>MULTISPECIES: chromosomal replication initiator protein DnaA [Klebsiella]

YLNNINGLLNDFCGADAPQLRFEVGAKPASSLQKGAVSPAAAAIPAAQVQTARAAPTIVRPGWDNVPAPAEPTYRSNVNVKHTFDNFVEGKSNQLARAAARQVADNPGGAYNPLFLYGGTGLGKTHLLHAVGNGIVARKPNAKVVYMHSERFVQDMVKALQNNAIEEFKRYYRSVDALLIDDIQFFANKERSQEEFFHTFNALLEGNQQIILTSDRYPKEINGVEDRLKSRFGWGLTVAIEPPELETRVAILMKKADENDIRLPGEVAFFIAKRLRSNVRELEGALNRVIANANFTGRAITIDFVREALRDLLALQEKLVTIDNIQKTVAEYYKIKVADLLSKRRSRSVARPRQMAMALAKELTNHSLPEIGDAFGGRDHTTVLHACRKIEQLREESHDIKEDFSNLIRTLSS

>WP\_004145090.1 MULTISPECIES: DNA polymerase III subunit beta [Klebsiella]

MKFTVEREHLLKPLQQVSGPLGGRPTLPILGNLLLQVADGALSLTGTDLEMEMVARVALVQPHEAGATTV

PARKFFDICRGLPEGAEIAVQLEGDRMLVRSGRSRFSLSTLPAADFPNLDDWQSEVEFTLPQATMKRLIE

ATQFSMAHQDVRYYLNGMLFETEGSELRTVATDGHRLAVCSMPLEASLPNHSVIVPRKGVIELMRMLDGG

DTPLRVQIGSNNIRAHVGDFIFTSKLVDGRFPDYRRVLPKNPDKHLEAGCDILKQAFARAAILSNEKFRG

VRLYVSENQLKITANNPEQEEAEEILDVTYAGTEMEIGFNVSYVLDVLNALKCENVRILLTDSVSSVQIE

DAASQSAAYVVMPMRL

>WP\_004150293.1 MULTISPECIES: DNA replication/repair protein RecF [Klebsiella]

MSLSRLLIKDFRNIEHADLALSPGFNFLVGANGSGKTSVLEAIYTLGHGRAFRSLQIGRVIRHEQDAFVL

HGRLQGEERETAIGLTKDKQGDSKVRIDGTDGHKVAELAHLMPMQLITPEGFTLLNGGPKYRRAFLDWGC

FHNEAGFFTAWSNLKRLVKQRNAALRQVSRYAQLRPWDLELIPLAEQISRWRAEYSAAIVEDMADTCQQF

LPEFTLTFSFQRGWEKETDYAEVLERNFERDRMLTYTAHGPHKADFRIRADGAPVEDTLSRGQLKLLMCA

LRLAQGEFLTRVSGRRCLYLIDDFASELDDARRGLLSSRLKATQSQVFVSAISAEHVMDMSDKNSKMFRV

EKGKITD

>WP\_004173845.1 MULTISPECIES: DNA topoisomerase (ATP-hydrolyzing) subunit B [Klebsiella]

MSNSYDSSSIKVLKGLDAVRKRPGMYIGDTDDGTGLHHMVFEVVDNAIDEALAGYCKDIVVTIHSDNSVS

VQDDGRGIPTGIHPEEGVSAAEVIMTVLHAGGKFDDNSYKVSGGLHGVGVSVVNALSQKLELVIQRDNKV

HKQMYEHGVPQAPLAVTGETDKTGTMVRFWPSLETFTNVTEFEYDILAKRLRELSFLNSGVSIRLRDKRD

GKEDHFHYEGGIKAFVEYLNKNKTPIHPNIFYFSTEKDGIGVEVALQWNDGFQENIYCFTNNIPQRDGGT

HLAGFRAAMTRTLNAYMDKEGYSKKAKVSATGDDAREGLIAVVSVKVPDPKFSSQTKDKLVSSEVKSAVE

QQMNELLSEYLLENPSDAKIVVGKIIDAARAREAARRAREMTRRKGALDLAGLPGKLADCQERDPALSEL

YLVEGDSAGGSAKQGRNRKNQAILPLKGKILNVEKARFDKMLSSQEVATLITALGCGIGRDEYNPDKLRY

HSIIIMTDADVDGSHIRTLLLTFFYRQMPEIVERGHVYIAQPPLYKVKKGKQEQYIKDDEAMDQYQISIA

LDGATLHTNANAPALAGEPLEKLVAEFNATQKMIGRMERRFPKALLKELIYQPTLTEADLADEQKVTRWV

NTLVSELNEKEQHGSQWKFDLHENKELQHFEPVIRVRTHGVDTDYPLDNEFIMGPEYRRICALGEKLRGL

MEEDAYIERGERRQPVASFEQALDWLVKESRRGLSIQRYKGLGEMNPDQLWETTMDPDSRRMLRVTVKDA

IAADQLFTTLMGDAVEPRRAFIEENALKAANIDI

>WP\_004151530.1 MULTISPECIES: sugar-phosphatase [Klebsiella]

MAIKLIAIDMDGTLLLPDHTISPAVKAAIAAARERGVNVVLTTGRPYAGVHSYLKELHMEQPGDYCITYN

GALVQKAGDGSTVAQTALSYDDYRFLEQLSREVGSHFHALDRNTLYTANRDISYYTVHESYVATIPLVFC

EAEKMDPEIQLLKVMMIDEPAILDQAIARIPAEVKEKYTVLKSAPYFLEILDKRVNKGTGVKSLADALGI

KPEEIMAIGDQENDIAMIEFAGVGVAMDNAIPAVKEAANFITKSNLEDGVAFAIEKYVLA

>WP\_075209882.1 hypothetical protein [Klebsiella pneumoniae]

MNIYHRLMLVTLPFASVQICAAAEPTAPLEPAYAYHGAEPADLSAPESRQPAAAASSSLLPLLGDEARKR

GYVLPLPFGVSINYMDMRQNINVDSINFTGLSLDGRNIDCGKDPVCKHAVNNIFANGPVSLDNAFQIGVG

HTRESSKTETLKLDAWLLPFMNVYGLVGHTEGHSISQIAVGLKGPNGKVVPLPGMQDLDFRLDFKGTTYG

MGTTLVGGVGNWFTVLDANYTQTRFDILDGSIDALTFSPRVGYRFSTPSVDALHLPAGKLNLWVGSMYQD

VQQEFKGSLSDLSMPSPMLQNMVNLANQDNNGRFDVKQHLQSPWNVLVGAQYELTQNFNITTEFGFAERN

SFFIAGEYRF

>WP\_016528946.1 BamA/TamA family outer membrane protein [Klebsiella pneumoniae]

MSRLFITFLLLMVCPTGSQAEALSREKIDGWLQHLGASDKFDASKGIDWGVMPGPFYTPELGLGIGTAVV

GLYRPDPQDTTSQNSTLTLSGYASSTGAFGLSVKNYTFFDRDLWRVFVDGSIANTPTYYWGQGFHAGDKD

NEKEKYTAQVLTLRPTLYRQLIDHVYLGAGWSLAAQNADEMDHDDRPKIENTPQGPSVFSSGASIDINWD

DRDFVPNPRRGQYANLRYTHYAPGLGSDTRFEEFQLHYSHYHALSEKSVLAWEVDGAFTQGEVPWSMMPL

LGSDERMRGYYQGRYRDKNVVSGQLEYRRQLTWRHGIVAWAGAGTMGPSLSSLNNGRWLPSAGVGYRFEF

KPRVNVRLDYGIGNGSSGFYFQVGEAF

>WP\_004145084.1 MULTISPECIES: D-galactonate utilization transcriptional regulator DgoR [Klebsiella]

MTLNKTDRIVISLGKQIVSGKYVPGSALPAEAELCEEFETSRNIIREVFRSLMAKRLIEMKRYRGAFVAP

RNQWNYLDTEVLQWVLENDYDPRLISAMSEVRNLVEPAIARWAAERATSSDLAEIESALNDMIANNQNRD

AFNEADIRYHEAVLQSVHNPVLQQLSVAISSLQRAVFERTWMGDEGNMPKTLQEHKALFDAIRHQDSDAA

EQAALTMIASSTRRLKEIT

>WP\_004145083.1 MULTISPECIES: 2-dehydro-3-deoxygalactonokinase [Klebsiella]

MTARYIAIDWGSTNLRAWLYQGEECLESRQSEAGVTRLNGRSPAAVLAEITQHWRDGATPVVMAGMVGSN

VGWKIAPYLPLPAAFSDIGQQLTAVGDNIWIIPGLCVSRDDNHNVMRGEETQLLGARALAPSSVYVMPGT

HCKWVLADRRQIHDFRTVLTGELHHLLLQHSLVGAGLPPQETSAAAFAAGLQRGINNPAVLPQLFEVRAS

HVLGALPREQVSEFLSGLLIGAEVATLSDTFAGQQAISLVAGSSLTSRYQQAFAAIGREVSAVAGDTAFQ

TGIRSIAYAVAN

>WP\_016530020.1 2-dehydro-3-deoxy-6-phosphogalactonate aldolase [Klebsiella pneumoniae]

MQWQTNLPLIAILRGITPDEALAHVGAVIDAGFDAVEIPLNSPQWEKSIPQVVDAYGEQALIGAGTVLQP

EQVDRLAAMGCRLIVTPNIQPEVIRRAVGYGMTVCPGCATASEAFSTLDAGAQALKIFPSSAFGPDYIKA

LKAVLPPEVPVFAVGGVTPENLAQWINAGCVGAGLGSDLYRAGQSVERTAQQAAAFVKAYREAVK

>WP\_016530021.1 galactonate dehydratase [Klebsiella pneumoniae]

MKITNITTYRLPPRWMFLKIETDEGIVGWGELVIEGRARTVEAAVHEFGDYLIGQDPARINDLWQVMYRG

GFYRGGPIMMSAIAGIDQALWDIKGKVLNAPVWQLMGGLVRDKIKAYSWVGGDRPAEVIDGIKKLRGIGF

DTFKLNGCEEMGIIDNSRAVDAAVNTVAQIREAFGNEIEFGLDFHGRVSAPMAKVLIKELEPYRPLFIEE

PVLAEQAEYYPRLAAQTHIPIAAGERMFSRFEFKRVLEAGGVAILQPDLSHAGGITECYKIAGMAEAYDV

GLAPHCPLGPIALAACLHVDFVSHNAVFQEQSMGIHYNKGAELLDFVKNKEDFNMEGGFFKPLMKPGLGV

EIDEARVIELSKNAPDWRNPLWRYEDGSVAEW

>WP\_046042092.1 MFS transporter [Klebsiella pneumoniae]

MVSGFAMPKIWRQIAMDISVTAVKTGRRRYLTLIMIFITVVICYVDRANLAVASAHIQEEFGISKAEMGY

VFSAFAWLYTLCQIPGGWFLDRVGSRLTYFIAIFGWSVATLLQGFATGLMSLIGLRAITGIFEAPAFPTN

NRMVTSWFPEHERASAVGFYTSGQFVGLAFLTPLLIWIQELLSWHWVFIVTGGIGIIWSLIWFKVYQPPR

LTKSISKAELDYIRDGGGLVDGDAPLKKEARQPLSKADWKLVFHRKLVGVYLGQFAVTSTLWFFLTWFPN

YLTQEKGITALKAGFMTTVPFLAAFFGVLLSGWLADKLVKKGYSLGVARKTPIICGLLISTCIMGANYTN

DPIWIMALMALAFFGNGFASITWSLVSSLAPMRLIGGVFNFVGGLGGITVPLVIGYLAQDYGFGPALVYI

SVVALIGALSYILLVGDVKRVG

>WP\_004150284.1 MULTISPECIES: DUF3748 domain-containing protein [Klebsiella]

MKQVTFAPRHHQLTNINTWTPDSQWLVFDVRPSGASFTGETIERVNVNSGTVETIYRATQGAHVGVVTVH

PTQERYVFIHGPERPDAQWQYDFHHRRGVVAFQGAVENLDAMDITPPYTPGALRGGSHVHVYSPNGQFVS

FTYNDHVLHERDPALDLRNVGVAAPYGPVTPQGQHPREYGGSHWCVLVSRTTPAPAPGSDEINRAYEEGW

VGNHTLAFIGDTLAENGDKVPELFIVDLPQDEAGWKQPGGAPLAGTATTMPAPPAGVSQRRLTFTHHRRY

PGLVNVPRHWVRANPQATAIAFLMRDDAGVVQLWLISPQGGEPRQLTHHASGIQSAFNWHPSGEWLGFAL

EDRIACCHAGTGDITFLTDTHAHAPSADAIVFSPDGKQIAWMEEVDGYRQLWVTQTGR

>WP\_004151524.1 MULTISPECIES: YceK/YidQ family lipoprotein [Klebsiella]

MKSRRLLKLVLFSGIISLSGCSSVMSHTGGKEGTYPGTRSSAQTLGDSDTNWGVKSLVALDMPFTAVMDT

LLLPWDMFRTDSSIKSRVEKSEKATLATNSVIPPAPMPAQ

>WP\_004151523.1 MULTISPECIES: heat shock chaperone IbpA [Klebsiella]

MRNFDLSPLYRSAIGFDRLFNLLENNQSQSNGGYPPYNVELVDENHYRIAIAVAGFAESELEITAQDNLL

IVKGAHAAEQKERTYLYQGIAERNFERKFQLAENIHVRGANLVNGLLYIDLERVIPEANKPRRIEIN

>WP\_004145074.1 MULTISPECIES: heat shock chaperone IbpB [Klebsiella]

MRNYDLSPLLRQWIGFDKLASALQTAGESQSFPPYNIEKSDDNHYRITLALAGFRQEDLDIQLEGTRLVV

KGTPQQPEKETTWLHQGLVSQAFSLSFTLADNMEVSGATFTNGLLHIDLTRNEPEQIAPQRIAISERPAL

NS

>WP\_046042103.1 putative transporter [Klebsiella pneumoniae]

MSEIALTVSVLALVAVVGLWIGNVKIRGVGFGIGGVLFGGIIVGHFVDQAGVALSSPMLHFIQEFGLILF

VYTIGIQVGPGFFASLRVSGLRLNLFAILIVILGGMVTAVLHKLFNIPLPVVLGIFSGAVTNTPALGAGQ

QILRDLGVPFEVVDQMGMSYAMAYPFGICGILLTMWLVRLFFRINVEKEAQRFEESSGNGHAHLHTINVR

VENPNLNQMAIQDVPMLNNDNIVCSRLKRGELLMVPAPGTLIQAGDLLHLVGRPEDLHNAQLVIGQEVAT

SLSTRGTDLKVERVVVTNEKVLGKKIRDLHVKQRYDVVISRLNRAGVELVASSSASLQFGDILNLVGRPE

AIDAVAAELGNAQQKLQQVQMLPVFIGIGLGVLLGSIPLFIPGFPAALKLGLAGGPLIMALILGRIGSIG

KLYWFMPPSANLALRELGIVLFLAVVGLKSGGDFVATLTQGDGLSWIAYGIFITAIPLLTVGILARMLAK

MNYLTLCGMLAGSMTDPPALAFANNLHATSGAAALSYATVYPLVMFLRIITPQLLAVLFWGLS

>WP\_004151520.1 MULTISPECIES: GntR family transcriptional regulator [Klebsiella]

MIYKSIADRLRLRLNSADFAIGSPLPGEKKLAEEFGVARMTIRKAIDLLVDWGLVVRRHGSGTYVARKDV

HHETSNLTGLAEVLRKQGKEVVSQVLAFEVMPAPPAIASLLRIKIDERIYFSRRVRYVDGKPLMLEDSYM

PVKLFRNLSLSHLEGSKFDYIEKECGIIISGNYETLTPVLADKQLARSMNVPEQTPLLRITSLSYSDSGE

FLNYSVMFRNASEYQVDYHLRRVQAQSPLA

>WP\_002923307.1 MULTISPECIES: alpha-glucoside-specific PTS transporter subunit IIBC [Klebsiella]

MLSQIQRFGGAMFTPVLLFPFAGIVVGIAIMLRNPMFVGEALTAPDSLFAQIVHIIEEGGWTVFRNMPLI

FAVGLPIGLAKQAQGRACLAVLVSFLTWNYFINAMGMTWGHFFGVDFSAEPTAGSGLTMIAGIKTLDTSI

IGAIVISGLVTALHNRYFDKPLPVFLGIFQGSSFVVIVAFLAMIPCAWLTLLGWPKVQLGIESLQAFLRS

AGALGVWVYIFLERILIPTGLHHFVYGPFIFGPAVVEGGLQVYWAEHLQAFSQSTEPLKTLFPEGGFALH

GNSKVFGSVGIALALYFTAAPENRVKVAGLLIPATLTAMLVGITEPLEFTFLFISPLLFAVHAVLAATMA

TVMYICGVVGNFGGGLLDQFLPQNWIPMFHHHASMMFIQIGIGLCFTALYFVVFRTLILRLNLKTPGREE

SEIKLYSKADYQAARGKTTAAAAPETRLGQAAGFLQALGGADNIESINNCATRLRIALVDMAKTQSDDVF

KALGAHGVVRRGNGIQVIVGLHVPQVRDQLENLMKDSLSTEHTTMTEAVS

>WP\_002923306.1 MULTISPECIES: 6-phospho-alpha-glucosidase [Klebsiella]

MKKFSVVIAGGGSTFTPGIVLMLLANQDRFPLRSLKFYDNDGARQETIAEACKVILKEQAPEIEFSYTTD

PQAAFTDVDFVMAHIRVGKYPMREQDEKIPLRHGVLGQETCGPGGIAYGMRSIGGVLELVDYMEKYSPNA

WMLNYSNPAAIVAEATRRLRPNAKILNICDMPIGIEGRMAQIVGLKDRKQMRVRYYGLNHFGWWTSIEDL

DGNDLMPKLREYVAKYGYVPPSNDPHTEASWNDTFAKAKDVQALDPQTMPNTYLKYYLFPDYVVAHSNPE

RTRANEVMDHREKNVFSACRAIIAAGKSTAGDLEIDEHASYIVDLATAIAFNTQERMLLIVPNNGAIHNF

DADAMVEIPCLVGHNGPEPLTVGDIPHFQKGLMSQQVAVEKLVVDAWEQRSYHKLWQAITLSKTVPSASV

AKAILDDLIAANKDYWPELH

>WP\_002923305.1 MULTISPECIES: DUF202 domain-containing protein [Enterobacteriaceae]

MKISRLGEAPDYRFSLANERTFLAWIRTALGFLAAGVGLDQLAPDFATPLIREILALLLCLFAGGMAIYG

YLRWLNNEKAMRLKQDLPYTRTLLVISILLLAVVAAVMLLVVYGG

>WP\_002923304.1 MULTISPECIES: DUF202 domain-containing protein [Klebsiella]

MADKRRARRESDPGLQPERTSLAWFRTLLGYGALMALAIKHSWHRAGLPFWLSIGVLAIVAVILWGYTRR

RHLMDVDDSDFLQPRAVRDKFLIALAVLSLAFLFAVTHLQPIVLFIRDMS

>WP\_004889115.1 hypothetical protein [Klebsiella pneumoniae]

MEAHHCHQPQAFYAQLRQQGLTAIHFIPQLAAGDAALWGEFLCAVFHRWVREDIGRINILLFSETLSAWC

GETLTQPGAPAANSACYGCPWLRLCRCGEQEDPLCAGYRQFYDFSGPYMRVMRDLRRQQRPPEALMPLLR

>WP\_016530744.1 D-serine ammonia-lyase [Klebsiella pneumoniae]

MKNADLTTLTATFPLVQDLIALKETTWFNPATTTLAEGLPYVGLTADDVQDAHARLQRFAPYLAAAFPET

AASGGIIESEVVAIPAMKRSLEQKFGQPISGELLLKKDSHLPISGSIKARGGIYEVLTHAEKLALEAGLL

TTADDYRKLLTPEFKQFFSQFSIAVGSTGNLGMSIGIMSARIGFQVTVHMSADARAWKKAKLRSHGVTVV

EYEEDYGVAVEQGRKAAESDPNCFFIDDENSRTLFLGYAVAGERLKAQFAQAGRVVDADHPLFVYLPCGV

GGGPGGVAFGLKLAFGDHVHCLFAEPTHSPCMLLGVYTGLHDQIAVQDLGIDNLTAADGLAVGRASGFVG

RAMERLLDGFYTLDDQTMYDMLGWLAKAENIRLEPSALAGMAGPQRVCASQAYHQLQGLGEQQLQQSTHL

VWATGGGMVPEEEMAQYLAKGR

>WP\_016530745.1 D-serine transporter DsdX [Klebsiella pneumoniae]

MESQIWVVSTLLISIVLIVLTIVKLKFHPFLALLLASFFVGAMMGMGPLEMVNAIESGIGGTLGFLAAVI

GLDTILGKMMEVSGAAERIGLTLQRCRWLSADVIMVLVGLICGITLFVEVGVVLLIPLAFSIAKKTNTSL

LKLAIPLCTALMAVHCVVPPHPAALFVANKLGADIGTVIVYGLLVGLIASLVGGPLFLRLLGNRLPFKPV

PAEFSNLDVREESTLPSLGATLFTVLLPIGLMLVKTVAELNMAKGGTLYTVLEFIGNPITAMFIAVFVAY

YMLGIRRQMGMGVLLTHTENGFGSIANILLIIGAGGAFNAILKSSGLADSLAVILSNLDMHPILLAWLVA

LILHAAVGSATVAMMGATAIVAPMLPLYPGVSPEIIAIAIGSGAIGCTIVTDSLFWLVKQYCGASLSETF

KYYTTATFIASLLALAATFLLSFII

>WP\_040146642.1 hypothetical protein [Klebsiella pneumoniae]

MTSKYAMGQINSSFSGSSGIIFLSSRLPIIARSA

>WP\_004150274.1 MULTISPECIES: DNA-binding transcriptional regulator DsdC [Klebsiella]

MDVLKTLGTRLLNGWQLSRLSTFEVAARHESFALAADELALTPSAVSHRINQLEEELGIQLFVRSHRKVE

LTREGKRVYWALKASLDGLNQEILDIKNQELSGSLTVYSRPSIAQCWLVPALGDFSRRYPAISLTVLTGN

DNVNLQRAGIDLAIYFDDAPSSQLSHHFLMDEAIVPVCTPYYARQLQLTSNPASLRHCTLLHDRQAWSND

SGTDEWFSWAQQFGIELPQSSGIGFDRSDLAVIAAMNHVGVAMGRKRLVQKRLESGELIAPFGDMTLKCH

QHYYVTTLPGRQWPKIDAFIEWLHSLT

>WP\_004181587.1 MULTISPECIES: multidrug efflux MFS transporter EmrD [Klebsiella]

MKRHKNFNLLLMLVLLVAVGQMAQTIYIPAIADMAVALNVREGAVQSVMAAYLLTYGISQLFYGPLSDRV

GRRPVILVGMSIFMLATLVAITTHSLPVLIAASAMQGMGTGVGGVMARTLPRDLYEGAQLRHANSLLNMG

ILVSPLIAPLLGGILDTLWSWRACYAFLLVLCAGVTFSMAKWMPETRPEGAPRTKLLASYKTLFGTGAFN

CYLLMLIGGLAGIAVFEACSGVLMGAVLGLSSMAVSILFILPIPAAFFGAWFAGRPNKRFPTLMWQSVIC

CLLAGLMMWIPGLLGIMTVWTLLVPAALFFFGAGMLFPLATSGAMEPFPFLAGTAGALVGGLQNIGSGVL

AWLSAMMPQTGQGSLGLLMMLMGLLILLCWLPLASRFTHHQQPV

>WP\_002923296.1 MULTISPECIES: DMT family transporter [Klebsiella]

MTLTVFCILLFAALLHASWNAIVKASGDKMYAAIGVSGSAALIALVMLPFAPQPALVSAPYLLASCALQV

VYTVLVAKTYQVSDMSQTYPLMRGTAPLLVAAISVLFLGDRLSPLAWLGIGVICLAILAMAFNGRASSRK

GIVLALINACFIAGYTLVDGTGVRLAGSALGYTLWTFFMNGFCLLCWAMVARRREASRYLRQHWKKGILG

GIGTMGSYGLALWAMTQAPLAVVAALRETSILFGALIAFIVLKEQLMPLRIVAACGIAAGAILLRLA

>WP\_002923294.1 MULTISPECIES: GNAT family N-acetyltransferase [Klebsiella]

MPPLLIAATTPDAPGFAALRIESLEQHFNMLRRLAENWQSGKNRFNAPGETLLGAFVNHQLVGVCGINSD

PFSPQPRAGRIRHLYISERYRRRGIGQQLLVSVITHSSAWFDFLNTHAPAQAWPFYERLGFRPVYDEPRV

THRLFCSL

>WP\_004145059.1 MULTISPECIES: type I toxin-antitoxin system toxin TisB [Klebsiella]

MCSLTTGDARMGGMDIIILILKLMVAVLQLLDAVLKQFR

>WP\_014343455.1 MULTISPECIES: hypothetical protein [Enterobacteriaceae]

MSKNKLNLYKHRFYVFTMDLFSSTKICAKDHSSAQKGRKQKTPPERGFYQHGYRW

>WP\_002923286.1 MULTISPECIES: ilvB operon leader peptide IvbL [Enterobacteriaceae]

MNATLIASTLLKTAPAAVVVVSVVVVVGNAP

>WP\_004173858.1 MULTISPECIES: acetolactate synthase large subunit [Klebsiella]

MASSGTTSNTMRFTGAQLVVHLLERQGITMVSGIPGGSILPIYDALSQSTQIRHILARHEQGAGFIAQGM

ARTEGKPAVCMACSGPGATNLVTAIADARLDSIPLVCITGQVPASMIGTDAFQEVDTYGISIPITKHNYL

VRDIAELPQVISDAFRIAQSGRPGPVWIDIPKDVQSATIELEALPEPGERAPAPAFAPESVREAAAMINA

AKRPVLYLGGGVINAPQAIRELAEKANLPTTMTLMALGMLPKAHPLSLGMLGMHGARSTNFILQEADLLI

VLGARFDDRAIGKTEQFCPNAKIIHVDIDRAELGKIKQPHVAIQGDVAEVLAQLNPQIEAQPREEWRQLV

ADLQREFPCAIPQESDPLSHYGLINAVAACVDDEAIITTDVGQHQMWTAQAYPLNRPRQWLTSGGLGTMG

FGLPAAIGAALANPQRKVICFSGDGSLMMNIQEMATAAENQLDVKIILLNNEALGLVHQQQSLFYQQGVF

AATYPGMINFMQIAAGFGLQTCDLNNEVDPQAALQAIIDRPGPALIHVRIDAQQKVYPMVPPGAANTEMV

GE

>WP\_002923283.1 MULTISPECIES: acetolactate synthase small subunit [Enterobacteriaceae]

MQKQCDNVILELTVRNHPGVMTHVCGLFARRAFNVEGILCLPIQGSEHSRIWLLVNDDQRLGQMISQIEK

LEDVTKVARNQSDPTMFNKIAVFFE

>WP\_002923282.1 MULTISPECIES: transcriptional regulator UhpA [Klebsiella]

MTTIALIDDHLIVRSGFAQLLGLEADFQVVAEFGSGREALTGLPGRGVQVCICDISMPDISGLELLSQLP

KGMATIMLSVHDSPALIEQALNAGARGFLSKRCSPDELIAAVRTVAAGGCYLTPDIAMKLAAGRQDPLTK

RERQVAEKLAQGMAVKEIAAELGLSPKTVHVHRANLLEKLGVSNDVELARRMFDSWQ

>WP\_004151519.1 MULTISPECIES: signal transduction histidine-protein kinase/phosphatase UhpB [Klebsiella]

MLSVIGCAFIFAAAWFCLWSISLHLVERADLAVLLFPFGLRLGLMLQCPRGYWPVLLGTEWLLILWLAQE

VALAHPIILMTGSLLTLLPVALISRYRQQRDWLTLLRQGGALMAAALLQSLPWLAEGDEGLNALLLTLTG

GLTLAPTCLVFWHYLTSTVWRPLGPALVAQPVNWRGRHLIWYLLLFTISLWLQLGLPAELSRFTPFCLAL

PIIALAWHYGWQGALIATLMNAIALIASQTWHDHPVDLLLSLLAQSLTGLLLGAGIQRLRELNQSLQSEL

ARNRRLAERLLETEESVRRDVARELHDDIGQTITAIRTQAGIVQRLAPDNASVRQSGQLIEQLSLGVYDS

VRRLLGRLRPRQLDDLPLEQAVRSLMREMELEDRGIVSHLDWRINEAGLSENQRVTLFRVCQEGLNNIVK

HASASAVTLQGWQQDERLMLVLEDDGCGLPPGSNLQGFGLTGMRERVTALGGTLTISCTHGTRVCVNLPL

RYA

>WP\_004145056.1 MULTISPECIES: MFS transporter [Klebsiella]

MFAFLKAPPDAAPISDKRELDARYRYWRRHILLTIWLGYALFYFTRKSFNAAVPEILASNVLTRSDIGLL

ATLFYITYGLSKFFSGIVSDRSDARYFMGLGLIATGVVNILFGFSSSLWAFALLWALNAFFQGWGSPVCA

RLLTAWYSRTERGGWWALWNTAHNVGGALIPMVVGAAALHYGWRAGMTIAGCLAILAGLYLCWRLRDRPQ

AVGLPAVGDWRHDALEIAQQQEGAGMSRKAILTRYVLANPYIWLLSLCYVLVYVVRAAINDWGNLYMSET

LGVDLVTANSAVTMFELGGFIGALVAGWGSDKLFNGNRGPMNLIFAAGILLSVGGLWLMPFASYVMQAAC

FFTTGFFVFGPQMLIGMAAAECSHKEAAGAATGFVGLFAYLGASLSGWPLAQVMDIWHWTGFFVVIAIAA

GISALLLLPFLNAQAPRTASEA

>WP\_002923280.1 MULTISPECIES: hexose-6-phosphate:phosphate antiporter [Klebsiella]

MLAFLNQVRKPTLDLPLDVRRKMWFKPFMQSYLVVFIGYLTMYLIRKNFNIAQNDMISTYGLSMTQLGMI

GLGFSITYGVGKTLVSYYADGKNTKQFLPFMLILSAICMLGFSASMGAGSTSLFLMIAFYALSGFFQSTG

GSCSYSTITKWTPRRKRGTFLGFWNISHNLGGAGAAGVALFGANYLFDGHVIGMFIFPSIIALIVGFIGL

RYGSDSPESYGLGTAEELFGEAISEEDKETEENAMTKWQIFVEYVLKNKVIWLLCFSNIFLYVVRIGIDQ

WSTVYAFQELKLSKEVAIQGFTLFEVGALVGTLLWGWLSDLANGRRALVACIALALIIATLGVYQHASNQ

YVYLASLFALGFLVFGPQLLIGVAAVGFVPKKAIGAADGIKGTFAYLIGDSFAKLGLGMIADGTPVFGLT

GWAGTFAALDAAAVGCICLMAIVAIFEERKIRREKKNRILQTA

>WP\_004181583.1 MULTISPECIES: DUF1198 domain-containing protein [Klebsiella]

MIWIGLATLVVVFVVGFRVLTSDSRRAIRRLSERLGITPVPLESMIDQLGKTAGNEYLRYLERPNEAHLQ

NAAQVLLIWQVAIVDASEKNLHYWYRLMQKARLAAPITEAQIRLAQGFLRELDPDMSDLHNLQQRYNDLF

LPEDGVHWLH

>WP\_004173862.1 MULTISPECIES: DNA-binding transcriptional regulator [Klebsiella]

MTAKNKYKSPAFEAIHSAASGLFSVGAIPQETMRHFDESCLGSVAALQPIEIKALREQLNVSQPVFARYL

NTSVSTVQKWETGAKRPSGMSLKLLSVVQKHGLKILL

>WP\_004151518.1 MULTISPECIES: type II toxin-antitoxin system RelE/ParE family toxin [Klebsiella]

MRIFKTKWFAREASSHGISDDELYQAIQSALQGKVVDLGGGVYKKRLNKNRDRAIILTKSAEYWFYTFLY

AKQDMANINHRELMGFRELAKHYANLSEEKTTVLVKSKELVEICDDSKK

>WP\_016532491.1 purine ribonucleoside efflux pump NepI [Klebsiella pneumoniae]

MSHSNEAKPHARDLARPNWSAVFAVAFCVACLITVEFLPVSLLTPMALDLGISEGMAGQSVTTTAFVAMF

SSLFITTVIGKTDRRYVVILFSLLLTLSCLLVSFADSFTLLLLGRACLGLALGGFWAMSASLTMRLVPMR

VVPKALSIIFGAVSIALVIAAPLGSFLGGLIGWRNVFNGAAVMGVLCTLWVLKALPSLPGESASQQQNMF

GLLKRPGVMAGMCAIFMAFAGQFAFFTYIRPVYMTLAGFDVDGLTLVLLSFGIASFIGTSLSSVLLKRSV

KAALAIAPLVLTACAVALVLWGESKIIASTVAIIWGFAFALIPVGWSTWITRSLSDQAEKAGSIQVAVIQ

LANTCGAAVGGIALDHLGLLSPLVLSGILMLFTGLLVAAKVKVNSPA

>WP\_046042128.1 2-aminoethylphosphonate--pyruvate transaminase [Klebsiella pneumoniae]

MTSRNYLLLTPGPLTTSRKVKEAMLFDSCTWDDDYNLGVVQTIRQQLVQLATPADGYTAVLLQGSGSYAV

EAVLGSVIGEQGKVLIVSNGAYGARMIEMAQLMGIACHPYDCGEVSRPDAAAIEQILQNDPAITHIAMVH

SETTTGMLNPIEEVAELAKRYDKRYIVDAMSSFGGIPLDIAALNIDYLISSANKCIQGVPGFAFVIAREA

ELAACKGRSRSLSLDLYAQWRCMEDNHGKWRFTSPTHTVLAFAQALKELAQEGGVSARHQRYRNNQRRLV

AGMRALGFRPLLDDSLHSPIITAFYSPDAPQYRFHTFYQKLKDQGFVIYPGKVSQSDCFRIGNIGEVYDA

DITALLAAIDNAMYWKQ

>WP\_016532492.1 MULTISPECIES: phosphonoacetaldehyde hydrolase [Klebsiella]

MNRISALILDWAGTTVDFGSFAPTQIFVEAFRQAFDIEITLEEARVPMGLGKWQHIEALGKLPAVDSRWQ

AKFGRAMTAADIDAIYAAFMPLQIAKVVDFSAPIAGVVDTIATFRAEGLKIGSCSGYPRPVMEKLVPAAA

AQGYAPDHWVATDDLAAGGRPGPWMALQNVITLGIDDVAHCVKVDDAAPGISEGLHAGMWSVGLAVSGNE

FGATWEEYQAMSKAEIATRRERAAGKLYAAGAHYVVDTLADLPEVIADINARLAKGERP

>WP\_004145049.1 MULTISPECIES: phosphonate utilization transcriptional regulator PhnR [Klebsiella]

MKSPSGEMPQYLMIKAQLQARIQNGALKSGDKLPSERELCALFNTTRITVRESLAQLEASGVIYRADRRG

WFVTPERLWLDPTQNTNFHKLCLEQGREPKTVLLDGRLAAVPLDVMAPLALQPFDQVYLLTRLRYADGRP

VCYCENHCLPARVPELLRHDLNGSLTEIYQTHYDLIYTSMHLSFYPTSMPPQAAEALGVMEGRPALLLRR

LNYDQHGRILDYDIEYWRHDSLRIEVDTH

>WP\_004173867.1 MULTISPECIES: 2-aminoethylphosphonate ABC transporter substrate-binding protein [Klebsiella]

MKLSRLALLSLFALTSSPVWADGVVTVYSADGLHDGDNSWYQSQFAAFTKATGIKVQYVEGGSGAIVERL

AKERTNPQADVLVTVPPFIQRAAKEQLLATFTPQGSAQIPGANDRYAPLVNNYLTFIYNSQLLKSAPASW

QDLLDSRYKNKLQYSTPGQAGDGTAVMLQAFHSLGGKDAGFAYLGKLQANNVGPSASTGKLTALVNKGEL

YVANGDLQMNLSQMARNPNVKIFWPADDKGERSALALPYTIGLVQNGPNSENGKKLINFLLDKPAQSSVS

ARSWGLPVRSDVAPDDANFKAAKAALDGVKSWEPNWDDVAVSLSADIARWHKVTDSE

>WP\_004150258.1 MULTISPECIES: 2-aminoethylphosphonate ABC transport system ATP-binding subunit PhnT [Klebsiella]

MLMKTTVTSSPSLAGTSGITLDSLRVSYHGNVVLKPLSLTIEPGEVLALIGPSGSGKTTVLRAIAGFVQP

AGGRILIGDTDVTQLPPYKRGLAMVVQNYALFPHMKVEDNVAFGLRAQKQPRGLIAERVTEALKIVGMAD

YATRYPHQLSGGQQQRVAIARAIAVRPRVLLLDEPLSALDAQIRHNMVEEIARLHRELPELTILYVTHDQ

TEALTLADKIGIMKDGSLIAHGETHELYHYPPNRFSAEFLGRANILQATALKDSPEPGLVSVSCGGGLIN

AFSRGGLHGNNKLLCIRPQHMSLAPRSATSNRLNATLTSVHWQGDLTHLLCDVAGEAVRIVMTHVNPLPR

AGDKLALYFEPGDAVLIEVQ

>WP\_046042131.1 2-aminoethylphosphonate ABC transporter permease subunit [Klebsiella pneumoniae]

MAQTLTLARPARNLRPYLWLALPLLVLATLFFYPLLLIAEQALRDASGNLSLETFWQVIDSKRFIGALLN

TLQIAVFATLGCLVLGSVLALILVFIPFPGSQLVGRVIDTFIALPTFLITLAFTFIYGSAGLLNGTLMAL

FAFELPPVDFLYSINGVILAEITVFTPLVMRPLMAGLRQIDKSQLEAASILGAHPLRVITHVIFPAALPA

LMAGGSLCLLLTTNEFGIVLFIGAKGVNTLPMMVYSKAILESDYSVACMIALINILLSLGLFMLYRLAAA

RTGVRS

>WP\_004145044.1 MULTISPECIES: 2-aminoethylphosphonate ABC transport system, membrane component PhnV [Klebsiella]

MLIWSRKGRAAAGALAVTLFAGVFLLPLAVILLSSLSKQWNGLLPTGFTFAHFVNAFRGAAWDSLFSSLM

VGFCASLLALLCGMWAALALRQYGATLQKYLGLAFYLPSAIPSVSVGLGILVAFSQGPLQMNGTFFIVLA

AHFVLISAFTFSNVTTGLARISADIENVASSLGASPWYRLRHVTLPLMTPWMISALALSLSLSMGELGAT

VMIYPPGWTTLPVTIFSLTDRGNIADGSALTIVLVGVTLLLMMKLERIARRLSQR

>WP\_022615681.1 carbohydrate porin [Klebsiella pneumoniae]

MNTVKKLPLAMAVVAALCPISVMAQEFTQEQIDAIVAKAVDKALADRQAKIDAAANKKVDVITNPETTAA

SPDMAIPFGLKFSGYARYGAHFQTGDQKYVGVDGSYNGASAIGRLGNESNGGEFQISKAFKSAQGAIWDL

NVMFDHWSDEVNLKKAYVGVTNVLESNPNAYIWAGRDFHQRPQQGINDYFWMNHDGQGAGVKNFDIGGVQ

FDVAAVSQVKSCSPEVMADETNPSRITCTGSSDTGDNGHYALTTKTHNIKAGPIDVEVYANYGFDSKAVD

SDARLEAWQGGLVLSHTNDSGVNKVILRYSDNSDNSVYNKTDDLTTVYASFEGSHKFTQQAQVEYLLAFH

DYDNGKDNADNRKNYGAIVRPMYFWNDVHSTWLEAGYQRVDYDQGGDNHGWKLTLSQNIAIGMGPEFRPM

LRFYVTGGQVDNEHTAKVNNTKDQQLDSLNVGGMFEAWF

>WP\_016530292.1 PTS lactose/cellobiose transporter subunit IIA [Klebsiella pneumoniae]

MMELEDAVMEIIVNAGQSRSLCFEALHAARTGNIDEARLLLNEADGYARRAHQMQTQLIGQDAGEARQPM

TLIMVHAQDHLMNSLLAREFSEELIHLYQR

>WP\_002923156.1 MULTISPECIES: PTS cellobiose transporter subunit IIC [Klebsiella]

MSSLYQSMIAVIEQSITPLAGRLGQQKYVIAIRDGFTAALPFMIIGSFMLVFIFPPFSPDTTNGFARGWL

DFSQHYREQLMLPFNLSMGVMTFFISVGIGASLGRQFQLDPVMSGLLAFMAFLLVAAPYADGKISTQYLS

GQGIFTALITAIYSTRVYAWLKQNNITIRLPKEVPTGVARSFEILIPVLVVIATLHPLNLFIEAQTGMIL

PQAIMHLLEPLVSASDSLPAILLSVLMCQIFWFAGIHGSLIVTGIMNPFWMANLSANQAALAAGTVLPHV

YLQGFWDHYLLIGGVGSTLPLAFLLLRSRATHLRTIGKMGIVPSFFNINEPILFGAPIIMNPMMFIPFVC

VPMVNAVLAYGATRLGWLSQVVSLTPWTTPAPIGASWAANWTLSPVVMCLICMVMSAVIYLPFLRAYERS

LMKTEVEKAKNSVPVAETVS

>WP\_004145041.1 MULTISPECIES: PTS sugar transporter subunit IIB [Klebsiella]

MYKIMLCCSAGMSTSLLVRKMVEAANERDLPVQIDAYGVSEFDMQFPQYQVVLLGPQVKYMLKTLSDKAA

SLNIPVQPIDTMDYGMQRGDNVLNYALSLIPAAH

>WP\_002923154.1 MULTISPECIES: LacI family transcriptional regulator [Klebsiella]

MSTINDVSRLAGVSKATVSRVLSGSRGVKEASRQAVLQAAEALNYRPNMIAQSLLSQSTGCIGVICAQDN

INQTTSYLYALEKQLSQHQKHLLLRFANTSHGVMNSLEELTCGLCDNVLIIGARFPLNINRPDVVLVDCL

DSEGDNSIQFDHAFAAETACHYLISQGRRQIALIHPQSSGFADQVLLGYKHALEKNFLPFNRNLVFLDNT

SPSVAVQELVNNATTLNFNALLVSDEQQAQRVVPQLQAFNRAVPQNVMVFSLAGSLQLPGIPTIPAIEYS

MDAMASRIVNWLTEKTDNPGGSPLRGDLIIPKH

>WP\_002923153.1 MULTISPECIES: aromatic acid/H+ symport family MFS transporter [Klebsiella]

MNHTNVVDVKAWIDTRPVSRFQWNVLLLCFIIIMLDGYDAAVMGFVAPALIEDWGISRAEMGPILGAAMF

GVAIGALVAGPLSDRYGRKRILLWSVALFALFSLAGAVAQSPTQLALMRFLTGLGLGAVMPNCVTLVAEY

MPERRKGVMITLMYSGFNVGSGLGGFIAAGLLSHYSWHSALVFGGVLPLVVLPFMIVMLPESAMNMVARR

LPGEQIARALNRLGGQFTAETVFQLNAPPITRSSKVAQLFRHGYARGTIALWLTYFMGLFVIYLLNGWLP

TILRSGGLSLQQAAMMTGLFQLGGPLGGILVGMLMDRASAKAVIAATYFLGCLCLLSQGVMDFGSAALSV

LIFISGMCINGAQNGLQAYSPAYYQTEIRATGVSWMHGIGRTGAILSSTLGGMLMLAVPGHSSIFLVLAL

PACLAGICILLHRMNHAKPRLTEAELDALSSPLEHR

>WP\_016530403.1 gallate dioxygenase [Klebsiella pneumoniae]

MANILGGIAVSHTPTIGFAVDHHKQQDPAWAPIFQSFEPLQRWLEEKKPDALVYIFNDHVTAFFFDHYST

FTLGIDSQYDVADEGGGPRCLPPVQGNAALSRHIGASLMADEFDMSFFMDKKLDHGLFSPLSALLPWDET

QGWPTAVIPLQIGVLQFPVPSARRCYKLGQALRRAIESFPEDINVAIVATGGLSHQVHGERCGFNNPDWD

AQFVDMLVNDPEKLTEMTLGEYAELGGMEGSEVIMWLVMRGALSANVTETWRDYYLPSMTGIATLILENN

ARLPPVDTLTRHRQHMAQQLAGVEKLPGTYPFTHERSLNGLRLNRFLHRLIEPAWRERFLQSPQSLYAEA

GLSEEEQQLLNARDWRGLIQYGASFFLLEKMGAVVGVSNLHIYAAMRGQTLEAFQQTRNQQVTYSVAGKR

>WP\_002923147.1 MULTISPECIES: LysR family transcriptional regulator [Klebsiella]

MLKRKHDKIINIMQLRFFCQVALRGSVSRAADDLFRTQSAITRAIRDLEAALNVTLFERHYSGMVPTEYG

KCILPRARRAIDDLQAIPALLQKHHTRSSGPLADAGWLFNTRRLAIFIQLYHVNHTQTVAQQLGITQPAV

SAALKVLEKGADSALFRRTPEGVRPTPAAELLYPPVSRALNELENIWSDLAARRGVLEGTVRIGALPLSR

TRLLPSAIAAFLAQHPGITLMTNESPYESLVADMRAGNIDFIIGALRQDEDLPDLCSEALFEEDMLILLR

NNHPLLRHPDPRSQLATAQWVLPRANAPARNLLDKAFVTLGLPLPQPTVETGDAAMVRGLLQGSDMLAAV

SASQMRFETDNGLLSVLPVPLPDTTRRIGLTFRAGSLPSPATQALLRFIYQQVQDGAV

>WP\_004211137.1 MULTISPECIES: 4-oxalmesaconate hydratase [Klebsiella]

MSHPVSEKSALVVSAHSADFVWRAGGAIALHALQGYQVHVVCLSFGERGESAKLWRKGNMTEEAVKQVRR

EEAQAAAAILGASVEFFDIGDYPLRADKETLFRLADVYRRIQPHFVLTHSLHDPYNYDHPLASHLAQEAR

IIAQAEGYRPGEKIVSAPPVYCFEPHQPEQCNWKPDVLLDITAVWEKKYQAIQCMQGQEHLWEYYTRVAL

QRGVQAKRNIGITAARDIVHGEAFQSIFPRVTENLA

>WP\_004145036.1 MULTISPECIES: 4-carboxy-4-hydroxy-2-oxoadipate aldolase/oxaloacetate decarboxylase [Klebsiella]

MNLLNKKGLVIRHLPRHDEAVLRRCEAAGVATLHEAWDRQGLMGPAIRPIQQGVSRAGNAVTVLVTPGDN

WMFHVAVEQCRAGDILVVAPTSPCGDGFFGDLLATSLQSRGVVGLVGDIGIRDSQTLREMGFAVWSRQVY

AQGTVKESLGSVNVPVICAGQLVQPGDVVVADDDGVVVLPHARVRDVLHKAEARMSNELAKRERMRNGEL

GLDIYAMRPRLAEKGLRYYDRADEVEE

>WP\_016530402.1 4-oxalomesaconate tautomerase [Klebsiella pneumoniae]

MAQRGIPCLWMRGGTSKAACFLADDLPADPVRRDAVLLAVMGSPDPRQIDGIGGADPLTSKVAIIRRSAR

PDADVDYLFAQVNVAAATVDYGQNCGNILAAVGPFAIERGLVRYDAPLTRVRIFMENTGQLAVAEIPCDA

DGVNYVGESRIDGVPGSASPILLHFLDVAGSSCGALLPTGRVRDRFDGIEVTCIDNGMPVILLRACDLGC

TGYETREQLDNDDALKRRLESIRLQAGPLMQLGDVSQRTVPKMTLIAEPRHGGAISSRTFIPHRCHASIG

VFGAVSVASACLLPGSVAQGLAQVAPGDTPLLSVEHPTGEFSVTLQLDADGALAGCGLLRTARLLFAGEV

FIPARVWPREE

>WP\_023279339.1 NAD(P)-dependent oxidoreductase [Klebsiella pneumoniae]

MTIAFIGFGEAGGILAADLAREHAVTMWDCKLNGPEREAMGKKARDSRVQVGNSLAQALEGATLVFSTVT

AGEALKVAQQAAALLQPGQYFLDLNSVAPETKRQAAEHFLPGAYIDVAVMAPVPPARLQTPLLIGGPQAE

AIAPRLQRLGLNARYGASTVGQVSAIKMCRSVMIKGLEALTTECLFAAREYGVEEEVLSSLHHSFPSLGW

TGAFPDYLISRVAEHGIRRSEEMEEVVKTLRDVGSAGIMSEAIAKSQRQLPEQMAARSLSYRQLTPFDWK

TLVARLK

>WP\_171819489.1 hypothetical protein [Klebsiella pneumoniae]

MVCLVTALSATSAWAESPLQRLQFEQQKQQVLKAVKEKCAPASHLSDNDFANKVLATDGNKNAVREATLA

KERNNQKSYQAAIDKIVCPAK

>WP\_004234160.1 MULTISPECIES: DMT family transporter [Klebsiella]

MIPLCHISLEEKMGSSKKGMLNVLIAAVLWGSSGVCAQFIMQESQMSSPFLTMTRLLFAGLILLMLGFVH

GDRIFRVLQNRRDALSLLFFSLFGALTVQFTFLMTIEKSNAATATVLQFLSPTIIVAWFALARKARPTPL

VLGAICTSLAGTFLLVTHGNPTTLSISPAALFWGIASAFAAAFYTTYPSTLIARYGTLPIVGWSMLFGGA

MLLPFYGGQGTDFVVNGSLLLAFFYLVVIGTSLTFSLYLNGAQKIGGAKAGILSCAEPLSSALLSLLLLG

ITFTLPDWLGTLLILASVVLIAIDSRRRVRAA

>WP\_046042135.1 PTS N-acetylmuramic acid transporter subunit IIBC [Klebsiella pneumoniae]

MAKITKEMIARILAHVGGAANVAQAGNCMTRLRLTLRDESLADSAAIRQIDGVMGVIVSDEQFQVVLGPG

KAQTAAEMMNGLLEAAPAAAPTLADVAAEKKQALKGKQTSAVQKFLAKFATIFTPLIPGFIAVGLLLGFA

TLAEQVFVLENAHPNASLVALIGYMKVFSKGMFTFLSILIGYNAQKAFGGSGVNGAIIASLFVLGYNPEA

TSGFYAGISTFFGHGIDPRGNIIGVLIAAILGAWVERQVRRVMPANLDMILTSAVTLLIMGAVTFTVIMP

IGGWLFTGMSWLFLHLNGNPFGSAVLAGLFLLAVMFGVHQGFVPVYFAQVDAQGFNSLFPILAMAGAGQV

GAALALFWRAKRDSLLRTQIKGAIIPGFLGIGEPLIYGVTLPRMKPFVTACLGGACGGFFVGLIAWLGLP

VGLNTVFGPSGLVALPLMTSGSGIYAGMAVYAGGLAVSYLCGFVLTWLFGSKNVDLS

>WP\_002923109.1 MULTISPECIES: N-acetylmuramic acid 6-phosphate etherase [Klebsiella]

MSIDLSKLLTERRNANSANIDTLSTLEMLTVINQEDQQVAQAITPYLPQIAEVVDKVAAALQAGGRLIYI

GAGTSGRLGILDASECPPTFGTRPEQVVGIIAGGHKAILSAVENVEDNKAQGAMDLQNLNFSNRDVLVGL

AASGRTPYVIGAMEYAHSQNAFVAIVSCNPHGEMAQLADVAITPVVGPEVVTGSTRLKAGTAQKLVLNMI

STGAMIRVGKVYSNLMVDVEATNAKLIERQVSIVMEATDCDRATAQKALEACGRHCKTAIVMVLADLSAA

EAQSLLAKNNGYIRKALSNT

>WP\_016531448.1 multidrug effflux MFS transporter [Klebsiella pneumoniae]

MARVSLSWALILGLLSGIGPLCTDFYLPALPEITQQLQATSTQTQLSLTAALIGLGLGQLFFGPLSDRIG

RLKPLALSLLLFIFSSAMCALTRDINMLIVWRFLQGFAGAGGSVLSRSIARDKYQGTLLTQFFALLMTVN

GIAPVLSPVLGGYVITAFDWRILFWTMAAIGGVLLVMSLAILRETRPATAAHASRQRPGQPVLKNRRFLR

FCLIQAFMMAGLFSYIGSSSFVMQSEYGMSAMQFSLLFGLNGIGLIIAAMIFSRLARRFSAESLLRGGLT

LAVSCAAIMLLFAWLHLPVLAMVGLFFTVSLMSGISTVAGAEAMSAVDAAQSGTASALMGTLMFVFGGIA

APLAGLGGETMLKMSLAMAICYLLALLLGLSKPRDAR

>WP\_004186228.1 MULTISPECIES: multidrug efflux RND transporter outer membrane subunit EefC [Klebsiella]

MFRLSFMFIALLTAGCVSLDPHYDRPAAPVPATLPGAHGESTAVVGDWQKVVNDARLKKVVSIALNSNRD

VQKALADIEAARAQYGETRASLFPTVDAELSHTRSKTVASGLSSASQADGAVSSFELDLFGKNQSLSRAA

RETWLASEFTAQNTRLTMIADLTTAWVTLATDNSNLALAQQTMDSAANSRNIVARQMAVGTASAGDLSSA

ESVYQQARASVASYRTLVAQDKNAINLLAGETVPESLLPGTLESLGDNSIALVPAGVSSSVLLRRPDIQE

AEHNLKSANADIGAARANFFPSISLTASAGVGSDSLSSLFSHGMQVWSFAPSISLPLFTGGSNLAQLRYA

EAEKKGLIATYEKSIQSAFKDVADALARRETLSEELDAQRQYVAAEQTSLDIAMKSYQAGVGDYLSVLTA

QRTLWSAKTTLLSLQQTDLNNRITLWQSLGGGAS

>WP\_004151514.1 MULTISPECIES: multidrug efflux RND transporter permease subunit EefB [Klebsiella]

MFSRFFVRRPVFAWVIAILIMLAGVLAIRTLPVGQYPDVAPPAVKISATYTGASAETLENSVTQVIEQQL

TGLDHLLYFSSTSSSDGSVSITVTFEQGTDPDTAQVQVQNKVQQAESRLPSEVQQSGVTVEKSQSSFLLI

LAVYDKTNRATSSDISDWLVSNMQDPLARVEGVGSLQVFGAEYAMRVWMDPTKLASYSLMPSDVQSAIEA

QNVQVSAGKIGALPSSNAQQLTATVRAQSRLQTPDQFKAIIVKSQADGSVVRLSDVARVEMGSEDYTATA

NLNGHPAAGIAVMMAPGANALDTATLVKSKIAEFQRQMPQGYDIAYPKDSTEFIKISVEDVIQTLFEAII

LVVCVMYLFLQNFRATLIPAVAVPVVLLGTFGVLALFGYSINTLTLFAMVLAIGLLVDDAIVVVENVERI

MRDEGLPAREATEKSMGEISGALVAIALVLSAVFLPMAFFGGSTGVIYRQFSVTIISAMMLSVVVALTLT

PALCGALLSHSKPHTKGFFGAFNRLWGRTEAGYQRRVLGGLRRGAVMMGAYALICGAMALAMWKLPGSFL

PVEDQGEIMVQYTLPAGATAVRTAEVRRQVTDWFLTKEKANTDVIFTVDGFSFSGSGQNAGMAFVSLKNW

SQRKGDDNTAQAIALRATKELGTIRDATLFAMTPPSVDGLGQSNGFTFELMASGGTDRDSLMKLRSQLLA

AANQSSELQSVRANDLPQMPQLQVDIDNNKAVSLGLSLSDVTDTLSSAWGGTYVNDFIDRGRVKKVYIQG

ESDARAVPSDLGKWFVRGSDNSMTPFSAFATTHWQYGPESLVRYNGSAAFEIQGENAAGFSSGAAMDKME

KLADSLPAGSTWAWSGISLQEKLASGQAMSLYAISILVVFLCLAALYESWSVPFSVIMVIPLGLLGAALA

ATLRGLSNDVYFQVALLTTIGLSSKNAILIVEFAESAVDEGYSLSRAAIRAAQTRLRPIVMTSLAFIAGV

LPLAIATGAGANSRVAIGTGIIGGTLTATLLAVFFVPLFFVLVKRLFTRQRPSQE

>WP\_016529678.1 MULTISPECIES: multidrug efflux RND transporter periplasmic adaptor subunit EefA [Klebsiella]

MKYIIAPIATALFLLSGCDNAQTSAPQQPTPEVGVVTLQSQPVPVVSQLTGRTTASLSAEVRPQVGGIIQ

KRLFTEGDMVKAGQALYQIDPSSYRATWNEAAAALKQAQALVVSDCQKAQRYASLVRDNGVSRQDADDAA

STCAQDKASVESKKAALESARINLNWTTVTAPIAGRIGISSVTPGALVSADQDTALATIRGLDTMYVDLT

RSSVDLLRLRKQSLASNSDTLSVTLTLEDGSTYQEKGRLALTEVAVDESTGSVTLRAIFPNPQHVLLPGM

FVRARIDEGIMNDAILAPQQGITRDAKGDATALVVDAANKVEQRTVETGDTYGDKWLVLSGLKAGDKLIV

EGTGKVAPGQTVKAVAVNNNGGNA

>WP\_004150240.1 MULTISPECIES: hypothetical protein [Klebsiella]

MIILIFPHYTIRRDNGKVFLLTFRTQKIKANNHGENKNIL

>WP\_014343452.1 MULTISPECIES: hypothetical protein [Klebsiella]

MLFVMISVINYLQYRAAEWLFSLSTFTKYSYFLHDYLP

>WP\_004173879.1 MULTISPECIES: GNAT family N-acetyltransferase [Klebsiella]

MTLIITKSINPDDQQELFAGLRQYNQQYLDAAQFGDLGIYSRDAQGVMQGGLIAKRKGNWLCIEYLWVSE

TTRGRGLGSELMQEAEQQAQAQGCSHLLVDTFSFQALPFYQKLGYQLQMSLPDFPHAGMQRHYLSKAL

>WP\_016529677.1 TetR/AcrR family transcriptional regulator [Klebsiella pneumoniae]

MTAQKDQDTPRRPGRPRGKKPGTANREQLMDIALTLFARDGAGRASLNAIAKEAGVTPAMLHYYFSSRDA

LVTQLIEERFMPLRNHISRIFVDHPQDPVLALTMMVETLGHMAEKNAWFAPLWMQEIIGEMPILRQHMDA

RFGEERFQVMLGTVRRWQQEGKINPALAPELLFTTVISLVLVPFSRIHSDPRLQAVNRQTIVSHALALMG

HGVGG

>WP\_017880064.1 MULTISPECIES: MFS transporter [Klebsiella]

MTTQVANPPVQSIRLLFSALLLVMLLSALDQTIVSTALPTIVGELGGLDKLSWVVTAYILSSTIAVPLYG

KFGDLFGRKIVLQVAIGLFLVGSALCGLAQNMTQLVLMRGLQGLGGGGLMVISMAAVADVIPPANRGRYQ

GLFGGVFGLATVIGPLIGGFLVQHASWRWIFYINLPLGLFALLVIGAVFHSSNKRSQHQIDWLGAIYLSM

ALLCIILFTSEGGSVHAWNDPQLWCILAFGIVGIIGFIYEERMAAEPIIPLALFRNRSFLLCSLIGFVIG

MSLFGSVTFLPLYLQVVKEATPTEAGLQLIPLMGGLLLTSIISGRIISRTGKYRLFPILGTLLGVTGMVL

LTRITIHSPLWQLYLFTGVLGAGLGLVMQVLVLAVQNAMPAQMYGVATSGVTLFRSIGGSIGVALFGAVF

THVLQSNLQQLLPEGAVLPPGMNPVAVQHLPADIRLDYLDAFGAAIHAAFLMAAGIMAVAFVLSWLLKEA

PLKTATH

>WP\_072200162.1 LysR family transcriptional regulator [Klebsiella pneumoniae]

MKNDNTGKVAIIFPQNGRIMDRLNAMALLVKVTELGSMSAAARALNMPLTTVSRHIGELESALGVRLLAR

TTRKLTLTDAGVDYVAAARRILEEVENAERQATGEYQEPKGELVISAPTMFGRQHVLPVISEFIARYPLI

RVRLLLSDRNADLVSDHVDLAVRIGDLADSSMVATRLGTMRIVACAHPALLAKYGEPQRPRDLAALPIIR

IESPMPYRGWRFRAAEREDQLINLPPVLSVTTPESAADAARLGVGVARLLHYQALDGLRHGELRLLLENV

EPDPAPVHLLYTARDLAPLKLRKFIDFAAPALRQALLRIAGAA

>WP\_002923018.1 MULTISPECIES: pyridoxamine 5'-phosphate oxidase family protein [Klebsiella]

MAATFLDIAITPDVMDVQHEMGSDSLWQTPRSRRQADRFGDSEAGMIATRDSFYLATVSQSGWPYIQHRG

GPPGFLHLLDDTTLAMADFGGNRQYITTGNLRGSDRACLFLMDYPRRARLKIYATVEVLAAEDHPQLLAQ

VAPANYRARIERLFLFHLQAFDWNCPQHITPRYSAQQVAEYSQNLQQRIHDLEQENQRLQQQLARRGE

>WP\_016529674.1 MULTISPECIES: nuclear transport factor 2 family protein [Klebsiella]

MTEQRPPLPPFTRDSAIQKVRAAEDGWNSRDAEKVALAYTVDSEWRNRSEFVHGRGQIVEFLQRKWRKEQ

QYRLIKELWAWQENRIAVRFAYEWCDDSGNWFRSYGNENWEFDKHGLMQTRYACINDLPISESERLFHWP

QGRRPDDHPGLSELGL

>WP\_004145017.1 MULTISPECIES: peroxidase-related enzyme [Klebsiella]

MSRLADIREQDATGKAADIFAGIKKAMGKVPNAYLTIGGHSPAALQQALAHNAMLHKGSLSAQQLEAINL

SVSEATGCDYCLAAHTLMAKKAGFSSEQIHALRRGEYAEEAQLDALVKFAQTLVTTTGTLPEADVAALRN

AGFSDQQVIEIISAISAILFTNMVNRVNDTVVDFPKAD

>WP\_016529673.1 AraC family transcriptional regulator [Klebsiella pneumoniae]

MDSLSHLLALLAPRCEVNLHCRFGGRWQAGHQQMRSGVVPWHVVLRGEGRLNVGGQTHHLRAGDVVLLPH

GSPHLMESLVEWGQVLPVAHRFNGTVTEMRAGPAERALEMLCGEFYFGPHVSWLFSEASTLIHLHTDARE

DCPELDALLNILVRESLAQRPGGSAIVRSLGDTLLVLLLRMLLGEQQPPGGLLRLMSDERLMPAVLAVMA

TPEQPWTLESMAARAFLSRATFARHFARVYHLTPQAWLSQLRMALAARLLRLERQTNLEVIAERCGFQSL

ASFSKRFKMRYGVTPGEWRRG

>WP\_002922973.1 MULTISPECIES: lipoprotein NlpA [Klebsiella]

MRLRLQAAAAVMLAGLALVGCDQKGNEAKHIKVGVINGAEQDVAEVAKKVAKEKYGLEVELVGFSGSLLP

NESTNAGDLDANVFQHRPFLEQDNKAHNYHLVAVGNTFVFPMAGYSRKIKSVAELKDGATIAIPNDPTNL

GRALLLLQKEKLITLKAGTGLLPTAVDITDNPRNLKIMELEGAQLPRVLDDPKVDVAIISTTYLQQTGLS

PVRDGIFIEDKNSPYVNIIVTREDNKDAQNVKEFMQSYQSPEVAKAAETIFNGGAVPGW

>WP\_002922972.1 MULTISPECIES: DMT family transporter [Klebsiella]

MVRQRQADLLLIAATVIAACGWIFSREAIAGMPVFAFLGLRFFFAALLLLPFCRGFRPQKQHWPKLIISG

LWFALNLCLWIYSVSTTASLGEGAFIMSLSMMFVPLTAWVMMKVRPPRAWWECLPIAVVGLGLLSLHMPI

AFHPSQGWFLLTALVQSIWFCYTSRCAREVPLIPLTTVQLAITGIVGLTISAAVERWDQPMTLPTLGWLV

ASIVIATSLRFGLQMKGQKYAAVASAAIIMVLEPLLTVIAAALWYGEQLPLQKIIGGVLILVAQLWFRWR

MLKP

>WP\_004186204.1 NUDIX hydrolase [Klebsiella pneumoniae]

MKKKLTAADMHDPQVIAETPWFSMRKVGIDVAPGERRDFYSIHYPRPAVGIVAIQDEKVLLIRHYRYLID

KVVWAIPSGGVDEEEDPAVAALRELREETGWQAQRVEEIIRFNPSYGSSDQLFITWLATGLRWVGMDADQ

DEVMETGWFTFDEINQLIARGEMPDGLSLVPLLQLMAQRRSGPLTA

>WP\_016529670.1 MBL fold metallo-hydrolase [Klebsiella pneumoniae]

MNITHIRNATQIIHYAGKRFLIDPMLADKGAWPGFPGTARSELRNPLVELPFSRDKIVDVDAVIVTHTHD

DHWDAAAIAAIPKTLPVFVQHEADAALLRSQGFQDLRLLSADSEFAGVRLLKTTSGQHGSDRTYAVPAMA

ERLGEACGVVFRHPQEKTLWLVGDTIWRDDIAADLLKLRPDVVVLNAGYAHVIGFGPIIMGKEDLLNVHF

ALPEAKIMAIHLEAVNHCLVSREEMRQYALDNQIADVVSIPQDGETVVY

>WP\_004145010.1 MULTISPECIES: helix-turn-helix domain-containing protein [Klebsiella]

MKLTDVAIVAVEGFSPFHYAVPCMLFGDSVSEIKRFNLHICAERPGLLRARDGFALYATGDYAALEQADI

VVVPYWGEVDRRPPQALLDSLVRARDNGAEIVGLCLGAFVLGYAGLLDGRRAATHWEFEQDFQRRFPQVQ

LDINALYVDDQRIITSAGTAAALDCCLYIIRQRFGSLAANQIARRMIVSPHREGGQAQFIAQPVPKNTRD

ARINCLLDYLQQHIAEPHSLDSLARVVAMSRRTLTRHFARATGMSITDWLTAERLRRSQTLLEAGDLPVE

QVAEAVGYLSAVTWRQQFKARFGVSPTEWRRTFRRGA

>WP\_016530861.1 NAD(P)-dependent alcohol dehydrogenase [Klebsiella pneumoniae]

MLINAIGTYSASQPLESMAITRRDPGPQDVQIAIAYCGVCHSDLHQARSEWAGTLYPCVPGHEIVGRVTA

VGNAVSRYAVGDLVGVGCMVDSCQQCEECAEGLENYCDHMVLTYNGPTQDAPGHTLGGYSQQIVVNERYV

LRITHPEAQLAAVAPLLCAGITTYSPLRHWHVGPGKKVGVVGIGGLGHMGIKLAHAMGAHVVAFTTSESK

RNAARALGADDVVVSRNDDEMAAHVKSFDFILNTVAAPHNLDAFTTLLKRDGTMTLVGAPATPHPSPEVF

NLIFRRRSIAGSMIGGIPETQEMLDFCAEHGIVADIELIRSDEINEAWERMVKGDVKYRFVIDSATLAG

>WP\_004151507.1 MULTISPECIES: winged helix-turn-helix transcriptional regulator [Klebsiella]

