQTQAVYDFVGRSPSELSLRAGQTLHVAPRDIQQTLNLLN

TGWALATTNGQTSGIIPISYVKSPQQMRQEMQDQMKPAQPQPELMNLSAAAFASPPLEQQMNYDFNLAAQ

QQAPLGPPSTTSAVLGEGFA

>gi|195025580|ref|XP\_001986084.1| GH21168 [Drosophila grimshawi]

MDNNLRSAIINESPMLATPYGNVRSLAAPPPVPQSPFQQQQSAYSGYGGGYGNVGSYGLGIGGYNGGGYG

GGYGGGYGGFGMGGLGGYGGRGYGGYSRFGSMNPNDPEQRFIQMAEASSRPAFQSIESLVSAIGNIASML

DSTFFALTSSFRAILGVAANFGRLRSVFGQFWASFAIFRGLRWIYRKILYWLRISHLDPSSKAFKKAFAK

ALNDNNMQESGAPHPPRKGTSAWPVLAFISFIFTAPYLIMKLLGTVTNTAQEEARNPAKWIAPIRTQAVY

DFQARNQGELTLRSGQTVQVAPREIQQTLQLLNSGWAIASINGQSSGLIPLNYVKSPQQLRQEQQEPVKP

PLQPQPELMNLSANAFPNPPFDQQMNYDFNLACQQQQPLGPPSTMAVTGLEDGFA

>gi|195021414|ref|XP\_001985390.1| GH14525 [Drosophila grimshawi]

MLSRVQDFLSRHRRKLIVTGVLVGGTIYAARYAQRKLVEYQERQAREFFERTRRVHHFESTERTCNQVIL

GMGEEMCQAVLAECSTDELLEQLRQNPANKLELWEQMKIVSFTRLATFVYASSMLVVALRVQLNLLGGYI

YRDIMTEQRQITDELKQQYLSLIRHFITFDGIRDLARFIRTQVVEVLKTMPLTRQLTLADTGQIFWSLQM

AINGDTRHDPNAHMSKYLLPDQIRLQQRSDCSPLLQQMYNETLDLLESEECIGVCAHNVSRGFVLSCDAI

AESMGQTLQHLAPGELQNQQPLGSSSSKPSNNNNLLNINTVLLALAKLIPIVSGLTSHGYDATARPQNLP

TQLLSFYVVSEKTKLLGANVYETFSSG

>gi|194872664|ref|XP\_001973058.1| GG15881 [Drosophila erecta]

MLSRLQDFLSRHRRKFIVTGVLVGGTIFAARYAQRRFVEFQEKQAREFFERTRRTTHFESTEKTCNQVIL

GMGEEMCQAVLRECSTDELLEQLRQNPKNKLELWEDMKIVAFTRLATYVYASSMLVIALRVQLNLLGGYI

YRDIMTEQKQITDELKQQYLSLIRHFITESGIRDLARYIRTQVIAVTKTLPLSQQLSLSDLEQLFWSLQM

AINADTRRDPNSRMSKYLLPNQNPSHSPLLQKMFNETLDLLESEDAIGVCSHNVSRGFVLACDAIAESMG

ETLQHLPPAEVQTQQEQNLKFNQAGSSGVSSSKSQNGLENNNLLNINRVLMALAKLIPIISGLTSRGFDT

TSRPHNLPTQLLTFYVIAEKTKTLGANVYESFSSA

>gi|194751553|ref|XP\_001958090.1| GF23687 [Drosophila ananassae]

MLSRLQDFLSRHRRKFIVTGVLVGGTIYAARYAQRRFVEFQERQAREFFERSRRMHHFESTEKTCNQVIL

GMGEEMCQAVLKECSTDELLEQLRQNPKNKLELWEDMKIVSFTRLATFVYASSMLVIALRVQLNLLGGYI

YRDIMTEQKQITDELKQQYLSLIRHFITESGIRDLARYIRTQVIAVVKSMPLTRQLSLNDMEQLFWSLQM

SINADPRRDPNSRMSKYLMPSQNPNHSPLLQQMFNETLDLLESEDAIGVCSHNVSRGFVLACDAIAESMG

ETLQHLSPAELKKQQENQQPLKFNQASGSSTPNMTSPTPENNNLLNINTVLMALAKVIPIISGITSRGYD

SAARPQNLPTQLLTFYVVAEKTKTLGANVYETFSSA

>gi|194754677|ref|XP\_001959621.1| GF12959 [Drosophila ananassae]

MVDNNNLRSAVISETPLLPPTTSAGAGLSGGTPPPEAVLRTPYGNVRALPGPAQPPPLPQSPFQQSQFGY

GGGYGGNSYGLGGFGGYNSGSFGYGGMGGFGSGYGFGGGYGGGFGGGYSRFGALGPNDPEQRFIQMAEAS

SRPAFQSIESLVSAIGNIASMLDSTFFALTSSFRAILGVAANFGRLRSVFAQFWTTFAIFRGLNWIYRKI

LYWLRISNLDPSSAAFKKAFAEALNENNSQSGGAPNVPRKGTSPWPVLAFLSFIFTAPYLIMKLLGTVTN

TAQEEARNPAKWVAPIQTQAIYDFLPRGQSELSLRAGQTLQVAPREIQQTLNLLNSGWALATTNGQTSGI

IPINYVKSPQQMRQELQGQAKVNQPQPGLMDLSSGAFPAPPMDSQMNYDFNLAAQQQEPLGPPSTTDAVL

EEGFA

>gi|91086101|ref|XP\_975792.1| PREDICTED: similar to CG4663 CG4663-PA isoform 2 [Tribolium castaneum]

MTSPLKPWESNSLQNASQIRSSHNLRDVPMAGRSAPVLPPLPRTSPMVASSAYSSYMPYSSGYSSLGYGM

PYRSSLYNSYGSYGGYNSYNMYGMGGYPSFGVNDDAERRFIQYAEESSRNTFASVESIVRAVNSISMMLD

NTFFAMTSSFRAVLSVADNFGRLRSMFGHIWYSINIFRLFNWLYRKFMWLIGRKVPNSATSLAWRQASGA

PPTGPAPGSSWPTLAFLGVLVSAPYIISKFLPKYEDKCDPANWKSPGVRAKAAFDFVARSQNEMSVQTND

ELTLAPTYVQEEMNLRNTGWAFAVANGRSGVVPLNYLVISKAGPREGTEEVPVPRVFNKTHTKRVSFGEN

QVFENVDLDDYVTGKKEIKGVDDIKNSVKEGVDDNKYSLKEVSDSKKDEQQNKGENEITNQVETKKVESN

>gi|91079218|ref|XP\_970039.1| PREDICTED: similar to peroxisomal biogenesis factor 3 [Tribolium castaneum]

MSVFSKVRNFFSRHRNKFIVGGVIIGGSIFLTRYAQQKLREWQEKEALEFLDRNRKHQHFESIGRTCNQT

ILNLALALNETISKNINTEEVIERLKTNPENKLALWNELKVLVFNKAACTIYANVMLVVTLKIQLSIIGG

YLYKDPTSLSSEMQERYLSLCQNLMDAGFSRLSRLVETNCRKVLEPVNLTKQLKLSDLEALFWSIQTAVA

THNDNPVENLRQYVLPELPVSDGIYEKMVKETAELLNSDEVKALVTHCTTRGFMVLAEQLSEFYTSNGVK

ENGKLPEGDEFTNPFNVKKPMAKVLPIMNGLFSKKSLPDQFLQQLIVYEKLQLLSANVYESFLS

>gi|189203705|ref|XP\_001938188.1| peroxisomal membrane protein PEX13 [Pyrenophora tritici-repentis Pt-1C-BFP]

MSSNAPPLPSVPDSLSTVANRNATNYSSMNNRYGSPYSTGYGGMNSYSSPYSSMGGGYGSMYGGMGGMGG

MYGGMGGMGMGMGGMYGGMGGMPGDPNSSLTQSFSQSTAATFQLIENIVGAFGGFAQMLQSTYMATHSSF

FAMVSVAEQFGNLRQTLGSVLGIYTVMRWIRTAIAKLTGRPLPADATALTPASFAAFNGRMPDGSPAPAK

PSKKPFIVFMLAVFGLPYLMGKLIKALARSQEAEEQRKMLENPQAGQPLDPNKLEFCRALYDFTPNANMQ

GMDLSVKKGDMVAVLSKSDPMGNASEWWKCRSRDGRMGYLPGIYLETIQRKTPAQITNGSPSGSLAGSRT

QTMTSSSAPNRTATMVESKVSDKVGPKVESKAGDMGVESFQKGAFYS

>gi|170587617|ref|XP\_001898572.1| Variant SH3 domain containing protein [Brugia malayi]

MLNATHHAVFNSFQAVFGALDEFGRLKTQIHCLLASTALLKWLRYIWQLLLKCLRLKVSGDAGMEEAWMG

VRKDSDALTTQEITSQLVPSNPFRWLPSLMFWLMAIGVPYLMYQSLGGMVDESMKWTTGNDGYYEALATE

DHYAEENDNISFKRGDILRVAPREYQPRKLGYILACSTGGKKVGLVPIKKIRLTRRVAESSAFTGQDAVQ

LFDDAHAFENNLYD

>gi|170108985|ref|XP\_001885700.1| predicted protein [Laccaria bicolor S238N-H82]

MATLDYVDVPAAATRLRAASISGFETNEIRPAPKITTSLPMPSPPPSPSVLRRRASSMSLDSLTSPTLSF

LPQLLLSSSLPSNPLGSPGTSTPKPVAKKKGEPTKPTLLSSKDPLSLPITTNNFKRFVAKVGPVFWLQDR

IEEILLWKRGWKVTTVWMLAYALLCYFPRLILLIPHISLIAIILATYPYPSAPGSDPLYTSSGSEPAENE

ALPPPPTEGSIPWQANIQGIQNLMGAFSDAFTLIEPYTYHLSLSPAHFSATRTQGSISTHPSPSSHSPYT

PHILTFLIVSFPPLLFLISLPAFPIRQVCLFVGLAPFAVTHPYGRALLPFIGPALRDLTPMVIKKAKVVK

GRITAAAKRQQQPQEDVVEDDSKGLLLPVSMMVQRLVDDDRLTDVVWNSELREVELWENERFGGAQDTPS

LSSSTSGPSPPQRGWSKQNLKPNERMAWTRGRDGWSGGVEGNGEVSFACSSNLTFSLSDGWAFVETEDWR

KDLSGDWSGCSADGDGWVYSNDTWQNPRPSPYVAGGGSVTRRRRWVRRVWFDASKVGSSPAVMVRY

>gi|170102673|ref|XP\_001882552.1| predicted protein [Laccaria bicolor S238N-H82]

GFGASYGGGLGSYGGMGSYGGMGSYGGAGSYGGIGSYGMGSYGGMNSYTGMGPYSGYGQGMGMGRLNPDG

TPSLTQTVEATTQSTFTLIQSIVQTFTGVAQMLESTFMATHSSFFAMIGVIDQFAKLRDALGGVLSLYGA

VRWLKATLTGRPTGTGGFNHHEFREFINGKQVQKPTQKASKKPLILFLLVVVGIPYAVTKLMKVLQERAV

ANGGALPGQLPPLDPASLTFVRAKYAFKPSNPNELELKEDEIVAVMGKMDQRTGAEGEWWKGRTREGREG

WFPKKWVEVLERR

>gi|119498501|ref|XP\_001266008.1| peroxisomal membrane protein (Pex3), putative [Neosartorya fischeri NRRL 181]

MIGATRRWFRRNRKGLAIGAGIIGAGYLAGQYVLSKITEARERMSSDRIARENLRRRFEQNQTDCTYTVL

ALLPTAAEGILEALPVEELTKELQKKRAERLARLQAGEGTVSDLSSVSPSAADDDRRSLSSFQSDGFVRT

SQLGEPSFDGEGPARVKRNKTQLWNEVKITSVTRSFTLIYTLSLLTIFTRIQLNLLGRRNYLSSVISLAT

PPADASTIKLEDHDDDLTQTLGNDFETNRRYLAFSWWLLHRGWKDLMNEVQAAVADAFGSLNPREDISVG

RLSELTLDIRKKVEGNTPEERRSRRWLPYLLPPREEEEHLLEESGVAGVTEPSTSQSASTLRHLLDETAD

LIESPTFGRVLQGLNDECFDLLMQNCIKEAFQSSPQASESVPQSFTSVATVVPQVKTADLKTKLANVLAV

MARQAHVIGNGTNPPNIYLTAMDQNVRNLEAFAAVIYSSNFDFQPPGAEQKAEQVTAERDRPDTSSTAPV

MVNKDDTQDFNQAGSSAVAEDNSAFEKAWGKAVEDGSSE

>gi|374587750|ref|ZP\_09660842.1| methyl-accepting chemotaxis sensory transducer [Leptonema illini DSM 21528]

MFFKADRKVSSISDDLMTEVMVRNNRRLFYSFLSILVLANVATLAIKIAGKGSAHLTYEAILIEFVFAAS

ALFIGFAISTKLKGHPASSYVSITGVILCLIAFQYVIFGATEIFATFYISFVLSVLYFNRNASLYNFILI

LGAQIALFILRPELKPVGPPSNLLVRFLVFVWVGVGATAGAAATKGLLTLAIEKQSEARETLANLRTMAT

AIVQTIETVRSQSEQQDRISDQLKGISEHQAASLQQIRAALAELAERADANNAIARSLNNETAASIQSVH

GLKAINASVQDGAGRILTNLNNVMAYSTNTSQQIRDSMDRFNQVQTRSGEIAAIVEVINDIAARVNLLSL

NAAIEAARAGEHGRGFAVVAEEISKLADATTKNAKEISSIIEENRSMILESSRMIADSSASMEKLDSAIN

VIKGEISGVGEQIRDVAGAVSAIESLNQSISETSRSIEASTEHQKNSTEEANRTTVGVSDYATKLVEVAR

EVHESSRATGRSVVQLEELAQKMAV

>gi|116235480|ref|NP\_149118.2| protein transport protein Sec16B [Homo sapiens]

MELWAPQRLPQTRGKATAPSKDPDRGFRRDGHHRPVPHSWHNGERFHQWQDNRGSPQPQQEPRADHQQQP

HYASRPGDWHQPVSGVDYYEGGYRNQLYSRPGYENSYQSYQSPTMREEYAYGSYYYHGHPQWLQEERVPR

QRSPYIWHEDYREQKYLDEHHYENQHSPFGTNSETHFQSNSRNPCKDSPASNSGQEWPGELFPGSLLAEA

QKNKPSLASESNLLQQRESGLSSSSYELSQYIRDAPERDDPPASAAWSPVQADVSSAGPKAPMKFYIPHV

PVSFGPGGQLVHVGPSSPTDGQAALVELHSMEVILNDSEEQEEMRSFSGPLIREDVHKVDIMTFCQQKAA

QSCKSETLGSRDSALLWQLLVLLCRQNGSMVGSDIAELLMQDCKKLEKYKRQPPVANLINLTDEDWPVLS

SGTPNLLTGEIPPSVETPAQIVEKFTRLLYYGRKKEALEWAMKNHLWGHALFLSSKMDPQTYSWVMSGFT

STLALNDPLQTLFQLMSGRIPQAATCCGEKQWGDWRPHLAVILSNQAGDPELYQRAIVAIGDTLAGKGLV

EAAHFCYLMAHVPFGHYTVKTDHLVLLGSSHSQEFLKFATTEAIQRTEIFEYCQMLGRPKSFIPSFQVYK

LLYASRLADYGLVSQALHYCEAIGAAVLSQGESSHPVLLVELIKLAEKLKLSDPLVLERRSGDRDLEPDW

LAQLRRQLEQKVAGDIGDPHPTRSDISGAGGTTTENTFYQDFSGCQGYSEAPGYRSALWLTPEQTCLLQP

SPQQPFPLQPGSYPAGGGAGQTGTPRPFYSVPETHLPGTGSSVAVTEATGGTVWEEMLQTHLGPGENTVS

QETSQPPDGQEVISKPQTPLAARPRSISESSASSAKEDEKESSDEADKNSPRNTAQRGKLGDGKEHTKSS

GFGWFSWFRSKPTKNASPAGDEDSSDSPDSEETPRASSPHQAGLGLSLTPSPESPPLPDVSAFSRGRGGG

EGRGSASSGGAAAGAGVGGLSGPESVSFELCSNPGVLLPPPALKGAVPLYNPSQVPQLPTATSLNRPNRL

AQRRYPTQP

>gi|145309311|ref|NP\_001034680.2| probable ubiquitin carboxyl-terminal hydrolase FAF-X isoform 4 [Homo sapiens]

