



-----MDRWYLGGSFPGDVPFYDY-----ETVRNGGLIFAGLAFIVGLLILLSRFR-----  
CGGNKRRQINEDEP-----

>gi|5174635|ref|NP\_005962.1|/1-67 fxyd3/FXYD domain-containing ion transport regulator 3 isoform 1 precursor  
[Homo sapiens]

-----NDLEDKNSPFYDW-----HSLQVGGGLICAGVLCAMGIIIVMSAKCK-----  
CKFGQKSGHHPGETPPLITPGSAQS-----

>gi|296841065|ref|NP\_001171892.1|/1-70 fxyd4/FXYD domain-containing ion transport regulator 4 precursor [Homo  
sapiens]

-----NDPFANKDDPFYDW-----KNLQLSGLICGGLLAIAGIAAVLSGKCK-----  
CKSSQKQHSPVPEKAIPLITPGSATTC-----

>gi|257195182|ref|NP\_001158077.1|/1-156 FXYD domain-containing ion transport regulator 5 precursor [Homo sapiens]

TLKDTTSSSSADSTIMDIQVPTRAPDAVYTELQPTSPPTWPADETPQFQTQTQOLEGTDGPLVTDPEETHKSTKAAHPTDDTTLSERPSPSTDVQTFQTLKPSGFHEDDP  
FFYDE-----HTLRKRGLLVAAVLFITGIIILTSGKCRQLSRLCRNRCR-----

>gi|258679520|ref|NP\_001158309.1|/1-77 FXYD domain-containing ion transport regulator 6 precursor [Homo sapiens]

CSFNQKPRAPGDEEAQVENLITANATEPQKAEN-----SAAEKEKEMDPFHYDY-----QTLRIGGLVFAVVLFSVGILLILSRCK-----

>gi|11612659|ref|NP\_071289.1|/1-80 FXYD domain-containing ion transport regulator 7 [Homo sapiens]

CRKADRSSESPTCKSCKSELPSAPGGGGV-----MATPTQTPTKAPEEPDPFYDY-----NTVQTVGMTLATILFLLGILIVISKVK-----

>gi|73620964|sp|P58550.2|/1-76 Putative FXVD domain-containing ion transport regulator 8 [Homo sapiens]

CSFNQKPQDPGDKEAQVENFITANAKEPQKAKN-----SAAKEKEIDPFHYNY-----QTLRIGGLVFDVVFLVPSCHLLSHRCK-----

>gi|37496592|emb|CAD88978.1|/1-74 phospholemman-like protein precursor [Squalus acanthias]

CKFNQNKRTRSNSGTATAQHLLQPGEATEC-----MDPEGPDNDERFTYDY-----YRLRVVGLIVAAVLCVIGIILLAGKCR-----

>gi|351705846|gb|EHB08765.1|/1-2174 Down syndrome cell adhesion molecule-like protein 1 [Heterocephalus glaber]