MSIPAASLSTDQALPSFYYGRQTKPLFAVESLLSAFLPASSPFALPRSTYYRFPPTQAESGLILLEEGIA

SLCHAENNMVISTIFAPSLLGLIDGYGVFNGIPEKHHCSLFAETDLRGRWIGHQAAVEILNAQNLWQEMA

HVLAQRLMVLSMRSQEMVGVDSYPMVRTLLTELADYPEEYRRQINALSFIQRRTNLSRSRVMSILAELRK

GGYITVHRGVLEKITRTLPAHF

>WP\_002922965.1 MULTISPECIES: antibiotic biosynthesis monooxygenase [Klebsiella]

MISLIAVLKAKPGQTDALRQALQALLLPTRQEPGNLDYALFQLRDAPDTFYMREAWQGQDALDAHVAMPY

FQAFMTQMESLLAEPLRLDFLTPVEP

>WP\_004181552.1 MULTISPECIES: zinc-binding alcohol dehydrogenase family protein [Klebsiella]

MKAIAITQAAADGNNIPSLTEIDLPIPTAHGRDLLVAVKAISVNPVDTKVRAGFQGDTPRVLGWDAVGVV

QSVGEEVTLFAPGDEVWYAGALGRAGSNSEYQLVDERLVAHKPRTLDNASAAALPLTAITAWELLFHRLG

VEEGGNAGDTLLIVGAAGGVGSILTQLASKLTAMTVIGTASRPESQQWVREAGAHHVIDHSKPLADELAR

IGITSVTHVASLTNTEQHFNALINALAPQGKLALIDDPETLDVVPLKAKSLSLHWEFMFTRSMFETDDMI

AQHQLLTRVAALIDNHTIKTTLGEHYGAITAANLQKAHRQLETGRAVGKIVLEGF

>WP\_002922963.1 MULTISPECIES: DUF3237 domain-containing protein [Klebsiella]

MTPELRHCFSITIQVDKPIIVSRSPQTGKRQLIPIVGGSVSGQLRGHVLPGGVDSQIIEPDGTCRLSARY

ALQVAEGTVYVENNGIRRVPAQYHDQLFADDMRFFSDIPPEAIYFRTVPTFEVDAPALSWLTTSLFICAG

GRTQDGVMLDFYQVG

>WP\_046042158.1 alpha-xylosidase [Klebsiella pneumoniae]

MKISDGNWLIQPGLNLIQPVQVYEVEQQGNEMVVYAAPRDVRERAWQLDTPLFTLRFFSPQEGIIGVRME

HFQGALDNGPHYPLNVQKDIHVEIENTAGFAELKSGSLSVRVTKGEFWGLDFLRDGVRITGSQLKNNGYV

QDSKTQRNYMFERLDLGVGETVYGLGERFTALVRNGQTVETWNEDGGTSTEQSYKNIPFYLTNRGYGVLV

NHPQRVSFEVGSEKVSKVQFSVEGEYLEYFVIDGPTPKAVLNRYTQFTGRPALPPAWSFGLWLTTSFTTN

YDEATVNSFIDGMAERHLPLHVFHFDCFWMKAFQWCDFEWDPQTFPDPEGMIKRLKAKGLKVCVWINPYI

GQRSPVFKELKEKGYLLKRPDGSLWQWDKWQPGLAIYDFTNPEARQWYADKLKGLVAMGVDCFKTDFGER

IPTDVQWFDGSDPQKMHNHYAFIYNELVWKVLKETVGEQEAVLFARSASVGAQQFPVHWGGDCYANYESM

AESLRGGLSIGMSGFGFWSHDIGGFENTAPAHVYKRWCAFGLLSSHSRLHGSKSYRVPWAYDDESCDVVR

HFTQLKCRMMPYLYRQAALANECGTPMLRAMLLEFPDDPACDYLDRQYMLGDSVLVAPVFSEAGEVQFYL

PEGHWTHLWHNDELPGSRWHKQHHDALSLPVYVRDNTLLALGNNDQKPDYAWHEGTAFQLFHLEDGREAR

CDVPAADGSTIFTLKARRQGNAIAVSGEGEARGWTLCLRNIPQVAGVQGGTQTGSELGVVVSAEGNTLTI

TL

>WP\_016530457.1 SIS domain-containing protein [Klebsiella pneumoniae]

MDVENIFRDVKLSKTEMTVLRFIQNDPEQCIRQGVRAVAEQCYSNPSSLVRLAKKLKFSGWLELVYFIKF

NITMPKLDVTNDIDYMSVQPEEALTPLLASLKQQRTLIHGSGFSQLIAQYIYNKFLVTGVNASLALWPDY

EILEQKNAACFDSIWIISKSGRSSSALNWVKALEGKEINLVCFTGDYQSPLAQAADTAFIIHDPQKFDDD

IYWSNPFFGYCILGFERLLKMWFTSLRSNS

>WP\_016530456.1 maltose-6'-phosphate glucosidase [Klebsiella pneumoniae]

MKLTVLGGGGVRSAFLAKSLAYNAHRIGLTEVVFLDNSADNLAIFGEIARYVFNTIRPDIQFSTTTDPVA

ALQDANYIITTLRVGGDESRIRDERIALEHNTLGQETTGAGGFAMAMRSIPAILGCEERDLSVECYGLNH

FSWFTHFTVRGEEVTERLIASPELYQKTAMQYFSPELVRLCDNQLLNEYLYYYYYRDEALKAIQGAGETR

GEQIARINQEMREALRTVDARTQPEAAFTIWMQHYLRRENSYMQNESRQEKFHTREPLTLRQFIEEPDTG

GYAGVALDILEAVNSTTTKRIVVSIQNNGTLDFLRPDDVIEISCDLSRDGLRPVTPVKVPTAQKNMIACV

KEYERLAVAAILQQDKSLAVRALMAHPLIGSYSLAKTLVEAYLDDEQFAAWR

>WP\_002922953.1 MULTISPECIES: PTS transporter subunit EIIC [Klebsiella]

MPEIRQRILENMQKFSRAMIGAVLFLPVIGLILALSSVLTNPTLIAETSFLHQLGQMLGDTFWPLFGNLG

LLFCVGISYGLAKDKKTEVALVSVMCFIMFLGANHSWLEHTHGLAEKINGEYYGTGQTQLLGFVVVDMGV

FLGIILGCTIAWVHNKVSAIELPGALSMYGGAKLTLVAMTPVVIFYAIAFTWIWPFMTHGISALTGFMKN

AGVAGVFVYGFFEKFLIPTGLHHFVWSPFQLTQIGGTLNVDGQVVSGTQAIFLAYMRHPDLTPVMNDALR

FSQQGMTTIFGLAGASLAFYHTAKPEKKAMAKAILLPAIITSMLTGITEPIEFTFLFVSPLLWVIHATLT

AASQAICDIFTVRPWGASGLIEFLIYNLPLPVSLTRWPGYVLIGIGQFAVYYVIFRTLVVKLNLKTPGRE

DDENVKLYSKAEYRQKVAQPQSVTDDIIRGLGGKENILSVDNCFTRLRVAVRDMARVDDTQLKNTGANGV

VRNRNEVQVIYGVKVGQVRSRVDNWLAEN

>WP\_004186173.1 MULTISPECIES: AsmA family protein [Klebsiella]

MKFLGKLILWLLVALLLVIIGAWFLLQTHWGARQASAWLSNGTGWQVSFDEMEHDFSSPLHVQLRNVTFG

REGKPATLVAKTVDIGFSTRQFSDPLHADEIVLNDGTLNLSPHSADLPFAADRLMLRNMAFNSPETGWAL

SAQRVTGGVSPWTPEAGNVLGKTAQIQMSAGSMTLNGVEASNVLIQGKIDQGEVTLSTLGADVARGTLTG

NAKRSADGSWRVDNLQLNEIRLQSPASLAEFFAPLTTVPSLQIGRLDITDARLQGPDWAVTDLDLSLRNL

TLSHGGWQSEDGTLSMNASEFIYGSLHLFDPILNAEFSPQGIALRQFSSRWEGGMVRTSGNWLRAGNALV

LDDTAFAGLEYTLPANWKQLWMTPLPAWLQSLTLKKFSASRNLIIDVDPAFPWQITALDGYGGELQLVKN

GSWGVWNGSATLNAAAATFNRIDVRRPSLKLNATASTVNITELSAFTERGILQATAAVSQLPQRQVNLSF

SGRGVPLNILQAWGWPSLPISGDGNLQLTASGSVQADAPLKPTINGQLSAVNMEKQQVAQIMRNGEVSPA

PAAPAPAPVTP

>WP\_002922950.1 MULTISPECIES: uracil-xanthine permease family protein [Klebsiella]

MSVNTAESENAQPVAHKPASELIYRLEDRPPLPQTLFAAFQHLLAMFVAVITPALLICQALGLPAQDTQH

IISMSLFASGVASIIQIKAWGPVGSGLLSIQGTSFNFVAPLIMGGTALKTGGADVPTMMAALFGTLMLAS

CTEMVLSRILHLARRIITPLVSGVVVMIIGLSLIQVGLTSIGGGYAAMADHTFGAPKNLLLAGIVLALII

ILNRQRNPYLRIASLVIAMAAGYLAAWFLDMLPANTAPTNSSLITVPTPLYYGLGIDWSLLLPLMLVFMI

TSLETIGDITATSDVSEQPVSGPLYMKRLKGGVLANGLNSFVSAVFNTFPNSCFGQNNGVIQLTGVASRY

VGFVVALMLIVLGLFPAVSGFVQHIPEPVLGGATLVMFGTIAASGVRIVSREPLNRRAILIIALSLAVGL

GVSQQPLILQFAPDWLKNLLSSGIAAGGITAIVLNLIFPPEKA

>WP\_016529540.1 sodium/glutamate symporter [Klebsiella pneumoniae]

MFHLDTLSTLVAATLVLLLGRKLVQTVPFLKKYTIPEPVAGGLLVALALLALKKSMDIEIDFDMSLKDPL

MLAFFATIGLNANLASLRAGGKVLGTFLIVVVGLLLLQNALGIGMATLLGLDPLMGLLAGSITLSGGHGT

GAAWSKLFVERYGFANATEVAMACATFGLVLGGLIGGPVARYLVKHSSSPDGTPDDQVAPTAFEKPDVGR

VITSLVLIESIALIAICLTLGKVVAQLLAGSVFELPTFVCVLFIGVILSNSLALAGLYRVFDRAVSVLGN

VSLSLFLAMALMSLKLWELASLALPMIIILAVQALAMALYAVFVTYRMMGKNYDAAVLAAGHCGFGLGAT

PTAIANMQAITDRFGPSHMAFLVVPLVGAFFIDIVNALVIKLYLLLPMFG

>WP\_002922944.1 MULTISPECIES: glycerol kinase GlpK [Klebsiella]

MTDKKYIVALDQGTTSSRAVVMDHDANIVSVSQREFEQIYPKPGWVEHDPMEIWASQSSTLVEALAKADI

NSDQIAAIGITNQRETVVVWERETGKPIYNAIVWQCRRTAEICEQLKRDGMEEYIRKATGLVVDPYFSGT

KVKWILDHVEGSRERAKRGELLFGTVDTWLIWKMTQGRVHVTDYTNASRTMLFNIHDLDWDDKMLDALDI

PRAMLPEVRKSSEVYGQTNIGGKGGTRIPIAGIAGDQQAALFGQLCVKEGMAKNTYGTGCFMLMNTGEKA

VTSTHGLLTTIACGPRGEVNYALEGAVFMAGASIQWLRDEMKLISDAFDSEYFATKVKDTNGVYVVPAFT

GLGAPYWDPYARGAIFGLTRGVNSNHIIRATLESIAFQTRDVLEAMQADSGIRLHALRVDGGAVANNFLM

QFQSDILGTRVERPEVREVTALGAAYLAGLAVGFWQNLDELQEKAVIEREFRPGIETTERNYRYSGWKKA

VKRALAWEEHDEA

>WP\_002922941.1 MULTISPECIES: aquaporin [Klebsiella]

MSQTSTLKGQCIAEFLGTGLLIFFGVGCVAALKVAGASFGQWEISIIWGLGVAMAIYLTAGVSGAHLNPA

VTIALWLFACFEGRKVVPFIISQFAGAFCAAALVYGLYYNLFLDYETTHHMIRGSVESLDLAGIFSTYPN

PHINFVQAFAVEMVITAILMGVILALTDDGNGIPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDIGP

KAFAWLAGWGDVAFTGGKDIPYFLVPLCAPVVGAALGAFSYRKLIGRHLPCDTCVEEEQQSPSSSTAQHK

ASL

>WP\_004150222.1 MULTISPECIES: septal ring assembly protein ZapB [Klebsiella/Raoultella group]

MTMSLEVFEKLESKVQQAIDTITLLQMEIEELKEKNNTLVQEVQSAQHGREELERENSQLKEQQQGWQER

LQALLGRMEEV

>WP\_002922936.1 MULTISPECIES: sulfate ABC transporter substrate-binding protein [Klebsiella]

MNKWGVGLTLLLASASVLAKDIQLLNVSYDPTRELYEQYNKAFSAHWKQETGDNVVIRQSHGGSGKQATS

VINGIEADVVTLALAYDVDAIAERGRIDKNWLKRLPDNSAPYTSTIVFLVRKGNPKQIHDWNDLIKPGVS

VITPNPKSSGGARWNYLAAWGYALHQNHGDQAKAQEFVKALYKNVEVLDSGARGSTNTFVERGIGDVLIA

WENEALLATNELGKDKFEIVTPSESILAEPTVSVVDKVVDKKGTRQVAEAYLKYLYSPEGQEIAAKNFYR

PRDPNVAKKYANEFPKLKLFTIDQEFGGWTKAQKEHFSNGGTFDQISQR

>WP\_020803798.1 MULTISPECIES: CDP-diacylglycerol diphosphatase [Klebsiella]

MKMRRVRYFLLALLVAILAALAGGYYWLHSGNPDALRKIVLQQCVPHQQQQQNPSPCAEVNLKGGYVLFK

DRNGPLQYLLMPTYRINGTESPLLLEPLTPNFFWQAWQGREIMSQRHGAPVPDNAVSLAINSRSGRTQNH

FHIHISCLRPDVRAQLDKDAAAISSRWLPLPGGLQGHEYLARRVTEAELAQRSPFLMLAEEVPEAREHMG

RFALAMAQQSDGSLVLLATERNLLTLNRASAEEIQDHRCAILNANH

>WP\_004151505.1 MULTISPECIES: SLC13 family permease [Klebsiella]

MSLWLTHPLFLPSLIVGVTIVLWATSLLPEFITALLFFAAAMMAKIAPPEVIFGGFASSAFWLVFSGFVL

GIAIRKTGLADRAAQALSARLTDSWPRMVASVVLLSYALAFVMPSNMGRIALLMPIVAAMARRAGIADGS

RGWFGLALAVGFGTFQLSATILPANVPNLVMSGAAEGSYGIHLNYVPYLLLHTPVLGWLKGAVLVALICW

LFPGKPHPPRDLAPLPPMSRDEKRLAWLLAVVLSLWVTESWHGVGPAWTGLAAAVITLLPRVGFINGEEF

ASGVNMRTCIYVAGILGLAIAVTQTGIGGAVGNALLQVMPLDKDNPFTSFLALTGITSALNFIMTANGVP

ALYTTFAQSFADATGFPLLSVIMIQVLGYSTPLLPYQASPIVVAMGLGKVPARAGMQLCLALAAVSYLIL

LPLDYAWYQLLGKL

>WP\_002922909.1 MULTISPECIES: triose-phosphate isomerase [Klebsiella]

MRHPLVMGNWKLNGSRHMVNELVANLRTELAGVSGCAVAIAPPEMYLDLAKRAAEGSHIHLGAQNVDVNL

SGAFTGETSAEMLKDIGAQYIIIGHSERRTYHKESDELIAKKFAVLKEQGLTPVLCIGETEAENEAGKTE

EVCARQIDAVLKTQGAAAFEGVVIAYEPVWAIGTGKSATPAQAQAVHKFIRDHIAKADAKIAEQVIIQYG

GSVNAGNAAELFTQPDIDGALVGGASLKADAFAVIVKAAEAAKKA

>WP\_002922908.1 MULTISPECIES: YiiQ family protein [Klebsiella]

MKKWTILWLSGLMGLAVGPHALSAESESTTAAAPYLLAGAPSFDQSISQFREKFNADNPKLPLNEFRSIA

TSRDRANLTRAASKINENLYASTALERGTLKIKSMQITWLPIQGPEQKAARTKALEYMSAMIRAFVPTFS

QAQSQQKLQKLLAAGKGKRYFADTEGAVRYVVADHGEKGLTFAIEPIKLALSETLEGNNK

>WP\_002922907.1 MULTISPECIES: DUF805 domain-containing protein [Klebsiella]

MTLQQWLFSIKGRIGRRDFWIWIAIWLVTMSALFTLAGSNLLNLQTAAFIIVCLLWPTAAVVVKRLHDRG

KSGLWALLMVLAWMLLAGNWAMLPQVWQWGVGRFVPTLIIVMMLIDLGAFVGTQGENKFGKETQDVRWKA

DA

>WP\_004173895.1 MULTISPECIES: ferredoxin--NADP(+) reductase [Klebsiella]

MADWVSGKVTKVEYWTDALFSLYVRAPVHPFTAGQFTKLGLEIDGERVQRAYSYVNAPGNPDLEFYLVTV

PEGKLSPRLAALKPGDEVLVVSEAAGFFVLEEVPDCDTLWMLATGTALGPYLSILQEGKDLERFNNLVLV

HAVRYAADLSYLPLMRELEQRYAGKLRIQTVVSRETVEGSLTGRVPFLIETGALEEAVGLPMTTDTSHVM

LCGNPQMVRDTQQLLKETRQMTKHLRRRPGHMTAEHYW

>WP\_002922903.1 MULTISPECIES: class II fructose-bisphosphatase [Klebsiella]

MKRELAIEFSRVTEAAALAGYKWLGRGDKNTADGAAVNAMRIMLNLVNIDGTIVIGEGEIDEAPMLYIGE

KVGTGKGDAVDIAVDPIEGTRMTAMGQANALAVMAVGDKGCFLNAPDMYMEKLIVGPGAKGAIDLNLPLE

ENLHNIARALNKPLGELTVTVLAKPRHDAVIAQLQQLGVRVFAIPDGDVAASILTCMPDSEVDVLYGIGG

APEGVVSAAVIRALDGDMQGRLLARHHVKGDNEENRRIGENELARCKTMGIEAGKVLRLDEMARSDNVVF

SATGITKGDLLDGITRKGNMATTETLLIRGKSRTIRRIQSIHYLDRKDPDIQQHIL

>WP\_004151504.1 MULTISPECIES: ATP-dependent DNA helicase RecG [Klebsiella]

MSGRLLDAVPLSSLTGVGAAQSSKLAKIGLHTVQDLLLHLPLRYEDRTHLYPIAELLPGVYATVEGEVLN

SNITFGGRRMMTCQISDGTGILTMRFFNFNAAMKNSLATGRRVLAYGEAKRGKYGAEMIHPEYRVQGDMS

TPELQETLTPVYPTTEGIKQATLRKLTDQALELLETCAISELLPPELAQGMMSLPEALRTLHRPPPSLQL

SELESGKHPAQQRLILEELLAHNLSMLALRAGAQRYHALPLGANDTLKNQLLASLPFKPTGAQARVTAEI

EHDMALDVPMMRLVQGDVGSGKTLVAALAALRAIVHGKQVALMAPTELLAEQHANNFRNWFEPLGIEVGW

LAGKQKGKARQAQQEAIASGEVQMIVGTHAIFQEQVQFNGLALVIIDEQHRFGVHQRLALWEKGQQQGFH

PHQLIMTATPIPRTLAMTAYADLDTSIIDELPPGRTPVTTVAIPDTRRSDIIDRVRNACTHEGRQAYWVC

TLIEESDLLEAQAAEATWEELKLALPELNIGLVHGRMKPAEKQAVMQAFKQGEMHLLVATTVIEVGVDVP

NSSLMIIENPERLGLAQLHQLRGRVGRGAVASHCVLLYKSPLSKTAQKRLQVLRDSNDGFVIAQKDLEIR

GPGELLGTRQTGNAEFKVADLLRDQAMIPDVQRIARHIHERYPLQAQALIERWMPETERYSNA

>WP\_004181538.1 MULTISPECIES: tRNA (guanosine(18)-2'-O)-methyltransferase TrmH [Klebsiella]

MNSKRYERICEMLARRQPDLTVCMEQVHKPHNVSAVIRTADAVGVHEVHAVWPSSRMRTMASAAAGSNSW

VQVKTHRTIADAVGHLKGQGMQILATHLSDKAIDFREIDYTRPTCILMGQEKTGITQEALALADQDIIIP

MIGMVQSLNVSVASALILYEAQRQRQNAGMYQRANSMLPPQEQQRLLFEGGYPVLARVARQKGLPYPHVN

EQGEVEADAAWWATMQAAR

>WP\_004150214.1 MULTISPECIES: bifunctional GTP diphosphokinase/guanosine-3',5'-bis pyrophosphate 3'-pyrophosphohydrolase [Klebsiella]

MYLFESLNQLIQNYLPEDQIKRLRQAYLVARDAHEGQTRSSGEPYITHPVAVACILAEMKLDYETLMAAL

LHDVIEDTPATYQDMEQLFGKSVAELVEGVSKLDKLKFRDKKEAQAENFRKMIMAMVQDIRVILIKLADR

THNMRTLGSLRPDKRRRIARETLEIYSPLAHRLGIHHIKTELEELGFEALYPNRYRVIKEVVKAARGNRK

EMIQKILSEIEGRLQEAGIPCRVSGREKHLYSIYCKMVLKEQRFHSIMDIYAFRVIVHDADICYRVLGQM

HSLYKPRPGRFKDYIAIPKANGYQSLHTSMIGPHGVPVEVQIRTEDMDQMAEMGVAAHWAYKEHGGESST

TAQIRAQRWMQSLLELQQSAGSSFEFIESVKSDLFPDEIYVFTPEGRIVELPAGATPVDFAYAVHTDIGH

ACVGARVDRQPYPLSQPLSSGQTVEIITAPGARPNAAWLNFVVSSKARAKIRQLLKNLKRDDSVSLGRRL

LNHALGGSRKLAEIPPENIQRELDRMKLASLDDLLAEIGLGNAMSVVVAKNLQQGEAAAAPVPANASNHG

HLPIKGADGVLITFAKCCRPIPGDPIIAHVSPGKGLVIHHESCRNIRGYQKEPEKFMAVEWDKETAQEFI

TEIKVDMFNHQGALANLTAAINTASSNIQSLNTEEKDGRVYSAFIRLTARDRVHLANIMRKIRVMPDVIK

VTRNRN

>WP\_000135058.1 MULTISPECIES: DNA-directed RNA polymerase subunit omega [Bacteria]

MARVTVQDAVEKIGNRFDLVLVAARRARQMQVGGKDPLVPEENDKTTVIALREIEEGLINNQILDVRERQ

EQQEQEAAELQAVTAIAEGRR

>WP\_002922664.1 MULTISPECIES: guanylate kinase [Klebsiella]

MAQGTLYIVSAPSGAGKSSLIQALLKTQPLYDTQVSVSHTTRAPRPGEVHGEHYFFVNHDEFRSMIGENA

FLEHAEVFGNYYGTSRKAIEQVLATGVDVFLDIDWQGAQQIRKSMPGARSIFILPPSKDELDRRLRGRGQ

DSEEVIAKRMAQAVAEMSHYAEYDYLIVNDDFDTALSDLKNIIRAERLRMSRQKQRHGALITKLLAD

>WP\_020864855.1 NAD-dependent DNA ligase LigB [Klebsiella pneumoniae]

MRKGGWWLALGMFSASVLATCPDWPPARGRQETSRLHQQIVAWKEAYWRQGASGVSDDVYDQLTLRLAQW

RQCFPGATPEDDDLPPPTGDARHPVAHTGVRKLADEDSVARWMKNKSDLWIQPKVDGVAVTLVYRQGRLV

QAISRGDGLRGEAWTARARQIPALEKVMTGELADSVLQGELFLRRDGHVQQQAGGMNARAKVAGLMMRAD

AAAALSQLDVFIWAWPDGPSDMRRRQKLLAQAGFKYSGQYTHPVSRIEQVAQWRQRWYRSPLPFVSDGVI

VREGREPPGRVWSPGKGEWLAAWKYPPASRVMQVRAIRFSIGRSGRLNVVAELEPQRLDDKRVQRVNVGS

VSRWQMLDIGVGDQLQISLAGQGIPRVDAVVWRTAERHKPTPPPAKFNALTCYFATHECSEQFLSRLIWL

SSKSALNVDGVGENLWRVIQQQNPMTHIFSWLALTVEQLQAVPGISAARGQHLWHQFDLVRKRPFIRWVL

AMGIPVPQGALAQLESENWHLLAAKSEAQWRTLPGVGEIRARQLVAFLHHPDVVALAQWLSGQRIPGF

>WP\_002922654.1 MULTISPECIES: trimeric intracellular cation channel family protein [Klebsiella]

MLLHVLYLIGITAEAMTGALAAGRRRMDTFGVIIIATATALGGGSVRDILLGHYPLGWVKHPEYVIIVAV

AAVLTTIAAPVMPHLRRLFLVLDALGLIVFSIIGAQIALDMGEGPVIASIAAVITGVFGGVLRDMFCKRI

PLVFQKELYAGISFAAAVLYIALQHYVSSHDVVVLATLLFGFTARMLALRWKLGLPVFHYTHDAH

>WP\_009308789.1 MULTISPECIES: chloride channel protein [Klebsiella]

MSVAAGNKNHLIRLIAVVLTGILAGLSGMVLALILHAIQHLAFGYSYGQIVGSVSFLQGVTESSWPRRIV

AIVAGGAVAGFGWWLLGRYGQRRVSIAAAVANPCVPMPAGTTTIHALLQIVTVALGSPLGREVAPREMGA

LGAGMVARKLRLLEDETRTLIACGAGAGLAAVYNVPLAGALFSLEVMLLSFSWEKTLAAIMTSAIAAWTA

TLGLGDESQYHFVSSALPHTFLWWAILAGPILGTGAWLFRKATSAARSRARSNWQMPVFCLLGFSLLAIL

SLYFPELPGNGKGPMQLALSDGLPLSMVAVLLVLKMVVILAVLRGGAEGGLLTPGLAVGGLVSLLLCALW

QLGFPGGDKSSFAVVGAAAFLAASMQMPLTAVALVMEFTHMDHSYLAPALLCAAGAFLTCRVLDKK

>WP\_004151500.1 MULTISPECIES: methylated-DNA--[protein]-cysteine S-methyltransferase [Klebsiella]

MKITDSMQCDIWYQALLERAVEFTGVFFVGVKTTGVFCISVCRARKPRRENVEFYNDFKSALDAGFRPCK

VCRPTENARTAPAFVEQALRLLREAPKVRLSDSELRQHDISPERVRRWFLQNHGITFQAFQRMQRLNMAL

QELKAGRSTTDVAFDSGYESLSGFGYTCKKLTGFAPSAQRQVVLIHRFTTPLGPMFVCATQRGICLLEFV

DRRALESEFSDLQRRFNASIIAGENAHTRQAQQEITEYFAGQRQSFEVALDTPGSEFQRAVWRRLQHVSF

GETTHYQSIAMEIGKPTATRAVAAANGANRVAIIIPCHRIIGKDGSMTGYGGGIARKIWLINHEATIREK

RG

>WP\_016530011.1 isocitrate lyase/phosphoenolpyruvate mutase family protein [Klebsiella pneumoniae]

MDFNALRQQHQPLLLANVWDASSAQAAQQAGYQALGSSSAAIAAMLGYEDGEEMSFDELFYVVSRIKTVS

ELPLSVDLEAGYGATTSHIIDNIRRLAHLGVSGINLEDSHVVDGTRRLDDAERFAVKLQEITRACPGLFV

NVRTDTFLLNVQDALVQTLYRGQLYAKHGACGFFVPCVTRAEDITAIVHHVPLPLNVMCMPELADFSTLS

TLGVKRISMGNFIYAATQARLKDLLCQVQTQHSFSGVF

>WP\_002922636.1 MULTISPECIES: YicC family protein [Klebsiella]

MIRSMTAYARREIKGDWGSAAWELRSVNQRYLETYFRLPEQFRSLEPVVRERIRARLTRGKVECTLRFEQ

DPSAQGELILNEKLAKQLVNAANWVKMQSDEGEINPVDILRWPGVMAAKEQDLDAIAADILAALDGALDD

FIVARETEGQALKALIEQRLEGVSGEVAKVRAHMPEILQWQRERLVAKLEDAEVQLENNRLEQELVLMAQ

RIDVAEELDRLEAHVKETYNILKKKEAVGRRLDFMMQEFNRESNTLASKSINAEVTNSAIELKVLIEQMR

EQIQNIE

>WP\_016530791.1 lysophospholipid acyltransferase family protein [Klebsiella pneumoniae]

MDAIFDRVVREFFPNTTIPFWKKWLFRTAFGNKVFSRLIYNERLVNKNGVEWVNAVVELLELKCESEHHQ

FNNIPEHGATVVISNHPTVIDGLSLIHTVSRVRSDIKIIANHVLPIIFPQVSELTIGIENMAGKMSHKKF

REMNDHLRKGGVLIICPAGKLANWSLSGLQEHKWNPGFLQLAMRNNAALVPIHITGANSKIYYLTATFWR

QLSNMMVIREALRHHGKTMKINIGQQIALSSFKEYNKDLSAAANVCLTHLQSIAKNGPAMLDTIAPQELE

PGKKELISAIEECEILRQFEDGRKLVIYRCNTNRTSPIIDELGRLRERCYRDIGAGTGNDRDNDVFDESY

YHIILWDPSDVEILGAYRVMPVGEQLAQHGVTGLYSNSLFKYHDNAYSCLEKCVEIGRGFIQKPYQKSKV

LDYLWQGIFDFIKRYPDYKYLLGVLTIPGAFPEKVQKLIISFYNIYFPSTADFCTPIALFTAENVQDDTP

FCGEDFRADWSMLNHLLREEGYELPWPFKQSAKWFSSGGSSILAFTKDYSFNSIAGLNLSSIDKLNESYV

KHYLRD

>WP\_065809828.1 MULTISPECIES: hypothetical protein [Klebsiella]

MLSGLLSHAVSISTDISIINTFIGFRIKTHPYAYHFPYHYGLD

>WP\_165456913.1 HlyD family efflux transporter periplasmic adaptor subunit [Klebsiella pneumoniae]

MLSGYSHGEFVYLSYSGNEKIERILINKGDNVATGQELVKIESFDAQNIFLRAEEKLSAESALLRNLESG

ERPEELDIIRSQIKKAQSAESQVKRQLGRYRNLYANHAISLAEWEDIRDELTQKGAQVEELINQLKARQL

PARQDEISKQRSMVAAAKLERDKALWDVQQTTIVSPVNAKVFDIIYRAGERPSAGKPIISLLPPENIKVR

FFIPEAKLGKFKIGSKVKLICDGCAEPIAGVINYISPEAEFTPPVIYSTKRREKLIFMAEAIPALQQAGR

MKIGQPFDVEIIGDE

>WP\_004152982.1 MULTISPECIES: ABC transporter ATP-binding protein [Klebsiella]

MNNLCIDVKNLNKHFGEHHVVKDFSLQVAKGEIYGFLGPNGSGKTTSIRMMCGLITPDSGEGTCLGMDIF

TQREKIKKKIGYMTQYFSMWGNLTIRENLLFIARLYSLDRRRDRVERALSELGLTARQHQLAKELSGGWK

QRMALAACMLHEPVLLFLDEPTAGVDPKARREFWQMLHQLSDRGISILVSTHYMDEAERCHKVAYLSYGR

LLANGTIASIIASQNLITMRTSGAGLTLLESQLQRLPDIEQTVIFGNQLYITSRDEAKLKSALFAFTQQG

YEFCKVDTNLEDAFTYLMKNNCEKN

>WP\_004150202.1 MULTISPECIES: ABC transporter permease [Klebsiella]

MVIKEIHELRRDKVSISMVLLTPLFQLIILGYAINMDPHNLPTALLNYDTERMSQIFVTEAQNTGYFSMI

PVDSEEAAQKAFVRGDVTFIVTIPEGFTRKLLRGEKPQLLIQGDAIDPITTGNALSALVQVAKSMFQHDL

PGDMRVVQKEDDFELIIHRMFNPEGITQFNTIPGIMGSILSTTLILMTALSITRERENGALENLLVSPLS

GLEVIIGKITPFVIIGLFQATLILIAAVLLFDIPLHGSVFLLFFVLLIYVFLCLSIGIGISGLAQNQLQA

LQMSSFYFIPSIMLSGFISPFISMPDWAKAIGSCLPLTYFIRLVKGIMLKGYSATALLPDLLPLIGLAVI

VIGVGLKSYRKTLD

>WP\_002922602.1 MULTISPECIES: ribonuclease PH [Klebsiella]

MRPAGRSANQVRPVTLTRNYTKHAEGSVLVEFGDTKVLCTASIDEGVPRFLKGQGQGWITAEYGMLPRST

HTRNAREAAKGKQGGRTMEIQRLIARALRAAVDLKALGEFTITLDCDVLQADGGTRTASITGACVALADA

LNKLVAAGKLKTNPMKGMVAAVSVGIVNGEAICDLEYIEDSAAETDMNVVMTEDGRIIEVQGTAEGEPFT

HEELLTLLALARGGIESIITTQKAALEN

>WP\_002922600.1 MULTISPECIES: orotate phosphoribosyltransferase [Klebsiella]

MKPYQRQFIEFALSKQVLKFGEFTLKSGRKSPYFFNAGLFNTGRDLALLGRFYAEALVDSGIEFDLLFGP

AYKGIPIATTTAVALAEHHDRDLPYCFNRKEAKTHGEGGNLVGSPLQGRVMLVDDVITAGTAIRESMEII

QAQGAQLAGVLISLDRQERGRGEISAIQEVERDYGCQVISIITLKELITYLEEKPEMAEHLASVRAYREA

YGV

>WP\_002922598.1 MULTISPECIES: nucleoid occlusion factor SlmA [Klebsiella]

MAEKQTAKRNRREEILQSLALMLESSDGSQRITTAKLAASVGVSEAALYRHFPSKTRMFDSLIEFIEDSL

ITRINLILKDEKDTTARLRLIVLLILGFGERNPGLTRILTGHALMFEQDRLQGRINQLFERIEAQLRQVM

REKKMREGEGYTLDETLLASQLLAFCEGMLSRFVRSEFKYRPTDDFDARWPLVAAQLQ

>WP\_019725185.1 MULTISPECIES: dUTP diphosphatase [Klebsiella]

MMKKIDVKILDPRVGQQFPLPTYATSGSAGLDLRACLDDAVELAPGATTLLPTGLAIHIADPSLAAVILP

RSGLGHKHGVVLGNLVGLIDSDYQGQLMVSVWNRSQQSFIIEPGERIAQMVFVPVVQAEFNLVESFDATD

RGEGGFGHSGRK

>WP\_004188117.1 MULTISPECIES: bifunctional phosphopantothenoylcysteine decarboxylase/phosphopantothenate--cysteine ligase CoaBC [Klebsiella]

MTLAGKKIVLGVSGGIAAYKTPELVRRLRERGAEVRVAMTEAAKAFITPLSLQAVSGYPVSDSLLDPAAE

AAMGHIELGKWADLVILAPATADLIARVAAGMANDLVSTICLATPSPVAVVPAMNQQMYRAQATQHNLQT

LATRGLLLWGPDSGSQACGDVGPGRMLDPLTIVDMAAQHFASPVKDLQHLNLMITAGPTREPLDPVRYIT

NHSSGKMGFAIAAAAAQRGANVTLISGPVSLPTPPFVQRIDVTTALEMEAAVQAGAQQQHIFIGCAAVAD

YRAAVIAEDKIKKQGDELTIKMVKNPDIVAGVAALKSHRPYVVGFAAETNNVEEYARQKRARKNLDLICA

NDVSQPNQGFNSDSNALHLFWQDGEKRLPLERKELLGQLLLDEIVTRYDEKNRR

>WP\_016529877.1 DNA repair protein RadC [Klebsiella pneumoniae]

MNGMENLMPREKMLQYGIETLTDVELLALFLRVGTRRQDVLSYAQALLQRFGSLYALLSADKAQLIAVDG

LGLAKYAQLKGIAELARRYFSSQLVEEAALVTPSMTREFLQSQLTEEEREIFMVIFLDNQNRVLKHSRLF

SGTLSHVEVHPREIVREAIKVNAAAVILAHNHPSGSPEPSQADRLITERVIKCCRFMEIRVLDHLVIGRG

AYVSFAERGWI

>WP\_000091955.1 MULTISPECIES: 50S ribosomal protein L28 [Bacteria]

MSRVCQVTGKRPVTGNNRSHALNATKRRFLPNLHSHRFWVESEKRFVTLRVSAKGMRVIDKKGIDTVLAE

LRARGEKY

>WP\_002922510.1 MULTISPECIES: 50S ribosomal protein L33 [Bacteria]

MAKGIREKIKLVSSAGTGHFYTTTKNKRTKPEKMELKKYDPVVRQHVIYKEAKIK

>WP\_016529878.1 MULTISPECIES: VWA domain-containing protein [Klebsiella]

MASFIPDVSFIDNSEQRTPLILVLDCSGSMQGQPIAQLNEGLKLLEEELKQDVIAAKRVRLLVIKYGGYD

ECELYGDWCDAMDFTAPVLEANGLTPTGQAVSLALDEIEAEKQRLKAAGVPYTRPWLFLMSDGEPTDNWQ

AAAQACRDAQAANKVAVFPISVGLEATESMGQFSRSGINGVKQLKGLQFRELFLWLSASMQVVSQSTPGG

KAQLPPTDSWSEISV

>WP\_042940972.1 MULTISPECIES: protein phosphatase 2C domain-containing protein [Klebsiella]

MGSSHRQNQLPCQDAFCYRNLGDRLVAVVCDGAGSAAYSEQGAAMVAHDLANRLATFTTAPDEKQLVALV

GSVRETVLLQAQAQDISPGDFACTVLAAWLGETASVIVHIGDGAAALGLDAEQHFSLPENGEYANQTWFL

TSDDWREHLHISPFSGRATRLVMMTDGVQPFALNRRGDALFSPFIDPVLRYLQQSSEAEGSEALRATLDD

PRTWAITGDDKTLLVALRHEP

>WP\_016529880.1 protein kinase [Klebsiella pneumoniae]

MNHKKLPVCYTEQRRAVRLGKLIKSGGAGSVYFLADDPSRVAKIYHPHTDTAYYQRKLSAMLAQRPEIPA

PAENASIVQLAWPDYLLYDERKRVVGFVMPVLDTQRTIELEYILQARQAKAHHLPEGIGAKVSLACNLAT

LVSTLHARQHRVIDMKPVNLRFYRDSLYIALLDCDGFSIQGEGERFPAGQFTPDYLAPEFQRIGQVPGEQ

EEAQDRFSLAVIIFQLLNHGIHPFSGRSISAKVPDDLPGRIAAGCYAYGINAAKSSVPVPGSTHHLLPVE

LRKLFDRAFSGSPARRPSADEWAQELRPYALRSTQKIILCHQKHQHFAGMPCLVCVRKKQVVAGIKQAKQ

RKQAETDRPRVAPVVRQPRRAPAAAVARQPTGPGPLTLLWRSIRSSVPSFAWHGALALMSTLIMGGLARS

FARLNDAGPAWFDIAALLIIFIWVAALIFRSIIRSKP

>WP\_016529881.1 hypothetical protein [Klebsiella pneumoniae]

MTLKLRYLILFFALLMAFVAPDLVSLLWSAPFRLMDKLPLLPAALNDPQRLYLYGLWLGGTIYFSALMWV

AVTRRNKGYLIVAVAQLVFVMGITLFKVPIGEQNQRRWQSMNQLETPAWSDFLYKRHARFIQIALQGGPL

DQHKITEQFLAQKKPLAALPLGWNEEDAEAADTLWQQALGYREREAKALPKMMDYLAWMPDRGDLTLATA

ILTLTSEADKAQAETAFRRAIAIAPENPDA

>WP\_016529882.1 TonB family protein [Klebsiella pneumoniae]

MAEGLKESPRQPALQQRLAAYIAQMPVDDRQILHILQARMQTRSCDLPLDKYATEQGEASKVLPLAKSIV

FKTAPVRSVSPINERFPGHVSIDSEHYGIRKESLQAMPYPAIHKYIKSATTILSLDTDASGELLNGVVEC

SSGIPEFDQAALYYAQQWRLGSHRQGKRVLLPVSFISDRVPPEEYYEEMEARAMRISRLAARHNKTAMES

ASKEMIAQFTRMKTLFPQQKLSAEEARQLQLIYLKKRDKTTKGRIESFTEMTQAMEALVDTHPYYAPLLK

DLAFRKSYASFEKKRATWSQLLALAPEDPQVWMAWGSVWADRDPELYMGAMIASMLLQPFTEDTEQKIEN

IKTKLLMRVGMGPRKAILSAKVYADYGDILGERAKGENTAKAAEILPASEKLDRQEAVAPLDPAQRMTVD

IDRDEVLNAALFNVEWKAPQRPDGQRVELTVDIDDTGMPTLVLVSKSSTVEQYDAQAVDMLWRWNFKPLP

DARRITVGVNFLH

>WP\_016529883.1 bifunctional DNA-formamidopyrimidine glycosylase/DNA-(apurinic or apyrimidinic site) lyase [Klebsiella pneumoniae]

MPELPEVETSRRGIEPHLVGATILHAVVRNGRLRWPVSEEIYRLSDVPVLSVRRRAKYLLLELPDGWIIV

HLGMSGSLRILSEELPAEKHDHVDLVMSNGKVLRYTDPRRFGAWLWTKTLEGHPVLAHLGPEPLSDEFNA

DYLQQKCAKKKTAIKPWLMDNKLVVGVGNIYASESLFSAGIHPDRLASSLSREECEQLVKVIKLVLLRSI

EQGGTTLKDFLQSDGKPGYFAQELQVYGRKGEPCRICGTPVVGTKHAQRATFYCRQCQK

>WP\_002922501.1 MULTISPECIES: pantetheine-phosphate adenylyltransferase [Klebsiella]

MSTKAIYPGTFDPITNGHIDIVTRAASMFDKVVLAIAASPSKKPMFSLDERIALAEQATAHLVNVEVIGF

SDLMANFARAQQANILIRGLRAVADFEYEMQLAHMNRHLMPTLESVFLMPCKEWSFISSSLVKEVARHQG

DVSHFLPANVHQALLNKLK

>WP\_016529884.1 glycosyltransferase family 2 protein [Klebsiella pneumoniae]

MSNRLSVVMIAKNAADLLPDCLGSVSWADEIIVLDSGSTDNTVELARRLGAQVYTHTDWRGYGIQRQRAQ

DYATGDWVLMIDTDERVTPELRQAILKVLDASQRGAIYSIARRNYFLGRFMRHSGWYPDRVLRLYERARY

RYNDNLVHESLDSLGAEVIPLTGDLLHLTCRDFAGFQQKQLAYAAAWALERHQKGKKTSMAGIFSHTLGA

FLKTLLLRGGVLDGKQGWLLAMVNAQYTFTKYTELWALSHGYSEKESS

>WP\_004145263.1 MULTISPECIES: lipid IV(A) 3-deoxy-D-manno-octulosonic acid transferase [Klebsiella]

MELLYTTLLYLIQPLVWLRLLLRSRKAPAYRKRWAERYGFCQNKVEPDGILLHSVSVGETLAAIPLVRAL

RHRYPSLPITVTTMTPTGSERAMSAFGKDVHHVYLPYDLPGAMNRFLNTVQPKLVIVMETELWPNMVAAL

HKRKIPLVIANARLSERSAKGYAKLGGFMRRLLSRITLIAAQNEEDGNRFLSLGLKRNQLAVTGSLKFDI

SVTPELAARAVTLRRQWAPHRKVWIATSTHDGEEQIILQAHKKLLETFPNLLLILVPRHPERFPDAREMV

QKAGMSFTLRSTGEIPSSSTQVVIGDTMGELMLLYGIADLAFVGGSLVERGGHNPLEPAAHAIPVLMGPH

TFNFKDICAKLQQDDGLITVTDADSLVREVSTLLTDEDYRLWYGRHAVEVLHQNQGALSRLLQLLQPYLP

QRSH

>WP\_004173909.1 MULTISPECIES: glycosyltransferase [Klebsiella]

MSQTPLLSIVAAVYNGEKFLAQFFECIEQQQLDSYELILVNDGSTDNSLAVIAEWQERLQNVQVLEQENQ

GVSVARNTGLAAASGKYLAFPDIDDKLYPGMYRTLLEMAEKEHLDIATCNGTYVYEKRRESHPIFPLDRL

PSTDVLPGHVWLKQALDSRKFLHVTWLNIYRHDFIRQHHFHFEPGLRHQDIPWTTEALLAAERVQYTSQQ

FYDYYIHSESVSHKPDNDDTLMRSARHYMKILEMLEAINQRYPDKVRHIAACRWQIAKEGLGIIHTFDSM

KDESKKHVIINEFFDRGIWRLIWKNACTFRLRWRLGRRYLRIKRYRHAG

>WP\_016529885.1 MULTISPECIES: glycosyltransferase [Klebsiella]

MRILFVIDGLPGGGAEKVVLTLAAQFLRDGDRVSLISLRDVCEYPLPEGLDYQVVADRCRKPWRKLTELS

RRARQLDAAVVRAEQQGQFDLVLSNLHKTDRIVARSRALRERNVWFCLHGVFSASYLGHRTGFDRWMKQQ

KIKRIYQGRNVVTVSDAVGRDLVEEFALRPAQLKTIYNPFDITALRAEAEADSERPDGDYLIHVGRFHPG

KRHDRLLEAYAQSGIDAPLVLLGQGKPEQEQRLRQLAKTLHIDDRVWFKGFQKNPLPWIKGARMLVLSSD

SEGFGNVVVEALLLHIPVASTRCPGGVTEILTGELARGLADLTSPALAQTMQSIYHNPPAIDDAALEKFS

VVSICQQYRQLQRT

>WP\_016529886.1 glycosyltransferase family 4 protein [Klebsiella pneumoniae]

MSKFRLALVRQKYRPDGGAERFVSRALEALDSSHLQLNVITREWQGPVKPDWQIHICNPRKWGRISRERG

FANAARELWQRESFDLVQSHERIPGCDLYRAGDGVHRRWLQQRSRILPAWKSRLLFADRYHRYVMQAERE

MYEDSHLRGVICNAEMIKREIIEDFGLPAEKIHVIYNAIDNQRFLPPDEETFAALRAKWQLPLQATCLIY

VGSGFERKGLAAAIRAIAPTDRYLLVVGKDKDQPRYQALAKSLNCEARVRFFGMQSETLPFYQMADGLLL

PTLYDPFPNVILEAMACGLPVITTTGCGGAEFIVDGHNGYVCDALDIPALQQAVMALPARALSSAEGGHA

RERIMACTSERLSTQLLSLYQDLVN

>WP\_004181527.1 MULTISPECIES: putative lipopolysaccharide heptosyltransferase III [Klebsiella]

MTPETLSRGPLNPARILVIKLRHHGDMLLITPLIHALKQQYPAASVDVLLYEETRDMLAANPDIHHIYGL

DRRWKKQGKRYQLKMQWQLIQTLRQQRYDMVLNLADQWPSAVISKLTGAATRIGFDFPKRRHPVWRYCHT

ALASTQQHNQLHTVQQNLSILAPLGLQLNDAPARMGYSEADWAASRALLPEDFREHYIVIQPTSRWFFKC

WREDRMSALINALSAEGYAVVLTSGPDAREKKMVDTIIAGCPQARLHSLAGQLTLRQLAAVIDHARLFIG

VDSVPMHMAAALGTPLVALFGPSKLTFWRPWQAKGEVIWAGDFGPLPDPDAINTNTDERYLDLIPTDAVI

AAAKKVLA

>WP\_016529887.1 polysaccharide deacetylase family protein [Klebsiella pneumoniae]

MHNPAFLITIDTEGDNLWQKHDSITTENARYLPRFQQLCEKYGFKPVYLTNYEMAIDPFYIEFARDVIAR

GTAEVGMHLHAWNSPPTEPLTADDWRHKPYLIEYSDAMMREKVDYMTRLLEDTFQTKMVSHRAGRWAFDE

RYARLLVEYGYQVDCSVTPRVNWKTAKGAPQGDGGTDYRRFPQHAYFLDENDISREGHSPLLEVPMSIQY

KHSAWMNSVKQGYDRLRGKVRSPSVHWLRPMGGNVETMKKVVEQTLTQGNDYVEYMLHSSEYMPGGSPTF

KNERDIERLYADLEAFFSWLAPQVKGMTLAEYYQRKC

>WP\_016529888.1 glycosyltransferase [Klebsiella pneumoniae]

MSDKRPLLSIIIPVFNNELYIKQTLTSVFEQIDNDVEVIIVNDGSTDNSAALIQKAIDEYQGTGDLHFIS

QQNAGVSVARNVALDKAQGRWIGFIDGDDLWCPHFLQTIKPLLLEDEGDLIDFQYHYFAQHPPTSSVPTL

VKRTDITQVNHDALYEIFRRSHWHIWSRIYRHELINQRRFHVGRRYEDMMFTPWLYLEAHHIISLDQVLY

WYRDNAQGITRNIQPSDVNDMVFALNQIIDNARTQPPSQMPSRIITPLIINCFNEIKGIHAKLYGFYNYS

EHTISTLKAAAGLLPSGSLSLKRRLHLRYPGLWKRVSQLRHILRRGR

>WP\_004901359.1 MULTISPECIES: O-antigen ligase family protein [Klebsiella]

MHRVLNTRLKIKNMVLNLAVLLYLFTFMLFYAAPVEMRKIYYLAGYLTFFVALLGCRSLTSWKNNRDIAG

ATALFGLTLLGWYALNFTHSEYWSIYDSYKETGKVLLITALIVFLVSNLRFSFPAERFSWLLIVAGLATN

AYAIYQGLEIESVRLQIELDRATVIAYIFTMTNIVMLAAILELKSQYRYFLFLLAALSGFAAIAYTETRA

ALLTFPVLIILLLIVHPRVRKKQLLKLGTAFIVMLALLAIAFHQKLTDRYQGLRNDVSQYQDNNSVSSIG

SRLAMFQSGLQAALDAPFGESAERRNDNIKRQVEKKPKLTGALDYMDVHMHNELIENFSLRGVGGVITLI

IFYATLLINAWRKCNVMQGMLTLSVIIYGLSDVIFFGKEAVIIFSTALILSILYQKIVIHKDENHE

>WP\_016529889.1 glycosyltransferase [Klebsiella pneumoniae]

MRKLHIINLEKMGGVERLFLQYIQDVTTNQDCIFCISNQIGPEIAQHLTGRKVTFVNRILNNYPIKFPPF

LRKYALQTKTWLANPEAIIVWDLVPVFVAKPTRGKVIYYDHGCSWRYPHNKKTMNFFAALDGTISASYAS

KRVMELRFNLSCPSQVLINRILPPANIFTGDKPLTAPLRLGIAARLVGLKGISVALLTLKNLLDRGINVT

LDIAGKGPDEHQFIQLAQKLGIAGNVNFLGFRDDLSDFFNSIHIYLSTPVTEPFGLSCLESLFYGVPVIY

PLIDGQPEVVKNGVCGIGITPDITPEAHFEQCGINVNFPYDVYFPGQDALHPPRLLAPEKCADAVLRIVN

GDYEAFRKNAFEHVKSNFDASVFMSDFNSTISEILDASRA

>WP\_046042178.1 lipopolysaccharide heptosyltransferase RfaC [Klebsiella pneumoniae]

MRVLIVKTSSMGDVLHTLPALTDAAQAIPGIRFDWVVEEGFAQIPSWHESVERVIPVAIRRWRKAWFSAP

IKAERQAFREAVQAVKYDAIIDAQGLVKSAALVTRLAHGVKHGMDWQTAREPLASLFYNRRHHIAKQQHA

VERTRELFAKSLGYAKPQTQGDYAIARHFLQHEASAAAPYLVFLHATTRDDKHWPETRWQELLDLLADSG

VHIKLPWGAPHEEARAKRLAEGREYVEVLPRMSLEQVAQVLAGARAVVSVDTGLSHLTAALDKPNFTLYG

PTDPGLIGGYGKNQHTLISPTKETKDISATTIMQAIQEVI

>WP\_004196077.1 MULTISPECIES: ADP-heptose--LPS heptosyltransferase RfaF [Klebsiella]

MKILVVGPSWVGDMMMSQSLYRTLRARYPQAIIDVMAPAWCRPLLSRMPEVNEAIPMPLGHGALAIGERR

KLGHSLRERRYDRAYVLPNSFKSALVPFFANIPLRTGWRGEMRYGLLNDARVLDKDAWPLMVERYVALAY

DNGVMRCAKDLPQPLLWPQLQVNEGEKSQACSAFNLSYDRPIVGFCPGAEFGPAKRWPHYHYAALAKKLI

DDGYQIALFGSAKDNEAGKEIIAALSSEQQAWCRNLAGETQLEQAVILIAACKAVVTNDSGLMHVAAALD

RPLVALYGPSSPDFTPPLSHKARVIRLITGYHKVRKGDAAEGYHQSLIDITPERVLQELNELLAEKTEHE

EA

>WP\_004210780.1 ADP-glyceromanno-heptose 6-epimerase [Klebsiella pneumoniae]

MIIVTGGAGFIGSNIVKALNDKGITDILVVDNLKDGTKFVNLVDLNIADYMDKEDFLIQIMAGEEFGEIE

AIFHEGACSSTTEWDGKYMMDNNYQYSKELLHYCLEREIPFLYASSAATYGGRTSDFIESREYEQPLNVY

GYSKFLFDEYVRQILPEANSQIVGFRYFNVYGPREGHKGSMASVAFHLNTQLNNGESPKLFEGSDGFKRD

FVYVGDVADVNLWFWENGVSGIFNLGTGRAESFQAVADATLAYHKKGSIEYIPFPEKLKGRYQAFTQADL

TNLRKAGYDKPFKTVAEGVTEYMAWLNRDA

>WP\_046042184.1 glycine C-acetyltransferase [Klebsiella pneumoniae]

MRGDFYKQLTSNLETARAEGLFKEERIITSAQQADITVGDSHVINFCANNYLGLANHPELIAAAKSGMDS

HGFGMASVRFICGTQDTHKQLEKKLADFLGMEDAILYSSCFDANGGLFETLLGPEDAIISDALNHASIID

GVRLCKANRFRYANNDMQELEARLKEAREAGARHVLIATDGVFSMDGVIANLQGVCDLADKYDALVMVDD

SHAVGFVGENGRGSHEYCDVMGRVDIITGTLGKALGGASGGYTAARKEVVEWLRQRSRPYLFSNSLAPAI

VAASIKVLEMVEEGADLRDRLWANARLFREKMTAAGFTLAGADHAIIPVMLGEAVVAQNFARELQKEGIY

VTGFFYPVVPKGQARIRTQMSAAHTPEQIERAVEAFTRIGKQLGVIA

>WP\_016529894.1 L-threonine 3-dehydrogenase [Klebsiella pneumoniae]

MKALSKLKAEEGIWMTDVPEPEVGHNDLLIKIRKTAICGTDVHIYNWDEWSQKTIPVPMVVGHEYVGEVV

GIGQEVRGFKIGDRVSGEGHITCGHCRNCRAGRTHLCRNTIGVGVNRPGCFAEYLVIPAFNAFKIPDNIS

DDLASIFDPFGNAVHTALSFDLVGEDVLVSGAGPIGVMAAAVAKHVGARNVVITDVNEYRLELAHKMGVT

RAVNVAKENLNDVMAELGMTEGFDVGLEMSGAPPAFRSMLDTMNHGGRIAMLGIPPSDMSIDWTKVIFKG

LFIKGIYGREMFETWYKMAALIQSGLDLSPIITHRFGIDDFQKGFDAMRSGQSGKVVLSWD

>WP\_016529895.1 glycosyltransferase family 2 protein [Klebsiella pneumoniae]

MLKLSVCLLTCNSARLLMEVLPPLLKVADECIVVDSGSTDETVAICQQFGLTVHHHAYKAHGAQMNYAIG

LASHDWVLCMDSDEILDNDVVTAIQALKAGEEPDPTCAWRLPRYWFVLGKQVRTIYPISSPDDPVRLFNR

QQARFNDRPVDDQVVGHASSVRLPGFVRHDTFYSLHEVFNKLNSYTTRLVKYQQIKPSLTRGIVSAIGAF

FKWYLFSGAWRYGKVGVVTGLYATFYSFLKYFKAWYAHEDNQAPVAQKRTDP

>WP\_016529896.1 divergent polysaccharide deacetylase family protein [Klebsiella pneumoniae]

MLQFRAIALAVAGSLALAAPAFAGKLSIVIDDFGYRPQTENQVLALPATISVAVLPNAPHAREMATKAHN

QGHEVLIHPPMAPLSKQPLEKDTLRPEMSSEEIERIIREAYGKVPYAVGLNNHMGSAMTSNLFGMQKVMQ

ALERYNLYFLDSVTIGNTQAMRAAQGTGVKVIKRKVFLDDTQNEADIRNQFNRAIALARRNGSAIAIGHP

HPTTVRVLQQMVYNLPPDITLVRPSSLLNEPQVDNSTPNYAQPPAQQTQQKPRNPFHGVKSCKPKRPLEP

VNASRFFTILSDSISQSALIQYYRLKWQGWDNPGN

>WP\_002922458.1 MULTISPECIES: murein hydrolase activator EnvC [Klebsiella]

MRGKAMYSTTWIAAAVRSVLYASALSAGVLLCASSAHADDRDQLKSIQADIAARQRAIKQQQQQRASLLA

QLKAQEEAIAAAARKLRETQDSLNQLNKQIDEMNAALAKLERQRASQERNLAAQLDAAFRQGPHTGIQMV

LSGEEGQRNQRMQVYFSYFNQARQETIAELKKTREEMAVQKSMLEEKQSQQQTLVYEQKAQQAKLEQARN

ERKKTLSGLESSIQQGQQQLSELRANESRLRGRIAQAEAAAKARADREARDAQAVRDRQQEASRKGTTYK

PTESERSLMSRTGGLGSPRGQAFWPVRGPLLHRYGEQLQGELRWKGMVIAASEGTEVRAIADGRVILADW

LQGYGLVVVVEHGKGDMSLYGYNQSALVSVGTQVRAGQPIALVGSSGGQGRPSLYFEIRRQGQAVNPQPW

LGR

>WP\_004152046.1 MULTISPECIES: 2,3-bisphosphoglycerate-independent phosphoglycerate mutase [Klebsiella]

MSVSKKPMVLVILDGYGYREDQQDNAIYSAKTPVMDALWAKRPHTLIDASGLEVGLPDRQMGNSEVGHVN

LGAGRIVYQDLTRLDVEIKERTFFANPVLTAAVDKAVAAGKAVHIMGLMSPGGVHSHEDHIMAMVELAAE

RGAEKIYLHAFLDGRDTPPRSAEKTLATFEAKFAALGKGRIASLIGRYYAMDRDNRWDRVEQAYDLLTLA

KGEFQADTAVAGLQAAYARDENDEFVKATVIRAAGQADAAMEDGDALIFMNFRADRAREITRAFVNADFD

GFARKKVVNLDFVMLTEYAADIKVACAYPPASLANTFGEWMAKHDKTQLRISETEKYAHVTFFFNGGVEE

PFKGEERILINSPKVATYDLQPEMSSAELTEKLVAAIKGGKYDTIICNYPNGDMVGHTGVMEAAVKAVEA

LDRCIDQVAQAVESVGGQLLITADHGNAEQMRDPATGQAHTAHTNLPVPLIYVGNKAVKAVNGGKLSDIA

PTMLSLMGMEIPQEMTGKPLFIVE

>WP\_002922436.1 MULTISPECIES: rhodanese-like domain-containing protein [Klebsiella]

MQEIMQFIGRHPVLSIAWIALLGAVVFTTFKGLMSKVKVITRGEATRLINKEDAVVVDLRQRDDFRKGHI

AGAINLLPSDIKANNVGELEKHKSQPIIVVDGSGMQAQEPASALNKAGFEKVFVLKEGIAGWSGENLPLV

RGK

>WP\_002922429.1 MULTISPECIES: glutaredoxin 3 [Enterobacteriaceae]

MANIEIYTKATCPFCIRAKALLNSKGVTFHELPIDGDAAKREEMIQRSGRTTVPQIFIDAQHIGGCDDLY

ALDSRGGLDPLLR

>WP\_002922428.1 MULTISPECIES: protein-export chaperone SecB [Klebsiella]

MSEQNSTEMTFQIQRIYTKDISFEAPNAPQVFQKDWQPEVKLDLDTASTQLAEGVYEVVLRVTVTAALGE

ETAFLCEVQQGGIFSIDGIEGTQMAHCLGAYCPNILFPYARECITSLVSRGTFPQLNLAPVNFDALFMNY

LQQQAGEGAEQHQDA

>WP\_016529899.1 NAD(P)H-dependent glycerol-3-phosphate dehydrogenase [Klebsiella pneumoniae]

MNALNAAMTVIGAGSYGTALAITLARNGHHVVLWGHDPKHIATLQHDRCNAAFLPNVPFPDTLHLESDLA

TALAASRDILIVVPSHVFGQVLRQIKPLMRSDARLVWATKGLEAETGRLLQDVAREALGDDIPLAVISGP

TFAKELAAGLPTAISLAATDPQFAEDLQRLLHCGKSFRVYINPDFIGVQLGGAVKNVIAIGAGMSDGIGF

GANARTALITRGLVEMSRLGAALGADPETFMGMAGLGDLVLTCTDNQSRNRRFGMMLGQGMDVQSAQDKI

GQVVEGYRNTKEVRVLAQRLGVEMPITEEIYQVLYCGKIAREAALTLLGRARKDERSSN

>WP\_002922426.1 MULTISPECIES: serine O-acetyltransferase [Klebsiella]

MPCEELDIVWNNIKAEARALADCEPMLASFYHATLLKHENLGSALSYMLANKLASPIMPAIAIREVVEEA

YAADPEMIASAACDIQAVRTRDPAVDKYSTPLLYLKGFHALQAYRIGHWLWTQGRRALAIFLQNQVSVSF

QVDIHPAAKIGRGIMLDHATGIVVGETAVIEDDVSILQSVTLGGTGKTSGDRHPKIREGVMIGAGAKILG

NIEVGRGAKIGAGSVVLQPVPPHTTAAGVPARIVGKPESDKPAMDMDQHFNGIHHTFEYGDGI

>WP\_004181521.1 MULTISPECIES: tRNA (uridine(34)/cytosine(34)/5-carboxymethylaminomethyluridine(34)-2'-O)-methyltransferase TrmL [Klebsiella]

MLNIVLFEPEIPPNTGNIIRLCANTGFSLHIIEPMGFTWDDKRLRRAGLDYHEFTAVQRYADYAAFVASA

QPQRLFALTTKGTPAHSAVSYQDGDFLMFGPETRGLPASILDALPPEQKIRIPMMPDSRSMNLSNAVSVV

VYEAWRQLGYPGAVLRS

>WP\_002922420.1 MULTISPECIES: FMN-dependent L-lactate dehydrogenase LldD [Klebsiella]

MIISAASDYRAAAQRILPPFLFHYIDGGAYAEHTLRRNVEDLSDVALRQRILRNMSDLSLETTLFNEKLA

MPTALAPVGLCGMYARRGEVQAAGAADDKGIPFTLSTVSVCPIEEVAPTIKRPMWFQLYVLRDRGFMRNA

LERAKAAGCSTLVFTVDMPTPGARYRDAHSGMSGPNAALRRYWQAVTHPQWAWDVGLNGRPHDLGNISAY

LGKPTGLEDYIGWLANNFDPSISWKDLEWIRDFWDGPMVIKGILDPEDARDAVRFGADGIVVSNHGGRQL

DGVLSSARALPAIADAVKGDITILADSGIRNGLDVVRMIALGADSVLLGRAYLYALATHGKQGVANLLNL

IEKEMKVAMTLTGAKSIREISRDSLVQNAEALQTFDALKQNNAA

>WP\_046042187.1 transcriptional regulator LldR [Klebsiella pneumoniae]

MIVMPKRLADDVARRVRALIEEQQLEAGMRLPAERQLAAQLGVSRNSLREALAMLVNEGVLLSRRGGGTF

VRFQHEPWSEQNIVQPLKTLLADDPDYSFDILEARHAIEASTAWHAAMRATDADKEKIRLCFEATQSEDP

DIASQADVRFHLAIAEASHNVVLLQTMRGFFDLLHSSVKQSRQRMYQVPPVFARLTEQHQAVMEAIVAGD

AEAARQAMMGHLGFVHGFDEDQARQARITRLPGDHNENSRENS

>WP\_002922413.1 MULTISPECIES: L-lactate permease [Klebsiella]

MNLWQQNYDPAGNIWLSSLIASLPILFFFFALIKLKLKGYIAATWTVAIALVVALLFYKMPVDRALASVV

YGFFYGLWPIAWIIIAAVFVYKISVKTGQFDIIRSSILSITPDQRLQMLIVGFSFGAFLEGAAGFGAPVA

ITAALLVGLGFNPLYAAGLCLIVNTAPVAFGAMGIPILVAGQVTGIDSFAIGQMVGRQLPFLTIIVLFWI

MAIMDGWRGIKETWPAVIVAGGSFAIAQYLSSNFLGPELPDIISSLVSLVCLTLFLKRWQPVRIFRFGDL

GASQVDMTLARTRYTAGQVIRAWSPFLFLTATVTLWSVPPFKALFAPGGAMYDFVINISVPFLDKMVARM

PPVVSAATPYAAVYKFDWLSATGTAILFAALLSIVWLRMKPKDALTTFAGTLKDLALPIYSIGMVLAFAF

ISNYSGLSSTLALALAHTGHAFTFFSPFLGWLGVFLTGSDTSSNALFAALQATAAQQIGVSDILLVAANT

TGGVTGKMISPQSIAIACAAVGLVGKESDLFRFTVKHSLIFTCMVGLITTLQAYVLTWMIP

>WP\_002922410.1 MULTISPECIES: YibL family ribosome-associated protein [Klebsiella]

MKEVEKNEIKRLSDRLDAIRHQQAELSLVEAADKYAELEKEKATLETEIERLRSVQSQKLSKEAQKLMSL

PFRRAITKKEQADMGKLKKSVRGLVVVHPMTALGREMGLKEMTGFARSEF

>WP\_002922402.1 MULTISPECIES: hypothetical protein [Klebsiella]