MTATTRGSPVGGNDNQGQAPDGQSQPPLQQNQTSSPDSSNENSPATPPDEQGQGDAPPQLEDEEPAFPHT

DLAKLDDMINRPRWVVPVLPKGELEVLLEAAIDLSKKGLDVKSEACQRFFRDGLTISFTKILTDEAVSGW

KFEIHRCIINNTHRLVELCVAKLSQDWFPLLELLAMALNPHCKFHIYNGTRPCESVSSSVQLPEDELFAR

SPDPRSPKGWLVDLLNKFGTLNGFQILHDRFINGSALNVQIIAALIKPFGQCYEFLTLHTVKKYFLPIIE

MVPQFLENLTDEELKKEAKNEAKNDALSMIIKSLKNLASRVPGQEETVKNLEIFRLKMILRLLQISSFNG

KMNALNEVNKVISSVSYYTHRHGNPEEEEWLTAERMAEWIQQNNILSIVLRDSLHQPQYVEKLEKILRFV

IKEKALTLQDLDNIWAAQAGKHEAIVKNVHDLLAKLAWDFSPEQLDHLFDCFKASWTNASKKQREKLLEL

IRRLAEDDKDGVMAHKVLNLLWNLAHSDDVPVDIMDLALSAHIKILDYSCSQDRDTQKIQWIDRFIEELR

TNDKWVIPALKQIREICSLFGEAPQNLSQTQRSPHVFYRHDLINQLQHNHALVTLVAENLATYMESMRLY

ARDHEDYDPQTVRLGSRYSHVQEVQERLNFLRFLLKDGQLWLCAPQAKQIWKCLAENAVYLCDREACFKW

YSKLMGDEPDLDPDINKDFFESNVLQLDPSLLTENGMKCFERFFKAVNCREGKLVAKRRAYMMDDLELIG

LDYLWRVVIQSNDDIASRAIDLLKEIYTNLGPRLQVNQVVIHEDFIQSCFDRLKASYDTLCVLDGDKDSV

NCARQEAVRMVRVLTVLREYINECDSDYHEERTILPMSRAFRGKHLSFVVRFPNQGRQVDDLEVWSHTND

TIGSVRRCILNRIKANVAHTKIELFVGGELIDPADDRKLIGQLNLKDKSLITAKLTQISSNMPSSPDSSS

DSSTGSPGNHGNHYSDGPNPEVESCLPGVIMSLHPRYISFLWQVADLGSSLNMPPLRDGARVLMKLMPPD

STTIEKLRAICLDHAKLGESSLSPSLDSLFFGPSASQVLYLTEVVYALLMPAGAPLADDSSDFQFHFLKS

GGLPLVLSMLTRNNFLPNADMETRRGAYLNALKIAKLLLTAIGYGHVRAVAEACQPGVEGVNPMTQINQV

THDQAVVLQSALQSIPNPSSECMLRNVSVRLAQQISDEASRYMPDICVIRAIQKIIWASGCGSLQLVFSP

NEEITKIYEKTNAGNEPDLEDEQVCCEALEVMTLCFALIPTALDALSKEKAWQTFIIDLLLHCHSKTVRQ

VAQEQFFLMCTRCCMGHRPLLFFITLLFTVLGSTARERAKHSGDYFTLLRHLLNYAYNSNINVPNAEVLL

NNEIDWLKRIRDDVKRTGETGIEETILEGHLGVTKELLAFQTSEKKFHIGCEKGGANLIKELIDDFIFPA

SNVYLQYMRNGELPAEQAIPVCGSPPTINAGFELLVALAVGCVRNLKQIVDSLTEMYYIGTAITTCEALT

EWEYLPPVGPRPPKGFVGLKNAGATCYMNSVIQQLYMIPSIRNGILAIEGTGSDVDDDMSGDEKQDNESN

VDPRDDVFGYPQQFEDKPALSKTEDRKEYNIGVLRHLQVIFGHLAASRLQYYVPRGFWKQFRLWGEPVNL

REQHDALEFFNSLVDSLDEALKALGHPAMLSKVLGGSFADQKICQGCPHRYECEESFTTLNVDIRNHQNL

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ELDMEPYTVAGVAKLEGDNVNPESQLIQQSEQSESETAGSTKYRLVGVLVHSGQASGGHYYSYIIQRNGG

DGERNRWYKFDDGDVTECKMDDDEEMKNQCFGGEYMGEVFDHMMKRMSYRRQKRWWNAYILFYERMDTID

QDDELIRYISELAITTRPHQIIMPSAIERSVRKQNVQFMHNRMQYSMEYFQFMKKLLTCNGVYLNPPPGQ

DHLLPEAEEITMISIQLAARFLFTTGFHTKKVVRGSASDWYDALCILLRHSKNVRFWFAHNVLFNVSNRF

SEYLLECPSAEVRGAFAKLIVFIAHFSLQDGPCPSPFASPGPSSQAYDNLSLSDHLLRAVLNLLRREVSE

HGRHLQQYFNLFVMYANLGVAEKTQLLKLSVPATFMLVSLDEGPGPPIKYQYAELGKLYSVVSQLIRCCN

VSSRMQSSINGNPPLPNPFGDPNLSQPIMPIQQNVADILFVRTSYVKKIIEDCSNSEETVKLLRFCCWEN

PQFSSTVLSELLWQVAYSYTYELRPYLDLLLQILLIEDSWQTHRIHNALKGIPDDRDGLFDTIQRSKNHY

QKRAYQCIKCMVALFSNCPVAYQILQGNGDLKRKWTWAVEWLGDELERRPYTGNPQYTYNNWSPPVQSNE

TSNGYFLERSHSARMTLAKACELCPEEEPDDQDAPDEHESPPPEDAPLYPHSPGSQYQQNNHVHGQPYTG

PAAHHMNNPQRTGQRAQENYEGSEEVSPPQTKDQ

>gi|145309309|ref|NP\_001034679.2| probable ubiquitin carboxyl-terminal hydrolase FAF-X isoform 3 [Homo sapiens]

MTATTRGSPVGGNDNQGQAPDGQSQPPLQQNQTSSPDSSNENSPATPPDEQGQGDAPPQLEDEEPAFPHT

DLAKLDDMINRPRWVVPVLPKGELEVLLEAAIDLSKKGLDVKSEACQRFFRDGLTISFTKILTDEAVSGW

KFEIHRCIINNTHRLVELCVAKLSQDWFPLLELLAMALNPHCKFHIYNGTRPCESVSSSVQLPEDELFAR

SPDPRSPKGWLVDLLNKFGTLNGFQILHDRFINGSALNVQIIAALIKPFGQCYEFLTLHTVKKYFLPIIE

MVPQFLENLTDEELKKEAKNEAKNDALSMIIKSLKNLASRVPGQEETVKNLEIFRLKMILRLLQISSFNG

KMNALNEVNKVISSVSYYTHRHGNPEEEEWLTAERMAEWIQQNNILSIVLRDSLHQPQYVEKLEKILRFV

IKEKALTLQDLDNIWAAQAGKHEAIVKNVHDLLAKLAWDFSPEQLDHLFDCFKASWTNASKKQREKLLEL

IRRLAEDDKDGVMAHKVLNLLWNLAHSDDVPVDIMDLALSAHIKILDYSCSQDRDTQKIQWIDRFIEELR

TNDKWVIPALKQIREICSLFGEAPQNLSQTQRSPHVFYRHDLINQLQHNHALVTLVAENLATYMESMRLY

ARDHEDYDPQTVRLGSRYSHVQEVQERLNFLRFLLKDGQLWLCAPQAKQIWKCLAENAVYLCDREACFKW

YSKLMGDEPDLDPDINKDFFESNVLQLDPSLLTENGMKCFERFFKAVNCREGKLVAKRRAYMMDDLELIG

LDYLWRVVIQSNDDIASRAIDLLKEIYTNLGPRLQVNQVVIHEDFIQSCFDRLKASYDTLCVLDGDKDSV

NCARQEAVRMVRVLTVLREYINECDSDYHEERTILPMSRAFRGKHLSFVVRFPNQGRQVDDLEVWSHTND

TIGSVRRCILNRIKANVAHTKIELFVGGELIDPADDRKLIGQLNLKDKSLITAKLTQISSNMPSSPDSSS

DSSTGSPGNHGNHYSDGPNPEVESCLPGVIMSLHPRYISFLWQVADLGSSLNMPPLRDGARVLMKLMPPD

STTIEKLRAICLDHAKLGESSLSPSLDSLFFGPSASQVLYLTEVVYALLMPAGAPLADDSSDFQFHFLKS

GGLPLVLSMLTRNNFLPNADMETRRGAYLNALKIAKLLLTAIGYGHVRAVAEACQPGVEGVNPMTQINQV

THDQAVVLQSALQSIPNPSSECMLRNVSVRLAQQISDEASRYMPDICVIRAIQKIIWASGCGSLQLVFSP

NEEITKIYEKTNAGNEPDLEDEQVCCEALEVMTLCFALIPTALDALSKEKAWQTFIIDLLLHCHSKTVRQ

VAQEQFFLMCTRCCMGHRPLLFFITLLFTVLGSTARERAKHSGDYFTLLRHLLNYAYNSNINVPNAEVLL

NNEIDWLKRIRDDVKRTGETGIEETILEGHLGVTKELLAFQTSEKKFHIGCEKGGANLIKELIDDFIFPA

SNVYLQYMRNGELPAEQAIPVCGSPPTINAGFELLVALAVGCVRNLKQIVDSLTEMYYIGTAITTCEALT

EWEYLPPVGPRPPKGFVGLKNAGATCYMNSVIQQLYMIPSIRNGILAIEGTGSDVDDDMSGDEKQDNESN

VDPRDDVFGYPQQFEDKPALSKTEDRKEYNIGVLRHLQVIFGHLAASRLQYYVPRGFWKQFRLWGEPVNL

REQHDALEFFNSLVDSLDEALKALGHPAMLSKVLGGSFADQKICQGCPHRYECEESFTTLNVDIRNHQNL

LDSLEQYVKGDLLEGANAYHCEKCNKKVDTVKRLLIKKLPPVLAIQLKRFDYDWERECAIKFNDYFEFPR

ELDMEPYTVAGVAKLEGDNVNPESQLIQQSEQSESETAGSTKYRLVGVLVHSGQASGGHYYSYIIQRNGG

DGERNRWYKFDDGDVTECKMDDDEEMKNQCFGGEYMGEVFDHMMKRMSYRRQKRWWNAYILFYERMDTID

QDDELIRYISELAITTRPHQIIMPSAIERSVRKQNVQFMHNRMQYSMEYFQFMKKLLTCNGVYLNPPPGQ

DHLLPEAEEITMISIQLAARFLFTTGFHTKKVVRGSASDWYDALCILLRHSKNVRFWFAHNVLFNVSNRF

SEYLLECPSAEVRGAFAKLIVFIAHFSLQDGPCPSPFASPGPSSQAYDNLSLSDHLLRAVLNLLRREVSE

HGRHLQQYFNLFVMYANLGVAEKTQLLKLSVPATFMLVSLDEGPGPPIKYQYAELGKLYSVVSQLIRCCN

VSSRMQSSINGNPPLPNPFGDPNLSQPIMPIQQNVADILFVRTSYVKKIIEDCSNSEETVKLLRFCCWEN

PQFSSTVLSELLWQVAYSYTYELRPYLDLLLQILLIEDSWQTHRIHNALKGIPDDRDGLFDTIQRSKNHY

QKRAYQCIKCMVALFSNCPVAYQILQGNGDLKRKWTWAVEWLGDELERRPYTGNPQYTYNNWSPPVQSNE

TSNGYFLERSHSARMTLAKACELCPEEVKKATSVQQIEMEESKEPDDQDAPDEHESPPPEDAPLYPHSPG

SQYQQNNHVHGQPYTGPAAHHMNNPQRTGQRAQENYEGSEEVSPPQTKDQ

>gi|45201311|ref|NP\_986881.1| AGR215Cp [Ashbya gossypii ATCC 10895]

MGSSRKYHAKFAQSRGQKPSLTFTTSPVVSQALYQFYPVLVIVDSVLNNMMWIQEDTCLGFVYLVLLYFS

AQTLYAEVDRTRAFESWMSFVSAGFLGLSAVYYVHSTLKEMQESEAPTVDDIVIVLESVLDKLQRLRVEV

LGSGLRRRLVVDVWAALKLVAVLTPLHWVLVRVLTPLECFTWFLVLASTYHSTWFQCTLLLCWRSLPVRV

AYYRFWRLSLRGRRSGQPLRYRVLSEDEVVPFPRALQRLSGAQLQLKLQSLLISDAAATVDMESTDYIKV

CIVEFCIDENERKWPKDGWSHTLLPYERQRYSLALDPQHRASPSPWRLQETVARDWHWVDDTWQHSPWSY

CDTEWNFLGSKDSIGCYTRHRTWKRRAFRIKG

>gi|45199018|ref|NP\_986047.1| AFR500Wp [Ashbya gossypii ATCC 10895]

MNSSGKETRAQFVDESHGLPHGGKSNQNLRSALKQRRPSGEGNSDYGSLVVSSPLLNSTPPTVTKSLVKL

YPYLVIADRALSTLTWTNDDVWESVLMVICYGAGVVYFERLIKFFGHLVIVGVLWGYSLLDKHVEETIRD

RPTLDDVVQMMSRVVAKSDLLLSPVSVLSGNDIKRLLLTMVFLSPIYVILTLFVIPPRKFVLVAGVYVLT

YHSSWSSVTRKLLWRFKLVRLLAFYVTGLDLSGVNKYQGGIFAAVHKKVKKLSGTNGADDGKPIRFTYVL

YENQRRWLAIGWTSNMLSYERSSWTDEFLNEAPPPEKFKLPEENGGMVWRWVDKTWRLDLTNDGAIHLPS

SRSKTTASPNSDDGFIYYDNTWKKPSTEDSFSKYTRRRRWIRTAELIKIDALGAAEGAHDELCSVTTDMG

SSPSRNVKFETSTPSSPRARKVSFSKVENVRVIHASTSASDKNNTRGELSERTKKEPSPEKAGGATESVA

KPQAPENDGKTDKKNV

>gi|302307865|ref|NP\_984634.2| AEL227Cp [Ashbya gossypii ATCC 10895]

MDSLRGHHTKERGSGHGRGECGVMQGMLLDKMMEKVLGMAIPPAGEAGGGAIESRVQAGRARPGLSVPIM

SRNFVQMNSRLSFPFQVVNEVIRIANWESTACTLSVGMLYSFVVLRPLVTLSSAPMFYILFAVMVPYYMQ

IHAPEPWEELGANPIPAAGPALKEPDLPRPVPELSKEFILNLTDLQNHMVLYVVCYDFITGLLAKFAFFA

DENVSAAAFVGLLVLGVFNMLFIESLFRWIPLKLLLLACGWGFLIMLHPSCRDACFDYISSEETRLKVLT

MTNKIEQLINDYWDYCEPRETRQAAIFEIQKFDRRTKEWRTAGFSSDDYTLLSKLRIAEEPIDSSATSLD

DVKPPLDWKWLGKYDWVLDLEPRQWVTDGFVQYVDIDAETKWVYDLNFDGTRGQYRRRRWIRLCTRNRSV

QENANVDTIDDDNSDDYELVDYSGCTGVSQNSMHGSVKSCHSISEPTDQIVVERLRSHTLSPAANASVSS

ADSTASATIATPNKNVEQGSRAIKSLTDFLNING

>gi|45188282|ref|NP\_984505.1| ADR410Cp [Ashbya gossypii ATCC 10895]

MVSKASRDQLRKYGAVSLASLLVAASIVAYRWWNAAPSIEVEKKLRRSVSRCVVVTQGIQNEDMIHDLLF

EDTVMLLAPGCTAEGRLKSASRENAYKVISCTTWQSVWACVRHFRKHTLLVRTSEVPSGVPADIGGYVSD

ISDI

>gi|45187737|ref|NP\_983960.1| ADL136Cp [Ashbya gossypii ATCC 10895]

MTWGGGPMKEDDRAKALESVAIGSKKRRSLLGEFLARKYERIMEAEERVADDEKARPCVTNRELVTNIAC

SLFDATWERLRTGKDQQRKTIDDDFDEFALRHELESSADSFWQEETSDNGAGMSDEEDTEEQRAAKLRAV

SQVQEQEHFIDILLDKMISAVLPEDLPEREQFTQRVQEPGRRRSHPISLIIMSRNLKIMTTKLGLIFEFQ

DSLVRLATWRNPSGTALSLILFSFACFNPMLVIILPMLYVLFGLMIPGYLHRHPLRRNFYLTKHSYGKSL

LATVATGGKPASWQSHDDVQEFDYNNLHTDTEEWERALHIKQTMEFIVNLRDLQNLMTASVKGIECAEKF

VYGDAGFKNEHHSTVLFLSGLLVVMGLWIIAPYINWSLTSAAGAWAALILIHPRVLPMVTAYINDDQLEK

GKVVIENVERYDILLDEKPEERYLELFEIYKQRLTSDEWDFYLLSSYAFDPTDKYRKSQRPPPGVTNIDE

VVPPSMWSFDRNSKWEVDYDVKGWAQERGLSLEINGEFLVDDSFKRRRLTRKVVRYANPARKPTV

>gi|196259774|ref|NP\_001124497.1| peroxisomal biogenesis factor 5 isoform d [Homo sapiens]

MAMRELVEAECGGANPLMKLAGHFTQDKALRQEGLRPGPWPPGAPASEAASKPLGVASEDELVAEFLQDQ

NAPLVSRAPQTFKMDDLLAEMQQIEQSNFRQAPQRAPGVADLALSENWAQEFLAAGDAVDVTQDYNETDW

SQEFISEVTDPLSVSPARWAEEYLEQSEEKLWLGEPEGTATDRWYDEYHPEEDLQHTASDFVAKVDDPKL

ANSEFLKFVRQIGEGQVSLESGAGSGRAQAEQWAAEFIQQQGTSDAWVDQFTRPVNTSALDMEFERAKSA

IESDVDFWDKLQAELEEMAKRDAEAHPWLSDYDDLTSATYDKGYQFEEENPLRDHPQPFEEGLRRLQEGD

LPNAVLLFEAAVQQDPKHMEAWQYLGTTQAENEQELLAISALRRCLELKPDNQTALMALAVSFTNESLQR

QACETLRDWLRYTPAYAHLVTPAEEGAGGAGLGPSKRILGSLLSDSLFLEVKELFLAAVRLDPTSIDPDV

QCGLGVLFNLSGEYDKAVDCFTAALSVRPNDYLLWNKLGATLANGNQSEEAVAAYRRALELQPGYIRSRY

NLGISCINLGAHREAVEHFLEALNMQRKSRGPRGEGGAMSENIWSTLRLALSMLGQSDAYGAADARDLST

LLTMFGLPQ

>gi|196259770|ref|NP\_001124495.1| peroxisomal biogenesis factor 5 isoform a [Homo sapiens]

MAMRELVEAECGGANPLMKLAGHFTQDKALRQEGLRPGPWPPGAPASEAVSVLEVESPGAASEAASKPLG

VASEDELVAEFLQDQNAPLVSRAPQTFKMDDLLAEMQQIEQSNFRQAPQRAPGVADLALSENWAQEFLAA

GDAVDVTQDYNETDWSQEFISEVTDPLSVSPARWAEEYLEQSEEKLWLGEPEGTATDRWYDEYHPEEDLQ

HTASDFVAKVDDPKLANSEFLKFVRQIGEGQVSLESGAGSGRAQAEQWAAEFIQQQGTSDAWVDQFTRPV

NTSALDMEFERAKSAIESDVDFWDKLQAELEEMAKRDAEAHPWLSDYDDLTSATYDKGYQFEEENPLRDH

PQPFEEGLRRLQEGDLPNAVLLFEAAVQQDPKHMEAWQYLGTTQAENEQELLAISALRRCLELKPDNQTA

LMALAVSFTNESLQRQACETLRDWLRYTPAYAHLVTPAEEGAGGAGLGPSKRILGSLLSDSLFLEVKELF

LAAVRLDPTSIDPDVQCGLGVLFNLSGEYDKAVDCFTAALSVRPNDYLLWNKLGATLANGNQSEEAVAAY

RRALELQPGYIRSRYNLGISCINLGAHREAVEHFLEALNMQRKSRGPRGEGGAMSENIWSTLRLALSMLG

QSDAYGAADARDLSTLLTMFGLPQ

>gi|196259776|ref|NP\_001124498.1| peroxisomal biogenesis factor 5 isoform d [Homo sapiens]