-----MAGLSTDDGGSSKGDVDPFHYDY-----ETVRNGGLIFAGLAFVVGLI ILLSKRFR-----  
CGGSRKPRFRCPNPWGTVVFNLPGLFAVEPELKGTCDFQGNKGPMLALDCGDLPLVLPVPHSVLGGQSWARGPRVIDAYLAMSSARLEDDVGTSLYFVNDLQVTFSSSVG  
VVP CPAAGSPSAALRWYLATGDDIYDVPHIRHVHANGTLQLYFPSPSAFNSFIHDNDYFCTAENAAGKIRSPNIRVKAVFREPYTVRVEDQSRMRGNVAVFKCLIPSSVQEY  
VSVVSWEKD TVSITPDQSTKSSLLTSAPQGNLGGWYLA AKLEEKRPVGVKERKSKWTAEPQEKTI GENRFFITHHGGLYISDVQKEDALSTYRCITKHKYSGETRQSN GARL  
SVTDPLVYVTLTPKKLKTGIGSTVILSCAL TGSPEFTIRWYRNTELVLVDEAISISIRGLSNETLLITSAQKSHSGAYQCFATRKAQTAQDFAIIVLEDGTPRIVSSFSEKVVNP  
GEQ'FLMCAAKGAPPTVTWALDDEPIVRDGSVRTNQY TMSDGT TISHMNV TGPQIR DGGVYRCTARNSVGS AEYQARINVRGPPSIRAMKNITAVAGRDTLINCRVIGYPY  
YSIKWYKDALLLPDNRHQQVVFENGTLKLTVDQKGMDEGEYLC SVLIQ PQLSISQSVHVAVKVPPLIQPFEPFPASIGQLLYIPC VVSSGDMPIRITWRKDGQVIISGSGVTI  
ESKEFMSSLQISSVSLKHNGNYTCIASNAATVSRERQLIVRVPFRFVQPNNQDGIYKAGV LNCSDGYPPPVMWKHAKGSGNPPQQYHPVPLTGRIQIILPNSLLIRHV  
LEEDIGYILCQASNGVGTDISKSMFLTVKIPAMITSHPTTIAIKGQAKELNCTARGERPIIIRWEKGD TVIDPDRVMRYAIATKDN GDEVVSTLKLKPADRGDSVFFSCHA  
INSYGEDRGLIQLTVQEPDPPELEIREVKARSMNLRWTRQRF DGN SIITGFDIEYKKNKSDSWDFKQSTRNISPTINQANIVDLHPASVYSIRMYSFNKIGRSEPSKELTIST  
EEAAPDGPMPMDVTLQPVTQSISQV TWKAPKKE LQNGVIRGYQI GYRENSPGSNQYSIVEMKATGDSEVYTLDNLKKFAQYGVVVQAFNRAGTGPSSSEINAT TLEDVPSQP  
PENVRALSVTSDVAVISWSEPPRSTLNGVLKGYRVI FWSLYVDGEWGMQNI TTRERVELRGM EKFTNYSVQV LAYTQAGDGVRS SVLYIQTKEDVPGPPAGIKAVPSSAS  
SVVSWLPPTKPNGVIRK YTIFCSPSGSQPAPSEYETSPEQLFYRI AHLNRGQOYLWVA AVTSAGRGNSEKVTIEPAGKAPAKIISFGGTVTPWMDVRLPCNSVGD P  
APT VKWTKDSEDAIPVSM DGHRLIHTNGTL LRAVKAEDSGY YCTATNTGGFDTIIVNLLVQVPPDQPR LTVSKTSASSITV TWIPGDNGGSSIRGFVLQYSVDNSEEWK  
DVFISSERSFKLDSLKCGTWYKVKLA AKNSVGSGRIS EIEAKTHGREPSFKDQHLFTHINSTHARLN LQGWNNGCPI TAI VLEYR PKGTWAWQGLRANNSAEVFLTEL  
REATWYELRM RACNSAGCGNETAQFATLDYD GSTIPP IKS AQGEGDDVKLFTIGCPVILATLGVALLFIRKKRKEKRLKRLRDAKSLAEMLI SKNNRSFDPVKGPPQGP  
RLHIDIPR VQLLIEDKEGIKQIGAVSSPSNGENHWPF GDSALDKGDDKATIPVTDAEFSQAVNPQS FCTGVSLHHPALI QSTGPLIDMSDIRPGTNPVSRKNVKS AHSTRNR  
YSSQWTLTKQASTPARTLTS DWRVTG SQHGVTVTESDSY SASLSQD TDKGRNSMVSTESASSTYEELARAYEHAKLEEQLQHAKFEITECFISDSSSDQMTGTNENADSM  
TSMSTPSEPGICRFTASPPKQDADRGNVAVPIPHRANKSDYCNLPLYPKSEAFFRKAEGRDYCNLPLYPKSEAFFRKAEGREPCPVVPPREASIRNLARTYHPQARHLTL  
DPASKPLGLPHGPPAAAATATLPQRTLAMPAPPAGTAPPAPGPTPAEPPAPPSTAPPAPSTEPFRVGGPHTKMGGSRDLSLLEMSTSGVGRSQKQAGAYSXS YTLV

>gi|431908274|gb|ELK11872.1|/1-343 Down syndrome cell adhesion molecule-like protein 1 [Pteropus alecto]

-----MEMVLIFLCSLLAPAVLASAPEQEKEKDPFHYDY-----QTLRIGGLVFAVVLFSVGI LLILSRCK-----  
CSFNQKPRAPGDEEAQVENLITANGGSPKGDVDPF SYDYETVRNGGLIFAALAFVVGLIIILTRPEDVGT--  
SLYFVNDLQVTFSSSVGVVVP CPAAGSPSAALRWYLATGDDIYDVPHIRHVHANGTLQLYFPSPSAFNSFIHDNDYFCTAENAAGKIRSPNIRVKAVFREPYTVRVEDQR  
SMRGNVAVFKCLIPSSVQEYVSVVSWEKD TVS IIPGKKKPWGHSSRGSWSGGEIKQSAELVVELTKILRLVLVSNLLLF GMLWPKSAFHLVWVHLCVGV-----