MAKIGDGVPRLIDKAVDFMASSQAFMEYLKKSPRLQHVPRDIPQDKEALFLQRLEYYRQLYRPTCDQTEP

ESER

>WP\_002922401.1 MULTISPECIES: mannitol operon repressor MtlR [Klebsiella]

MHNLARPTSRPLRLLSDMQAMMEETQAFENRVLERLNAGKTVRSFLIATVELLTEAVNILVLQVFRKDDY

AVKYAVEPLLEGSGPLGDLSVRLKLIYGLGVISRAEYEDAELLMALREELNHDGNEYSFTDDEIIGPFGE

LHCVAALPPTPQFDDSDAELLAMQKLRYQQMVRSTMVLSLTELISRISLKKAFQKSTL

>WP\_004145239.1 MULTISPECIES: mannitol-1-phosphate 5-dehydrogenase [Klebsiella]

MKALHFGAGNIGRGFIGKLLADAGIELTFADVNQTVLDALNARHSYQVHVVGENEQVDTVSGVNAVSSIG

DEVVDLIAEVDLVTTAVGPVVLERIAPAIAKGLAQRKAQGTERPLNIIACENMVRGTTQLKGHVFNALAE

EDKAWVEAHIGFVDSAVDRIVPPSASATHDPLEVTVETFSEWIVDKTQFKGALPTIPGMELTDNLMAFVE

RKLFTLNTGHAITAYLGKLAGHQTIRDAILDEKIRAVVQGAMEESGAVLIKRYAFDPQKHAAYIQKILGR

FENPYLKDDVERVGRQPLRKLSAGDRLIKPLLGTLEYGLPHRNLVKGIAAAMHFRSEDDPQAQELAALIA

DKGPQAALAQISGLDAASDVVAEAVNDYNAEK

>WP\_016529902.1 PTS mannitol transporter subunit IICBA [Klebsiella pneumoniae]

MSSDIKIKVQSFGRFLSNMVMPNIGAFIAWGIITALFIPTGWLPNETLAKLVGPMITYLLPLLIGYTGGK

LVGGERGGVVGAITTMGVIVGADMPMFLGSMIAGPLGGYCIKKFDNWVDGKIKSGFEMLVNNFSAGIIGM

ILAILAFLGIGPAVEVLSKILAAGVNFMVAHDMLPLASIFVEPAKILFLNNAINHGIFSPLGIQQSHELG

KSIFFLIEANPGPGMGVLLAYMFFGRGSAKQSAGGAAIIHFLGGIHEIYFPYVLMNPRLILAVILGGMTG

VFTLTILNGGLVSPASPGSILAVLAMTPKGAYFANIAAIIAAMAVSFVVSAVLLKTSKVKEEDNIEAATR

RMHDMKAESKGASPLAAGNVTNDLSHVRKIIVACDAGMGSSAMGAGVLRKKVQDAGLSNISVTNSAINNL

PPDVDLVITHRDLTERAMRQVPQAQHISLTNFLDSGLYTSLTERLVAAQRHIDNEVKVTDSLKDSFDDTN

NNLFQLGADNIFLGRKAATKEEAIRFAGEQLVKGGYVEPEYVQAMLDREKLTSTYLGESIAVPHGTIEAK

DRVLKTGVVFCQYPEGVRFGEEEDEVARLVIGIAARNNEHIQVITSLTNALDDETVIERLAKTTSVDEVL

ALLNK

>WP\_004145238.1 MULTISPECIES: glutathione S-transferase [Klebsiella]

MKLIGSYTSPFVRKISVILLEKRIPFEFVNESPYSESNGVARYNPLGKVPALVTDDGECWFDSPVIAQYL

ELLGVAPPMIPADPRAALRMRQLEALADGVMEAAQALVREKARPGAQQSEQELLRQREKVARGLDRLEAC

AADGTLRGDEVNLATISTACAIAYLNFRRVAPGWCATRPQLVKLVDALFQRASFARTEPPRT

>WP\_032103599.1 L-seryl-tRNA(Sec) selenium transferase [Klebsiella pneumoniae]

MTTEIRALYTRLPAIDRLLRDPAFSSLLAQHGHSQVVAQLRQMLDEAREQIRQYQTLPDWSHDWPSACAQ

RLTAGRQSALRPVFNLTGTVLHTNLGRAIQAESAVEAVASAMRAPVTLEYDLDDAGRGHRDRAIADLLCQ

ITGAEDACIVNNNAAAVLLMLAATASGREVVVSRGELVEIGGAFRIPDVMRQAGCQLHEVGTTNRTHAKD

YRQAVNDNTALLMKVHTSNYSIEGFTKAVDEAELAAIGRELDVPVVADLGSGSLVDLSQYGLPKEPMPQE

MIAAGVSMVSFSGDKLLGGPQAGIIVGKRALIAQLQSHPLKRALRADKMTLAALEATLRLYQHPEALREK

LPTLRLLTRPAEEIRRLAERLQPDLAAHYADFAVSVAACQSQIGSGSLPVDRLPSAALTFTPHDGRGSRL

EALAARWRALPCPVIGRIYDGRLWLDLRCLENETRFMEMLLR

>WP\_004173923.1 MULTISPECIES: selenocysteine-specific translation elongation factor [Klebsiella]

MIIATAGHVDHGKTTLLQAITGVNADRLPEEKARGMTIDLGYAYWPQPDGRVLGFIDVPGHEKFLSNMLA

GVGGIDHALLVVACDDGVMAQTREHLAILQLTGKPTLTVALTKTDRVAAARVAEVQAEVEQTLGELGFDA

VAFFPTAAAENIGIAELRSHLLQLAERPRPQQQRFRLALDRAFTVKGAGLVVTGTALSGEVRVGDTLWLT

GVNTPMRVRGLHAQNQAVEQAHAGQRIALNIVGDAQKEAVHRGDWLLSSPPPEPAERVIVELQCHTPLSQ

WQPLHIHHAASHITGRVSLLEGNLAELVLDTPLWLADNDRLVLRDISARLTLAGARVVTLDPPRRGKRKP

EYLQWLHALAAVGADDAQALELHLQRDAVRLEHFAWARQLSEAGMAALIQRPDYLQAGQRLLSAPLAARW

QRKLLDALARYHEQHRDEPGPGRERLRRIALPMEDEALVLLLIEQMRESGLVHSHHGWLHLPEHKAGFTD

EQQAVWQKVETLFGDDPWWVRDLAREVHVEESLMRAVLRQAAQQGMITAIVKDRYYRNDRIVQFAQRVRE

LDRLRGSTCAADFRDTLNVGRKLAIQILEYFDRIGFTRRRGNDHILRDKALFR

>WP\_002922360.1 MULTISPECIES: 4Fe-4S binding protein [Klebsiella]

MNQFLIANAQRCIGCRTCEVACAVAHQQAQDVAALSTNHFAPRIRVVKSGDISTAMACRQCEDAPCASVC

PQGAIQRDNDVWWVDQRRCIGCKSCMVACPYGAMTVTVMNQQAQALKCDLCHHRAEGPACVAACPTQALR

VMVPAELEALCAQKRQRLALA

>WP\_002922359.1 MULTISPECIES: valine--pyruvate transaminase [Klebsiella]

MTFSLFGDKFTRHSGITRLMEDLNDGLRTPGAIMLGGGNPAQIPEMNDYFQQLLADMLDNGKALDALCNY

DGPQGKSELLALLANMLRDELGWEIEPQNIALTNGSQSAFFYLFNLFAGRRADGTTRKVLFPLTPEYIGY

ADAGLEEDLFVATRPNIELLPEGQFKYHVDFEHLQVTEETGMICVSRPTNPTGNVITDEELIKLDALANQ

HGVPLVIDNAYGVPFPGIIFSDARPLWNPNIVLCMSLSKLGLPGSRCGIIIANEKIITAISNMNGIISLA

PGGIGPAMMCEMIKRQDLLRLSETVIKPFYYQRVQETIAIIRRYLPEERCLIHKPEGAIFLWLWFKDLPI

STELLYQRLKKRGVLMVPGDYFFPGLDKPWPHTHQCMRMNYVPDPQKIEAGVKILAEEVEFAWREQEA

>WP\_004901315.1 MULTISPECIES: alpha-amylase [Klebsiella]

MKLAALATLFVPGMAFAAWTTTDFPAFTEEGTGRFISQKVVEKGTRPLQLNFDQQCWQPSGGIKLNQMLS

MEPCRGTPPQWRIFRQGLYTLEVDTRSGTPTMMISLEEKETSAAAPQIRQCPKWDGKPLTIDVSKTFAEG

SKVRDFYSGNVATVSGGKITLQPAFGSNGLLLLERAETAAPAPFDWHNATVYFVLTDRFVNGNPANDNSY

GRHKDGMQEIGTFHGGDLQGLTSKLDYLQQMGVNALWISSPLEQIHGWVGGGTKGDFPHYAYHGYYTQDW

SKLDANMGTEADLRRLVDEAHKRGIRILFDVVMNHAGYATLADMQEFQFGSLYLQGDELKKTLGERWTDW

KPGAGQTWHSFNDYINFSDKAGWEKWWGKKWIRTDIGDYDNPGYDDLTMSLAFLPDLKTESKEVSGLPNF

YSHKPDTAAKAIPGYTPRDYLTHWLSQWVRDYGIDGFRVDTAKHVEMDAWQQLKTQATAALAEWKKANPD

KALDAAPFWMTGEAWGHGVMQSDYYRHGFDAMINFDYQDQAAKAATCMANIDLTWQQMADKLQSFNVLSY

LSSHDTRLFREGGTTAAELLLLAPGAVQIFYGDESSRPFGPTGSDPLQGTRSEMNWQDVNGKAARSVTHW

QKIGQFRARHPAIGMGKQTTLSMPRGYGFVRESGEDKVMVIWAGQQQ

>WP\_004188166.1 MULTISPECIES: protein bax [Klebsiella]

MISNPIRRYGAAILMLLTCIFSGSVLATTHTATKSHKAPTVKKISSTKVSSKQEYSRNSVKSSSLPDLRK

YPSGTPRKKAFLRTVMPYITKQNQAITADRNWLISKQYDARWSPTEKARLKDIASRYKVKWSGNTRHVPW

NALLERVDIIPNSMVATMAAAESGWGTSRLARENNNLFGMKCGAGRCRGAMKGYSQFESVEQSVQAYVTN

LNTHPAYSSFRKSRLQLRKADQEVTASTMIHKLKGYSTKGSSYNNYLFAMYQDNQRLIAAHL

>WP\_016530898.1 MULTISPECIES: XylR family transcriptional regulator [Klebsiella]

MFEKRHRITLLFNANKAYDRQVVEGVGEYLQASQLEWDIFIEEDFRARIENIKEWLGDGVIADYDDPEIE

KLLADVHVPIVGVGGSYHQPEQYPPVHYIATDNAALVESAFLHLKEKGVHRFAFYGLPISSGKRWAVERE

YAFCQLVAKEKYRGVVYQGLETAPENWQHAQNRLADWLQTLPPQTGIIAVTDARARHVLQACELLHIPVP

EKLCVIGIDNEELTRYLSRVALSSVAQGTRQMGYQAAKLLHRLLNNEALPLQRQLIPPMRVVERRSTDYR

SLNDPSVIQAMHYIRNNACKGIKVEQVLDAVGISRSNLEKRFKEEVGETIHTVIHSEKLEKARSLLVSTS

LSINEISQMCGYPSLQYFYSVFKKEYDVTPKEYRDRHSEVML

>WP\_002922349.1 MULTISPECIES: sugar ABC transporter permease [Klebsiella]

MSKNTSSEIKLTPTAPAALPALKGLNLQVFVMIAAIVVIMLFFTWVTDGAYLSARNISNLLRQTAITGIL

AVGMVFVIISAEIDLSVGSMMGLLGGAAAIFDVWLGWPLPLTILVTLVMGLLLGAWNGWWVAYRKVPSFI

VTLAGMLAFRGILIGITNGTTVSPTSPAMSQIGQSYLPDGIGFGIGVVGMAVFIVWQWRGRMRRQALGLA

TSSSTAAVGRQAITAVIVLGAIWLLNDYRGVPTPVLILAALLLAGLFMATRTAFGRRIYAIGGNLEAARL

SGINVERTKLAVFAINGLMVAIAGLILSSRLGAGSPSAGNIAELDAIAACVIGGTSLAGGIGSVAGAVMG

AFIMSALDNGMSMMDVATFWQYIVKGAILLLAVWMDSATKRRA

>WP\_002922346.1 MULTISPECIES: xylose ABC transporter ATP-binding protein [Klebsiella]

MTWLLEMKNITKTFGAVKAVDNVSLRLNAGEVVSLCGENGSGKSTLMKVLCGIYPHGSYEGEIIFAGETL

QANHIRDTERKGIAIIHQELALVKHLTVLENIFLGAEISRHGLLDYETMTLRCQKLLAQVNLPISPDTRV

GDLGLGQQQLVEIAKALNKQVRLLILDEPTASLTEQETATLLAIVRDLQNHDIACIYISHKLNEVKAISD

TICVIRDGQHIGTRDASGMSEDDIITMMVGRELTALYPSEPHAHGEEILRVEHLTAWHPVNRHIKRVNDV

SFSLRRGEILGIAGLVGAGRTEAVQCLFGVWPGRWQGEIFIDGQPVSISNCQQAIAHGIAMVPEDRKKDG

IVPVMAVGKNITLAALNQFTGAMSSLDDAAEQHCIQQSIQRLKIKTSSPELAIGRLSGGNQQKAILARCL

LLNPRILILDEPTRGIDIGAKYEIYKLINQLVQQGIAVIVISSELPEVLGLSDRVLVMHEGRLKANLVNQ

HLTQEQVMEAALRSERHVEEHVV

>WP\_004152040.1 MULTISPECIES: D-xylose ABC transporter substrate-binding protein [Klebsiella]

MKIKNLCLTLCASSLLLASMAGMAKEVKIGMAIDDLRLERWQKDRDIFVNKAESLGAKVFVQSANGNEET

QMSQIENMINRGVDVLVIIPYNGQVLSNVIKEAKQEGIKVLAYDRMINNADIDFYISFDNEKVGEMQAQS

LVDKVPQGNYFLMGGSPVDNNAKLFRAGQMKVLKPYVDDGKIKIVGDQWVDGWLPENALKIMENALTANN

NKIDAVVASNDATAGGAIQALTAQGLAGKVAISGQDADLAGVKRIISGTQTMTVYKPITTLATNAAEIAV

ELGNDKQPKADTTLNNGLKDVPSRLLTPIEVNKENIDATVIKDGFHKKSEL

>WP\_002922139.1 MULTISPECIES: xylose isomerase [Klebsiella]

MQTYFDQLDRVRYEGPKSTNPLAFRHYNPDELVLGKRMEDHLRFAACYWHTFCWNGADMFGVGSFDRPWQ

QPGDALEMAKRKADVAFEFFHKLNVPYYCFHDVDVSPEGASLKEYSNNFARMVEVLAEKQQQSGVKLLWG

TANCFTNPRYGAGAATNPDPEVFSWAATQVVTAMNATHQLGGENYVLWGGREGYETLLNTDLRQEREQIG

RFMQLVVEHKHKIGFKGTLLIEPKPQEPTKHQYDYDASTVYGFLKQFGLEKEIKLNIEANHATLAGHSFH

HEIATAIALGLFGSVDANRGDPQLGWDTDQFPNSVEENALVMYEILKAGGFTTGGLNFDAKVRRQSTDKY

DLFYGHIGAMDTMALSLKVAARMIEDGELDKRVARRYAGWNGELGQQILNGQMTLSDIAQYAAQHQLAPQ

HRSGQQEQLENLVNHYLFDK

>WP\_046042192.1 xylulokinase [Klebsiella pneumoniae]

MYIGIDLGTSGVKAILLNEQGEVVASHTEKLTVSRPHPLWSEQDPEQWWLATDTAMKALGAQHSLRDVKA

LGIAGQMHGATLLDKSLQVLRPAILWNDGRCAEECQLLEDKVSASRQITGNLMMPGFTAPKLLWVQRHEA

AVFSQVDKVLQPKDYLRLRMTGELASDMSDAAGTMWLDVARRDWSDEMLAACDLSRDAMPALFEGSDVTG

QLRPEVAQAWNMPPALVVGGGGDNAAGAVGVGMADAGQAMLSLGTSGVYFAVSEGFLSKPESAVHSFCHA

LPGRWHLMSVMLSAASCLDWAAKLTGLASVPALIAAAQTADESAGPVWFLPYLSGERTPHNNPQAKGVFF

GLTHQHGPAELARAVLEGVGYALADGMDVVHACGIKPQSITLIGGGARSAYWRQMLADISGLQLDYRTGG

DVGPALGAARLAQLAVHDEADRPGLLKPLPLEQAHRPDDRRVAHYAPQRETFRQIYQQLKPLMS

>WP\_016529858.1 hypothetical protein [Klebsiella pneumoniae]

MITKRNIARGMMATGSLVYLLGIWRTCPLFRGKGYFLGVLVMGMFAVLAHQRASQWQEQDDGFIALCRLV

LLLSVGLLLVGAWYVPADWHEKAVYIAAWFVCLYGASATPERTRIARAMQKTE

>WP\_004188180.1 MULTISPECIES: YiaB family inner membrane protein [Klebsiella]

MMENKHATYSPAFHLISWIALIGGIVTYLVGLWNADMQLNEKGYYFAVLVLGLFAAASYQKTVRDKYEAI

PTTALYYTTCLVVFVIAVGLLVIGLWNATLLLSEKGFYGLAYFLSLFGAVAVQKNVRDVWDPTRLREPLS

VTEEGPET

>WP\_016529859.1 acyltransferase [Klebsiella pneumoniae]

MQEKIHWITNLRGIACMMVVMIHSTSWYITHPHAITLLQWDIANLLNSASRVSVPLFFMISGYLFFGERS

AQPRHFWRIGLCIAFYSALSLLYITLFTHINVELSLKNLLQKPVFYHLWFFFAITVIYLLSPLLQVKSTS

STMLLALMAILGILANPNMVSVKAAGIEWLPVNLYINGDTFYYVLYGVLGRAIGTLNTDKKWLTPLCAAL

FIAAVWVISRGTLHELRWRGDFGDTWYLYCGPAVFVCAVTLLTLAKNWLNARPLPGIACIARHSLGIYGF

HALIVHALRASHLELSRWPLLDIVWIFSAALLGSLLLSGLVQRIDSRRLVS

>WP\_072198203.1 YsaB family lipoprotein [Klebsiella pneumoniae]

MKGVVSVMLVLLLAGCSETVSPPTQKAQRARITPQTTLNMAQLCKDQAAIRYNTQTQFVDVNHFEQFQAS

YELSGRTGKNERFICSFDPDGQFMHLSMR

>WP\_002922128.1 MULTISPECIES: glycine--tRNA ligase subunit alpha [Klebsiella]

MQKFDTRTFQGLILTLQDYWARQGCTIVQPLDMEVGAGTSHPMTCLRALGPEPMATAYVQPSRRPTDGRY

GENPNRLQHYYQFQVVIKPSPDNIQELYLGSLKELGMDPTIHDIRFVEDNWENPTLGAWGLGWEVWLNGM

EVTQFTYFQQVGGLECKPVTGEITYGLERLAMYIQGVDSVYDLVWSDGPLGKTTYGDVFHQNEVEQSTYN

FEYADVDFLFTCFEQYEKEAQQLLALETPLPLPAYERILKAAHSFNLLDARKAISVTERQRYILRIRTLT

KAVAEAYYASREALGFPMCNKNK

>WP\_002922127.1 MULTISPECIES: glycine--tRNA ligase subunit beta [Klebsiella]

MSENTFLVEIGTEELPPKALRSLAESFAANVTAELDNAGLAHGKVEWFAAPRRLALKVANLAAAQADREV

EKRGPAIAQAFDAEGKPSKAAEGWARGCGITVDQAERLTTDKGEWLLYRAHVKGESTEALLPNMIASSLA

KLPIPKLMRWGASDVHFVRPVHTVTLLLGDKVIPATILGIPSDRVIRGHRFMGEPEFTIDHADQYPQILL

ERGKVIADYEQRKAKIKADAQEAARKIGGQADLSESLLEEVTSLVEWPVVLTAKFEEKFLAVPSEALVYT

MKGDQKYFPVYDNAGKLLPNFIFVANIESKDPQQIISGNEKVVRPRLADAEFFFNTDRKKRLEDNLPRLE

TVLFQQQLGTLRDKTDRIQALAGWIAEQIGADVNHATRAGLLSKCDLMTNMVFEFTDTQGVMGMHYARHD

GEAEDVAVALNEQYQPRFAGDALPSNPVACAVAIADKMDTLAGIFGIGQHPKGDKDPFALRRAALGVLRI

IVEKNLDLDLQTLTEEAVRLYGEKLTNANVVDDVIDFMLGRFRAWYQDEGYGVDTIQAVLARRPTRPADF

DARMKAVSHFRTLEESSALAAANKRVSNILAKSDETLNDIVHASVLKEAAEIKLAGNLVVLRDKLQPYFA

AGRYQDALIELAALREPVDEFFENVMVNAEDKDVRINRLTLLSKLRELFLQVADISLLQ

>WP\_087661561.1 MULTISPECIES: IS3 family transposase [Klebsiella]

MSRRKYTFQQRLEVVMHYFATDEGYRLTSARFNVPRTQVRIWVAAYDAYGEEGLKPRDKGVSIDPDIRVE

AVKAVLTGQISQTQAAAKFNVAGSASVGKWMKVFSEHGEEGLRSLRVGKKRALHMIDDPVALEVELERSK

DKRIQELEQKVRRLELRILYLKKFESLSSVRDKVRIIDELRQHYSFDQLLQIAQIPRSTFYYHLKALRSP

GKYDEVKCRIKEIYDENLGRYGYRRIALALRREGGALNHKVVQRLMNVLRLKAAIRVKRYSSWRGEHGRA

ADNILQRNFKASRPNEKWVTDVTEFAVSGRKLYLSPIIDLFNNEVISYSISEHPTMPMIDDMLIKAFARL

DAGTNPVLHSDQGWQYRHRWYQYQLREFGIIQSMSRKGNCLDNACAECFFGTLKSECFYTSKFKDIDELK

IVIEDYIRYYNTRRISLKFKGLSPVEYRLKSYPGRN

>WP\_004901287.1 MULTISPECIES: GFA family protein [Enterobacteriaceae]

MNGSCLCGTIEFELTHKPAVFYRCHCSLCRKQSGVGYNLATLVKDSEFRWIKGKNCVASWSKPTGYRTDF

CNVCGSTVPNSLRDVPYVWVPVGLIDERLDMECAGDFCTDDAMPWDETRSPSGHAGPVESLASLLKCLKL

NS

>WP\_003026799.1 MULTISPECIES: DUF1778 domain-containing protein [Bacteria]

MKSDVQLNLRAKESQRALIDAAAEILHKSRTDFILEMACKAAENVILDRRVFNFNDEQYAEFIDMLDAPV

EDEPAINKLLARKPQWDV

>WP\_115217266.1 IS3 family transposase [Klebsiella pneumoniae]

MIDVLGPEKRRRRTTQEKIAIVQQSFEPGMTVSLVARQHGVAASQLFLWRKQYQEGSLTAVAAGEQVVPA

SELAAAMKQIKELQRLLGKKTMENELLKEAVEYGRGKKVDSARALIARGWGVSFVSRCLRVSRAQLHVIL

RRTDDWKDGRRSRHTDDTDVLRRIHHVIGELPTYGYRRVWALLRRQTEPDGMPAINAKRVYRIMRQNALL

LERKPAVPPSKRAHTGRVAVKESNQRWCSDGFEFRCDNGEKLRVTFALDCCDREALHWAVTTGGFDSETV

QDVMPGAVERRFGSELPASPVEWLTDNGSCYRANETRQFARMLGLEPKNTAVRSPESNGIAESFVKTIKR

DYISIMPKPDGLTAAKNLAEAFEHYNEWHPHSALGYRSPREYLRQRASNGLSDNRCLEI

>WP\_227504837.1 GNAT family N-acetyltransferase [Klebsiella pneumoniae]

MTSLKTSIKTITYLSDIGCLEIQGASLITAPEPLSSAHQLAEFVSGETVLDEWLKQRGLKNQALGAARTF

VVCKKGTKQVAGFYSLATGSVNHTEATGSLRRNMPDPIPVIILARLAVDVSLRGKGLGADLLHDAVLRCY

RVAENIGVRAIMVHALTEEAKNFYIHHGFKPSQTQPRTLFLRLPQ

>WP\_002922102.1 MULTISPECIES: type I toxin-antitoxin system toxin HokA [Enterobacteriaceae]

MPQKYLLFGLVVICFTILLLTWMVRDSLCELQRRQGNIELVAFLACDIKQ

>WP\_046042196.1 ATP-binding cassette domain-containing protein [Klebsiella pneumoniae]

MAHCAHIPAFVLHQVTCQFATGQTLFGPLSVSLEPSLCGLVGRNGVGKTRLLAGLDSPAGGHIERAAAVA

WVAQQPTLTPETTLATLLGYASVFAALSRLEQGQGLADDFDLLDGHWDLTDRLSLAFREADLPPFSADRP

AFSLSGGERMKALLCGAFVSGADYLLLDEPTNHLDRQGREWLYHQLESWQGGALIASHDRELLTRMPRII

ELTPTVLRSYGGNYDEYQRQRMAEQQAARAALEHAVTDRRRTRARMHKEHDAAQRRSAQTLRTVDTLNIA

SFERVKYKGAAKERPGALRRQHREQNSSLNAAVQQARERVEEETPVMFTLPGSEVAAGKQVLVVESLQLD

HAPAAPLNWRIDGPMRIALKGPNGCGKTTLLKTLLGLEQAASGDVRLSVSAAYLDQHLTQLDLSLSVMAH

LSLEDTPLDEGLLRTRLAQLQLGADKVTLPLSALSGGERLKAALACVLWRREPAQLLLLDEPTNHLDLAS

TQAIESALAAFPGAMLVVSHDEAFLQGLKLTHSLAWRETSWHFSLL

>WP\_000014594.1 MULTISPECIES: RNA chaperone/antiterminator CspA [Bacteria]

MSGKMTGIVKWFNADKGFGFITPDDGSKDVFVHFSAIQNDGYKSLDEGQKVSFTIESGAKGPAAGNVTSL

>WP\_002921931.1 MULTISPECIES: HTH-type transcriptional regulator [Gammaproteobacteria]

MEYKDPVFELLSSLEHIVFKDDNQKLTSNRKSTVFSEFEQLRKGTGLKIDDFANVMGVSVAMVREWESRR

VRPSPTELKLMRLIQANPQLSRQLLD

>WP\_004901270.1 MULTISPECIES: aromatic acid/H+ symport family MFS transporter [Klebsiella]

MTKTTIDIQAFINEHPFTRYQWMILALCFITVAMDGFDTAIIGFIASDLVQEWGVEKSALGPVMSAALVG

LAVGALTAGPLADRIGRKKVLIMSIVVFGGFSLLTAFATSLNQLTLLRFLTGLGLGAAMPNAATLMSEYA

PERRRALLVNLMFVGFPMGSSLGGFLSAWMIPHYGWQSVLVLGGVMPLLLAVALIFLLPESVRYLVVKQH

PAQRIAAILRHIAPLPKAVEFVLREAGQVKEKSAIGVIFSPRYAVGTVMLCLTYFMGLLIFYLLTSWLPL

LIRETGASMSQASIITALFPLGGGIGVLILGALMDKINPNKVVAVGWLLTGVFVCLVGFSTSSLALMGVM

VFIAGSIMNGAQSSMPALAAGFYPTQGRATGVAWMLGIGRFGGILGAFSGAFLMQAQLSFETIFTLLAIP

AFLSAFALLIKYRVSKSVPATTDEARSLQKA

>WP\_002921929.1 MULTISPECIES: DUF3053 domain-containing protein [Klebsiella]

MATGKSCSRWFAAMAALLMVVSLSGCFDKEGDQRKAFIDFLQNTAMRSGERLPTLTADQKKQFGPFVSDY

AVIYGYSQQVSQAMDAGLRPVVDSVNAIRVPQDYMTQREPLRQANGALGVLSQQLQNAKMQADAAHGALK

QADDLKPVFDQVYAKVVTAPADALQPLIPAAQIFTQQLVQVGDFVAQQGTQVSFVANGIQFPTSQQASQY

NALIGPLAAQHQAFNQAWTAAVNATR

>WP\_004186083.1 glyoxylate/hydroxypyruvate reductase GhrB [Klebsiella pneumoniae]

MKPSVILYKTLPDDLLQRLEEHFSVTQVKNLRPETVSQHAEAFAQAEGLLGSSEKVDAALLEKMPKLRAT

STVSVGYDNFDVEALNARRVLLMHTPTVLTETVADTVMALVLSTARRVVEVAERVKAGEWTKSIGPDWFG

TDVHHKTLGIVGMGRIGMALAQRAHFGFGMPILYNARRQHPQAEERFNARYCDLDTLLQEADFVCLILPL

SEETHHLFGQAQFAKMKSSAIFINAGRGPVVDEQALIAALQNGEIHAAGLDVFEHEPLAKDSPLLSLPNV

VALPHIGSATHETRYNMAACAVDNLINALNGNVEKNCVNPQVK

>WP\_002921927.1 MULTISPECIES: MFS transporter [Klebsiella]

MNSSTNATKRWWYIMPIVFITYSLAYLDRANFSFASAAGITEDLGITKGISSLLGALFFLGYFFFQIPGA

IYAERRSVRKLIFICLILWGGCASLTGIVHNIPALAAIRFILGVVEAAVMPAMLIYISNWFTKSERSRAN

TFLILGNPVTVLWMSVVSGYLIQAFGWREMFIIEGVPAVIWAFCWWVLVKDKPSQVSWLAESEKAALQEQ

LDREQQGIKAVRNYGEAFRSRNVILLCAQYFAWSIGVYGFVLWLPSIIRSGGENMGMVEVGWLSSVPYLA

ATIAMIVVSWASDKLQNRKLFVWPLLLIGGLAFIGSWAVGANHFWVSYTLLVVAGAAMYAPYGPFFAIIP

EMLPRNVAGGAMALINSMGALGSFCGSWFVGYLNGATGSPAASYIFMGVALFASVWLTLIVKPANNQNLP

LGAHHA

>WP\_002921921.1 MULTISPECIES: sugar kinase [Klebsiella]

MENLDVITIGEAMAMFVATETGDLAEVEHFMKRVAGAELNVATGLARLGLKVGWVSRVGNDSFGRFVLQS

LAKEGIDSHAVAIDNRFATGFQMKSKVENGTDPIVEYFRKGSAASHLSPDDFRADYFTSARHLHLSGVAA

ALSESSYALLEHAAKVMKAEGKTLSFDPNLRPVLWKSEAEMVEKLNRLAFQADWVLPGLKEGVILTGQQT

PEGIADFYLSRGVKAVVIKTGCDGAWFKSASGEQGTVDAIKVDNVVDTVGAGDGFAVGVISALLEGKTLL

QAVNRGNKIGSLAIQVQGDSEGLPTRDALGE

>WP\_002921919.1 MULTISPECIES: hypothetical protein [Klebsiella]

MARKIIVVTAAYGNDHVKSLGGQAAVLPFIANAGADGVEIRRELCSAEELNALPSLAATIERHGLLACYS

APQALFTDNGELNPDLPTLLAEAQTLNALWLKLSLGHFLHNQQLDELRDILSDSGMALVVENDQTDCGQL

APMQRFKAACRVHQLPITLTFDMGNWLWVGDSPEEAARHLAPAVSYIHVKAAEPHHEKFRAVPPDQAAER

WLALLDNLPADAPRGIEFPLTGHDLTAVTRRYVNLLRED

>WP\_002921918.1 MULTISPECIES: LacI family DNA-binding transcriptional regulator [Klebsiella]

MAKAARATISDVAKAAKTGKTSISRYLNGEKHLLSDDLLSRIEKAIAELDYRPSLMARGLKHGRTRLIGL

IIADITNPYSVNVMSGIEAACREKGFTLLVCNTNNELDQELHYLDLLRSYQVEGIVVNAVGMREDGLNRL

QQSALPMVLIDRKIPDFACDVVGLDNAQAATTATEHLVEKGFEAILFLSEPLGSVNTRRERLSAFRATLA

RHHGVVAENAEVQLNDGAMLDNVLRQFHARHRGMRKAVISANGALTLQVARALKRVGLIWGSDIGLLGFD

ELEWAELAGVGITTLKQPTWQIGYAAVEQVIRRIAGTNDPIRERVFSGELIVRGSTSR

>WP\_046042200.1 OmpA family lipoprotein [Klebsiella pneumoniae]

MKKRVLMIAALVSGTLAISGCTTNPYTGEREAGKSGIGAGIGSLVGAGVGALSSSKHDRGKGALIGAAAG

AALGGGIGYYMDVQEAKLRDKMQGTGVSVTRNGDNIVLNMPNNVTFDSNSANLKPAGANTLTGVAMVLKE

YEKTAVNVVGYTDSTGSKDLNMRLSQQRADSVASALITQGVAANRIRTTGMGPANPIASNSTAEGKAQNH

RVEITLSPLQ

>WP\_029884694.1 molybdopterin guanine dinucleotide-containing S/N-oxide reductase [Klebsiella pneumoniae]

MPTSSATKTILTAAHWGPMLVETDGENVLSSRGALATPFANSLQTAVRDQVHSKTRVRYPMVRKGFLASP

DKPQGVRGQDEFVRVSWEQALDLIDAQHRRIRDSYGPASIFAGSYGWRSNGVLHKAATLLQRYMSLAGGY

TGHLGDYSTGAAQAIMPYVVGGNEVYQQQTSWPLVLEHSEVVVLWSANPLNTLKIAWNASDEQGIPWFDR

LRQSGKRLICIDPMRSETVDFFGDSMEWIAPHMGTDVALMLGIAHTLVENDWQDDAFLTRCTSGYDIFAR

YLTGESDGVAKTAEWAAAICGVKADKIRELAQLFHENTTMLMAGWGMQRQQYGEQKHWMLVTLAAMLGQI

GTPGGGFGLSYHFANGGNPTRRAAVLGSMQGSVAGGVDAVEKIPVARIVEALENPGAEYQHNGMARRFPD

IRFIWWAGGANFTHHQDTNRLIQAWQKPELIVISECFWTAAARHADIVLPATTSFERNDLTMTGDYSNQH

LVPMKQVVAPRDEARDDFAVFADLSERWEAGGRERFTEGKSDLQWLETFYQMAARRGAQQQVTLPPFAEF

WQANQLIEMPEEPENARFARFAAFRADPQANPLKTASGKIEIHSPTIAAFGYADCPPHPMWLEPGEWHGN

AEAGQLQLLSAHPAHRLHSQLNHTALRERYAVAGREPVTIHPQDAQARGIVDGDLVRVWNARGQVLAGAV

VTEGIRPGVICLHEGAWPDLDPQVGICKNGAVNVLTKDIPTSRLGNGCAGNTALAWLEKYTGPALPLTAF

DPPANA

>WP\_015959126.1 MULTISPECIES: N-acetyltransferase [Klebsiella]

MIRKWDTKDTAPLLALWLDSTIHAHPFISESYWRDSVAVVRDVYLPAASTWVWEQDGELKGFVSVLDSRF

VGALFVAPGATRQGIGRALLDEVKQHYAWLSLEVYQKNESAVSFYHAQGFRIEDCAWQDDTQHPTWIMRW

PADQMP

>WP\_002921914.1 MULTISPECIES: DNA-3-methyladenine glycosylase I [Klebsiella]

MQRCGWVSQDPLYIEYHDTEWGVAQKEGRQLFEMICLEGQQAGLSWITVLKKRQNYRQAFHQFDPVRVAA

MGDDDIERLLQDTGIIRHRGKIQAIIGNARAYLAMEENGESFTDFVWSFVDNAPQVTRAATLAEIPTTTP

ASDALSKALKKRGFKFVGSTICYSFMQACGLVNDHVTGCFCHPGGQDDPQVGH

>WP\_004220756.1 MULTISPECIES: lipase [Klebsiella]

MSCVSGANAWQQEYIAIDTKSNTSERYTWDSDHQPRYEDILAERMKSSETPGGLALNQGLAPPDSGRGLS

IGWNYPLANGVTSGPVASLRSDVTAPTVRSAGEAGYVNTLGWRMDYQALWGVHPWAQVSYNQSLASDVWA

PMSRAREGGWSDVTLGADMRLGSHVAAWATLSQADNLPSGENTLYLMGVSANF

>WP\_002921907.1 MULTISPECIES: MFS transporter [Klebsiella]

MNAANRQSTRWLTLIGTIITQFALGSVYTWSLFNSSLSDKLGEPVSQVAFSFGLLSLGLALSSSVAGKLQ

ERFGVKRVTMASGILLGLGFFLTAHSSSLMMLWLSAGVLVGLADGAGYLLTLSNCVKWFPERKGLISAFS

IGSYGLGSLGFKFIDSHLLATVGLEKTFVIWGAIVLVMIVFGATLMKDAPNHPAATAANGVVENDFTLAE

SMRKPQYWMLAVMFLTACMSGLYVIGVAKDIAQGMVHLDVATAANAVTVISIANLSGRLVLGILSDKISR

IRVITIGQVVSLVGMAALLFAPLNALTFFAAIACVAFNFGGTITVFPSLVSEFFGLNNLAKNYGVIYLGF

GIGSICGSLIASLFGGFYVTFCVIFALLILSLALSTTIRQPKSTVYNEAHA

>WP\_032105386.1 kdo(2)-lipid A phosphoethanolamine 7''-transferase [Klebsiella pneumoniae]

MKYIRTMTQQKLSFWLALYIGWFMNVAVFFRRFDGYAQEFTFWKGLSGVVELVATVFVTFFLLRLLSLFG

RRIWRILATLIVLFSAAASYYMTFLNVVIGYGIIASVMTTDIDLSKEVIGWHLILWLVAVSAPPLLFIWS

NRCRHTLLRQLRTPGQRVKNVLIVVLAGLIVWGPIRLLELRQHDVERHSEVDMPSYGGVIANSYLPSNWL

SALGLYAWAQVDESSDNKSLINPAKKFTYVAPEGLDDTYVVFIIGETTRWDHMGILGYSRNTTPELEKEK

NLVAFRGYSCDTATKLSLRCMFVREGGAEDNPQRTLKEQNVFAVLHQLGFSGNLYAMQSEMWFYSNTMAN

NIAYREQIGAEPRNRGKSVDDMLLVDEMKRGMAQGNASGKHLIILHTKGSHFNYTQRYPRSFAQWKPECV

GVDNKCSKAELINSYDNSVAYVDHFIVSVLDQLRDKKAIVFYAADHGESINEREHLHGTPRKMAPPEQFR

VPMMVWMSDKYLENPDHAAAFAHLQQQAAMKVPRRHVELYDTIMGCLGYTSPDGGINENNNWCRWKK

>WP\_032105387.1 ankyrin repeat domain-containing protein [Klebsiella pneumoniae]

MKVIKGLVLLCLMMLAGCQSEEETSQFLLACKYDAPATIAAMLDNGIDVDGQDKTGLSGLMVAAAENRRD

VVELLLKRRAKPNLQTRQGVTALMLAAARGSDTAIIGDLLQAGASVNQTSIDKSTALMSAISDGGDVRND

YQHILAMKKPDAPVEEESTLDKIVGVTAAKSLATGNRALMTEDMALQLAPGAFKKNVDEIVALLLKHGAD

VKAVNASGESAFFLAVDHARSAETITTLANAGADTSLADKSGTTPLMLAAAGDDPDLVLALSASGVEVDK

PNREGLTALQVAAGQGAPAVIAALVQRGAKLDQLSANDLSPLMLAVKMNNKANVEALLAAGASVNLSNKA

GYTAIGYSRAGEVRQLLLAQHAELKGQAAHMAQSELQFCANAFADKLAYSDIARAVNNDTRPDIMRHQQS

CPELGELTMLLGEFTFTPAGATYLGEPVTCKVSEYRKTFEVNCR

>WP\_016529074.1 ABC transporter substrate-binding protein [Klebsiella pneumoniae]

MSISLKKSGMLKLGLSLVAMTVAASVQAKTLVYCSEGSPEGFNPQLFTSGTTYDASSVPIYNRLVEFKTG

TTEVIPGLAEKWEVSADGKTYTFHLRQGVKWQDNKDFKPTRDLNADDVVFSFDRQKNTNNPYHKVSGGSY

EYFEGMGLPDLISEVKKVDDNTVQFVLTRPEAPFLADLAMDFASILSKEYADNMLKAGTPEKVDLNPIGT

GPFQLLQYQKDSRILYKAFPGYWGTKPKIDRLVFSITPDASVRYAKLQKNECQVMPYPNPADIARMKEDK

NITLLEQPGLNVGYLSFNTEKKPLDNVKVRQALTYAVNKEAIIKAVYQGAGQSAKNLIPPTMWGYNDDVK

DYTYDPEKAKQLLKEAGMEKGFTIDLWAMPVQRPYNPNARRMAEMIQADWAKVGVQAKIVTYEWGEYLKR

AKAGEHQTVMMGWTGDNGDPDNFFATLFSCAAAKDGSNYSRWCYKPFEDLIQPARATDDHNKRIELYKQA

QVVMHDQAPALIIAHSTVYEPVRKEVKGYVVDPLGKHHFDNVSVE

>WP\_002921786.1 MULTISPECIES: dipeptide ABC transporter permease DppB [Klebsiella]

MLQFILRRLGLVIPTFIGITLLTFAFVHMIPGDPVMIMAGERGISPERHAQLLAEMGLDKPLWQQYAHYI

WGVLHGDLGISLKSRIPVWQEFVPRFKATLELGVCAMIFAVAVGIPVGVLAAVKRGSIFDHTAVGLALTG

YSMPIFWWGMMLIMLVSVQLNLTPVSGRISDTVFLDDTLPLTGFMLIDTAIWGEQGDFIDALMHMILPAI

VLGTIPLAVIVRMTRSSMLEVLGEDYIRTARAKGLTRMRVIVIHALRNAMLPVVTVIGLQVGTLLAGAIL

TETIFSWPGLGRWLIDALQRRDYPVVQGGVLLVATMIILVNLLVDLLYGVVNPRIRHKK

>WP\_004145207.1 MULTISPECIES: dipeptide ABC transporter permease DppC [Klebsiella]

MSQVTENKVIAAPVPMTPLQEFWHYFKRNKGAVVGLVYVVVMIVIAVFANFLAPYNPADQFRDSLLAPPF

WQDGGSMAHLLGTDDVGRDILSRLMYGARLSLLVGCLVVVLSLILGVVLGLVAGYFGGVVDSIIMRVVDI

MLALPSLLLALVLVAIFGPSIVNASLALTFVALPHYVRLTRAAVLVEVNRDYVTASRVAGAGAMRQMFVN

ILPNCLAPLIVQASLGFSNAILDMAALGFLGMGAQPPTPEWGTMLSDVLQFAQSAWWVVTFPGVAILLTV

LAFNLMGDGLRDALDPKLKQ

>WP\_002921785.1 MULTISPECIES: dipeptide ABC transporter ATP-binding protein [Klebsiella]

MALLNVDKLSVHFGDENAPFRAVDRISYSVKQGEVVGIVGESGSGKSVSSLAIMGLIDYPGRVMADKLEF

NGRDLQRISEKERRQLVGAEVAMIFQDPMTSLNPCFTVGYQIMEAIKVHQGGNKQTRRQRAIDLLNLVGI

PDPASRLDVYPHQLSGGMSQRVMIAMAIACRPKLLIADEPTTALDVTIQAQIIELLLDLQQQENMALVLI

THDLALVAEAAHKIIVMYAGQVVETGDAKDIFRAPRHPYTQALLRALPEFAQDKARLASLPGVVPGKYDR

PNGCLLNPRCPYATDKCRSEEPALADLTGGRQSKCHYPLDDAGRPGL

>WP\_002921784.1 MULTISPECIES: dipeptide ABC transporter ATP-binding subunit DppF [Klebsiella]

MSTQKAATPQPLLQAIDLKKHYPVKKGLFAPERLVKALDGVSFTLERGKTLAVVGESGCGKSTLGRLLTM

IEIPTGGELYYQGQDLLKHDPQAQKLRRQKIQIVFQNPYGSLNPRKKVGQILEEPLLINSSLSKEQRREK

ALAMMAKVGLKTEHYDRYPHMFSGGQRQRIAIARGLMLDPDVVIADEPVSALDVSVRAQVLNLMMDLQQD

LGLSYVFISHDLSVVEHIADEVMVMYLGRCVEKGTKDQIFNNPRHPYTQALLSATPRLNPDDRRERIKLT

GELPSPLNPPPGCAFNARCRRRFGPCTQLQPQLKDYGGQLVACFAVDQDENPQKSHA

>WP\_004145206.1 MULTISPECIES: hypothetical protein [Klebsiella]

MAGSFSPAVDKTWRLRILPQFMSRSQSILRRLSEKISLSVHFYRIKEKLKWFRFILSLI

>WP\_016531323.1 cellulose biosynthesis protein BcsO [Klebsiella pneumoniae]

MSHYDDLQRFQEKTRTQNLNFQDLSSQAATREHGDWAILNQLNPGAEKPSSLALGGSVSAPLPQSVPADL

FRQVEAAVAAAPTSDPVVSAASAAPATSQPVVETAAAAPEPVRQEPAPTPAPSIPVSEPAMAPPPRMAPR

PAPAAENYAHLFAAKSAEPVAKNKDQPLKSLLERIATCR

>WP\_004901226.1 MULTISPECIES: UDP-forming cellulose synthase catalytic subunit [Klebsiella]

MKKSLFWLLALVLSPVAVLVVITPMDSQKQYIFGLLSIGILFLMGFSKRRSVSVIMVVTSLLMSTRYMYF

RLTQTLHFNSSIEAILGMGLFLAEVYIWVMLLLNYLQTVWPLKRGIVPLPDDMSKWPTVDIYIPSYNEPL

EVVRDTVLAAQCIDYPKDKMKIYLLDDGKRSEFAVFAADVGVGYITRNDNKHAKAGNLNHALTLTQGELI

CVFDCDHVATRVFLQATVGGFLKDPMLALVQTPHYFYSPDPFERNLSVGRNIPNEGMLFYGPIQQGNDNW

NATFFCGSCAVIRREALAQIGGFAVETVTEDAHTALKFQRLGWKSAFLDIPLAAGLATERLVVHVIQRTR

WARGMTQIFRVDNPLFGRGLTFQQRLCYLSAMLYYQFALPRVVFVTAPLAYLLFNLNIIYSSASLIVSYA

LPHLFLAIYVGSRMNGRYRYSFWGEIYDIVLAFHLVLPTLVTMIFPKRGKFNVTDKGGLLDVGYFDFTVV

RPHLVVACLLALGVIVGIVRAIGHDYFGSDPNVIALNVGWGIYSLIFLLAAIAVARETRQVRKTIRIDVD

IPVVIHYASGIVSRSHTADLSMGGCRVVALDNRHLEDDIEEIELILQSGAISIPAQLVTSDERFLRLKFD

EDIPLSRRRELVRVVLARADAWINPPRPQDNPFRSFFTILRCVFELFWLTWKTRRSQRNRATVAKTAQED

GTL

>WP\_002921529.1 MULTISPECIES: hypothetical protein [Gammaproteobacteria]

MMTENNNPVVMTWFQQQQTPAGWFDLLIIMIEGMLNNAGELESQPFLRQMGASLAETHPLPASETVGDLE

ANINRLLTHFHWGVVTIDVGEDGLRLRHQALPVSRDEAGRVRWCNAFCAILEGLYSRWLQSQGGSAHVIL

QRERVFSVSDVQFLYYHP

>WP\_004188233.1 glycosyl hydrolase family 8 [Klebsiella pneumoniae]

MPLRALVAVIVTTVVMLVPRAWADTAWERYKARFMMPDGRIIDTANGNVSHTEGQGFAMLLAVANNDRPA

FDKLWQWTDNTLRNKSNGLFYWRYNPVAPDPIADKNNASDGDTLIAWALLRAQKQWQDKRYAIASDAITA

ALLKSTVVTFAGRQVMLPGVKGFNLNDRLNLNPSYFIFPAWRAFAERTHLTAWRTLQSDGQALLGQMGWG

KSHLPSDWVALRADGKMLPAKEWPPRMSFDAIRIPLYLSWADPHSALLAPWKAWMQSYPRLQTPAWINVS

TNEVAPWYMAGGLLAVRDLTLGEPQEAPQIDDKDDYYSASLKLLVWLAKQDQR

>WP\_002921518.1 MULTISPECIES: cellulose biosynthesis protein BcsF [Enterobacteriaceae]

MMSLADILQLVVLCALLFFPLGYLTRHYQRRIRTTLRLMFFKPRYVKPAGVLRRGTTVKQGKANK

>WP\_002921513.1 MULTISPECIES: cellulose biosynthesis protein BcsR [Enterobacterales]

MPAKDPAVPTDATLGYTFQNDFLALSRAFSLPDIDYHDISRREQLNAALKRWPLLAEFAEKK

>WP\_002921510.1 MULTISPECIES: cellulose biosynthesis protein BcsQ [Klebsiella]

MAILGLQGVRGGTGVTSITAALAWALQLLGESVLAIDASPDNMLRFFFNTDIHHQDGWARALLDGRDWRD

AGLRYTQHIDLLPFGQLSAGERENVDQLQPTLGAIAEAVQQLQGQYRWLLLDLPAGYSPLTRELLTLCDR

SLVVVHPDANSHIRLHQQPLPANGDILINDLRVGSQLQEDLYQLWLESQPRILPVTIHRDEAMAECLAAK

QPLGEYRQDSLAAEEVLTLANWCLIHYSAGRAA

>WP\_002921508.1 MULTISPECIES: UDP-forming cellulose synthase catalytic subunit [Klebsiella]

MIRLSTLLLAPPVGERLRARYDDYRQHGASWLSASLGCLWASLVWALMPLETPRWQAILARHETYFPHIN

PHRPRPLDPLRYLLQSLWLLTTRVPEPEKKVNWRSLAALEGVHGRYTQWLEKLPEQMNARTGHLDKQKEL

AHLNPKLRRAILGGVTFCSLVLALMCITQPFNPLSQFIFLMLLWGVALLVRRIPGRFSALMLIVLSLTVS

CRYIWWRYTSTLNWNDPVSLVCGIILLFAETYAWVVLVLGYFQVVWPLNRQPVPLPEDMDLWPTVDIFVP

TYNEDLNVVKNTIYASQGIDWPKDKLNIWILDDGGREAFRQFAKDVGVHYIARTSHEHAKAGNINNALKY

AKGEFVSIFDCDHVPTRSFLQMTMGWFLKEKELAMMQTPHHFFSPDPFERNLGRFRKTPNEGTLFYGLVQ

DGNDMWDATFFCGSCAVIRRGPLDEIGGIAVETVTEDAHTSLRLHRRGYTSAYMRIPQAAGLATESLSAH

IGQRIRWARGMVQIFRLDNPLFGKGLKLVQRVCYANAMLHFLSGIPRLIFLTAPLAFLLLHAYIIYAPAL

MIALFVLPHMIHASLTNSKIQGKYRHSFWSEIYETVLAWYIAPPTFVALINPHKGKFNVTAKGGLVEEEY

VDWVISRPYIYLVLLNLVGVAVGIWRFMYGPENEILTVWVSIVWVFYNLIILGGAVAVSVESKQVRRSHR

VEMSMPAAIAREDGHLFSCTVHDYSDGGLGIKINGDAQVLEGQNARLLLKRGQQEYAFPVRVARVNGSEV

GLQLLPLTNQQHIDFVQCTFARADTWALWQDSFPEDKPMESLLDILKLGFRGYRHLAEFSPPSVKVVFRA

LTSLVAWIASFVPRRPERAAPTLSADPAMAQQ

>WP\_071829969.1 cellulose biosynthesis cyclic di-GMP-binding regulatory protein BcsB [Klebsiella pneumoniae]

MKRKLSWMCAVAVGMCSWYPLVSYAAPAAVANAAPVVQPQAATPAAPIVVGEPTATLAEPTAPAALAENV

PQREVKLSFATIAPPPGSIVLRGSRPDASVEFGMRSDELVANALLNLEYTPSPSLLPVQSQLKVYLNDEL

MGVLPVTKEQLGKKIRAQLPIDPLYITDFNRVRLEFVGHYRDVCENPASSTLWLDVGRESYLDLTYQSLK

VNNDLSHFPVPFYDPRDNRPLKLPMIFPGSPAVTQQQAAAIVASWFGSKAGWRGQQFPVYFNELPDRNAI

VFATNDKRPDFLRDHPPVKAPTIEMIDNPNDPYVKLLVIFGRDDNDLLLAAKGIAQGNILFRGSSVTVDG

IKTLQPRQPYDAPNWVRTDRSVTFAELKTYEQQLQSSGLVPDAITVALNLPPDLYLLRANGIDMDLKYRY

TMPPVKDSSRMDISLNDQFLQSFSLNSSQDVNKLILRLPVLQGLLDGKSEVTIPALRLGAVNQLRFDFQY

MNPMPGGSIDNCITFQPVQNHVVIGDDSTIDFSKYYHFIALPDLRVFANAGFPYSRMADLSDTLVVVPKA

PTQGQVATLLQALGGIGSQTGLAAINLQMTDDGNQIKNKDADLLLIGAIPSSLKDDTKINLLVEATKSWV

KMPMRHYDLASIYPDDEARTPNTRTDITSSGPMAAVIGFQSPYNDQRSVVALLADSPRGNELLTNALNDS

GKRAAMFGSVAVIRESGVNSLRVGDIYYVGHLPWFERIWFALSNHPILLAIFAAISIVLLAWVLWRMLRI

ISRRRLSLDDE

>WP\_046042211.1 cellulose synthase complex periplasmic endoglucanase BcsZ [Klebsiella pneumoniae]

MMKVLCGAVLSALLLAAGQVGAACQWPAWEQFKQAYVSPEGRVIDPSDARKISTSEGQSYGLFFALAAND

RAGFDKLLTWTQNNLAEGDLKQHLPGWLWGKKDDEEWTLLDSNSASDSDLWIAWALLEAGRLWQQPQYTE

TGKALLARIVAEETVAVPGLGTMLLPGKVGFADDSGWRFNPSYLPPQLATYFVRFGAPWPALRDSNLRLL

LETAPKGFTPDWVRYEKGKGWQLKTEKPPIGSYDAIRVYLWVGMLHNGDKQKARLLQRFAPMAAQTTEQG

VPPEKVNIATGKTSGQGPVGFSAAMLPFLQDDEARSVQRQRVADNYPGADAYYSAVLTLFGQGWDQHRFR

FTASGELQPDWNQECASSH

>WP\_046042212.1 cellulose synthase complex outer membrane protein BcsC [Klebsiella pneumoniae]

MRKLSLSLLTLSLGVALLPLAQAATTPAQEHLLEQVRLGEASNREDLVRQSLYRLELIDPNNPELIAARM

RYLLRQGDAAGAQKELERLTKLAPDSPELKASRNEMKSNTGEGRQALQQARLLGVAGKVDEAIAAYEKLY

GGVPDDVDVAIEYWTLVARLPSRHSEGVSQLKKLNASAPGNVSLLTSLAKQMFADNKPQEGFAYLAEMAR

SASGRGIAADMWFSEVKSMPVSKASVQALQQFLLQFPTGSVAANARVLLDQQQAQLQDPTFRARSEGLAA

VKSGNTTQAVADLQKAVQADSRDSDAVGALGQAYSQRGDRARAVAQLSKAIAMDPDSPNRGKWDSLLQTN

RYWLLIKQGDNALKAGQLSQAQNYYAQAQRVDRTDSYAVLGLGDVAAARKEAAAAERYYQQALRLDRGNN

LAVRGLANLYRAESPEKASAWIAGLPPAQRRSIDDIERSLTNDRLEKQAQALESQGNWAQAAEVQRRRLA

LDPDSVWITYRLARDLVSAGERQEADALMRTMVNRQPQDAERVYASGLYLSGNDQDDLALAQIAALPRSA

WTDNIRELEARLQSDRVLRQANQLRDSGDEAQAIALIKRQPASVRYDLTLADWAQQRGDSQTAIADYQRV

LRQEADNGDARLGLAEVYLAEGDKPAARAQVMQLKGAETESMNMQRRVALARAGLGDTADAQRIFNQIVP

QAKAQPPSMESALVLRDAARFATQSGAPQQALTHYREAMVASGITPAQPQDNATFTRLTRNDSHDDWLKR

GIRSDAADLYRQQDLNVTLEHDFWGSSGTGGYSDLKAHTTMLQVDAPLADGRMFFRTDLVNMDAGSFSTH

SDGSYSPSWGTCGEIACTSGSINQTDSGASVAVGWKNDTWSGDIGTTPMGFNVVDVVGGLSYSSDVGPVG

YTVNVHRRPISSSLLSFGGQKDSSSHTGATWGGVRADGGGLSLSYDRGEAHGIWSSLGADSLTGKNVADN

WRVRWMTGYYYKVINENNRRVTVGLNNMIWHYDKDLSGYTLGQGGYYSPQEYLSFAVPVTWRQRTENWSW

ELGGSVSWSHSRTQTQARYPLLNLIPSDYRQRASELTEEGSSSHGFGYTARALVERRVTSNWFVGAAVDI

QQAKDYTPSHALLYVRYSAAGWQGDLDMPPQPLVPYADW

>WP\_004151429.1 MULTISPECIES: biofilm formation regulator HmsP [Klebsiella]

MRVSRSLTIKQMAMVASVSMAFVLVFCTILLFHFVQQSRFTTATQLESIARSVREPLSAAILKADIPEAE

AILSRIQPAGIVSRADVVLPNQFQALRMRFIPERPVPVTVTRLFELPVQISLPIYSLERPANPQPLAYLV

LQADSYRMYKFVMSALATLVTAYLLLVLMLTVALTWCINRLMVRPLRRIARELNDLSQQERLGHQLTLPR

LHHDDEIGMLVRSYNRNQQSLVRQHDELSIQSTRFPVSELPNKAFLLAMLEQTVARPQSAALIVVACETL

QDAAGVLKESQREMLLLTLVEKLRAAIPPQMVLAQVSGYDFAILADGLAEPWQAVTLSKQVLTIINERLP

LHGLQLRPYASVGIAMFHAGLSAEQFYRRAVSAAVTARRKGKNQIEFFDPEQMEKAQRRLMEEHDIMTAL

DNQQFAIWLQPQVACASGEICGAEVLLRQRQADGSWSLPPALIERIESCGLIIPVGYWVMEEACRQLAAW

QSQGIMLPLSVNVSLLQLLEHDRGEEMLKLIARYRIAPGTLILEVTESCRMDDPQDVMARLRPLREAGVQ

IALDDFGMGYAGLHQLQQMKALPVDILKIDKVFIDMLPEDVSMVPAMIQLARGLSLRIVAEGVENDAQRR

WLQAAGVEVLQGHLFGCALPQEAFSARYLSPVREDENL

>WP\_002921438.1 MULTISPECIES: dicarboxylate/amino acid:cation symporter [Klebsiella]

MKTSIFKSLYVQVLTAIAIGILLGHFYPELGAQMKPFGDAFVKLIKMVIAPVIFCTVVTGIAGMESMKAV

GRTGAVALLYFEVVSTIALIIGLIIVNVVQPGAGMNVDPSTLDAKAVAVYAEQAKDQGVVAFLLDVIPGS

VIGAFASGNILQVLLFAVLFGFALHRLGSKGQLIFNVIESFSQVIFGIINMIMRLAPIGAFGAMAFTIGK

YGVGTLVQLGQLIICFYITCILFVVVVLGSIARATGFSIFKFIRYIREELLIVLGTSSSESALPRMLDKM

EKLGCRKSVVGLVIPTGYSFNLDGTSIYLTMAAVFIAQATNSHMDIFHQITLLVVLLLSSKGAAGVTGSG

FIVLAATISAVGHLPVAGLALILGIDRFMSEARALTNLVGNGVATVVVAKWVKELDAKQMDDVLNNRVPA

NKTHELSS

>WP\_004145185.1 MULTISPECIES: insulinase family protein [Klebsiella]

MQGTTIKLLTGGLLMVAAAGYVQAEALQPDPAWQQGTLANGLSWQVLATPQRPSDRIEVRLSVNIGSLSE

STQQSGFSRFIPRLALTQSGSLPTMQARSLWQQSIDPKRPLPPAIVSYDYTMFNLSLPNNRNDLLKEALS

WLADASGKLAITPESINHALQGSDMVATWPLDTKEGWWRYRLKGSTMLGHDPAAPLKQPIDVAQLKDFYQ

KWYTPDAMTLIVVGNVDSRSVAEQINKTFGDLKGKRETPAAVPTLSPLPTVPVSIMTNAVRQDKLSIMWD

APWQPIRDSAALQRYWRDDLAREALFWHVQQSLSKNNVKDIGLGFDCRVLYQRAQCAINIDSPGERLNNN

LSVVSRELAKVRDNGLPQEEFDALIAQKSLELQKLFATYARTDTDILMSQRMRSLQNQVVDIAPEQYQKL

RQEFLNSLTVDMLNQYLRQQLSQDMALVLQQPKGEPEYNMKELQATWEKLMAPNPAATATSGSADTVDAH

SEASDIPPGQ

>WP\_004901196.1 MULTISPECIES: sugar kinase [Klebsiella]

MSKKIAVIGECMIELSEKNGAVNRGFGGDTLNTSVYIARQTDASALSVHYVTALGTDAFSQQMLDSWQQE

NVNTDLIQRMADRLPGLYYIETDDTGERTFYYWRNEAAAKFWLESDRAAAICEELATFDYLYLSGISLAI

LSPASRDKLFTLLRECRANGGKVIFDNNYRPRLWASQAETQQVYQEMLACTDIAFLTLDDEDALWGEKPV

AEVIARTHAAGVEEVVVKRGAEACLVSVSGQPLREVPAVRLAKEKVVDTTAAGDSFSAGYLAVRLTGGDA

ESAARRGHLTASTVIQYRGAIIPREAMPQ

>WP\_016532624.1 AsmA family protein [Klebsiella pneumoniae]

MSRTRKTLVIITGTILLLIVLFFIVLATFDWNRLKPTINQKVSAELNRPFAIRGDLGVVWERQPDERGWR

SWIPWPHVHAEDIVLGNPPAIPQVTMIHLPRVEATLAPLALLSKTVYLPWIKLEQPDVRLIRLAEDNNNW

TFQLAGDKRTSGDSAPSSWSFRLDNILFDRGTIAIDDKITRSDITILVDPLGKPLPFSEVTGTKDRHSAA

KPGDYVFGLSLKGRYKGQPVTGNGKIGGMLALRSASAPFPLQGDFHSGNTRVAFSGTVSDPLNVGGIDLR

LKFAGDSLRDLYALTGVLLPETPSFSTDGRLRADFMQKNRMRFNYQNFNGRIGDSDIHGSLTYTTGKPRP

KLSGDMESKQLRLADLGPLIGVDSGKGTKKSAARQAGDRPQPAGKVLPADRFETDKWQVMDADVRFKGRR

IEHGGTLPISDLSTHVILEDGDLRLQPVRFGLANGSIAGSVHLQGDKKPLQGEANLQARRLKLKALMPNV

EMMQKTLGEMNGDVQLRGSGNSVAALLGNSNGNLKLLMNDGLISRNLMEILGLNVGNYLIGQIFGDEEVR

VNCAAANIDVTNGVARPQIFAFDTENALINVTGTASFASEQLDLTIDPESKGFRVITLRSPLYVRGTFKS

PQAGVKAGPLIVRGAVAAALATLVTPAAALLALISPAEGDSNQCRTILSQMKK

>WP\_004150118.1 MULTISPECIES: MHS family MFS transporter [Klebsiella]

MQATATTLENTQETAPVNSRNKVVVASLIGTAIEFFDFYIYATAAVIVFPHIFFPQGDAAAATLQSLATF

AIAFVARPIGSALFGHFGDRVGRKVTLVASLLTMGISTVVIGLLPGYESIGIVAPMLLALARFGQGLGLG

GEWGGAALLATENAPARKRALYGSFPQLGAPIGFFFANGTFLLLSWLLTDQQFMEWGWRVPFIFSAVLVI

IGLYVRVSLHETPVFAKVAAAKKQVKIPLGTLLTKHVRVTVLGTFIMLATYTLFYIMTVYSMTFSTGAAP

NGLGLPRNEVLWMLMMAVIGFGVMVPVAGLLADAFGRRKSMIIITTMIILFALFAFKPLLGSGNPLLVFA

FLLLGLSLMGLTFGPMGALLPELFPTEVRYTGASFSYNVSSILGASVAPYIAAWLQGNYGLAAVGTYLAA

MAALTLIALLLTHETRHQSL

>WP\_002921337.1 MULTISPECIES: inner membrane protein YhjD [Klebsiella]

MTPENDDRRPPQEPDTQPEKSKSTLEALNDTAVGQKASQALKTVTGTAAKVQRNPVIAHLLRAAERFNDR

LGNQFGAAITYFSFLSMIPILMVSFAAAGFVLAWHPTLLQDIFDKILQNVSDPTLAATLKNTINTAVQQR

TAVGLVGLLVALYSGINWMGNLREAIRAQSRDVWERRPQDEEKIWVKYFRDLISLIGLLVALIITLSITS

VAGSAQQMIISALYLDNIEWLKPAWRLIGLAISIFANYLLFFWIFWRLPRHRPRRKALFRGTLIAAIGFE

IIKIVMTWTLPALVKSPSGAAFGSVLGLMAFFYFFARLTLFCAAWIATAEYKDDRRMPGKTHR

>WP\_004145179.1 MULTISPECIES: LysR family transcriptional regulator [Klebsiella]

MDKIHAMQLFIRVADLESFSRAAETLALPKGSVSRQIQALESHLGVRLLHRTTRRVQLTQDGMVYYERAK

DLLSNLDELDGMFQHDPASISGRLRVDMPVGFAKKMVIPHLPTFLQQYPGIELELSSSDRLVDVIREGFD

CVVRVGALKDSGLIARPLGKLTQINCASPDYLARFGYPQSLEDLADHALIHYASTLGVRPPGFEVMIDGA

VRWVKTGGILTVNSTETYQAACIAGLGIIQVPRTGVREALRAGDLIEILPQYRAEPLPVSLIYPHRRNLS

RRVNLFMEWLGGLMKAYVD

>WP\_002921336.1 MULTISPECIES: SDR family oxidoreductase [Klebsiella]

MTQRIALVTGGSRGLGKNAALKLAAKGTDILLTYHSNRQAALDVVAEIEQKGVKAAALALNVGDSTTFDA

FASEVAQVLAQKWGRTTFDYLLNNAGIGLNAPFAETSEAQFDELMNIQFKGPFFLTQRLLPLLQDGGRIL

NVSSGLARFALPGYAAYAAMKGAMEVLTRYQAKELGGRGISVNIIAPGAIETDFGGGEVRDNAEVNRHIA

AQTALGRVGLPDDIGDAIAALLSDELAWMNAQRVEVSGGMFL

>WP\_004901185.1 MULTISPECIES: GNAT family N-acetyltransferase [Klebsiella]