MAMRELVEAECGGANPLMKLAGHFTQDKALRQEGLRPGPWPPGAPASEAASKPLGVASEDELVAEFLQDQ

NAPLVSRAPQTFKMDDLLAEMQQIEQSNFRQAPQRAPGVADLALSENWAQEFLAAGDAVDVTQDYNETDW

SQEFISEVTDPLSVSPARWAEEYLEQSEEKLWLGEPEGTATDRWYDEYHPEEDLQHTASDFVAKVDDPKL

ANSEFLKFVRQIGEGQVSLESGAGSGRAQAEQWAAEFIQQQGTSDAWVDQFTRPVNTSALDMEFERAKSA

IESDVDFWDKLQAELEEMAKRDAEAHPWLSDYDDLTSATYDKGYQFEEENPLRDHPQPFEEGLRRLQEGD

LPNAVLLFEAAVQQDPKHMEAWQYLGTTQAENEQELLAISALRRCLELKPDNQTALMALAVSFTNESLQR

QACETLRDWLRYTPAYAHLVTPAEEGAGGAGLGPSKRILGSLLSDSLFLEVKELFLAAVRLDPTSIDPDV

QCGLGVLFNLSGEYDKAVDCFTAALSVRPNDYLLWNKLGATLANGNQSEEAVAAYRRALELQPGYIRSRY

NLGISCINLGAHREAVEHFLEALNMQRKSRGPRGEGGAMSENIWSTLRLALSMLGQSDAYGAADARDLST

LLTMFGLPQ

>gi|196259772|ref|NP\_001124496.1| peroxisomal biogenesis factor 5 isoform c [Homo sapiens]

MAMRELVEAECGGANPLMKLAGHFTQDKALRQEGLRPGPWPPGAPASEAASKPLGVASEDELVAEFLQDQ

NAPLVSRAPQTFKMDDLLAEMQQIEQSNFRQAPQRAPGVADLALSENWAQEFLAAGDAVDVTQDYNETDW

SQEFISEVTDPLSVSPARWAEEYLEQSEEKLWLGEPEGTATDRWYDEYHPEEDLQHTASDFVAKVDDPKL

ANSEGTSDAWVDQFTRPVNTSALDMEFERAKSAIESDVDFWDKLQAELEEMAKRDAEAHPWLSDYDDLTS

ATYDKGYQFEEENPLRDHPQPFEEGLRRLQEGDLPNAVLLFEAAVQQDPKHMEAWQYLGTTQAENEQELL

AISALRRCLELKPDNQTALMALAVSFTNESLQRQACETLRDWLRYTPAYAHLVTPAEEGAGGAGLGPSKR

ILGSLLSDSLFLEVKELFLAAVRLDPTSIDPDVQCGLGVLFNLSGEYDKAVDCFTAALSVRPNDYLLWNK

LGATLANGNQSEEAVAAYRRALELQPGYIRSRYNLGISCINLGAHREAVEHFLEALNMQRKSRGPRGEGG

AMSENIWSTLRLALSMLGQSDAYGAADARDLSTLLTMFGLPQ

>gi|21361204|ref|NP\_000310.2| peroxisomal biogenesis factor 5 isoform b [Homo sapiens]

MAMRELVEAECGGANPLMKLAGHFTQDKALRQEGLRPGPWPPGAPASEAASKPLGVASEDELVAEFLQDQ

NAPLVSRAPQTFKMDDLLAEMQQIEQSNFRQAPQRAPGVADLALSENWAQEFLAAGDAVDVTQDYNETDW

SQEFISEVTDPLSVSPARWAEEYLEQSEEKLWLGEPEGTATDRWYDEYHPEEDLQHTASDFVAKVDDPKL

ANSEFLKFVRQIGEGQVSLESGAGSGRAQAEQWAAEFIQQQGTSDAWVDQFTRPVNTSALDMEFERAKSA

IELQAELEEMAKRDAEAHPWLSDYDDLTSATYDKGYQFEEENPLRDHPQPFEEGLRRLQEGDLPNAVLLF

EAAVQQDPKHMEAWQYLGTTQAENEQELLAISALRRCLELKPDNQTALMALAVSFTNESLQRQACETLRD

WLRYTPAYAHLVTPAEEGAGGAGLGPSKRILGSLLSDSLFLEVKELFLAAVRLDPTSIDPDVQCGLGVLF

NLSGEYDKAVDCFTAALSVRPNDYLLWNKLGATLANGNQSEEAVAAYRRALELQPGYIRSRYNLGISCIN

LGAHREAVEHFLEALNMQRKSRGPRGEGGAMSENIWSTLRLALSMLGQSDAYGAADARDLSTLLTMFGLP

Q

>gi|398366261|ref|NP\_011755.3| Pex21p [Saccharomyces cerevisiae S288c]

MPSVCHTSPIEKIIQQGHRIQNDSLIPSKRTKLAHTELTAHYATEDSHVEKHFLHNGSNFDGIDNVRYQN

QPSPLTFITPNNTVDSSDWVPQFSSMKIDDSLEFSSEYKRLYSNYESQQRLNSSRQHLPFKNCMIRKTSC

TYPPQKTLRQQRQGNRDNPTDAFQFDAEFQVLEREIQKERYEPITRRDEKWFDQDQSELQRIATDIVKCC

TPPPSSASSSSTLSSSVESKLSESKFIQLMRNISSGDVTLKKNADGNSASELFSSNNGELVGNRHIFVKD

EIHKDILD

>gi|398365241|ref|NP\_009727.3| Pex32p [Saccharomyces cerevisiae S288c]

MDTNSKTKVQTENKKIKAKFIHNHGQKPSLIQITPPMISSTLFHAYPLLLIFDNALANIMWLSDDKCLTF

IYLTSIWLTISFFIPVETEASHFLPFTKILRLWLGIISGAFLFLSFMYYIVSLIASLRDTEPPTLDEIVV

LLESVLDKLEVLRNELNVWKKLKLSFDGVNKECSGKRLFCRLFLFGTIFQIIIMRYISPGTYTRFFIITG

LIYNTSSFQATLRLLWRFTAVRNFYYLGIESFKISSFLPKHLKMEQIIPLSQGRAITVPLVEVLPKLLRD

KKGDDHIHILQLLLNEQKDNFGNEDLKILEIEVYENQRRWYQNKNWSTKLLPYERQNYCIEIKNTDGTLT

MRSCLPPDGLGEEELPNNWHWINDNWDGTDWIYSDSAWKEIGQYSSLESFTRSRKWKRRLFHL

>gi|398364395|ref|NP\_011362.3| Pex14p [Saccharomyces cerevisiae S288c]

MSDVVSKDRKALFDSAVSFLKDESIKDAPLLKKIEFLKSKGLTEKEIEIAMKEPKKDGIVGDEVSKKIGS

TENRASQDMYLYEAMPPTLPHRDWKDYFVMATATAGLLYGAYEVTRRYVIPNILPEAKSKLEGDKKEIDD

QFSKIDTVLNAIEAEQAEFRKKESETLKELSDTIAELKQALVQTTRSREKIEDEFRIVKLEVVNMQNTID

KFVSDNDGMQELNNIQKEMESLKSLMNNRMESGNAQDNRLFSISPNGIPGIDTIPSASEILAKMGMQEES

DKEKENGSDANKDDNAVPAWKKAREQTIDSNASIPEWQKNTAANEISVPDWQNGQVEDSIP

>gi|6325145|ref|NP\_015213.1| Pex25p [Saccharomyces cerevisiae S288c]

MSQFGTTDIVSGSETPPYSGASYQDAQDDNTHPHSSDAGAEKFSAGSGSESHTESSRSDDEDSQAKTKMV

DNITILKYILDSLSGRDKLAKIIKYALDILKLFIEKSKRNLTVLDPSVLTYYTKILKNLTVKVALRHPIT

VIKVLLLSLLRNFDKKIDFISQQLSTFRYILRFGGTPFRVCSFLGKFNKTRKCNFQIDQIKKIWFNEASL

REFLDLYYGIFDELDLLYKLKIWTNKSFYSFVSRQESLAWQYDILLSLKDHWLNLQSLQKRQLELEVQLK

VQNNALLLSPILMHQAHKDDGSQSPIRKQLLNDLNVNNDAEVLIHKQLKAIKDEKTLVYLDIARLSFDCM

ANTSDILNLKTPKGTYAVLSLGSGLTGLVKLWITTKRSLCSSKD

>gi|6324115|ref|NP\_014185.1| Pex17p [Saccharomyces cerevisiae S288c]

MTSINSFPRNIDWPSNIGIKKIEGTNPTVNAIKGLLYNGGSIYAFLYFVIAMFVEPTLQKQYQQRNDFSL

FVLLRLRRIIAQLQKRLVMTPVSSLGFNEQNNFVERSTQTSDDNIIREDNSHWAEMIYQLQNMKQELQYF

NRSSGQPSESIDDFVFQIKMVTDQVELTDRSRAFSNKSRNIIQGIREIKGWFVNGQVPR

>gi|6323668|ref|NP\_013739.1| Pex12p [Saccharomyces cerevisiae S288c]

MSFYSNLPSAGQSSRGSSTSGRNGVGLEPLYPTIFEIMSSQEIDSLLPASIRYLLANHLVANFPNRYTLR

LNKYFFEWFQAIKGFVEWYHLKTYNSTFIDRFYGLQLFSSRDRNLALTQCLNPKGQSEWPQGLQLNQQQK

SVIFLEKIILPYITAKLDEILEKISMNNIFSSDETENKWPKRAFLRIYPFIKKLLALSNLLVKLLFLTKR

TGSVSLLQYLFKIEYTTVRPLSSELSGLKETKGMDNRLRKTNISSIFALMQGQLSIIPRFLTFMGSQFFP

TFIFVLRVYQWWTTQDMTTKLQKRVNDLDEDIPRPPFSSHSDKTEDKEGVSEACPVCEKTVQNPCVLETG

YVACYPCAISYLVNNEGHCPVTNKKLLGCTYNKHTNKWEVVTGIRKLLI

>gi|6322250|ref|NP\_012325.1| Pex2p [Saccharomyces cerevisiae S288c]

MSRVAQLDSIALDKELYGQFWSEFNAAFNTSEHKEEWELALNTVVFMCATRFLPHYGSSCTYGSALSGVV

FQCRKRTLYVVTVLAGYVWKKITHIIFNGPHCGNQMMWLKLYKWVNLLYHGCDVTNFLRFLAAEGPNARA

FLSPLYRAFNVHSTRLIRDGSAIASEFYSNSVFAGLEYQNRQLLWNALLELFSNTLLTKRGLLTFVKKPP

RSRSTTTYKTVCPRCGGFPTNPYQIACCRANYCYVCVVKALEWSMCDACGSSGRLTASPVY

>gi|6321441|ref|NP\_011518.1| Pex31p [Saccharomyces cerevisiae S288c]

MSEINNENLEPTSSTVAESTESKNKHIRSALRKRRGKLSAQTYEEDQEAILSSPLLTSTPKTVSRSLVRL

YPYLIVVDNFLSIITWSNDNVSANLLGIFLFTVCVLYFGFITRYFGHLMIVGIIWVYLLIDKHVQETMAS

CPSLDDIIHVMDRVSMKSSAVLSPITILSAQDVRRLLFTIAFLSPVYIFLTVFVLSPNYLMLIGGLYVLT

YHSKLIRRMRRYLWKFRVVRLLVFFITGLDLGGPDNNRRLFASVNKKIRSFVWNEVGNTSNTKKTVLFKV

ALFENQRRWLGIGWTSTMLSYERASWTDEFLNTSPSPEVFTLPEEQSGMAWEWHDKDWMLDLTNDGIIQL

PASAAKTKVKPGADEGFIYYDNTWNNPSATDTYKKYTRRRRWIRTATVTTTYDDEPTVEKATPNSHALKS

EENNRVRKRKVSFSTANEVHIIPSSDSSKLIQISDVSMSPSL

>gi|6323356|ref|NP\_013428.1| Pex30p [Saccharomyces cerevisiae S288c]

MSGNTTNVHETRAKFAETLQPRIGGNTTKVIRAALEKNEAESGVSEDNDNGSLEKVNVATSPLLTSTPPT

ISKALVKLYPYLILIDEFLNVVTWTGKNIWSSVLMLCLFITTVEYFETLVKYFGHLAIIAILWGYSLLDN

YIEGTLSSSPTLEDIALLMNRVSLKSDILLSPMVNLGTQDIQRLLYTTVILSPIYVMITWLLLPPRSLML

MVGMFLLTYHSPWSKVARRLLWKFKIVRLLVFYVTGLDLGGINKDQGIFATVQKQVKKLASTENSNGVLS

DSKPIRFTYVLYENQRRWLGIGWKPSMLSYERTPWTDEFLNEAPSPENFHLPEETNTMVWRWVDKTWRLD

MTNDGAIQVPNSKARTSADPSPDEGFIYYDNTWKKPSKEDSFSKYTRRRRWVRTAELVKTSDFDESVINS

NRNSAIEQKVEENSTNGLTAEQELGSNKQEKDNAKKVGEPTTEETKEFAEASNINEGEFERISSTDEEVL

KSRARDRLAKVLDDTEEKEQSNPTIGRDSKKAV

>gi|6321954|ref|NP\_012030.1| Pex18p [Saccharomyces cerevisiae S288c]

MNSNRCQTNEVNKFISSTEKGPFTGRDNTLSFNKIGSRLNSPPILKDKIELKFLQHSEDLNQSRSYVNIR

PRTLEDQSYKFEAPNLNDNETSWAKDFRYNFPKNVEPPIENQIANLNINNGLRTSQTDFPLGFYSQKNFN

IASFPVVDHQIFKTTGLEHPINSHIDSLINAEFSELEASSLEEDVHTEEENSGTSLEDEETAMKGLASDI

IEFCDNNSANKDVKERLNSSKFMGLMGSISDGSIVLKKDNGTERNLQKHVGFCFQNSGNWAGLEFHDVED

RIA

>gi|6320226|ref|NP\_010306.1| Ses1p [Saccharomyces cerevisiae S288c]

MLDINQFIEDKGGNPELIRQSQKARNASVEIVDEIISDYKDWVKTRFELDELNKKFNKLQKDIGLKFKNK

EDASGLLAEKEKLTQQKKELTEKEQQEDKDLKKKVFQVGNIVHPSVVVSNDEENNELVRTWKPEDLEAVG

PIASVTGKPASLSHHEILLRLDGYDPDRGVKICGHRGYFFRNYGVFLNQALINYGLQFLAAKGYIPLQAP

VMMNKELMSKTAQLSEFDEELYKVIDGEDEKYLIATSEQPISAYHSGEWFEKPQEQLPIHYVGYSSCFRR

EAGSHGKDAWGVFRVHAFEKIEQFVITEPEKSWEEFEKMISYSEEFYKSLKLPYRIVGIVSGELNNAAAK

KYDLEAWFPYQKEYKELVSCSNCTDYQSRNLEIRCGIKKMGDREKKYVHCLNSTLAATQRALCCILENYQ

TEDGLVVPEVLRKYIPGEPEFLPFVNELPKNSTSSKDKKKKN

>gi|6319263|ref|NP\_009346.1| Pex22p [Saccharomyces cerevisiae S288c]

MPPPSRSRINKTRTLGIVGTAIAVLVTSYYIYQKVTSAKEDNGARPPEGDSVKENKKARKSKCIIMSKSI

QGLPIKWEEYAADEVVLLVPTSHTDGSMKQAIGDAFRKTKNEHKIIYCDSMDGLWSCVRRLGKFQCILNS

RDFTSSGGSDAAVVPEDIGRFVKFVVDSDVEDVLIDTLCN

>gi|392885618|ref|NP\_491602.2| Protein FERL-1 [Caenorhabditis elegans]

MTDKEKLLKVKQKFKRGDSSSDVDSGPERDRDEDDSDNESRNTSKTSKSSKNGKSGKSTGTSEMTELLND

GGSDIELLPDNGKNFEKRKLQDTDKSCTWNVLVRIIEAKGVSTGSARVRTIFDGKSKMTRTVTHAIPKWR

QNILYTMKNQPLEKLAAKVLTFRLVRPTALGESSVGEFSCYLSEVIRSPDRSLIAKWVALGFPGMSDEEP

DDIAYENCGFLKVTLSVYRIDESPPTLIDDGGKEQIWSGIRVFSVEQLIRKMINERKIKKKQRFYVMVQC

GAHKTKTTMESAFLDEDANIASIIFSLFDKKGRGKTCIGKATLPMKMIYEPGVAGYLPTFGPAFLNVFDC

ERVSRFSIFSRKMRGSQLDGSRFVGRLFIAIDCVEYMEKANAQIMHLDYSQIMEAESICKNLKWYNCFCS

MSLVNKIDPQFASDPVCIMMSIGSFGSTSNEDKKCNSSTVPTYPERDEHECCSFAWGNLRPVAEVNAPWE

VIDRRIEMSNVLMKMTNMLDSMISEIRHISSGAVDQIASVGIESLECLEQQIESASKFLRRINHVNSNAL

DRHILDYRKEKILKLREHFEKEAFSIDYSDGEVDAKLLRMLLQIRSMTLELAEDVQMTIPPVLIKMMSHG

KLIGFAKIPISEIFQSDDEAQSGEWCGRTRAINIQWPTLVDQRNRKREHVAVLHAKMWFGRTDQLTKWKE

HVQPADIERFIVLYEVQTKEPTLKWKDESDIYDGKWVKTKEVPPLENEWNAVGPWIVMNTRQTFVPKLGQ

HTAHDKAFEIQKRAETGTWKHFQYTDCYADELKPKDLDKHVKGWQVGSWDQDKFRNNGDEKGCVYSTNGV

FIGSGVLPDREEKVHHNFRKRCIERPRKHEGYNKEFEDFARFRKLIGNDKWEVSWNFE

>gi|193202784|ref|NP\_001122477.1| Protein FER-1, isoform b [Caenorhabditis elegans]