>gi|431908274|gb|ELK11872.1|/1-343 Down syndrome cell adhesion molecule-like protein 1 [Pteropus alecto]

-----MEMVLIFLCSLLAPAVLASAPEQEKEKDPFHYDYQTLRIGGLVFAVVLFSVGI LLILSRCKCSFNQKPRAPGDEEAQVENLITANGGSPKGDVDPF SYDY-----  
ETVRNGGLIFAALAFVVGLIIILTRPEDVGT--  
SLYFVNDLQVTFSSSVGVVVP CPAAGSPSAALRWYLATGDDIYDVPHIRHVHANGTLQLYFPSPSAFNSFIHDNDYFCTAENAAGKIRSPNIRVKAVFREPYTVRVEDQR  
SMRGNVAVFKCLIPSSVQEYVSVVSWEKD TVS IIPGKKKPWGHSSRGSWSGGEIKQSAELVVELTKILRLVLVSNLLLF GMLWPKSAFHLVWVHLCVGV-----

>gi|537176875|gb|ERE75212.1|/1-894 transmembrane protease serine 13-like protein [Cricetulus griseus]

MPFILFAECFPPSKDTSSRFPSKDTSSRFPSKDTSSGFSSKDVSPGFPSKDISSPGISSPGFSSPGFSCSGFSSSGFPKDISSRSITFQVIVGQVVICQVSLYDILPNESVP  
CLSLSKFSWQEAQRQLPLIGCVILLISLVISLILLFYFWRGHTGIKYKEPLESCPSHAVRCDGVVDCMKMSDELGCVRFDWDRSLKVIYSGSSGEWLPVCSSSWNDSKRT  
CQQLGFDSAYRTEVTHRDIANSFLLSEYNSTIQESLYRSKCPSQRYVSLQCSHCGLRALTGRIVGGALTSESKWPWQISLHFGATHICGGTLIDAQWVLTAAHCFVVTREK  
VLEGWKVYAGTSNLHQLPEAVSIQIIINGNYTDEQDDYDIALIRLSKPLTSAHIHPACLPMHGQTFSLNETCWI TGF GKTKETDEKTS PFLREVQVNLIDFKKCN DY SVY  
DNYLTPRMMCAGDLRGGRDSCQGDSSGGPLVCEQNNRWYLAGVTSWGTGCGQRNKPGVYTKVTEVLPWIYSKMEEPDVFLYPLEGRCGFPSSSDTPNSTWINKKCYLRD TME  
TVLILCSLLAPAVLASAAEKEKEKDPFYDY-----  
QTLRIGGLVFAVVLFSVGIILLISGSAKGPEDPFHYDYETVRKGG LIFAGLAFVVG LILLTRPEDVGTSLYFVNDSLQQVTFSSSVGVVPCPAAGSPNAALRWYLATGDD  
IYDVPHIRHVHANGTLQLYFPSPAFNSFIHDNDYFC TAENAAGKIRSPNIRIKAVFREPYTVRVEDQRSMRGNVAVFKCLIPSSVQ EYVSVVSWEKDTV SITPENWMDSGK  
KSSKMVGLTGVLAGAIVWGMVYEADTFCLAC YRPGTWLSGRILAFAPIIVHACLWLQLSEKDTATRHQK RVAEGGSKT-----

>gi|10957338|ref|NP\_058362.1|/1-348 hypothetical protein R27\_p149 [Salmonella enterica subsp. enterica serovar Typhi]

MITFSMDES GYTG YDLLHKEQKFQ GASSILINHDDASRLIKEYFPK LQADELKYSSLKRRDSNRKPLFELQKHLLSNYPCITCVGDKRFL LILMFIDYAVEPFY YDS-----  
GINLYEDGGNFSMAMVYVGPAYYGS AFDDVLLQFQ NAMKEKTLDSVSL LISKIRRLDWQRLKEFFG PLAFNHPDCIDAIMTDGISTDASFTILNALISRTEMSSGEYAI  
EHDRSKNLLTYNERLNF LINC DKEGFKHSEIATISFPLNLK KVVYQIDSKESPSVQLCDVLIGACIESVYQLMDSKVLNQN SVLSLYQDSQLIHFIPDIDFEGQKFRKGSQ  
SEEYLTFIQNEYSSKL-----