MPELLTPRLRCSPLQLDDWSFFLSLQQDPQVMLYVADPRPQAAIREAFDSRLPPWTPGDEHWLCLVVRDR

LTHTPLGLTGYQHHQRDIAEVGFLFAPAAQGRGYGYESLRALCDYAFTTGGVRRLTASVTAGNETSKQLL

LKAGFRLEGELRENYWLNGRWHNDWLFGRLRGEGDAP

>WP\_004150117.1 MULTISPECIES: alpha,alpha-trehalase [Klebsiella]

MFSQKLRHVEDDELRIDIDPCYEADPYELKLDEMIDAEPEPEVIEGLPASDALTPADRYLELFTNVQKSR

IFADSKTFPDCAPKHDPLDILRNYRKVKRQPDFDLRQFVEDNFWLPESQSDIYISDPSLTLKEHIDKLWP

VLTREPQDHIPWSSLLALPQAYIVPGGRFSETYYWDSYFTMLGLAESGREDLLKCMADNFAWLIETYGHI

PNGNRTYYLSRSQPPVFALMVELFEEDGVRGAKRYLDHLKMEHAFWMDGAESLIPHQAYRHVVRMPDGSL

LNRYWDDRDTPRDESWREDVETARHSGRPANEVYRDLRAGAASGWDYSSRWLRDITRLASIRTTQFIPID

LNAFLFKLETTIANLSGLKGDRETETAFRQKAQDRRAAVNRYLWDDENGCFRDYDWRREQLALFSAASIV

TLYVGLATHEQAERLADAVRARLLTPGGIMATEYESGEQWDKPNGWAPLQWMAIQGFKRYGQDPLGDEIA

WSWLQTVNHFYKQHHKLIEKYHIATGVPHEGGGGEYPLQDGFGWTNGVVRRLIGLYGEPT

>WP\_016529215.1 iron-containing alcohol dehydrogenase [Klebsiella pneumoniae]

MLTPFTVLMPANIRFGRGQAESAAPWLAQQGGPILLVHGASPQRAAFLRQQLEALQLAVTTLAISREPWL

SDIEQGVQLAREKGIRAVVSLGGGAVIDAGKAIAALVPAVGPVIDYLEVVGTGRQLEASPLPFVAIPTTA

GTGAEVTKNAVINVPEQQRKVSLRDDRMLPDLAILDPALTDNAPRSITLSSGLDALTQVIEPWLCSRATP

FTDALCQQAIPRGIRALKILMEQECPASRDEMAWVSLCGGLALANAGLGVIHGLAGPLGGLSRASHGALC

GSLLPFGLALNESQINDPGLRQRVNDVRRWLADGLDVPVDQVWDSLREWSHRAGLGTLRDLGVARDALEP

AALAASTSSSMKANPVSLSGEQLLEMLEAAWE

>WP\_002921273.1 MULTISPECIES: glutathione S-transferase [Klebsiella]

MLTILGKRSSINVRKVLWTCEEAGLAYQQEDYGSGFKPLDTPEFQRLNPNSLVPVLLDDDFVLWESNSIC

RYLARKAERWDLLPAEPQPAAEVEHWMDWQATEFNTAWRHAFMGLVRKDPRFQDPVAIKESIAAWTHCVR

IVEAQLQRTGAWIAGERFTLADIVLGLSVHRWKMTPFAHPEMPAVERWYMALNQRPAFMRHGNNGVA

>WP\_046042215.1 glutathione-disulfide reductase [Klebsiella pneumoniae]

MSKHYDYLAIGGGSGGIASINRAAMYGQKCALIEAKELGGTCVNVGCVPKKVMWHAAQIREAIHLYGPDY

GFDTTINHFDWEKLVASRSAYIDRIHTSYDNVLGKNKVDVIKGFARFVDAHTVEVNGEIITADHILIATG

GRPSHPDIPGVEYGINSDGFFELPALPKRVAVVGAGYIAVELAGVINGLGAETHLFVRKHAPLRSFDPLI

VETLVEVMNAEGPQLHTNAIPKAVVKNADGSLTLELEDGRSQTVDCLIWAIGREPATDNFNLAATGVKTN

DKGYIIVDKFQNTNVPGIYAVGDNTGAVELTPVAVAAGRRLSERLFNNKPEEHLDYSNIPTVVFSHPPIG

TVGLTEPQAREQYGDDAVKVYKSSFTAMYTAVTSHRQPCRMKLVCVGPEEKIVGIHGIGFGMDEMLQGFA

VALKMGATKKDFDNTVAIHPTAAEEFVTMR

>WP\_002921269.1 MULTISPECIES: 23S rRNA (adenine(2030)-N(6))-methyltransferase RlmJ [Klebsiella]

MLSYRHSFHAGNHADVLKHTVQSLIIESLKEKEKPFLYLDTHAGAGRYQLSGEHAERTGEYLEGIARIWQ

QDDLPAELEPYISVVEHFNRNGQLRYYPGSPLIARQLLREQDSLQMTELHPSDFPLLRAEFQKDSRARVD

KADGYQQLKAKLPPVSRRGLILIDPPYEIKTDYQAVVTGINEGYKRFATGTYALWYPVVLRAQIKRMIKE

LEATGIRKILQIELAVRPDSDQRGMTASGMIVINPPWKLEQQMNNVLPWLHSKLVPTGTGHATVSWIVPE

>WP\_016529354.1 MULTISPECIES: phosphatase PAP2 family protein [Klebsiella]

MKRQLSLLAVALLLAQPVLAKDIPLNRAAALANSVTPAASSQAYDDLEQQALAQLRHALQGNAATLTRDR

LARTKQNQTQADTAWLKASGYDFQTRANQQAGIALLSAFSTLPETVVKQNLATVTAINRDAVQTTRRQAL

ADAEGISYLYFLSDALGPRLGKAFLTAYDQGALGKAAALIKASEVSTGEAKKHFNNPRPFLVQGNTIHLV

PDDVVVKDNQPYTADGGSFPSGHTNTGYTDALLLAAMIPERYDALVARGARYGYSRIVLGVHYPLDVIGS

RMVAERNVAHYLNDPHYRVLFNEARDQLRAALAKACGTSLAECAKSSVKDDPWRDPAMRDFSRFTMTYDL

PQQKGPQPRLQVPEGAEVLLEDALPHLSAAQRRALMVNTALPAGYPLSGTTPEQQFWQRLNLSAAWEMAQ

KRQ

>WP\_004151426.1 MULTISPECIES: oligopeptidase A [Klebsiella]

MTNPLLTPFSLPPFSAIKPEHVVPAVTKALEDCRAAVESAVAHGAPYSWENLCQPLAEVDDVLGRIFSPV

SHLNSVKNSPELREAYEQTLPLLSEYSTWVGQHEGLYKAYRDLRDGDNYATLNTAQKKAVDNALRDFELS

GIGLPPEAQKRYGEIAARLSELGNQYSNNVLDATMGWNKLVTDVADLAGMPESALAAAQAQAQAKEQEGY

LLTLDIPSYLPVMTYCDNQALREEMYRAYSTRASDQGPNAGKWDNSPVMAEILALRHELAQLLGFDSYAY

KSLATKMAKDPQQVLDFLTDLAKRARPQGEKELAQLRAFAKAEFGVDELQPWDIAYYSEKQKQHLYSISD

EQLRPYFPENKAVSGLFEVVKRIYGITAKERTDVDVWHPEVRFFELYDEHNELRGSFYLDLYAREHKRGG

AWMDDCVGQMRKLDGSLQKPVAYLTCNFNRPVNGKPALFTHDEVITLFHEFGHGLHHMLTRIDTAGVSGI

SGVPWDAVELPSQFMENWCWEPEALAFISGHYETGEPLPQELLEKMLAAKNYQAAMFILRQLEFGLFDFR

LHAEYKPEQGAKILETLAEIKKQVAVVPGPTWGRFPHAFSHIFAGGYAAGYYSYLWADVLAADAFSRFEE

EGIFNRETGQSFLDNILSRGGSEEPMELFKRFRGREPQLDAMLEHYGIKG

>WP\_004151425.1 MULTISPECIES: 16S rRNA (guanine(1516)-N(2))-methyltransferase RsmJ [Klebsiella]

MKICLIDETGAGDGALSVLAARWGLEQDDDNPMALALTTEHLELRKRDEPKLGGIFVDFVGGAMAHRRKF

GGGRGEAVAKAVGIKGDYLPDVVDATAGLGRDAFVLASVGCRVRMLERNPVVAALLDDGLARGYADAEIG

GWLQERLQLIHASSLTALTDITPRPQVVYLDPMFPHKQKSALVKKEMRVFQSLVGPDLDADGLLAPARQL

ATKRVVVKRPDYAPPLAEVATPNAVVTKGHRFDIYAGTPE

>WP\_016529351.1 dipeptide/tripeptide permease DtpB [Klebsiella pneumoniae]

MNTTAPTGLLQQPRPFFMIFFVELWERFGYYGVQGILAVFFVKQLGFSQEQAFITFGAFAALVYGLISIG

GYVGDHLLGTKRTLVLGAIVLAIGYFMTGMSLLKPQLIFIALGTIAVGNGLFKANPASLLSKCYPPKDAR

LDGAFTLFYMSINIGSLLSLAPVIAEKFGYAVTYNLCGAGLIIALLVYFACRGMVKDIGSEPDHRPLSLR

NLALVLAGTVVMIFLCAWLMHNVMIANLVLIVLSVVVIAFFFREAFRLDKTGRNKMFVAFILMIEAVLFY

ILYAQMPTSLNFFAINNVHHEILGFTINPVSFQALNPFWVVVASPVLAAIYTHLGHKGKDLTMPVKFTLG

MFLCALGFLTAAAAGMWFADAQGLTSPWFIVLVYLFQSLGELLISALGLAMVAALVPQHLMGFILGMWFL

TQAAAFLLGGYVATFTAVPENITDPLQTLPVYTNVFSKIGLVTLGVTVVMALMVPWLNRMINTPASAE

>WP\_004145166.1 MULTISPECIES: universal stress protein UspA [Klebsiella]

MAYKHILIAVDLSPESKVLVEKAVSMARPYNAKVSLIHVDVNYSDLYTGLIDVNLGDMQKRISEETHHAL

TELSTNAGYPITETLSGSGDLGQVLVDAIKKYDMDLVVCGHHQDFWSKLMSSARQLINTVHVDMLIVPLR

DEEDE

>WP\_002921203.1 MULTISPECIES: universal stress protein UspB [Klebsiella]

MISTIALFWALCVVCVVNMARYFSSLRALLVVLRGCDPLLYQYVDGGGFFTSHGQPSKQMRLVWYIYAQR

YRDHHDDEFIRRCERVRRQFILTSALCGLVVVSLIALMIWH

>WP\_002921200.1 MULTISPECIES: inorganic phosphate transporter PitA [Klebsiella]

MLHLFAGLDLHTGLLLLLALAFVLFYEAINGFHDTANAVATVIYTRAMRSQLAVAMAALFNFFGVLLGGL

SVAYAIVHMLPTDLLLNMGSAHGLAMVFSMLLAAIIWNLGTWYFGLPASSSHTLIGAIIGIGLTNALMTG

TSVVDALNIPKVIGIFASLIISPIVGLVIAGGLIFLLRRYWSGTKKRARIHLTPAEREKKDGKKKPPFWT

RIALILSAIGVSFSHGANDGQKGIGLVMLVLIGVAPAGFVVNMNASGYEITRTRDAVNNVETFFQQRPEL

LKKATGVDQLVPSPDTNTAANGEFHCHPANTINALDRVKTMLTGVENYESLKPEQRGQLRRIMLCISDTT

DKVAKLPDVSADDQRLLKKLKTDMLSTIEYAPIWIIMAVALALGIGTMIGWRRVATTIGEKIGKKGMTYA

QGMSAQMTAAVSIGLASYTGMPVSTTHVLSSSVAGTMLVDGGGLQKKTVTSILMAWVLTLPAAIILSGVL

YWLSLKLI

>WP\_016529349.1 MULTISPECIES: NAD(P)/FAD-dependent oxidoreductase [Klebsiella]

MERFDAIVVGAGAAGMFCAAQAGQLGCRVLLLDNGKKPGRKILMSGGGRCNFTNMYVEPAAYLSQNPHFC

KSALARYTQWDFIELVGKYGIAWHEKTLGQLFCDDSAEQIVNLLLAECEKGGVQIRLRSEILSVERDEQG

YRLQVNGETLMTKKLVIASGGLSMPGLGASPFGYKVAEQFGLKVLPTRAGLVPFTLHKPLLEQLQVLSGV

SVPSTITAENGTLFRENLLFTHRGLSGPAVLQISSYWQPGEFVTVNLLPDCDLDDFLNEQRSAHPNQSLK

NTLAMQLPKRLVECLQQLGQIPDVTLKQLNVRDQQTLVETLTAWRVQPNGTEGYRTAEVTLGGVDTNELS

SRTMEARKAPGLYFIGEVMDVTGWLGGYNFQWAWSSAWACAQALVEG

>WP\_002921192.1 MULTISPECIES: magnesium transporter [Klebsiella]

MSSIQLCAAHQATSGFDGDAIVQYMRTDFITLQEHLSVHEAREHFISQLASDDIPGQVFVVAGKKLRGSL

SVKKLLQETDINQSIRHLMDSCLFRVKPDDERQQVIAELSERGLDLVPVVDKGELVGCLMEKEIAHLLED

DVTEDAQLQGATLPLEKPYLEISPWTLWKKRSVWLLLLFVAEAYTSSVLQHFEEALESAIALAFFIPLLI

GTGGNSGTQITSTLVRSMALGEVRLRDMGRVIRKEVSTSFLIALTLGLAGCLRAWMMGIGMEITLIVSLT

LVCITLWSAIVSSVIPMVLKRIGIDPAVVSAPFIATLIDGTGLIIYFKIAQYFLGLN

>WP\_002921188.1 MULTISPECIES: nickel-responsive transcriptional regulator NikR [Klebsiella]

MQRVTLTLDDDLLAALDALSARRGYHNRSEAVRDILRDALNQDPPSPESRRGYAVLSYVYEHEKRELASR

LVATQHHHHDLSVATLHVHISHDDCLEIAVLKGDMAEVQHFADDVIAQRGVRHGHLQCLADD

>WP\_004173958.1 MULTISPECIES: nickel import ATP-binding protein NikE [Klebsiella]

MNLLSATGVSHDYPHHGRVLHAIHLAIAPGETVALLGRSGCGKSTLARMLVGLETPQHGDIAWRGTPLAA

LKGEAIGAFRRDIQLVFQDAFSAVNPRKTVREIVSEPLRHLLCLSREARARRVEEMLLAVDLAPSLLDKR

PAQVSGGQLQRVCLARALAVRPQLLILDEAVSNLDLLLQAEIIALLKRLQAQFDTACLFITHDLRLVERF

CQRVLVMEHGRIVETATVSLPLRLRSPAGQALQQAVLPPFPATLLNEAMPCSA

>WP\_004173959.1 MULTISPECIES: nickel import ATP-binding protein NikD [Klebsiella]

MPQKIQLEQISLAADRPLVSDVSFTLRRGQVLALLGSSGCGKSLTCAAALGLLPPGVRQTAGRVLLDGIP

VHGEQLRGATIATIMQNPRSAFNPLQTMAAHARETCRAAGRETNDAVLLAAMEEVGLDNPRALLKRYPFE

MSGGMLQRMMVALALLSRAPFIIADEPTTDLDAIAQARILDLLADIVARRGLGLLLVTHDMGVVARLAHH

VTVMENGRLVEHCDVNTLFSAPRHPLSQRLLAAHLALYGLEKTP

>WP\_004151422.1 MULTISPECIES: nickel ABC transporter permease subunit NikC [Klebsiella]

MRGLQSFRWPVKLAMLVIALLAVIAIGSGWWLPWDPAAIDLQQRLLPPGAAHWLGTDHLGRDIFSRLLAA

TRVSLGAVMACLLLVLLIGLAVGGCAGLLGGRADRGLMRIAELFMTFPTSILSFFMVGVLGTGLTNVILA

IALSHWAWYARMVRNLVVSLRQREFILAARLSGASQWRLFSDHLAGAVIPSLLVLASLDIGHMMLHVAGM

SFLGLGVSAPTAEWGVMINDARQYIWTQPLQMVWPGLALFISVMAFNLLGDALRDRLDPHLIAEHSH

>WP\_002921105.1 MULTISPECIES: nickel ABC transporter permease subunit NikB [Klebsiella]

MLRYILRRLLLLIPLLLAASAIIFLLLRLGAGDPALDYLRLSNLPPTEEMVASTRELLGLNQPLAMQYLH

WLWRALHLDFGLSYATQRPVLDDLLHFLPATLLLTGAALALILVTSLPLGIWAARHRDRLPDYIVRLIAF

LGVSMPNFWLAFLLVMLFSVHLQWLPAMGYGDWQHLILPAVSIAFMSLAINARLLRASMLDAASQRHVIW

ARLRGLSARQVERRHILRNATLPVVTAMGMHIGELIGGTMIIENIFAWPGVGRYAVSAIFNRDYPVIQCF

TLMMVTVFVLANLAVDVLNAALDPRLRRHEEVSA

>WP\_046042218.1 nickel ABC transporter substrate-binding protein [Klebsiella pneumoniae]

MSIIRLTLLALVACVPLLAQAAPYQLTTAWPVNVGPLNPHLYTPNQMFAQSMVYEPLVKYQADGSVQPWL

ATRWRHSADGKTWWFTLRDDVAFSNGEPFNAQAAAANFQAVLANRQRHAWLELANQITDVRALSTTELQI

TLKSAYAPLLQELALPRPFRFIAPSQFIDGGTARGIKAPIGTGPWRLASSQLNQRDVLVRNERYWGRKPA

LQQITIKVIPDATSRAVAFETGEIDMLYGDEGLLPLDTFERFRHHPGYVTRLSAPAETVMLALNASQGPT

REQAVREALNYAVDKQTLVDSVLYGTQQVADTLFAPSVPYAPQNLTPRRYDPTKARALLEQAGWQQLEGQ

PWRQKAGQPLAIELAFIGTDALAKSMAEIIQANLRQVGVQVTLVGEEESSIYARQREGRFGMIFNRTWGA

PYDPHAFLSSMRVPSHADYQAQRGLPDKALIDKEISEVLTTGDEAQRRKLYHDVLTRLHQDAVYLPISYV

SLMSVARQEVGEIPFAPVTSEIPFDQITPVTP

>WP\_004151421.1 MULTISPECIES: LysR family transcriptional regulator [Klebsiella]

MHKTTLEQWALLEKVVELGSFARAAEETNRSQSSVSYNLALLQERLGVALLAPSGRRAVLTPAGELLLNQ

VKPLLQAFAYVETHAATLRNGARTRLDLVVDSIFPRQRLFAILRQFQQRYPQTQVRLTEVLENLDDESAA

RTEADVMVLTRRQDITGRGEWLMNIDFIAVAHRDHPLAALDGPLEDSALAPWPLVRIADQGGDSQAPRDA

WTFSTIDAAIDAVMYQVGFGWLPEERIRPHLDQGVLKRLPLSHGARRATPLHLIVKRDLAPIDEQVATLL

ALFRTP

>WP\_004181483.1 MULTISPECIES: phenolic acid decarboxylase [Klebsiella]

MMSTFDKHDLSGFIGKHLVYTYDNGWNYEIYVKNGHTLDYRIHSGIVGNRWVKDQEAYIVRVGESIYKIS

WTEPTGTDVSLIVNLGDKLFHGTIFFPRWIMNNPEKTICFQNDHIPLMNSYRDAGPAYPTEVIDEFATIT

FIRDCGADNDEVINCPASELPADFPANL

>WP\_016532496.1 UDP-4-amino-4-deoxy-L-arabinose aminotransferase [Klebsiella pneumoniae]

MSDFLPFSRPSMGDAELAALREVLASGWITTGPKNQALEAAFCQLTGNRHAIAVSSATGGMHVTLMALGI

GPGDEVITPSQTWVSTLNMICLLGATPVMIDVDNDNLMIIPDAVEAAITSRTKAIIPVHYAGAPADIDAI

RAVGERHGISVIEDAAHAAGTHYKGRHVGWQGTAIFSFHAIKNMTCAEGGLIVTDDDELASRIRSLKFHG

LGVDAYDRQTHGRAPQAEVITPGFKYNLADINAALALVQLEKLSHANQRRTEIAQRYLRELADTPFKPLS

VPAWEHQHAWHLFIIRVDEAACGISRDALMEKLKAMGIGTGLHFRAAHTQKYYRERFPEVSLPNTEWNSA

RICSLPLFPDMTDDDVTRVISALRQLSGR

>WP\_002921035.1 MULTISPECIES: undecaprenyl-phosphate 4-deoxy-4-formamido-L-arabinose transferase [Klebsiella]

MLTYPPVKKVSVVIPVYNEQDSLPELLRRTDAACATLGRQYEILLIDDGSSDDSARMLTEAAEAEGSHVV

AVLLNRNYGQHSAIMAGFSHVTGDLIITLDADLQNPPEEIPRLVAKADEGYDVVGTVRQNRQDSIFRKTA

SKMINRLIQRTTGKAMGDYGCMLRAYRRHIIDAMLNCHERSTFIPILANTFARRAVEIPVMHAEREFGDS

KYSFMRLINLMYDLVTCLTTTPLRLLSIFGSVIALLGFAFGLLLVVLRLAFGPQWAAEGVFMLFAVLFMF

IGAQFVGMGLLGEYIGRIYNDVRARPRYFIQRVVRQPETASKEEDRS

>WP\_016532497.1 bifunctional UDP-4-amino-4-deoxy-L-arabinose formyltransferase/UDP-glucuronic acid oxidase ArnA [Klebsiella pneumoniae]

MKAVVFAYHDMGCTGIQSLLDAGYDIAAIFTHPDNPGENHFFGSVARLAAEQGIPVWAPEDVNHPLWIER

IREMKPDVLFSFYYRNLLGDEILNLAPKGAFNLHGSLLPKYRGRAPLNWVLVNGESETGVTLHRMVNRAD

AGDIVAQQAVAIGADDAALTLHRKLCAAATELLSRALPAILAGTTDERPQDHSQATYVGRRTPEDGRLDW

ELPAQTLHNLVRAVSDPWPGAFGYAGANKFIVWKSRVRHDLPAAKPGTVLSIAPLIVACQDGALEIVTGQ

TERGVYMQGAQLAQALGLVSGAVISSKPVEAIKRRTRVLILGVNGFIGNHLTERLLQDDNYEIYGLDIGS

DAINRFLDCPRFHFVEGDISIHSEWIEYHIKKCDVVLPLVAIATPIEYTRNPLRVFELDFEENLKIIRDC

VKYNKRIIFPSTSEVYGMCTDKNFDEDSSNLVVGPINKQRWIYSVSKQLLDRVIWAYGDKNGLKFTLFRP

FNWMGPRLDNLNAARIGSSRAITQLILNLVEGSPIKLIEGGKQKRCFTDISDGIEALFRIIENKDGRCDG

QIINIGNPDNEASIKELAEMLLACFERHPLRDRFPPFAGFREVESSDYYGKGYQDVEHRKPSIRNAKRCL

NWEPKVEMEETVEHTLDFFLRTVELVDDKNP

>WP\_021469881.1 MULTISPECIES: 4-deoxy-4-formamido-L-arabinose-phosphoundecaprenol deformylase [Klebsiella]

MKQVGLRIDVDTFRGTRDGVPRLLELLGRHGIQASFFFSVGPDNMGRHLWRLIKPKFLWKMLRSRAASLY

GWDILLAGTAWPGRRIGAGNEAVIRAAAESHEVGLHAWDHYSWQAWSGVWPQERLALEVERGLLELERII

GRPVTCSAVAGWRADQRVVKAKESFDFLYNSDCRGTRPFLPQLGSGVSGTVQIPVTLPTWDEAVGTAVDI

AGFNRYLLDCIHRDAGVPVYTIHAEVEGIAYADQFNELLTMAAEEEIQFCPLSQLLPADFSELPSGKVVR

GELAGREGWLGREQLLTSGI

>WP\_046042221.1 lipid IV(A) 4-amino-4-deoxy-L-arabinosyltransferase [Klebsiella pneumoniae]

MKSIRYGVSLIALFALYYLLPLNFRLLWQPDETRYAEISREMLATGDWVVPHFLGLRYFEKPIAGYWINS

IGQWLFGHNNFGVRFGSVFAITMTALLVAWLAWRIFRDKRVAILSLIIFLTAMLVYAIGTYAVLDPMITL

WLALAMCSFWGAVQAHSRSGKILGYVLLGVACGMGVMTKGFLALAVPVVGVLPWVIARKRWREVLTYGWL

AVIVCTLVVLPWGLAIAQREPDFWRYFFWVEHIQRFAEKDAQHKAPFWYYIPFLIAGSLPWLALLPGALK

RGWLERDEARGALYLLGWVAMPFLFFSIAKGKLPTYILPCFAPLSILMARYALEAAKTGAKALRINGMIN

LGVGLLGLIAVLVVSPWGFMHKPVWTKIELYKCLLAAIAFAVWALMGWLAMKDSGRRWSLAALCPLGLAL

LVGFAIPDRVIDSKQPQFLVDIVSESLQPSRYVLTNNVGIAGGLAWELKRSDIIMFDKQGELKYGLDWPD

AQGSFVSQAGFADWLAAHRQQGPVSLVLLMDKGESMLDLPLPKPDNAYELGRVVFLQYLPQ

>WP\_002920864.1 MULTISPECIES: 4-amino-4-deoxy-L-arabinose-phosphoundecaprenol flippase subunit ArnE [Enterobacteriaceae]

MSVWICLVCASLLSCAGQLCQKQATRPSRRGRRSRHILFWLGMALLCLGCGMLLWLSVLQSIPVSIAYPM

LSLNFVWVTLAGWGIWHEPVARRHWLGVGLIVVGIVILGTSV

>WP\_016532502.1 4-amino-4-deoxy-L-arabinose-phosphoundecaprenol flippase subunit ArnF [Klebsiella pneumoniae]

MGFFWALLSVGLVSAAQLLLRSAMVALPPLTDIAAFLQHLLHFQPGTFGLFFGLLGYLLSMVCWYFALHR

LPLSKAYALLSLSYILVWAAAIWLPGWHEPFYWQSLLGVAIIVAGVLTIFWPVKRR

>WP\_016532503.1 AI-2E family transporter [Klebsiella pneumoniae]

MSPPQADKAGLHILLKLAALVIILAGIHAAADILVQLLLALFFAIVLNPLVTWFIRRGVRRPFAITLVVT

AMLVMLTALLGVLAASLNDFVAMLPDFNRALTRKILQLQEYLPFLNLHINPERMLRRMDSERLMTWATTL

MTQLSGAMASIVLLVMTVIFMLFEVRHLPYKLRFVLNNPRLHIAGLHRALKGVTHYLALKTLISLWTGLI

VWLGLLAMGVQFALMWGVLAFLLNYVPNIGSAISAIPPMLQALLFSGIYECLLVGALFLVVHMVLGNMVE

PRMMGHRLGMSTLVVFLSLLVWGWLLGPVGMLLSVPLTSVCKIWMETTVGGSKLAILLGPGRPKSRLPG

>WP\_016532504.1 MFS transporter [Klebsiella pneumoniae]

MPEPVAEPALNGLRLNLRIVSVVIFNFASYLTIGLPLAVLPGYVHDVMGFSAFWAGLVISLQYFATLLSR

PHAGRYADLLGPKKIVVFGLGGCFLSGLSYLLAAWGSGWPLISLLLLCLGRVILGIGQSFAGTGSTLWGV

GVVGSLHIGRVISWNGIVTYGAMAMGAPLGVLCYSHIGLSGLAGVIMAVALVAILCALPRAAVKAAKGKA

MSFRAVLGRVWPYGMALALASAGFGVIATFITLFYDAKGWDGAAFALTLFSCAFVGARLLFPNAINRLGG

LNVAMLCFSVEAIGLLLVGFADTPMMAKIGTFLTGAGFSLVFPALGVVAVKAVPQHNQGSALATYTVFMD

LSLGVSGPLAGLLLAWTGISMIYLAAAGLVMAALLLGWRLKKRPPVSEPEASAPGQ

>WP\_016532505.1 DcrB family lipoprotein [Klebsiella pneumoniae]

MRNLVKYVGIGLLVMGLAACDNSDSKAPTVGAAAESNASGQAISLLDGKLSFTLPAGMADQSGKLGTQAN

NMHVYSDATGQKAVIVIVGDSTNEDLAVLAKRLEDQQRSRDPQLQVVSNKPLEIKGHTLQQLDSIISAKG

QTAWSSVILGKVDDKLLTLQITLPADNQQQAQTEAESIINTLTIQ

>WP\_002920860.1 MULTISPECIES: 7-cyano-7-deazaguanine/7-aminomethyl-7-deazaguanine transporter [Klebsiella]

MNPFTTVQRKKALVWLSLFHLLVITSSNYLVQLPISIFGFHTTWGAFSFPFIFLATDLTVRIFGAPLARR

IIFAVMVPALAISYGISALFYMGEWQGFAALGTFNLFVARIAVASFMAYALGQILDVHVFNRLRQSRRWW

LAPTASTLFGNISDTVAFFFIAFWRSPDPFMAAHWGEIALVDYSFKVLISIIFFLPMYGVLLNMLLKRLA

DKSDLSALQPS

>WP\_002920858.1 MULTISPECIES: sulfurtransferase TusA [Gammaproteobacteria]

MSELFSTPDHTLDALGLRCPEPVMMVRKTVRTMPVGETLLIIADDPATTRDIPGFCRFMEHELVAQETEA

LPYRYLIRKSH

>WP\_046042224.1 Zn(II)/Cd(II)/Pb(II) translocating P-type ATPase ZntA [Klebsiella pneumoniae]

MSTPDAQDKKVPQFSSFTMRPATAPAESCCTDHACATESAPAAEALSDARYSWQVDGMDCAACARKVETA

VRQVPGVSQVQVLFATEKLLVNAEGDVRAQVENAVRQAGYTLRDADAPAAEQTRGSLLRDNLPLLTLVIM

MALSWGLEQANHPAGQLAFIATTLVGLWPVARQALRLIKSGSWFAIETLMSVAAIGALFIGATAEAAMVL

LLFLIGERLEGWAASRARQGVSALMALKPDTAIRLRNGVRETVAQRDLRPGDVIEVAAGGRLPADGQLLS

PFASFDESALTGESVPVERQAGERVAAGATSVDRLVQLTVISEPGDSAIDRILKLIEEAEERRAPIERFI

DRFSRIYTPAIMVVALLVAIVPPLFFASAWLPWIYKGLTLLLIGCPCALVISTPAAITSGLAVAARRGAL

IKGGAALEQLGQVRQVAFDKTGTLTVGQPQVTSVIATAEVDDNALLALAAAVEQGSSHPLAQAIVREAQR

RQLSIPLASGQRALAGSGIEAEVNGCRILICAASKAAPAEHEAQIQQLESAGQTVVLVMRGETLLGILAL

RDTLRDDARQAVDALHQLGVQGVILTGDNPRAAAAIASELGLEFRAGLLPADKVNAVIALNADAPLAMVG

DGINDAPAMKAATIGIAMGSGTDVALETADAALTHNRLTGLAQMISLARATHANIRQNIAIALGLKGIFL

VTTLLGLTGLWLAVLADTGATVLVTANALRLLRKKL

>WP\_004173987.1 MULTISPECIES: lysoplasmalogenase [Klebsiella]

MLWSFIAVCFSAWLYVDASYRGPAWRRWVFKPVTLILLLLLAWQAPMFNAISYLVLAGLCASLLGDALTL

LPRQRVMYAVGAFFLSHLLYTIWFASQLTLSFFWPLPLVLLVFGALLMAVIWSRLEEMKMPVLTFIGMTL

VMVWLAGELWFARPTNTALSGFAGAALLLLSNAVWLVSHYRRRFRADNAIAAAFYFAGHFLIVRALYL

>WP\_004173989.1 MULTISPECIES: DUF2500 domain-containing protein [Klebsiella]

MPLFFVLVVAVIVVAASFRYVQQRREKQANDAAPLLQKRVIVSNKREKVINDRRSRQQTVTPAGSEMRYE

ASFRPENGGLEVVFRLDAPQYHALSVGDRGMLSYKGTAFVAFTPDP

>WP\_002920822.1 MULTISPECIES: DUF1145 family protein [Gammaproteobacteria]

MLINLGRLLMLCVWAFLLLNLFQPFPKPLNIFVNVALIFMILMHGLQLTLLKATQPKEAPPLSRFEQIRI

FIFGVFELVAWQKKLKATLKK

>WP\_002920820.1 MULTISPECIES: 16S rRNA (guanine(966)-N(2))-methyltransferase [Gammaproteobacteria]

MKKPNHAGSGQIRIIGGQWRGRKLPVPESPGLRPTTDRVRETLFNWLAPSIVDAHCLDCFAGSGALGLEA

LSRYAASTTLLEMERGVAQQLQKNLATLKADRGKVITTNTLSFLSQPGTPHQIVFVDPPFRQGLLEETLR

LLETQGWLADEALVYVESEVENGLPPVPANWQLYREKVAGQVAYRLYQREAQGEHHAD

>WP\_046042226.1 signal recognition particle-docking protein FtsY [Klebsiella pneumoniae]

MAKEKKRGFFSWLGFGQKEQAQETETEQKVEEQQAVAEEIPAVETPAEPSAPKADPEAFAEDVVEVTETV

VESEKAHLAEPASAQEEEWVETPALTEETPVVEPEPAVSEPPEQPAVVEPLAEEVIAEPVVAEAVAEQPV

EGIVVQPQETEAPEEDAPLSDEELEAQALAAEAAEEAAVVVPAPEDEAPLEALAQEQEKPTKEGFFARLK

RSLLKTKQNLGSGFISLFRGKKIDDDLFEELEEQLLIADVGVETTRKIITNLTEGASRKQLRDAEALYGL

LKEEMGEILAKVDEPLNVEGKTPFVILMVGVNGVGKTTTIGKLARQFEQQGKSVMLAAGDTFRAAAVEQL

QVWGQRNNIPVIAQHTGADSASVIFDAIQAAKARHVDVLIADTAGRLQNKSHLMEELKKIVRVMKKLDVD

APHEVMLTIDASTGQNAISQAKLFHEAVGLTGITLTKLDGTAKGGVIFSAADQFGIPIRYIGVGERIEDL

RPFNAGDFIEALFARED

>WP\_002920817.1 MULTISPECIES: cell division ATP-binding protein FtsE [Klebsiella]

MIRFEQVSKAYLGGRQALQGVTFHLQPGEMAFLTGHSGAGKSTLLKLICGIERPSAGKIFFSGHEISRLK

SREVPFLRRQIGMIFQDHHLLMDRTVYDNVAIPLIIAGASGDDIRRRVSAALDKVGLLDKAKNFPIQLSG

GEQQRVGIARAVVNKPAVLLADEPTGNLDEALSEGILRLFEEFNRVGVTVLMATHDLGLISSRPYRVLTL

SDGHLHGGIRGE

>WP\_004173994.1 MULTISPECIES: permease-like cell division protein FtsX [Klebsiella]

MNKRDAMNQIRQFGSKFDRLRNAAGGGGGGRNAPKRPKAAPNPASRKSNVFNEQVRYAWHGALQDLKSTP

LATFLTVMVIAISLTLPSVCYMVYKNVSSAASQYYPSPQITVYLEKTLDDDAAARVVGQLQAEQGVDKVN

YLSRDEALGEFRNWSGFGGALDMLEENPLPAVAIVVPKLDFQSTEALNTLRDRVTRIQGVDEVRMDDSWF

ARLSSLTGLVGRVSAMIGVLMVAAVFLVIGNSVRLSIFARRDTINVQKLIGATDGFILRPFLYGGAMLGF

SGAFLSLILSEILVMRLSSAVTEVAKVFGTQFELSGLGFDECLLMLIVCSMIGWVAAWLATVQHLRHFTP

D

>WP\_002920815.1 MULTISPECIES: RNA polymerase sigma factor RpoH [Klebsiella]

MTKEMQTLALAPVGNLESYIRAANTWPMLSADEERELAEKLHYQGDLEAAKKLILSHLRFVVHIARNYSG

YGLPQADLIQEGNIGLMKAVRRFNPEVGVRLVSFAVHWIKAEIHEYVLRNWRIVKVATTKAQRKLFFNLR

KTKQRLGWFNQDEVEMVARELGVSSKDVREMESRMAAQDMTFDMSSDDESDSQPMAPVLYLQDKTSNFAD

GIEDDNWEEQAANKLTDAMQGLDERSQDIIRARWLDEDNKSTLQELADRYGVSAERVRQLEKNAMKKLRA

AIEA

>WP\_046042228.1 PLP-dependent aminotransferase family protein [Klebsiella pneumoniae]

MRSLVGDLVLVRLQEERDPLLHKRLYNALRRAILDGSLAPQSRLPPSRDLAGELGVSRNTILTTYEQLLA

EGYVVSRRGSGTFVAQTAPESSLTAKGQQENSSIAAPTAHLSRQGQHLLGQVSASPRQWGAFIPGVPDVN

AFPHPLFSKIQARISRRPKPERLSYSCNGGTPELQQALVDYLRVSRGVHCQSDQILITEGIHQAIDLVTR

MLCDNGDLAWVEEPSYWGIRHVLTMNDVRAEPLTVDANGLCPPETVDDAPRLIFVTPSHQYPLGAVMSLE

RRQRLLALARQQGSWIVEDDYDSEFRFSGQPIPALQGLVADAPVVYIGTFSKTLYPGLRLGYVVIPRPLV

SDLKHAHAELYRGGHSLIQMALAEFITAGHYSAHIRRMRLLYSRRRAFLTELIQRHCMPYALSDFSDNAG

LHLILNLPAEADDVAIAREANARHILVRPLSRYYLTAARKKGLLMGFASQPEEQMASAFSVLLGCLQTHC

PQMLLLREDAEKQNAPT

>WP\_002920814.1 MULTISPECIES: 4-aminobutyrate--2-oxoglutarate transaminase [Klebsiella]

MKSSELNQRRQQATPRGVGVMCNYFVEKAENATLWDIEGNEVIDFAAGIAVLNTGHRHPKVVAAVADQLQ

AFTHTAYQIVPYESYVSLAERINDLAPIDGPAKTAFFTTGAEAVENAVKIARAYTGRPGLITFGGGFHGR

TFMTMALTGKVAPYKIGFGPFPGSVYHGVYPNAAHGVTTADALKSLERIFKADIAPDQVAAIILEPIQGE

GGFNVAPADFMQALRDLCDTHGILLIADEVQTGFARTGKLFAMQHYEVKPDLMTMAKSLAGGFPLSGVVG

RAEVMDAPAPGGLGGTYAGNPLAVAAAHAVLDVIAEEQLCQRAEQLGSHLQEVLNQARATCPAIVDVRGR

GSMVAVEFNDPQTGEPSPEFTRLVQQKAQENGLLLLSCGVYGNVIRFLYPLTIPDAQFSKALDILARVLK

S

>WP\_032104698.1 MULTISPECIES: amino acid permease [Klebsiella]

MSENSTFSPVLTGRERTAVPAKSLSFIEGVSMIVGTNIGAGVLSIAYASSKAGFLPLLFWLVLVGSLTTV

TMLYVAESTLRTRKHLQLSGLSKRYVGGFGALMMFLSVCVNSVGALTAYMTGSGKLLHSLFGISPALGSV

LFFVPAAGVLYLGLKAIGRGEKFISIGMVVMISVLVIATLLKETTRVGYLLDGNWLYMVPVFNVVAFCFS

AQYIVPEMARGFADKPEKLPKAIMVGMALTFTLLALVPLSVISLNGLDNISDVATISWGRALGEWAFFSA

NLFALCAMLTSYWGLGGSFLTNIFDQFRLGNDEQPARRLMVLLVVAIPPFVLAYSGMVSFVNALYFAGVF

SGVILSIMPILMLKGARQRGDLTPGWTCPAWMTHPLIQCFIVLLYLCSAAYAIASAVGYLPAGW

>WP\_002920812.1 MULTISPECIES: branched chain amino acid ABC transporter substrate-binding protein LivJ [Klebsiella]

MNMKGKALLAGCIALVMSSAALAEDIKIAVVGAMSGPVAQYGDQEFTGAEQAVADINAKGGIKGNKLQIV

KYDDACDPKQAVAVANKVVNDGIKYVIGHLCSSSTQPASDIYEDEGILMITPAATAPELTARGYKLILRT

TGLDSDQGPTAAKYILDKVKPQRIAVVHDKQQYGEGLARAVQDGLKKGGANVVFFDGITAGEKDFSTLVA

RLKKENIDFVYYGGYHPEMGQILRQARAAGLKTQFMGPEGVANVSLSNIAGESAEGLLVTKPKNYDQVPA

NKPIVDAIKAKKQDPSGAFVWTTYAALQSLQAGLNQSDDPAEIAKYLKGATVDTVMGPLSWDQKGDLKGF

EFGVFTWHANGTATDAK

>WP\_002920810.1 MULTISPECIES: aspartate 1-decarboxylase autocleavage activator PanM [Klebsiella]

MKLTIIRLQHFSDQDRIDLGKIWPSQDLSTLTLDENHRLYAARFNERLLGAVRVTLRGVEGELSDLCVRE

VTRRRGVGQYLVEETLRDNPAINSWRVADHGVEDRGVMAAFMQALGFSAQQNGWEKH

>WP\_004150079.1 MULTISPECIES: high-affinity branched-chain amino acid ABC transporter substrate-binding protein LivK [Klebsiella]

MKRNAKTIVAGIVALAMSHAAMAKDIKVAVVGAMSGPVAQWGDMEFNGARQAIKDINASGGIKGDKLVAV

EYDDACDPKQAVAVANKIVNDGIQYVIGHLCSSSTQPASDIYEDEGILMISPGATNPELTQRGYQYIMRT

AGLDSSQGPTAAKYIVEKVKPQRIAIIHDKQQYGEGLARSVQDNLKKAGANIVFFDGITAGEKDFSALLA

RLKKENIDFVYYGGYYPEMGQMLRQARSVGLKTVFMGPEGVGNASLSNIAGAAAEGMLVTMPKRYDQDPA

NSAIVNALKAEKKDPSGPYVWITYAAVQSLAQAMDRTGSQQPLDLINDLKAHGAKTVIGPLTWDEKGDLK

GFEFGVFQWHADGSSSAAK

>WP\_002920807.1 MULTISPECIES: high-affinity branched-chain amino acid ABC transporter permease LivH [Klebsiella]

MSEQFLYFLQQMFNGVTLGSTYALIAIGYTMVYGIIGMINFAHGEVYMIGSYVSFMIIAALMMMGIDTSW

LLVAAGFVGAIVIASAYGWSIERVAYRPVRNSKRLIALISAIGMSIFLQNYVSLTQGSRDVALPSLFNGQ

WVVGHSDSFSATITTMQLVIWVVTFIAMLALTLFIRYSRMGRACRACAEDLKMASLLGINTDRVIALTFV

IGAAMAAVAGVLLGQFYGVINPYIGFMAGMKAFTAAVLGGIGSIPGAMIGGLILGIAEALSSAYLSTEYK

DVVSFALLILVLLVMPTGILGRPEVEKV

>WP\_004174005.1 MULTISPECIES: branched chain amino acid ABC transporter permease LivM [Klebsiella]

MKPMQIAMALLSAVMFFILAGVFMGVQLELNGTKLVVDTAADIRWQWIFIGTAVVFFFQLLRPLFQKAVK

NVSGPKFIMPAIDGSTVKQKLFLIALLVIAVAWPFMVSRGTVDIATLTMIYIILGLGLNVVVGLSGLLVL

GYGGFYAIGAYTFALLNHYYGLGFWTCLPLAGLVSAAAGFLLGFPVLRLRGDYLAIVTLGFGEIVRILLL

NNTEITGGPNGISQIPKPTFFGLEFSRSAREGGWDTFSNFFGVKYDPSDRVIFLYLVALLLVVLSLFVIN

RLLRMPLGRAWEALREDEIACRSLGLSPTRIKLTAFTISAAFAGFAGTLFAARQGFVSPESFTFAESAFV

LAIVVLGGMGSQFAVILAAILLVVSRELMRDFNEYSMLMLGGLMVLMMIWRPQGLLPMTRVQLKLKNGQA

KGEQA

>WP\_002920803.1 MULTISPECIES: high-affinity branched-chain amino acid ABC transporter ATP-binding protein LivG [Klebsiella]

MSQPLLSVSGLMMRFGGLLAVNNVSLELREREIVSLIGPNGAGKTTVFNCLTGFYKPTGGTILLRDQHLE

GLPGQQIARMGVVRTFQHVRLFREMTVIENLLVAQHQQLKTGLFSGLLKTPAFRRAQSEALDRAATWLER

IGLLEHANRQASNLAYGDQRRLEIARCMVTQPEILMLDEPAAGLNPKETKELDELIAELRNHHNTTILLI

EHDMKLVMGISDRIYVVNQGTPLANGTPEEIRNNPDVIRAYLGEA

>WP\_004145133.1 MULTISPECIES: high-affinity branched-chain amino acid ABC transporter ATP-binding protein LivF [Klebsiella]

MENAMLTFDNVSAHYGKIQALHNVSLHIKQGEIVTLIGANGAGKTTLLGTLCGDPRASSGRIVFDGKDIT

DWQTAKIMREAVAIVPEGRRVFSRMTVEENLAMGGFFADRDQFQTRIKWVYELFPRLHERRIQRAGTMSG

GEQQMLAIGRALMSQPRLLLLDEPSLGLAPIIIQQIFDTIEQLREQGMTIFLVEQNANQALKLADRGYVL

ENGHVVLEDTGDALLANEAVRSAYLGG

>WP\_004174006.1 MULTISPECIES: type II toxin-antitoxin system Phd/YefM family antitoxin [Gammaproteobacteria]

MRTVNYSEARQNLADVLESAVTGVPVTITRRGHKSAVIISAEEFERYQAARMDDEFAAIMAVHGDEIREL

ADK

>WP\_002920796.1 MULTISPECIES: sn-glycerol-3-phosphate ABC transporter substrate-binding protein UgpB [Klebsiella]

MISLRHTALGLALSLAFAGQALAVTTIPFWHSMEGELGKEVDSLAQRFNAANPDYKIVPVYKGNYEQSLS

AGIAAFRTGNAPAILQVYEVGTATMMASKAIKPVYQVFSEAGIKFDESQFVPTVAGYYTDSKTGHLLSQP

FNSSTPVLYYNKDAFKKAGLDPDQPPKTWQDLAAYTAKLKAAGMKCGYASGWQGWIQIENFSAWHGLPVA

TKNNGFDGTDAVLEFNKPEQVKHIALLEEMNKKGDFSYFGRKDESTEKFYNGDCAITTASSGSLADIRQY

AKFNYGVGMMPYDADVKGAPQNAIIGGASLWVMQGKDKETYTGVAKFLDFLTKPENAAEWHQKTGYLPIT

TAAYDLTRQQGFYDKNPGADIATRQMLNKPPLPFTKGLRLGNMPQIRTIVDEELESVWTGKKTPQQALDS

AVQRGNQLLRRFEQATKS

>WP\_002920792.1 MULTISPECIES: sn-glycerol-3-phosphate ABC transporter permease UgpA [Klebsiella]

MSSSRPVFRSRWLPYVLVAPQLIITLIFFIWPAGEALWYSLQSVDPFGLSSQFVGLDNFVALFHDPYYLD

SFWTTIKFSALVTVSGLLISLFFAALVDYVVRGSRFYQTLMLLPYAVAPAVAAVLWIFLFNPGRGLITHF

LGELGYDWNHAQNSGQAMFLVVFASVWKQISYNFLFFFAALQSIPRSLVEAAAIDGAGPIRRFFKLALPL

IAPVSFFLLVVNLVYAFFDTFPVIDAATAGGPVQATTTLIYKIYREGFAGLDLSASAAQSVVLMFLVIIL

TVVQFRYVESKVRYQ

>WP\_004145129.1 MULTISPECIES: sn-glycerol-3-phosphate ABC transporter permease UgpE [Klebsiella]

MIENRRGLTIFSHTMLILGIAVILFPLYVAFVAATLDNKSVFETPMTLIPGGHLLENMKTIWVNGVGVNS

APFWLMMLNSFIMAFAITVGKIVVSMLSAFAIVWFRFPLRNLFFWMIFITLMLPVEVRIFPTVEVIANLN

MLDSYAGLTLPLMASATATFLFRQFFMTLPDELIEAARIDGASPMRFFRDIVLPLSKTNLAALFVITFIY

GWNQYLWPLLIIQDVNLGTAVAGIKGMIATGEGTTQWNQVMAAMLLTLIPPVVIVLAMQRAFVRGLVDSE

K

>WP\_004150074.1 MULTISPECIES: sn-glycerol-3-phosphate import ATP-binding protein UgpC [Klebsiella]

MAGLKLQAVSKSWDGKTQVIQPLTLDVADGEFIVMVGPSGCGKSTLLRMVAGLERVTSGDIWIDRKRVTE

MEPKDRGIAMVFQNYALYPHMSVEENMAWGLKIRGMGKGLIAERVQEAARILELDGLLKRRPRELSGGQR

QRVAMGRAIVRDPAVFLFDEPLSNLDAKLRVQMRLELQQLHRRLKTTSLYVTHDQVEAMTLAQRVMVMNK

GVAEQIGTPVEVYEKPASRFVASFIGSPAMNLLEGRISDDGGRFELAGGMQLPTNHEHRRHAGRKMTLGI

RPEHFILSSQAQGGIPLLMDTLEILGADNLAHGRWGEQKLVVRLPHQQRPAAGSTLWLHLPLEHLHLFDG

ETGQRA

>WP\_016531888.1 MULTISPECIES: glycerophosphodiester phosphodiesterase [Klebsiella]

MSNWPYPRIVAHRGGGKLAPENTLAAIDVGARYGHTMIEFDAKLSKDGQIFLLHDDNLERTSNGWGVAGE

LAWDDLLKVDAGSWFSREFKGEPLPLLSQVAERCRRHGMMANIEIKPTTGLGPQTGRVVALAARDLWQGM

TAPLLSSFEIDALEAAQEAAPELPRGLLLDEWRDDWRELTTRLGCVSIHLNHKLLDAARVASLKQAGLHI

LVYTVNKPQRAAELLRWGVDCICTDAVDVIGPNFQP

>WP\_004150073.1 MULTISPECIES: DUF2756 family protein [Gammaproteobacteria]

MKAILFLAALMPLGVLAQPININNNPNQPGYVVPSQQRMQNEMKIQQQQQQSMLKQDLNNQTRSQQQHLQ

NQLQTNQQRAAQGGNLNAPQQVRPNNNGGMLRQTNP

>WP\_004150072.1 MULTISPECIES: gamma-glutamyltransferase [Klebsiella]

MIKTTIWRQVVIAALLAGGSFTVAANPPPPPPVSYGVEEDVFHPVRARQGMVASVDALATRVGVDILRQG

GNAVDAAVAVGYALAVTHPQAGNIGGGGFMMLRTKDGKTTAIDFREMAPEQATRDMFLDDQGNPDSKKSL

TSHLASGTPGSVAGFSLALEKYGTMPLNKVIRPAIKLAEEGFIVNDALADDLKTYGSEVIPQHENSKAIF

WKNGEPLKKGDRLVQKNLGKSLELIAEHGPDAFYKGAIADQIADEMKKHGGLITKADLAGYKAVERTPVS

GEYRGYEVYSMPPPSSGGIHIVQILNILENFDMQKYGFGSADAMQVMAEAEKHAYADRSEYLGDPDFVNV

PWQALTSKAYAKAIAAEIDVNKAKPSSQIRPGKLAPYESNQTTHFSVVDKDGNAVAVTYTLNTTFGTGIV

AGDSGILLNNQMDDFSAKPGVPNVYGLVGGDANAVEPKKRPLSSMSPTIVVKDGKTWLVTGSPGGSRIIT

TVLQMVVNTIDFGMNVAEATNAPRFHHQWLPDELRVEKGFSPDTLKLLEAKGQKVALKEAMGSTQSIMVG

PDGMLYGASDPRSPDDLTAGY

>WP\_025861230.1 N-acetyltransferase [Klebsiella pneumoniae]

MIRHAEPRDAEPLRMLMAHPEVYHDTLQIPYPSMEAWQEKLQPRPHTFHLVATLDEQVAGHLSLHVEPRP

RRSHVATFGMAVAAGHQGCGIGSALMREMIDLCDNWLRVERIELTVFADNAPAIAVYKKYGFEIEGTGRR

YALRNGEYVDAYYMARIK

>WP\_016531890.1 polymer-forming cytoskeletal protein [Klebsiella pneumoniae]

MDKQYLAINGALFFWLLALIAWSVDASALARLAAACALIAFLLHSQRNKINAMFIKKNKTEPQISEAATP

PAINPEPEAVASKKHETTVIASGVHFVGNIVASGHVYIHGQVTGNIEAKENLIKVMREGQVEGNVSCREL

IIDGKVQGQCHGDSITIEEHGHLEGTLAYRALAIKKGGVFSGRAELLAAAENKSHILGLVADAPSKADAE

PVRPQSA

>WP\_016531891.1 oxidoreductase [Klebsiella pneumoniae]

MTLHCAFIGFGKSTTRYHLPYVLHRKDRWQVAHIYRRRAKPEEQAPQYSHIHFTSDLDEVLNDPLVKLVV

VCTHADSHFEYAKKALEAGKNVLVEKPFTPTLEEAKTLFALANSKGLTVTPYQNRRFDSCFLTTKKVIES

GKLGELVEIESHFDNYRPLAETNPGGPQNGEFYGLGVHTLDQIISLFGRPDHVSYDLRSLRNKANPDDTF

EAQLFYGDMKAIVKTSHLVQIDYPKFIVHGHKGSFVKYGIDQQETSLKANIMPGEPGFGADDSVGELVYV

NEAGEMVREAVPLESGDYGRVYDALYDTLVNSQPNYVKETDVLTNMEILQRGFEQPSPATITLTR

>WP\_002920779.1 MULTISPECIES: pirin family protein [Klebsiella]

MIYLRKANERGHANHGWLDSWHTFSFANYYDPNFMGFSALRVINDDVIDAGQGFGTHPHKDMEILTYVLE

GAVEHQDSMGNKEQVPAGEFQIMSAGTGVRHSEYNPSKTDRLRLYQIWIIPEETGITPRYEQRRFDAAQG

KQLVLSPDARDGSLKVYQDMELYRWALLKDEQSVHQIAAERRVWIQVVKGEVTINGTKATTSDGLAIWDE

QAISVHADSDSEILLFDLPPV

>WP\_002920777.1 MULTISPECIES: gluconate operon transcriptional repressor GntR [Klebsiella]

MKKKRPVLQDVADLVGVTKMTVSRYLRNPEQVSEALRGKIAVALDELGYIPNRAPDILSNATSRAIGVLL

PSLTNQVFSEVLRGIESVTDAFGYQTMLAHYGYKPEMEEKRLESMLSWNIDGLILTERTHTPRTLKMIEV

AGIPVVELMDSRSPCLDIAVGFDNFEAARQMTAAIIARGHRHVAYLGARLDERTIIKQKGYEQAMLDAGM

TPYSVMVEQSSSYSSGIELMRQARREYPQLDGIFCTNDDLAVGAAFECQRLGLKIPDDMAIAGFHGHDIG

QVMEPRLASVLTPRERMGRIGAERLLARIRGEAITPKMLDLGFTLSPGGSI

>WP\_002920775.1 MULTISPECIES: gluconokinase [Klebsiella]

MSTTNHDHHVYVLMGVSGSGKSAVASEVAHQLHAAFLDGDFLHPRSNITKMASGEPLNDDDRTPWLQALN

DAAFAMQRTNKVSLIVCSALKKSYRDILRKGNPNLSFIYLKGDFDVIESRLKARKGHFFKTQMLVTQFET

LQEPGADESDVLIVDIDQPLEGVVASTIEVINKGSH

>WP\_002920773.1 MULTISPECIES: gluconate transporter [Klebsiella]

MSTLTLVLTAVGSVLLLLFLVMKARMHAFVALMVVSIGAGLFSGMPLDKIAATMEKGMGGTLGFLAIVVA

LGAMFGKILHETGAVDQIAVKMLKSFGHNRAHYAIGLAGLICALPLFFEVAIVLLISVAFSMARHTGTNL

VKLVIPLFAGVAAAAAFLLPGPAPMLLASQMHADFGWMILIGLCAAIPGMIIAGPLWGNFISRYVELHIP

DDVTEPHLGEGKMPSFGFSLALILLPLVLVGLKTIAARFVPVGSTAYEWFEFIGHPFTAILVACLVAIYG

LAVRQGMAKDRVMEICGHALQPAGIILLVIGAGGVFKQVLVDSGVGPALGEALTGMGLPIAITCFVLAAA

VRIIQGSATVACLTAVGLVMPVIEQLNYSGAQMAALSICIAGGSIVVSHVNDAGFWLFGKFTGASEAQTL

KTWTMMETILGTTGAIVGMIAFQLLS

>WP\_020325126.1 MULTISPECIES: hypothetical protein [Klebsiella]

MIAEQSEKQLILHIVHRRWSSSKAQRLSGKSPGEWNIFRRYFIDPDYGLSVKSGAFPLAKKKRQTQSQQG

LTRDTSIVVALIRANSWQGKEGKRAAYCKEARVSSVTLAFYFPRAGDERA

>WP\_002920570.1 MULTISPECIES: aspartate-semialdehyde dehydrogenase [Klebsiella]

MKNVGFIGWRGMVGSVLMQRMVEERDFDAIRPVFFSTSQLGQPAPSFGGSTGGTLQDAFDLDALKALDII

VTCQGGDYTNEIYPKLRASGWQGYWIDAASSLRMKDDAIIILDPVNQDVITAGLNNGVKTFVGGNCTVSL

MLMSLGGLFAQDLVEWVSVATYQAASGGGARHMRELLSQMGQLHNHVAAELADPASAILDIERKVTSLTR

SGELPVDNFGVPLAGSLIPWIDKQLDNGQSREEWKGQAETNKILATSSVIPVDGLCVRVGALRCHSQAFT

IKLKKDVSIPTVEELLAAHNPWAKVVPNDREITMRELTPAAVTGTLTTPVGRLRKLNMGPEYLSAFTVGD

QLLWGAAEPLRRMLRQLA

>WP\_004150069.1 MULTISPECIES: 1,4-alpha-glucan branching enzyme [Klebsiella]

MSNHIDRDVINALIAGHFADPFSVLGMHRTDAGLEVRALLPDATDVWVIEPKTGRKVGKLECLDSRGFFS

GVLPRRKNAFRYQLAVTWHGQQNLIDDPYRFGPLLQDLDVWLLSEGTHLRPYETLGAHAATMDGVTGTRF

SVWAPNARRVSVVGQFNYWDGRRHPMRFRKESGIWELFVPGAHNGQLYKFELIDAHGNLRVKADPYAFES

QMRPESASLICDLPPKVEQPADRRAANQFDAPISIYEVHLGSWRRHTDNNFWLSYRELADQLVPYAKWMG

FTHLELLPVNEHPFDGSWGYQPTGLYAPTRRFGTRDDFRYFINAAHAAGLNVILDWVPGHFPADDFALAS

FDGTSLYEHSDPREGYHQDWNTLIYNYGRREVSNYLVGNALYWIERFGIDALRVDAVASMIYRDYSRKAG

EWIPNEYGGRENLEAIEFLRNTNRILGEQTPGAVTMAEESTDFAGVTRPPAGGGLGFWFKWNLGWMHDTL

DYMKLDPVHRRYHHDKMTFGMLYNYTENFVLPLSHDEVVHGKKSILDRMPGDAWQKFANLRAYYGWLFAF

PGKKLLFMGNEFAQGREWNHDVSLDWHLLEGGDNWHHGVQRLVRDLNHTYRHHKALHELDFDPYGFEWLV

VDDHERSVFVFVRRDRAGNEIIVASNFTPVPRHDYRFGINQPGRWREALNTDSMHYHGSNQGNGGVVESD

AIASHGREHSLSLTLPPLATIWLVREAQ

>WP\_004174015.1 MULTISPECIES: glycogen debranching protein GlgX [Klebsiella]

MTSLAAGKPAPLGASYDGKGVNFALFSAHAERVELCVFDEQGNEQRFDLPARSGDIWHGWLAAAGPGLRY

GYRVHGPWDPAQGHRFNPAKLLIDPSAHRVEGDLPDDERLHGGMWQPDRRDSAAVAPKSQVVDLRYDWRG

DKPPRTPWGETVIYEAHVKGLTLLNPQLPEAIRGTYKALGHPAMIAYFKSLGISALELLPVAQFASEPRL

QRMGLSNYWGYNPLAWFALDPRYASDPDRALDEFRDAVKALHAAGIEVILDIVLNHSAEIDLEGPTVSLR

GIDNRSYYWVREDGDYHNWTGCGNTLNLSHPGVVEWARQCLRFWVDECHVDGFRFDLASVMGRTPEFRQD

APLFEAIRRDSVLSQVKLIAEPWDIGPGGYQVGNFPPLFAEWNDHFRDSARRFWLQQNVSLGDFAQRFAA

SSDLFARDGKPPSATVNLVTAHDGFTLRDCVCFNQKHNEANGEENRDGTNNNYSNNHGIEGLEANFAVIE

RRRASAHALLTTLLLAQGTPMLLAGDEQGHSQHGNNNAYCQDNALTWLDWRQANPGLTAFTAALIHLRRR

IPALTRNRWWQEGDGNVRWLNRNAQPLTAAEWQQGAACMQIQLSDRWLLTLNATAEVVDMVLPEGEWRAV

PPFAGEDNPVIMAVWHGPAHGVCVFQRS

>WP\_002920566.1 MULTISPECIES: glucose-1-phosphate adenylyltransferase [Klebsiella]

MVRLEKNDPLMLARQLPIKSVALILAGGRGTRLKDLTIKRAKPAVHFGGKFRIIDFALSNCINSGIRRIG

VITQYQSHTLVQHIQRGWSFFSEEMNEFVDLLPAQQRVHGENWYRGTADAVTQNLDIISRYKAEYVVILA

GDHIYKQDYSRMLIDHVEKGARCTVACMPVPIEEASAFGVMAVDENEKIIEFVEKPANPPAMPTDPTKSL

ASMGIYVFDAAYLYELLEEDDRNENSSHDFGKDIIPKITEAGMAYAHPFPLSCVQSDPNAEPYWRDVGTL

EAYWKANLDLASVTPELDMYDQNWPIRTHMESLPPAKFVQDRSGSHGMTLNSLVSGGCIISGSVVVQSVL

FPRVRVNSFCNIDSAVLLPDVWVGRSCRLRRCVIDRACVIPEGMVIGENAEEDARRFYRSEEGIVLVTRD

MLRKLGHKQER

>WP\_002920564.1 MULTISPECIES: glycogen synthase GlgA [Klebsiella]

MQVLHVCSEMFPLLKTGGLADVIGALPAAQIAEGIDTRVLLPAFPDIRRGVVDAQVVTRRDTFAGRITLL

YGHFNGVGIYLIDAPHLYDRPGSPYHDTNQHAYPDNVLRFALLGWVGSEMASGLDPFWRPDVVHAHDWHA

GLTPAYLAARGRPAKSVFTVHNLAYQGMFYSWHMNDIELPWSFYNMHGLEFNGQISFLKAGLYYADHITA

VSPTYAREITEPQYAYGMEGLLRQRHHEGRLSGILNGVDDGIWSPQNDLLLPMRYDRDTLEEKAENKRQL

QIAMGLKVDDKAPLFAVVSRLTSQKGLDLVLEALPGLLEQGGQLALLGAGDPVLQEGFLAAAAEHPGKVG

VQIGYHEAFSHRIMGGADVILVPSRFEPCGLTQLYGLKYGTLPLVRRTGGLADTVADSSLENLADGLATG

FVFEDSNALSLLRAIRRAFVLWSRPSLWRYVQRQAMNMDFSWQVAANSYRELYQRLM

>WP\_002920561.1 MULTISPECIES: glycogen phosphorylase [Klebsiella]

MNVPFSYASPTLSVEALKHSIAYKLMFIIGKDPAIANKHEWLNATLFAVRDRMVERWLRSNRAQLSQEVR

QVYYLSMEFLIGRTLSNALLSLGIYDDVSSALAEMGLDLEELIDEENDPGLGNGGLGRLAACFLDSLAAL

GLPGRGYGIRYDYGMFKQNIVDGRQKESPDYWLEYGNPWEFERHNTRYKVRFGGRIQQEGKKTRWIETEE

IIAEAYDQIIPGFDTDATNTLRLWSAQASSEINLGKFNQGDYFAAVEDKNHSENVSRVLYPDDSTYSGRE

LRLRQEYFLVSATVQDILSRHYMLHKTYDNLADKIAIHLNDTHPVLSIPELMRLLIDEHKFSWDEAFEVT

CQVFSYTNHTLMSEALETWPVDMLGKILPRHLQIIFEINDYFLKTLQEQYPNDTDLLSRTSIIDESNGRR

VRMAWLAVVVSHKVNGVSELHSRLMVESLFAEFAKIFPMRFINVTNGVTPRRWLALANPPLSKVLDEHIG

RTWRTDLSQLDELKQHIDYPMVNQAVRQAKFENKQRLASYIAQQLNVVVNPKALFDVQIKRIHEYKRQLM

NVLHVITRYNRIKADPQAEWVPRVNIFAGKAASAYYMAKHIIHLINDVAAVINNDPQIGDKLKVVFIPNY

SVSLAQLIIPAADLSEQISLAGTEASGTSNMKFALNGALTIGTLDGANVEMQEHVGEENIFIFGNTAEEV

EELRRSGYKPREYYEQDEELHQALTQIGTGVFSPAEPGRYRDLLDSLINFGDHYQVLADYRSYVDCQDRV

DELYQNPEEWAYKAMLNIANMGYFSSDRTIQEYAKYIWHIDPVRL

>WP\_016529833.1 MULTISPECIES: type II toxin-antitoxin system RelE/ParE family toxin [Klebsiella]

MWDVETTDTFDTWFELQSRALKEDMLATMLILSEFAPQLGRPYVDTVKDSTFQNMKELRVQHHGLPIRAF

FAFDPLRKAIVLCAGDKDGMNEKRFYKEMITLADREFSQHLTKER

>WP\_016529832.1 helix-turn-helix domain-containing protein [Klebsiella pneumoniae]

MATLKELMAKQSPESQQRIAAKAAEIRQSVALNLLREELQMSQTEMAAAMGVKQPTIAKMEQTDNAPRLS

TLKRYIAALGGELSINVTLPTGKKVSFNL

>WP\_002920554.1 MULTISPECIES: glycerol-3-phosphate dehydrogenase [Klebsiella]