MTRTVTHAIPKWRQNILYTIKNQPLEKLAAKVLTLRLVRPTALGESSVGEFSCYLSEVIHSPDRSVIAKW

VALGFPGMDDEEPDDIAYENCGFLKVTLSVYRIDESPPTLIDDDGKEQIWSGAHLIDYTLKIRVFSVEQL

IRQMINERKIKKKQRFYVMVQCGAHKTETTMESAFLDEDANIASVKFEQEIYLPIQWPTVISEIIFSLFD

KKGRGKTCIGKATLPMKMIYEPGETGYLPTFGPAFLNVFDCERVTRFSIFSRKMRGSQQDGSRFVGRLFI

AIDCVEYMEKANAQIMHLDHSPIMEAESICKNLEWYNCFCSMSGLNMINPQFASDPVCIMMSIGSFGSTS

NEFRSCNSSTLPAEPNWDGCKYFTMPWGNLRPVAEVNAPWEVIEHRIEMSNVLMKMTNMLDTMIWEVRRI

GNKAIDHVSSVGMEALECLEQQIDSASKYLGRINPVSSNALDRHILDYRKEKILKLREHFEKEAFSIDYS

DGEVDAKLLRMLLKIRSMTLELAEDVQMTIPPVLIKMMSHGKLIGFAKIPISEIFQSDDEAQSGEWCGRT

RAINIQWPTLVDQRNRKREHVAVLHAKMWFGRTDQLTKWKEHVQPADIRRFMEMYEVQTKGLALKWKDEA

DIYDGKWEKTNEVPLENGWNAVGHWIVMNTRHMFVPKLGQHTVHDKAFEIQKRTEDGTWKHFKYTDCYAD

ELKPKDLDKHAKGWEVGSWAQDKFRNNGDEKGWVYSTNGVFFGSGVLTDREEKVHHNFRKRCIKRPRKHE

GYNKELEDFEHFRTTMGNENWEYSPSKKEGPYHDLEDRTDRIRRRRYVREVENKDPDSEDPRFRVYEYQM

QTGKWQLRCYIMWGNDLLPVVKNSSRAFVRISFAQYSKQTLLVDNSQNPIWNETVMFKSVLIAGGTRDIM

KYPPVVSVEVVGECSNNEEANLGHFETKPNVICGNTDVRGTPQWFPLKFSNGRTRGAVLACFELYSEEDK

DLIPLEPKCKHNYKERSEIPTEFRPQFDKFHVQFLCWGVRNLKKHKLLAVRRPFVGLTIGDQEFTLQPLK

DVRRDPNFPEPMIVFGEVILPSALELSPPLIINLFDARAFNRQPLVGSCLVSDLHKYVSHIVPKVKSDHA

ERWEQLDLVITEEFDQIIRMVRVPTLTTDPMVPLDWWSRYYASMSQFHRSPGYPESGMEYVRIFRRPLEQ

MNGYNNFSDFLDTFPFVKSMKGDFDDPEEKEKAGELKCRLLISKLKKGKPPAAINTVVDFVGPTRCLVRV

YIIEANGLISNARKGRVDSYVKLHCGKQNVNLKKNYRSECCDPIFGERVDMTVTIPLEKDLKITVMGKRR

ILSDQEIGSTTIDLENRLLTKWRATGGLSGQFTVQGELQWRDQMTPMEILKSYCYKMMLSVPKIESRQTE

RGEEKGITIEKITFWFSEVLHVFENEEIAMLNSQRQKAGKENFSDGSDQQNEDVSDGSWDEEDLEREKEK

LKWEKHRSKGKPLKKVTTEKAETADGELRKKAKMRIMGSQLQTIALFILRQMNLVPEHVESRPLFSDKGG

RTQKGELRMFVDIFPMEYGAIPAPFNIAPRKPINYQLRIAVMDVRGAIPVKRSFAEPVSDLYVKAFINGM

TKGHKTDTHFRVLDGTGEFNWRFLLNFDYNPWEKKVVAYTKNRFFCKPVEELVDPILVIELWDKNKFRKD

RLLGDIELDLLDFIEGIGSPSDVGVYSTKKRQRGVKCPKCCTRRGCLCKCCIFCFETKCLCGKRKVKKKP

FPKPVLFVEPEGYDDTVNIFESRNLYGWWPMLTEEYPHEEPQNAKKKNDDVGKDPKWIMGLVEMDMLLLT

KQEADQEPAGKKRSEPNHSPFLEKPDRKSWANSWLVSRIKPCIKYFWHYYGLQILLWLIIIVILILTIFV

LLHTWPTILAEIIKAIF

>gi|17535903|ref|NP\_495658.1| Protein T01H3.2 [Caenorhabditis elegans]

MPFEYIWTVSANGVACRIPSPSDPRCISEIEWKEIPCSDGSAICTIVASPTSAFAIDRSGRVLILVLPTH

LAIRERAEIYNNQRWIGIWRGTFFIDRPRFSDESGRVSIDPSANEIDPGWSWEDNWHPHLDPRKYDKEGW

QYSLSFLAPKWDKQCRMYHLVRRRVLKRNVRYTSHDQWIEMSNEETRMFTELAIGGMDVMGEGGMILFAL

GSDGNIYRRDGIHPSCPSGRSWQLISKVTFKDCESDDVTLISASPSLATLMAITWDGKMFHRVGITRQNQ

NGFSWKSIPTPKNKAVISASIGTRTMWCITADGCVWFVRLDIDEKLKEHKMENITSESYQMTTQGGISKI

SVTRNDQVFCVSTREKIEVRTGIEPREPSGKRFERIVDRGEPNDQKWISIHTGSVLFDKIPDYFMSSSSL

KSKMEVLQFKKADWRLQILERLQETSDRSWSLMNSVNGVGIDSPEELEGPNTPRQIRCQLMQGELFRSVN

ITILNNNLQIYGDNSLSKSIDTSSIKSVLPCFQRLPQKYLLYVFIGANSDSECFAFTDEKSRTTFQSILE

TIIRDYICSSTRNSFGDCMWSISSEGVVRWHCLAEMSKESKFEKRVNPGESRGLVVDGLFESVDCGVKGS

VWAINQSGNLYSLSSNYNPLSSHSTTHDYKMTDQITLKMFEYQKHAVFRGFISFQGSQKGISAWMCDNKP

CPPSPSSLPSTNWSWIDSAWQLEEDTWKYSNNIDGVYSYNEKAQGKARRRVWRRQAKFELNKSPWCHVES

PPIQCVRVSKIESCEGTIVVVVLTKDGHILIRNGVDREHFTGTNWTEILTDSPISSMHLQWEGMKLWCAT

YDGTILSRSLTNSKSSSFLSSSDWRHLDLDTSVITDNISPKAVNDIELTGYSDILYVRIKFILFRIDTKN

ETISDAYPMDNLQQAVVSARGSICLRGTNITVVRDWRVVPYTDRKATIIAMRDVERATNMGCRVESIAFY

>gi|194018488|ref|NP\_000278.3| peroxisome biogenesis factor 6 [Homo sapiens]

MALAVLRVLEPFPTETPPLAVLLPPGGPWPAAELGLVLALRPAGESPAGPALLVAALEGPDAGTEEQGPG

PPQLLVSRALLRLLALGSGAWVRARAVRRPPALGWALLGTSLGPGLGPRVGPLLVRRGETLPVPGPRVLE

TRPALQGLLGPGTRLAVTELRGRARLCPESGDSSRPPPPPVVSSFAVSGTVRRLQGVLGGTGDSLGVSRS

CLRGLGLFQGEWVWVAQARESSNTSQPHLARVQVLEPRWDLSDRLGPGSGPLGEPLADGLALVPATLAFN

LGCDPLEMGELRIQRYLEGSIAPEDKGSCSLLPGPPFARELHIEIVSSPHYSTNGNYDGVLYRHFQIPRV

VQEGDVLCVPTIGQVEILEGSPEKLPRWREMFFKVKKTVGEAPDGPASAYLADTTHTSLYMVGSTLSPVP

WLPSEESTLWSSLSPPGLEALVSELCAVLKPRLQPGGALLTGTSSVLLRGPPGCGKTTVVAAACSHLGLH

LLKVPCSSLCAESSGAVETKLQAIFSRARRCRPAVLLLTAVDLLGRDRDGLGEDARVMAVLRHLLLNEDP

LNSCPPLMVVATTSRAQDLPADVQTAFPHELEVPALSEGQRLSILRALTAHLPLGQEVNLAQLARRCAGF

VVGDLYALLTHSSRAACTRIKNSGLAGGLTEEDEGELCAAGFPLLAEDFGQALEQLQTAHSQAVGAPKIP

SVSWHDVGGLQEVKKEILETIQLPLEHPELLSLGLRRSGLLLHGPPGTGKTLLAKAVATECSLTFLSVKG

PELINMYVGQSEENVREVFARARAAAPCIIFFDELDSLAPSRGRSGDSGGVMDRVVSQLLAELDGLHSTQ

DVFVIGATNRPDLLDPALLRPGRFDKLVFVGANEDRASQLRVLSAITRKFKLEPSVSLVNVLDCCPPQLT

GADLYSLCSDAMTAALKRRVHDLEEGLEPGSSALMLTMEDLLQAAARLQPSVSEQELLRYKRIQRKFAAC

>gi|124378039|ref|NP\_055681.1| protein transport protein Sec16A [Homo sapiens]

MQPPPQTVPSGMAGPPPAGNPRSVFWASSPYRRRANNNAAVAPTTCPLQPVTDPFAFSRQALQSTPLGSS

SKSSPPVLQGPAPAGFSQHPGLLVPHTHARDSSQGPCEPLPGPLTQPRAHASPFSGALTPSAPPGPEMNR

SAEVGPSSEPEVQTLPYLPHYIPGVDPETSHGGHPHGNMPGLDRPLSRQNPHDGVVTPAASPSLPQPGLQ

MPGQWGPVQGGPQPSGQHRSPCPEGPVPSGVPCATSVPHFPTPSILHQGPGHEQHSPLVAPPAALPSDGR

DEVSHLQSGSHLANNSDPESTFRQNPRIVNHWASPELRQNPGVKNEHRPASALVNPLARGDSPENRTHHP

LGAGAGSGCAPLEADSGASGALAMFFQGGETENEENLSSEKAGLSGQADFDDFCSSPGLGRPPAPTHVGA

GSLCQALLPGPSNEAAGDVWGDTASTGVPDASGSQYENVENLEFVQNQEVLPSEPLNLDPSSPSDQFRYG

PLPGPAVPRHGAVCHTGAPDATLHTVHPDSVSSSYSSRSHGRLSGSARPQELVGTFIQQEVGKPEDEASG

SFFKQIDSSPVGGETDETTVSQNYRGSVSQPSTPSPPKPTGIFQTSANSSFEPVKSHLVGVKPFEADRAN

VVGEVRETCVRQKQCRPAAALPDASPGNLEQPPDNMETLCAPQVCPLPLNSTTEAVHMLPHAGAPPLDTV

YPAPEKRPSARTQGPVKCESPATTLWAQSELPDFGGNVLLAPAAPALYVCAKPQPPVVQPPEEAMSGQQS

RNPSSAAPVQSRGGIGASENLENPPKMGEEEALQSQASSGYASLLSSPPTESLQNPPVLIAQPDHSYNLA

QPINFSVSLSNSHEKNQSWREALVGDRPAVSSWALGGDSGENTSLSGIPTSSVLSLSLPSSVAQSNFPQG

SGASEMVSNQPANLLVQPPSQPVPENLVPESQKDRKAGSALPGFANSPAGSTSVVLVPPAHGTLVPDGNK

ANHSSHQEDTYGALDFTLSRTLENPVNVYNPSHSDSLASQQSVASHPRQSGPGAPNLDRFYQQVTKDAQG

QPGLERAQQELVPPQQQASPPQLPKAMFSELSNPESLPAQGQAQNSAQSPASLVLVDAGQQLPPRPPQSS

SVSLVSSGSGQAAVPSEQPWPQPVPALAPGPPPQDLAAYYYYRPLYDAYQPQYSLPYPPEPGAASLYYQD

VYSLYEPRYRPYDGAASAYAQNYRYPEPERPSSRASHSSERPPPRQGYPEGYYSSKSGWSSQSDYYASYY

SSQYDYGDPGHWDRYHYSARVRDPRTYDRRYWCDAEYDAYRREHSAFGDRPEKRDNNWRYDPRFTGSFDD

DPDPHRDPYGEEVDRRSVHSEHSARSLHSAHSLASRRSSLSSHSHQSQIYRSHNVAAGSYEAPLPPGSFH

GDFAYGTYRSNFSSGPGFPEYGYPADTVWPAMEQVSSRPTSPEKFSVPHVCARFGPGGQLIKVIPNLPSE

GQPALVEVHSMEALLQHTSEQEEMRAFPGPLAKDDTHKVDVINFAQNKAMKCLQNENLIDKESASLLWNF

IVLLCRQNGTVVGTDIAELLLRDHRTVWLPGKSPNEANLIDFTNEAVEQVEEEESGEAQLSFLTGGPAAA

ASSLERETERFRELLLYGRKKDALESAMKNGLWGHALLLASKMDSRTHARVMTRFANSLPINDPLQTVYQ

LMSGRMPAASTCCGDEKWGDWRPHLAMVLSNLNNNMDVESRTMATMGDTLASRGLLDAAHFCYLMAQAGF

GVYTKKTTKLVLIGSNHSLPFLKFATNEAIQRTEAYEYAQSLGAETCPLPSFQVFKFIYSCRLAEMGLAT

QAFHYCEAIAKSILTQPHLYSPVLISQLVQMASQLRLFDPQLKEKPEEESLAAPTWLVHLQQVERQIKEG

AGVWHQDGALPQQCPGTPSSEMEQLDRPGLSQPGALGIANPLLAVPAPSPEHSSPSVRLLPSAPQTLPDG

PLASPARVPMFPVPLPPGPLEPGPGCVTPGPALGFLEPSGPGLPPGVPPLQERRHLLQEARSPDPGIVPQ

EAPVGNSLSELSEENFDGKFANLTPSRTVPDSEAPPGWDRADSGPTQPPLSLSPAPETKRPGQAAKKETK

EPKKGESWFFRWLPGKKKTEAYLPDDKNKSIVWDEKKNQWVNLNEPEEEKKAPPPPPTSMPKTVQAAPPA

LPGPPGAPVNMYSRRAAGTRARYVDVLNPSGTQRSEPALAPADFVAPLAPLPIPSNLFVPTPDAEEPQLP

DGTGREGPAAARGLANPEPAPEPKVLSSAASLPGSELPSSRPEGSQGGELSRCSSMSSLSREVSQHFNQA

PGDLPAAGGPPSGAMPFYNPAQLAQACATSGSSRLGRIGQRKHLVLN

>gi|209571464|ref|NP\_001129365.1| probable ubiquitin carboxyl-terminal hydrolase FAF-X isoform 1 [Rattus norvegicus]

MTATTRGSPVGGNDNQGQAPDGQSQPPLQQNQTSSPDSSNENSPATPPDEQGQGDAPPQIEDEEPAFPHT

DLAKLDDMINRPRWVVPVLPKGELEVLLEAAIDLSKKGLDVKSEACQRFFRDGLTISFTKILTDEAVSGW

KFEIHRCIINNTHRLVELCVAKLAQDWFPLLELLAMALNPHCKFHIYNGTRPCESVSSSVQLPEDELFAR

SPDPRSPKGWLVDLLNKFGTLNGFQILHDRFINGSALNVQIIAALIKPFGQCYEFLTLHTVKKYFLPIIE

MVPQFLENLTDEELKKEAKNEAKNDALSMIIKSLKSLASRVPGQEETVKNLEIFRLKMILRLLQISSFNG

KMNALNEVNKVISSVSYYTHRHGSSEEEEWLTAERMAEWIQQNNILSIVLRDSLHQPQYVEKLEKILRFV

IKEKALTLQDLDNIWAAQAGKHEAIVKNVHDLLAKLAWDFSPEQLDHLFDCFKASWTNASKKQREKLLEL

IRRLAEDDKDGVMAHKVLNLLWNLAHSDDVPVDIMDLALSAHIKILDYSCSQDRDTQKIQWIDRFIEELR

TNDKWVIPALKQIREICSLFGEAPQNLSQTQRSPHVFYRHDLINQLQHNHALVTLVAENLATYMESMRLY

GRDNEDYDPQTVRVGSRYSHVQEVQERLNFLRFLLKDGQLWLCAPQAKQIWKCLAENAVYLCDREACFKW

YSKLMGDEPDLDPDINKDFFESNVLQLDPSLLTENGMKCFERFFKAVNCREGKLVAKRRAYMMDDLELIG

LDYLWRVVIQSNDDIASRAIDLLKEIYTNLGPRLQVNQVVIHEDFIQSCFDRLKASYDTLCVLDGDKDSI

NCARQEAVRMVRVLTVLREYINECDSDYHEERTILPMSRAFRGKHLSFIVRFPNQGRQVDDLEVWSHTND

TIGSVRRCILNRIKANVAHTKIELFVGGELIDPGDDRKLIGQLNLKDKSLITAKLTQISSNMPSSPDSSS

DSSTGSPGNHGNHYSDGPNPEVESCLPGVIMSLHPRYISFLWQVADLGSSLNMPPLRDGARVLMKLMPPD

STTIEKLRAICLDHAKLGESSLSPSLDSLFFGPSASQVLYLTEVVYALLMPAGAPLADDSSDFQFHFLKS

GGLPLVLSMLTRNNFLPNADMETRRGAYLNALKIAKLLLTAIGYGHVRAVAEACQPGVEGVNPMTSVNQV

THDQAVVLQSALQSIPNPSSECMLRNVSVRLAQQISDEASRYMPDICVIRAIQKIIWTSGCGGLQLVFSP

NEEVTKIYEKTNAGNEPDLEDEQVCCEALEVMTLCFALIPTALDALSKEKAWQTFIIDLLLHCHSKTVRQ

VAQEQFFLMCTRCCMGHRPLLFFITLLFTVLGSTARERAKHSGDYFTLLRHLLNYAYNSNINVPNAEVLL

NNEIDWLKRIRDDVKRTGETGVEETILEGHLGVTKELLAFQTPEKKFHIGCEKGGANLIKELIDDFIFPA

SNVYLQYMRNGELPAEQAIPVCGSPATINAGFELLVALAVGCVRNLKQIVDSLTEMYYIGTAITTCEALT

EWEYLPPVGPRPPKGFVGLKNAGATCYMNSVIQQLYMIPSIRNGILAIEGTGSDVDDDMSGDEKQDNESN

VDPRDDVFGYPQQFEDKPPLSKTEDRKEYNIGVLRHLQVIFGHLAASRLQYYVPRGFWKQFRLWGEPVNL

REQHDALEFFNSLVDSLDEALKALGHPAMLSKVLGGSFADQKICQGCPHRYECEESFTTLNVDIRNHQNL

LDSLEQYVKGDLLEGANAYHCEKCNKKVDTVKRLLIKKLPPVLAIQLKRFDYDWERECAIKFNDYFEFPR

ELDMEPYTVAGVAKLEGDNVNPESQLIQQNEQSESEKAGSTKYRLVGVLVHSGQASGGHYYSYIIQRNGG

DGEKNRWYKFDDGDVTECKMDDDEEMKNQCFGGEYMGEVFDHMMKRMSYRRQKRWWNAYILFYERMDTID

HDDEVIRYISEIAITTRPHQIVMPSAIERSVRKQNVQFMHNRMQYSLEYFQFMKKLLTCNGVYLNPPPGQ

DHLSPEAEEITMISIQLAARFLFTTGFHTKKIVRGSASDWYDALCILLRHSKNVRFWFAHNVLFNVSNRF

SEYLLECPSAEVRGAFAKLIVFIAHFSLQDGPCPSPFASPGPSSQAYDNLSLSDHLLRAVLNLLRREVSE

HGRHLQQYFNLFVMYANLGVAEKTQLLKLSVPATFMLVSLDEGPGPPIKYQYAELGKLYSVVSQLIRCCN

VSSRMQSSINGNPSLPNPFGDPNLSQPIMPIQQNVVDILFVRTSYVKKIIEDCSNSDETVKLLRFCCWEN

PQFSSTVLSELLWQVAYSYTYELRPYLDLLLQILLIEDSWQTHRIHNALKGIPDDRDGLFDTIQRSKNHY

QKRAYQCIKCMVALFSSCPVAYQILQGNGDLKRKWTWAVEWLGDELERRPYTGNPQYTYNNWSPPVQSNE

TSNGYFLERSHSARMTLAKACELCPEEEPDDQDAPDEHESPPPEDAPLYPHSPGSQYQQPYTGPAAHHMN

NPQRTGQRAQENYEGSEEVSPPQTKDQ

>gi|8394121|ref|NP\_058930.1| peroxisome biogenesis factor 2 [Rattus norvegicus]