>gi|510919487|ref|WP\_016240412.1|/1-348 hypothetical protein [Escherichia coli]



>gi|497293115|ref|WP\_009607332.1|/1-225 DNA damage-indicible protein DnaD [Turicibacter sp. HGF1]

MMYDLWEKKLLDFNTLLLTIIYKELELNEQEFVVICLLANLIQTNPGGWTFADISKQMTLDDGSCSLLFIGLVERKYILVSSKTDEFGKRFEYSLSPFLTRIEKHLKQKKNQ  
SKSTQREEIFTLLEQEFGLSPLDIETIHMWMTEDNFDPELIKLAIEVNANQIKSIRYIDKILLEWKKKNITVVEEAKRQLIQFRQRKQSPMATNNEAPVVDPNFYDW--  
-----MNE-----

>gi|479339333|ref|YP\_007850551.1|/1-279 Sugar phosphate isomerases/epimerases [Clostridium cf. saccharolyticum K10]

MKLVSFERLSVLNLHYFYSLDYFLDRMVDLGIKNVELLGGHQMWLDPNEYQDPEPILKKLQSRNLHCPVFTPNCRFGYQFGVKEPELRKKTFGFFSNGIKLAAALGAKY  
MEANSGWGYWDEPEEEGLKRAIEMHQLAEVAEQNNITIVAESLRPQESRIGYSLSQMKRLFDGVNHPNFKVMVDLTAMSVAGESIQDWFVDVFGTENIAHAHFQDCNPYGHY  
IWGQGRNLREDLEVMVKNGYEGYFTQELTDPAYYLDPFYYDK-----KNVQNLRMYMED-----

>gi|558688197|ref|YP\_008826316.1|/1-284 Hypothetical protein EfmE4452\_2428 [Enterococcus mundtii QU 25]

-----MYYQLEYDKVMVDDPFYYEE-----



KNTWVDGLSLFLRFDPIFEIDSTTKSKEQTLELSNERAYLPHLVKVSYDKKKKIVSFHEHEEIKGKYKVARYYMDTCPKPRPSRYDKKEPTEEEEKRLEEAIYKLMDDLDKG  
IQYESEYQQSEISKEEFYFIVKKYGFIVDDSSLQNCISYGWYEIDILPEGVVVQNSQSKHSNGITKRLEENVLEVQRHEQILSTKTGEMKFEYRKECLAFMNRTEFLENQI  
EFLLNQELFEQEKVMESYVQLINEWEHFNRFLKQDGLYIS-----

>gi|544852827|ref|WP\_021267398.1|/1-281 putative lipoprotein [Bacteriovorax sp. BAL6\_X]

-----MKLLAVAALGTLVSCGGSGSGSSSTYGKYSPTYVTAQGFVSALNSVDPYYDL-----  
NTLEKDYDLSLREDFVYFDAKYNEFVAVDITYLRTLAYWDYYSNNQGLADEFRDVQSDDAWDFGIIGDGGDDYEIVDYVGSDFVFGDPVFEGFDTGYYEDEEETMDTGLM  
AANDDELQMFNKASLYSQAFKLPADKALSLVTMEKEIKKMLENAKDGELEQDQQAIAANNIKHFTGKSIEEFMAAKNDLGAREQVIDDVAGHLGTTTTQNIEDVILPELLSIE  
L-----

>gi|345005911|ref|YP\_004808764.1|/1-321 small GTP-binding protein [halophilic archaeon DL31]

MTFEDLPTPRSEELLDKAFSRASRTGRAKAPYEAQEAAMLRTAANILSDNLENVVTAWPDFDYVDPFYEL-----  
ADAIVDVRDLRQALSEVTWASRQIGELRSEYTTKIRNSDITDARKHRKQAFARIADIMDEIEDLLFVGEARDQLKTLDPDIRPDEPAIVVAGYPNVGKSSFVNHVTNARNEI  
RSYPFTTKAVQVGHFEYDRVRHQIVDTPGLLDRPEAERNIEKQAVSALEHLADAVLFVVDASGECGYPLESQLELRDEVLERFDVPVLTVCNKSDRSRDVEADLYMSVTED  
ENVDAVLKQVVEAIDWEPDIPASRE-----

>gi|551258028|ref|WP\_022878263.1|/1-493 polygalacturonase [Microbacterium sp. B19]