METKDLIVIGGGINGAGIAADAAGRGLSVLMLEARDLACATSSASSKLIHGGLRYLEHYEFRLVSEALAE

REVLLKMAPHIAFPMRFRLPHRPHLRPAWMIRIGLFMYDHLGKRTSLPGSTGLRFGAESVLKPEIVRGFE

YSDCWVDDARLVLANAQMVVRKGGEVRTRTRAISAKRENGLWVVEAEDIDSGEKFTWKARGLVNATGPWV

KQFFDEGMHLRSPYGIRLIKGSHIVVPRVHTQKQAYILQNEDKRIVFVIPWMDEFSIIGTTDVEYKGDPK

AVAIDDKEINYLLNVYNAHFKKTLSRDDIVWTYSGVRPLCDDESDSPQAITRDYTLDIHDENGQAPLLSV

FGGKLTTYRKLAEHALEKLTPYYKGIGPAWTKTAVLPGGDIGGDRDDYAAKLRRRFPFISESLARHYART

YGSNSEWILKEASALSDLGEDFGHEFYEAELKYLVEHEWVRSLDDAIWRRTKQGMWLTAEQQARISEWLA

QHAGKSELSLAS

>WP\_002920552.1 MULTISPECIES: thiosulfate sulfurtransferase GlpE [Gammaproteobacteria]

MEQFECINVEEAHQKLHQQTAVLVDIRDPQSYAMGHTPGAFHLTNDTLGAFMRDNDFDTAVMVMCYHGNS

SKGAAQYLLQQGFDKVYSVDGGFDAWHRHFPAEVARGTF

>WP\_004151408.1 MULTISPECIES: rhomboid family intramembrane serine protease GlpG [Enterobacteriaceae]

MLMITSFANPRVAQAFVDYMATQGIILTIQQHTQSDVWLADESQAGRVRAELARFLENPADPRYLAASWQ

SGQTNSGLRYQRFPFFATLRHNAGPFTWAILLICIAVFILQNLLGDQPVMIWLAWPYDPSLQFEAWRYFS

HAFMHFSLMHILFNLLWWWYLGGAVEKRIGSGKLVVITVISALLSGFVQHQFSGPWFGGLSGVVYALMGY

VWLRGERDPQSGIYLQRGLILFSLVWLIAGWFDVFGMAIANGAHVAGLATGLAMAFVDTLHGRKRA

>WP\_002920548.1 MULTISPECIES: DeoR/GlpR family transcriptional regulator [Enterobacteriaceae]

MKQTQRHDAIIELVKKQGYVSTEELVEQFAVSPQTIRRDLNDLAEQKMILRHHGGAALPSSSVNTSWHDR

KATQTAEKERIARRVASEIPDGATLFIDIGTTPEAVAHALLDHNDLRIVTNNLNVANTLMVKEDFRIILA

GGELRSRDGGIIGEATLDFISQFRLDFGILGISGVDSDGSLLEFDYHEVRTKRAIIENSRHVMLVVDHTK

FGRNAMVNMGSISMVDAVYTDVLPPAGVLKVITDNNLQLELC

>WP\_016529568.1 HTH-type transcriptional regulator MalT [Klebsiella pneumoniae]

MLIPSKLSRPVRLEHTVVRERLLAKLSGANNYRLVLITSPAGYGKTTLISQWAAGKNDLGWFSLDEGDNQ

QERFASYLIAAIQQATGNHCAASEAMVQKRQYASLSSLFAQLFIELADWQRPLYLVIDDYHLINNPVIHD

AMRFFLRHQPENMTLVVLSRNLPQLGIANLRVRDQLLEIGSQQLAFTHQEAKQFFDCRLTSPIEADDSSR

LCDDVAGWATALQLIALSARQNNSSAQHSARRLAGINASHLSDYLVDEVLNNVDARTRNFLLKSSLLRSM

NDALIVRVTGEENGQMQLEEIERQGLFLQRMDDSGEWFRYHPLFGSFLRQRCQWELAVELPEIHRAAAES

WMAQGFPSEAIHHALAAGDAKMLRDILLNHAWGMFNHSELGLLEQSLAALPWSNLLENPRLILLQAWLMQ

SQHRYSEVNTLLARAEQEMSVEMDTAMHGDFNALRAQVAINDGDQDEAERLSMVALEELPLANYYSRIVA

TSVHGEVLHCKGKLTKSLAVMQQTEQMARRHDVWHYALWSIIQQSEILFAQGFLQAAWESQEKAFQLVRE

QHLEQLPMHEFLLRIRSQLLWAWARLDEAEACARQGMDVLSTYQPQQQLQCLALMVQCSLARGDLDNARS

HLNRLENLLGNGHYHSDWVSNADKVRVIYWQMTGDKTAAANWLRQTPKPEFANNHFLQSQWRNIARAQIL

LGDFEPAEMVLEELNENARSLRLMSDLNRNLLLLNQLYWQSGRKSEAQKALLEALTLANRTGFINHFVIE

GEAMAQQLRQLIQLNTLPELEQHRAQRILRDINQHHRHKFAHFDEGFVERLLNHPEVPELIRTSPLTQRE

WQVLGLIYSGYSNEQIAGELDVAATTIKTHIRNLYQKLGVAHRQDAVQHAQQLLKMMGYGV

>WP\_004151407.1 MULTISPECIES: maltodextrin phosphorylase [Enterobacteriaceae]

MSQTTFNKAQFQAALTRQWQHFGLQSASEMTQRQWWRAVSGALAELLAAQPVAKPAQGQRHVNYISMEFL

IGRLTGNNLLNLGWYEGVSDALKGYDVNLTDLLEEETDPALGNGGLGRLAACFLDSMATVGQSATGYGLN

YQYGLFRQSFDDGQQMEAPDDWGRSSYPWFRHNEALDVQVGIGGKVSKNGEWQPAFVITGEAWDLPVLGY

RNNVAQPLRLWQAKHAHPFNLTKFNDGDFLRAEQQGIDAEKLTKVLYPNDNHQAGKKLRLMQQYFQCACS

VADILRRHHLAGRKLAELADYEVIQLNDTHPTIAIPELLRVLIDEHQLSWDDAWAITSKTFAYTNHTLMP

EALECWDEKLVKALLPRHMQIIKEINDRFKQLVDKTWPGDKQVWAKLAVVHDKQVRMANMCVVGGFAVNG

VAALHSDLVVKDLFPEYNQLWPNKFHNVTNGITPRRWIKQCNPALASLLDETLKKEWANDLDQLINLEKY

ADDAAFRQTYRDIKQANKVHLAEFVKQRTGIEINPQAIFDIQIKRLHEYKRQHLNLLHILALYKEIRENP

QSDRVPRVFLFGAKAAPGYYLAKNIIFAINKVAEAINNDPKVGDKLKVVFLPDYCVSAAEKLIPAADISE

QISTAGKEASGTGNMKLALNGALTVGTLDGANVEIAEQVGEENIFIFGHTVEEVKALKAKGYDPLKWRKK

DKLLDAVLKELENGTYSNGDKHAFDQMLHSLLQGGDPYLVLADFEAYVAAQKRVDELYRDEEAWTRAAIL

NTARCGMFSSDRSIRDYQQRIWQAKR

>WP\_002920543.1 MULTISPECIES: 4-alpha-glucanotransferase [Enterobacteriaceae]

MESKRLDNAALAAGISPSYINAHGKPQSIAAVTKQRLLDAMHRSTAATKVAVNPLPNVKIFTHGKKMSLP

VAGRGEYQWILTTEDGKQYQGKTRGGETLPLPAKLPEGYHSLTLTQEGERWHCRTIVAPARCYEPQPLKE

GKKLWGTCVQLYTLRSEKNWGIGDFGDLRAMLPEIARRGGSFIGLNPIHALYPANPESASPYSPSSRRWL

NVIYIDVNAVEDFQRSEEAQAWWQSPATQQALQAARETDDVDYTAVTTLKMTALRMAWKQFSRREDEQMT

AFREFVLREGESLYWQAAFDALHAWQVQQDPLRWGWPAWPKAFQDIDSPEVKAFCVEHEDDVSFYLWLQW

LAWSQFAACWETSQRDGMPIGLYRDLAVGVAEGGSETWCDRELYCLKASVGAPPDILGPLGQNWGLPPMD

PHIIAARAYEPFIDLLRANMQNCGALRIDHVMSVLRLWWIPYGETADHGAYVQYPVDDLLSLLALESQRH

RCMVIGEDLGTVPVEIVSKLRNSGVYSYKVLYFESDAEKTFRAPALYPEQSMAVATTHDLPTLRGYWESG

DLTLGKALGLYPDEVVLRGLYQDRELAKQGLLDALHKYGCLPKRAGHKASLMSMTGILNRGMQRYIADSN

SALLGLQPEDWLEMATPVNIPGTSTEYPNWRRKLSVTLEQMFADERVNKLIKDLDKRRKAASKKAAS

>WP\_002920542.1 MULTISPECIES: gluconate transporter [Klebsiella]

MPLVIVAIGVALLLLLMIRFKMNGFIALVLVALAVGLMQGMPLDKVIVSIKNGVGGTLGSLALIMGFGAM

LGKLLADCGGAQRIATTLINKFGKKHIQWAVVLTGFTVGFALFYEVGFVLMLPLVFTIAASARIPLLYVG

VPMAAALSVTHGFLPPHPGPTAIATIFHADMGKTLLYGTILAIPTVILAGPVFARFLKGIDKPIPEGLHN

PKVFTEEEMPGFGVSVWTSLVPVILMAMRAVAEMILPKGHAFLPIAEFFGDPVMATLIAVLIALFTFGLN

RGRSMEQINDTLTSSIKIIAMMLLIIGGGGAFKQVLVDSGMDKYIASIMHESNMSPLFMAWSIAAVLRIA

LGSATVAAITAGGIAAPLIATTGVSPELMVIAVGSGSVIFSHVNDPGFWLFKEYFNLTIGETIKSWSVLE

TIISVCGLVGCLLLGMVV

>WP\_002920540.1 MULTISPECIES: Fe-S biogenesis protein NfuA [Klebsiella]

MIRISDAAQAHFAKLLANQEEGTQIRVFVINPGTPNAECGVSYCPPDAVEDTDTALKFEQLTAYVDELSA

PYLEDAEIDFVTDQLGSQLTLKAPNAKMRKVSDDAPLMERVEYLLQSQINPQLAGHGGRVSLMEITDDGL

AILQFGGGCNGCSMVDVTLKEGIEKQLLNEFPELKGVRDLTEHQRGEHSYY

>WP\_004185961.1 MULTISPECIES: DNA utilization protein GntX [Klebsiella]

MLTAHSLCWLCQMPLAVARWGICSRCSRALLACPPLCPQCGLPAAASRHPCGRCLQKPPPWHRLVAVNDY

RPPLSGLVQQLKFHHRPELGPALARLLLQRLLQRDDLPPVDALVGVPLWHRRRWRRGYNQCDELCRPLAR

WRGCVWHREGLTRQRAGAVQHSLNARQRRQNLKNAFQLEFAVQGLHIALVDDVVTTGSTVAEISRLLLRN

GAATVQVWCLCRTL

>WP\_004174021.1 MULTISPECIES: pimeloyl-ACP methyl ester esterase BioH [Klebsiella]

MNDIWWQTIGEGDCHLVLLHGWGLNAQVWDCITPQLASHFTLHLVDLPGYGRSGGFGAMSLEAMAQRVLE

QAPPQAVWLGWSLGGLVASQVAIMRPERVQALVTVASSPCFAARDDWPGIKPEVLAGFQQQLSDDFQRTV

ERFLALQTMGTESARQDARALKQAVLSLPMPSAEALNGGLEILRTVDLRQALVRLPMPFLRLYGRLDGLV

PRKIVPLLDDLWPESESILFDKAAHAPFVSHPAAFCEPLLALKTRLG

>WP\_002920510.1 MULTISPECIES: DUF1471 domain-containing protein [Enterobacteriaceae]

MKLVTGMVASLVIGTLSFGAFAAKEIQKEDVAKMNLTKVGSITTSRTTSPMDARRDLSKKADELGGKYFV

VIAGQKNEKTVHANADVYK

>WP\_002920509.1 MULTISPECIES: [Fe-S]-dependent transcriptional repressor FeoC [Enterobacteriaceae]

MASLMEVRDMLALQGRMEAKQLSARLQTPQPLIDAMLERMEAMGKVVRISETSEGCLSGSCKSCPEGKAA

CRQEWWALR

>WP\_014906839.1 MULTISPECIES: Fe(2+) transporter permease subunit FeoB [Klebsiella]

MQKLTVGLIGNPNSGKTTLFNQLTGARQRVGNWAGVTVERKEGIFATTDHQVTLVDLPGTYSLTTISSQT

SLDEQIACHYILSGDADMLINVVDASNLERNLYLTLQLLELGIPCVVALNMLDIAEKQQVRIDIDALAAR

LGCPVIPLVSTRGRGIEALKIALDRHQANSDLELVHYPQPLLREADLLAQQMSAQIPPRQRRWLGLQMLE

GDIYSRAYAGDAADKLDIALANLSDEIDDPALHIADARYQTIAAICDAVSNTLTAEPSRFTAAMDKVILN

RFLGLPIFLFVMYLMFLLAINIGGALQPIFDAGSVAIFVHGIQWLGYTLHFPDWLTVFLAQGIGGGINTV

LPLVPQIGMMYLFLSFLEDSGYMARAAFVMDRLMQALGLPGKSFVPLIVGFGCNVPSVMGARTLDAPRER

LMTIMMAPFMSCGARLAIFAVFAAAFFGQNGALAVFSLYVLGIVMAILTGLMLKHTIMRGEASPFVMELP

VYHVPHIKSLIIQTWQRLKGFVLRAGKVIVIVSIFLSALNSFSLSGKVVDNINDSALASVSRVITPVFKP

IGVHEDNWQATVGLFTGAMAKEVVVGTLNTLYTAEDIQNEEFNPQTFSLGEELLAAVDETWQGLKDTFSL

SVLANPIEASKGDGEMATGAMGVMGSKFGSAAAAYSYLIFVLLYIPCISVMGAIARESSRGWMTFSILWG

LNIAYSLSTLYYQTVSFSDHPRYSLVCILAVVLFNVVLFGLLRRARSRVDVSLLATRKTPASCCSSPAGD

CH

>WP\_002920506.1 MULTISPECIES: ferrous iron transporter A [Enterobacteriaceae]

MQFTPDSAWKITGFSRDISPAYRQKLLSLGMLPGSSFHVVRVAPLGDPVHIETRRVSLVLRKKDLALIEL

EAVAQ

>WP\_004150056.1 MULTISPECIES: RNA-binding transcriptional accessory protein [Klebsiella]

MMNDSLCRIIAGELQARAEQVEAAVRLLDEGNTVPFIARYRKEVTGGLDDTQLRNLETRLGYLRELEDRR

QAILKSIAEQGKLTDALEKAINTTLSKTELEDLYLPYKPKRRTRGQIAIEAGLEPLADLLWNEPAHDPEA

EAAKYIDADKGVADSKAALDGARYILMERFAEDAALLAKVRDYLWKNAHLVSTVVSGKEEEGAKFRDYFD

HHEPIATVPSHRALAMFRGRNEGVLQLSLNADPQFDEPPKESHGEQIIIDHLGLRLNNAPADSWRKGVVS

WTWRIKVLMHLETELMGTVRERAEDEAINVFARNLHDLLMAAPAGLRATMGLDPGLRTGVKVAVVDATGK

LVATDTIYPHTGQAAKAAVAVAALCEKYNVELVAIGNGTASRETERFFLDVQKQFPKVTAQKVIVSEAGA

SVYSASELAAQEFPDLDVSLRGAVSIARRLQDPLAELVKIDPKSIGVGQYQHDVSQTQLARKLDAVVEDC

VNAVGVDLNTASVPLLTRVAGLTRMMAQNIVAWRDENGQFQNRQQLLKVSRLGPKAFEQCAGFLRINHGD

NPLDASTVHPEAYPVVERILAATQQALKDLMGNSSALRHLKAVDFTDEKFGVPTVTDIIKELEKPGRDPR

PEFKTAKFADGVETMNDLLPGMILEGAVTNVTNFGAFVDIGVHQDGLVHISSLSDRFVEDPHTVVKAGDI

VKVKVMEVDLPRKRIALTMRLDEQPGDSNARRGGGQERPQGNRPAAKAAKPRGREAQPAGNSAMMDALAA

AMGKKR

>WP\_002920503.1 MULTISPECIES: transcription elongation factor GreB [Klebsiella]

MKTPLITREGYEKLKQEMDYLWRQERPEVTKKVTWAASLGDRSENADYQYNKKRLREIDRRVRYLTKCLE

QLKIVDYSPQQEGKVFFGAWVEIENDEGDIKRFRIVGYDEIFGRKDYISIDSPMARALLKKEVGDLAIVN

TPAGEASWYVNEIEYVK

>WP\_001157751.1 MULTISPECIES: two-component system response regulator OmpR [Enterobacterales]

MQENYKILVVDDDMRLRALLERYLTEQGFQVRSVANAEQMDRLLTRESFHLMVLDLMLPGEDGLSICRRL

RSQSNPMPIIMVTAKGEEVDRIVGLEIGADDYIPKPFNPRELLARIRAVLRRQANELPGAPSQEEAVIAF

GKFKLNLGTREMFREDEPMPLTSGEFAVLKALVSHPREPLSRDKLMNLARGREYSAMERSIDVQISRLRR

MVEEDPAHPRYIQTVWGLGYVFVPDGSKA

>WP\_002920333.1 MULTISPECIES: two-component system sensor histidine kinase EnvZ [Klebsiella]

MKRVRFSPRSSFARTLLLIVTLLFVSLVTTYLVVLNFAILPSLQQFNKVLAYEVRMLMTDKLQLEDGTQL

VVPPAFRREIYRELGISLYSNEAAEDAGLRWAQHYEFLSQQMAHQLGGPTEVRVEVNKSSPVVWLKTWLS

PNIWVRVPLTEIHQGDFSPLFRYTLAIMLLAIGGAWLFIRIQNRPLVDLEHAALQVGRGIIPPPLREYGA

SEVRSVTRAFNHMAAGVKQLADDRTLLMAGVSHDLRTPLTRIRLATEMMGEQDGYLAESINKDIEECNAI

IEQFIDYLRTGQEMPMELADLNAVLGEVIAAESGYEREIATALQAGEIPVRMHPLSIKRALANMVVNAAR

YGNGWIKVSSGSEASRAWFQVEDDGPGIKPEQREHLFQPFVRGDSARSTSGTGLGLAIVQRIIDNHNGRL

EIGSSERGGLLIRAWLPVHRMLAPMKPARES

>WP\_004210368.1 phosphoenolpyruvate carboxykinase (ATP) [Klebsiella pneumoniae]

MRVNHGLTPQDLKAYGINDVQDIVHNPSYDMLFQEELDPNLEGYERGVLTTLGAIAVDTGIFTGRSPKDK

YLVRDDTTRDTVWWSDKGKGKNDNKPLSQETWQHLKGLVTQQLSGKRLFIVDAFCGANADTRLSVRFITE

VAWQAHFVKNMFIRPSDEELAEFVPDFIVMNGAKCTNPQWKEQGLNSENFVAFNLTERIQLIGGTWYGGE

MKKGMFSIMNYLLPLKGIASMHCSANVGEKGDVAIFFGLSGTGKTTLSTDPKRRLIGDDEHGWDDDGVFN

FEGGCYAKTIKLSEAAEPDIYHAIRRNALLENVVVRADGTVDFDDGSKTENTRVSYPIDHIDNIVKPVSK

AGHATKVIFLTADAFGVLPPVSRLTADQTQYHFLSGFTAKLAGTERGVTEPTPTFSACFGAAFLSLHPTQ

YAEVLVKRMQAAGAQAYLVNTGWNGTGKRISIKDTRAIIDAILNGSLDNAETFTLPMFNLQIPTALPGVD

THILDPRSTYGSPEQWQEKADQLAKLFIENFEKYTDTPAGAALVAAGPQR

>WP\_171819464.1 Hsp33 family molecular chaperone HslO [Klebsiella pneumoniae]

MIMTQHDQLHRYLFENYAVRGELVTVSETLEQILANHTYPQPVKTVLAELLVATSLLTATLKFAGDITVQ

LQGDGPLQLAVINGNNQQQLRGVARVQGEIADDADLKTMVGNGYLVITISPEEGERYQGVVGLEGDTLAA

CLEDYFQRSEQLPTRLIIRTGDHEGQPMAGGMLLQVMPAQDAQTADFEHLTTLTETIKAEELFTLPANDV

LWRLYHEEEVTVYDPQSVEFKCTCSRERCAGALKTLPDEEIDSILADEGEIDMHCDYCGNHYIFNAMDIA

EIRNNASPADPQVH

>WP\_002920326.1 MULTISPECIES: ribosome-associated heat shock protein Hsp15 [Klebsiella]

MKEKPTETVRLDKWLWAARFYKTRALAREMIEGGKVHYNGQRSKPGKIVELDAMLTLRQGNDERTVRIIG

ITEQRRPASEAVNLYEETAESIEKREKMALARKMNALTMPHPDRRPDKKERRDLMRFKHGESE

>WP\_016530730.1 intracellular growth attenuator family protein [Klebsiella pneumoniae]

MGTFLIFLTALLICVLLIGWWYRAHARRRRLPLLHAFSDATTRQLPADERQAIEKYVAELSHAQQVPASG

ATSAPVALALNEQSDTVYAVTRAITRYGITTDAPNKWRYFLDSVEVHLPPFWEQHINDENSVELIPTDSL

PLVITLNGHSLSDYRQEAQSYALERASATQASIRGEESEQVELRQIRRETPEEHALNRPDGLREAILIVA

SFLFFYFSLIGPAVFTPWLVAAGLLLLAAGLWGIYAPPRRAALREIHCLRGVPKRWGLFGENDQEQINNI

SLGIIDLIYPRHWQPWIAQDLGQQTDIDIYLNRHVARQGRYLSLHDEVKNFPLQYWLRSAIIAAGALVVV

IMLWASVPLNMPFKFTLSWLKGAQTIEATTVSQLEKAHVRIGDTLRLTGTGMCNIRTPGSWSAKEDSPFL

PFDCSQIVWNDAPPLPLPESDIVSKATALMQSVQRQLHPETDDDSRVSPALRSAIQKSGMVLLDDFGDIV

QKTNDLCSAKDDCLRLKNALVNLGNTRNWETLTKRATAGKLDGVNVLLRPVSAESLENLVTTSTAPFVIR

ETSRAAQALNSPAPGGFLIASDEGSVLVNQPWPAVSLYDYPAHEQWGELRRLAGMLMHTPFHAEGIVTNL

FTDANGTQHINLHRIPDRSGLWRYLGITLLLSMVGCMAYHAVQALRRYQRHRQRMEEIQKYYESCLNPVL

LPSSDSQD

>WP\_002920321.1 MULTISPECIES: ADP compounds hydrolase NudE [Klebsiella]

MSKSLQKPTILNVETVARSRLFNVESVDLEFSNGVRRVYERMRPSTREAVMIVPIVDDHIILIREYAVGT

ESYELGFSKGLIDPGETVDEAANRELKEEVGYGANKLTFLKKLSMAPSYFSSKMNIMVAEDLYPESLPGD

EPEPLPQVRWPLAQLMSLLDEEDFNEARNVSALFLVREWLQAQGRL

>WP\_004185951.1 MULTISPECIES: peptidoglycan glycosyltransferase/peptidoglycan DD-transpeptidase MrcA [Klebsiella]

MKFVKYLLILAVCCVLLGAGSIFGLYKYIEPQLPDVATLKDVRLQIPMQVYSADGELIAQYGEKRRIPVT

LQQIPPELVKAFIATEDSRFYEHHGVDPVGIFRAASVAMFSGHASQGASTITQQLARNFFLSPEKTLMRK

IKEAFLAIRIEQLLNKDEILELYLNKIYLGYRAYGVGAAAQVYFGKPIDQLTLSEMAVIAGLPKAPSTFN

PLYSMDRATARRNVVLSRMLSEGYITQAQYDEARSEPIDASYHAPKIAFSAPYLSEMVRQEMVNRYGEQA

YEDGYRVYTTITRKNQQAAQQAVRNNVLDYDMRHGYRGPASVLWKVGETPWETKKIVDSLKRQSGYGPLF

PAVVTSANAQEAVALLANGDSVSLTMEGVRWARRFISDTQQGATPRKVNDVVQAGQQIWVRKVGDSWWLS

QLPDVNSALVSINPQNGAIIALVGGFDFNQSKFNRATQALRQVGSNIKPFLYTAAMDKGLTLASMLNDVP

ISRWDAGAGSDWRPKNSPPQYAGPIRLRQGLGQSKNVVMVRAMRAMGVDYAAEYLQRFGFPAQNIVHTES

LALGSASFTPLQVARGYSVMANGGFLVNPFFISKIENDQGGVLFEERPKIACPQCDLPVIYGDTPKSNVL

ENKDVEDVATSAEPQNGNVPPQPQLEQANQSLVAQSGAQEYAPHVINTPLAFLIKSALNSNIFGEPGWMG

TGWRAGRDLQRHDIGGKTGTTNSSKDAWFSGYGPGVVTSVWIGFDDHRRDLGRTTASGAIKDQISGYEGG

AKSAQPAWDSFMKSVLEGVPEEPLTPPPGIVTVNIDRSTGQLANGGNSRAEYFIEGTQPTQQAVREVGTT

LTDGGGETHELF

>WP\_046042236.1 hypothetical protein [Klebsiella pneumoniae]

MAFRNWRLGMHIQQDSIAIVALLHERSHWALRRWWRIPLPPGLVRQGMVADVSALGSRLAAWRRELPAQH

QVSIAFPAVRTLQKRLPYPQFALREREQATWVASAMSQQLAMPASALCIDYAPSSRDDGWQVTAAQRLDI

NVLRELAGRLRLRVAAIVPDASALGAFFPWMTAADQGLAWRDEKHWLWATREAWGSDACADVGSLSQLAG

QLQVLLRLCIDAGDEASRFDVWQVIHRRQPPLPADGDRYAIALGLALGGGRHDACR

>WP\_046042238.1 pilus assembly protein PilN [Klebsiella pneumoniae]

MTHVVNLLPWRDLRRRQRLRYVLLLTIGIVLLGGMGLLVSRTARLQRDFLATLHTTADAQLLASLKQREQ

AMREAWQQHQRQRQQYQRRSAIAAWQPRLQALAADLPAQAWLTRLEYQGVLLTLDGLALNLKALTSVEAA

LTRVAGFAPAKAGGTQRDAEGRWQFSFTLTGARADAD

>WP\_004151403.1 MULTISPECIES: hypothetical protein [Klebsiella]

MRINLRGAWTGLPILLAMGLSGGGVALWRDLRPPQAAVTRDAALQTQWRRIMALRIPGEENPGARIDTQS

FSPIAIPLSGAKLIAWRPQGSGGEMELTLSWSTVPALFSWLARCGMNPRSFSLGREAQTLRLRLLLEAED

ER

>WP\_002920279.1 MULTISPECIES: HofP DNA utilization family protein [Klebsiella]

MSGKRWIFLWLPLSLLAAERDPFQPVEDPCRTAQLSQWRYGGAVGDEAGWTGFLQDGNGKWRRVRMDEQL

PTGWRVSRLTAGELDIVTSSGCEPPAWRWQREGKQHDAMDKPAASAAAAGGGPRRPQ

>WP\_004174030.1 MULTISPECIES: DNA uptake porin HofQ [Klebsiella]

MMRWISLLLLLLPLAVAPAARNDKPVSLVIDDAPVAQVLQALAEMNHKNLVVAPDVSGTLSLRLQKVPWS

QALRAVADSAGLSLQQQGTVIYAHTQAWQKANQAQREAEQEKRLQNLPLQAESVTLHFADAEELAKSGGK

LLSARGHLMADKRTNRLLIRDDARHLPALKAWAQEMDLPVGQVELAAHIVSMSETSLRELGVKWRLAEAG

SPPGSGQITTLSSDVSVNDASTRAGFNIGKINGRLLELELSALERKQQVEIIASPRLLASHMQPASIKQG

SEIPYQVSSGESGATSVEFKEAVLGMEVTPTVLQQGRVRLKLRISENTPGQVLKQENGEALAIDKQEIET

LVEVRSGETLALGGIFSQKNKTARDSVPLLGDIPVLGRLFRRDGKDNERRELVVFITPRILAVR

>WP\_002920267.1 MULTISPECIES: shikimate kinase AroK [Enterobacteriaceae]

MAEKRNIFLVGPMGAGKSTIGRQLAQQLNMEFYDSDQEIEKRTGADVGWVFDVEGEEGFRDREEKIINEL

TEKQGIVLATGGGSVKSRETRNRLSARGVVVYLETTIEKQLARTQRDKKRPLLQVDAPPREVLEALADER

NPLYEEIADVTIRTDDQSAKVVANQIIHMLESN

>WP\_004150047.1 MULTISPECIES: 3-dehydroquinate synthase [Klebsiella]

MERLTVTLGERSYPITIAAGLFNDPASFLPLKSGDQAMLVTNETLAPLYLDTVRSALEQSGVNVDSVILP

DGEQYKSLAVMDTVFTALLQKPHGRDTTLVALGGGVIGDLTGFAAASYQRGVRFIQVPTTLLSQVDSSVG

GKTAVNHPLGKNMIGAFWQPVSVVVDLNCLKTLPKRELASGLAEVIKYGVILDGEFFSWLENNIDALLAL

DDTAMAYCIRRCCELKAEVVAADERETGLRALLNLGHTFGHAIEAEMGYGNWLHGEAVAAGMVMAARTSE

RLGQFRAQDTQRIIELLKRAGLPVRGPQEMSAQAYLPHMMRDKKVLAGEMRLVLPLAIGSSELRGGVPHD

VVLGAIADTQQAQQ

>WP\_016529309.1 cell division protein DamX [Klebsiella pneumoniae]

MDDFKPEDDMKADRNDRRAGRSRQSSERDADPHINFDDVDLDADEGRPTRAGKARREREEEEFEEELDAQ

DEEMLEEQPVERRPRKRKKAPAKPASRQYIMMGVGILVLLLLIVGIGSALKSPSSSSQQTASGEKSINLS

DDQSASMPAAGQDQTAAANSTSQQDVTVPPIAANPTQGQAAVAPQGQQRIEVQGDLNNALTQQQGQLDGA

VANSTLPTEPATVAPIRNGANGTAAPRQATERQTAATPRPAERKHTVIEAKPQSKPQAVAKTPVESKPVQ

QKHVESTATTAPAKTSVSESKPVATAQSKPTTTTAAPAATAAAAAPAAKSGKTAGDVSSMKTAPSGHYTL

QLSSSSNYDNLNNWAKKEKLDKYVVYETSRNGQPWYVLVSGIYASKDEAKRAVTSLPADVQAKNPWAKPL

HQVQADLK

>WP\_002920260.1 MULTISPECIES: adenine-specific DNA-methyltransferase [Klebsiella]

MKKNRAFLKWAGGKFPLLDDIKKHLPEGECLIEPFVGAGSVFLNTDFSRYILADINSDLIGLYNIVKLRT

DEYVAAAREMFTPENNVAERYYLYRDEFNQSQDPLRRAVLFLYLNRHGYNGLCRYNLRGEFNVPFGRYKK

PYFPEAELYHFAEKAQNAEFYCESYEECMQRADSRTVVYCDPPYAPLTATANFTAYHTNSFNLEQQVLLA

QKAESLMKKRIPVLISNHRTPLTQEWYKNAAETHIVKVRRSISSNGGTRKKVDELLALYRPPKTK

>WP\_002920259.1 MULTISPECIES: ribulose-phosphate 3-epimerase [Klebsiella]

MKQYLIAPSILSADFARLGEDTAKALAAGADVVHFDVMDNHYVPNLTIGPMVLKSLRNYGITAPIDVHLM

VKPVDRIIPDFAEAGASIITFHPEASEHVDRSLQLIKEHGCKAGLVFNPATPLSYLDYVMDKLDVILLMS

VNPGFGGQSFIPQTLDKLREVRQRIDASGYDIRLEVDGGVKASNIGEIAAAGADMFVAGSAIFGQPDYKQ

VIDQMRSELAKVSHG

>WP\_004188345.1 MULTISPECIES: phosphoglycolate phosphatase [Klebsiella]

MDKLQAIRGIAFDLDGTLVDSAPGLTSAVDNALYALELPVAGEERVITWIGNGADVLMERALTWARQERA

TLRAAMGKPSVDDHDIPQDEQLRILRKLFDRYYAEAAEEGSFLFPAVADTLGALHAKGLPLALVTNKPTP

FVAPLLDALDIAKYFTVVIGGDDVQNKKPHPEPLLLVAEKLSLAPAELLFVGDSRNDIQAAKAAGCCSVG

LTYGYNYGEPLALSEPDYLFDQFNELLPALGLPHSETQELKHD

>WP\_002920253.1 MULTISPECIES: tryptophan--tRNA ligase [Klebsiella]

MTKPIVFSGAQPSGELTIGNYMGALRQWVNMQDDYHCIYCIVDQHAITVRQDPQQLRKATLDTLALYLAC

GIDPQKSTIFVQSHVPEHAQLGWALNCYTYFGELSRMTQFKDKSARYAENINAGLFDYPVLMAADILLYQ

TNQVPVGEDQKQHLELSRDIAQRFNAIYGDIFKVPEPFIPKSGARVMSLLEPTKKMSKSDDNRNNVIGLL

EDPKSVVKKIKRAVTDSDEPPVVRYDLKEKAGVSNLLDILSAVTGKTIPELEQHFEGKMYGHLKGEVAEA

VSGMLIDLQERYHRFRNDEAFLNQVMKDGAEKASARASQTLKAVYEAIGFVAKP

>WP\_002920252.1 MULTISPECIES: siroheme synthase CysG [Klebsiella]

MDHLPIFCQLRQRDCLLVGGGDVAERKARLLLDAGANVTVNALDFTPQFQVWADSQMLTLVQGEFIPSLL

DNCWLAIAATDDETVNQQVSEAAEARRIFCNVVDAPRQASFIMPSIIDRSPLMVAVSSGGTSPVLARLLR

EKLESILPLHLGQLARYAGHLRARVKQQFATVGERRRFWEKLFVNDRLAQSLANDDRQAVADTTEQLLTE

PLEHRGEVVLVGAGPGDAGLLTLKGLQQIQQADVVVYDRLVSDDIMNLVRRDADRVFVGKRSGYHCVPQE

EINQILLREAQKGRRVVRLKGGDPFIFGRGGEELETLCEAGIPFSVVPGITAASGCSAYSGIPLTHRDFA

QGVRLVTGHLKTGGELDWANLAVEKQTLVFYMGLNQAPAIREKLIAHGMAEDMPAAIVENGTAVTQKVVS

GTLGQLDILAQQMASPALIIVGRVVGLRDKLNWFSNH

>WP\_002920249.1 MULTISPECIES: nitrite reductase small subunit NirD [Enterobacterales]

MSQWVNICSIDDILPATGVCALLGQQQVAIFRPYHDDRVFAISNIDPFFNASVLSRGIIAEHDGALWVAS

PLKKQRFRLSDGLCMEDASHSIARFDARVKDGHVQLKA

>WP\_002920243.1 MULTISPECIES: nitrite reductase large subunit NirB [Klebsiella]

MSKVRIAIIGNGMVGHRFIEELLDKAPAGQFDITVFCEEPRIAYDRVHLSSYFSHHTAEELSLVREGFYE

KHGVKVLVGERAITINRQEKVIHSSAGRTVFYDKLIMATGSYPWIPPIKGAETQDCFVYRTIEDLNAIES

CARRSKRGAVVGGGLLGLEAAGALKNLGVETHVIEFAPMLMAEQLDQMGGEQLRRKIESMGVKVHTSKNT

KEIVQQGTEARKTMHFADGSELQVDFIVFSTGIRPRDKLATQCGLAVAQRGGIMVNDSCQTSDPDIYAIG

ECASWNNRVYGLVAPGYKMAQVAVDHLLGSENSFTGADLSAKLKLLGVDVGGIGDAHGRTPGARSYVYLD

ESKEVYKRLIVSADNKTLLGAVLVGDTSDYGNLLQLVLNAIELPENPDSLILPAHAGSGKPSIGVDKLPD

SAQICSCFDVSKGDLIAAINKGCHTVAALKAETKAGTGCGGCIPLVTQVLNAELAKQGIEVNNNLCEHFA

YSRQELFHLIRVEGIKTFDELLEKHGQGYGCEVCKPTVGSLLASCWNEYILKPQHTPLQDSNDNFLANIQ

KDGTYSVIPRSAGGEITPEGLVAVGRIAREFNLYTKITGSQRIGLFGAQKDDLPEIWRQLIEAGFETGHA

YAKALRMAKTCVGSTWCRYGVGDSVGFGVELENRYKGIRTPHKMKFGVSGCTRECAEAQGKDVGIIATEK

GWNLYVCGNGGMKPRHADLLAADLDRDTLIKYLDRFMMFYIRTADKLTRTAPWLDNMEGGIDYLRSVIID

DKLGLNDHLEEELARLRAAFACEWTETVNNPAAQTRFKHFINSDQRDPNVQVVPERDQHRPATPYERIPV

TLVEEKA

>WP\_016531177.1 cytosine deaminase [Klebsiella pneumoniae]

MTAAPLWLIQNVRLADRDGLWQIAIDKGRFGEITPMGEAHDESYEVLNARGGLAIPPFIEPHIHLDTTQT

AGEPNWNQSGTLFEGIERWAERKALLSHEDVKARAWKTLKWQIANGVQFVRTHVDVFDPTLTALKAMLEV

KQEVAPWVELQIVAFPQEGILSYLNGEALLEEALKLGADVVGAIPHFEFTREYGVESLHIAFRLAQQYDR

PLDIHCDEIDDEQSRFVETVAALALKAGIGPRVTASHTTAMHSYNGAYTSRLFRLLKLSGINFVANPLVN

IHLQGRFDDYPKRRGITRVKELLAAGINVCFGHDDVFDPWYPLGTGNMLQVLHMGLHVCQLMGYQQINDG

LQLITDNSARTFGLEDYGIVSGNPANLIILPAENGFEAVRCQVPVRWSIRQGRVIATTQPAQSWIQTDRG

GEELSFMRNSPLADAKGPKA

>WP\_002920240.1 MULTISPECIES: MFS transporter TsgA [Klebsiella]

MTNSNRIKLTWISFFSYALTGALVIVTGMVMGNIADYFHLPVSSMSNTFTFLNAGILISIFLNAWLMEIV

PLKTQLRFGFILMVLAVAGLMLSHSLALFSASMFVLGLVSGITMSIGTFLITHMYEGRQRGARLLFTDSF

FSMAGMIFPMVAAVLLARSIEWYWVYACIGLVYVAIFVLTFGCDFPVLGKKAQSENSQPVVKEKWGIGVL

FLSVAALCYILGQLGFISWVPEYAKSLGMSLGDAGKLVSDFWMSYMIGMWSFSFILRFFDLQRILTVLAG

LATVLMYLFINGSPEHMPWFILTLGFFSSAIYTSIITLGSQQTRVASPKLVNFILTCGTIGTMLTFVVTG

PIVAASGPLAALHTANGLYAVVFVMCFILGFVSRHRQNNAQAASH

>WP\_002920238.1 MULTISPECIES: peptidylprolyl isomerase A [Klebsiella]

MLKSTLAAMAAVFAISAFSPAMAAKGDPHVLLTTSAGNIELELNSQKAPISVDNFLKYVNSGFYNNTTFH

RVIPGFMVQGGGFNEQMQQKQPNPPIKNEADNGLRNTRGTIAMARTADQDSATSQFFINVADNAFLDHGQ

RDFGYAVFGKVVKGMDVADKISQVQTHNVGPYQNVPTKPVVILSAKVLP

>WP\_002920231.1 MULTISPECIES: YhfG family protein [Enterobacteriaceae]

MRPLTDKQKSRLWEQTRNTNFQASRRLEGVTVPLVTLTAEEALARLATLRREYER

>WP\_002920230.1 MULTISPECIES: putative adenosine monophosphate-protein transferase Fic [Klebsiella]

MSDKFGDERDPYLYPALNVLRNRLGIRQAKNLQQAAFEMTALRAATLPLGPRVRGLPYLCAIHHQLYQDL

FDWAGRLREVNLYLGDTPFCHFARIEEEGNALMQALEQEDYLSGLPRDTFIERLSWFYGEINVLHPFRLG

NGLTQRIFFEQLAIHAGYLLNWRDVDPAGWSAACQQSAMGDLAPLVAIFRKVVSEARESE

>WP\_002920229.1 MULTISPECIES: aminodeoxychorismate synthase component 2 [Klebsiella]

MILLIDNYDSFTWNLYQYFCELGAEVLVRRNDALTLEEIAALAPEKIVISPGPCTPDEAGISLAVIRHYA

GKTPLLGVCLGHQAIAQAFGATIVRAAQVMHGKTSLIEHNGEGVFQGLNNPLTVTRYHSLVIDPPTLPSE

FNVTARSASGEIMGIRHREWDLEGVQFHPESILSEQGHQLLANFLKR

>WP\_004174049.1 MULTISPECIES: aspartate aminotransferase family protein [Klebsiella]

MATEQPAITRATFDEVILPIYAPAEFIPVKGKGSRVWDQQGKEYIDFAGGIAVTALGHCHPALVAALHQQ

GETLWHTSNVFTNEPALRLGRKLVEATFAERVVFMNSGTEANETAFKLARHYAVTRHSPYKTKIIAFHNA

FHGRSLFTVSVGGQPKYSDGFGPKPADIVHVPFNDLQAVKAVMDDHTCAVVVEPIQGEGGVTAATPAFLQ

GLRELCDQHQALLVFDEVQCGMGRTGSLFAYMHYGVTPDILTSAKALGGGFPVSAMLTTHEIASAFHAGS

HGSTYGGNPLACAVANAAFDLINTPAVLDGVSAKRELFVKHLQRLDAEFDLFSDIRGMGLLIGAELKPQH

KGRARDFLYAAADAGVMVLNAGPDVMRFVPSLIIDEQDITEGMARFAQAVAKVING

>WP\_016531180.1 YccS/YhfK family putative transporter [Klebsiella pneumoniae]

MWRRLIYHPEVNYALRQTLVLCLPVAIGLLLGHLQQGLLFSLVPACCNIAGLDTPHKRFFKRLIIGGCLF

AGCSLVVQLLLAQAIPLPFILSGLALLLGVTAEISSLHARLLPASLIAAIFTLSLAGNMPIWEPLLIYAF

GTLWYGVFNWFWFWLWREQPLWESLSLLYRELADYCEAKYSLLTQHTDPSTALPPLLTRQQKVVDLITQC

YQQMHMLAANQRNDHKRLLRAFQMGLDLQEHISVSLHQPEEVQKLVERSHAEAVIRWNAQTVAARLRVLA

DDMLYHRFPKRFQMDKQIEALEKIARQHPDNPVGHFCAWHFSRIARVLHTQRPLYARDLMADKERRLPLL

PALKNYLSLKSPALRNAARISVMLSVASLMGNALHLPKPYWILMTVLFVTQNGYGATRVRIVHRAAGTLA

GLTIAGLTLHFHVPESYTLSGMLLITLLSYLIIRKHYGWAMVGFTVTAVYTLQLLTLNGEQFIIARLIDT

LIGCLIAFGGMVWLWPQWQSGLLKKNAHDALEADQQAIRLILSADPKAPALAYQRMRVNQAHNALYNSLN

QAMQEPGFNTHYLEDMKLWVTHSQFIVEHINAMTTLAREHTMLTPDLAQRYLESCEIALQRCQQRLDSDG

PGSAGDANIMESPESEAPIGPLSTLEQHLQRILGHLNTMHTISSVAWRQRPHHGIWLRKISR

>WP\_000242758.1 MULTISPECIES: cAMP-activated global transcriptional regulator CRP [Enterobacterales]

MVLGKPQTDPTLEWFLSHCHIHKYPSKSTLIHQGEKAETLYYIVKGSVAVLIKDEEGKEMILSYLNQGDF

IGELGLFEEGQERSAWVRAKTACEVAEISYKKFRQLIQVNPDILMRLSSQMARRLQVTSEKVGNLAFLDV

TGRIAQTLLNLAKQPDAMTHPDGMQIKITRQEIGQIVGCSRETVGRILKMLEDQNLISAHGKTIVVYGTR

>WP\_002920158.1 MULTISPECIES: OsmC family protein [Klebsiella]

MQARVKWVEGLTFIGESASGHQILMDGNSGDKAPSPMEMVLMAAGGCSAIDVVSILQKGRHDVTNCEVKL

TSERREEAPRLFTHINLHFIVTGKALKDAAVSRAVDLSAEKYCSVALMLEKAVNITHSYEVIEA

>WP\_046042248.1 phosphoribulokinase [Klebsiella pneumoniae]

MSAKHPVIAVTGSSGAGTTTTSLAFRKIFAQLNLHAAEVEGDSFHRYTRPEMDMAIRKARDQGKHISYFG

PEANDFGLLEQTFVDYGRHGKGQSRKYLHTYDEAVPWNQVPGTFTPWQPLPEPTDVLFYEGLHGGVVTPQ

HDVASHVDLLVGVVPIVNLEWIQKLIRDTSERGHSREAVMDSVVRSMEDYINFITPQFSRTHINFQRVPT

VDTSNPFAAKAIPSLDESFVVLHFRNLQNIDFPWLLAMLQGSFISHMNTLVVPGGKMGLAMELIMTPLVE

RLMEGRKIG

>WP\_002920151.1 MULTISPECIES: YheU family protein [Proteobacteria]

MIIPWQDLDPETLDNLIESFVLREGTDYGEHERSLADKVADVKQQLKRGEAVLVWSELHETVNIMPRALF

NG

>WP\_024264627.1 MULTISPECIES: hydrolase [Klebsiella]

MTPPENDSREFHPMRGVGNRHLQTMLPRLIRRKLRFTPHWQRLELPDGDFVDLAWSEDPHQARHKPRLVV

FHGLEGSLHSPYAHGLIHAAMQRGWLGVVMHFRGCSGEPNRNHRIYHSGETEDGTWFLHWLKREFGPAPT

AAVGYSLGGNMLGCLLAEEGDRCPLDAAVIVSAPFMLEACSYHMDKGFSRVYQRYLLNLLKANASRKLKA

YPGSLPVDLRQLKGMRRIREFDDMITAKIHGFADALDYYRQCSAMPRLSDITKPTLIIHAKDDPFMDHHS

IPPQEQLPANVEYQLTEQGGHVGFVSGTLRKPEMWLERRIPDWLNRWLEVPV

>WP\_016532008.1 MULTISPECIES: ABC transporter ATP-binding protein [Klebsiella]

MIVFSSLQIRRGVRVLLDNATATINPGQKVGLVGKNGCGKSTLLSLLKNEISADGGSMTFPGNWQLAWVN

QETPALPQPAIDYVIDGDREYRQLEAALQLANERNDGHAIATVHGKLDAIDAWTIRSRAASLLHGLGFSN

EQLERPVSDFSGGWRMRLNLAQALICRSDLLLLDEPTNHLDLDAVIWLEKWLKGYTGTLILISHDRDFLD

PIVDKIIHIEQQTMFEYTGNYSSFEVQRATRLAQQQAMYESQQQRVAHLQSYIDRFRAKATKAKQAQSRI

KMLERMELIAPAHVDNPFHFSFRQPESLPNPLLKMEKVSAGYGERIILDSIKLNLVPGSRIGLLGRNGAG

KSTLIKLLAGELQPVSGEIGLAKGIKLGYFAQHQLEFLRADESPLQHLARLAPQELEQKLRDYLGGFGFQ

GDKVSEETRRFSGGEKARLVLALIVWQRPNLLLLDEPTNHLDLDMRQALTEALIDFEGALVVVSHDRHLI

RSTTDDLYLVHDGKVEPFDGDLEDYQQWLSDSQKQESQSGEAPKESGNSAQARKDQKRREAELRSQTQPL

RKEIARLEKEMDKLNAQLASAEEKLGDSELYDASRKAELTECLQQQASAKSGLEECEMAWLEAQEQLERM

LQEG

>WP\_004151401.1 MULTISPECIES: glutathione-regulated potassium-efflux system ancillary protein KefG [Klebsiella]

MMSQTAKVLLLYAHPESQDSVANRVLLEPALQLPNVTVHDLYAHYPDFFIDIAYEQDLLRQHEVIVFQHP

LYTWSCPALLKEWLDRVLSRGFASGAGGNELAGKYWRSVITTGEPESAYRRDANRYPMNDILRPFELTAG

MCRMHWMSPIIVYWARRQQPEELRSRALAYRDWLANPIAAGGVHGGI

>WP\_004150031.1 MULTISPECIES: glutathione-regulated potassium-efflux system protein KefB [Klebsiella]

MAGSDLLLAGVLFLFAAVIAVPLASRLGIGAVLGYLLAGIAIGPWGLGFISDVDEILHFSELGVVFLMFI

IGLELNPAKLWRLRSSIFGVGAAQVMLSAAILGGLLMTTGFSWQAAVVGGIGLAMSSTAMALQLMREKGM

SRSEAGQLGFSVLLFQDLAVIPALALVPLLAGSADEHVNWLTVGMKVLAFAGMLIGGRYLLRPVFRFIAS

SGVREVFTAATLLLVLGSALFMEALGLSMALGTFIAGVLLAESEYRHELEIAIDPFKGLLLGLFFISVGM

ALNLGVLYTHLLWVAVSVAVLVAVKMLVLYLLARLYGLRSSERMQFAGVLSQGGEFAFVLFSLPASQRLF

QHDQMALLLVAVTLSMMTTPLLMKGIDKLLSRRLNPADDTGEAPWVEDDKPQVIIVGFGRFGQVIGRLLM

ANKMRITVLERDISAVNLMRNYGYKVYFGDATQLELLRSAGAEEAQSIVITCNEPEDTMRLVEMCQQHFP

HLHILARARGRVEAHELLQAGVTQFSRETFSSALELGRKALITLGMHPHQAQRAQLHFRRLDMRMLRELM

PVHTDTVQISRVREARRELEEIFQREMQKESRQLDGWDEFE

>WP\_002920143.1 MULTISPECIES: YheV family putative metal-binding protein [Gammaproteobacteria]

MAVRKRFIAGAKCPACQAQDSLAMWRENNVDVVECVKCGHQMREADKEAREHVRKEEQVIGIFHPD

>WP\_002920140.1 MULTISPECIES: peptidylprolyl isomerase [Klebsiella]

MKVAKDLVVSLAYQVRTEDGVLVDESPVSAPLDYLHGHGSLISGLENALDGHEVGDKFDVAVGANDAYGQ

YDENLVQRVPKDVFMGVDELQVGMRFLAETDQGPVPVEITEVEDDHVVVDGNHMLAGQNLKFNVEVVAIR

EATAEELEHGHVHGAHGHDHDHDHGHDGCCGGHGHDHGHDHGKGGCGGHGGCGCH

>WP\_002920136.1 MULTISPECIES: SlyX family protein [Enterobacteriaceae]

MHDSTLETRLAELESRLAFQEITIEDLNKTVTAHEIEMAKMREHMRLMIEKLKATQPSHIASQAEETPPP

HY

>WP\_004150030.1 MULTISPECIES: FKBP-type peptidyl-prolyl cis-trans isomerase [Klebsiella]

MKSLFKVTLLATTMAVALNAPLTFAADTATKAAPAAESKSAFKNDDQKSAYALGASLGRYMENSLKEQEK

LGIKLDKSQLIAGVQDAFADKSKLSDQEIEQTLQAFETRVKTAAQQKMEKDATENEAKGKAFRDNFAKEK

GVKTSKTGLLYKVEKEGAGDAPKDSDTVVVNYKGTLIDGKEFDNSYTRGEPLSFRLDGVIPGWTEGLKNI

KKGGKIKLVIPPDLAYGKTGVPGIPANSTLVFDVELLDIKPAPKADAQPEAAGDAKAADAKADAKK

>WP\_002920130.1 MULTISPECIES: transcriptional regulator [Gammaproteobacteria]

MSRSLLTNETSELDLLDQRPFDQTDFDILKSYEAVVDGLAMLIGSHCEIVLHSLQDLKCSAIRIANGEHT

GRQIGSPITDLALRMLHDMTGADSSVSKCYFTRAKSGVLMKSVTIAIRNRDHRVIGLLCINMNLDVPFSQ

IMSTFIPPETPEVNSPVNFASSVDDLVAQTLEFTIEEVNADRSVSNNAKNRQIVLNLYEKGIFDIKDAIN

QVADRLNISKHTVYLYIRQFKSGDFQGLDK

>WP\_016528954.1 sulfurtransferase complex subunit TusD [Klebsiella pneumoniae]

MRFALTVTGPAYGTQQASSAWQFAQAVLQEGHELACVFFYREGVLNANQLTAPASDEFDLVRGWQSLHDE

HGVALHICVAAALRRGVTDEREAQQLALPGHNLQPGFSLSGLGALAEAALTCDRMVQF

>WP\_004174061.1 MULTISPECIES: sulfurtransferase complex subunit TusC [Klebsiella]

MKRVAFVFSSAPHGSAAGREGLDALLATSALTDDIGVFFVGDGVFQLLPEQRPGAVLARDYIATFKLLSL

YDIDQCWLCADSARERGLDPATPWVVDVECLAPDALRARLHEFDVILRF

>WP\_002920119.1 MULTISPECIES: sulfurtransferase complex subunit TusB [Enterobacteriaceae]

MLHTLSVSPWHADIAAMLRLMEHGDDLVLLSDGVTAAIADGRFLEILQSAPITLYVLQDDVDARGLAGQI

ADSVGRVSYTDFVRLTVKHAGQLAW

>WP\_002920115.1 MULTISPECIES: 30S ribosomal protein S12 [Enterobacteriaceae]

MATINQLVRKPRARKVAKSNVPALEACPQKRGVCTRVYTTTPKKPNSALRKVCRVRLTNGFEVTSYIGGE

GHNLQEHSVILIRGGRVKDLPGVRYHTVRGALDCSGVKDRKQARSKYGVKRPKA

>WP\_002920113.1 MULTISPECIES: 30S ribosomal protein S7 [Enterobacteriaceae]

MPRRRVIGQRKILPDPKFGSELLAKFVNILMVDGKKSTAETIVYSALETLAQRSGKSELEAFEVALENVR

PTVEVKSRRVGGSTYQVPVEVRPVRRNALAMRWIVEAARKRGDKSMALRLANELTDAADNKGTAVKKRED

VHRMAEANKAFAHYRW

>WP\_002920103.1 MULTISPECIES: elongation factor G [Klebsiella]

MARTTPIARYRNIGISAHIDAGKTTTTERILFYTGVNHKIGEVHDGAATMDWMEQEQERGITITSAATTA

FWSGMAKQYEPHRVNIIDTPGHVDFTIEVERSMRVLDGAVMVYCAVGGVQPQSETVWRQANKYKVPRIAF

VNKMDRMGANFLKVVGQIKTRLGANPVPLQLAIGAEEGFTGVVDLVKMKAINWNDADQGVTFEYEDIPAD

MQDLADEWHQNLIESAAEASEELMEKYLGGEELTEEEIKKALRQRVLNNEIILVTCGSAFKNKGVQAMLD

AVIDYLPSPVDVPAINGILDDGKDTPAERHASDDEPFSALAFKIATDPFVGNLTFFRVYSGVVNSGDTVL

NSVKAARERFGRIVQMHANKREEIKEVRAGDIAAAIGLKDVTTGDTLCDPDAPIILERMEFPEPVISIAV

EPKTKADQEKMGLALGRLAKEDPSFRVWTDEESNQTIIAGMGELHLDIIVDRMKREFNVEANVGKPQVAY

REAIRAKVTDIEGKHAKQSGGRGQYGHVVIDMYPLEPGSNPKGYEFINDIKGGVIPGEYIPAVDKGIQEQ

LKAGPLAGYPVVDMGIRLHFGSYHDVDSSELAFKLAASIAFKEGFKKAKPVLLEPIMKVEVETPEENTGD

VIGDLSRRRGMLRGQESEVTGVKIHAEVPLSEMFGYATQLRSLTKGRASYTMEFLKYDDAPNNVAQAVIE

ARGK

>WP\_004152415.1 MULTISPECIES: bacterioferritin-associated ferredoxin [Enterobacterales]

MYVCLCNGVSDKKIRQVVRQFQPQSFQQLRKFVPVGNQCGKCVRAAREVMEDELTTMPEFKEIA

>WP\_002919971.1 MULTISPECIES: bacterioferritin [Klebsiella]

MKGDVKIISYLNKLLGNELVAINQYFLHARMFKNWGLMRLNDIEYHESIDEMKHADKYIERILFLEGIPN

LQDLGKLGIGEDVEEMLRSDLRLELEGAQNLREAIAYADSVHDYVSRDMMIEILADEEGHIDWLETELDL

IGKIGLQNYLQSQIKVSD

>WP\_042941280.1 A24 family peptidase [Klebsiella pneumoniae]

MLAALPFLLCYSGLTVALCHQDLRHGLLPDRYTCPLLWSGLLFYLCLAPHQLHDAVRGAIAGYLSLAAIY

WLYRGIRGYEGLGYGDIKYLAALGAWHGWRLLPQLVLVASLLAGIAWAGAGLYASCGGRSKWRRSNPLPF

GPFLAAAGFWCGWQTLASLTL

>WP\_001181005.1 MULTISPECIES: 30S ribosomal protein S10 [Bacteria]

MQNQRIRIRLKAFDHRLIDQSTAEIVETAKRTGAQVRGPIPLPTRKERFTVLISPHVNKDARDQYEIRTH

KRLVDIVEPTEKTVDALMRLDLAAGVDVQISLG

>WP\_002919796.1 MULTISPECIES: 50S ribosomal protein L3 [Bacteria]

MIGLVGKKVGMTRIFTEDGVSIPVTVIEVEANRVTQVKDLANDGYRAIQVTTGAKKANRVTKPEAGHFAK

AGVEAGRGLWEFRLADGEEFTVGQNISVELFADVKKVDVTGTSKGKGFAGTVKRWNFRTQDATHGNSLSH

RVPGSIGQNQTPGKVFKGKKMAGQLGNERVTVQSLDVVRVDAERNLLLVKGAVPGATGSDLIVKPAVKA

>WP\_002919794.1 MULTISPECIES: 50S ribosomal protein L4 [Bacteria]

MELVLKDAQSALTVSETTFGRDFNEALVHQVVVAYAAGARQGTRAQKTRAEITGSGKKPWRQKGTGRARS

GSIKSPIWRSGGVTFAARPQDHSQKVNKKMYRGALKSILSELVRQDRLIVVEKFSVEAPKTKLLAQKLKD

MALEDVLIITGELDENLFLAARNLHKVDVRDANGIDPVSLIAFDKVVMTADAVKQVEEMLA

>WP\_000617546.1 MULTISPECIES: 50S ribosomal protein L23 [Bacteria]

MIREERLLKVLRAPHVSEKASTAMEKTNTIVLKVAKDATKAEIKAAVQKLFEVEVEVVNTLVVKGKVKRH

GQRIGRRSDWKKAYVTLKEGQNLDFVGGAE

>WP\_002919786.1 MULTISPECIES: 50S ribosomal protein L2 [Bacteria]

MAVVKCKPTSPGRRHVVKVVNPELHKGKPFAPLLEKNSKSGGRNNNGRITTRHIGGGHKQAYRIVDFKRN

KDGIPAVVERLEYDPNRSANIALVLYKDGERRYILAPKGLKAGDQIQSGVDAAIKAGNTLPMRNIPVGST

VHNVEMKPGKGGQLARSAGTYVQIVARDGAYVTLRLRSGEMRKVEADCRATLGEVGNAEHMLRVLGKAGA

ARWRGVRPTVRGTAMNPVDHPHGGGEGRNFGKHPVSPWGLQTKGKKTRSNKRTDKFIVRRRSK

>WP\_001138115.1 MULTISPECIES: 30S ribosomal protein S19 [Bacteria]

MPRSLKKGPFIDLHLLKKVEKAVESGDKKPLRTWSRRSTIFPNMIGLTIAVHNGRQHVPVFVSDEMVGHK

LGEFAPTRTYRGHAADKKAKKK

>WP\_002919773.1 MULTISPECIES: 50S ribosomal protein L22 [Bacteria]

METLAQHRHARSSAQKVRLVADLIRGKKVSQALDILTYTNKKAAVLVKKVLESAIANAEHNDGADIDDLK

VAKIFVDEGPSMKRIMPRAKGRADRILKRTSHITVVVSDR

>WP\_002919766.1 MULTISPECIES: 30S ribosomal protein S3 [Bacteria]

MGQKVHPNGIRLGIVKPWNSTWFANTKEFADNLDSDFKVRQFLTKELAKASVSRIVIERPAKSIRVTIHT

ARPGIVIGKKGEDVEKLRKVVADIAGVPAQINIAEVRKPELDAKLVADSITSQLERRVMFRRAMKRAVQN

AMRLGAKGIKVEVSGRLGGAEIARTEWYREGRVPLHTLRADIDYNTSEAHTTYGVIGVKVWIFKGEILGG

MAAVEQPEPAAQPKKQQRKGRK

>WP\_002919759.1 MULTISPECIES: 50S ribosomal protein L16 [Bacteria]

MLQPKRTKFRKVHKGRNRGLAQGTDVSFGTFGLKAVGRGRLTARQIEAARRAMTRAVKRQGKIWIRVFPD

KPITEKPLEVRMGKGKGNVEYWVALIQPGKVLYEMDGVPEELAREAFGLAAAKLPIKTTFVTKTVM

>WP\_002919754.1 MULTISPECIES: 50S ribosomal protein L29 [Bacteria]

MKAKELREKSVEELNAELLNLLREQFNLRMQAASGQLQQTHLLKQVRRDVARVKTLLTQKAGA

>WP\_002919751.1 MULTISPECIES: 30S ribosomal protein S17 [Bacteria]

MTDKIRTLQGRVVSDKMEKSIVVAIERMVKHPVYGKFIKRTTKLHVHDENNECGIGDKVEIRECRPLSKT

KSWTLVRVVEKAVL

>WP\_002919748.1 MULTISPECIES: 50S ribosomal protein L14 [Bacteria]

MIQEQTMLNVADNSGARRVMCIKVLGGSHRRYAGVGDIIKITIKEAIPRGKVKKGDVLKAVVVRTKKGVR

RPDGSVIRFDGNACVILNNNSEQPIGTRIFGPVTRELRTEKFMKIISLAPEVL

>WP\_000729185.1 MULTISPECIES: 50S ribosomal protein L24 [Bacteria]

MAAKIRRDDEVIVLTGKDKGKRGKVKNVLSSGKVIVEGINLVKKHQKPVPALNQPGGIVEKEAAIQVSNV

AIFNAATGKADRVGFRFEDGKKVRFFKSNSETIK

>WP\_001096200.1 MULTISPECIES: 50S ribosomal protein L5 [Bacteria]

MAKLHDYYKDEVVKKLMTEFNYNSVMQVPRVEKITLNMGVGEAIADKKLLDNAAADLAAISGQKPLITKA

RKSVAGFKIRQGYPIGCKVTLRGERMWEFFERLITIAVPRIRDFRGLSAKSFDGRGNYSMGVREQIIFPE

IDYDKVDRVRGLDITITTTAKSDEEGRALLAAFDFPFRK

>WP\_002919667.1 MULTISPECIES: 30S ribosomal protein S14 [Bacteria]

MAKQSMKAREVKRVALADKFFAKRAELKAIISDVNATDEDRWNAVLKLQTLPRDSSPSRQRNRCRQTGRP

HGFLRKFGLSRIKVREAAMRGEIPGLKKASW

>WP\_002919665.1 MULTISPECIES: 30S ribosomal protein S8 [Bacteria]

MSMQDPIADMLTRIRNGQAANKAAVTMPSSKLKVAIANVLKEEGFIEDFKVEGDTKPELELTLKYFQGKA

VVESIQRVSRPGLRIYKKKDELPKVMAGLGIAVVSTSKGVMTDRAARQAGLGGEIICYVA

>WP\_002919662.1 MULTISPECIES: 50S ribosomal protein L6 [Bacteria]

MSRVAKAPVVVPAGVDVKINGQVITIKGKNGELTRTLNDAVEVKHADNALTFGPRDGYADGWAQAGTARA

LLNSMVIGVTEGFTKKLQLVGVGYRAAVKGNVVNLALGFSHPVDHQLPAGITAECPTQTEIVLKGADKQV

IGQVAADLRAYRRPEPYKGKGVRYADEVVRTKEAKKK

>WP\_000358960.1 MULTISPECIES: 50S ribosomal protein L18 [Bacteria]

MDKKSARIRRATRARRKLQELGATRLVVHRTPRHIYAQVIAPNGSEVLVAASTVEKAIAEQLKYTGNKDA

AAAVGKAVAERALEKGIKDVSFDRSGFQYHGRVQALADAAREAGLQF

>WP\_002919545.1 MULTISPECIES: 30S ribosomal protein S5 [Bacteria]

MAHIEKQAGELQEKLIAVNRVSKTVKGGRIFSFTALTVVGDGNGRVGFGYGKAREVPAAIQKAMEKARRN

MINVALNHGTLQHPVKGTHTGSRVFMQPASEGTGIIAGGAMRAVLEVAGVRNVLAKAYGSTNPINVVRAT

IDGLENMKSPDMVAAKRGKSVEEILGK

>WP\_001140434.1 MULTISPECIES: 50S ribosomal protein L30 [Bacteria]

MAKTIKITQTRSAIGRLPKHKATLLGLGLRRIGHTVEREDTPAVRGMVNAVSFMVKVEE

>WP\_002919516.1 MULTISPECIES: 50S ribosomal protein L15 [Bacteria]

MRLNTLSPAEGSKKAGKRLGRGIGSGLGKTGGRGHKGQKSRSGGGVRRGFEGGQMPLYRRLPKFGFTSRK

AMITAEIRLSDLAHVEGDVVDLNALKAANIIGVQIEFAKVILSGEVTRPVTVRGLRVTKGARAAIEAAGG

KIEE

>WP\_002919515.1 MULTISPECIES: preprotein translocase subunit SecY [Bacteria]

MAKQPGLDFQSAKGGLGELKRRLLFVVGALIVFRIGSFIPIPGIDAAVLAKLLEQQRGTIIEMFNMFSGG

ALSRASIFALGIMPYISASIIVQLLTVVYQPLAELKKEGESGRRKISQYTRYGTLVLAIFQSIGIATGLP

NMPGMQGLVINPGFAFYFTAVVSLVTGTMFLMWLGEQITERGIGNGISIIIFAGIVAGLPPAIAHTIEQA

RQGDLHFLLLLLVAVLVFAVTFFVVFVERGQRRIVVNYAKRQQGRRVYAAQSTHLPLKVNMAGVIPAIFA

SSIILFPATITSWFGGGTGWNWLTTISLYLQPGQPLYVLLYASAIIFFCFFYTALVFNPRETADNLKKSG

AFVPGIRPGEQTAKYIDKVMTRLTLVGALYITFICLIPEFMRDAMKVPFYFGGTSLLIVVVVIMDFMAQV

QTLMMSSQYESALKKANLKGYGR

>WP\_000868187.1 MULTISPECIES: 50S ribosomal protein L36 [Bacteria]

MKVRASVKKLCRNCKIVKRDGVIRVICSAEPKHKQRQG

>WP\_002919259.1 MULTISPECIES: 30S ribosomal protein S13 [Bacteria]

MARIAGINIPDHKHTVIALTAIFGIGKTRSKAICAETGIAENVKISELSEEQIDILREAVGKFVVEGDLR

REITLSIKRLMDLGCYRGLRHRRGLPVRGQRTKTNARTRKGPRKPIKK

>WP\_002919257.1 MULTISPECIES: 30S ribosomal protein S11 [Bacteria]