MAAREESTQSANRVLRISQLDALELNKALEQLVWSQFTQCFHGFKPGLLARFEPEVKAFLWLFLWRFTIY

SKNATVGQSVLNIQYKNDSSPNPVYQPPSKNQKLLYAVCTIGGRWLEERCYDLFPNRHLASFGKAKQCMN

FVVGLLKLGELMNFLIFLQKGKFATLTERLLGIHSVFCKPQSMREVGFEYMNRELLWHGFAEFLVFLLPL

INIQKLKAKLSSWCIPLTSTAGSDSTLGSSGKECALCGEWPTMPHTIGCEHVFCYYCVKSSFLFDMYFTC

PKCGTEVHSVQPLKSGIEMSEVNAL

>gi|19115812|ref|NP\_594900.1| peroxisomal membrane protein Pex22 (predicted) [Schizosaccharomyces pombe 972h-]

MLGQGLIFISLAFVAHALEIPISCAVSHNEQTEIFPHGTIDIPEMTFRPSDSQIDWSNLSHSDFVQCGVY

EDSTNTWLAGASKYKIDEIKTLPKVPRDHYIILCDSSESNEIAKFTQVVHSFDFSSDSESAVVEQLHPSS

PIPILTTAVRKKGSRPSKPQKEKQGNKQGSKTEESPNVDEDELESEPEEKTFFQKYGLYLIPILFLIIMS

GNNANQQAANTAK

>gi|308198098|ref|XP\_001386837.2| predicted protein [Scheffersomyces stipitis CBS 6054]

MSDDKYRSTATKVLSSVYQASSDFADAHQGQNRGAAAGTAAALLSMGIDRVNRTGKSASRSGSLDLDYTD

EQLEHIRQMASSAEENELKKHRDHFVDKLMDKMLKYTIPDDSPDKAIFEQKINDPSRSERPNLSIRILLS

NFKKLAGKMGMFFELQYGIIHIITWRKPTKTLTALVLYTTICLWPHLVVTYPLIFLLFGIIVPGYLHRHP

MRTPELIKVKKRGQSLFSFLNEGAGEHSIIDDLLSDSVLGDEGLRPTFSGSEESSDVLQISPSEVISETS

VSTDDSKKPIAKSQLALLINMRDLQNLTTDLLNGMDLAEKSWFETFGFKDEHLSTFIFYGVAAATSVVLF

LGQFIPWRLIFIQSGWAGILLCHPKSKTFLVELSNAKKARAAKAPQPEEIIESEVKKFETNDIIVDDAPE

RRIVEIFELQKKSILHEKWTFYSYSGNIFDTKKKTRLAGKRPGGVDHLSKVVPPKDWLFDFGFANKWTID

YEPQEFLRQRSLESKNLVIREGEKSGWIYDKDVESQSSDITYEFRRRRLYRECLRYGRAPKGSRKS

>gi|145342435|ref|XP\_001416188.1| Novel AAA ATPase [Ostreococcus lucimarinus CCE9901]

MARSREILECFFPVCQFSFQQYENNLCDDCTRPSEMHNANFMLLMLDSPKAHGAALRHTMLRRIQRVFAK

QQVTWTGFQVTLPCEGSPRIKKPSFSLQVAKISSRDGNHLLYEPVDTRIVVKARENEFVPYKHTMVVSQD

FRARFEAVKSALIRLSSPLNCSSGRLASDTPLLLKQSSKHFLRWLQSKLQSSVRMQSRVISCQYLVLLKS

QKQISLIIERALTGIDSDTALILEDVDVLVKDKDGLNLQCLLSTLNDIADFRTIQGSFHTFIIGTTAEFK

VHSDLHRHFPLQIPSPSQDSDVHVQQIRRDEGLKQIRLKVQSALSIGGHRQQKAMRIVPLSTSQQNNGNV

RWDDVGGLEDIKAALCDMLKWPIKFPKLFKNYSKGALLHGPPGTGKTLIAKAASVESGLTFFNVKGPELL

GMYVGESEKCVRELFNKARELAPALIFFDEFDSLCMVDAPPGTLISRVISQVVTELDSLKGSQVFVLAAS

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RAWIKAAKRAIAYNSTGIVVQTMDFY

>gi|302914878|ref|XP\_003051250.1| predicted protein [Nectria haematococca mpVI 77-13-4]

MDDFTTEIIASGRAFDSPESPERHRRVSAGSHDEEPVVEAEATTPAPPQKTGLRGGLAAIRQKASLQDRL

VEKLLQQVIPADKDDPNDVAFAADDHAPTQTERPNFNITTMSYNFRRFNARIGVVFKFQARVGRILCWHR

ASHTLSLLAVYTFVCLDPYLLCVLPVAILLLGVFIPAFLARHPAPPKGTLSSEQNVGYSPRGPPLAPAAT

VKPVKELSKDFFRNMRDLQNSMDDFSEGHDKVVAFLVPVTNFSDEALSSALFLFLFAGGIFMTIAAQLIP

WRFVFLLGGWAVIGMGHPYVARLLAVAHRERLQPQEAKARSWLDDWIAKDVILDSSPETREVEIFELQRK

IAGGSGEWEPWLFCPSPYDPLSQPRIAGERPRGTRFFEDVMPPEAWEWSEKKWALDLWSREWVEERIITG

VEVETEGERWVYDIYDERDERTGVVDPPIHDKGKQKAAAAKPSWEEGEDGSGRRGDWRRRRWVRLVKRKA

APVQPV

>gi|115473295|ref|NP\_001060246.1| Os07g0608900 [Oryza sativa Japonica Group]

MGSSEMAFGLYYHLPKRAAGIRYVFIGKPMIQRPRYQILGIFLLIQLCILGAERLRRSNLSTIASSINQI

SSGSYPSSRGGTFFF

>gi|115462951|ref|NP\_001055075.1| Os05g0275700 [Oryza sativa Japonica Group]

MTDPETLPSPSASTDSSSPPPDAWAAEYRRLLPQWESMRDSSKIAIPISISRVNQFDAARLDVEMSAMLK

EQLVKVFSLVKPGLLFQYEPELDAFLEFLIWRFSIWVDKPTPGNALMNLRYRDERAAPITGKEVRTGLEG

PGLSVSQKVLYCISTVGGQYIWSRLQSFSAFRRWGDSEQRPLARRAWGLVQHAEGLYRASSFFNLLLFLY

GARYKTIVERILKARLVYESPNMNRAVSFEYMNRQLVWNEFSEMLLLLLPLLNSSSVKKFLLPFSKDKSA

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>gi|115473293|ref|NP\_001060245.1| Os07g0608800 [Oryza sativa Japonica Group]

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RGIALEDSQLDDHSESDSSSIGTAAQPSPIRNSPSRSLSFSHLSRLRGRVHTLWEWVLRKWPSMLPFAQD

FIQLTIRTNLMFFYFEGLYYHLPKRAAGIRYVFIGKPLNQRPRYQILGIFLLIQLCILGAERLRRSNLST

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GHVFCWSCIMEWCNEKPECPLCRTPITHSSLICIYHSDF

>gi|295671687|ref|XP\_002796390.1| integral peroxisomal membrane protein [Paracoccidioides sp. 'lutzii' Pb01]

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PAVLAAADGAPPTVAAFAPTTISGLSLASRQRSTIVVHRKSPLLVATPPPVTRALAYSHPFLLPLNRLAG

LLSWTTGDPWESFLLVACFCATVLYGDVILLWAGPILVVLGLILAMYSRRYSPLSSTGLTGEKHGSHGVG

DGASQHLKSLDEIVETLRTFTTRCNILLEPLLELTDFLSTQRTATSATTRPALTSLTIRVVLMTPVWILL

TLPPFRLITPRRVILSVGTVIITWHSKPARISRVILWRSLTVRRICSVVTGLPFSTTPSPISRDSDATSK

SSILSLNLFRRKSSNYASAISMKQRRANSSGVRFTFILYENQRRWLGVGWTYSLFAYERAAWTDEHLNPA

PSIDDFELPEVEGGNAKWKWVPGSEWRIDTVPSDFSSKRSFKSSQKDNGGNSDNDEGWIYYDSKWSDGRR

GKDGWGRYTRRRKWCRDAELVEITPSTESTPPPSSTEEQGSSSSLPQTNNSKGDDDISDTEGRTSPPSDS

RKPRQRRWFGSSELSKALASPPGSASSLPLSNGDSLSTALATGADSGTMAKQPSPSIPNVRATSYSNSFP

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>gi|294658956|ref|XP\_461288.2| DEHA2F21758p [Debaryomyces hansenii CBS767]

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FAQSLSLSDKHQVTLNLKLNNFETTQINLEPVTSSDWELVELHAQILEDKLLSQSRCVSLNQVLVVYPSQ

TTSAKLIVTDIGTKDHNYAKISPMCEVAIAPKVRVKKAESTSGKSTKSSKSSRAEDYSNLPSVLKRGISL

PHNIFSDLPSHSNPDGYEIYVNFNEVIHSLNKAEYVAVSIVPGPNSKQNIVGSGNQNPEQNQNQNQTLTK

ENSKEKISSPLKETKRVIAKLVNCPKCPSNTVGLSAKLAVALNVEYQVGSIVVLNPSVKHISKKPSSFVI

HPYILQTKKTDQINLNSIEKKDKNTKLLQALTTLFYNEESPINNSPITNYIKLPIVPHLLPNGGLLKFKR

NDDVNAWIKPFTFSDEKKQIKLETGEELIRNQSFIQEIKSESEEKDEVIGLDNMIEEALDSITINKNSGT

LIYGNSGSGKTSMLNLIASKINSDYGYHTKYISCEKIMNENFNSLSNNHAMKWIQECSWHKPSLLILDNL

DKILPAEMEHVDSAVSNQLTEFLITRLQKIYSQHNSNLSILISATSKEALNKLLFQCHLLEHFHHLSPPD

KNTRLDIINGYITDKLGCNIQFDVMDMVSETEGYLPNDLKILCDRIYHESLFSQAQSASQNNLKIAKEHF

EKALKGYTPSNLRGVKLQKSSISWSDIGGLKDAKNILLETLEWPTKYAPIFANCPLRLRSGILLYGYPGC

GKTLLASAIAGQCGLNFISIKGPEILNKYIGASEQSVRELFERAQSAKPCILFFDEFDSIAPKRGHDSTG

VTDRVVNQMLTQMDGAEGLDGVYVLAATSRPDLIDSALLRPGRLDKSVICDMPSFEDRLDILESITTKMD

LMEDVNLKQIAEKTAGFSGADMQGLGYNAYLKAVHVKLSNDELQAVKGEKHNTKDKISFDFFQVNSEKLK

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KIYNQFVSGRDGNMPDGTPNNEVGGRTTLM

>gi|294658425|ref|XP\_460760.2| DEHA2F09174p [Debaryomyces hansenii CBS767]

MSKVNDNALPFADASTIVRAHQKDTYFESSYRSQVQDVLHLFKGQRFINTHPEEITVAAKSLYLMLTTLI

GARTLGEEYVDLIYVNRSGKRFPQLLSKLGFILSYALLPYLFTRLVRKYKPKDGDESSKPKDGTKDWLVQ

FFSSYPKVLDTLMNLHIAIFYFKGEFYSLSKRIFGLRYAFGHNKDPKKLRLARGDYSLLGGIILLQFFVK

SLIKFKSYIDDKNKVNQPENEENEKNVNAIFKISQLENFRDKVTTNNKLYKQINVDLSNPDHLPYLPENS

RACMLCLSPMTNPSAASCGHLFCWECIVDWVRDHPECPLCRQQCLEQNLLPLK

>gi|294657662|ref|XP\_459967.2| DEHA2E15224p [Debaryomyces hansenii CBS767]

MDQVSNFFENILTVEANEKESDAKGKTTQNELKQSKLMSDKSKRKSESDFAFWTHKKEGNDEQKSTNTLL

TDKLMEKIISMVIPMNVKDQGALNERLEMQKTRPPLSVNLISKNSILLNSRLSVPFETIDGVIKFFNWDN

SSFTVGILLVITHIILNPYLILVLPLLLILINIMVPHYLVLHPTDRSVLNSMYFQRNPVPDDGPALRESE

IPKPVPEFSNEFILNLTDLQNHMLLYVVTYDLILWGTKEFLFYKDENISSVVFLGLLILGLHNLFVLPKV

VPILFWYLPIRFMLVISIWAVAILFHPVVRNRLLNWMYNEETRLYFVNLDNQIEEFLLDLIVKVDDEQVK

IETKQVEIFELQRYDKTSKIWELNGFTNDFYTINSPMRKLKQEYLKGKNNDKNDDEEDGEKSENVDINTV

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QSSIKDINQSNSGSVYSDYLL

>gi|294657353|ref|XP\_002770444.1| DEHA2E08184p [Debaryomyces hansenii CBS767]

MDAANCGPSNALQNLSKHTQRDNTLQNEIIRNQPQQGNGFRNQAIVDQRLNQDFQQFSNGQAFNQYQPEP

VHQQFHQHHRQHNQAQHSQHHPQQGWVQDFSKMSINQQPRHQAGNIQNGKVQNDWHQQFMNQTSQHPAQN

NVAYQPQHQMGGFRMNMRTNLSNSLYQTRGNVPEHKEMHKMEEENQIFDAQFDQMERELQHENMSNEQTA

EVQMDGNEFEKEQFAKTAKQVQESMLKGENAETNAKFQNSNFLKLMSSISNRSVELSAEGDKLVSKQSGE

DIRDNPEVVTSQTPTPVPVSQYDQYTNHIPMSQDDMPTQEPQTSHLPDPLAHIKKGSIEGDVSPFQAAQI

VTGNQVKTSDWMEDDDWLDMTEDAPFPVMGGPQRMPPKHPRNNIMSDEWQEVYDDYKHDDDFN

>gi|294654580|ref|XP\_456637.2| DEHA2A07172p [Debaryomyces hansenii CBS767]

MSGKQSNHNGENLGNKSSGSKVHSSPNSGKVEGSGESKDNTAEIRAVFTSSDSKQDEESKSRPQTSPLLS

STPPSVAKSLVRSYPYLLIVNKFLSIITWTNDDYWINIILVCLYSLAILYFENLVTWSGHLIIVGIITLY

ALLNNKIIEETNLHPTLDDVVQALTTTCIKADMLLNPITSLSLTAYDIKRLLFTTVFLTPLYLIVTFLLV

KPRIILLFTGLHILTYHSSYSRVARKMLWKIKLVRVLCFYLTGLDFSQARNHSLFAAAFAKVHKNAGHSL

DLSSEASNKPVRFTYVIYENQRRWLGIGWTSNLLSYERTPWTDEFLNESSSLESFQLPNNENNDYSFGAQ

QSQQLSGSDTTWRWVDKTWRLDLTNDGAITLQNNKRSKTTANPATDEGYIYYDNTWKKPSTEDSFSKYTR

RRRWIRTAELVFNGSSDKTPSTEEEISSNSASIPGSSNSTTGAETGNSTKSAKKRKSLRFVDPESDTTDE

KTDGPESLAQVEKELAADEQDTKDLKRGVEELTSMAQEADFAGKKND

>gi|50405875|ref|XP\_456578.1| DEHA2A05874p [Debaryomyces hansenii CBS767]

MVADTILYHPTFGKLTRFLDSTPKREKCFRLVVYLSRFLSYYLQRQGFSPDVVNIFKDLKHHITIIRKGM

RFLKPLNHLQAAAQTFDNKLMDPVLQKTTVIKNLGYVGYLSLDSITWLKLMNILSAKRFPTISTWSSRFW

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ITSIMGLHDLWKSSK

>gi|294659651|ref|XP\_462048.2| DEHA2G11880p [Debaryomyces hansenii CBS767]

MTDKYDESLYASFQPSDAKLLTSSSHTQLLTEYPILSSALSNIFPYLLLIDNFLEIVTWTNEDPYQNFIL

IVLYSVIIMYWQILSFIIMPILISVTFACFVWSISSIIYDSKFNEKPTIDEVLHTLHNITIRFEMLLRPI

QHFPMKKRNFVKAFIMTFLLTPIHVLLVKYVIPPQKVLWLTGLFMLTYHSAWSFSIRRLLWRSVYIRIFA

FYVTGLNIKLDRTNQNHFMNISIIHSPNTSDIEDFDENQKPLQLLGDFKILKKTVISPTQLRQVVTFEIL

ENERRWVGVGWSKFVLPGDRPSYCYEQSMKPSPSISNDESFNFPIFENDLYTYSWEWLETNWKVDKEFNK

GKGSEGWVYYDNNWSTESYSDGFSKFTRSRKWVRKATLTIDKQDTVYDE

>gi|294654342|ref|XP\_456395.2| DEHA2A01298p [Debaryomyces hansenii CBS767]

MEYYSSLDASQLDSEIPTLFELISASQLESLLSPSLRYILVHYASKYPYLLLKVANNFEELNLFFRTFIE

WYFMSYWQGSFTENFYGLKRVSQTPLSDSKYKSSKLTQLVPSMIEDRRSLSGLQRFASIFEITGVSYLSE

KFNYWYEIWYPKYVTNQLVPNDPTNRADIYRTEFKRRFVKLYPILQSIFRTGNFITTLLYLSGSSKSPTL

LTILFKINYSRLNQYDYSKHEPKVASKKDTPNKIAPPTLAASIFRILNKNITKPSWRLINFILGTFFPVA

IFMLKFLEWYSNSNFASKIAKTQGNMLDSLLPPPSSLSRKRRLEDKPKKVYNSGKTCPLCKDEISNPAII

ETGYVFCYSCIYNYLAQSHKIISEKARLRREEMDSDTEESDNEKEDQNEKVDANATQEEKITIDVNKGGR

CPITGKKLLGCKWNGLKEEWEIEGIRRLIF

>gi|50423677|ref|XP\_460423.1| DEHA2F01386p [Debaryomyces hansenii CBS767]