MWAAFGAMIVVVALVACGCVPEPLTQSATPTPVSTESGPGDRRS VSRPQLPKTTCATVSARLDMPAGVAADAQEAAPPDTTTLRQQALDACTQDGDIVAVKLVASTSGH  
DFLSAPLTIPOGVSLVLDNVTLYASRKPQDYQIAGATTGGSVAESGRGCRPFLTSSARNVGVQSIP SANGSLGRIDGRGGMQMWGSTESWWDIAEVARDGGFQNPRLLOQT  
DGADNVVSDIELRSAAGYHVYASHGDGFTAWGVVRVTPATARN TDGIDVDGTTNVTIANSFISAGDDGIGIKASTQRTAHVSVFGNHL YGTHGLSIGALTAGGVDDVVRIG  
NTITGVDAFGMASETSVGIRIKSATRFGGKVEQVHYKDTCIDQVQRPIDIDPFYFDM-----  
EGKTTPTWFTGISIDGLAAVNSPPGAVTRNLGLDGDHPLVLTMSNVQVDAARVRSNAEIAANGVTFGGEPALDGPVNIATARTAPSAPCTFPPFPND-----

>gi|383765969|ref|YP\_005444950.1|/1-1000 hypothetical protein PSMK\_08940 [Phycisphaera mikurensis NBRC 102666]

MIHLPSFLGRLALVASAASVASPAAAGALRADFHRLSPGEVRAEIRWPDWTLSPHAPEGTRIAVEDDRLVLQDDSQENAAVLSLTGDASREPQVVEIRFSLRVDAPAREAGD  
PEGSAFAFLRFGPAYGEDLGFLRVILPGDAAEAGRAFVDASSGDELVRPSGSAGASIP LAEPVDVVLRLDPAAGTYAVRFGGEEVLGATLAGGVEPRLGVFSVHTPSRGRA  
GISLGDLVIEPVGADADADAAGAAPAWPTRAEPPELLSLLNDVLDLGGRLVETPGFDLQDEGAEFQFQPHLYYWPVRDEAGITAWRSEVEKEWIGRHLYSLRAFPVESNRRY  
VVSALVKSFRDRANNEIDLGLEMLTMNHERLPAERVAGLPADTASDPDNVDGWVRWEYAFVTANYDEPVKARFILRHNI GYTDHEAIDLRLAQVKLIELPVEPHAVEGDGSD  
LVTFRGGPGNLPMAVESVEEDGGVFTVRTTGKFTIDTDAGRIAARQRIDFRDLFDADLSLPLAGLQLVRHDDTVAVLRNEHLAIGVQC DGMAAVAPLSPMAVLATARIGG  
AFNRLGRGSVYAGDDFGGF AINTYPVIGSGTTVDFEPVTSGLWFEGLARNDTETMAEAGEASRPGWQIRWDLKPGERIFLSGFPCRPFDWERSFSEHYQLTHRENEVEGYDD  
PWYDVVDVLI LWDFHQRSWGMADNYTPYDAELTQEHIRAIQAEGMKVMPYNSAWFHRTDPEVWVESARRMVEDEGFEGMYS DGLPAVEWL VG YEEMRMLREGVLPDGP I  
RVHDSL PQSGRHVAEYAPVYTYASTTYQAEHVST DAGPGWPVRYVINSWRQSN AIGDIKGDKWRGFGGDTPEQQTRSLAGFIWNARPGSGAPNYMQDVKPVWDALEADW  
REHGDDPFYYDR-----  
HYLPLAQELTGFRIGRAAMP IVAEDGDQVELSKTATGDGVAI RYTLTGSEPTAASAAYDGPVALPEGATLKAVTLAEGLEPSAVAVHPLPED-----

>gi|225714002|gb|AC012847.1|/1-179 Cuticle protein 7 [Lepeophtheirus salmonis]

-----MAKNNVLVLFGLLYSFALSTALSDPFYYDT-----  
NYDSYINQERYITPPRYIPEQNQP VYAPIPEQAPIHEPVAHAVVSNAPASQYVVA TQFHSQDEFGNANFGYSNESSALEESRDEYGNVVGSYV DATGINRHVSYVADD  
GGFRITSTNNLPEDTPEVAAAKALHFDALKQRGLYLY-----

>gi|602631564|ref|XP\_007422682.1|/1-227 PREDICTED: placenta-expressed transcript 1 protein [Python bivittatus]