MAKAPIRARKRVRKQVSDGVAHIHASFNNTIVTITDRQGNALGWATAGGSGFRGSRKSTPFAAQVAAERC

AEAVKEYGIKNLEVMVKGPGPGRESTIRALNAAGFRITNITDVTPIPHNGCRPPKKRRV

>WP\_002919224.1 MULTISPECIES: 30S ribosomal protein S4 [Bacteria]

MARYLGPKLKLSRREGTDLFLKSGVRAIDTKCKIEQAPGQHGARKPRLSDYGVQLREKQKVRRMYGVLER

QFRNYYKEAARLKGNTGENLLALLEGRLDNVVYRMGFGATRAEARQLVSHKAIMVNGRVVNIASYQVKAN

DVVSIREKAKKQSRVKAALELAEQREKPTWLEVDAGKMEGTFKRQPERSDLSADINEHLIVELYSK

>WP\_002919219.1 MULTISPECIES: DNA-directed RNA polymerase subunit alpha [Bacteria]

MQGSVTEFLKPRLVDIEQVSSTHAKVTLEPLERGFGHTLGNALRRILLSSMPGCAVTEVEIDGVLHEYST

KEGVQEDILEILLNLKGLAVRVQGKDEVILTLNKSGIGPVTAADITHDGDVEIVKPQHVICHLTDENAAI

SMRIKVQRGRGYVPASARIHSEEDERPIGRLLVDACYSPVERIAYNVEAARVEQRTDLDKLVIEMETNGT

IDPEEAIRRAATILAEQLEAFVDLRDVRQPEVKEEKPEFDPILLRPVDDLELTVRSANCLKAEAIHYIGD

LVQRTEVELLKTPNLGKKSLTEIKDVLASRGLSLGMRLENWPPASIADE

>WP\_002919206.1 MULTISPECIES: 50S ribosomal protein L17 [Bacteria]

MRHRKSGRQLNRNSSHRQAMFRNMAGSLVRHEIIKTTLPKAKELRRVVEPLITLAKTDSVANRRLAFART

RDNEIVAKLFNELGPRFASRAGGYTRILKCGFRAGDNAPMAYIELVDRAEPKAEAAAE

>WP\_002919204.1 MULTISPECIES: DUF1992 domain-containing protein [Klebsiella]

MWLLDQWAERHILDAQTKGEFDNLPGSGEPLTLDDDSHVPAELRAGYRLLKNAGCLPPELEQRKEALALA

DLLNGVRQDDPRHAELSKRLALLELKLRQAGLNTDFLRGEYADALLQKINQE

>WP\_004185894.1 MULTISPECIES: Zn(2+)-responsive transcriptional regulator [Klebsiella]

MYRIGELAKLADVTPDTIRYYEKQQMMDHDIRTEGGFRLYSDNDLQRLRFIRYARQLGFTLEAIRELLSI

RIDPEHHTCQESKGIVQARLSEVEARIKELQTMRRSLQRLNDACCGTAHSSVYCSILEALEQGASNGNGG

R

>WP\_016530588.1 alternative ribosome-rescue factor A [Klebsiella pneumoniae]

MSRYQHTKGQIKDNAIEALLHDPLFRQRVEKNKKGKGSYQRKDKHAGRVDREASGKQANRFFTTGLLLSL

LIKNGCSVLSADREFRSAELLL

>WP\_004145325.1 MULTISPECIES: large-conductance mechanosensitive channel protein MscL [Enterobacteriaceae]

MSFLKEFREFAMRGNVVDLAVGVIIGAAFGKIVSSLVADIIMPPLGLLIGGIDFKQFAVTLRDAQGDVPA

VVMHYGVFIQNVFDFIIVAFAIFMAIKLMNKLNRKKEEAPAAPPAPSKEEVLLSEIRDLLKEQNNRS

>WP\_002919153.1 MULTISPECIES: Trk system potassium transporter TrkA [Klebsiella]

MKIIILGAGQVGGTLAENLVGENNDITLVDTNGDRLRSLQDKFDLRVVQGHGSHPRVLREAGADDADMLV

AVTSSDETNMVACQVAYSLFNTPNRIARIRAPDYVRDAEKLFNSEAVPIDHLIAPEQLVIDNIHRLIEYP

GALQVVNFAEGKVSLAVVKAYYGGPLVGNALSTMREHMPHIDTRVAAIFRHDRPIRPQGSTIVEAGDEVF

FIAASQHIRAVMSELQRLEKPYKRIMLVGGGNIGAGLAHKLEKDYSVKLIERNQQRAAELAEKLQHTIVF

YGDASDQELLAEEHIDQVDLFIAVTNDDEANIMSAMLAKRMGAKKVMVLIQRRAYVDLVQGSVIDIAISP

QQATISALLSHVRKADIVGVSSLRRGVAEAIEAVAHGDESTSRVVGRSIDEIKLPPGTIIGAVVRGNDVM

IANNNLRIEQGDHVIMFLTDKKFISDVERLFQPSPFFL

>WP\_004150007.1 MULTISPECIES: methionyl-tRNA formyltransferase [Klebsiella]

MSQSLRIIFAGTPDFAARHLDALLSSEHQVVGVFTQPDRPAGRGKKLMPSPVKVLAEAHNLPVFQPSSLR

PQDNQRLVADLGADIMVVVAYGLILPKAVLEMPRLGCINVHGSLLPRWRGAAPIQRSLWAGDSETGVTIM

QMDVGLDTGDMLYKLSCPITAEDTSGSLYDKLAELGPQGLLATLAQLANGTARPEVQDESLVCHAEKLSK

EEARIDWSLSAAQLERCIRAFNPWPMSWLEIDGQPVKVWRASVIAEAAHAEPGTIVAATKQGIQVATGDG

ILSLESLQPAGKKAMSAQDLLNSRREWFIPGTRLA

>WP\_004150006.1 MULTISPECIES: peptide deformylase [Klebsiella]

MAVLQVLHIPDERLRKVAEPVKEVNAEIQRIVDDMFDTMYAEEGIGLAATQVDIHQRIIVIDVSENREEQ

LVLINPEMLEKDGETGIEEGCLSIPEQRALVPRAEKVKIRALDRNGKPFELEADGLLAICIQHEMDHLVG

KLFIDYLSPLKQQRIRQKVEKLDRLRSRA

>WP\_016530584.1 MULTISPECIES: DNA-protecting protein DprA [Klebsiella]

MTPDEIWLRLMKVSSLYGDRMVEIAQRLCAAASVDREALHAVGMTAAQAKLFFRLDEHELDETRRWLEQP

DHHLLRGDDPRYPLRLKAIADYPGALLVSGGLALLHSAQLAVIGSRSHSWYGACWGKLFSETLAHKGITI

TSGLALGIDGVAHRGALAAEGKTIAVLGNGLSQVYPRRHATLARQIIDNGGTLVSEFPLVTPPLPAHFPR

RNRIISGLSLGVLVIEAALRSGSLVTVRCALEQGRDVFALPGPIGNPGSEGPHWLIKQGAVPVTSPEDIV

EYWHNELAWLTDTSDSINICVDQPSVALPFPELLANVGDEVTPVDVVAERAGQSVPVTVAQLLELELAGW

IAAVPGGYVRLRRASHVRRTHVFV

>WP\_002919137.1 MULTISPECIES: DUF494 family protein Smg [Klebsiella]

MFDVLMYLFETYIHSEAEMRVDQDKLTRDLTDAGFEREDIYNALMWLEKLADYQEGLVEPMQLASDPLSL

RVYTEEECQRLDASCRGFLLFLEQIQVLNLETREMVIERVLALDTAEFELEDLKWVILMVLFNIPGCENA

YQQMEELLFEVNEGMLH

>WP\_004145330.1 MULTISPECIES: topoisomerase DNA-binding C4 zinc finger domain-containing protein [Klebsiella]

MTKSALFSVRKNEPCPQCGAELVIRSGKHGPFLGCSHYPDCDYIRPLKSQADGHIVKVLEGQECPSCGAV

MVLRQGRFGMFIGCSRYPECEHTELIDKPDETAIACPQCGQGHLVQRRSRFGKTFHSCDRYPDCQFVINF

KPVAGECPECHYPLLIEKKTAQGLRRFCASKQCGKPIPAE

>WP\_002919132.1 MULTISPECIES: L-threonylcarbamoyladenylate synthase type 1 TsaC [Klebsiella]

MNNNLPSEAVAHAVAVLKNEHVIAYPTEAVFGVGCDPDSETAVMRLLELKQRPVEKGLILIAASFEQLKP

YIDDSRLSDSQREAIFSCWPGPVTFVFPARPETPRWLTGRFDSLAVRVTNHPLVIELCEAYGKPLVSTSA

NLTGQPPCRTTAEVHAQFGDSFPVVDGATGGRQNPSEIRDALTGELFRQG

>WP\_002919126.1 MULTISPECIES: shikimate dehydrogenase [Klebsiella]

METYAVFGNPIAHSKSPAIHQLFARQLGITHPYGRVLAPLDDFVSSLNQFFAEGGKGANVTVPFKEEAFA

RADELTERAALAGAVNTLKRLEDGRLLGDNTDGIGLLSDLERLGFIKPRQRILLVGAGGASRGVLLPLLS

LGCAVTIVNRTYSRARELATLFAHTGSVSAREMDTLSGETFDLIVNATSSGIDGDVPAIPASIVNADVYC

YDMFYQKGPTPFLHWCQQYGAVHCADGLGMLVAQAAHAVLLWHGVLPAIAPVIETLQQELNA

>WP\_002919125.1 MULTISPECIES: DUF1488 domain-containing protein [Enterobacteriaceae]

MNQAIQFPDRESWDAERQGVVFPALVNGMQLTCAISGQILQQRFGAEGPAQWLAAFQEHRWDLEEEAEAL

IRDGQEDAQGWIWLS

>WP\_002919123.1 MULTISPECIES: gamma carbonic anhydrase family protein [Klebsiella]

MSAQLRPYKAFFPQIGLRVMIDASSVVIGDVRIADDVSVWPLVAIRGDVNYVSIGQRSNIQDGSVLHVTH

KSSYKPEGNPLIIGEDVTVGHKVMLHGCTIGNRVLVGMGSILLDGVVVGDDVMIGAGSLVPQNKQLESGY

LYFGNPVKQIRPLTEAEREGLKYSANNYVKWKNEYLDQDNQIQP

>WP\_002919103.1 MULTISPECIES: membrane protein [Enterobacterales]

MKKYLIVALLASLLAGCAHDSPCVPVYDSQGRLVHTNTCMKGTTEDNWETAGAIAGGAAAVAGLTLGIVA

LTR

>WP\_016529116.1 efflux RND transporter permease subunit [Klebsiella pneumoniae]

MSKFFIHRPVFAWVLAIIMMIAGGLAILQLPIAQYPTIAPPAVAISATYPGADAQTVQDTVTQVIEQNMN

GIDNLMYMSSTSDSAGSVTITLTFKSGTDPDIAQVQVQNKLQLATPLLPQEVQQQGISVEKSSSSFLLVA

GFISDNPTTTQDDISDYVASNVKDPISRLNGVGDVQLFGAQYAMRVWLDGNLLNKYNLTPVDVINALQVQ

NDQIAAGQLGGTPALKGQQLNASIIAQTRLKDPQEFGKVTLRVNADGSVVHLKDVARIELGGENYNVVAR

INGKPASGLGIKLATGANALDTATAIKAKLAELQPYFPQGMKVVYPYDTTPFVKISIHEVVKTLFEAIIL

VFLVMYLFLQNMRATLIPTIAVPVVLLGTFAVLSMFGYSINTLPMFGMVLAIGLLVDDAIVVVENVERVM

VEEKLSPKEATEKSMSQIQGALVGIAMVLSAVFVPMAFFGGSTGAIYRQFSITIVSAMALSVLVALVLTP

ALCATLLKPASAEHHEKKGFFGWFNARFDQSVNHYTNSVSGILRGTGRYLVIYLLIVVGMAVLFMRLPTS

FLPDEDQGVFLTMIQLPSGATQERTQKVLDTVTDYYLHNEKANVESVFTVNGFSFSGQGQNSGMAFVSLK

PWEARSGDKNSVESIIKRATVAFSQIKDAMVFPFNMPAIIELGTATGFDFELIDQGGLGHTALTQARNQL

LGMVKQHPDQLVRVRPNGLEDTPQFKLDVDQEKAQALGVSLSDINETISAALGGYYVNDFIDRGRVKKVY

VQADAHFRMLPSDINNMYVRSANGEMVPFSAFVTSRWIYGSPRLERYNGLPSMEILGEASPGKSTGEAMA

LMETLASKLPSGIGYDWTGMSYQERLSGNQAPALYAISLIVVFLCLAALYESWSIPFSVMLVVPLGVIGA

LLAATLRGLNNDVYFQVGLLTTIGLSAKNAILIVEFAKDLMEKEGKGIIEATLEASRMRLRPILMTSLAF

ILGVMPLVISHGAGSGAQNAVGTGVMGGMLTATLLAIFFVPVFFVVVRRRFTRHAE

>WP\_002919101.1 MULTISPECIES: efflux RND transporter periplasmic adaptor subunit [Klebsiella]

MTTHARVTLLSGLIISALLLTGCDNSDNQQPHAQAPQVTVHVVNSAPLSVTTELPGRTSAFRVAEVRPQV

SGIILKRNFVEGSDVEAGQSLYQIDPATYQAAWNSAKGDEAKAEAAAAIAHLTVKRYVPLLGTKYISQQE

YDQAVATARQADADVIATKAAVETARINLAYTKVTSPISGRIGKSSVTEGALVTNGQSDALATVQQLDPI

YVDVTESSNDFMRLKQESLQRGGDTKSVELVMENGQAYPLKGSLQFSDVTVDESTGSITLRAIFPNPQHV

LLPGMFVRARIDEGVDPQAILVPQQGVTRTPRGDASVMLVNDKNQVETREVVATQAVGDKWLITSGLKPG

DKVIVSGLQKVRPGVTVKAEAERAAPAVQ

>WP\_016530888.1 acrEF/envCD operon transcriptional regulator [Klebsiella pneumoniae]

MARKTREEAQRTRQLLIESAIQQFALRGVTNTTLTDIADAAGVTRGAVYWHFASKTELFNEMWQQQPPLR

DLIQPSQAIEYEQEPLNALRERFIAGLRYIAANPRQRALMQILYQRCEFSSDMLSEYEIRQRIGFNYSLI

GGILQCCVRNNILPAETNIEMILIVLHSAFSGLIKNWLLDPQRFDLYQQAPALVDNIMAVVCAARLSGGS

ALRLVNQ

>WP\_000462905.1 MULTISPECIES: DNA-binding transcriptional regulator Fis [Bacteria]

MFEQRVNSDVLTVSTVNSQDQVTQKPLRDSVKQALKNYFAQLNGQDVNDLYELVLAEVEQPLLDMVMQYT

RGNQTRAALMMGINRGTLRKKLKKYGMN

>WP\_004144972.1 MULTISPECIES: tRNA dihydrouridine synthase DusB [Klebsiella]

MRIGHHQLRNRLIAAPMAGITDRPFRTLCYEMGAGLTVSEMMSSNPQVWESDKSRLRMVHIDEPGIRTVQ

IAGSVPEEMAAAARINVESGAQIIDINMGCPAKKVNRKLAGSALLQYPDQVKSILTAVVNAVDVPVTLKI

RTGWEPEHRNCVEIAQLAEECGIQALTIHGRTRACLFNGDAEYDSIRAVKQKVSIPIIANGDITDPLKAR

AVLDYTGADALMIGRAAQGRPWIFREIQHYLDTGELLPPLPLAEVKRLLCAHVRELHDFYGQAKGYRIAR

KHVSWYLQEHAPDDQFRRTFNAIEDASEQLEALEAYFENFA

>WP\_004144971.1 MULTISPECIES: 50S ribosomal protein L11 methyltransferase [Klebsiella]

MPWIQLKLNTTGANAEDLSDALMEAGSVSITFQDTHDTPVFEPLPGETRLWGDTDVIGLFDAETDMKAVV

AQLEQHPLLGAGFAHKIEQLEDKDWEREWMDNFHPMRFGERLWICPSWRDVPDENAVNVMLDPGLAFGTG

THPTTSLCLQWLDGLDLNGKTVIDFGCGSGILAIAALKLGAAKAIGIDIDPQAIQASRDNAQRNGVSERL

ELYLPQDQPESMKADVVVANILAGPLRELAPLISVLPVSGGLLGLSGILASQAESVCEAYADLFTLDPVV

EKEEWCRITGRKN

>WP\_004181435.1 MULTISPECIES: sodium/pantothenate symporter [Klebsiella]

MQFEVIIPLIAYLVVVFGLSLYAMRKRASGSFLNEYFLGSRSMGGFVLAMTLTATYISASSFIGGPGAAY

KYGLGWVLLAMIQLPAIWLSLGVLGKKFAILARRYNAVTLNDMLFARYQSRLLVWLASLSLLVAFVGAMT

VQFIGGARLLETAAGIPYDTGLLIFGVSIALYTAYGGFRASVLNDTMQGMVMLIGTIVLLVGVIHAAGGV

GHAVETLQSIDVKLVSPQGAEDILSPTFMASFWVLVCFGVIGLPHTAVRCISYKDSKAVHRGIIIGTIVV

AILMFGMHLAGALGRAVIPDLTVPDLVIPTLMVKVLPPFAAGIFLAAPMAAIMSTINAQLLQSSATIIKD

LYLNWRPDQATNEKRLKRMSAGITLLLGVLLLLAAWRPPEMIIWLNLLAFGGLEAVFLWPLVLGLYWERA

NAAGALSAMIVGGVLYAVLATLKVQFLGFHPIVPALLLSLLAFVAGNRFGRPAPQPPILTTDK

>WP\_002918740.1 MULTISPECIES: YhdT family protein [Klebsiella]

MDKRFVQAHKEARWALWLTLLYLAAWLAAAYLPGVAIGFTGLPHWFEMACLLVPLLFILLCWAMVKLIFR

DISLEDDDAV

>WP\_002918738.1 MULTISPECIES: acetyl-CoA carboxylase biotin carboxylase subunit [Klebsiella]

MLDKIVIANRGEIALRILRACKELGIKTVAVHSTADRDLKHVLLADETVCIGPAPSVKSYLNIPAIISAA

EITGAVAIHPGYGFLSENANFAEQVERSGFIFIGPKADTIRLMGDKVSAITAMKKAGVPTVPGSDGPLGD

DMDANRAHAKRIGYPVIIKASGGGGGRGMRVVRSDAELAQSISMTKAEAKAAFNNDMVYMEKYLENPRHI

EIQVLADGQGNAIYLAERDCSMQRRHQKVVEEAPAPGITPELRRYIGERCAKACVDIGYRGAGTFEFLFE

NGEFYFIEMNTRIQVEHPVTEMITGVDLIKEQLRIAAGQPLSIKQDEVVVRGHAVECRINAEDPNTFLPS

PGKITRFHAPGGFGVRWESHIYAGYTVPPYYDSMIGKLICYGESRDVAIARMKNALQELIIDGIKTNVDL

QMRIMSDENFQHGGTNIHYLEKKLGLQEK

>WP\_002918736.1 MULTISPECIES: acetyl-CoA carboxylase biotin carboxyl carrier protein [Klebsiella]

MDIRKIKKLIELVEESGISELEISEGEESVRISRSAPAASYPVMQQAYAAPMMQPQAPAAATAAPAAAAE

APAKAEISGHIVRSPMVGTFYRTPSPDAKAFVEVGQKVNVGDTLCIVEAMKMMNQIEADKAGVVKAILIE

SGQPVEFDEPLVVIE

>WP\_004174104.1 MULTISPECIES: type II 3-dehydroquinate dehydratase [Klebsiella]

MAVKFHILLLNGPNINMLGTREPEKYGPLTLAEIVNRLTSEAAALNVSLDHLQSNAEHALIDRIHQAKDN

VDYILINPAAFTHTSVAIRDALLAVNIPFIEIHLSNVHAREPFRQHSYLSDVAAGVICGLGADGYSYALQ

TAVKRLSQSH

>WP\_016529298.1 protein-methionine-sulfoxide reductase heme-binding subunit MsrQ [Klebsiella pneumoniae]

MRFTVKQIVWLKVLLHLAGFLPLVWLFWAGHQGYLSADPAKDIQHFTGRMALKFLLATLLVSPLARYAKQ

PLSIRVRRLLGLWCFAWATLHLSSYTLLELGINNLALLGSEIITRPYLTLGMISWAILLALAVTSTQAMQ

RKLGRRWQLLHNFVYLVAILAPIHYLWSVKIVSPQPVIYALLAAGLLTWRYKKFRQWWRSIR

>WP\_004211677.1 MULTISPECIES: protein-methionine-sulfoxide reductase catalytic subunit MsrP [Klebsiella]

MKRKKLTEADVTAESVFMLKRRQVLKMLGISATALSLPAAAQADLLDWFKGNDRPPAPAGKALEFAKPAE

WQANLTLTPEDKVAGYNNFYEFGLDKADPAANAGSLRTDPWTLTIGGEVAKPLTLDHDDLTKRFPLEERI

YRMRCVEAWSMVVPWVGFPLHKLLALVEPTSSARYVAFKTLYAPDQMPGQKDRFIGGGLAYPYVEGLRLD

EAMHPLTLLTVGVYGKALPPQNGAPVRLTVPWKYGFKGIKSIVSIELTRERPPTTWNLAAPDEYGFFANV

NPHVDHPRWSQASERFIGAGGVLDVKRQPTLLFNGYADEVASLYRGMNLRENF

>WP\_004144963.1 MULTISPECIES: hypothetical protein [Klebsiella]

MRRRRGFVILRLKLKRFWRRPQAGDDWQIFSANYTRYRHTFTDNTHSIARLAIFDSMRRALKG

>WP\_002918686.1 MULTISPECIES: RNase E specificity factor CsrD [Klebsiella]

MRLTTKFSAFITLLTSLTIFVTLIGASLSFYNGIENKVENRVQAVATMLDNRLITTSFDKLEPQLDELMT

PIEIVHIDFMLNGKPLYSHSRPDSYRPLGSHEQFREITVQSLKHPGITLHLVYVDPMVNYFRSLSITAPL

SISIGFMVVIIFFAVRWIRRQLAGQELLELRSTRILSGERGPQVRGSVYEWPASTSSALDMLLSELQFAS

DQRSRMDTLIRSYAAQDSKTGLNNRLFFDNQLATLLEDQEKVGAYGIVMMIRLPEFDLLRDNWGRAAAEE

HYFTLINLLSTFIMRYPGALLARYHRSDFAVLLPHRTLKEADSIAGLLLKAMDALPPTRILDRDDMMHIG

ICSFRSGQSAAQVMEHAEAATRNAVLQGSNSWSVYDDTLPEKGRGNVRWRTLIEQMLSRGGPRLYQKPAV

TRDGRVHHRELMSRMYDGKEEVIAAEYMPMVLQFGLAEEYDRLQVTRLLPFLGFWPEENLALQLSVESLI

RPRFQRWLRDALMQCEKSQRQRIIFELAEADVCQYIGRLQPVMRLVNALGVRVAVVQAGLTLVGTSWIKQ

LDAELIKLHPGLARNIEKRSENQLLVQSLVEACKGMPMQVFATGVRSRSEWLVLSQCGVTGGQGEFFAAS

QPLDTNVKKYSQRYSV

>WP\_002918653.1 MULTISPECIES: rod shape-determining protein MreB [Enterobacteriaceae]

MLKKFRGMFSNDLSIDLGTANTLIYVKGQGIVLNEPSVVAIRQDRAGSPKSVAAVGHEAKQMLGRTPGNI

AAIRPMKDGVIADFFVTEKMLQHFIKQVHSNSFMRPSPRVLVCVPVGATQVERRAIRESAQGAGAREVFL

IEEPMAAAIGAGLPVSEATGSMVVDIGGGTTEVAVISLNGVVYSSSVRIGGDRFDEAVINYVRRNYGSLI

GEATAERIKHEIGSAYPGDEVREIEVRGRNLAEGVPRGFTLNSNEILEALQEPLTGIVSAVMVALEQCPP

ELASDISERGMVLTGGGALLRNLDRLLMEETGIPVVVAEDPLTCVARGGGKALEMIDMHGGDLFSEE

>WP\_004149974.1 MULTISPECIES: rod shape-determining protein MreC [Klebsiella]

MKPIFSRGPSLQIRLILAVLVALGVIIADSRLGTFSQIRTYMDTAVSPFYFVSNGPRELLDSVSQTLATR

DQLELENRALRQELLLKNSDLLMLGQYKQENARLRELLGSPLRQDEQKMVTQVISTVNDPYSDQVVIDKG

SVNGVYEGQPVISDKGVVGQVVAVAKMTSRVLLICDATHALPIQVLRNDIRVIAAGNGCTDDLQLEHLPA

NTDIRVGDVLVTSGLGGRFPEGYPVGVVSSVKLDTQRAYTVIQARPTAGLQRLRYLLLLWGADRNGANPM

TPEEVHRVANERLMQMMPQVLPAPDAMGPQMPAPATGLTPPQPSQPAGGQ

>WP\_002918648.1 MULTISPECIES: rod shape-determining protein MreD [Klebsiella]

MASYRSQGRWVIWLSFLIALLLQIMPWPADISVFRPNWVLLILLYWILALPHRVNVGTGFVMGAILDLIS

GSTLGVRALSLSIVAYLVALKYQLFRNLALWQQALVVMLLSLAVDIIVFWAEFLVINVSFRPEVFWSSVV

NGILWPWLFLLMRKVRQQFAVQ

>WP\_002918646.1 MULTISPECIES: Maf-like protein [Klebsiella]

MTTLYLASGSPRRQELLTQLGLAFERLVPGIEEQRQPQESAQHYVVRLAREKAQAGVAMATRDLPVLGAD

TIVILNGEVLEKPRDAEHAAAMLRLLSGHTHQVMTAVALADKQQTLDCLVVTEVTFRRLSEQDIADYVAS

GEPLDKAGAYGIQGLGGCFVRKINGSYHAVVGLPLVETYELLSNFNSLRKGKG

>WP\_002918644.1 MULTISPECIES: ribonuclease G [Klebsiella]

MTAELLVNVTPSETRVAYIDGGILQEIHIEREARRGIVGNIYKGRVSRVLPGMQAAFVDIGLDKAAFLHA

SDIMPHTECVAGEEQKQFTVRDISELVRQGQDLMVQVVKDPLGTKGARLTTDITLPSRYLVFMPGASHVG

VSQRIESEAERERLKKVVAEYCDEQGGFIIRTAAEGVHEQEMAADAAYLKRVWTKVMERKKRNQTRYQLY

GELALAQRVLRDFADAQLDRIRVDSRLTYEALLEFTAEYIPEMTSKLEHYSGRQPIFDLFDVENEIQRAL

ERKVELKSGGYLIIDQTEAMTTIDINTGAFVGHRNLDDTIFNTNIEATQAIARQLRLRNLGGIIIIDFID

MNNEDHRRRVLHSLEQALSKDRVKTSINGFSQLGLVEMTRKRTRESVEHVLCNECPTCHGRGTVKSVETV

CYEIMREIVRVHHAYDSDRFLVYASPAVAETLKGEESHALAEVEIFVGKQVKVQIEPLYNQEQFDVVMM

>WP\_032105137.1 AsmA2 domain-containing protein YhdP [Klebsiella pneumoniae]

MRRLPGILLLTVATLIVIVALLVSGLRLVLPQLDAWRPQLLEKISTLTGTPVDASQITASWQTFGPTLDA

RDIHVGLKDGGTMAVKRVTLALDVWQSLLHMRWQFRDLTFWQLQVHTNTPIQTNDGGESLKTDRISDLFL

RQFDHFTLRDSHLSFLTLSGQRAELAVPQLTWLNGRNRHRAEGQLSLSSLTGQHGVMQVRMDLRDEDGLL

NKGRVWLQADDIDVKPWLGRWMQDNIALKSARFSLEGWMTIEKGDVASGDVWLKKGGASWQGDNEVHHLS

VDNLTAHLSHDKQSWAFYIPDTRIAIDDKPWPSGALAMAWIPAQDVGGDDRQRSDELRIRASNLALSGLS

GLQPFADKLAPSLGELWRTTQPGGKINLLALDIPLQATEKTRFQAQWSDLAWKQWKLLPGAEHFSGSLNG

SVEHGELRAHMAKALMPYAGVFRAPLEIAAGEATLSWVKNDKGFMLDGRDIDVQATGVRARGGFRYLQPQ

GDDPWLGILAGISTNDGGQAWRYFPENLMGKALVDYLSGAIKAGQASDATLVYGGNPHLFPYPHNEGQFQ

VYVPLKNATFAFQPDWPALTGLNIDLNFINNGLWMRADKAMLGNVTASNLDAAIPDYAQEKLLIDADIKG

PGKEVGPYFNTTPLKESLGAALDSLQLDGDVSARLHLNIPLDGEMTTAKGDVRLQNNSLFIKPLDTTLQN

LSGNFSFVNGDLNSQTLSATWFNQPLNLNFSTREGEKAFLVDVGMNANWQPSRTGLLPKAVSEALSGSVP

WDGKVAIELPYHGNASYKVDINGDLKNVSSRLPSPVSKPAGEPLPVKINVAGGLSSFDLTGSVGAKNHIN

SRWLLNHKLTLDRAILTTDSKGHSPLPDQPGIELNLPPMDGAQWLALFENGAANEVSSSVLFPPRIVLRT

PSLALAGQQWNNVSLMSQPVAGGSQVEAQGREINATLTMRDNAPWLANVRYLYFNPASASGQNATENVAP

QTATRLDFHGWPDLQLRCAECWLWGQKYGRIDGDVAIEGDTLTLSNGLVDTGFGRLTTNGVWVNAPSGVR

TSLKGRLHGNKTDAFADFFGVSTPVKDSPFDIDYDLHWRAPPWSPDVASLNGIIKSHLGKGQFTDLSTGH

AGQLLRLLSVDALLRKLRFDFSDTFSEGFYFDSINSTAWIKDGVLHTDDTLVDGLEADIAMKGSVDLVRR

QLDLQAVVAPEISATVGVAAAFAVNPIVGAAVFAASKVLGPLWNKVSILRYRITGPIDQPQINEVLRQAR

SNKKQ

>WP\_004144958.1 MULTISPECIES: metalloprotease TldD [Klebsiella]

MSLNLVSEQLLSANGLNHQDLFAILGQLTERRLDYGDLYFQSSYHESWVLEDSIIKDGSYNIDQGVGVRA

VSGEKTGFAYADQISKLALEQSAQAARTIVRDTGNGKVQTLGAVEHRALYTSIDPLQSMTREEKLDILRR

VDKVARAADQRVQEVSASLSGVYELILVAATDGTLAADVRPLVRLSVSVLVEEDGKRERGSSGGGGRFGY

DYFLASQEGDVRADAWAKEAVRMALVNLSAVAAPAGMLPVVLGAGWPGVLLHEAVGHGLEGDFNRRGTSV

FSGHMGELVASELCTVVDDGTIADRRGSVAIDDEGTPGQYNVLIENGILKGYMQDKLNARLMGVAPTGNG

RRESYAHLPMPRMTNTYMLAGQSTPQEIIESVDYGIFAPNFGGGQVDITSGKFVFSTSEAYLIEKGKVTK

AVKGATLIGSGIETMQQISMVGNDLRLDNGVGVCGKEGQSVPVGVGQPTLKVDNLTVGGTA

>WP\_002918641.1 MULTISPECIES: HTH-type transcriptional activator AaeR [Klebsiella]

MERLKRMSVFAKVVELGSFTAAARQLQMSVSSISQTVAKLEDELQVKLLNRSTRSLGLTEAGKIYYQGCR

RMLFEAQDVHEQLYAFNNTPIGTLRIGCSSTMAQNVLARITAKMLKEYPGLSVNLVTGIPAPDLIADGLD

VVIRVGALQDSSLFSRRLGSMPMVLCAAKSYLAQAGNPEKPADLAGHAWLEYSVRPDNEFVIIAPEGIST

RLTPQGRFVTNDPMTLVRWLTAGVGIAYVPLMWAIEEINRGELEILLPSYQSDPRPVYALYTEKDKLPLK

VQVCINYLTEYFVDVAKIYQGMHGRGIAR

>WP\_002918640.1 MULTISPECIES: p-hydroxybenzoic acid efflux pump operon protein AaeX [Bacteria]

MSLFPVIVIFGLSFPPIFFELLLSLAIFWLVHRLLVPTGIYDFVWHPALFNTALYCCLFYLISRLFV

>WP\_002918639.1 MULTISPECIES: p-hydroxybenzoic acid efflux pump subunit AaeA [Klebsiella]

MKTLTRNILRTAITVILVILAFVAIFRAWVYYTASPWTRDARFSADIVAIAPDVSGLISQVNVKDNQLVK

KDQVLFVIDQPRYQKALAQAEADVAYYQTLAQEKRVEAGRRNKLGVQAMSREEIDQANNVLQTVEHQLAK

AVASRDLARLDLERTVIRAPADGWVTNLNVYTGEFITRGSTAVALVKENTFYVMAYLEETKLEGVRPGYR

AEITPLGSSKTIKGTVDSIAAGVTNASSSSDSKGMASVDSNLEWVRLAQRVPVRIRLDHQQGNLWPSGTT

ATVVITGQEDRDTSQANFFQKLAMRLREFG

>WP\_002918632.1 MULTISPECIES: p-hydroxybenzoic acid efflux pump subunit AaeB [Klebsiella]

MGTYTIAPRHLRFAIKLACAVVLALFVGFHFQLETPRWAVLTAAIVAAGPAFAAGGEPYSGAIRYRGMLR

IAGTFIGCIAALVIIILMIRAPLLMMLVCCLWAGFCTWVSSLVKVENSYAWGLAGYTALIIIITIHTNPM

LAPQFAVERCSEIVIGIVSAIVADLLFSPRSIKKEIDLELDNLLIAQYKLMQLCVAHGEKEEVDQAWGAL

VRRTTALEGMRSNLIMESSRWAKANQRLKAINTLSLTLITQACETYLIQNSRPEMVTDDYRELFAEPVET

VQDVHQQLKRMRRFLTWKGEHNTPVTIYSWVGAATRYLLLKRGVVGNTKISRIEDGVLRGETVVKVESAE

RHHAMVNFWRTSVSCILGTLFWLWTGWTSGSGAMVMIAVVTALAMRLPNPRMVAIDFLYGTLAALPLGTL

YFLVIMPATQQSMLLLCISLAAMAFFIGIEVQKRRLGSLGALASTINILVLDNPMQFQFSQFLDSALGQI

VGCFLALMVILIVRDNSRARTGRVLLNQFVSAAVSSLTTNSARRKENHLPALYQQLFLLLNKFPGDVARF

RLALTLIIAHQRLRDAPVPVNDDLSAFHRQLRRTADHVISAGSDDKRRRYFTQLLAELDVYQEKLRVWEA

SPQVTEPVRRLVEMLHKYQHVLTSS

>WP\_016529685.1 barstar family protein [Klebsiella pneumoniae]

MTTYTFDFDEIAEQQDFYREFSRTFELAQDKVNNLDSLWDAVTGGLLPLPLDIEFIHLNDKQRRCFGALI

LLFDEAEEELEGELRFNARQA

>WP\_002918627.1 MULTISPECIES: DUF1471 family stress response protein YhcN-B [Enterobacterales]

MKRAMIIASLGLASLLSFGASAAVQQVNAEQAQNLQSMGTISVSQVGSAPMDMRQELAAKAEKEGASSYR

IIEARTGDSWHATAELYK

>WP\_002918626.1 MULTISPECIES: peroxide/acid stress response protein YhcN [Klebsiella]

MKIKTTVAAISILSVVSFGAFAADIINSEQAQGREAIGTVSVGAVASSPMDMHEMLNKKAQEEGASSYRI

IEARTGDHWHATAELYK

>WP\_002918625.1 MULTISPECIES: transcriptional regulator ArgR [Klebsiella]

MRSSAKQEELVKAFKALLKEEKFSSQGEIVQALQEEGFENINQSKVSRMLTKFGAVRTRNAKMEMVYCLP

AELGVPTTSSPLKNLVLDIDYNDAVVVIHTSPGAAQLIARLLDSLGKAEGILGSIAGDDTIFTTPARGFT

VKDLHDAILVLFEQEL

>WP\_002918570.1 MULTISPECIES: malate dehydrogenase [Klebsiella]

MKVAVLGAAGGIGQALALLLKTQLPSGSELSLYDIAPVTPGVAVDLSHIPTDVKIKGFSGEDATPALEGA

DVVLISAGVARKPGMDRSDLFNVNAGIVKNLVQQIAKTCPQACIGIITNPVNTTVAIAAEVLKKAGVYDK

NKLFGVTTLDIIRSNTFVAELKGKSATEVEVPVIGGHSGVTILPLLSQIPGVSFSDQEIADLTKRIQNAG

TEVVEAKAGGGSATLSMGQAAARFGLSLVRAMQGEKGVVECAYVEGDGHYARFFSQPLLLGKNGVEERQS

IGKLSAFEQQALEGMLDTLKKDIALGEDFVNK

>WP\_009309620.1 MULTISPECIES: GntR family transcriptional regulator [Klebsiella]

MKKIERKQTRDQIAQMIRYQILSGAMKAGDELTQESIAEQLGLSRMPVREALQSLEQEGFLVRLPNRHMQ

VSTLAVEDVSHIFRVIAVMAAELFALVPANQGEVLRARAQELARPGENTRELAFHQLLISYLDNRYLAKA

YQQFLDGYISYVILYLKENGQESALILSELANAIGNGEGGKIAQTTQRYFLMLAEIMRQHMKDWESAEA

>WP\_004181429.1 MULTISPECIES: GntR family transcriptional regulator [Klebsiella]

MQKPKLGKIKLLSAKEQVAAVLRKAILSRDLVEGQEITLEGIARLVGVSSMPVREAFQILAADGLIQVRP

NKGAVVLGINEQTIREHYEIRAVLESEAVAKASRPGTDISRIAQVHYAAEKALADNNSAEYSDLNQAFHM

EIWSAAGNEKMKMLLCNMWNGLSMGHKVTEEEYAVISIREHKAILQALEQHNEALARQRMHEHIIRSMEN

MLTRYLPDTTT

>WP\_004181428.1 MULTISPECIES: SLC13 family permease [Klebsiella]

MEPITITLCLLVFAIIMFVWEKVPLAVTSMVVCVALVLTGVLDLKQAFAGFIDSNVILFVAMFIVGGALF

ETGMANKVGGVITHFAKTEKQLIFIIMVVVGVMSGFLSNTGTAAVLIPVVIGVAAKSGFTRSRLLMPLVF

AAALGGNLSLIGAPGNLIAQSALQNIGSGFGFFEYAKVGLPMLVCGILYFLTIGYKFLPNNSNSSEVGSI

GEQRDYSHVPRWKQILSLVVLIATILGMIFEKQTGISLTVAGCIGALVLVITGVLTEKQAYKAIDSQTIF

IFGGTLALAKALEMTGAGKLVADQVIGLLGNNSSPFMLLVVVFALSVVMTNFMSNTATVALLVPVSLSIA

AGMGADPRAVLMATVIGSSCAYATPIGMPANMMVLSAGGYKFVDYAKSGIPLIIVSTIVSLILLPILFPF

HP

>WP\_004181427.1 MULTISPECIES: L(+)-tartrate dehydratase subunit alpha [Klebsiella]

MSKSEQISRMTDIMARFVGYTGKVLPDDVTAKLQDLHKKETSQLADVIFTTMIENQRLAKELDRPSCQDT

GVIQFLVECGANFPLIGELEALLRESVIKATIDSPLRHNSVETFDEYNTGKNVGKGTPTVFWEIVPNSDQ

CSIYTYMAGGGCSLPGKAMVLMPGAGYEGVTRFVLDVMTSYGLNACPPLLVGVGVATSVETAALLSKKAL

MRPIGSHNDNERAALLEKMLEDGINKIGLGPQGMSGNTSVMGVNIENTARHPSTIGVAVNVGCWSHRKGH

IVFDKDLNYTITSHTGVAF

>WP\_004188410.1 MULTISPECIES: L(+)-tartrate dehydratase subunit beta [Klebsiella]

MTKKILTTPIKDEDLADIKAGDIIYLNGHIVTCRDVAHRRLIEGGRELPVNVAGGAILHAGPIVRPIKGT

EDKFEMVSVGPTTSMRMEKFEKEFIAKTGVKLIVGKGGMGKGTEEGCMEHKALHCVFPAGCAVVAAVCVE

EIEDAQWRDLGMPETLWVCRVKEFGPLIVSIDTHGNNLFEQNKVIFNQRKEIVADEICKHVSFIK

>WP\_014906863.1 MULTISPECIES: oxaloacetate decarboxylase subunit gamma [Klebsiella]

MTDNAILLGEGFTLMFLGMGFVLVFLLLLIFAIRGMSLAVNRLFPEPSAAPAAAPAAVAPADDFARLKPA

IVAAIHHHRRLHP

>WP\_046044004.1 sodium ion-translocating decarboxylase subunit beta [Klebsiella pneumoniae]

MESLNALIQGMGLMHLGAGQAAMLLVSLLLLWLAIAKKFEPLLLLPIGFGGLLSNIPEAGLALTALESLL

AHHDPAQLAVIAAKLHCAPDVHAIKAALALALPSVQGQMESLAVDMGYSAGVLAIFYKVAIGSGIAPLVI

FMGVGAMTDFGPLLANPRTLLLGAAAQFGIFATVLGALTLNYFGIISFTLPQAAAIGIIGGADGPTAIYL

SGKLAPELLGAIAVAAYSYMALVPLIQPPIMKALTTDKERKIRMVQLRTVSKREKILFPAVLLLLVALLL

PDAAPLLGMFCFGNLMRESGVVERLSDTVQNALINIVTIFLGLSVGAKLVADKFLQPQTLGILVLGVIAF

CVGTAAGVLMAKLMNVFSRHKINPLIGSAGVIGSAIAAGVMLKYVLAM

>WP\_004181422.1 MULTISPECIES: hypothetical protein [Klebsiella]

MNEGIACCPENRTSTREAVVDAMLASGDELAQLQPALNLLSPPLNATPGEALLASCYEAGADHNADEATR

AVSALPAAVVRSATPSLQRSGLLCMAAGALSARQLPLTHNRLCDVAGQFARAIPEGDEEAGSGFYTVRSV

SLPVYRRLRRDNHSHSVCLQQALLHLLAWKSESPWARQQAQRLLWQGGVLGEKGEFALLTLDDELRERQI

VWPALRSLLAVTGFLVRFPAGPVFSD

>WP\_002918568.1 MULTISPECIES: outer membrane-stress sensor serine endopeptidase DegS [Klebsiella]

MPGKLLRSVLIGLLVGGLLLALMPSLRQWQLAPTTQNDTADDSPASYNAAVRRAAPAVVNVYNRALNSTS

HNQLTLGSGVIMDQRGYILTNKHVINDADQIIVALQDGRVFEALLVGSDSLTDLAVLKINATGGLPVIPI

NPKRTPHIGDVVLAIGNPYNLGQTITQGIISATGRIGLNPTGRQNFLQTDASINHGNSGGALVNSLGELM

GINTLSFDKSNDGETPEGIGFAIPFQLATKIMDKLIRDGRVIRGYIGISGREIAPLHAQGGGIDQIQGIV

VNDVAPDGPAAQAGIRANDVIISVNDKPAVSALETMDQVAEIRPGSEIPVVIMRDDKKITLHIAVQEYPA

TN

>WP\_004174125.1 MULTISPECIES: serine endoprotease DegQ [Klebsiella]

MKKQTLLLSALALSIGLSLSVLPPAAASLPTQVPGQGALPSLAPMLEKVLPAVVSVQVEGTASPTLNMPE

ELKKYFGDNAPQEQAQPFEGLGSGVIIDAAKGYVLTNNHVINQAQKISVQLNDGREFDAKLVGSDEQSDI

ALLQLIKPDHLTQIAIADSDKLRVGDFAVAVGNPFGLGQTATSGIISALGRSGLNLEGLENFIQTDASIN

RGNSGGALLNLNGELIGINTAILAPGGGSIGIGFAIPSNMAKTLADQLIQFGEIKRGLLGIKGMEMSADI

AKAMNLNVQRGAFVSEVLPNSGSAKAGIKSGDVIVSLNGKPLNSFAELRSRIATTEPGTKVKLGLLRDGK

PVDVEVTLDKSTSSTASAELIIPALQGASFSDGQMKDGTKGVVIDNVDKGSAAAQVGLHKDDIIIGLNRQ

RIHSIAELRKALEGKPPVIALNVIRGNESIYLLLR

>WP\_002918565.1 MULTISPECIES: Z-ring associated protein ZapG [Klebsiella]

MTWEYALIGLVVGIIIGAVAMRFGNRKLRQQQALQYELEKNKAELEEYREELVSHFARSAELLDNMAHDY

RQLYQHMAKSSNNLLPDSMADANPFRNRLEESEASNDQAPVQMPRDYSEGASGLLRGGAKRD

>WP\_004144945.1 MULTISPECIES: cell division protein ZapE [Klebsiella]

MQSLSPTSRYLLALKEGSHQPDDVQQEAVSRLDTIYQELQTQPAPVASGGGLRAKFGKLLGKREPAAGTA

PVRGLYMWGGVGRGKTWLMDLFYQSLPGERKQRLHFHRFMLRVHEELTTLQGHSDPLEIVADRFKAETDV

LCFDEFFVSDITDAMLLGGLMKALFARGITLVATSNIPPDELYRNGLQRARFLPAIDAIKQHCDIMNVDA

GIDYRLRTLTQAHLWLSPLNNDTREQMDKLWLALAGAPRAAGPTLEINHRELPTLGVENQTLAASFATLC

VDARSQHDYIALSRLFHTVMLFDVPVMTAQLESEARRFIALVDEFYERHVKLVVSAAVPLYDIYQGERLK

FEFQRCLSRLQEMQSEEYLKRPHMP

>WP\_002918559.1 MULTISPECIES: 50S ribosomal protein L13 [Enterobacteriaceae]

MKTFTAKPETVKRDWYVVDATGKTLGRLATELARRLRGKHKAEYTPHVDTGDYIIVLNAEKVAVTGNKRE

DKMYYHHTGHIGGIKEATFEEMIARRPERVIEIAVKGMLPKGPLGRAMYRKLKVYAGNEHNHAAQQPQVL

DI

>WP\_000829818.1 MULTISPECIES: 30S ribosomal protein S9 [Enterobacteriaceae]

MAENQYYGTGRRKSSAARVFIKPGNGKIVINQRSLEQYFGRETARMVVRQPLELVDMVEKLDLYITVKGG

GISGQAGAIRHGITRALMEYDESLRSELRKAGFVTRDARQVERKKVGLRKARRRPQFSKR

>WP\_135801240.1 MULTISPECIES: hypothetical protein [Klebsiella]

MDKTAVIHKHSAGSRHFFSISRIPSPQRLQNLVNYHPIFCPNAGDCSFFVLFVNEGDIALMGFLHLAGHE

WPAAVQNSEYTWRFSWLSLPTNVR

>WP\_002918467.1 MULTISPECIES: stringent starvation protein A [Klebsiella]

MAVAANKRSVMTLFSGPTDIYSHQVRIVLAEKGVSFEIEHVEKDNPPQDLIDLNPNQSVPTLVDRELTLW

ESRIIMEYLDERFPHPPLMPVYPVARGESRLYMQRIEKDWYSLMNTIQSGTAAQADAARKQLREELLAIA

PVFTQKPYFLSDEFSLVDCYLAPLLWRLPVLGVELVGAGAKELKGYMTRVFERDSFLASLTEAEREMRLG

RG

>WP\_002918465.1 MULTISPECIES: ClpXP protease specificity-enhancing factor [Klebsiella]

MDVSQLTPRRPYLLRAFYDWLLDNQLTPHLVVDVTLPGVLVPMEYARDGQIVLNIAPRAVGNLELANDEV

RFNARFGGVPRNVSVPLAAVLAIYARENGAGTMFEPEAAYDEDVSSLNDDDVAPESESETVMSVIDGDKP

DNHDDDPDDTPPPRGGRPALRVVK

>WP\_004188425.1 MULTISPECIES: N-acetylmannosamine-6-phosphate 2-epimerase [Klebsiella]

MSLLAQLDQRIRHHGGLIVSCQPVPGSPLDNPAIVAAMALAAEQAGAVALRIEGLANLQAVRPLVTVPVI

GLIKRDLPDSPVRITPWLEDIDALAQGGADIIAIDGTQRQRPASVSALLAEIHQLGKVAMADCSSLDDAL

ECWQLGAEIVGTTLSGYTAEETPDEPDLALVQCLSVAGCRVIAEGRYNTPAQAAEAMRCGAWAVTVGSAI

TRLEHICGWYNTALKAAVCPANEQ

>WP\_002918461.1 MULTISPECIES: glutamate synthase small subunit [Klebsiella]

MSQNVYQFIDLQRVDPPKKPLKIRKIEFVEIYEPFSEGQAKAQADRCLSCGNPYCEWKCPVHNYIPNWLK

LANEGRIFEAAELSHQTNTLPEVCGRVCPQDRLCEGSCTLNDEFGAVTIGNIERYINDKAFEMGWRPDLS

DVKPTGKTVAIIGAGPAGLACADVLTRNGVKAVVFDRHPEIGGLLTFGIPAFKLEKEVMTRRREIFTGMG

IEFKLNTEVGRDVQLDDLLKEYDAVFLGVGTYQSMRGGLDNEDAPGVYDALPFLIANTKQIMGFGETADE

PYVSMEGKRVVVLGGGDTAMDCVRTSVRQNAAHVICAYRRDEENMPGSKREVKNAREEGVEFQFNVQPLG

VEVNANGKVCGVKMARTEMGQPDAKGRRRAEIVPGSEHVVPADAVVMAFGFRPHSMEWLAKHSVELDSQG

RIIAPEGSENAFQTSNPKIFAGGDIVRGSDLVVTAIAEGRKAADGILNYLEV

>WP\_002918458.1 MULTISPECIES: glutamate synthase large subunit [Klebsiella]

MLYDKSLERDNCGFGLIAHIEGEPSHKVVRTAIHALARMQHRGAILADGKTGDGCGLLLQKPDRFFRIVA

EERGWRLAKNYAVGMLFLNKDPELAKAARRIVEEELQLETLSIVGWRDVPTNEGVLGEIALSSLPRIEQI

FVNAPAGWRPRDMERRLFIARRRIEKRLQEDKDFYVCSLSNLVNIYKGLCMPADLPRFYLDLADLRLESA

ICLFHQRFSTNTVPRWPLAQPFRYLAHNGEINTITGNRQWARARTYKFQTPLIPDLHDAAPFVNETGSDS

SSMDNMLELLLAGGMDIVRAMRLLVPPAWQNNPDMDPELRSFFDFNSMHMEPWDGPAGIVMSDGRYAACN

LDRNGLRPARYVITKDKLITCASEVGIWDYQPDEVVEKGRVGPGELMVIDTRAGRILHSAETDDDLKSRH

PYKEWMEKNVRRLVPFEDLPDEEVGSRQLDDDTLASYQKQFNYSAEELDSVLRVLGENGQEAVGSMGDDT

PFAVLSSQPRIIYDYFRQQFAQVTNPPIDPLREAHVMSLATSIGREMNVFCEAEGQAHRLSFKSPILLYS

DFKQLTTMEEEHYRADVLDITFNPAEASLSETVKALCDKAEQMVRDGTVLLVLSDRNIAKDRLPVPAPMA

VGAIQTRLVDKSLRCDANIIVETASARDPHHFAVLLGFGATAIYPYLAYETLAKLVDSKAIDKPYRAVML

NYRNGINKGLYKIMSKMGISTIASYRCSKLFEAVGLHRDVSELCFQGVVSRIGGASFDDFQQDLLNLSKR

AWLARKPLAQGGLLKYVHGGEYHAYNPDVVRTLQQAVQSGEYSDYQQYAKLVNERPAATLRDLLALNPGE

DAISIDEVEPAKELFKRFDTAAMSIGALSPEAHESLAEAMNSIGGFSNSGEGGEDPARYGTNKVSRIKQV

ASGRFGVTPAYLVNADVIQIKVAQGAKPGEGGQLPGDKVTPYIAKLRYSVPGVTLISPPPHHDIYSIEDL

AQLIFDLKQVNPKAMISVKLVSEPGVGTIATGVAKAYADLITIAGYDGGTGASPLSSVKYAGCPWELGLV

ETQQALVANGLRHKIRLQVDGGLKTGLDIIKAAILGAESFGFGTGPMVALGCKYLRICHLNNCATGVATQ

DDKLRKNHYHGLPFKVTNYFEFIARETRELMAQLGVKRLVDLIGRTDLLKELDGFTAKQQKLDLGKLLET

AEPHPGKALYCTENNPPFDNGVLNAQLLQQAKPYVDEKQSKTFWFDIRNTDRSVGASLSGYIAQTHGDQG

LAGDPIVAHFSGTAGQSFGVWNAGGVELHLTGDANDYVGKGMAGGLLAIRPPVGSAFRSHEASIIGNTCL

YGATGGRLYAAGRAGERFAVRNSGAITVVEGIGDNGCEYMTGGIVCVLGKTGVNFGAGMTGGFAYVLDED

GDFRKRVNPELVEVLDVDSLAIHEEHLRGLITEHVQLTGSQRGEEILANWPAFSAKFALVKPKSSDVKAL

LGHRSRSAAELRVQAQ

>WP\_002918453.1 MULTISPECIES: MFS transporter [Klebsiella]

MGKNIRWIIVLLLFLVYMINYLDRVALSITVPMIEKDLALNAEQFGIIFGSFFFGYAVFNFIGGLAVDKF

GATLVMGLAVGLWSLFCGLTAVATGFYSMLVLRVLFGMAEGPICASANKMINGWFPKKQAATAVGFLSAG

SPLGGAVAGPIVGYLALAFGWRPAFMIIFAIGIVWMIAWFFIAANSPEKHKKVSQEELKLINKMKEEEVA

LETIENQTAHSLGYYLKQPIILVTAFAFFCYNYILFFFLSWFPSYLVQQHHLDIKQMSLTTMIPWIVGFV

GLALGGYISDKIFKLTGRLLLSRKIVLVVCLLMAAICVGLAGTVSSVVPAVLLMSVSIFFLYVTGAIYWA

IIQDVVHKSRVGGASGFIHLIGSVSGIVGPIVTGYIVQSTGKFDSAFVLAGTIAALGALLVLFVIKTPRV

TMKASQA

>WP\_002918451.1 MULTISPECIES: Zn-dependent oxidoreductase [Klebsiella]

MRSVVVKEPGQLNIESRPVPVPGAHEVRVKIAFAGICGSDVHIYHGHNPFAKYPRVIGHEFYGIIDAVGE

QVSPARIGERVAVDPVVSCGHCYPCSVGRPNVCTQLQVIGVHRDGGFSDYACVPAKNAWRIPEAISDRQA

TMVEPFTIAANITAQLQPTAQDIALVYGAGPMGLTIIQALKGVYGVKQVIVVDRIAERLQMARENGADLT

LDNTDQPLAEQLAQRQLAPTLVIDAACHPAILQEAILLASPAARIGILGFSGEASTLTQQSITSKEISIF

SSRLNSGRFPLVIDWMEKGLIRPEALITHCMPLEQVKEAMEIFANDRKTCCKVLLQLG

>WP\_004188429.1 mannonate dehydratase [Klebsiella pneumoniae]

MQMTMRWFGPEEDKISLEHIRQVPGVEGVVGALYDVAVGEVWPVDKIERLVDQAHAAGLKMEVIESVNIH

DDIKIGLPTRDRYIANYQQTIRNLARFGVKVICYNFMPVFDWMKTDMNYVLPDGSLTMAFEKKDIDKRLE

DVVKEVLENSNGFALPGWEPERLAEVQTLFAKYSAVDDQKLRENLVYFLQAVIPVCEEVGVKMAIHPDDP

PYSIFGLPRVVKNRDDLDWICRAVDSPANGITLCTGSIAEDPDNDVYAILAEFTRRKRIHFAHVRNIKLM

QDKDFYECAHPSEYGSLDMYKVMQALYDNGFDGYIRPDHGRFIWGETGRPGYGLFDRALGVTYLKGLWEA

LSKR

>WP\_002918444.1 MULTISPECIES: aerobic respiration two-component sensor histidine kinase ArcB [Klebsiella]

MKQIRMLAQYYVDLMMKLGLVRFSMLLALALVVLAIVVQMAVTMVLHGQVESIDVIRSIFFGLLITPWAV

YFLSVVVEQLEESRQRLSRLVDKLEEMRERDLKLNVQLKDNIAQLNQEIGEREKAEAERETTLEQLKIEM

KEREETQIQLEQQSSFLRSFLDASPDLVFYRNEDKEFSGCNRAMELLTGKSEKQLIHLKPQDVYSEEAAE

KVLETDEKVFRHNVSLTYEQWLDYPDGRKACFEIRKVPYYDRVGKRRGLMGFGRDITERKRYQDALERAS

RDKTTFISTISHELRTPLNGIVGLSRILLDTELTSEQEKYLKTIHVSAVTLGNIFNDIIDMDKMERRKVQ

LDNQPVDFTSFLADLENLSGLQAQQKGLRFVLEPSLPLPHKVITDGTRLRQILWNLISNAVKFTPQGGGV

NVRVRYDEGDILHFEVEDSGIGIPEAEQDKIFAMYYQVKDSHGGKPATGTGIGLAVSRRLARNMGGDISV

TSQPGKGATFTLTVHAPAIAEEVEDTLAEDDMPLPALNVLLVEDIELNVIVARSVLEKLGNSVDVAMTGK

AALEMFEPGEYDLVLLDIQLPDMTGLDISRELKQRFAADELPPLVALTANVLKNKKEYLDAGMDDVLSKP

LSVPALTAMIKKFWDAPDEEAQEAPAADLHKADAVLDTDMLEQYIELVGPKLINDGLAVFEKMMPGYMSV

LESNLTARDQKGIVEEGHKIKGAAGSIGLRHIQQLGQQIQTPDLPAWSDNVAEWVEEMKSEWQNDVAVLK

AWVAKASKK

>WP\_004181418.1 MULTISPECIES: isoprenoid biosynthesis glyoxalase ElbB [Klebsiella]

MKKIGVVLGGCGVYDGSEIHEAVITLLAIARNGAQAVCFAPDKPQRDVINHLTGEAMPEQRNVLVEAARI

ARGDILPLAQARAETLDALIVPGGFGAAKNLSSFAAEGSECQVDPDLRALALAMHQTGKPLGFMCIAPAM

LPKIFAFPLRITIGTDLDTADVVEEMGAEHVPCPVDDIVVDEDNKVVTTPAYMLAEDIAQAATGIEKLVA

RVLALSA

>WP\_004144927.1 MULTISPECIES: monofunctional biosynthetic peptidoglycan transglycosylase [Klebsiella]

MRLRIAPFALLKRLALRLLLIAAVFWGGGIALFSVLPVPFSAVMLERQVSAWLSGDFHYLAHSDWVAMDK

ISPWMGLAVIAAEDQKFPEHWGFDVSAIEKALAHNERHETRIRGASTLSQQTAKNLFLWDGRSWLRKGLE

AGLTVGIETVWSKKRILTVYLNIAEFGDGIFGVEAAAQRYFHKPASQLTPGEAALLAAVLPNPIRYRADA

PSGYVRSRQAWILRQMRQLGGEGFMREHKLY

>WP\_002918431.1 MULTISPECIES: PTS phosphocarrier protein NPr [Bacteria]

MTVKQTVEITNKLGMHARPAMKLFELMQNFDAEVLLRNDEGTEAEANSVIALLMLDSAKGRQIEVEASGP

QEVEALAAVIALFNAGFDED

>WP\_002918428.1 MULTISPECIES: RNase adapter RapZ [Klebsiella]

MVLMIVSGRSGSGKSVALRALEDMGFYCVDNLPVVLLPDLARSLADRNISAAVSIDVRNMPESPEIFEQA

MQNLPECFSPQLLFLDADRNTLIRRYSDTRRLHPLSSKNLSLESAIDEESDLLEPLRSRADLIVDTSEMS

VHELAEMLRTRLLGKRERELTMVFESFGFKHGIPIDADYVFDVRFLPNPHWDPKLRPMTGLDKPVAAFLD

RHTEVHNFIYQTRSYLELWLPMLETNNRSYLTVAIGCTGGKHRSVYIAEQLADYFRSRGKNVQSRHRTLE

KRKS

>WP\_004144926.1 MULTISPECIES: PTS IIA-like nitrogen regulatory protein PtsN [Klebsiella]

MMNNDSALQLSNVLNQECTRSQVHCQSKKRALEIISELAAKQLSLPPQVVFEAILTREKMGSTGIGNGIA

IPHGKLEEDTLRAVGVFVQLETPIAFDAIDNQPVDLLFALLVPADQTKTHLHTLSLVAKRLADKAICRRL

RAAQSDEELYEIITEAGSSDDA

>WP\_002918423.1 MULTISPECIES: ribosome hibernation promoting factor [Enterobacteriaceae]

MQLNITGHNVEITPAMREFVTAKFSKLEQFFDRINQVYIVLKVEKVTQIADANLHVNGGEIHASAEGQDM

YAAVDGLIDKLARQLTKHKDKLKQH

>WP\_002918420.1 MULTISPECIES: RNA polymerase factor sigma-54 [Klebsiella]

MKQGLQLRLSQQLAMTPQLQQAIRLLQLSTLELQQELQQALESNPLLEQTDLHDEVEAKEVEDRESLDTV

DALEQKEMPDELPLDASWDEIYTAGTPSGNGVDYQDDELPVYQGETTQTLQDYLMWQVELTPFTDTDRAI

ATSIVDAVDDTGYLTIQIEDIVDSIGDDEIGLEEVEAVLKRIQRFDPVGVAAKDLRDCLLIQLSQFAKET

PWLEEARLIISDHLDLLANHDFRTLMRVTRLKEEVLKEAVNLIQSLDPRPGQSIQTSEPEYVIPDVLVRK

VSGRWTVELNADSIPRLKINQQYAAMGNSARNDADGQFIRSNLQEARWLIKSLESRNDTLLRVSRCIVEQ

QQAFFEQGEEYMKPMVLADIAQAVEMHESTISRVTTQKYLHSPRGIFELKYFFSSHVNTEGGGEASSTAI

RALVKKLIAAENPAKPLSDSKLTSMLSEQGIMVARRTVAKYRESLSIPPSNQRKQLV

>WP\_016529639.1 LPS export ABC transporter ATP-binding protein [Klebsiella pneumoniae]

MATLTAKNLAKAYKGRRVVEDVSLTVNSGEIVGLLGPNGAGKTTTFYMVVGIVPRDAGNIIIDDEDISLL

PLHARARRGIGYLPQEASIFRRLSVYDNLMAVLQIRDDLTSEQREDSAKELMEEFHIEHLRDSLGQALSG

GERRRVEIARALAANPKFILLDEPFAGVDPISVIDIKRIIEHLRDSGLGVLITDHNVRETLAVCERAYIV

SQGHLIAHGTPQQILEDEQVKRVYLGEDFRL

>WP\_002918415.1 MULTISPECIES: lipopolysaccharide ABC transporter substrate-binding protein LptA [Klebsiella]

MKFRTNKLSLKIALAGALLAASLPALAKTGDTDQPIHIESDQQSLDMQGNVVTFTGNVVVTQGTIKINAD

KVVVTRPGNEKGKEVIEGFGNPATFYQMQDNGKPVKGRASKMRYELQNDYVVLTGNAYLEQLDSNIKGDK

ITYLVKEQKMQAFSDKGRRVTTVLVPSELQDKSGNQQKKSN

>WP\_002918413.1 MULTISPECIES: LPS export ABC transporter periplasmic protein LptC [Klebsiella]

MSKTRRWVIILLSLLALILIGLNLANTDDTAQPEVNPNDPTYKSEHTDTVVYSPEGALSYRLIAEHVEYF

SDQEVSWFTKPVMTTFDTNKVPTWSVRADKAKLTNDRMLYLYGHVEVNALAPDSQLRKITTDNAQINLVT

QDVTSDDMVTLYGTTFNSSGLKMRGNLRSKNAELIEKVRTSYEIQNKQTQP

>WP\_002918405.1 MULTISPECIES: 3-deoxy-manno-octulosonate-8-phosphatase KdsC [Klebsiella]

MNNADAQLATCYGPVSQAFVDRAAKIRLLILDVDGVLSDGLIYMGNHGEELKAFNVRDGYGIRCALTSGI

EVAIITGRKAKLVEDRCQTLGITHLYQGQSDKLLAFRDLTDKLHVRPEEVAYIGDDLIDWPVMAEVGLSV

AVADAHPLLLPRANYVTRINGGRGAVREVCDLLLLAQGKLDEAKGQSI

>WP\_002918399.1 MULTISPECIES: arabinose-5-phosphate isomerase KdsD [Klebsiella]

MSQIDLPTDFDFQQAGRQVLEIEREGLAQLDQYINEDFTHACETIFRCGGKVVVMGMGKSGHIGRKMAAT

FASTGTSAFFVHPGEAAHGDLGMVTPQDVVIALSNSGESNEILALIPVLKRQQVKLICITSRPESSMARA

ADIHLCVKVPKEACPLGLAPTSSTTAALVMGDALAVALLEARGFTAEDFALSHPGGALGRKLLLRVNDIM

HTGDEIPHVGLQATLRDALLEITRKNLGMTAICDDDMNIIGIFTDGDLRRVFDTGVDMRDASIADVMTRG

GIRIRPGTLAVDALNLMQSRHITCVLVADGDHLLGVVHMHDLLRAGVV

>WP\_016531106.1 calcium/sodium antiporter [Klebsiella pneumoniae]

MLLATALLIIGLLLVVYSADRLVYAASILCRMLGIPPLIIGMTVVSIGTSLPEIMVATAASLHGQTDLAV

GTALGSNITNILLILGLAALLRPFTVHSDILRRELPLMLLVSVLAGLVLYDGQLTRLDGLFLLALALLWL

LFTIKIARLAERQGSDSLTREQLAELPREGSLPVALLWLGVAMIVMPIATRMVVDNSTVLANYFAISELT

VGLTVVAIGTSLPELATAIAGARKGEDDIAIGNIIGANILNIALVLGLPALIAPGSFATEAFTRDYGVML

LVSLIFAVLCWRRQQQPGRLVGALLVGGFVVWLAMLFWTAPLFVE

>WP\_004150950.1 MULTISPECIES: phospholipid ABC transporter ATP-binding protein MlaF [Klebsiella]

MSQTQANLVEVRGIRFSRGDRVIFDDISLSVPRGKITAIMGPSGIGKTTLLRLIGGQIPPDRGEILFDGE

NVPQMTRSRLYTVRKRMSMLFQSGALFTDLNVFDNVAYPLREHTHLPPALLHTTVMMKLEAVGLRGAAKL

MPSELSGGMARRAALARAIALEPDLIMFDEPFVGQDPITMGVLVKLISELNSTLGVTCIVVSHDVPEVLS

IADYAYIVADKKIVAHGSAQSLRENTDPRVRQFIDGIADGPVPFRYPAGDYHHDLLGIGS

>WP\_004150949.1 MULTISPECIES: lipid asymmetry maintenance ABC transporter permease subunit MlaE [Klebsiella]