MPQAQIRKTQRNPKLWIAALVAASIVTISYKVYSSYIAEENIEDKKTEGDGGVEEKLRIAKRYTKKSIAL

TLSHSVLSSQLPLNEILLNSENVTFILPPNLSMDDLVCNIGNADEVERYNLPKTLLNNYKLLHCSNIDGY

FNILKNLKPDTLLVCSEDLGIANNVPRDLHRFVKEIINIDQNKDDIYKKLSSIFIK

>gi|50420887|ref|XP\_458984.1| DEHA2D11858p [Debaryomyces hansenii CBS767]

MLSFRTAGYNGYGVQYSPFFDNKLAVATSANYGLVGNGRLFILGIEPNGSIGNPISWETQDGLFDVAWSE

IHENQVVAASGDGSIKIFDITVPNFPVMNYREHTKEVFSVNWNLVDKSNFVSASWDGTMKIWSPQRQESL

LTLSPKVDYTTKTSPVAQTAKPPLSHQQQHQQLNTTNCIYNASFSPHSPSTIISCNGSSHVQVWDIRSPH

PLQLDYIAHGGLEALSCDWNKYKSTIVASAGTDKSIRIWDLRMITGIDHPNSNSPMPAYHTIGPTPLNQL

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EPGWAASTGWDEMVYIWDSKRLA

>gi|260947698|ref|XP\_002618146.1| hypothetical protein CLUG\_01605 [Clavispora lusitaniae ATCC 42720]

MARKRNTRTWVALALATSVAAVAYKIYQEWLPNEDEQRESSNVKKIKSKYANKSVTLTLSHSVLNSDSSL

EEILLNSNNVTFILPPYLSVDDLQCNISGKRSMVVPEILQDNYKLLKCSNMQGYFQLLKNLRPDILIVCT

DDLGITEQIPKDLGRFVGKVVTIDQEKDKARTVLSEYF

>gi|255716150|ref|XP\_002554356.1| KLTH0F03322p [Lachancea thermotolerans]

MIVNKIDGDKLDNDLYSHLWALYDDKIKPTSNREEFKLLLKTLAFHFSTKSNGIQTTTYGSALAGTSFQT

AKLSLFAANILMPYLVQKLQTFLYNADNNLLPKIRIVETLISVWSLSTFIQLLSGSPKQYLSIFHKIFRI

KISTFMQSQFYQNTITASMEFQNTQLLYNALLQLLNNQVSQSKLIQKLLRSSTKKGIKRQNAFNCPYCDE

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>gi|255715137|ref|XP\_002553850.1| KLTH0E08602p [Lachancea thermotolerans]

MSEHPKERETRARFVEEPTARLGGKTNKVLRSALKNRGKKALGESEQEEVESSPLLTSTPPTVSKALVRL

YPYLIITDKVLSIITWTNDDIWPSVLVVVGYITSVLYFQNILKYFGHLVLVGILGCYSLLDMFVEESIKD

RPTLDDIVHIITCVNAKADLLLSPIAVLTGNDVKRLLFTTIFLSPLYVIITLFIFPPRRLLLFGGVYLLT

YHSAWSRVSRKLLWKFKLVRLLVFYITGLDLSGVNKNQGIFAAVQSKVKKMSSTRGISEEGKPIRFTYVL

YENQRKWLGIGWTSNMLSYERAPWSDEFINEAPSPENFRLPEENMGMTWRWVDRTWRLDLTNDGAIQLPS

SRPKTSAQPNSDEGFIYYDNTWKKPSTEDSFSKYTRRRRWIRTAELLRGDVLDVGGIMSSASAVDPTPQN

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SGITERSSARDLNVDPPPTSPPGAAVETKKHV

>gi|255714599|ref|XP\_002553581.1| KLTH0E02112p [Lachancea thermotolerans]

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PPSSELAKKTIEHRVEASRNRPGLSVPIMSRNFVQLNSRLGPPFQVIDEVIKIFNWTNTAYTLSVLSLFT

YTVMKPLPTLTSIPIFYLLFGVMVPQYLKIHKPDSSLVFASNPVPATGPPLVKAEVPKPVPEFSKEFILN

LTDLQNHMLLYVSAFDFVNGILARFAFFTDESTSSAAFLALLVLAWFNALFMDTLSRFIPLKSLLIISGW

ALALALHPRYRDHFLSKIYSEETRLRALMISSKVEKRVNEYFQYREPRELRQASIFEVQKLDTSIKTWGL

VGYSTDHYALFSDYRISEKGLEDASHTLEEVKAPLEWEWTKGSKWVQDLDPVSWVASEFVDYVDIDVEAK

WVYDACLDGSRGDYRRRRWIRQCTRIAEQISVSENTSSDTTDDVYQQGQFNGYASSFAPETVSGSTGVPK

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>gi|255713676|ref|XP\_002553120.1| KLTH0D09416p [Lachancea thermotolerans]

MESQLYEGFHSSQRLVDEFNMLQDNQPISFTEKDSSDEESTAEESQELQEVKHSHAVHHSAVVVRNIDVL

NHIFGTLGGKDRLAKILKYVLDLVKLFVSRSRIGITRWDPQVLEHYSKVLAQLNLRLLLRHPATIAKIMV

VAGLRNFEAKASLVSSNLSLFRQILRFGGTPFRVAALWSKINLTTHQIAAARAKPASAADSHTLAVINKL

WLNEASLGDFIDLYYGVMDELMLLHKFKVWHHPGLYTWVAKHESLSWYYDIMLGLKKNWCSLQQLNRAQL

ELSIQEQVKKRALELSSRLQGKTASPIKQQLLQDLQTGQEHNDQFSKRIRDIERQRRVVILDLVRLSFDF

LADTTDVFNLKTPPGTYAVLSLASGLTGLVKLWGNAKRELSESVV

>gi|255713572|ref|XP\_002553068.1| KLTH0D08184p [Lachancea thermotolerans]

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KLTLESYYLKTWDATFIEVFYGLKRINASDAVLLRTLQSNPPVEIPMRLTRFQRRAVLCEKVLAPYVALK

LDLLHSKLLARSLLQHPPAQEMGQRVRESLRTLYLRFYPLLKKLLFVLNLAVKLYFLSGRTGSTSLLDLI

LNIQYTRLSKYDYSRNDRSSTAPGQAVRSRPQRLNRSALLFLCRASFSKIKNLLKLSVSQMLPAFIFLLR

VFQWWSSQDLSGEIQRRLNNIDKDIPPPPGRFEKNTEGTCRICNGPIRNPAVIGTGYVFCYPCILDYLPQ

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>gi|255712051|ref|XP\_002552308.1| KLTH0C01826p [Lachancea thermotolerans]

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GITIDEDYDQFAQFVPSESSDGFWKDENFRQEYELGSELGSSQTSEPEKMAEKPKSERTRGTQEHFIDIL

LDKMISTILPENFPEREHFSQRLNDPDRKRRQKLSATILASNLKILTTKLGSIFELQDSVIRLVAWRNPS

GTITMLIMVTMICFNPIYLAVIPLLYVLYGLMVPGYMHRHPPRRTNFLSRKQYGRSLIVSLTSGGKRTHN

YLNEDIREYDYNLEADPQDVKKAHNIKQSMEFVVNLRDLQNSMSAMVSLSNSIERFVYGTAGFKDEHRST

VLFLAGLGALLLSGIISPFINWSALLAALAWLSMVAIHPKVRPKLAQVVKKEQLDRGKEALKRTERYDVI

LDEQPEVRVIEIFEIFKKEALSNNWSFVKYSSSVFDPRDSFRKAQVLPPGVDELECVCPPLTWSFDANSV

WEIDYNVGGWSTERCLNLQIDDQFLVDDAFKRRRLTRKVLRYASPARKPSYK

>gi|255715585|ref|XP\_002554074.1| KLTH0E13706p [Lachancea thermotolerans]

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STNILTVQDGASFARRAVESWVGTMSCVLLLLSFVYYISSVLHELNADEPPTLEDIIVMVETVVYKLEVI

RDDLREPLKMSSQELVTVLVFITPVHWLLMKYLFSSNDYLVFLVLFCSVYHSSWCQCTLRLLWRSLYVRQ

LLSLVCGRTRDAGGIGQAAFYVVNNSGIQVPRYTSPLEDLSSSSFSNRVRKALDGVYDPDLVSKHSSTPV

SAKVVEFRIDENQRKWPLDGWTQNMLPYERSKFTASQDPASAECSSPWKFQESLGREWCWLDDAWKPEPW

LYCDTHWIARGENDSLDCYTRRRMWKRRAFQCSH

>gi|255714625|ref|XP\_002553594.1| KLTH0E02464p [Lachancea thermotolerans]

MANSRKLEFADASAIVQSHQKDDQIESILTSKLADATRAIKGQYFSNVYSKEISTCAKLLYLALTTLRGR

RTLGEEYVDLLHVNRNGEKLPRMLQRLLFVLSHALIPYAYYKILGRLSRSKDAGGQNENGLQTPKSTLRK

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QFVTRNVPPIVTWLKKELIVSPLSDKTSSEIQNNASLVITGVPSKDIVNHVDLQDPAELSFIPSESRKCI

LCLSLMVDPSCAPCGHLFCWDCLLNWSKERPECPLCRQTCQTQSILPIR

>gi|255712125|ref|XP\_002552345.1| KLTH0C02684p [Lachancea thermotolerans]

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VAKNSILICYVERTIAKFKIQRLVPETLDIARLGTDTLVVISPMLNKSRIPNGKPKNHLEAFVTHSPHIL

RSICWDEDLKGYSVGVSPGDIKSPLAFVSIVRNPLEGKVQEDRPSDDTAIECAQRIAVKVVVIEHLESSQ

AVVSDLAWESLGVRKKNGEKVKIEYISNHVAAATPTVFIHPVDRSQDASDVVLNGENSYFDESFSEQIKT

MFSGCVLTDKAYLPSKLAYFELVSEHGKHVQFCEWNENKMGIKILDSAVRISRREPEQEAPKIHKEPLGF

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TAKNRDQLNQLLFSRHTISKTWPLTPPNKDQRRIFFENFVAEKSLQLSDDLDESMMAIETEGYSPQDILL

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TKYAPIFSECPLRLRSGILLYGYPGCGKTMLASAVAQQCGLNFISIKGPEILNKYIGASEQNIREIFERA

QAAKPCILFFDEFDSIAPKRGHDSIGVTDRVVNQMLTQMDGAEGLEGVYVLAATSRPDLIDSALLRPGRL

DKSILCGLPDERERLEILEAVVSSGNMELEPDCHLSSAAAATDGMSGADLQGLCYNAYLKAVHRSMASAP

LKEEKQTATRPSFEYFTLDETKGLPVEFLDRLQQKSANSDKPEDERAASGAPKISIQDLLEASSETKPSI

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>gi|255712017|ref|XP\_002552291.1| KLTH0C01430p [Lachancea thermotolerans]

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DAWVNQFSNMHIKDPLSFSSEYQRLYSSYEQPQAVRPAQPQTLHAVQPQYQRQFYPSSYSQSLSQQFSQS

FTADNSALFDSEFDQIEQEEAAQQQQQQQQQGPAAQDTATAVPALDDEQAKFQQAATEIYARLSPGPQTP

PEMEAKLHNPKLQNSKFLGLMRRISDGVVTLQNDQNSQKYTQLYSPTTGEVVGNEYFPVVDAILEP

>gi|254585799|ref|XP\_002498467.1| ZYRO0G10978p [Zygosaccharomyces rouxii]

MSDNSAKDRETRAQFVDEPTNRIGGNTTKVIRSALKKRSGSGQDDSDDSGAIVSSPLLTSTPPTISKALV

KLYPNLIVVDRTLSLLTWTSDDIWPSVLMVLSYMAVILYFETIAKYFGHLVVVAIMWGYSQLDNHVEETL

STHPTLDDIVYVMNRVITKADILLSPITILSAQDIRKLLFTTAFLSPIYVIITLFILPPRKLLFIGGIYV

LTYHSSWSKVTRRLLWRFKLVRLLVFYVTGLDLGGISRSQGIFAAVHKQMNNLSGTNNDSDEGWPIRFTY

VLYENQRRWLGIGWTSSMLSYERSPWTDEFFNEAPPPDQFQLPDENTGMVWRWVDKTWRLDNTNDGAIQL

SSTKPKTTASPNADEGFIYYDNTWKKPSTEDSFSKYTRRRRWVRTAELLKIKNVEGTESPNITVDSTSHN

STSQAANTDTGGSGHSTAIAPENSNHQNGSKPHENLKRRGVSFSDVQNVHIVPLENEDEDESKNESSNDD

GNYHDNQLDAENKNESTPLLRD

>gi|254579232|ref|XP\_002495602.1| ZYRO0B15246p [Zygosaccharomyces rouxii]

MSAPRKREIMKTYFTKRYEKVLDSLMVADTTAAVATLVNGDSKRASGLPNLEVVHGVASSLFNASLEKLK

PNKDKEDLTLEKATESSDEFWKDENFKQEIHSESPNSYIETDQDQDQEASKVEAKTRQHFIDIFVEKLIA

KMVPERLPERERLFQSNSEDEKLGYQTVSATKLTQNLKDLSAKTGGMFETQDTIVRLLTWRNPSGTITML

ILLTMICFNPMCFLVFPLLYIMYAMMVPGYMRRHPLRRTLYPIRRANGKSLLRELANGGIPKSSQPPYSF

DLYRTNSDSLKDENVNNGAELVANIRDFQNATTSLLSFLSSLEKFKYGTAGFKDERFSTLVFLAYFIGFC

ILGLVSPYINWSLVISFALWFGMLVIHPKTLPRIKKHINTNPVHHSKRTIRDSEKYDVILDEPPEVRFVE

IFEIYEQGITPRHWEFFKISSQVFDSSDKFRKLQKPPPGVDSLSEVLPPKTWSFDENSQWEVDYDAEKWA

FERGLLLPIQEEFLTDDMFKRRRLTRKVLRYANPIRKPFYKYK

>gi|254577673|ref|XP\_002494823.1| ZYRO0A10472p [Zygosaccharomyces rouxii]

MSTCVSLKVRKVNLHYKTVHQPKSDMAKEASDYYCRAHFIYHHGQKPSLTLVTPATMSSVLHRIYPLLLI

ADATLSNLMWICEDLCLPFIHLVMVLMVVNFLCEDLQVDISHIAQLWLGLMSLFFLAFSVAYYILTLYQD

LLYESEPPTVDDIVIVLESVVDKLETIQHEGLSVNKRRALQLAVLLTPLHWGLIKLVSMKNYCMGFTLMC

ILYHSNWFQCTLKLFWRILLTRKVYYGLERLFNGHGPFPKKPVDFFRAISSSEYIYRMALPHDVKALHSH

KLQLRLQQLFPWDKPLHNDENGSDLMVIEFKINENQRKWQADGWTARMLPYERTKYSIELGGKINTCHSP

WQFQESDLKNWSWLDDCWRPTDWIYSDTNWDFKGVHDSLDCCTRTRAWKRRVYRLME

>gi|254579407|ref|XP\_002495689.1| ZYRO0C00638p [Zygosaccharomyces rouxii]

MTQRKSNGTIRWVRMAGTAAILAVGIGAAIYAWSQSSSLSQTDDNQGKSVQKTKGPSKAIIITKSVAQVE

GIDWIKLLQEDVVLLVPPGIPFLEDRDEEESPAHRYKIIRCDTMIGLWSCVKHLQKEQLLYVEEEIADGL

PNDLTRYVKELVNCKDSEHLKASCV

>gi|254577257|ref|XP\_002494615.1| ZYRO0A05610p [Zygosaccharomyces rouxii]

MSVKLGSGKPSGSSSGGATSTGSSSAGNGSGSSLSSAGIQKLLTDNLVEKIMRMALPPGSDVAINSLAKR

KQFAKDRPGLSVNTMSRNFRLMNARLSQPFAILDEIIEVFSWANPAYTISIMLIYTHAVMKPLPTLTSLP

IFYLLFGVMVPHYLYMHKPNYSMYLDGNPTPAQGLPLRKPVVPKPVPELSQEFILNLTDLQNHMMIYVSF

YDFISVWLTKFAYFTNEKISTAVFFILLVVGLINALFLDTLSKHLPVKGFFVAFGWFLAFMLHPKFREWF

LSRVNSEETRLRVLTLTNRFENIINEHLRYTEVRENKLVSVFEIQKFSEKDKCWVLVGFSNDDYTLFSDL

RIEQEDIALHCAPTLEEVKPPVEWEWVEAEDSWALDLEPIEWVEQGFIQYVDIDMGTKWVYDLTLEGKRG

GYRRRMWTNVCARQMDYHYVDTNGEEEEVVEEDDMVNLARVENYSHGHRRVSRDSMSGSSTHSEETKPAI

DRSESNNSINSVISPASPKKLPKGESFSGLGSLTDLLNMTV

>gi|254571411|ref|XP\_002492815.1| Peroxisome assembly protein 22 [Komagataella pastoris GS115]

MKSTKRNTFFGLAALGALGLGYSVYKSFITSDKSSSLINLGINQERKSYTRQKVAIIVSESILAIQLPIQ

EILKNTKDVVFVLAPTIAKDEFLRENEVDSGLSFKVIETGTAIGCFHVLKHIKATYNIFNLHDFLPSSTK

TSSDNEQLTFDLEEYVNLHLNNFLQNVVELPSDSTSIQETVNQYIYN

>gi|242219155|ref|XP\_002475360.1| predicted protein [Postia placenta Mad-698-R]