-----MAWLKLTMQFLFLGASLVLPAYSQQPPCEIVRKTVAQGSFRLDVPDPLYEPE-----  
GAIYTVSVTGAEKATSVILQIVPPENSSGGSWEEEHQTIHCSATESVMQKNFSGPGTQIRWRSRPRAPSAGSAQIRAFVSVFVNGTLLLRKILEGELVTSMSSSVSQPTSSPH  
KPTLHSNPSDVHLHLNNTTVHHNFASSHQWTKDPHSSVSVAQASSFLLTILQLLSISLGYKLLT-----

>gi|496134146|ref|WP\_008858653.1|/1-1058 type III restriction endonuclease subunit R [Dialister succinatiphilus]

-----  
MADIIDLKDGVEKVISRDFDKKLTAKALADKEIWADREDVDAQEAVGYLSSYLEKLIIRLCLKDIADENQDHCVKDELALTNELVEKLASRIANLGDGHDVTAEQFILKSLEH  
RANKIARKKWEVPATSLVNSFLFTNSRNDVSMIHELNREIMTCDRMDMLISFIRFSGLSLILPCLRQFTAGGGHLRVVTTTYMGATDPKAVKVLSELPNTEVRI SYNVKETR  
LHAKSYMFYRDSGFSTAYVGSSNLSRAAIADGMEWNMKVTEQDLPGI IAKMKATFDTYWHSDEFQPFQVSDFDKLSRAIDRERGRKEEGSDTTYSDIEPYPYQAVLDALR  
TERLGKGRWHNLVVAATGTGKTAISAFDYRNFYQSRKGRKARLLFIAHREIILKQISISCFRQVMKDPNFGQLAVGNYHAARSEHLFMSIQTFNSQKFWKMDPFYYDM-----  
-----  
IIVDEFHHAAGYQKLLTWFHPKILLGLTATPERMDGKSILNYFGGHMAAEIRLPDAIERLLCPHFYFGIDDPVLSNWKWTGGHYDIEELENVYTGEALASQRARAI I  
QALERYTADMVDKALGFCVSKKHAHFMADYFNROGIKALALDADSPKDVRNAARQKLESGDITIIIFVVDLFNEGVDIPAVNTVFLRPTNSMTIFLQQLGRGLRFLPEKDC  
LTVLDFAQANRRYDFASRYASLLGKSHVVIKKEIQDGFPHVPGKCSIQLEEIAARHVLENINSRLRKNFYMVMVKELASATGHIPTLEEFFKATAIHPHTFYNEKHTFAR  
LLADAGLIPDFPVTEEEVLRKALPRVLSMDSPKWISFMKCYETMPALTEMEKKYLRMWQLTLYPEGGKWTCAPAVEDAVRRFRGQHELTDEIKALLRWQYDSIDI IPEKP  
DLPYQTPLEVYCNYSRDQLFAALGFAKPGSIREGVKYLTPENSDDVVTAPTDFLVTLNKSEKFEFSDTTLYEDYSIDRQTFHWQSQTSTTPESKTGQRYIHQRDNGTTVLLFV  
RSAQDAYKSSMAYTFLGPAHLMRWEGSQPMTI IYHLDNPIPAKYITKTDSAGVL-----

>gi|545543093|ref|XP\_005635989.1|/1-1066 PREDICTED: ankyrin repeat and MYND domain-containing protein 1 isoform X2 [Canis lupus familiaris]