MLFNALAALGHRGIKTTATFGRAGLMLFNAVVGKPEFRKHAPLLVRQLYNVGVLSMLIIIVSGLFIGMVL

GLQGYLVLTTYSAETSLGMLVALSLLRELGPVVAALLFAGRAGSALTAEIGLMRATEQLSSMEMMAVDPL

RRVISPRFWAGVISLPLLTIIFVAVGIWGGALVGVSWKGIDGGFFWTAMQNAVDWRMDLVNCLIKSLVFA

ITVTWIALFNGYDAIPTSAGISRATTRTVVHASLAVLGLDFVLTALMFGN

>WP\_002918387.1 MULTISPECIES: outer membrane lipid asymmetry maintenance protein MlaD [Klebsiella]

MQTKKTEIWVGVFLLVALLAALFVCLKAANVTSLRTEPTYRLYATFDNIGGLKARSPVRIGGVVVGRVAD

ITLDPKTYLPRVELDIDERYNHIPDTSSLAIRTSGLLGEQYLALNVGFEDPDLGTTILKDGGTIQDTKSA

MVLEDLIGQFLYNSKGGDNQNSGNDKAEAEGHTDATPAAGTTH

>WP\_002918386.1 MULTISPECIES: phospholipid-binding protein MlaC [Klebsiella]

MFKRLLMVAMLVIAPLTAVQAADQSNPYKLMNEAAQKTFDRLKNEQPKIKANPNYLRDIVDQELLPYVQV

KYAGALVLGRYYKEATPAQREAYFAAFREYLKQAYGQALAMYHGQTYQIAPEQPLGSATIVPIRVTIIDP

NGRPPVRLDFQWRKNTQTGNWQAYDMIAEGVSMITTKQNEWSDLLRTKGVDGLTAQLKAISAQPITLEQK

K

>WP\_004185850.1 MULTISPECIES: lipid asymmetry maintenance protein MlaB [Klebsiella]

MSGQLSWTREGETLALHGELDQDLLVPLWEARAQATAGTAIIDLSQTTRVDTAGLALLVHFMALIRRQGR

EAQLVGKSENLQTLIGLYNLPADLI

>WP\_004144910.1 MULTISPECIES: BolA family iron metabolism protein IbaG [Enterobacteriaceae]

MENHEIQTVLMNALPLQEVHVSGDGSHFQVIAVGEMFDGMSRVKKQQSVYAPLMEYIADNRIHALSIKAF

TPQEWARDRKLNGF

>WP\_002918382.1 MULTISPECIES: UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Klebsiella]

MDKFRVQGPTRLQGEVTISGAKNAALPILFSALLAEEPVEIQNVPKLKDIDTTMKLLSQLGAKVERNGSV

WIDAGPVDVFCAPYDLVKTMRASIWALGPLVARFGQGQVSLPGGCAIGARPVDLHISGLEQLGAEIKLEE

GYVKASVSGRLKGAHIVMDKVSVGATVTIMSAATLAEGTTIIENAAREPEIVDTANFLNALGAKITGQGS

DRITIEGVQRLGGGVYRVLPDRIETGTFLVAAAISGGKILCRNAQPDTLDAVLAKLRDAGADIETGEDWI

SLDMHGNRPKAVNVRTAPHPGFPTDMQAQFTLLNLVAEGTGVITETIFENRFMHIPELIRMGAHAEIESN

TAICHGVKQLSGAQVMATDLRASASLVLAGCIAEGTTIVDRIYHIDRGYERIEDKLQALGANIQRVKGE

>WP\_002918381.1 MULTISPECIES: DNA-binding transcriptional regulator SfsB [Enterobacteriaceae]

MDKFIDWHPADIVAGLRKRGTSLAAESRRHGLSSSTLANALTRPWPKGELIIATALETQPWVIWPSRYHD

PVTHEFIDRTQMMRQKKIDK

>WP\_016530973.1 octaprenyl diphosphate synthase [Klebsiella pneumoniae]

MNLEKINELTAQDMAGVNATILEQLNSDVQLINQLGYYIVSGGGKRIRPMIAVLAARTVGYQGSAHVTIA

ALIEFIHTATLLHDDVVDESDMRRGKATANAAFGNAASVLVGDFIYTRAFQMMTQLGSLKILEVMSEAVN

VIAEGEVLQLMNVNDPDITEENYMRVIYSKTARLFEAASQCAGLLADCTAEEERALQDYGRYLGTAFQLI

DDLLDYSSDGERLGKNVGDDLNEGKPTLPLLHAMHHGTPDQSAMIRGAIEQGNGRHLLDAVLETMATCGS

LEWTQKRAEEEADKAIAALQILPDTPWREALIGLAHIAVQRDH

>WP\_002918379.1 MULTISPECIES: 50S ribosomal protein L21 [Bacteria]

MYAVFQSGGKQHRVSEGQTVRLEKLDIATGEAVEFAEVLMIANGEEIKIGVPFVEGGVIKAEVVAHGRGE

KVKIVKFRRRKHYRKQQGHRQWFTDVKITGISA

>WP\_002434222.1 MULTISPECIES: 50S ribosomal protein L27 [Bacteria]

MAHKKAGGSTRNGRDSEAKRLGVKRFGGEAVLAGSIIVRQRGTKFHAGTNVGCGRDHTLFALTDGKVKFE

VKGPKNRKFISIVAE

>WP\_004149938.1 MULTISPECIES: DMT family transporter [Klebsiella]

MKQQAGIGIILALTTAMCWGALPIAMKQVLEVMAPPTVVFYRFLMASIGLGAILAIKGKLPPMRIFRKPR

WLVLLAIATGGLFGNFILFSSSLQYLSPTASQVIGQLSPVGMMVASVVILKERMRGTQVVGALMLLSGLV

MFFNTSLIEIFTRLTDYTWGVIFGVAAATVWVSYGVAQKVLLRRLASQQILFLLYTLCTIALLPLAEPGV

ISRLSSWQLACLIFCGLNTLVGYGALAEAMARWQAAQVSALITLTPLFTLLFSDLLSMAWPDVFARPMLN

LIGYLGAFVVVAGAMYSAIGHRLWGRWRKREAVVPLPRSGE

>WP\_002918377.1 MULTISPECIES: Obg family GTPase CgtA [Klebsiella]

MKFVDEATILVVAGDGGNGCVSFRREKYIPKGGPDGGDGGDGGDVWLEADENLNTLIDYRFEKSFRAERG

QNGQSRDCTGKRGKDVTVKVPVGTRVIDQGTGETMGDMTKHGQRLMVAKGGWHGLGNTRFKSSVNRTPRQ

KTMGTPGDKRDLQLELMLLADVGMLGMPNAGKSTFIRAVSAAKPKVADYPFTTLVPSLGVVRMDNEKSFV

VADIPGLIEGAAEGAGLGIRFLKHLERCRVLLHLIDIDPIDGSDPVENARIIIGELEKYSEKLASKPRWL

VFNKIDLMDKAEAEAKAKAIAEALGWEEKFYLISAASQQGVKELCWDVMTFIIENPIVQAEEEQKPEKVE

FMWDDYHRQQLEEAEAEAEDDEDWDDDWDEDDEEGVEFIYKR

>WP\_002918376.1 MULTISPECIES: serine-type D-Ala-D-Ala carboxypeptidase [Klebsiella]

MRFPRFIIGLTAGIALSAQAANIDEYINQLPAGANLAFMAQKVGASTPEIDYHSQQMALPASTQKVITAL

AALLQLGPDFRFTTTLETKGSLDGGVLKGDLIARFGGDPTLKRQDIRNMVATLKKAGVQRIEGNVLIDTS

VFASHDKAPGWPWNDLTQCFSAPPAAAIVDRNCFSVSLYSAQKPGDVAFIRVASYYPVTMFSQVRTLARG

SSEAQYCELDVVPGDLNRYTLTGCLPQRSEPLPLAFAIQDGASYAGAILKAELAQAGITYSGTLLRQTLA

NEPGTVLATSQSAPLHDLLRIMLKKSDNMIADTVFRTIGHARFGVPGTWRAGSDAVRQILRQQAGVDLGN

TIIADGSGLSRHNLIAPATMMQVLQYIAQHDTELNFISMLPLAGHDGSLQYRAGLHQAGVDGKVSAKTGS

LQGVYNLAGFITTASGQKMAFVQYLSGYAVEPADQRNRRIPLVRFESRLYKDLYQNN

>WP\_002918375.1 MULTISPECIES: transcription elongation factor GreA [Enterobacteriaceae]

MQAIPMTLRGAEKLREELDYLKSVRRPEIIAAIAEAREHGDLKENAEYHAAREQQGFCEGRIKDIEAKLS

NAQVIDITKMPNNGRVIFGSTVSVLNLDTDEEQTYRIVGDDEADFKQNLISVNSPIARGLIGKEQDDVVT

IRTPGGEVEYEITKVEYL

>WP\_016530974.1 ribosome assembly RNA-binding protein YhbY [Klebsiella pneumoniae]

MNLSTKQKQHLKGLAHPLKPVVMLGNNGLTEGVLAEIEQALGHHELIKVKIASEDRETKALIVEAIVRET

GACIVQVIGKTLVLYRPTPERKISLPR

>WP\_002918373.1 MULTISPECIES: 23S rRNA (uridine(2552)-2'-O)-methyltransferase RlmE [Klebsiella]

MTGKKRSASSSRWLQEHFSDKYVQQAQKKGLRSRAWFKLDEIQQSDKIFKPGMTVVDLGAAPGGWSQYAV

TQIGNSGRIIACDLLPMDPIVGVDFLQGDFRDELVLKALLERVGDSKVQVVMSDMAPNMCGTPAVDIPRA

MYLVELALEMSRDVLAPGGSFVVKVFQGEGFDEYLREIRSLFTKVKVRKPDSSRARSREVYIVATGRKP

>WP\_002918372.1 MULTISPECIES: ATP-dependent zinc metalloprotease FtsH [Klebsiella]

MAKNLILWLVIAVVLMSVFQSFGPSESNGRKVDYSTFLQEVNQDQVREARINGREINVTKKDSNRYTTYI

PVNDPKLLDNLLTKNVKVVGEPPEEPSLLASIFISWFPMLLLIGVWIFFMRQMQGGGGKGAMSFGKSKAR

MLTEDQIKTTFADVAGCDEAKEEVGELVEYLREPSRFQKLGGKIPKGVLMVGPPGTGKTLLAKAIAGEAK

VPFFTISGSDFVEMFVGVGASRVRDMFEQAKKAAPCIIFIDEIDAVGRQRGAGLGGGHDEREQTLNQMLV

EMDGFEGNEGIIVIAATNRPDVLDPALLRPGRFDRQVVVGLPDVRGREQILKVHMRRVPLAPDIDAAIIA

RGTPGFSGADLANLVNEAALFAARGNKRVVSMVEFEKAKDKIMMGAERRSMVMTEAQKESTAYHEAGHAI

IGRLVPEHDPVHKVTIIPRGRALGVTFFLPEGDAISASRQKLESQISTLYGGRLAEEIIYGPEHVSTGAS

NDIKVATNLARNMVTQWGFSDKLGPLLYAEEEGEVFLGRSVAKAKHMSDETARIIDQEVKSLIERNYGRA

RQLLNDNMDILHAMKDALMKYETIDAPQIDDLMARREVRPPAGWEEPGSSNNSDNNGTPRAPRPVDEPRT

PNPGNTMSEQLGDK

>WP\_002918371.1 MULTISPECIES: dihydropteroate synthase [Klebsiella]

MKLVAQGSTLDLSHPHVMGILNVTPDSFSDGGAHNSLIEAVKHANLMINAGATIIDIGGESTRPGAAEVS

VEEELARVIPVVEAIAQRFEVWISVDTSKAEVIRQSARAGAHIINDIRSLTEPGALQAAAETGLPVCLMH

MQGQPKTMQEAPKYEDVFADVERFFNEHIVRCEQAGIAKEKLLLDPGFGFGKNLSHNYQLLARLGEFHHF

GLPLLVGMSRKSMVGQLLNVGPSERLNGSLACAVIAAMQGAQIIRVHDVKETVEALRVVEATLAAKGKKR

YE

>WP\_002918370.1 MULTISPECIES: phosphoglucosamine mutase [Klebsiella]

MSNRKYFGTDGIRGRVGDAPITPEFVLKLGWAAGKVLARHGSRKIIIGKDTRISGYMLESALEAGLAAAG

LSASFTGPMPTPAIAYLTRAFRAEAGIVISASHNPFYDNGIKFFSIEGTKLPDDVEEAIEAEMEKELTCV

DSAELGKASRIVDAAGRYIEFCKGTFPNELSLGTLKVVVDCAHGATYHIAPNVFRELGAQVIAMGCEPDG

LNINEEVGATDVRALQARVLAEKADLGIAYDGDGDRVIMVDHEGNKVDGDQILYIIAREGLRQGQLRGGA

VGTLMSNMGLELALKQLGIPFARAKVGDRYVLEMLQEKGWRIGAENSGHVILLDKTTTGDGIVASLQVVA

AMVRNHMSLHDLCSGMKMFPQLLVNVRFTEGSGNPLENEHVKAVTAEVEAALGKRGRVLLRKSGTEPLIR

VMVEGEHEDQVHEFAHRIAEAVKSV

>WP\_002918369.1 MULTISPECIES: preprotein translocase subunit SecG [Bacteria]

MYEALLVVFLIVAIGLVGLVMLQQGKGADMGASFGAGASGTLFGSSGSGNFMTRMTGILAALFFIISLAL

GNINSNKTSKGSEWDNLSAPKTEQTQPTAPAQPTSDIPH

>WP\_014906872.1 MULTISPECIES: hypothetical protein [Gammaproteobacteria]

MRRYFQDNTALISRLNHSLKSHYLQDVERRDVFDRHSEAYKVYGALTRLEQMASMNEVYRKENNVAGLQE

INRVLKSVPLTS

>WP\_016530976.1 YfaZ family outer membrane protein [Klebsiella pneumoniae]

MKSIAATMVAVTIALGASSAACAAVNLHGEAGAEFTNLSASFGAGEPGMTFSSQWAHSDNDGDSVGLGMG

YNFNLGPFLMTLGGKAVYLNPKDGDEGYAIAAGGGAELPLGQYFTLFGEGYYSPDSMSSGVEDYVEANAG

VRLNVLPSLNIEAGYRYIDMAGKDGNRDNTLADGAYAGVNFRF

>WP\_004174150.1 MULTISPECIES: winged helix-turn-helix transcriptional regulator [Klebsiella]

MNIKPPIRPQKTIDRLIDVLEPHATPVNAIARKRLTWEYKGKTQLFIFKKGELSIIRNSDRLLMVTVYEP

HLFGVAEMLQPSRSHSLRAEVSCELLRIDHDLASALFRQHNLWEEVTSLLAYHTSYMVYRDDLVLQQRTY

SVIRNHLLEMMLLSEETRQRVSILEYIQDRTLLSRSSILNVLSALKKGGYIAFARGGYLQNIVSLPEKF

>WP\_004144895.1 MULTISPECIES: argininosuccinate synthase [Klebsiella]

MTTILKHLPVGQRIGIAFSGGLDTSAALLWMRKKGAVPYAYTANLGQPDEDDYDAIPRRAKEYGAEGARL

IDCRKQLVAEGIAAIQCGAFHNTTGGLTYFNTTPLGRAVTGTMLVAAMKEDGVNIWGDGSTYKGNDIERF

YRYGLLTNAELQIYKPWLDSDFINELGGRHEMSEFMIACGFDYKMSVEKAYSTDSNMLGATHEAKDLEFL

NSSVKIVNPIMGVKFWDENVKIPAEEVTVRFEQGHPVALNGKTFADDVEMMLEANRIGGRHGLGMSDQIE

NRIIEAKSRGIYEAPGMALLHIAYERLLTGIHNEDTIEQYHAHGRQLGRLLYQGRWFDSQALMLRDSLQR

WVASQITGEVTLELRRGNDYSILNTVSDNLTYKAERLTMEKGDSMFTAEDRIGQLTMRNLDITDTREKLF

GYAQSGLLSASSATGLPQVENLENKGK

>WP\_002918364.1 MULTISPECIES: ribosome maturation factor RimP [Klebsiella]

MSTLEQKLTEMLTAPVEALGFELVGIEFIRGRTSTLRIYIDSEDGINVDDCADVSHQVSAVMDVEDPITV

AYNLEVSSPGLDRPMFTAEHYQRFTGEEVALVLRMAVQNRRKWQGIIKAVDGEMITVTVEGKDEVFALSN

IQKANLVPHF

>WP\_002918252.1 MULTISPECIES: transcription termination factor NusA [Klebsiella]

MNKEILAVVEAVSNEKALPREKIFEALESALATATKKKYEQEIDVRVEIDRKSGDFDTFRRWLVVEEVTQ

PTREITLEAARFEDESMNVGDYVEDQIESVTFDRITTQTAKQVIVQKVREAERAMVVDQFREHEGEIITG

VVKKVNRDNITLDLGNNAEAVILREDMLPRENFRPGDRIRGVLYAVRPEARGAQLFVTRSKPEMLIELFR

IEVPEIGEEVLEIKAAARDPGSRAKIAVKTNDKRIDPVGACVGMRGARVQAVSTELGGERIDIVLWDDNP

AQFVINAMAPADVASIVVDEDKHTMDIAVEAGNLAQAIGRNGQNVRLASQLSGWELNVMTVDDLQAKHQA

EAHAAIDTFTKYLDIDEDFATVLVEEGFSSLEELAYVPMKELLEIDGLDEATVEALRERAKNALTTLALA

QEESLGDNKPADDLLNLEGLDRALAFKLAARGVCTLEDLAEQGVDDLADIEGMTDEKAGELIMAARNICW

FGDEA

>WP\_002918250.1 MULTISPECIES: translation initiation factor IF-2 [Klebsiella]

MTDVTIKALASEIQTSVDRLIQQFADAGIRKSADDSVTSQEKQTLLTHLNREHGSAPDKLTLQRKTRSTL

NIPGTGGKSKSVQIEVRKKRTFVKRDPQEAERLAAEEQAQREAEEQARREAEEAAKREAQLKAEREAAEQ

AKREVADKAKREAAEKDKVSNQHTDEMTKTAQAEKIRRENEAAELKRKSEEEARRKLEEEARRVAEEARR

MAEENEKNWSETSDSPEDSSDYHVTTSQHARQAEDDNDREVEGGRGRSRSSKAARPAKKGNKHAESKADR

EEARAAVRGGKGGKHRKGSALQQGFQKPAQAVNRDVVIGETITVGELANKMAVKGSQVIKAMMKLGAMAT

INQVIDQETAQLVAEEMGHKVILRRENELEEAVMSDRDTGAAAEPRAPVVTIMGHVDHGKTSLLDYIRST

KVASGEAGGITQHIGAYHVETDNGMITFLDTPGHAAFTSMRARGAQATDIVVLVVAADDGVMPQTIEAIQ

HAKAAQVPVVVAVNKIDKPEADPDRVKNELSQYGILPEEWGGESQFVHVSAKAGTGIDDLLDAILLQAEV

LELKAVRNGMASGAVIESFLDKGRGPVATVLVREGTLHKGDIVLCGFEYGRVRAMRDELGREVLEAGPSI

PVEILGLSGVPAAGDEVTVVRDEKKAREVALYRQGKFREVKLARQQKSKLENMFANMTEGEVHEVNIVLK

ADVQGSVEAISDSLLKLSTDEVKVKIIGSGVGGITETDATLAAASNAILVGFNVRADASARKVIEAESLD

LRYYSVIYNLIDEVKAAMSGMLSPELKQQIIGLAEVRDVFKSPKFGAIAGCMVTEGTIKRHNPIRVLRDN

VVIYEGELESLRRFKDDVNEVRNGMECGIGVKNYNDVRVGDMIEVFEIIEIQRSID

>WP\_002918248.1 MULTISPECIES: 30S ribosome-binding factor RbfA [Klebsiella]

MAKEFGRPQRVAQEMQKEIAIILQREIKDPRLGMMTTVSGVEMSRDLAYAKVYVTFLNDKDEAAVKAGIK

ALQEASGFIRSLLGKAMRLRIVPELTFFYDNSLVEGMRMSNLVTSVVKHDDERRVNPDDSKED

>WP\_004144892.1 MULTISPECIES: tRNA pseudouridine(55) synthase TruB [Klebsiella]

MSRPRRRGRDVHGVLLLDKPQGASSNDVLQKVKRIYNANRAGHTGALDPLATGMLPICLGEATKFSQYLL

DSDKRYRVIAKLGQRTDTSDADGQVVEERPLTFSDEQLAAALDSFRGETQQVPSMYSALKYQGKKLYEYA

RQGIEVPREARPITVYELLFIRREGDELELEIHCSKGTYIRTIIDDLGEKLGCGAHVIFLRRLAVSKYPV

ERMVTLEQLQALVDEAAAQDIPAAQLLDPLLMPMDSPASDYPLVNIPETSAVYFKNGNPVRQSGAPLNGL

VRVMESESGKFLGMGEIDDEGRVAPRRLVVEYPA

>WP\_002918244.1 MULTISPECIES: 30S ribosomal protein S15 [Bacteria]

MSLSVEAKAKIVSEFGRGENDSGSTEVQVALLTAQINHLQGHFAEHKKDHHSRRGLLRMVSQRRKLLDYL

KRKDVARYSALIERLGLRR

>WP\_004150944.1 MULTISPECIES: polyribonucleotide nucleotidyltransferase [Klebsiella]

MLNPIVRKFQYGQHTVTLETGMMARQATAAVMVSMDDTAVFVTVVGQKKAKPGQDFFPLTVNYQERTYAA

GKIPGGFFRREGRPSEGETLIARLIDRPVRPLFPEGFVNEVQVIATVVSVNPQVNPDIVAMIGASAALSL

SGIPFNGPIGAARVGYINDQYVLNPTQEELKSSKLDLVVAGTEAAVLMVESEAELLSEDQMLGAVVFGHE

QQQIVIQNINDLVKEAGKPRWDWQPEAVNEALNARVAALAESRLSDAYRITDKQERYAQVDVIKSETIAT

LVAEDETLDANELGEILHAIEKNVVRSRVLAGEPRIDGREKDMIRGLDVRTGVLPRTHGSALFTRGETQA

LVTATLGTARDAQNIDELMGERTDSFLFHYNFPPYSVGETGMVGSPKRREIGHGRLAKRGVLAVMPTIEE

FPYTVRVVSEITESNGSSSMASVCGASLALMDAGVPVKAAVAGIAMGLVKEGDNFVVLSDILGDEDHLGD

MDFKVAGSRDGISALQMDIKIEGITKEIMQVALNQAKGARLHILGVMEQAINAPRGDISEFAPRIHTIKI

NPDKIKDVIGKGGSVIRALTEETGTTIEIEDDGTVKIAATDGDKAQHAIRRIEEITAEIEVGRIYNGKVT

RIVDFGAFVAIGGGKEGLVHISQIADKRVEKVTDYLQMGQEVPVKVLEVDRQGRVRLSIKEATEQTPSAA

APEAPAAEQGE

>WP\_002918241.1 MULTISPECIES: lipoprotein NlpI [Klebsiella]

MKPFLRWCFVATALTLAGCSSTAWRKDAVLAVPLQPTLQQEVILARMEQILASRALSDDERAQLLYERGV

LYDSLGLRALARNDFSQALAIRPDMPEVFNYLGIYLTQAGNFDAAYEAFDSVLELDPTYNYAHLNRGIAL

YYGGRAKLAQDDLLAFYQDDPNDPFRSLWLYIAERKLDEKRALEALRERLNKSDKEQWGWNIVEFYLGDI

SEKELMTRLKADATDNTSLAEHLSETNFYLGKYYLSLGDKDSATALFKLAVANNVHNYVEHRYALLELSL

LGQEQDDLAESDQQ

>WP\_085903200.1 MULTISPECIES: protein YrbN [Enterobacterales]

MKITVNFHDELCRLAAINFEAHVLHG

>WP\_016529474.1 MULTISPECIES: DEAD/DEAH family ATP-dependent RNA helicase [Klebsiella]

MAEFETTFADLGLKAPILEALTDLGYEKPSPIQAECIPHLLDGRDVLGMAQTGSGKTAAFSLPLLNNIDP

ELRAPQILVLAPTRELAVQVAEAMTEFSKHMRGVNVVALYGGQRYDVQLRALRQGPQIVVGTPGRLLDHL

KRGTLDLSKLSGLVLDEADEMLRMGFIEDVETIMAQIPEGHQTALFSATMPEAIRRITRRFMKEPQEVRI

QSSVTTRPDISQSYWTAYGMRKNEALVRFLEAEDFDAAIIFVRTKNATLEVAEALERNGYNSAALNGDMN

QALREQTLERLKDGRLDILIATDVAARGLDVERISLVVNYDIPMDSESYVHRIGRTGRAGRAGRALLFVE

NRERRLLRNIERTMKLTIPEVELPNAELLSKRRLEKFAAKVQQQLESSDLDQYRALLAKIQPTAEGEELD

VETLAAALLKMAQGERSLIVPPDAPMRPRREFRDRDDRFDRRGDRNDRGPRGDREDRPKRERRDVGDMEL

YRIEVGRDDGVEVRHIVGAIANEGDISSRYIGNIKLFASHSTIELPKGMPGEVLQHFTRTRILNKPMNMQ

LLGDAQPRTERRGGGERREGGRGFGGERREGGRGFGGERREGRRFSGERREGRAPRRDDASAPRRDDSAG

RRRFGGDA

>WP\_004185824.1 MULTISPECIES: tryptophan permease [Klebsiella]

MATLTTTATRPSLFGGVVIIGGTIIGAGMFSLPVVMSGAWFFWSLAALVFTWFCMLHSGLMILEANLNYR

IGSSFDTITKDLLGKGWNLVNGVSIAFVLYILTYAYISASGSILHHTFSELSLKVPARAAGFGFALLVAF

IVWMSTKAVSRMTAIVLGAKVITFFLTFGSLLGHVEPTTLFNVAEKNASYAPYLLMTLPFCLASFGYHGN

VPSLMKYYGKDPRTIIRCLTYGTLLALGLYVVWLLVTMGNIPRPQFIDIAQKGGNIDVLVQALSGVLNSR

SLDLLLVVFSNFAVASSFLGVTLGLFDYLADLFGFDDSAMGRFKTALLTFIPPMIGGLVKPDGFLYAIGY

AGLAATIWAAIVPALLARASRKRFGSPQFRVWGGTPMIVLILLFGLGNAVVHILSSVNLLPVYQ

>WP\_002918234.1 MULTISPECIES: LLM class flavin-dependent oxidoreductase [Klebsiella]

MTDKSVPFSVLDLAPIPQGSSAKEAFTHSLDLARLAESRGYHRYWLAEHHNMVGIASAATSVLIGYLAAN

TTTLHLGSGGVMLPNHSPLVIAEQFGTLNTLYPGRIDLGLGRAPGSDQPTMRALRRHMSGDVDNFPRDVA

ELVDWFDARDPNPHVRPVPGYGERIPVWLLGSSLYSAQLAAQLGLPFAFASHFAPDMLFQALHLYRSNFK

PSARLEKPYAMVCINIIAADSNRDAEFLFTSMQQAFVKLRRGETGQLPPPVENMHQLWSASEQYGVQQAL

SMSLVGDKTKVRHGLESILRETEADEIMVNGQIFDHQARLHSFDLAMQVKEELLG

>WP\_002918233.1 MULTISPECIES: U32 family peptidase [Klebsiella]

MKYSLGPVLYYWPKETLEDFYQQAANCSADTIYLGEAVCSKRRATKVGDWIEMAKTLAASGKQVVLSTLA

LVQASSELGELKRYVDNGEFLIEASDLGVVNLCAERKLPFVAGHALNCYNAVTLRLLRKQGMVRWCMPVE

LSRDWLANLLTQCEELGIRNQFEVEVLSYGHLPLAYSARCFTARSEDRPKDECETCCIKYPTGRSMLSQE

NQQVFVLNGIQTMSGYVYNLGNELTSMHGLVDMVRLSPMGNETFAMLEAFRANENGAAPLDLTSNSDCNG

YWKRLPGLVLQA

>WP\_002918232.1 MULTISPECIES: U32 family peptidase [Klebsiella]

MELLCPAGNLPALKAAIENGADAVYIGLKDDTNARHFAGLNFTEKKLQEAVSFVHQHRRKLHIAINTFAH

PDGYARWQRAVDMAAQLGADALILADIAMLEYAAERYPHIERHVSVQASATNEEAIRFYHRNFDVARVVL

PRVLSIHQVKQLARATPVPLEVFAFGSLCIMAEGRCYLSSYLTGESPNTVGACSPARFVRWQQTPQGLES

RLNEVLIDRYQDGENAGYPTLCKGRYLVDGERYHALEEPTSLNTLELLPELMAANIASVKIEGRQRSPAY

VTQVAKVWRQAIDRCKADPQNFVPQSAWMETLGAMSEGTQTTLGAYHRKWQ

>WP\_002918231.1 MULTISPECIES: SCP2 domain-containing protein [Klebsiella]

MLDKLRSRLVHFGPSLMSVPVKLAPFALKRQVLEQVLSWQFRQALAEGELEFLEGRWLSIHVRDIGLLWY

TSVVDGRLVVSQQADADVSFSADASDLLMIAARKQDPDTLFFQRRLVIEGDTELGLYVKNLMDAIELEQM

PKALRVMLLQLADFVEAGLKSPQKPEQTSVGEAC

>WP\_002918229.1 MULTISPECIES: N-acetyltransferase [Klebsiella]

MLIRVEIGIDAPGIDALLRRTFGRDAEAQLVHDLREDGLITLGVVATDDEGQVIGYVAFSPVAVEGEELQ

WVGLAPLAVDERYRGQGIGRQLVYEGLDSLNEFGYAAVVTLGDPDLYRRFGFEPAARFDLRCRWPDSAEA

FQVHRLADDALDGVHGQVEYSEHFNRL

>WP\_016529428.1 GIY-YIG nuclease family protein [Klebsiella pneumoniae]

MTVCWFLYLIRTADNRLYTGITTDVPRRFRQHQAGKGAKALRGKGDLQLAFSHEVGEHSLALRLEYRIKQ

LTKREKERLVAGEDAFETLLARLKDD

>WP\_002918223.1 MULTISPECIES: YhbP family protein [Bacteria]

MDTLAAIGRWLSKQHVVTWCVSREDELWCANAFYVYDPDTVAFYLLSEEHTRHGQMTGQRAKVAGTVNGQ

PKTVALIRGVQFKGEIRRLSGDEEARMRQRYVKRFPVARMLSAPVWEIRPDEIKFTDNTLGFGKKLHWRR

DAGAEQA

>WP\_002918221.1 MULTISPECIES: type 1 glutamine amidotransferase [Klebsiella]

MSKKIAVLITDDFEDSEFTSPAEAFKLAGHQVITIEKQAGKTVKGKQGEAEVAIDRAIDDVTPGEFDALL

LPGGYSPDQLRGDERFVTFTRDFVNGGKPVFAICHGPQLLISADVIRGRKLTAVKPIVVDVKNAGGEFYD

QEVVVDNEQLVTSRTPDDLPAFNREALRLLGAGITPPV

>WP\_016531003.1 NAD(P)H-binding protein [Klebsiella pneumoniae]

MSQVLLTGATGLVGGHLLRLLQNEPRISTIAAPTRRPLAPAEGVFNPHDPQLTDALAQVVDPVDIVFCCL

GTTRREAGSKEAFVHADYTLVVDTALTGKRLGAQHMLVVSAMGANAHSPFFYNRVKGEMEAALIEQDWPR

LTIARPSMLSGEREKKRANETFLAPLFRLLPGNWKSIAARDVATALLAEALSPTHEGVRILTSSELRERA

ARQAE

>WP\_004188467.1 MULTISPECIES: permease [Klebsiella]

MAGQSSSQAASPFQWWKPALFFLVVIVGLWYVKWQPYYGKAFTAAETHSIGKSILAQADANPLMAAWDYA

MVYFLAVWKAAVLGVLLGSLIQVLIPRDWLLRTLGQSRFQGTLLGAIFSLPGMMCTCCAAPVAAGMRKQQ

VSMGGALAFWMGNPLLNPATLVFMGFVLGWQFALVRLVAGLATVLTVATLVQKWVKEAATQPVAVPAAPS

EATQGGFFSRWLRALWTLFWNTIPVYILAVLVLGAARVWLFPHADGVVDNTLFWVIAMAIAGCLFVIPTA

AEIPIVQTMMLAGMGTAPALALLITLPAVSVPSLIMLRKAFPAKALWLTGGLVALCGAIVGALALV

>WP\_002918214.1 MULTISPECIES: division/outer membrane stress-associated lipid-binding lipoprotein [Klebsiella]

MKALSPLAILLSALLLQGCVAAAVVGTAAVGTKAATDPRTVGTQVDDSTLELRVNSALSKDEQIKKQARI

NVTAYQGKVLLTGQSPTPDLSARAKQIAMGVEGTTEVFNEVRQGQPIGLGTASSDTWITTKVRSQLLSTD

QVKSSNVKVTTENSEVFLMGLVTDREGRAAADIASRVSGVSRVTTAFTYIK

>WP\_002918211.1 MULTISPECIES: DnaA initiator-associating protein DiaA [Enterobacteriaceae]

MLDRIKACFTESIQTQIAAAEALPDAISRAAMTLVQSLLNGNKILCCGNGTSAANAQHFAASMINRFETE

RPGLPAIALNTDNVVLTAIANDRLHDEIYAKQVRALGHAGDVLLAISTRGNSRDIVKAVEAAVTRDMTIV

ALTGYDGGELAGLLGQQDVEIRIPSHRSARIQEMHMLTVNCLCDLIDNTLFPHQDD

>WP\_002918206.1 MULTISPECIES: YraN family protein [Klebsiella]

MAQVPAGKNRSGQLSKQTGDAWENQARRWLEGQGLRFIAANARERGGEIDLIMRDGTVTVFIEVRYRRSA

RYGDAAASVTPQKQQRLLKAARLWLCRQNGSFETVDCRFDVVAFTGNDIQWLKNAFGE

>WP\_046042292.1 penicillin-binding protein activator [Klebsiella pneumoniae]

MVPSTFLRSKPARCLPVLLATLIFAGCGTHTQDQSAAFMQGTSQANSSFYLQQMQQSTNDSKTNWQLLAI

RALLQEGKKQQAIDLFNQLPANLNSTQAREQSLLAVEVKLAQNDYQAARNLLAKIDPTSLEQPQQARYWQ

AQIDASQGKPSLTLLRALIAQQPLLSDAKQRQKNIDATWQALTSMPQDQANALVINADENILQGWLDLQR

MWFDNRNDPTLLKAGVKDWQTRYPQNPGAKMLPTALVNMQNYKPASINKIALFLPLNGQASIFGRTIQQG

FEAAKNGAPSVTGSAVPAQVAQAANVSGNDDVVSPSQAEISDLTAAGSRADPVQAPTQDQAAPAAEPAAQ

APATSATPQTTASPATQPVTAPAAQPQPVVATAANPSAELKIYDTTSQPISQLLAQAQQDGATLVVGPLL

KENVEEVIKSNTPLNVLALNQPEKVESRANLCYFALSPEDEARDAARHIHQQGKQTPLLLVPRGALGDRV

VSAFADEWLKLGGASVLQQRFGSTAELRAGVNGGGGIALSGTPVSTLPSAQNSILGSADEMPVSSGGSVD

AAYILATPEQIAYIKPMIAMRNGSQSNVTLYASSRSAQGTAGPDFRLEMEGLQYSEIPMLAGSNPSLMQQ

ALSAVRNDYSLARLYAMGADAWSLANHFTQMRQTPGFELNGNTGDLTANQDCVINRKLSWLKYQQGKIVP

AS

>WP\_046042294.1 16S rRNA (cytidine(1402)-2'-O)-methyltransferase [Klebsiella pneumoniae]

MKQHESADNSQGQLYIVPTPIGNLSDITQRALEVLQAVDLIAAEDTRHTGLLLQHFAINARLFALHDHNE

QQKAETLLAKLKEGQNIALVSDAGTPLINDPGYHLVRTCREANIRVVPLPGPCAAIAALSAAGLPSDRFC

YEGFLPAKSKGRRDTLKALEEEPRTLIFYESTHRLVESLEDICAVLGEFRYVVLARELTKTWESIHGAPI

GELVAWVKEDENRRKGEMVLIVEGFKAQEEALPAAALRTLALLQAELPLKKAAALAAEIHGVKKNALYKY

ALEQQGE

>WP\_046042296.1 galactarate dehydratase [Klebsiella pneumoniae]

MADIAIRQQSPTAFYIKVDPTDNVAIIVNDRGLTAGTRFPDGLTLVEHIPQGHKVALVDIPAHGEIIRYG

EVIGYAVRDIPQGSWIDESLVELPTAPPLNTLPLATKVPEQLPPLEGYTFEGYRNADGSVGTKNLLGITT

SVHCVAGVVDYVVKIIERDLLPNYPNVDGVVGLNHLYGCGVAINAPAAVVPIRTIHNIALNPNFGGEVMV

IGLGCEKLQPERLLQGTEDVKSIPVDSASIVSLQDEKHVGFKSMVDDILQVAERHLAKLNQRQRETCPAS

ELVVGMQCGGSDAFSGVTANPAVGYASDLLVRCGATVMFSEVTEVRDAIHLLTPRAINEEVGKRLLEEMA

WYDNYLDMGKTDRSANPSPGNKKGGLANVVEKALGSIAKSGKSAIVEVLSPGQRPTKRGLIYAATPASDF

VCGTQQVASGITVQVFTTGRGTPYGLMAVPVIKMATRTELANRWYDLMDINAGTIATGEETIEDVGRKLF

EFILDVASGRKKTFSDQWGLHNQLAVFNPAPVT

>WP\_016531008.1 MFS transporter [Klebsiella pneumoniae]

MILDSTLDEKKGIPTRYLILLMIFVVTAVNYGDRATLSIAGTEVAKELGLSAVSMGYIFSAFGWAYLLMQ

IPGGWLLDKFGSKKVYSYSLFFWSRFTFLQGFIDVFPLAWAGVSMFFMRFMLGFSEAPSFPANARIVAAW

FPAKERGTASAIFNAAQYFSLALFSPLLGWLTFALGWEHVFTVMGIIGFVLTIIWVKFVHNPTDHPRMSA

AELKYISEGGAVVDMDHKKEATPAAGPKMDYIRQLLTNRMMLGVFFGQYFLNTITWFFLTWFPIYLVQDK

GMSILKVGFVASIPALFGFAGGVLGGLFSDYLIGRGCTLTFARKLPIVLGMLLASSIILCNYTASTPLVI

TLMALAFFGKGFGALGWPVISDVAPKEIVGLCGGVFNVFGNVASIATPLVIGYIVSELHSFNGALIFVGG

SALMMMVCYLFVVGDIKRMELQK

>WP\_016531009.1 2-dehydro-3-deoxyglucarate aldolase [Klebsiella pneumoniae]

MDNAIFPNKFKAALAAHQVQIGCWCALANPISTEVLGLAGFDWLVLDAEHAPNDVTTLIPQLMALKGSSS

AQVVRVPTNEPIIIKRMLDIGFYNFLVPFVETAEQAAQAVASTRYPPEGIRGVSVSHRGNMFGTVPDYFA

QSNKNISILVQIESQTGVDNVEAIAATEGVDGVFVGPSDLAAALGHLGNAAHPEVQRAIQYIFASAKKHG

KPSGILAPVEADARRYLEWGATFVAVGSDLGVFRSATQKLADAFKK

>WP\_002917952.1 MULTISPECIES: 2-hydroxy-3-oxopropionate reductase [Klebsiella]

MTIKVGFIGLGIMGKPMSKNLLKAGYSLVVSDRNPEAIADVIAAGAETATTPKAIAEQCEVIITMLPNSP

HVKEVALGENGIIEGAKPGTVVIDMSSIAPLASREISEALKAKGIDMLDAPVSGGEPKAIDGTLSVMVGG

DKAIFDKYYDLMKAMAGSVVHTGDIGAGNVTKLANQVIVALNIAAMSEALTLATKAGVNPDLVYQAIRGG

LAGSTVLDAKAPMVMDRNFKPGFRIDLHIKDLANALDTSHGVGAQLPLTAAVMEMMQALRADGLGTADHS

ALACYYEKLAKVEVTR

>WP\_004900844.1 MULTISPECIES: glycerate 2-kinase [Klebsiella]

MKIVIAPDSYKESLSASEVAQAIEKGFREIFPDAQYVSLPVADGGEGTVEAMIAATQGKEHFAWVTGPLG

ERVKACWGMSGDGVTAFIEMAAASGLGLVPPDKRNPLITTSRGTGELILQALEHGAERIIIGIGGSATND

GGAGMMQALGARLCDAEGQEIGHGGGSLSRLSRIDLSAIDPRLRDRMIHVACDVTNPLVGERGASRIFGP

QKGATEAMIVELDRNLAHYADVIKASLQVDVKSIPGAGAAGGMGAALMAFLNAELRSGIEIVTEALKLEE

QIHDCSLVVTGEGRLDSQSVHGKVPVGVARVAKKYRKPVIGIAGSLTHDVGVVHQHGIDAVFSVLTSVST

LEEAFRGAFDNIYRASRNIAATLQVGMTTEG

>WP\_004150939.1 MULTISPECIES: OB-fold putative lipoprotein [Enterobacterales]

MLLRFRVLPLVFVISLLSGCGLASKAFYSAGDKLFQPGDDAVASMQTYSVAQFLQPFTLNPAKASSDYLG

KWVKVRGVIVDIRRKSGIAGSYYFIVTMRDEQNKTDKRLTFNFGSHNSADVEALSNGSVATIVGQVHQVQ

DSTIPTLQNPKVVK

>WP\_004149907.1 MULTISPECIES: Spy/CpxP family protein refolding chaperone [Klebsiella]

MKLITRIAFATLLTTGFSITAQAADVKAAPAPAQDPIVQHLKLTNDQVAKIKSLHQQLESNVQQISQQEI

KDGALINVIDSGKWDEKAVNDQLAAFSKIDQQVRYYRVKYYFEVNKVLTPEQRTQVKKDLADALSE

>WP\_002917926.1 MULTISPECIES: hypothetical protein [Klebsiella]

MSKKKNRKKASPTPLAPVQPQVAGAASFGYDEMLSELEAIVAEAEIRLRDEESLA

>WP\_002917925.1 MULTISPECIES: pirin family protein [Klebsiella]

MITTRTAKQCGQADFGWLQARYTFSFGHYFDPKLLGFASLRVLNQEVLAPGASFQARTYPKVDILNLILE

GEAEYRDSDGNHVQAKAGEALLIATQPGVSYSEHNLSKEQSLTRMQLWLDACPQRENPLQQKINVADATL

QLLASPEGGDNSLQLRQQAWVYHIALEKGEQINVQLHGPRAYLQSIHGSVHAVAQEQQKQALTCGDGAFI

RDEANITLVADTPLRALLIDLPV

>WP\_004144865.1 MULTISPECIES: LysR family transcriptional regulator [Klebsiella]

MAKERALTLEALRVMDAIDRRGSFAAAADELGRVPSALSYTMQKLEEELDVVLFDRSGHRTKFTNVGRML

LERGRVLLEAADKLTTDAEALSRGWETHLTIVTEALVPTPDLFPLIEKLATKSNTQLSIITEVLAGAWER

LEQGRADIVVAPDMHFRSSSEINSRKLYSVLSVYVAAPDHPIHQEPEPLSEVTRVKYRGVAVADTARERP

VLTVQLLDKQPRLTVSTIEDKRQALLAGLGVATMPYPLVEKDIAEGRLRVVSPEYTNEIDIIMAWRRDSM

GEAKSWCLREIPKLFAGR

>WP\_002917923.1 MULTISPECIES: DUF805 domain-containing protein [Bacteria]

MDWYLKVLKNYIGFGGRARRKEYWMFILVNLILTGVLSIIDKMLGWQRAGGEGILTTIYGVLVFLPWWAV

QFRRLHDTDRSAWWLLLLLIPVIGWLVILIFNCQRGTEGNNRFGPDPKPFSY

>WP\_002917922.1 MULTISPECIES: glutathione S-transferase family protein [Klebsiella]

MGQLVDGVWQDTWYDTKSTGGRFKRSVSAFRNWLTADGAAGPSGEGGFAAEKDRYHLYVSLACPWAHRTL

IMRKLKGLEPFLPVSVVNPLMLENGWTFDDSFPEATGDTLYQHDFLYQLYLHADPHYTGRVTVPVLWDKK

QQTIVSNESAEIIRMFNTAFDGLGARAGDYYPPALREQIDELNGWIYDNVNNGVYKAGFATSQQAYDEAV

DAVFTSLERLEQILGQHRYLTGNQLTEADIRLWTTLVRFDPVYVTHFKCDKRRISDYLNLYGFLRDIYQM

PGIAETVSFPHIRHHYYRSHKTINPTGIISIGPQQDLNEPHGRDQRFR

>WP\_002917920.1 MULTISPECIES: DoxX family protein [Klebsiella]

MKKLEDVGVLVARILMPILFITAGWGKITGYAGTQQYMEAMGVPGALLPLTILLEFGGGLAILFGFLTRT

TALFTAGFTLLTAFLFHSNFAEGVNSLMFMKNLTIAGGYLLLAITGPGAFSIDRVLNKKW

>WP\_002917918.1 MULTISPECIES: YqjK-like family protein [Klebsiella]

MNGRQERERQKTQLLRQIQQQRLELSACRRHWHEATAPLDRGWHTLLSLRSWLMVGSGLMAVWSVRHPHF

LMRWTKRGLGLWSTWRLVRGILRQSAVR

>WP\_002917917.1 MULTISPECIES: phage holin family protein [Klebsiella]

MANTQHTQGPGQRVFSIGQRIVTLLVEMVETRLRLVVVELEEEKANLFQLLIMTGLTLLFAAFGLMSLLV

LVIWAVDAQYRLHVMIATTVVLLLAAAIVGILTLRKARRSTLLRLTRKELENDRALLEEDKS

>WP\_002917916.1 MULTISPECIES: YqjD family protein [Bacteria]

MAKENVTDDLRAELKTLADTLEEVLNSSADKSKEEMGKLRSKAESALKESRARLGETSEAILRQTRETAA

RADDYVRENPWTGVGIGAAVGLVLGVLLSRR

>WP\_004144860.1 MULTISPECIES: DUF1090 domain-containing protein [Klebsiella]

MKHRIALLLVLTSLSASALAASPCQEKEQDIQREISYAEKHHNQSRIDGLNTALRQVRENCSDSKLKADH

QQKIAKQREEIAERQRDLQEARKKGDADKINKRQHKLNEAQQELKTLESRDY

>WP\_004218213.1 MULTISPECIES: EnvZ/OmpR regulon moderator MzrA [Klebsiella]

MKRPSLRQFSWLLGGSLLLGALFWLWLAVQQQEATLAIRPVGQGIGMPDGFSVWHHLDANGIRFKSITPQ

KDGLLIKFDSTAQGAAAKEVLGRALPHGYIIALLEDDNSPTAWLSRLRDAPHRLG

>WP\_002917909.1 MULTISPECIES: DedA family protein [Klebsiella]

MELFTQLLNALWAQDYETLANPSMIGMLYFVLFMILFLENGLLPAAFLPGDSLLVLVGVLIAKGAMGFPE

TLLLLTAAASLGCWLSYIQGRWLGNTRIVQNWLSHLPSHYHQRAHHLFHKHGLSALLIGRFIAFVRTLLP

TIAGLSGLNNARFQFFNWMSGLLWVLILTSLGYLLGKTPVFLKYEDQLMSCLMLLPVALLVFGLIGSLVV

LWKKKYRSRG

>WP\_002917907.1 MULTISPECIES: transcriptional regulator ExuR [Klebsiella]

MEIIEPRRLYQQLAAELKTRIEQGVYLVGDKLPAERFIADEKNVSRTVVREAIIMLEVEGYVEVRKGSGI

HVISNHPKYQQVADESLEFANYGPFELLQARQLIESNIAEFAATQVTKQDIMKLMEIQEKARNEKCFRDS

EWDLQFHVQVALATQNSALAAIVEKMWTQRVHNPYWKKLHEHIDLRTVDNWCDDHDQILKALLRKDPNAA

KLAMWQHLENTKQMLFNETSDDFEFNADRYLFAENPVVHLDTAVNGAK

>WP\_004174208.1 MFS transporter [Klebsiella pneumoniae]

MRKIKGLRWYMIALVTLGTVLGYLTRNTVAAAAPTLMEELHISTQQYSYIIAAYSAAYTVMQPVAGYVLD

ILGTKIGYAFFAIAWAVFCGSTALAGSWGGLALARGAVGAAEAAMIPAGLKASSEWFPAKERSIAVGYFN

VGSSIGAMIAPPLVVWAIVMHSWQMAFIISGVLSFAWAIAWLIFYKHPRDQKKLSDEERDYIIGGQESQH

QTNNAKKMSPWQILRNRQFWGIALPRFLAEPAWGTFNAWIPLFMFKVYGFNLKEIAMFAWMPMLFADLGC

IVGGYLPPLFQRWFGVNLIVSRKMVVTMGALLMIGPGMIGLFTSPYVAIALLCIGGFAHQALSGALITLS

SDVFGRNEVATANGLTGMAAWLASTMFALVVGALADTIGFSPLFAVLAVFDLLGALVIWTVLKNKPADDD

STPLSSRKPATQS

>WP\_002917899.1 MULTISPECIES: glucuronate isomerase [Klebsiella]

MTSFMTEDFLLDTEFARRLYHDYAKDQPIFDYHCHLPPQQVAENYRFKNLYDIWLKGDHYKWRAMRTNGV

PERLCTGDASDREKFDAWAATVPHTIGNPLYHWTHLELRRPFGITGKLLSPSTADEIWDQCNDLLAQDAF

SARGIMKQMNVKMVGTTDDPIDSLEHHAAVAKDNSFDIKVLPSWRPDKAFNIELATFNDYMAKLGEVSDT

DIRRFADLQSALTKRLDHFAAHGCKVSDHALDVVLFAEATDAELDDILARRLAGETLSEHEVAQFKTAVL

VFLGAEYARRGWVQQYHIGALRNNNLRQFKLLGPDVGFDSINDRPMAEELSKLLSKQNEENLLPKTILYC

LNPRDNEVLGTMIGNFQGEGMPGKMQFGSGWWFNDQKDGMERQMTQLAQLGLLSRFVGMLTDSRSFLSYT

RHEYFRRILCQMIGRWVAAGEAPADIALLGEMVKNICFNNARDYFAIELN

>WP\_032103056.1 altronate dehydratase family protein [Klebsiella pneumoniae]

MQYIKIHSQDNVAVALTDIAAGSVVTIDNDSVTLGQDIVRGHKFALRAIAKGENVVKYGLPIGHALADIA

PGEHVHAHNTRTNLSDLDAYRYQPDLVAQPPQPADREVQIYRRANGDVGVRNELWILPTVGCVNAMARQM

QNRFLKETYGAEDIDGVHLFSHTYGCSQLGDDHINTRTMLQNMVRHPNAGAVLVVGLGCENNQVEAFRET

LGEFDPQRVHFMVCQHQDDEVEAGIEHLHQLYEVMRQDKRQPGKLSELKFGLECGGSDGLSGITANPMLG

RFSDYVIANGGTTVLTEVPEMFGAEQLLMSHCRDEATFDKLVTMVNDFKQYFIAHDQPIYENPSPGNKAG

GITTLEDKSLGCTQKAGSSQVVDVLRYGERLKVHGLNLLSAPGNDAVATSALAGAGCHMVLFSTGRGTPY

GGFVPTVKIATNSELAAKKKHWIDFDAGQLLHGKTMPQLLEEFVDAIVAFANGKPTCNEQNDFRELAIFK

SGVTL

>WP\_016530910.1 serine/threonine transporter SstT [Klebsiella pneumoniae]

MTTRTPSSGWLSRLAQGSLVKQILIGLVLGVLLALVSKPAAIAVGLLGTLFVGALKAVAPVLVLMLVMAS

IANHQHGQKTSIRPILFLYLPGTFSAALTAVLFSFLFPSTLHLTTAADSITPPSGIVEVLRGLLMSMVSN

PIDALLNANYIGILVWAVGLGFALRHGNDTTKNLINDVSHAVTFIVKVVIRFAPLGIFGLVSSTLATTGF

ETLWGYAQLLLVLVGCMLLVALVINPLLVFWKIRRNPYPLVLTCLRESGVYAFFTRSSAANIPVNMALCE

KLNLDRDTYSVSIPLGATINMAGAAITITVLTLAAVHTLNIPVVLPTALLLSVVASLCACGASGVAGGSL

LLIPLACNMFGIPNDVAMQVVAVGFIIGVLQDSCETALNSSTDALFTAAACMAEDDQLAKNALRG

>WP\_004185787.1 TerC family protein [Klebsiella pneumoniae]

MNTVGTPLLWGGFAVVVAIMLAIDLLLQGRRGSHSMTMKQAAGWSILWVTLSLLFNAAFWWYLVQTQGRA

VADPQALAFLTGYLIEKALAVDNVFVWLMLFSYFAVPPALQRRVLVFGVLGAIVLRTIMIFAGSWLISQF

DWLLYVFGAFLLFTGVKMALAKEDDSGIGDKPLVRWIRSHLRMTDKIESERFFTRKNGVLFATPLLLVLI

LVELSDVIFAVDSIPAIFAVTTDPFIVLTSNLFAILGLRAMYFLLAGVAERFSMLKYGLSVILVFIGVKM

LIVDFYHIPVAISLGVVGGILAVTLLINAWVNRQHDKQRKLPE

>WP\_004144843.1 MULTISPECIES: M48 family metallopeptidase [Klebsiella]

MTKLIYLQGYPESLLAQVTTLIEQGRLGEVLQKRYPQGHDVNSDKALYQYTQDLKNRFLRGAAPINKVMY

DSKIHVLNNALGLHTAISRVQGGKLKAKAEIRVATVFRDAPEAFLRMIVVHELAHLKEKDHNKAFYQLCC

HMEPQYHQLEFDTRLWLTHLSLNRSA

>WP\_004144842.1 MULTISPECIES: XRE family transcriptional regulator [Klebsiella]

MNVKVNITTDSGSDVDQVSRAVATRLKAYRKAKKMSLDELSRRASISKGMLVEMEKEAANPSIAILCKLA

AALGVSVADIVNVASEPALHIIPAEQIPTLWQGPLGGSARLLAGTAGPNMIELWRWEMQPGEAFASPGHP

ATTFELLHVEAGALTLTLGETCRTVAAGESAVARTEIEHGYRNEGTAPLVFTMTVAELPS

>WP\_002917889.1 MULTISPECIES: B3/4 domain-containing protein [Klebsiella]

MRSVTPSIESAVSRLAPGFRALSIVVESAPVADPAVAEQALAEACLAVQQDDVPWAQAHLAAWDEAFSAF

GAKAKRTPCSAQALRKRVLKEGSLPAIDPVVDIYNAISIRYAVPVGGENLAAYRGEPRLAIARGDEPFDT

LKSAEPVVEYPEPGEVIWRDDIGVTCRRWNWRQGVRTRLDSGAQTMWFILESLPAMPLSALHEAGERLVG

YLQQLMPGARASITLLRADDEGDLR

>WP\_016531665.1 23S rRNA (guanine(1835)-N(2))-methyltransferase RlmG [Klebsiella pneumoniae]

MSQAELNGELFTLERFPPNAEEEALQAWEAADEYLLQQVNDVDGLTLIFNDGFGALACALADRNPVSIND

SFISELATRHNLRMNGIDEESVRFQDSLSPLPAAPALVLIKVPKQLALLEQQLRALREVVTPETRIIAAA

KARDVHNSTLALFEKILGTSTTSLAWKKARLIHCVFTAPELADAPQTYSWKLDGTPWTIHNHANVFARSG

LDIGARFFLQHLPSDLEGEIADLGCGNGVIGLQALAQNPNASVMFTDESHMAVASSRLNVERNLPDDIAR

CEFMVNNSLSGIEPDRFTAILCNPPFHQQHAITDHIAWQMFNDARRSLKYGGELYVVGNRHLDYFRKLKR

AFGNCTTIATNNKFVILKATKVRKQR

>WP\_016531664.1 NADPH-dependent 2,4-dienoyl-CoA reductase [Klebsiella pneumoniae]

MSRYPSLFAPLELGFTTLKNRVLMGSMHTGLEELPDGAQRLAAFYAERARHGVALIVTGGIAPAPSGVTM

AGGAVLNDASHLAHHRHITDAVHQEGGKIALQILHTGRYSYQPALVAPSALQAPINRFTPHELSHDEILT

LIDDFAHCAQLAREAGYDGVEVMGSEGYLINEFLAARTNQRDDQWGGDYARRMRFAVEVVKAVRQRAGHD

FIIIYRLSMLDLVNDGSTLAEVTELAKAIEAAGATIINTGIGWHEARIPTIATPVPRGAFSWVTRKLKGA

VSIPLITTNRINDPQVAEDILARGDADMVSMARPFLADAEFISKAQDDRADQINTCIGCNQACLDRIFVG

KVTSCLVNPRACHETLMPVLPANAPKRLAVVGAGPAGLAFAVNAAARGHHVTLFDALPEIGGQFNIAKQI

PGKEEFHETLRYYRTMLDLHGVDLRLNTHVTTDDLLAFDETILATGIAPRLPAIDGIDHPKVLSYLDVLR

DKAPVGAKVAIIGCGGIGFDTAMFLSQSGVATSQDIGEFCREWGIDTSLQTAGGLSAEGPQLSKSPRQIV

MLQRKASKPGEGLGKTTGWIHRATLLARGVKMIPAVSYEKIDDEGLHVTIGGERQLLAVDQVVICAGQEP

RRELADPLRAAGKTVHLIGGCDVAAELDARRAIAQGTKLALAI

>WP\_046042307.1 autoinducer-2 kinase [Klebsiella pneumoniae]

MSYLLALDAGTGSIRAVIFDLNGRQLAVGQAEWKHLSVDNVPGSMEFDLTTNWQLACQCIRQALDAARLS

AADIQSVACCSMREGIVLYDRNGEAIWACANVDARASREVAELKEIHDYRFESEVYEVSGQTLALSAMPR

LLWLAHHRPDIYRKAATITMISDWLAAKLSGELAVDPSNAGTTGMLDLFSRDWRPALLDMAGLRADMLSP

VKETGTLLGAVTEAAAQQSGLRAGTPVVMGGGDVQLGCLGLGVVHAGQTAVLGGTFWQQVVNLPQVRTDP

QMNIRVNPHVIPGMAQAESISFFTGLTMRWFRDAFCAEEKLIAERLGVDAYSLLEEMASRVPAGSHGVMP

IFSDAMHFKQWYHAAPSFINLSIDPEKCNKATLFRALEENAAIVSACNLAQISQFSGVTFESLVFAGGGS

KGALWSQILSDVTGLPVRVPVVREATALGCAIAAGTGAGLYDDMASTGERLVSWHREFTPNPQHRELYQE

MMSKWQTVYADQLGLVDSGLTTSMWQAPGLERRQRVASSPSP

>WP\_004144837.1 MULTISPECIES: transcriptional regulator LsrR [Klebsiella]

MSEKRITEENRYAGLALAEEELVARVAWCYYHDGLTQNDIGERLGLPRLKISRLLEKGRQSGVIRVQINS

RYEGCLALESELQQRFGLKIARVLPALNTPPMNTRLGIGAAQSLMGILQPGQLLAVGFGEATMSCLQHLS

GFIGSQQVRLVTLSGGVGPYMTGIGQLDAACSVSIIPAPLRVSSAEVAEILRRESSVRDVILAATAADAA

VVGIGAIDQRRDATILRSGYISEGEQLMYARKGAVGDILGYFLQADGRPVEGLEIHRELLGVTLDELAQL

PTIVGVAGGEEKAQAIYAALIGKRINGLVTEETTARAVLTLAS

>WP\_046042309.1 autoinducer 2 ABC transporter ATP-binding protein LsrA [Klebsiella pneumoniae]

MKPLLEARQIRKQFSGVAVLKGIDFTLCAGQVHALMGGNGAGKSTLMKIIAGVETPDSGELTIGDRAFAR

LSPALAHQLGIYLVPQEPMLFPNLSVRENILFRLPKRADTTARLQEKLQQLNCQINLDASASTLEVADQQ

MVEILRGLMREARILILDEPTASLTPGETERLFSQIRALQALDVGIVFISHKLPEIRQLASHISVMRDGA

VVLSGEAATYRDEQLISAMTPASRDHTLSDTQKLWLALPGNRRTQAQDFPVLRVEDLTGEGFIDLNLEIR

AGEIVGLAGLVGSGRTEFAETLYGLRPPRAGRIWLENREISNDSTRARLASGLVYLPEDRQVSGLFLDAP

VRWNTVMFNQPSWWQQGKREAAVVERYHRALGIKLADGDQPVRTLSGGNQQKVLLARCLEANPLLLIVDE

PTRGVDVSARADIYQLLKSVAVQNVAVLMISSDLDEFIGLADRVLVMHQGRYSGELARQAVTVDRMMTLA

FGGQA

>WP\_004181392.1 MULTISPECIES: autoinducer 2 ABC transporter permease LsrC [Klebsiella]

MKTLLKNRELSAFFAIVALFVVLVALNPAYFSLQTLAMIFSSSQILCLLALGATLVMLTRNIDVSVGSTV

GLCAIAVGVALNNGYGLATAIAFALAIGALAGAFNGLLVVGLRIPAIVATLGTLGLYRGVMLLWTGGKWI

EGLPDSLKSLSEPAFIGVSPLGWLVLALLLAGGWLLSRTAFGRDFYAVGDNLAAARQLGVAVNRTRMLAF

TLNGMLAACAGIVFAAQIGFVPNQTGSGLEMKAIAACVLGGISLLGGTGTLLGAFLGAFFLTQIDTVLVL

FRLPAWWNDFIAGLVLLGVLVLDGRLRQALARHQRALKYSRFQPGNKGGKQVARFPERKSKEVA

>WP\_016531103.1 ABC transporter permease [Klebsiella pneumoniae]

MKLKLNWESALLALLIVEILLFGALNPRMLDLNMLLFSTSDFICIGIVALPLTLVIISGGIDISLGSTIG

LCAIALGVMTQAGWPLWLAVSLTLLLGLLCGVFNAALIHYTGISPLVITLGTLYLYGGGALLLSGMAGAT

GYEGIGGFPDSFTAFANLTLAGLPLPLVLFAIITFFFWLLTHRGRFGRHLFLLGQNPRAARYAALSVNGI

PYVLYGLVGVASAVAALVMVSYFGSARSDLGRDLLMPALTAAVLGGANIYGGSGSILGTALAALLVGYLQ

QGLQMVGIPNQVSSALSGALLVVVVMGRSLSLHREWVRATWRRLFSHKTIGA

>WP\_016531102.1 autoinducer 2 ABC transporter substrate-binding protein LsrB [Klebsiella pneumoniae]

MKLKLIVLALAMSVVTAQAADRIAFIPKLVGVGFFTSGGNGAKEAGKALGVDVTYDGPTEPSVSGQVQLI

NNFVNQGYNAIIVSAVSPDGLCPALKRAMQRGVKVLTWDSDTRPECRSIYINQGTPQQLGGLLVEMAEKQ

VTKPTAKVAFFYSSPTVTDQNQWVKEAKAKIEKEHPQWQIVTTQFGYNDATKSLQTAEGILKAYPDLDAI

IAPDANALPAAAQAAENLKRQGVAIVGFSTPNVMRPYVERGTVKAFGLWDVVQQGRIAVNVADRLLKKGD

LNVGDSVEVKDIGSLKVEPNSVQGYQYEAKGNGIVLLPERVVFSKENINNYDF

>WP\_002917724.1 MULTISPECIES: 3-hydroxy-5-phosphonooxypentane-2,4-dione thiolase [Klebsiella]

MADLDDIKEGKDFGIDRPQQNTLYTLKGCGSLDWGMQSRLARIFNPHSNRTVMLAFDHGYFQGPTTGLER

IDLSIAPLFADTDVLMCTRGVLRSQVPAATNKPVVLRASGGNSILSELSNECVAVAMEDALRLNVCAVAA

QVYIGSEYEHQSINNIIKLVDAGNRYGMPVLAVTGVGKEMTRDARYFSLASRIAAEMGAQFVKTYFVEEG

FEKVTASCPVPIVIAGGKKLPEHEALEMCWRAIDQGASGVDMGRNIFQSSAPRAMLKAVKKVVHENLNAR

EAYQFWQEEKQGELK

>WP\_002917723.1 MULTISPECIES: (4S)-4-hydroxy-5-phosphonooxypentane-2,3-dione isomerase [Klebsiella]

MNVTLVEINIKPERVDEFLEVFRANHEGALQEPGNLRFDVLQDPEVKTRFFIYEAYKDDEAVLAHKKTPH

YLACVEKLEEMMSQPRQKRSFIGLLPQV

>WP\_042941333.1 putrescine aminotransferase [Klebsiella pneumoniae]

MNRLPSSASALACSAHALNLIEKRTLDHEEMKALNQEVREYFKEHVNPGFLEYRKSVTASGDYGAVEWQA

GGLNTLVDTQGQEFIDCLGGFGIFNVGHRNPVVVSAVENQLAKQPLHSQELLDPLRAMLAKTLAALTPGK

LKYSFFCNSGTESVEAAIKLAKAYQSPRGKFTFIATSGAFHGKSLGALSATAKSTFRKPFMPLLPGFRHV

PFGDINAMRTMLSECKKTGDDVAAVILEPIQGEGGVILPPTGYLPAVRKLCDEFGALLILDEVQTGMGRT

GKMFACEHENVQPDILCLAKALGGGVMPIGATVATEEVFSVLFDNPFLHTTTFGGNPLACAAALATINVL

LTQNLPAQAAQKGDMLLDGFRLLAQEYPDLVNEVRGKGMLMAIEFVDNEIGYDFASEMFRQRVLVAGTLN

NAKTIRIEPPLTLTLEQCEQVLKAARKALAALRVSVEEA

>WP\_002917718.1 MULTISPECIES: PadR family transcriptional regulator [Klebsiella]

MRHHHEEGRGPRGRHGDPSEHGDHGRRGGGRRQRFFGHGELRLIILDILSRSASHGYELIKEIETLTQGN

YSPSPGVIYPTLDLLQDQGLISVEDDNGRKKILISEEGKQLHAENQEHLAHIQERLQARMVGCELRRDPQ

MKRALENFKAVLDLKVNQQASSAAQLKQIIGIIDRAAMEISQLD

>WP\_023283007.1 glycerone kinase [Klebsiella pneumoniae]