MATLNYVDIPSYATRLPSNPRADTARPSPKVITALPRPELSSSAASSPVSSQPLSSTLSPSKLALNSIPQ

LLLSSTLSIPANASATPRSNSSISGTGGAKGVPRLLSGRDPLSIPITTVNFRRFVSKVGPVFWLQDRLEE

IVMWRKGSKYTGVWMATYAFLCYFPRLFLLLPYVIVLSVIIATHPALNHPDEYDCEEAKAPIPPPPQTAE

GSVDWLANVQAIQNLMGAFRQTFLPALHNLFRRLLRARLACLVDNDRLDDRHWRAELREAELFENERWNA

GTGTGAEDDGEWAKGHLKPGERKAWTRGRDGWSGVDEDGASDVSSKLTFALEPGWAFVETEDWRPDVEGA

WAVLASADDDEDIELCIRVFTAPRWSPSCRWTSEGFGLSWCHCATLAKAHVGGHAYGLDCVPCGTEDLWH

SSQFRRSTPELVSLLYKGDWTFSVSSSVSIRFPLLRYSLSSEWIDPGVRSMTATTEGIPHLGHGPECPRV

VTARALSTSGVLNKVVTVSESDYLLHASQNKMIRSVGPAIEIMDTRI

>gi|242221835|ref|XP\_002476657.1| predicted protein [Postia placenta Mad-698-R]

MSRLSRISWARYDRHWRAELREVELFENERWNVGTGTGAEDDGEWAKSHLKPGERKAWTRGRDGWSGVDE

DGASDVSSKLTFALEPGWAFVETEDWRPDVEGEWAVPANADDAGWVYTNDSWLDPRPLPLSEWKIAGMTR

RRRWTRRVYYDPSVATQ

>gi|224015477|ref|XP\_002297392.1| predicted protein [Thalassiosira pseudonana CCMP1335]

MNASLKNHGCNSSKAKAKPMDTQPKIPRPYTSWLIYFQLQREWILQKQLGVVSASTEEYAFTTTDPSYEG

PPLPSRFQDLKLPIDWWKPGKGRRRKRLHRKSHGLISFHELSRMIGDSWKEVDVETRAFCDCLSAISMKK

YRELKASVADATAYVADATIGKTKKNKSGKEFKYSSPNRARANPIKKKGKRRVQDCRKCFASRTVAIVDD

EYRD

>gi|159486976|ref|XP\_001701512.1| predicted protein [Chlamydomonas reinhardtii]

MGRAATLDSVWPADGDPKTLLCVRVPCLAAELFKTLFVDPELQVQLHKQRNDSPLVETAWVASRDQLPPE

LYTWQAGGQRNEPGASLRFRKVRFESPPTALASKPFQNEETHVLTHWAPDQLYVLEAVSNTSAPYGDKFS

VFFKYIIRPDASSPGTASCVLHLLFCVDFLPSMNRMMKPVIAKAIFRSVLGGLRPGTADVAEAELPPGGL

LAGALASYSSSSGEESESEEDEAEGEGDEDKARKRHHHHHHHAFASAAPIPAPPTGPTPGAHPGMAAAPG

LLSVFSQQLVYKDQVVLLADLVGAGLRSVTHSELGAQALAALLTVWLISLAVLTSLALVAAINWALIRGS

EAAGKPGGTASMVWEQVVPQLPAGWRWVEDEWQIDLDGTEVEAVDGDGWSYALDFYLLKYPPPPQAGKCS

LKHFVRRRRLFRTRVRLPDRSLLDSDGSDLLGLQLQPLSPDARTRRPVAGAPLPAGPERKAGGGATAPAV

AVRTAVAGYAASPHAEHDSEPAARVSTEGYVLSPKTEVKAHDPLGALLQDEAAALAEPSSAAGGEGAALK

GAAIVGQEERGPAVGAEGEAGGTPTRADTGASGAGKQQARAARRTAAAHGHGSGAGAEGSGSAGDQAEED

LGGGAVVAADLVD

>gi|237835765|ref|XP\_002367180.1| zinc finger (C3HC4 RING finger) protein, putative [Toxoplasma gondii ME49]

MYELVTGTSSRDMLESMSAGVDRARSEENQAHAVVPTSPAASLANTDEAPVLHSGEYEVNSTTHPRRHPE

FRNTNIEETKERREIEDDGNVSCDEKANGMACLFCQGKCRGPTATACGHIYCWRCITRWILQQQRDQTAA

ACPVCR

>gi|237831105|ref|XP\_002364850.1| peroxisomal-type ATPase, putative [Toxoplasma gondii ME49]

MCPGRCCLGLTNSAPGVGSLSTSFSPLFTYETLRKLPPDSKFSSSISASPDRASSPTVGDELSLHNEKSA

VSIPRTRHRSAKSALKQDTQISNSSVEDPCGKQDESAARWRGGTDERVPLPTDQGFAARLAANALANVRG

CPGGQDALSSLSGNLFLAPEWERKVQHCLRWFYVEYIELGTQDLDVPASGVRTVLPPPVGVVSRQSTGLF

LQGRTTSRRLIPFGAHHCLRCPPSPVLPAIQEPLARFLSFATFLLNQSSTSTEGRSDRAAILLKGPRGSG

KRTLARHACQQLGFHFKEIDGLALSQGASGTAAAAGGDAPIGADMHRLQVARELIEAIHSTDETCSSPIL

QVSPTEVAEICTGLSAAEVHSLFHRVLHAKVAALRQAQSPAATGVVHPQETCKIPPIETMTATDFRRAVK

AFRSDTVDTTVPTVHWQDVGGIETAKQEIRDYISLPLERPELFDGLKTRGGILLFGPPGTGKTLLAKAVA

TECGVNFISVKGPELLNMYIGESEKNVRMVFQKARACKPSVLFFDELDALLPRRGRTSDSAGVLDRIVAQ

LLAEIDGLPSNVFVIGSTNRIELIDKAVLRAGRLDRCVYIGIEQNRIPLLETLTRHMTLEETCQDPTDPS

SCTGSICSARRRLLETVNNLLPPQFTGADCKSLCSIAGLLAAKEKINFLNDMSGKSLVFHDELLKEEKLQ

RRLIV

>gi|237835147|ref|XP\_002366871.1| peroxisomal biogenesis factor 11 domain-containing protein [Toxoplasma gondii ME49]

MALSKERDEVAHLVKFWSSTEGRDKSTKCLQYGSRTLASFLVTRNPKVAAKFAALNGTASDGRKIFRLGK

FLNEYVKVKAILIAFLRSRCKSAKLCWDDCQITQLLQLISRSGFLCYWVLDNLLLLSKIKFLGFDTKKLA

KLCGVFWFIGLLGSLANEARTLRRVQDEEQSHLDTLEREEARQDDKNFEACARETTKTLRKLRQEKTATS

LNIIKNAADLVVASNLAQIPHKIFGQPFPEGSVGTAGFISGAISCYQMYD

>gi|210075963|ref|XP\_505069.2| YALI0F06226p [Yarrowia lipolytica]

MAPRKTRLPAVIGAAAAAAAVAYLVYSFVAKSNSDQDTFDSSVQSSSKSSTKSPKSTATNSKITVVVSQE

LVQSQLVDFKHLMSVHPNLVVIVPPMVANKFHRALKSSVGHDHGVKVIRCDTDVGVIHVIKHIRPDLALI

ADGVGDNIQGEIKRFVGSSEALSGDVNLAAERLTGL

>gi|50554873|ref|XP\_504845.1| YALI0F01012p [Yarrowia lipolytica]

MSSVLRLFKIGAPVPNVRVHQLDASLLDAELVDLLKNQLFKGFTNFHPEFRDKYESELVLALKLILFKLT

VWDHAITYGGKLQNLKFIDSRHSSKLQIQPSVIQKLGYGILVVGGGYLWSKIEGYLLARSEDDVATDGTS

VRGASAARGALKVANFASLLYSAATLGNFVAFLYTGRYATVIMRLLRIRLVPSQRTSSRQVSYEFQNRQL

VWNAFTEFLIFILPLLQLPKLKRRIERKLQSLNVTRVGNVEEASEGELAHLPQKTCAICFRDEEEQEGGG

GASHYSTDVTNPYQADCGHVYCYVCLVTKLAQGDGDGWNCYRCAKQVQKMKPWVDVDEAAVVGAAEMHEK

VDVIEHAEDNEQEEEEFDDDDEDSNFQLMKD

>gi|50552149|ref|XP\_503549.1| YALI0E04620p [Yarrowia lipolytica]

MASQKRLIKELAAYKKDPNPCLASLTADGDSLYKWTAVMRGTEGTAYENGLWQVEINIPENYPLQPPTMF

FRTKICHPNIHFETGEVCIDVLKTQWSPAWTISSACTAVSAMLSLPEPDSPLNIDAANLVRCGDESAMEG

LVRYYVNKYASGN

>gi|50551763|ref|XP\_503356.1| YALI0D27302p [Yarrowia lipolytica]

MSDKEKKKSSATHAAFPPSTASQPQSMSPLLSSTPPTVTKALAQAYPYILASDKVLGLLTWTEDDQWQSF

LLVAVYVTVVMYYEYLVIYCGHILAVGFIWAFVYIRQSVERRQTSEPSLDAIVHTLTNVTTKANLLLLPI

TSLSLTPRDVTRLAFTTLFLSPLYMFGAYFFLGPRKFLLTTGVFFLTYHSMAARVTRAVIWKSKAIRLVT

FYLTGLDFSNTKRNLGAFGFTQSPLSVQSKDGKPVRFTYVLYENQRRWLGIGWTANLLAYERTPWTDEFL

NEVTPPSEFKLPDTEGTGMKWQWVDPTWRLDCTNDGALVIIGNKALSTPDPSPSEGWIYYDNTWKRPTAD

DSFSKYTRRRRWVRTAELITVTKPTDVVVTVEEDGVTDAAGDVEIITTETEEKVRRRKGIRFEEDS

>gi|50547523|ref|XP\_501231.1| YALI0B22660p [Yarrowia lipolytica]

MSHEEDLDDLDDFLDEFDEQVLSKPPGAQKDATPTTSTAPTTAEAKPDATKKSTETSGTDSKTEGADTAD

KNAATDSAEAGAEKVSLPNLEDQLAGLKMDDFLKDIEADPESKAQFESLLKEINNVTSATASEKAQQPKS

FKETISATADRLNQSNQEMGDMPLGDDMLAGLMEQLSGAGGFGEGGEGDFGDMLGGIMRQLASKEVLYQP

LKEMHDNYPKWWDEHGSKVTEEKERDRLKLQQDIVGKICAKFEDPSYSDDSEADRAVITQLMDEMQETGA

PPDEIMSNVADGSIPGGLDGLGLGGLGGGKMPEMPENMPECNQQ

>gi|50556438|ref|XP\_505627.1| YALI0F19580p [Yarrowia lipolytica]

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KGLTDDVSAEKLRGGKIADSDGNVMSDASDSELDTDGPEPINPHAKLSVKLMDKMLALALPPKSAAVAKR

VRIQQGQDPFSMNLMGKNFRGVTSRFTIIYETYYTVLEILMWKRPSFTLGVMAIYSFICLHPRLLFITPL

AYIMFCVMVPAYASRHYDVQENYLTTQWPTIEPKIPAPAPEFSRDFYINMVDTQNAMTDFIRTYDIVAGI

LAHLIYFAGDESLSAAIYFVGMLGVAIFYVYGDTILRIMPWRFFFFVFGWAVILLLNPMLHRIVLREYKK

LPHETREKFTPEAVKEVIDELARDEFLYHTADDVRVIEVFELQELDVHTRQWKTATYVAHPHIPSMLHEP

NYYADPDDLGLSPTASAGSVDSESRILPQFRHTNGIPDRTFSPPPTTMGEAIRNIEEEVSMATYGVSSLH

QIPAPPGVYSLEEVLPPTGWTFLEVPERDMLSSLPRSSDWEMDYMPEQWVAWWGAWRKYLEIDQDEKWVY

DILPDGFRGTWRRRRWTSLCKRKSYLKSNVVGRVGERREHD

>gi|50552646|ref|XP\_503733.1| YALI0E09405p [Yarrowia lipolytica]

MIPSCLSTQHMAPREDLVQSAVAFLNDPQAATAPLAKRIEFLESKDMTPEEIEEALKRAGSGSAQSHPGS

VVSHGGAAPTVPASYAFQSAPPLPERDWKDVFIMATVTVGVGFGLYTVAKRYLMPLILPPTPPSLEADKE

ALEAEFARVQGLLDQVQQDTEEVKNSQVEVAKRVTDALKGVEETIDQLKSQTKKRDDEMKLVTAEVERIR

DRLPKNIDKLKDSQEQGLADIQSELKSLKQLLSTRTAASSGPKLPPIPPPSSYLTRKASPAVPAAAPAPV

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NSAVKKPAPKASIPAWQLAALEKEKEKEKE

>gi|50552468|ref|XP\_503644.1| YALI0E06831p [Yarrowia lipolytica]

MASCGPSNALQNLSKHASADRSLQHDRMAPGGAPGAQRQQFRSQTQGGQLNNEFQQFAQAGPAHNSFEQS

QMGPHFGQQHFGQPHQPQMGQHAPMAHGQQSDWAQSFSQLNLGPQTGPQHTQQSNWGQDFMRQSPQSHQV

QPQMANGVMGSMSGMSSFGPMYSNSQLMNSTYGLQTEHQQTHKTETKSSQDAAFEAAFGAVEESITKTSD

KGKEVEKDPMEQTYRYDQADALNRQAEHISDNISREEVDIKTDENGEFASIARQIASSLEEADKSKFEKS

TFMNLMRRIGNHEVTLDGDKLVNKEGEDIREEVRDELLREGASQENGFQSEAQQTAPLPVHHEAPPPEQI

HPHTETGDKQLEDPMVYIEQEAARRAAESGRTVEEEKLNFYSPFEYAQKLGPQGVAKQSNWEEDYDF

>gi|50549581|ref|XP\_502261.1| YALI0D00891p [Yarrowia lipolytica]

MNKYLVPPPQANRTVTNLDLLINNLRGSSTPGAAEVDTRDILQRIVFILPTIKNPLNLDLVIKEIINSPR

LLPPLIDLHDYQQLTDAFRATIKRKALVTDPTISFEAWLETCFQVITRFAGPGWKKLPLLAGLILADYDI

SADGPTLERKPGFPSKLKHLLKREFVTTFDQCLSIDTRNRSDATKWVPVLACISIAQVYSLLGDVAINYR

RFLQVGLDLIFSNYGLEMGTALARLHAESGGDATTAGGLIGKKLKEPVVALLNTFAHIASSCIVHVDIDY

IDRIQNKIILVCENQAETWRILTIESPTVMHHQESVQYLKWELFTLCIIMQGIANMLLTQKMNQFMYLQL

AYKQLQALHSIYFIVDQMGSQFAAYDYVFFSAIDVLLSEYAPYIKNRGTIPPNKEFVAERLAANLAGTSN

VGSHLPIDRSRVLFALNYYEQLVTVCHDSCVETIIYPMARSFLYPTSDIQQLKPLVEAAHSVILAGLAVP

TNAVVNAKLIPEYMGGVLPLFPGVFSWNQFVLAIQSIVNTVSPPSEVFKTNQKLFRLVLDSLMKKCRDTP

VGIPVPHSVTVSQEQEDIPPTQRAVVMLALINSLPYVDIRSFELWLQETWNMIEATPMLAENAPNKELAH

AEHEFLVLEMWKMISGNIDQRLNDVAIRWWYKKNARVHGTL

>gi|50549031|ref|XP\_501986.1| YALI0C18689p [Yarrowia lipolytica]

MPSISHKPITAKLVAAPDATKLELSSYLYQQLFSDKPAEPYVAFEAPGIKWALYPASEDRSLPQYTCKAD

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RVRLCEPVNQGKVVKGTTKLTVAKEQETIQPADEAADVAFDIAEFLDFDTSVAKTRESTNLQVAPLEGAI

PTPLSDRFDDCESRGFVKSETMSKLGVFSGDIVSIKTKNGAERVLRLFAYPEPNTVKYDVVYVSPILYHN

IGDKEIEVTPNGETHKSVGEALDSVLEAAEEVKLARVLGPTTTDRTFQTAYHAGLQAYFKPVKRAVRVGD

LIPIPFDSILARTIGEDPEMSHIPLEALAVKPDSVAWFQVTSLNGSEDPASKQYLVDSSQTKLIEGGTTS

SAVIPTSVPWREYLGLDTLPKFGSEFAYADKIRNLVQISTSALSHAKLNTSVLLHSAKRGVGKSTVLRSV

AAQCGISVFEISCFGLIGDNEAQTLGTLRAKLDRAYGCSPCVVVLQHLESIAKKSDQDGKDEGIVSKLVD

VLADYSGHGVLLAATSNDPDKISEAIRSRFQFEIEIGVPSEPQRRQIFSHLTKSGPGGDSIRNAPISLRS

DVSVENLALQSAGLTPPDLTAIVQTTRLRAIDRLNKLTKDSDTTLDDLLTLSHGTLQLTPSDFDDAIADA

RQKYSDSIGAPRIPNVGWDDVGGMEGVKKDILDTIETPLKYPHWFSDGVKKRSGILFYGPPGTGKTLLAK

AIATTFSLNFFSVKGPELLNMYIGESEANVRRVFQKARDAKPCVVFFDELDSVAPQRGNQGDSGGVMDRI

VSQLLAELDGMSTAGGEGVFVVGATNRPDLLDEALLRPGRFDKMLYLGISDTHEKQQTIMEALTRKFRLA

ADVSLEAISKRCPFTFTGADFYALCSDAMLNAMTRTANEVDAKIKLLNKNREEAGEEPVSIRWWFDHEAT

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>gi|50548901|ref|XP\_501921.1| YALI0C16841p [Yarrowia lipolytica]

MGLLEKTLFAEGEPFSYDGNNRGKRKLRPMDGSSLPLENTDFSAETLDRLVGRNVVSPASDYFHLGESGE

VSEEVRARRELRDRRLAAEEERERGARAARKRAEKETWKEIEQKYGEGKEPVVGDLRRHVSKDEDGNAKE

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SSIDSRDFSRPVQFCNEVGVPDPSWQSHDVSDPEEISAPILPRFESLKKSTKGKKIGGGRKGRRRAAIEE

EANNGGERSEKRSVLSSRRNKGKEVDDGYESTATGKSRRPSVATNATLSPSFGAVSDFSDMDSDVEGICG

LESGMASRNRSSVSVNSKHASLLSKASAKSKAASFKSTTGNPSTGKPAYVSKIISEEEYINDYYRKNYGH

DAPKVEEPVAEETGLHHVKSTKSIKIDEPESVIEKRQSQVDPLYRPKPLPEPRKSGESSRSVKSNKSGKS

GLPHISRGVAMMMTGLSPTNSTPASMRDSISPEGSEGWRSRESLVSRSRAASLAPSINRDSWSRAPSTNR

GSVSRAPSLSRDDSRTQSFMSRDHPHLSRLRSSFRHSSDDSSAYPASMDLNLPQGRTISNPDISIHHPLF

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GVSGDNPEVRPLSEAASQKGYVLDVIYENQRGMFVFGHPFFSSNSLLNFDRKPWTTLDNKAAPGDPQSYP