MENGNSSGFYYEIPNVGISQNPVASSCTPAASEDLRILESSRTMEMFFSKRDVDPSPPEEEEEESQGPPEQDLKEAYIQLVQGMQEWDPDGCVYRGDFGLDMKLGHGFEFSWP  
TGESYRGQFYRDHRHGLGTYLWPDGSSFTGMFYLSSREGYGTMYLKTRLFQGLYKADQRFGPGVETYPDGSQDVLWGFREHLIKLCTEVPGGFSIHSYPEYS AFLTRSPASI  
SLSDEERVEREPHEGEDPFYYDY-----  
KRFLLDDDLTLPEMYIYSTDNSHLPVTCSEFRKELDARVFLNDIPPFVEDGEPWFIKNETPLMVRIQKQAYKYRNKRAHGSWGMGAVLEGDRSGFARCGPKERLAEDMILRA  
REGSYDWWYVIGILRDGLASADVADAKGYTALAAAALHCHNDIVNLLLDNGADVNFKFTDEGLTVLSMCFLLYYPSRSFKPNIAERTAPKQRRRRHVQEHAWTVAQTEASPARG  
APAASTRPPGSPRAHLQEAQSPVVPNPSRSSSLPEAAKEPSLEEWVPTPGSQEQRSVSVSGSEEDGLSAGTQPSRESPPDGGNPQKWEVPSPRGSVSDLEKGMVGVAGSPDRCT  
PGSQEMDFESDVCVHNYTIELSQDLLEKSAQAHSTLKSQSLGATGSVKGTMRMALAMIERRSRWQTIKLLLRGADPNLCCVPMHVLFVAVKAGDVAVRLLLENGAGTDI  
RLPAELGALTPHIAAALPGEQVVKVTELLHVAVDVADARAADQDDVYQPGKLDLLPSSLKLSNEAGPASVYHSQRASAPDEGGRTALHVACEREDSYKCARDVVRLLLSHK  
ANPNMLWSGHSPLSLSIASGNLIVKELLSHGADPNLLTKGLSALCVACDLYEHQRSTDSKLALIDQLIKYGADILRPVRLTQGDVAVGTAVDYGFKFYQDRKIAHC  
PFHMLTPAEREVVFVARRLLEYMGFQLRRAVFAKESQWDPKVLNLSKRAELTPYQRMKRKSTSVSKALHLEEQLVPPFFKFCYQCGRSIGVRLAPCTRICYGILTCISKYCKTK  
AWSDFHKRDCGTLASAIVPCPGPHLEDLPWRVEETQ-----

>gi|497283516|ref|WP\_009597733.1|/1-1080 TonB-linked outer membrane protein, SusC/RagA family [Alistipes]

MKICTNFLNLLKVCMCVALAFAALETRAQGEAFVSGTVKDasGQPVIgATVFDTTTQKGDVTSTTGSFSLQVVPGSVLKVSFVGYAEQSAKVVAGKTTYDFVLES DALEIE  
ELVVVGYGTQKKASLTGAISAINNEEIIITTKNENVQNMLTGKvAGLRVRONSSEPGQFNtSMDirGFGAPLIVIDGvPRDNMARLDPEDIEQVSVLKDASAAIYGvKGGNGV  
VLITTKKGDKGRVININYSGNISWQRPSNFPDLVDAADWMTLYNEKYTMHsvDNMSPVQYSQEDIAAYRNGEKKSYNWKDAVFRNSAPQTQHTVVSASGNDKVTFFYTS LGYQ  
YQESFLQHTPIYDYKTYLRANINAKIAKNTLTDVNLAGHMDEKKSNSFSSSDIVRSTWLFPTLPDPFYDD-----  
EQTMHTKDDNTGIVNPLAMIDKDANGYQSLISRWFQSAFSLRWDMPFLPGLYAKGFFSYDYIMNDNKFYRKAFNTYTSTGAATSFLKGDADHYFVQRNYYGKEHRQWHVQV  
GYDRTFGRHSVSGMLLFEDQHKVGDNFYGSREVVLPMQVVFVGDGETQQFNQSSGGGSLYDYAYQSLAGRFNYDFGGKYLAEFVFRYDASSRFPDGLRWVFFPSVSVGWRI  
SEENFWKESLDFIENLIRASYGKTYDGDLYEFLTGFTYPSGGAILGGDYVNGSVPKGIANKDITWQTIKMFDIGLDFSAWNGKLGTLFDYFRHRDGLYARRNLSLPG  
SVGASLPLENLNSDRDTGFEELELSHRNRVGDYSYAVKGNVSFTRRKTLYERAESGNSYLNRQNNDRFNSIWWGYEGGRTISWDQLYINPVYIGRGSVMGDYLYEDWNG  
DGWINDLDVHPIGYTDMVPMVNFGLTISASWKGIDFSLWQSGKPLHRRSRVSAAGALVAYQRHFGTHGPLASGRSDGQSLRSRHEVGRIRLYGLDGKSQLGAWVAECP  
LPASEESRNLFAAQEVADEGGYRECPDLQRLQPADDRSGLSRPGLVHSSVWGRGQYGIILSDQDLYRTERQILKQKNETSEILSPDLCGRIRRVHRFGYTAEKY  
LQ-----

>gi|149237779|ref|XP\_001524766.1|/1-1125 hypothetical protein LELG\_03798 [Lodderomyces elongisporus NRRL YB-4239]

MAKALEYTSRGDwalGLVIANFSGPESFARIASEYARNTFPFSKANNKVMHIMPIILKVIAGNVQSVIQLDITIVQNEGDYASLHWKEIVSTVAISGLKAKEFLIEFGKFL  
INRNNLLGGEISFILAGLPFGQGFMAITSGHHSMTQVYEAILNINTALQFPHLLPKLKHASTLADYGLINESQKYIDSLNSNIKSLGNKSPFVNQNLILEFQNLITRLR  
DLGSSDQGGWFGGKMSKVNLDKVVWQIDKFIvGGGEDTNKLSGDTGVFSKFSPIsRTSSTLEFSTMPFASPSMKGPEQFERRTYTSNTSFMPPQQLDTHASTNSVYKYAP  
GNTLGNRQTHGAGSERYPFAGNMSQPNLHEPLHHHHHQHQHQHLVFLNLQVQQGQNKVQSPPLASKVYYPYGNPIGHLSNSSIGSIPHLNIGAPSHSGATGTASGTATGT  
AGLNATKALPGHKPQOSISSVISGESIISNTPVSASHQSHQSHQSHQLHQDGEKISTIQESPELYPSQNSQKHLKSPVTEVPEIKEPEVQAPPPKMAKAKSAPPRSNPYA  
PTAGANAQAKQRNKYGPVDFSTPSKDTTSSKYGPTSSQSNTSKYRAELGNDFKSSFHPPQDVKNNTYNGENVDTKTALAPVVKHKVDSTKVDEEQIDRESQDVGGVQKNE  
HDFETNQEANLGPNAESSQFDIYDYPGNDYKPTASTPPRRKPTKNVPHIEDSFNSVLESPPSGITPARPLTLNQGVASNFDPMRMSNFSTISAGHRVRELDGYPiPGSPD  
ETTRANSVFGAPPVTAGAVHGIPATVNSTTNAAAAAAAAAAATVAVASQGGTYGFSRSLSQSALYQQYEVQDITVRDYVPIAEEDDEDDEDLKQKQKQKQEEEKRA  
KEQKLREEQEAKELKKQLRSQMSGDGSKEGWNGWLGSKNDGKPKPIRAKLGEKVNPFYYDE-----  
KHKRWLDRTKPIEEQLNAGKAPPPPSMKKPGASAADGGLSSPSTASGVTPTSITPSGPPRAKTPLSRNGQGIPLSANEASDSSALAPVSGVPPAPSTRPGRPKTSGA  
PGAGAGAKTAPSSNTLANASLDDLLSMNESSTVGRKPRRAGRNNYINVLDK-----

>gi|251771646|gb|EES52221.1|/1-727 Hemolysin activation/secretion protein-like protein [Leptospirillum ferrodiazotrophum]

MFFKDRPGGFPLSTKVRNIK MVRQASWCLSLVLMVFPDPVVRASDCISTGSLSVIMMDCAPAVAGPEKPGAKKEEPDRFD RDWTLRIRAPQGDWHSSIRASVALWVEKRLY  
PNATKEEKALMSVAIQHLARMGFVKAVKESDLIRVNVTAKT LNRIAATLDEALRRGHLYHVSRIIVAGGSEKENQFASAQLPVPENGI V DSEGMSAKLFSLSQIPGFTR  
ADGMMVPAIATRNVSFSLPHILI IHS DRKWARDIRRQV FLLVANLVIDMKNPLAKKIVKTL SGRLSRLDWPL LKIQQEAKET YRVEAPS LLLNLT LKNILLQAATLGRVSD  
SVIENPKQLSTGNIFAPLPEALEFDN FLVHLTPTPTFSGSQIEIDNYGYAPTGA VTLN AIGNVNNALLAGGLFTV GASTTFGGMNSGSLGYSFP IGLYVRAGMDLFAMNYK  
IGLGLSPWGSVNTQAL TALGVSGSNYSGDLWINQAI VQKEDRKLVLKETIFLKEFQDSYSP TVQND RSLVGGILDLSGSRALGRLNLSFDLSDTEYDLSQSGSSPVNPFY  
YDT-----  
QGFQNYITGNGQVGFAPTPKYSMTLGTVDQOYIGGGTLDPMLQATLGGMANVMVLPTASLFGN NLYVGT LTFTRTDSVDAGAFYTS GFFDAGEI SGI GTSFGAMGPVEESF  
SSKHFFARIDA AVPVGPLPVQGLGNSITALTGGNIGQGGIPIQLWLSIGLRE-----