LPNTNWQWAWKYWYIDMSGDVDDHGWSYSWFFRSRRWHGSHVWFHSWVRRRRWIRVRKTREFNKSEAITG

RLERPIRIHDSLLEAKQRGDANRAAHKASSGAVVTNSAAHDFMHAKYSVLVESAASAATWGDFWEVFTAC

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DERIG

>gi|50547683|ref|XP\_501311.1| YALI0C01023p [Yarrowia lipolytica]

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VTFLQKWKGVRFIHQYKEELETASKFAYLGLCTLVGSKTLGEEYTNLMYTIRDRTALPGVVRRFGYVLSN

TLFPYLFVRYMGKLRAKLMREYPHLVEYDEDEPVPSPETWKERVIKTFVNKFDKFTALEGFTAIHLAIFY

VYGSYYQLSKRIWGMRYVFGHRLDKNEPRIGYEMLGLLIFARFATSFVQTGREYLGALLEKSVEKEAGEK

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ISEWVREKPECPLCRQGVREQNLLPIR

>gi|68482295|ref|XP\_714905.1| likely peroxisomal import RING finger complex component Pex2 [Candida albicans SC5314]

MIPISYPSPRVSQLDAGILDSELFSLLKEQLSSIFQLHSTSRYSFSQHPELYSLLLNLLIFRLTVWKSGS

SYGSSLQNLKLTDSRSGKIIGSSRKALLGAVIIGGYLYKKLESYLFFLDESSTQNSHSTLDKLKNYLLIN

RTSILSGLENSLKIANLVNFTFFLVNGQYSSLVNRILGIIETPISSDLLKFNGSNVNYEFQNRQLVWNVM

TEFLVFILPLLQLRKLGRMTRKLLGRSKNSLDVQSGNVPTLTSYTNLPVSECAICHDNNNQASQTGGRTF

PSAGPVTNPYITNCGHVYCYVCISTRFNMIKVNGEDMPCLRCGKRLEWFEEFGLADGAVDEDAIVLSFEN

DESDEQEEESDEEGSITSEKEVHSYEPELSQNRIQRHLSERSTIFDDQSADEFSEDEYSEEEEFDADEMM

>gi|68482168|ref|XP\_714968.1| likely peroxisomal import RING finger complex component Pex2 [Candida albicans SC5314]

MIPISYPSPRVSQLDAGILDSELFSLLKEQLSSIFQLHSTSRYSFSQHPELYSLLLNLLIFRLTVWKSGS

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RTSILSGLENSLKIANLVNFTFFLVNGQYSSLVNRILGIIETPISSDLLKFNGSNVNYEFQNRQLVWNVM

TEFLVFILPLLQLRKLGRMTRKLLGRSKNSLDVQSGNVPTLTSYTNLPVSECAICHDNNNQASQTGGRTF

PSAGPVTNPYITNCGHVYCYVCISTRFNMIKVNGEDMPCLRCGKRLEWFEEFGLADGAVDEDAIVLSFEN

DESDEQEEESDEEGSITSEKEVHSYEPELSQNRIQRHLSERSTIFDDQSADEFSEDEYSEEEEFDADEMM

>gi|68480621|ref|XP\_715696.1| hypothetical protein CaO19.1933 [Candida albicans SC5314]

MEQVSSILSNILSVEEGTTQSHPQSKTSSNRSSIDESSETLSKKPQRRSKDFDFSSFWKTSDKEQDTTNG

EDRKNDFETIGDKTSKKTLSNSLESEGNATTIPLPAPSSSSSAQYMADKLMEKVISMMISNEVVDEQTSK

ILQDRIEMQKQRPPLSIALMQNNSNELHRRNSDMYIFIDHVQKFFSWQDPFYTVAWLLIITHLILNPYLF

TVLPLVQLITSTLVPHYLMIYPPDGVANQEYLEVNPKPSDKPLNLYKVPKPVPLFSREFFMNFTDTQNFM

TLNIKLFDFTVWLTSDYLYFKNEQITSGIYVICIAMIFGNLYLLPYIVPFLLNHFIIVQLYFIFNIWAIT

AILHPYPRGLLLEWIYKEDTRLNVQHFVNKIEDKLTKFIVKTPTLEQSITNTDLQHTTKDIGSSNEILED

NDTKYVEIYELQKLNTKNKMWEAVGFTPNFYTTNDMIRRYNSAIQELEQNDKSHTHSNEDPQEPHKLPLL

KRDTLSEISPPQNYKFIPSEKWKIDYDISTWVENNLIQDLVIIDDDEKWAYDVITETNQDQKQEIEGKQL

DKAINEMTMNEIEKFTDLTKSTEFFRRRRWIRKVTRMNYKDLKEESVPISSISAWV

>gi|68472786|ref|XP\_719458.1| potential peroxisomal import complex protein Pex12 [Candida albicans SC5314]

MEYYSSLDASQLDSERPTLFELISANQLESLLSPSLRYILVHYASKYPRYLLQLTNNFDELNLLLRSFIE

WYFLTYWQGTFTENFYGLKRVSQTPLSQGEYNSSRLTQLVPSMIEERRKLSKLQKLVSLFEVTGVSFVSE

KLNYCYEVWYTKYVTNQLNTSDTLTTQENVKIKIKRKFVEIYPYLQSAYRAANFITTLLYLSGSSKSPTL

LTYLFRINFSRLNQYDYSKNEPKQPLNDSKKPNRIHPPTAIEYILRLLSNNVTKPSWKAIKFVLGTFFPV

AIFTLKFLEWWNNSDFSSKLSKNLGNVLDFTLPPPSSLTSALRSYKNEEKKDSGTEIKQQKKKQYKSGKV

CPLCKKELTNPAIIETGYVFDYSCIYNYLEKSHIIVSKKLQTKQKDEEDDNIYSEDESEDENIENEKKEE

AKEKENVVIDINKGGRCPITGRRLLGCKWNPIKEEWEIEGIRRLIF

>gi|170092179|ref|XP\_001877311.1| predicted protein [Laccaria bicolor S238N-H82]

MAGMSSAAATSAVPLLSDFLSSVPSQLTTALIHLAPYISLLKRTAVVISWRSSWFESWLVVGGCFFLPLV

LLVILPFTNRRQNARPSNALAPVTEYALQAIITDLTIIQSLFPQFAPLPAISLSILLRVVILSYIPYLFL

TCYLSLSVIFAVVGTVILTWRAPWATILRATVWRSAWFRWTLYAGWARLTGQPLPSRTLSLQPKISSTNP

VRSIRFLFTIYENQRWWMGLDWTAALLPGERPSWCSAAQHPVSPPNAFSLPNITTVYLPDGNGRTLKRTA

TWKWEEPEWRVLVRKSGGGLSRIERPLPAIKEDNSNGSRLLKAAGMFRESGSLGNVSSTPPDKISDEGQP

EDVEDGIEEESSTDADGWVYGDNKWEGQGSRGGMGKYTRYRRWTRVAFLSEIVDVVDTDCVGITREPTSS

LDAVPPTNILDIPTNVDNPPENPLRQRLKLALAKGATQSVVP

>gi|169614854|ref|XP\_001800843.1| hypothetical protein SNOG\_10577 [Phaeosphaeria nodorum SN15]

MASDEQDTFANREAPIPLLQVHPADDSTPKILTPSTEHGHSRRLSASKLKDKLESLGDKSGRDSAGRMGD

KMFNLNDASSSTRVKDRRSRTYVARPNFSIPTMSSNFRRFNSRIGVAFILQNRLIHLFTWAEPTQTLSFL

FVWTFLCVDPYLLPVLPLASLLFFVMVPSFLTRHPEPEVHVGDADLWQGSLSGPPLANARTIKPAPEFSK

DFFRNMRDLQNCMEDFSTIHDAVLAFLTPLTNFSNENLSSMLYILLLLLSCTLFISAHLLPWRLIFLAIG

YTLTALGHPTIQDLLATPENEKLLSDTEHEGRSFLLTISKADIELEPTQESREVEIFELQHRALHDEHGE

YEGFMFSSSPYSPLSPARISGDKPRGTPFFEDVLPPRGWRWADKKWTLDLLSREWVEDRCVTGVEVEIEG

ERWVTDLHYEVLESDGEREKAKRARLQKKPGRGAQTGVGES

>gi|169598632|ref|XP\_001792739.1| hypothetical protein SNOG\_02121 [Phaeosphaeria nodorum SN15]

MSSPSRPSNDASSPLPTGDPNPPTYASFTPSTLGQSTPQTKLRSAILVHQKSPLLAATPPQITRVLAYSH

PFILPLNKLVGLLTWTTGDPWESFLLVASFWAIVMYGDAVTRYAGPIIVVSGLILGMYTRRYSPLSSTGW

TGEKGQKVHKRAESESDIKHHKSLEDIVDMSLSWHSRPARVTRTLMWRSRMVRKTCAFLTGLDFGDTISA

DKKGAPPLPPRKKSTQEVAASLAAKRRPESTGVRFTFSIYENQRRWLGIGWTSSMLAYERASWTDEHLNA

VPPKDQFELPEVEGGQSRWRWVQGSSWKIETGGDTKTTTKDDAGWIYYDNKWRDGRRGLDGWGRYTRRRK

WYRDAELVESTPSTEVTPVPTPKHAPVDDDQLAKFPSNLSVSTADTTLVDDAASVVSDTDAASTKSKRSW

FKKKRRSKSTSGSVSGITVASAGTEGSRRSEEEDVHSPLERTREDDWRGVDDIRQHLDI

>gi|170083945|ref|XP\_001873196.1| predicted protein [Laccaria bicolor S238N-H82]

MTSLSPPPPTLIQDDPSAADLARKRFAPRARFLSLPSLRSPPSKPSLKPSTETTTLEIDSTNIDTPINLD

NSALINDDYSKDLYQWAVIYENQRGMTLFSTPYYSKLSLLPTDPSPFTLPDNSYKRSEQPPVSFEEYPLP

DGNWHWVSRCWMIDMRSDSGEVQHDGFEYNWMFRKHNWRAQVGFVSAGGWVRRRRWVRLMLRPGRKVIGC

TDGISVPSSSNVKSGYLRQGQSTPSLFPPSVLTSITDVVDDWSEMDPSDVWIGDDPDANWQRCHKLMKKF

GRDGRKLELWRLWFGFYHPEHKHKFLETDEKGKRRDKQWTEDEGPLPSEALASDALSRESVTIAPREAVI

PVLRKYGQTLLHSFTYPESRVQFLKVLANADLLLELNATFGVDSTNIEFWSYASSLEVVAKSPVKDMAVA

DCSM

>gi|154272277|ref|XP\_001536991.1| predicted protein [Ajellomyces capsulatus NAm1]

MKKRRADSSGVRFTFILYENQRRWLGIGWTYSLFTYERAAWTDEHLNPVPQKDDFELPEVEGGSARWRWV

PGSEWRIDNSPSDVPTKKSSKSIQNTSGNGAGEDEGWIYYDNKWNDGRRGQDGWGRYTRRRKWCRDAELV

EVSPSTEVTPPPSPTPEKGPSSSSSQSIKHQYEDNLLETERNNCPPCDSCKVRKRRWFGSSELSRALASS

PGSTSSVHNSESGSAAIATSTGASANASASSTAMKVPWPSSSNITNVRPTSISTSYNHSHSSYANSFDNA

GGAGSCSSRNSFTSRRRSRPGANSMTLADADGESLSRSIRDQEIEEAENAVDSFGSRPGGAAERTERGWG

LGDDAHMGLS

>gi|71000221|ref|XP\_754814.1| peroxisome biosynthesis protein (PAS8/Peroxin-6) [Aspergillus fumigatus Af293]

MDFPHHDRASVQPRRRRRNVAKRRLRNRAPISARLALDSQLRGSVGILSEDLANDLFQPPSVTDDDGIRY

LAISPYTPGSSAVEDLAWTIVPVRLESLDRSRPSPLPHSTVLFPDSADSLQPFIQTLTKLEPTRHPLQAQ

RIVEIRALDVIPLHLDTVYVTVERDLLRNHDDVQSRFGGGFTTNMHGPNGLWAKAGKGFEPKRFTKKAAA

EVEERLTAAVREALGTQKVVHTGDVLPLPLPPHPITYAPAPPAHISFCEPVSQGLLASTTKIVLIQARPQ

GHRAQRSLRSRPGLLKQVAEDEADDTSNEQFYSAAEDKPSESGTELESTTPPDDSETEGSVGNASDTSDD

SLEDMISLTAPELPQPPSGVLSSITSATPRAGGRRLDGIHTPGSVASNFTSATLRPGRGPGKVFKAEGLL

RGIPIELLHPRPREDDDPESFIYVDISTLAKIGCFSGDWVRIEATEEPQANMFSSIQLGSFNEHDEEHGN

WRPVKIYGLPGLPSAKPRYSINQSSDRRPSISQRPPQRLTPSVYTSPLLLNNLENTKYVRISPMAFATGN

GPSKSAVLHQVKASSARQPPLAKEVNLLKVSTPLSMDRVLQPALFAGLKQYFESKRRILKSGDLVGISVD

EGFGRAVFSGAAATDASTPDEDLTIRFNQANESAQGVKKVGVAWFRVAHVVPGKSEDQDEDDQWGGVAVI

DSATTRMVQAGSDISRVPGILENGWEYWLGVKSVPKSISNAPGPHGLVTEPPQPFIPPLQKRIRELMAVA

TSPRAIQLGMKPVVILLRSQQRHIGKTTVATRACADIGLHTFPIDAYDILTEGGANGGDVKTEAYLKARA

ERAFHCGPHCTALLIKHIEVLTADRIVSAMAEILADARVVIATTTDVEQIPEGIRSMFTHEFEMTAPEEK

EREGILRNAVAERSIRLSPDVDLGSVALKTAALVAGDLVDVVERASAIRTARLEKLAETASKVAPESNVS

VRDVLVSGGDAARGVTKADFDAAVEAARKNFADSIGAPKIPNVKWEDVGGLTNVKDALVETIQLPLERPE

LFAKGMKKRSGILFYGPPGTGKTLLAKAIATEFSLNFFSVKGPELLNMYIGESEANVRRVFQRARDARPC

VVFFDELDSVAPKRGNQGDSGGVMDRIVSQLLAELDGMNGGEENSGGVFVIGATNRPDLLDTALLRPGRF

DKMLYLGVSDTHEKQATILEALTRKFTLDPEVSLRRVADRLPLTYTGADLYALCSDAMLKAITRKATAVD

EKIKQLPGGPVSTAYFFDHLATPDDVAVMVTEEDFNRAQSEMVPSVSAKELEHFERIRRQFESDDKKQEP

QSTGPGSKAPQTIGDALEALRLGSQLDGFIDGPVTNGDHPSPGSGKGKGKAGPAMMRSASGQSTNSKGKG

KCRNKTVSGGDGESDSSPDVANGDDDYIVRTDHLVNSTDAAK

>gi|70983600|ref|XP\_747327.1| peroxisomal targeting signal-1 receptor (PEX5), putaitve [Aspergillus fumigatus Af293]

MSFLGGAECSTAGNPLSQFTKHVQDDKSLQRDRLVGRGPGGVQESMRSRSMMGGQDQMMDEFAAQQPGQI

PGTAPQPFAMEQLRRELDHFQTTPPRTGSPGWAAEFDTGEHARMEAAFAGPTGPLMNNGSAFTPAEFARF

QQQSRVGMPQTSSPATSVSPVMAGYQRMGMMRPSYTPMGMQQQPAEAATQDKGKGRMVELDDENWEAQFA

EMETAGNQTLDDEANAAIEAELNDLDRSVPTTDTGNAQDYDAFESVWQRLGDYMFEEENVFRNVANPFEE

GVKIMREGGNLSLAALAFEAAVQKDPQHVQAWTMLGSAQAQNEKELPAIRALEQALKIDPNNLDALMGLA

VSYTNEGYDSTAYRTLERWLSVKYPQIIDPKDLSSDADLGFTDRQILHERVTDLFIKAAQLSPSGEHMDP

DVQVGLGVLFYCAEEYDKAVDCFSAALASTESGTVNQKEQLHLLWNRLGATLANSGRSEEAIQAYEQALT

INPNFVRARYNLGVSCINIGCYPEAAQHLLGALSMHRVNQSTNLYDTLRRVFSQMGRRDLADMVVAGMDV

NVFRKEFDF

>gi|70990514|ref|XP\_750106.1| peroxisome biosynthesis protein (Peroxin-2) [Aspergillus fumigatus Af293]

MSSTNFAAAQERVLERRRLREAEARKRLAEQQRASPLNHPALNRLPYPLNRIPQSGVTLWNSIKGREGSR

PAFRVGQVDAELLDEELLGLLKGQVGNALKYFGPQLREDWSHEIQFALRAILFKLSIWDHNASYGAALQG

LRYVDSRSKGPVHSTPTKWQKSLYGLLTVGGRYAWEKWESWLISQEGGYEEPSRDVRMLARLTGLVSTTH

SIAAFVSFLVFLVNGRYRTLVDRILRIRLTPPSAQSAREVSFEYLNRQLVWHAFTEFLLFLLPLVGISRW

RRWLSRAWRKAISAIRSRDDDEVEVEKRGELAFLPERTCAICYKDQNPASTSENDIITASAGGIVGSAQT

DITNPYETVPCGCIYCFVCLVQKVEGEEGEGWICLRCGEIVKKCKPWNGDVLEEVRPSTTSGKIVGFAMD

ENAVTQGPVSGQGPKTLAEELSASHEVGQDEALDHSDQWSKVDKDEEEAELDEEVNESA

>gi|146322958|ref|XP\_755628.2| peroxisomal membrane anchor protein [Aspergillus fumigatus Af293]

MSDIKPKSPSIPQWQQPAAATTNTGNSTSTPSPSSDETPRSELIEQAKKFLQDDSIRDAPIDRKIAFLES

KGLRSEEIDSLLANSRETDSSTNLAEGSKSTPDSTTSSTSNESQSPKEPSALSPISSASSPTTPAAPTAT

KNSTPRDVPPIITYPEFLMQQSKPPPLVTLRSILYTLYGAAGLGASLYGASEYLVKPMLATLTSARVELA

QTANANLQKLNEKLEQNVSRIPPHLSAKDTKQTEPADSEDDEQDSVTSDPTELFHRDVATQTSQDLDVST

LPHKAGYHPADEATPDPTATVNTHIKRLENITSHLREVASSEKESGALDDSMRTRLNELHHYLDGLLYGR

SSYSSVTAYGVYSTPGLETTSGPSVGISKAEEDAMASFRADIRGVKGALLSARNFPASRGRIGSGILSGR