MSQFFFNQRASLVNDVIEGTIIASPWNNLACLESDPAIRVVVRRDLNKNNVAVISGGGAGHEPAHVGFIG

KGMLTAAVCGDLFASPSVDAVLTAIQAVTGEAGCLLIVKNYTGDRLNFGLAAEKARRLGYNVEMLIVGDD

ISLPDNKQPRGIAGTILVHKVAGYFAERGFNLATVLREAQYAASHTASIGVALASCHLPQEADSAPRHQA

GHAELGMGIHGEPGASTIATQNSAEIVNLMVEKLTAALPETGRLAVMLNNLGGVSVAEMAILTRELANTP

LQARIDWLIGPASLVTALDMKGFSLTAIVLEESIEKALLSDVETASWQKPVQPRTINVVPSTLDSARVDF

TPSANPQVGDYVAQVTGALIDLEEHLNALDAKVGDGDTGSTFAAGAREIAERLERQQLPLNDLPTLFALI

GERLTVVMGGSSGVLMSIFFTAAGQKLGQGASVAEALNAGLEQMKFYGGADEGDRTMIDALQPALAALLA

EPENLQAAFAAAQAGADRTCQSSKAGAGRASYLNSDSLLGNMDPGAHAVAMVFKALAER

>WP\_032103066.1 dihydroxyacetone kinase phosphoryl donor subunit DhaM [Klebsiella pneumoniae]

MVNLVIVSHSARLGEGVGELARQMLINDGCKLAIAAGIDDPDSPIGTDPLKVMEAIESVADTDHVLVMMD

IGSALLSAETALDLLDPAIAAKVRLCAAPLVEGTLAATVSAASGAGIDKVIADAMSALEAKRVQLGLPSP

TSDAAPAPMLADDGDTKSVSVIINNHNGLHVRPASKLVAALAGFNADLLLEKNGKCVKPDSLNQIALLQV

RRNDKLRLLARGPDADAALAAFQALAADNFGESPAAQPAAAPATPERVEGAALRYPLALIQPLRPAAADA

AREQQRLRQAIDQTLADLIALTELAENKFNADIAAIFAGHHTLLDDDDLFDAANDRLLTEQCSAEWAWHQ

VLMELSQQYRQLDDPYLQARYIDIEDILQRTLRHLQGVQERVPTPGEPTIIIADNIYPSTVLQLDASFVK

GLCLRDGSEQAHGAIIARAAGIAWLSQQGEALNSVQPGETIVLDMRHQRLIRD

>WP\_004181378.1 MULTISPECIES: dihydroxyacetone kinase subunit DhaL [Klebsiella]

MSLNRTQIVDWLYRCGDIFTKESDFLTGLDKEIGDADHGLNMHRGFSKVVEKLPSIADKDIGFILKNTGM

TLLSNVGGASGPLFGTFFIRAAQVTQAHQSLTLDELYLMIREGADGVVNRGKAEPGDKTMCDVWLPVVDS

LRQSSEQHLSIAAALDAACEVAERAAHATITMQARKGRASYLGERSIGHQDPGATSVLFMVQMLAAAAKE

>WP\_002917682.1 MULTISPECIES: dihydroxyacetone kinase subunit DhaK [Klebsiella]

MKKLINRVEDVLNEQLQGLAKAHPQLTLHQDPLYVTRTDAPVAGKVALLSGGGSGHEPMHCGYIGQGMLS

GACPGEIFTSPTPDKMFECAMQIDGGEGVLLIIKNYTGDILNFETATELLHESGIKVTTVVVDDDVAVKD

SLYTAGRRGVANTVLIEKLVGAAAERGDSLEACAELGRRLNNLGHSIGIALGACTVPAAGQPSFTLKDDE

MEFGVGIHGEPGIDRRRFSSLDQTVDEMFDTLLENGAYSRTLRQWDTVKGAWQEVQQSKTALQNGDRVIA

LVNNLGATPLSELYGVYNRLAQRCEASGIIIERNLIGSYCTSLDMAGFSITLLKVDDETLTLWDAPVHTP

ALNWGN

>WP\_032415719.1 MULTISPECIES: hypothetical protein [Klebsiella]

MFDPLFSRSRQKISKKFFSTRFASYPDRRLWQKKKSAPARIFTISSAKTFHKETKSGSNVS

>WP\_002917681.1 MULTISPECIES: glycerol dehydrogenase [Enterobacteriaceae]

MLKVIQSPAKYLQGPDAAVLFGQYAKNLAESFFVIADDFVMKLAGEKVVNGLQSHDIRCHAERFNGECSH

AEINRLMAILQKQGCRGVVGIGGGKTLDTAKAIGYYQKLPVVVIPTIASTDAPTSALSVIYTEAGEFEEY

LIYPKNPDMVVMDTAIIAKAPVRLLVSGMGDALSTWFEAKACYDARATSMAGGQSTEAALSLARLCYDTL

LAEGEKARLAAQAGVVTEALERIIEANTYLSGIGFESSGLAAAHAIHNGFTILEECHHLYHGEKVAFGTL

AQLVLQNSPMDEIETVLGFCQRVGLPVTLAQMGVKEGIDEKIAAVAKATCAEGETIHNMPFAVTPESVHA

AILTADLLGQQWLAR

>WP\_002917680.1 MULTISPECIES: dihydroxyacetone kinase operon transcriptional regulator DhaR [Enterobacteriaceae]

MTVQTQDTGKAVSSVIAQSWHRCSKFMQRETWQTPHQAQGLTFDSICRRKTALLTIGQAALEDAWEFMDG

RPCALFILDESACILSRCGEPQTLAQLAALGFRDGSYCAESIIGTCALSLAAMQGQPINTAGDRHFKQAL

QPWSFCSTPVFDNHGRLFGSISLCCLVEHQSSADLSLTLAIAREVGNSLLTDSLLAESNRHLNQMYGLLE

SMDDGVMAWNEQGVLQFLNVQAARLLHLDAQASQGKNIADLVTLPALLRRAIKHARGLNHVEVTFESQHQ

FVDAVITLKPIVEAQGNSFILLLHPVEQMRQLMTSQLGKVSHTFEQMSADDPETRRLIHFGRQAARGGFP

VLLCGEEGVGKELLSQAIHNESERAGGPYIAVNCQLYADSVLGQDFMGSAPTDDENGRLSRLELANGGTL

FLEKIEYLAPELQSALLQVIKQGVLTRLDARRLIPVDVKVIATTTVDLANLVEQNRFSRQLYYALHSFEI

VIPPLRARRNSIPSLVHNRLKSLEKRFSSRLKVDDDALAQLVAYSWPGNDFELNSVIENIAISSDNGHIR

LSNLPEYLFSERPGGDSASSLLPASLTFSAIEKEAIIHAARVTSGRVQEMSQLLNIGRTTLWRKMKQYDI

DASQFKRKHQA

>WP\_016529557.1 cob(I)yrinic acid a,c-diamide adenosyltransferase [Klebsiella pneumoniae]

MYRIYTRTGDKGTTALYGGSRIEKDHIRVEAYGTVDELISQLGVCYATTRDAGLRESLHQIQQTLFVLGA

ELASDARGLTRLSQTIGEEEISALERLIDRNMAESGPLKQFVIPGKNLSSAQLHVARTQARRLERLLTAM

DRAHPLREALKRYSNRLSDALFSMARIEETRPDACA

>WP\_016529556.1 glycerol dehydratase reactivase beta/small subunit family protein [Klebsiella pneumoniae]

MSLSPPGVRLFYDPRGHHAGAINELCWGLEEQGVPCQTITYDGGGDAAALGALAARSSPLRVGIGLSAAG

EIALTHAQLPADAPLATGHVTDSGDHLRTLGANAGQLVKVLPLSERN

>WP\_004150927.1 MULTISPECIES: 1,3-propanediol dehydrogenase [Enterobacterales]

MSYRMFDYLVPNVNFFGPNAISVVGERCQLLGGKKALLVTDKGLRAIKDGAVDKTLHYLREAGIEVAIFD

GVEPNPKDTNVRDGLAVFRREQCDIIVTVGGGSPHDCGKGIGIAATHEGDLYQYAGIETLTNPLPPIVAV

NTTAGTASEVTRHCVLTNTETKVKFVIVSWRNLPSVSINDPLLMIGKPAALTAATGMDALTHAVEAYISK

DANPVTDAAAMQAIRLIARNLRQAVALGSNLQARENMAYASLLAGMAFNNANLGYVHAMAHQLGGLYDMP

HGVANAVLLPHVARYNLIANPEKFADIAELMGENITGLSTLDAAEKAIAAITRLSMDIGIPQHLRDLGVK

EADFPYMAEMALKDGNAFSNPRKGNEQEIAAIFRQAF

>WP\_015875176.1 MULTISPECIES: heme-binding protein [Klebsiella]

MNKSQQVQTITLAAAQQMAAAVEKKATEINVAVVFSVVDRGGNTLLIQRMDEAFVSSCDISLNKAWSACS

LKQGTHEITSAVQPGQSLYGLQLTNQQRIIIFGGGLPVIFNEQVIGAVGVSGGTVEQDQLLAQCALDCFS

AL

>WP\_016529555.1 propanediol/glycerol family dehydratase large subunit [Klebsiella pneumoniae]

MKRSKRFAVLAQRPVNQDGLIGEWPEEGLIAMDSPFDPVSSVKVDNGLIVELDGKRRDQFDMIDRFIADY

AINVERTEQAMRLEAVEIARMLVDIHVSREEIIAITTAITPAKAVEVMAQMNVVEMMMALQKMRARRTPS

NQCHVTNLKDNPVQIAADAAEAGIRGFSEQETTVGIARYAPFNALALLVGSQCGRPGVLTQCSVEEATEL

ELGMRGLTSYAETVSVYGTEAVFTDGDDTPWSKAFLASAYASRGLKMRYTSGTALMGYSESKSMLYLESR

CIFITKGAGVQGLQNGAVSCIGMTGAVPSGIRAVLAENLIASMLDLEVASANDQTFSHSDIRRTARTLMQ

MLPGTDFIFSGYSAVPNYDNMFAGSNFDAEDFDDYNILQRDLMVDGGLRPVTEAETIAIRQKAARAIQAV

FRELGLPPIADEEVEAATYAHGSNEMPPRNVVEDLSAVEEMMKRNITGLDIVGALSRSGFEDIASNILNM

LRQRVTGDYLQTSAILDRQFEVVSAVNDINDYQGPGTGYRISAERWAEIKNIPGVVQPDTIE

>WP\_002917672.1 MULTISPECIES: propanediol/glycerol family dehydratase medium subunit [Enterobacterales]

MQQTTQIQPSFTLKTREGGVASADERADEVVIGVGPAFDKHQHHTLIDMPHGAILKELIAGVEEEGLHAR

VVRILRTSDVSFMAWDAANLSGSGIGIGIQSKGTTVIHQRDLLPLSNLELFSQAPLLTLETYRQIGKNAA

RYARKESPSPVPVVNDQMVRPKFMAKAALFHIKETKHVVQDAEPVTLHVDLVRE

>WP\_002917670.1 MULTISPECIES: glycerol dehydratase small subunit DhaB3 [Gammaproteobacteria]

MSEKTMRVQDYPLATRCPEHILTPTGKPLTDITLEKVLSGEVGPQDVRISRQTLEYQAQIAEQMQRHAVA

RNFRRAAELIAIPDERILAIYNALRPFRSSQAELLAIADELEHTWHATVNAAFVRESAEVYQQRHKLRKG

S

>WP\_016529554.1 diol dehydratase reactivase subunit alpha [Klebsiella pneumoniae]

MPLIAGIDIGNATTEVALASDDPQARAFVASGIVATTGMKGTRDNIAGTLAALEQALAKTPWSMSDVSRI

YLNEAVPVIGDVAMETITETIITESTMIGHNPQTPGGVGVGVGTTIALGRLATLPAAQYAEGWIVLIDDA

VDFLDAVWWLNEALDRGINVVAAILKKDDGVLVNNRLRKTLPVVDEVTLLEQVPEGVMAAVEVAAPGQVV

RILSNPYGIATFFGLSPEETQAIVPIARALIGNRSAVVLKTPQGDVQSRVIPAGNLYISGEKRRGEADVA

EGAEAIMQAMSACAPVRDIRGEPGTHAGGMLERVRKVMASLTGHEMSAIYIQDLLAVDTFIPRKVQGGMA

GECAMENAVGMAAMVKADRLQMQVIARELSARLQTEVVVGGVEANMAIAGALTTPGCAAPLAILDLGAGS

TDAAIVNAEGQITAVHLAGAGNMVSLLIKTELGLEDLSLAEAIKKYPLAKVESLFSIRHENGAVEFFREA

LSPAVFAKVVYIKEGELVPIDNASPLEKIRLVRRQAKEKVFVTNCLRALRQVSPGGSIRDIAFVVLVGGS

SLDFEIPQLITEALSHYGVVAGQGNIRGTEGPRNAVATGLLLAGQAN

>WP\_046042320.1 aquaporin [Klebsiella pneumoniae]

MNQTSTLTGQCVAEFLGTGLLIFFGAGCVAALRVAGASFGQWEISIIWGLGVAMAIYLTAGVSGAHLNPA

VTIALWLFACFERRKVLPFIVAQTAGAFCAAALVYGLYRQLFLDLEQSQHIVRGTAASLNLAGVFSTYPH

PQITFIQAFAVETTITAILMAMIMALTDDGNGIPRGPLAPLLIGLLIAVIGASMGPLTGFALNPARDFGP

KLFTSLAGWGSIAFTGGLAIPYFLVPLLAPVVGAIIGAFLYRKLIGRHLPCECGIDE

>WP\_002917655.1 MULTISPECIES: acid-activated periplasmic chaperone HdeB [Klebsiella/Raoultella group]

MNLPKALVLTVAATTFCLMTSPAFAVEETTPQNMTCQEFMDMNPKSMTPVAFWVVNRNTDFSGGDYVDWH

EVETVSVPKMLQECHKNPAAKLGDLSAVIKK

>WP\_002917651.1 MULTISPECIES: HdeD family acid-resistance protein [Klebsiella]

MFMFSHYTLNAFSPRVFIRYKRHACLMAVLLFICGACCLAWPLVAGWYLATVTGMLLMICGFYSLYSLIV

FRQQHWKSRLVALIFAIAWIVLGLSFVVNPLNGMSSLAILFGFLFVLGGISRIVNGCQTRKQSGAGWNIF

IGLLDLLIACLWLAMNPQQSWLFITAFIGVEMIFSAIGLLVLRNKMKHAQA

>WP\_004144810.1 MULTISPECIES: YfdX family protein [Klebsiella]

MLTDFNQESTMKKVILASLLATMMSTSPVWATDSATAAPAAAATTQVQKEAADVLQVAVQGANAMRDIQF

ARLALFHGQPDSAKKLTDDAAALLAADDASWAKFVKTDAKAKMIADRYVIINASIALSEDYVATPEKESA

IQSANEKLAKGDQKGAIDTLRLAGIGVIENQYLMPLNQTRKAVAQAQELLKAGKYYEANLVLKGAEEGIV

VDSEMLVAGN

>WP\_020864858.1 transporter substrate-binding domain-containing protein [Klebsiella pneumoniae]

MAVRLILSVVVGLALSLSPAAYAMKQLELKSHSHIAAIDIPLSGKEKAWLAAQPTLTVGTWLPERTPIVY

DGDEKSYQGINADYLALMAHSLGLKVIIRQYDTEQQALTALADRQVDTLLTQVAHRDALAPSLDQSAPLL

KTWPTLVTSLKSPLPPLTTDRRVTLACTRDCAFFDIIQQAFPNAKITLYDSDYQALASVVSGENQYFIGN

NITTGHCISKYFSQSLVIAHYFRQQEQHNRFVTRDDRPELHQLLDRFIHAVDSDTAMRIMQNWLNRGDLS

FLNTPLTFSPEEQRWLQKHRRVRLLVNPYFPPFTLVDNEDELRGIMADMLNIVSLQTGLQFDPILVRNRQ

ALAKRMEKEDWAIMPAATLTPQPQAYVTLSDPLINVAFVLVARGSAPDQHLLTRSARIALPVGPIAAHDL

KARFPLINWVETDNVGVAMKMVEEGEVDAAVASELSARYMIDHYYPQGLHYTRIDGLPVAAIRLAIPRDE

PVLAAILNKALQVIPPRDILQMTEKWSKISSQQIENWSQYSRQFYQLIAFALVLIAISLGWGLSLCREVR

KRKDSQQRLEEELAQKEALSCALEREKDKAIQATKAKSRFLASMSHELRTPVSAIVGFLELLAKPELNVG

QRKEALELAGSTAQTLLGLIGNILDIDKIESGKYQVTPQWSDVAQLVSQQCHTFDALAQQKGIDLHYHNA

LQEGTMLWVDPQALRQILNNLIGNALKFTVEGAIQVSCRLTPANETQGELALMVSDSGCGISEAEQATLF

HRYAQARQGRQQTGSGLGLVICKELVALMQGRLEMVSRPGVGTTFTITLPVKASRCAIHAPQASPARPQA

LPGLAILIADDHPTNRLLLKRQLSTIGYSVDEACDGEEAENKLASKHYDLLITDLNMPKKDGLELAASLR

RRYPGLVIWGVTASALPQSREACLASGMNMCLFKPVSVQTLSHELSRLAVGRSSPHATRHLKLSVLSENT

GGDQALMNEMLETFRDASAADLQAAGQAIARHEPQIFLRALHRLHGSAQILGITRQLAGVSESGRFASKG

AHSCCSAVMVQRITGVMREIDGEIDALIGR

>WP\_004174237.1 MULTISPECIES: acid-sensing system DNA-binding response regulator EvgA [Klebsiella]

MNAIIIDDHPLARIAIRNLLDSNGITVAAELDSGAHAVQTAESMQPDLLIVDVDIPELSGIEVLEQLRKR

RYQGTIIIISAKNELFYGKRSADCGANGFVSKKEGMNNILAAIDAANNGYSYFPFSLERFCTHGITDQDR

LDTLSTQEMKVFRYILSGVDYTTIGSKMNISNKTVSTYKVRLMDKLGCSTLLELYDFAQRNKIG

>WP\_026005884.1 HdeA/HdeB family chaperone [Klebsiella pneumoniae]

MAKEKRAFWRKWVWKHLMAGITVLAMSCAAVGKDVVPDEARTRDMMRCQDYLQLDPRAWTPMVIWLMNDP

FSLEPPEWTDFHEAELVLTPILTEICRQEPDVWLTSLRERLNSYQQVRSLN

>WP\_004185740.1 hypothetical protein [Klebsiella pneumoniae]

MKEAAAFAFNVDASQVTISDTRQQDVKTNFVVTIGKTSHRCYVTKAAEPKLYGLIPLGGGSTVSDAICAG

ANPTLASKTCDALSQKAGRC

>WP\_002917636.1 MULTISPECIES: G/U mismatch-specific DNA glycosylase [Klebsiella]

MISDILAPGLRVVFCGINPGKSSAHTGFHFAHPGNRFWKVIHQAGFTDRQLRPEEELQLLDTRCGITMLV

ERPTVQASEVALQELRSGGRELVRKIEEYQPQALAVLGKQAFELAFNQRGAKWGKQAMTIGTTQVWVLPN

PSGLNRATLDKLVAAYRELDDALATRGQ

>WP\_004174339.1 MULTISPECIES: RNA polymerase sigma factor RpoD [Klebsiella]

MEQNPQSQLKLLVQRGKEQGYLTYAEVNDHLPEDIVDSDQIEDIIQMINDMGIQVMEEAPDADDLMLAEN

TADEDAAEAAAQVLSSVESEIGRTTDPVRMYMREMGTVELLTREGEIDIAKRIEDGINQVQCSVAEYPEA

ITYLLEQYDRVEAEEARLSDLITGFVDPNAEEDMAPTATHVGSELSQEEMDDDEDEDEDEDADDNSDDDN

SIDPELAREKFAELRTQYELTRDTIKAKGRSHAAAQEEILKLSEVFKQFRLVPKQFDYLVNSMRSMMDRV

RTQERIIMKLCVEQCKMPKKNFITLFTGNETSETWFNAAVAMNKPWSEKLLEVKEDVQRGLQKLQQIEEE

TGLTIEQVKDINRRMSIGEAKARRAKKEMVEANLRLVISIAKKYTNRGLQFLDLIQEGNIGLMKAVDKFE

YRRGYKFSTYATWWIRQAITRSIADQARTIRIPVHMIETINKLNRISRQMLQEMGREPTPEELAERMLMP

EDKIRKVLKIAKEPISMETPIGDDEDSHLGDFIEDTTLELPLDSATTESLRAATHDVLAGLTAREAKVLR

MRFGIDMNTDHTLEEVGKQFDVTRERIRQIEAKALRKLRHPSRSEVLRSFLDD

>WP\_004149864.1 MULTISPECIES: DNA primase [Klebsiella]

MAGRIPRVFISDLLARTDIVDLIDARVKLKKQGKNFHACCPFHNEKTPSFTVNGEKQFYHCFGCGAHGNA

IDFLMNYDKLEFVETVEELAAMHNLEVPYEAGNGPSQIERHQRQNLYQLLDGLNAFYQQSLMQPAADPAR

QYLAKRGLSSEVITRFAIGYAPPGWDNVLKRFGGNQENRQSLIDAGMLVTNDQGRSYDRFRERVMFPIRD

KRGRVIGFGGRVLGDALPKYLNSPETDIFHKGRQLYGLYEAQQDNPEPPRLLVVEGYMDVVALAQYDINY

AVASLGTSTTADHIQLLFRVTNNVICCYDGDRAGRDAAWRALETALPYMTDGRQLRFMFLPDGEDPDTLV

RKEGKAAFEARMEQAQPLSTFLFNSLLPQVDLSTPDGRAQLSTLALPLITQVPGETLRIYLRQELGNKLG

ILDDAQLERLMPKQAENGAPRPAPQLKRTTMRILIGLLVQNPDLAPLVPPLEGLDSRKMPGLSLFSELVK

SCLAQPGLTTGQLLEQYRGTKEAATLEKLSMWDDIADKDIAEQTFTDSLNHMFDSLLELRQEELIARDRT

HGLSSEERRELWTISQELAKK

>WP\_001144069.1 MULTISPECIES: 30S ribosomal protein S21 [Bacteria]

MPVIKVRENEPFDVALRRFKRSCEKAGVLAEVRRREFYEKPTTERKRAKASAVKRHAKKLARENARRTRL

Y

>WP\_002916879.1 MULTISPECIES: tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex transferase subunit TsaD [Klebsiella]

MRVLGIETSCDETGIAIYDDQQGLLANQLYSQVKLHADYGGVVPELASRDHVRKTVPLIQAALKEAGLTA

KDIDAVAYTAGPGLVGALLVGATVGRSLAFAWNVPAIPVHHMEGHLLAPMLEDNPPAFPFVALLVSGGHT

QLISVTGIGQYELLGESIDDAAGEAFDKTAKLLGLDYPGGPMLSKMASQGTEGRFVFPRPMTDRPGLDFS

FSGLKTFAANTIRSNGDDEQTRADIARAFEDAVVDTLMIKCRRALEQTGFKRLVMAGGVSANRTLRAKLA

EMMQKRGGEVFYARPEFCTDNGAMIAYAGMVRLQTGAKAELGVTVRPRWPLAELPAA

>WP\_004181356.1 MULTISPECIES: cytosine permease [Klebsiella]

MSSLDLNPELPATTRTSGSRETLEDYTLRYAPLSFRRWGPGVVAVTALGGIAYLADFSIGASIGMAWGTS

NAIYSILVAALVIFLTGIPLAITAARYNIDLDLITRSAGFGYFGSVITSIIFAGFTFIFFALEGSIMAQG

LLVGLGIPLWMGYLIATLMVLPLVVYGMKALTRLQVWTTPLWLVLMVVPVVWLIVKDPQLVDGFLHFAGK

NSASTVDITAIMLGAGVCLSLIMQIGEQIDYLRFMPPKTAENRKSWWLAVFSAGPGWVVLGAIKQIIGAF

LGFYLLTRFPAVHNTEPVQQFVSVFDNLVPGWLALTLAVVLVVISQIKINVTNAYSGSLAWTSAWTRTTK

RYPGRIIFVVVNLAIALALMEGDMFSALSWILGFYSNFAIAWVVVVATDITFNKGLLKLAPAQPEYRRGM

IYNVNPVGVVSFGLAAGLSICAFFGLLGATLAPFSPLIALVVAFVMTPLMGLLTRGRYYIKQVDDGIAEP

RYDAAGNASTTVYQCVSCEEEYERPDVMHSHKHQGAICSLCKSME

>WP\_002916877.1 MULTISPECIES: urease accessory protein UreG [Bacteria]

MNSYKHPLRVGVGGPVGSGKTALLEALCKAMRDTWQLAVVTNDIYTKEDQRILTEAGALAPERIVGVETG

GCPHTAIREDASMNLAAVEALSEKFGNLDLIFVESGGDNLSATFSPELADLTIYVIDVAEGEKIPRKGGP

GITKSDFLVINKTDLAPYVGASLEVMASDTQRMRGDRPWTFTNLKQGDGLSTIIAFLEDKGMLGK

>WP\_016532672.1 MULTISPECIES: urease accessory protein UreF [Klebsiella]

MSTAEQRLRLMQLASSNLPVGGYSWSQGLEWAVEAGWVPDVAAFERWQRRQMTEGFFTVDLPLFARLYRA

CEQGDIAAAQRWTAYLLACRETRELREEERNRGAAFARLLSDWQPDCPPPWRSLCQQSQLAGMAWLGVRW

RIALPEMALSLGYSWIESAVMAGVKLVPFGQQAAQQLILRLCDHYAAEMPRALAAPDGDIGSATPLAAIA

SARHETQYSRLFRS

>WP\_002916875.1 MULTISPECIES: urease accessory protein UreE [Klebsiella]

MLYLTQRLEIPAAATASVTLPIDVRVKSRVKVTLNDGREAGLLLPRGLLLRGGDVLSNEEGTEFVQVIAA

DEGVSVVRCDDPFMLAKACYHLGNRHVPLQIMPGELRYHHDHVLDDMLRQFGLTVTFGQLPFEPEAGAYA

SESHGHHHAHHDHHAHSH

>WP\_046042331.1 urease subunit alpha [Klebsiella pneumoniae]

MSNISRQAYADMFGPTVGDKVRLADTELWIEVEDDLTTYGEEVKFGGGKVIRDGMGQGQMLAADCVDLVL

TNALIVDHWGIVKADIGVKDGRIFAIGKAGNPDIQPNVTIPIGAATEVIAAEGKIVTAGGIDTHIHWICP

QQAEEALVSGVTTMVGGGTGPAAGTHATTCTPGPWYISRMLQAADSLPVNIGLLGKGNVSQPDALREQVA

AGVIGLKIHEDWGATPAAIDCALTVADEMDIQVALHSDTLNESGFVEDTFAAIGGRTIHTFHTEGAGGGH

APDIITACAHPNILPSSTNPTLPYTLNTIDEHLDMLMVCHHLDPDIAEDVAFAESRIRRETIAAEDVLHD

LGAFSLTSSDSQAMGRVGEVILRTWQVAHRMKVQRGALAEETGDNDNFRVKRYIAKYTINPALTHGIAHE

VGSIEVGKLADLVVWSPAFFGVKPATVIKGGMIAIAPMGDINASIPTPQPVHYRPMFGALGSARHHCRLT

FLSQAAAANGVAGRLNLRSAIAVVKGCRTVQKADMVHNSLQPNITVDAQTYEVRVDGELITSEPADVLPM

AQRYFLF

>WP\_002916872.1 MULTISPECIES: urease subunit beta [Bacteria]

MIPGEYHVKPGQIALNTGRATCRVVVENHGDRPIQVGSHYHFAEVNPALKFDRQQAAGYRLNIPAGTAVR

FEPGQKREVELVAFAGHRAVFGFRGEVMGPLEVNDE

>WP\_002916871.1 MULTISPECIES: urease subunit gamma [Bacteria]

MELTPREKDKLLLFTAALVAERRLARGLKLNYPESVALISAFIMEGARDGKSVASLMEEGRHVLTREQVM

EGVPEMIPDIQVEATFPDGSKLVTVHNPII

>WP\_016532675.1 urease accessory protein UreD [Klebsiella pneumoniae]

MHGTVLPPLKKGWQATLDLRFHQAGGKTVLASAQHVGPLTVQRPFYPEEETCHLYLLHPPGGIVGGDELT

ISAHLAPGCHTLITMPGASKFYRSSGAQALVRQHLTLAPQATLEWLPQDAIFFPGANARLFTTFHLCASS

RLLAWDLLCLGRPVIGETFSHGTLSNRLEVWVDDEPLLVERLQLQEGELSSVAERPWVGTLLCYPATDAL

LDGVRDALAPLGLYAGASLTDRLLTVRFLSDDNLICQRVMRDVWQFLRPHLTGKSPVLPRIWLT

>WP\_004144529.1 MULTISPECIES: short-chain dehydrogenase [Bacteria]

MPCNVAPLQNQDKTAAMSIDRREFIPVIRNAYVIRNPERRDGREGKAA

>WP\_020324810.1 MULTISPECIES: hypothetical protein [Klebsiella]

MERQKLRWRLAARRNPIRRLFRRAQAADQDIDGKDYPGE

>WP\_004144530.1 MULTISPECIES: glycerol-3-phosphate 1-O-acyltransferase PlsY [Klebsiella]

MSAIAPGLVLLAYLCGSISSAILVCRLAGLPDPRDSGSGNPGATNVLRIGGKGAAVAVLIFDVLKGMLPV

WGAWALGLTPFWLGLVAIAACVGHIWPVFFHFRGGKGVATAFGAIAPIGLDLTGVMAGTWLLTILLSGYS

SLGAIVSALIAPFYVWWFKPQYTFPVSMLSCLILLRHHDNIQRLWRRQESKIWTRVKKKKTPEQK

>WP\_004150923.1 MULTISPECIES: bifunctional dihydroneopterin aldolase/7,8-dihydroneopterin epimerase [Klebsiella]

MDIVFIEQLSVITTIGVYDWEQTIEQKLVFDIEIAWDNRKAAASDDVSDCLSYADISERVIAHVEGGKFA

LVERVAEEVADLLLETFQSPWVRIKVSKPGAVARAANVGVIIERGLNLKQNFSGHTC

>WP\_004144532.1 MULTISPECIES: undecaprenyl-diphosphate phosphatase [Klebsiella]

MSDIHSLLVAAILGVVEGLTEFLPVSSTGHMIIVGHLLGFEGDTANTFEVVIQLGSILAVVVMFWRRLFG

LIGIHFGKPPAHEGQGSGRLSLIHILLGMIPAVVMGLIFHDTIKSLFNPVNVMYALIVGGVLLIAAEVLK

PKQPRAVGIDDMTYRQAFVIGCFQCLALWPGFSRSGATISGGMLMGVSRYAASEFSFLLAVPMMMGATVL

DVYKSIGFLNMGDVPMFAVGFVMAFIVALIAIKTFLQLIKRISFIPFAIYRFIVAAAVYVVFF

>WP\_016532678.1 multifunctional CCA addition/repair protein [Klebsiella pneumoniae]

MKSYLVGGAVRDALLGLPVKDRDWVVVGATPQQMLDAGYQQVGRDFPVFLHPQSREEYALARTERKSGAG

YTGFTCYAAPDVTLEADLLRRDLTVNALAQDADGAIIDPYGGQNDLRQRLLRHVSPAFSEDPLRVLRVAR

FAARYAHLGFRIAEETQALMAAMVEAGELAHLTPERVWKETESALTTRNPQVFFQTLRDCQALKVLFPEI

DALYGVPAPAKWHPEIDTGLHTLMTVTMAAMLSPDVDVRFATLCHDLGKGLTPKALWPRHHGHGPAGVKL

VEQLCARLRVPNDIRDLAKLVAEYHDLIHTLPILQPKTLVKLFDSIDAWRKPQRVQQIALTSEADVRGRT

GFEASDYPQRRLLLEAWEVAQSVSTKEVVAAGFKGAEIREELTRRRIAAVAQWKEQRCPQPQG

>WP\_002916862.1 MULTISPECIES: TIGR04211 family SH3 domain-containing protein [Klebsiella]

MPKLRLITFTLLALSAATAVHAEEKRYVSDELNTWVRSGPGDNYRLVGTINAGEEVSVLQTNDSTSYAQI

RDSNGRTAWIPLKELSNEPSLRTRVPDLENQVKTLTDKLNNIDATWNQRTADMQKKVAGSDSVINALKDE

NQKLKNELVVAQKKVNAANLQLDDKQRTIIMQWFMYGGGVLGVGLLLGLVLPHLVPSRKRKDRWMN

>WP\_004174351.1 inorganic triphosphatase [Klebsiella pneumoniae]

MAQEIELKFIVAQDGVETLREQLNALEAKHTPAGQLLNIYYETADNWLRRHDMGLRIRGDQGRYEMTLKI

AGRVVGGLHQRPEYNIPLDKPELALERLPAEVWPQGELPAALAEHVQPLFSTDFARERWVIQEGKSEIEI

ALDRGEVKAGEHQEPICELELELLAGETADLLRLAHRLLESGVLRQGSLSKAARGYHLAQGNNERPVTRL

AVLPVAAKASVEQGLEAALESALAHWLYHDEIWLRGNAKAKAEILLAIARVRHALVLFGGIVPRKATTHL

RALLNDADAVLLAADTADEALFRTEVVGAKLALTEWLIQRGWRPFLNEAGEKKIAGSFKRFADIHLSRVA

AELRSAVQHLAVEDAADQLPKLSRDIDSVQLLAGAYGDAVAPWLENWQELQRAIEHDDRSVFEYFRRQAL

AAEPFWLHSGKR

>WP\_004174352.1 bifunctional [glutamate--ammonia ligase]-adenylyl-L-tyrosine phosphorylase/[glutamate--ammonia-ligase] adenylyltransferase [Klebsiella pneumoniae]

MMPLSPQLQQHWQTVADRLPADFPVAELSPQARSVMAFSDFVEQSVIAQPGWLNELADSAPAAEEWRHYE

AWLQERLQAVTDEAGLMRELRLFRRQMMVRIAWAQALSLVREEETLQQLSVLAETLIVAARDWLYAACCK

EWGTPCNAEGQPQPLLILGMGKLGGGELNFSSDIDLIFAWPEHGATRGGRRELDNAQFFTRLGQRLIKAL

DQPTQDGFVYRVDMRLRPFGDSGPLVLSFAALEDYYQEQGRDWERYAMVKARIMGDNDGAYASELRAMLR

PFVFRRYIDFSVIQSLRNMKGMIAREVRRRGLKDNIKLGAGGIREIEFIVQVFQLIRGGREPALQQRALL

PTLAAIDELHLLPEGDAMLLRAAYLFLRRLENLLQSINDEQTQTLPQDELNRARLAWGMHTDDWETLSAQ

LANHMANVRRVFNELIGDDEAQSPDEQLAEYWRELWQDALEEDDASPALAHLNDADRRSVLALIADFRKE

LDRRTIGPRGRQVLDQLMPHLLSEICSRADAPLPLARITPLLTGIVTRTTYLELLSEFPGALKHLITLCA

ASPMVASQLARHPLLLDELLDPNTLYQPTATDAYRDELRQYLLRVPEEDEEQQLEALRQFKQAQQLHIAA

ADIAGTLPVMKVSDHLTWLAEAILDAVVQQAWGQMVARYGLPTHLHDRQGRGFAVVGYGKLGGWELGYSS

DLDLVFLHDCPAEVMTDGEREIDGRQFYLRLAQRIMHLFSTRTSSGILYEVDARLRPSGAAGMLVTTADA

FADYQQNEAWTWEHQALVRARVVYGDPALQARFDAIRRDILTTPREGATLQTEVREMREKMRAHLGNKHP

NRFDIKADAGGITDIEFITQYLVLRYASDKPKLTRWSDNVRILELLAQNDIMDEEEARALTHAYTTLRDA

LHHLALQELPGHVAPEAFSREREQVSASWQKWLMA

>WP\_046042336.1 bifunctional D-glycero-beta-D-manno-heptose-7-phosphate kinase/D-glycero-beta-D-manno-heptose 1-phosphate adenylyltransferase HldE [Klebsiella pneumoniae]

MKVTLPEFERAGVLVVGDVMLDRYWYGPTSRISPEAPVPVVKVENIEERPGGAANVAMNIASLGATSRLV

GLTGIDDAARALSQALANVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLDFEEGFSGVDPQPMHERIQQA

LGSIGALVLSDYAKGALTSVQTMIRLAREAGVPVLIDPKGTDFERYRGATLLTPNLSEFEAVVGKCQDEA

QIVERGMKLIAEFELSALLVTRSEQGMTLLQPGRPPLHMPTQAQEVYDVTGAGDTVIGVLAATLASGNTL

EEACYFANAAAGVVVGKLGTSTVSPVELENAVRGRAESGFGVMSEEELKQAVAAARKRGEKVVMTNGVFD

ILHAGHVSYLANARKLGDRLIVAVNSDASTKRLKGETRPVNPLEQRMIVLGALEAVDWVVSFEEDTPQRL

IAGILPDLLVKGGDYKPEQIAGSEEVWANGGEVLVLNFEDGCSTTNIIKKIQKDSDK

>WP\_004144536.1 MULTISPECIES: hypothetical protein [Klebsiella]

MVHAHTPSAVDVLISHMPFTHFSIYAYLNAICTKNALNMIIYCAKSFST

>WP\_004174354.1 MULTISPECIES: cell surface composition regulator GlgS [Klebsiella]

MNHNDMYSMKNFDFLARSFARMHAQGQPIDLQAIVGNMDEEHREWFCQRYELYCRQVSSQAEAAH

>WP\_004174355.1 MULTISPECIES: accessory factor UbiK family protein [Klebsiella]

MIDPKKIEQIARQVHESMPKGLRDLGEDVEKKIRQALQSQLTRLDLVSREEFDVQTQVLLRTREKLALLE

QRLNDLENRPATTPGSEEQQ

>WP\_004185664.1 MULTISPECIES: 3,4-dihydroxy-2-butanone-4-phosphate synthase [Klebsiella]

MNQTLLSSFGTAFERVEHALDALREGRGVMVLDDEDRENEGDMIFAAETMTVEQMALTIRHGSGIVCLCL

TEERRKQLDLPMMVENNTSAYGTGFTVTIEAAEGVTTGVSAADRVTTVRAAIADGAKPSDLNRPGHVFPL

RAQPGGVLTRGGHTEATIDLVTLAGFKPAGVLCELTNDDGTMARAPECIKFAQQHNMAVVTIEDLVAYRR

EHERKAS

>WP\_002916852.1 MULTISPECIES: zinc transporter ZupT [Klebsiella]

MSSPLILTLLAGSATFIGAIFGVIGQKPSNRLLGFSLGFAAGIMLLISLMEMLPAALAAEGMSPLLGYGM

FVVGLLGYFGLDRLLPHAHPQDLMTPAMPRPRNLRRTAILLTLGISLHNFPEGIATYVTASNNLELGMGV

ALAVALHNIPEGLAVAGPVYAATGSRSKAVLWAGLSGMAEILGGVLAWLILGSLVSPLVMGAIMAAVAGI

MVALSVDELMPLAKEIDPQSNPSYGVLCGMSVMGLSLVVLQTMGIG

>WP\_004174357.1 MULTISPECIES: 4,5-DOPA dioxygenase extradiol [Klebsiella]

MSRTRMPALFLGHGSPMNVLEDNRYTRAWAQLGETLPRPKAIVVVSAHWFTRGTGVTAMEAPKTIHDFGG

FPQALYDTHYPAPGSPALAQRLVELLSPVPVTLDTEAWGFDHGSWGVLIKMYPQADIPMVQLSIDSTKPP

AWHLEMGRKLASLRDEGIMLVASGNVVHNLRTARWHGENTPYPWAESFNNYVKANLQWQGLDEQHPLVNY

LAHEGGSLSNPTAEHFLPLLYVLGTWDGVEAMTIPVDGIEMGSLSMLSVLVGA

>WP\_004900674.1 MULTISPECIES: glutathionylspermidine synthase family protein [Klebsiella]

MERVSITERPDWREKATEYGFNFHTMYGEPYWSEEAYYKLTLAQVEKLEAVTAELHQMCLQVVEKVIASD

ELMTKFRIPKHTWGFVRQSWKTNQPSLYSRLDLAWDGVGEPKLLENNADTPTSLYEAAFFQWIWLEDQLN

AGKLPAGSDQFNSLQEKLIDRFGELREQFGFQLLHMACCRDTVEDRGTVQYLQDCAAEAGLATEFLYVED

IGLGEKGQFTDLQDQVIGNLFKLYPWEFMLREMFSTKLEDAGVRWLEPAWKSIISNKALLPMLWEMFPNH

PNLLAAYFSEDAHPEMEKYVIKPIFSREGANVSIVENGKVVEAVEGPYGEEGTIVQAFYPLPKFGDSYTL

IGSWLINDQPAGIGIREDRALITQDLSRFYPHIFVE

>WP\_002916849.1 MULTISPECIES: DUF1190 family protein [Klebsiella]

MKRTKNINHSSFRKSWSARHLTPVALAVTAVFMLAGCEKSDETVSLYQNADDCSAANPGKAAECTTAYTN

AVKEAERTAPKYATREDCVAEFGEGQCQQTPAQAGVAPENQAQAQSSGSFWMPLMAGYMMGRLMGGGMAQ

QQPLFSSKNPASPAYGQYTDASGKSYGAAQPGRTMNVPKTAMAPKPATTTTVTRGGFGESVAKQSTMQRS

AAGSTSSSRSMGG

>WP\_004150921.1 MULTISPECIES: outer membrane channel protein TolC [Klebsiella]

MKKLLPILIGLSLTGFSAMSQAENLLQVYQQARISNPDLRKSAADRDAAFEKINEARSPLLPQLGLGADY

TYTNGYRDSNGVNSNVTSGSLQLTQVLFDMSKWRALTLQEKTAGIQDVTYQTDQQTLILNTATAYFKVLA

AIDTLSYTEAQKQAIYRQLDQTTQRFNVGLVAITDVQNARSQYDAVLANEVTARNDLDNAVEGLRQVTGN

YYPELASLNVNGFKTNKPQAVNALLKEAENRNLSLLQARLSQDLAREQIRQAQDGHLPTLNLSASTGVSN

TRYNGSKTNTPLAYNDSDNGQNQIGLNFSLPLYQGGAVTSQVKQAQYNFVGASEQLESAHRSVVQTVRSS

FNNVNASISSINAYKQAVVSAQSSLDAMEAGYSVGTRTIVDVLDATTTLYNAKQQLSNARYNYLINELNI

KSALGTLNEQDLVALNNTLGKPISTSADSVAPENPQQDATADGYGNTTAAVKPASARTTQSSGSNPFRQ

>WP\_016532683.1 ADP-ribose diphosphatase [Klebsiella pneumoniae]

MSKPTQQGITFSKNDVEIIARETLYRGFFSLDLYRFRHRLFNGGMSREITREIFERGHAAVLLPFDPVRD

EVVLVEQIRIAAYDTSESPWLLEMVAGMIEAGETVEDVARREALEEAGLEVGRTKPILSYLASPGGTSER

LSILVGEVDASTAKGIHGLAEENEDIRVHVVSREQAYQWVEEGKIDNAASVIALQWLQLHYHNLRNEWTK

>WP\_002916847.1 MULTISPECIES: DUF1249 family protein [Enterobacterales]

MKRYTPDFPEMMRLCETNFAQLRRLLPRTDAAGEKVSYQVGSAQYRLTIVESTRYTTLVAIEQTLPAVSY

WSLPSMTVRLYHDAMVAEVCSSQQIFRFKARYDYPNKKLHQRDEKHQINQFLADWLRYCLAHGAMAIPVC

>WP\_002916846.1 MULTISPECIES: 3',5'-cyclic-AMP phosphodiesterase [Klebsiella]

MESLLNLPLAGEARVRILQITDTHLFAEKHETLLGINTWDSYQAVLSAIHASQRPCDLIVATGDLAQDHS

SAAYQHFAEGIASFAAPCVWLPGNHDFQPAMYSTLQEAGISPAKRVFLGDRWQILLLDSQVFGVPHGELS

DFQLEWLEHKLAEAPERYTLLLLHHHPLPAGCSWLDQHSLRNAGALDSALSAWPRVKHLLCGHIHQELDL

DWNGRRMMATPSTCVQFKPHCANFTLDTVSPGWRWLELHPDGTLTTEVCRLEGAAFHPDIASEGY

>WP\_002916845.1 MULTISPECIES: esterase YqiA [Klebsiella]

MATLLYLHGFNSSPRSAKATALKTWLAQHYPEITMVVPELPPYPAETAELLESIVLEHGGEPLGVVGSSL

GGYYATWLSQCFMLPAVVVNPAVRPFELLNNFLGHNENPYTGQQYVLESRHIYDLKVMQIDPLEAPDLLW

LLQQTGDEVLDYRQAVHYYASCRQTVEEGGNHAFVGFDDHFTQIIEFLGLR

>WP\_002916844.1 MULTISPECIES: DNA topoisomerase IV subunit B [Klebsiella]

MTQSSYNADAIEVLTGLEPVRRRPGMYTDTTRPNHLGQEVIDNSVDEALAGHAKRVEVILHADQSLEVID

DGRGMPVDIHPEEGVPAVELILCRLHAGGKFSNKNYQFSGGLHGVGISVVNALSKRVEVNVRRDGQVYSI

AFENGEKVEDLHVTGTCGKRNTGTSVHFWPDESFFDSPRFSVSRLTHLLKAKAVLCPGVEIVFRDQVNNS

EQSWCYADGLNDYLSEAVNGLPLLPEKPFVGAFSGETEAVDWALLWLPEGGELLTESYVNLIPTMQGGTH

VNGLRQGLLDAMREFCEYRNILPRGVKLSAEDIWDRCAYVLSVKMQDPQFAGQTKERLSSRQCAAFVSGV

VKDAFSLWLNQNVQAAELLAEMAISSAQRRLRAAKKVVRKKLTSGPALPGKLADCTAQDLNRTELFLVEG

DSAGGSAKQARDREYQAIMPLKGKILNTWEVSSDEVLASQEVHDISVAIGIDPDSDDLSQLRYGKICILA

DADSDGLHIATLLCALFVRHFRTLVKEGHVYVALPPLYRIDLGKEVYYALTEEEKTGVLEQLKRKKGKPN

VQRFKGLGEMNPMQLRETTLDPNTRRLVQLVISDEDEQQTTAIMDMLLAKKRSEDRRNWLQEKGDMADLE

V

>WP\_002916842.1 MULTISPECIES: antibiotic biosynthesis monooxygenase [Klebsiella]

MLTVIAEIRTRPGQHHRQAVLDQFAKIIPTVLQEAGCHGYAPLVDHAAGVSFQTTAPDSIVMVEQWESVA

HLEAHLQTPHMKAWSEAVKGDVLETSIRILQAGV

>WP\_002916840.1 MULTISPECIES: NAD(P)H-dependent oxidoreductase [Klebsiella]

MSNILIINGAKKFAHSNGQLNDTLTEVAESYLRDAGHDVKSVRAESEYDVKEEVQNFLWADVVIWQMPGW

WMGAPWTVKKYMDDVFTEGHGSLYASDGRTRSDASKKYGSGGLVQGKKYMLSLTWNAPMEAFTDKDQFFH

GVGVDGVYLPFHKANQFLGMEALPTFIANDVIKMPDVPRYIAEYRKHLAEIFG

>WP\_046042343.1 two-component system sensor histidine kinase QseC [Klebsiella pneumoniae]

MKRLARLRLRLTLLFAVLTTAAWGMASVIAWQQTSKKLDKLFDTQQLLFARRLSVMHFDELRAPPALLGE

KKKVRHGHIDDDALAFAIFTRDGKMVLNDGENGEDIQWNSQREGFSDGYLRDDDDEWRFLWLTTADGRYR

IAVGQEWDYRREMAMDIVTSQLTPWMVALPLMFVLLIVLLSRELAPLKNLARTLRLRAPDSADSLSVEKI

PAEVRPLVEALNQLFRRTHDVMLRERRFTSDAAHELRSPLAALKVQTEVAQLSLDDPEGREKALDQLHQG

IDRATRLVDQLLTLSRLDSLAQLDDVQKVAIADLLQSAVMEMYHPAQQSGIELRLHLNASHIVRTGQPLL

LSLLVRNLLDNAVRYSPRGSQVDITLNAREFRVRDNGPGISPQALSRIGERFYRPPGQEAPGSGLGLSIV

RRIASLHGMQVDFANARDGGFEARVYW

>WP\_004174368.1 two-component system response regulator QseB [Klebsiella pneumoniae]

MRILLVEDDKLIGDGIKAGLSKMGFSIDWFTAGLEGKNALYSAPYDAAILDLTLPGIDGLDILREWRDRG

RHEPVLILTARDALSQRVEGLRLGADDYLCKPFALIEVAARLEALIRRAHGQSSSELRHGKVILDPNRLT

ASLDGESLALKPKEFALLELLMRNAGRVLPRKLIEEKLYTWDDEVSSNAVEVHVHHLRRKLGSDFIRTVH

GIGYTLGDA

>WP\_002916833.1 MULTISPECIES: YgiW/YdeI family stress tolerance OB fold protein [Klebsiella]

MKKIAAMTAIIALVSMPVLAAGQGGFTGPSTTTTTQAGGFTGPSGAVTTVANAKSLRDDTWVTLRGKIVE

RISDDLYKFQDASGVINVDIDHKRWNGVTVGPQDTVEIQGEVDKDWNSVEIDVKQIRKIAP

>WP\_002916831.1 MULTISPECIES: AraC family transcriptional regulator [Klebsiella]

MNDIKASPAYVGRFQRVCRYIARHLDEPLSLETLSAIAHSSPYHFHRQFSAYTGIPLYRYIQWLRLRRAC

WRLAFNPRDKVIDIALDAGFQNAESFSRAFRTAFDQSPTQFRQQPDWAEWHRRVPKHTLQEQTSMDVNII

SCPSTRIAVLQHRGSPDLVNATAARFIAWRKTSGLSPVATSDTWGIAWDDPQTTPQEAFRFDICGTVDRP

VGENAFGVINGEIPGGRCAVVRHHGSLDTLANSVWFLYRDWLPASGETLRDFPVYFRYLNFVHEVAEHEL

QTDIYLPLA

>WP\_004181324.1 MULTISPECIES: DNA topoisomerase IV subunit A [Klebsiella]

MSDMAERLALHEFTENAYLNYSMYVIMDRALPFIGDGLKPVQRRIVYAMSELGLNASAKFKKSARTVGDV

LGKYHPHGDSACYEAMVLMAQPFSYRYPLVDGQGNWGAPDDPKSFAAMRYTESRLSKYAELLLSELGQGT

VDWVPNFDGTLQEPKMLPARLPNILLNGTTGIAVGMATDIPPHNLREVAKAAITLIEQPKTTLDELLDIV

QGPDFPTEAEIITSRAEIRKIYQNGRGSVRMRAVWSKEDGAVVISALPHQVSGAKVLEQIAAQMRNKKLP

MVDDLRDESDHENPTRLVIVPRSNRVDMEQVMNHLFATTDLEKSYRINLNMIGLDGRPAVKNLLEILSEW

LVFRRDTVRRRLNHRLEKVLKRLHILEGLLVAFLNIDEVIEIIRTEDEPKPALMSRFGISETQAEAILEL

KLRHLAKLEEMKIRGEQSELEKERDQLQAILASERKMNNLLKKELQADADAFGDDRRSPLHEREEAKAMS

EHDMLPSEPVTIVLSQMGWVRSAKGHDIDAQGLSYKAGDSWKASAKGKSNQPVVFIDTTGRSYAIDPITL

PSARGQGEPLTGKLTLPPGATVEHMLMESDDQKLLMASDAGYGFVCTFNDLVARNRAGKALITLPDNAHV

MPPLVIEDESDMLLAITAAGRMLMFPVSDLPQLSKGKGNKIISIPAAEAAAGQDGLAHLFVLPPQSTLTI

HVGKRKIKLRPEELQKVTGERGRRGSLMRGLQKIDRVEIDSPRRAAAGDSEE

>WP\_002916826.1 MULTISPECIES: 1-acylglycerol-3-phosphate O-acyltransferase [Klebsiella]

MLFIFRVIFVVIYCIVVCVLGCLYCLFSPRNPKHVATFGHLFGRLSPVFGLKVELRKPADAESYGNAIYI

ANHQNNYDMVTASNIVQAPTVTVGKKSLLWIPFFGQLYWLTGNLLIDRNNRTKAHGTIAEVVNAFKKRKI

SFWMFPEGTRSRGRGLLPFKTGAFHAAIAAGVPIIPVCVSNTSNKIKLNRWNNGLVIVEMLPPVDTTQFG

KDNVRALATHCRELMAAKIADLDNEVAEREAAGKQ

>WP\_046042347.1 cell division protein FtsP [Klebsiella pneumoniae]

MSLSRRQFIKASGVALCAGAAPLKAHAAGQQPALPVPPLLESRRGQPLFLTLQRSHWSFTPGTRAPVWGI

NGRYMGPTIRVWNGDDVKLIYSNRLTENVAMTIRGLQVPGPLIGGAARMMSPNADWAPVLPIRQSAATLW

YQANTPNRMAKQVYNGLAGMWLVEDEVSKNLPIPNHYGVDDFPVIIQDKRLDNFGTPEYSEPGSGGFVGD

TLLVNGVQSPYVEVSRGWVRLRLLNASNSRRYQLQMSDGRLLHVISGDQGFLPAPVSLKQLSLAPGERRE

ILVDMTNGDEVSITCGEAASIVDRIRGFFEPSSILVSTLVLTLRPTGLLPLVTDSLPVRLLPTELLSGTP

IRSRDITLGDDPGINGQLWDPQRIDITAQQGTWERWTVRADRPQSFHIEGVMFQIRNVNGSSPFPEDRGW

KDTMWVDGQVELLVYYAQPSWPHFPFQYLSQTLELADRGSIGQMLVNTAP

>WP\_004144550.1 MULTISPECIES: GNAT family N-acetyltransferase [Klebsiella]

MTPVILSRQQLDQLWEIDRSEIIDTLYRLDNGQLRAYREYYDVRGWDPHDRQVYTPIHEACYDRGGIFFA

FFDDEQMIAAAALDTLPRGMNGELRQLLFFYVGAGKRGQGWGRRLFQYALHQLPEMGASGLYISSIPNKN

TVDFYLAQGCRLADKPDPALFALEPEDIHLVCDRL

>WP\_002916796.1 MULTISPECIES: 2,5-didehydrogluconate reductase DkgA [Klebsiella]

MTHPTVIKLHDGNLMPQLGLGVWKAGNEEVVSAIHKALEVGYRSFDTAAAYQNETGVGNALHSAGVNRDE

LFITTKLWNDDQKRPHEALKESLSKLKLDYVDLYLIHWPVPAIGHYVEAWQALIELQQQGLTKSIGVCNF

QVPHLQKLIDETGVAPVINQIELHPLMQQRQLHAWNATHKIQTESWSPLAQGGEGVFDQKVIHQLADKYG

KTPAQIVIRWHLDSGLVVIPKSVTPSRIAENFDVWDFRLDKDELGAIAKLDQGKRLGPDPDQFGG

>WP\_004144551.1 MULTISPECIES: alcohol dehydrogenase [Klebsiella]

MNNFDLHTPTRILFGKGAIEKLREQIPAEARVLITYGGGSVKKTGVLDQVLTALNGLDVLEFGGIEPNPS

YETLMNAVKLAREEKVTFLLAVGGGSVLDGTKFIAAAAHYDADIDPWEILETYGSKIASAIPMGSVLTLP

ATGSESNKGAVISRKTTGDKRAFMSSHVQPQFAILDPVYTYTLPPRQVANGVVDAFVHTVEQYVTYPVDG

KIQDRFAEGILLTLIEDGPKALQEPENYNVRANIMWAATQALNGLIGAGVPQDWATHMLGHELTAMHGLD

HAQTLAIVLPALWNEKRDAKREKLLQYAERVWNITEGSDDQRIDAAIAATRQFFEQMGVPTRLSDYGLDG

SSIPALLAKLEEHGMTKLGEHQDITLDVSRRIYEAAR

>WP\_004144552.1 MULTISPECIES: AraC family transcriptional regulator [Klebsiella]

MQHAEICRTLTEKINLLKDKHEMLSSLLPDVRLLYGTQPGPRTPVMYQPGIVFLFSGHKIGYINERTFRY

DTNEYLLLTVPLPFECETFATPEVPLAGMRLNVDILQLQELLMDIGEDPLFQPAVASSGINSAVLSEDIL

CAAERLLDVMERPLDARILGKQIVREILYYVLTGPCGGALLALVSRQTHFSLISRVLKHIESQYTENLSV

DRLAAEANMSVSAFHHNFKAVTSTSPLQYLKNYRLHKARMLMIHDGMKASAAAMRVGYESPSQFSREFKR

YFGLTPGEDAARIRTMQGM

>WP\_002916791.1 MULTISPECIES: DedA family protein [Klebsiella]

MVVIQEIVAALWQHDFAALANPHVVGVVYLVMFATLFLENGLLPASFLPGDSLLLLAGALIAKGVMDFVP

TIAILTAAASLGCWLSYVQGRWLGNTQTVKGWLAHLPHKYHQRATCMFDRHGLLALLAGRFLAFVRTLLP

TMAGISGLPNRRFQFFNWLSALLWVCVVTGLGYALSMIPFVKRHEDQVMTCLMILPIALLLAGLLGTLFV

VIKKKYCSA

>WP\_004149836.1 MULTISPECIES: cystathionine beta-lyase [Klebsiella]

MADKHLDTALVNAGRSKKYTQGSVNSVIQRASSLVFDTVEAKKHATRNRANGELFYGRRGTLTHFSLQEA

MCELEGGAGCALFPCGAAAVANTILAFVEQGDHVLMTNTAYEPSQDFCTKILAKLGVTTSWFDPLIGADI

ARLVRPETRVVFLESPGSITMEVHDVPAIVAAVRQVAPEAIIMIDNTWAAGILFKALDFGIDISIQAGTK

YLIGHSDAMVGTAVANARCWPQLRENAYLMGQMLDADTAYMTSRGLRTLGVRLRQHHESSLRIAEWLAQH

PQVARVNHPALPGSKGHEFWKRDFTGSSGLFSFVLSKRLNDAELAEYLDNFSLFSMAYSWGGFESLILAN

QPEQIAHIRPDAEVDFSGTLIRLHIGLENVDDLQADLAAGFARIV

>WP\_004174395.1 MULTISPECIES: tol-pal system-associated acyl-CoA thioesterase [Klebsiella]

MGNNLMQADLSVWGMYHHADIVVKVVMIGLILASVVTWAIFFGKGAEILASKRRLKREQQQLAEARSLDQ

ASDIASAFEAKSLTTQLINEAQNELELSAGAEDNEGIKERTGFRLERRVAAVGRHMGRGNGYLATIGAIS

PFVGLFGTVWGIMNSFIGIAQTQTTNLAVVAPGIAEALLATAIGLFAAIPAVVIYNIFARMIGSYKASLG

DVAAQVLLLQSRDLDLSASGVKPVRSAQKLRVG

>WP\_002916785.1 MULTISPECIES: TonB system transport protein ExbD [Klebsiella]

MAMRLNENLDDNGEMHEINVTPFIDVMLVLLIIFMVAAPLATVDVKVNLPASSSQPQPRPEKPIYLSVKA

DKSMFLGNDPVTEANMINALDSLTAGKKDTTVFFRADKTVDYETMMKVMDTLHQAGYLKIGLVGEETVKA

K

>WP\_004105804.1 MULTISPECIES: TIGR00645 family protein [Klebsiella]

MERFLENAMYASRWLLAPVYFGLSLGLIALTIKFFQEIFHILPHIFSVSESDMILTLLSLVDMTLVGGLL

VMVMFSGYENFVSQLDINEGKEKLSWLGKMDATSLKNKVAASIVAISSIHLLRVFMDAKNVPDNKLMWYV

IIHLTFVLSAFVMGYLDRLTKVKH

>WP\_004144560.1 MULTISPECIES: dienelactone hydrolase family protein [Klebsiella]

MTRLTAKDFPQQLLEYYDYYAHGKISKREFLQLAGKYTVGGMTALALFNLLKPDYALAEQVPFTDPDIRP

EYIHYPSPDGHGEVRAYLVTPTKIADKAPAVVVVHENRGLNPYIEDVARRVAKAGYIALAPDGLSAVGGY

PGNDDEGRALQQKVDPVKLMNDFFAAVAFMANYPQATGKVGITGFCYGGGVSNAAAVAIPELACAVPFYG

RQPPLKEVDKIKAPLLLHYAGLDSGINEGWPAYEQALKEHHKVYEAYFYQGVNHGFHNDSTPRYDRAAAD

LAWQRTLAWFEKYLR

>WP\_002916743.1 MULTISPECIES: DUF2623 domain-containing protein [Klebsiella]

MENHFGKGLMAGLQASYADTAAHAANFCADYKRGFVLGYSHRMFEKTGDRQLSAWEAGILTRRYGLDRDM

VMDFFKEGGSGMAMRYFLAGYRLES

>WP\_016531363.1 glutathione-dependent disulfide-bond oxidoreductase [Klebsiella pneumoniae]

MSEQNYQPPKVWEWKQNSGGAFANINRPVSGATHERVLPVGTHPLQLYSLGTHNGQKVTIMLEELLALGV

SGAEYDAWLIRIGEGDQFSSGFVEINPNSKIPALSDHSTTPPTRVFESGNILLYLAEKFGFFLPKDPAGR

TETLNWLFWLQGAAPFLGGGFGHFYNYAPVKIEYAIDRFTMEAKRQLDVLDKQLARGRYVAGEEYTIADM

AVWPWYGNVVLGNVYNAAEFLDAGSYKNVLRWAQDVGNRPAVKRGRIVNRTNGPLNEQLHERHDARDFDT

QTEDKRQA

>WP\_004150918.1 MULTISPECIES: thioredoxin domain-containing protein [Klebsiella]

MSTPSHLNAQPLVWGHGPRTFEVFLEPTCPYSVRAFNKLDDLLDEVGADNVTIKIRLQSQPWHLFSGVIV

RCILAASTLPHGREQAHKVMQAVADHREEFEFTDHCSGPNMNATPQQIIERIERYSHVLLGAAFARPELQ

DVIKWHSKYARQNGIHVSPTFMVNGLVQPDLGSGDDVSVWAARIMA

>WP\_004217169.1 MULTISPECIES: hypothetical protein [Bacteria]

MFFCYITDNDITFVSGCRVIFLNGTISETNEWYHRYTSVW

>WP\_002916740.1 MULTISPECIES: bifunctional glutathionylspermidine amidase/synthase [Klebsiella]

MSKGSTSSDAPFGTLLGYAPGGVAIYSSNYSSLNPQDYPDDATFRSYIGNEYMGHKWQCVEFARRFLFLT

YGFVFTDVGMAYEIFSLRFLREVVNDNILPLQAFANGSRRPPIAGSLLIWQKGGEFKHTGHVAVITQLVG

NKVRIAEQNVIHSPLPQGQQWTRELTLEVNDGRYTIKDTFADTEILGWMIQTADTEHSLPQPVLPGEAMA

IKGARLPNNGQFRGKWLNEKDPLQKAYVAANGHFINQDPYQYFTISESAEQELIKATNELHLMYLHATDK

VMKDDNLLALFDIPKILWPRLRLSWQRRRHHMITGRMDFCMDERGLKVYEYNADSASCHTEGGLILEQWL

KQGYYGTGHNPAEGLLDELAGAWKHSRARPFVHIMQDKDLEENYHAQFIQRSLTQAGFESKILFGLDELR

WDAAGQLIDADGRLVNCVWKTWAWETAIEQVREVSAEEYAAVPIRTGHPQNEVRLIDVLLRPEVLVFEPL

WTVIPGNKAILPVLWSLFPHHRYLLDTDFEVNDELAKTGYAVKPISGRCGNNIDLIGPQDELLDKTSGQF

VDRKNIYQQLWCLPKVDGKYIQVCTFTVGGNYGGTCLRGDSSLVVKKESDIEPLIVLKDKA

>WP\_004149825.1 MULTISPECIES: PLP-dependent aminotransferase family protein [Klebsiella]

MHDRRLAARAGELKPSAVRELLKHSKLPGVISLGGGIPAPELFDTEGLELAVQKVMSERFNDAFQYGLTE

GYPPLRQAVSEICHSRGVACSAAQVYITSGSQQSLDIVARTLLDPGDTIVVERPTYLAALQVFQLAQANI

LSVDTDDDGMLVEQLADLLETTRVKAVYLVPTFGNPGGKTLSEARRRRLVELAKKYDFVILEDDPYGEIS

FTDAVRRPLYQHAVELGCEDQVVYTSTFSKILAPGMRIGWIVMPDWLAQQTVIVKQAADLHTNMLSQVIT

AEYLSLNRLDNQIALIREDYRKKCVALADALESRLGEHLEFSRPQGGMFLWARFRYPFDTMEWMKKTLEN

GVVYVPGEAFYHDKPDTRTLRLSYSTVSEAGLLTAVERLAASL

>WP\_002916738.1 MULTISPECIES: hypothetical protein [Klebsiella]

MPVIIASSVKEAKALINGGKYREIILNFDIDADDFFSLASHSAGTKISIADRNDRSPVESAK

>WP\_004185642.1 MULTISPECIES: hypothetical protein [Klebsiella]

MLKKLSLIIPLLALIALLVWWFTPHYTEEDEAYYRAVFCIIDHDDSRQFLHDMQNIVEGGNSDYALHKTH

YLPALGQRMLDTWRQLSPQEQQALRQDKQRCGEILREKQQGKSS

>WP\_004174410.1 MULTISPECIES: short chain dehydrogenase [Klebsiella]

MKIIVIGASGTIGRAVSEELSQRHEVIRVGRTRGDYQVDITSQESVEALFAQTGEVDAIVSTTGNLHFGP

LSTMTDSQFNLGLQDKLLGQIRLALVGQHFLRDGGSITLVSGIVAQEPIAQGVNATTVNAGLEGFVRAAA

CELPRGIRINLISPTVLSESLAAYGDFFPGFPSVPAAAVAQAYRRSIEGVQTGRIYPVGY

>WP\_021314148.1 LysR family transcriptional regulator [Klebsiella pneumoniae]

MDKLRGMETFIAVVECGSFTGAASRLGLSAVMVGKYIAQLESQLATRLLERNTRRQSLTDAGRVYFDEAK

RVMEQVSIAESAVERLRLAPAGTLRVSAPTSFGASVIAPLTATFLQVWPAVRVELDLTNRMVDLVDEGFD

LAIRIGEIHQEDLVARYLAPYRMVICAAPAYLARYGTPGRPEDLADHLCLSHTVWTARNEWRLPGVEGEV

RWKRDAVLRCNDGYALRQAAIAGAGLLMQPEVLLADALASGSLVRVLEAWTPQPRPVHLLWRQDRRPLPK

LTQFIAHLQQGMADALTTTRASE

>WP\_016531357.1 PLP-dependent aspartate aminotransferase family protein [Klebsiella pneumoniae]

MSSIHTLSVHSGTFTDSHGAVMPPIYATSTFAQPAPGQHTGYEYSRSGNPTRHALETAIADLENGTRGYA

FASGLAAISTVLELLDKDSHLVAVDDVYGGTYRLLENVRRRSAGLQVSWVKPDDLAGIEAAIRPDTRMIW

VETPTNPLLKLADLSAIAAIARRHNLISVADNTFASPAIHRPLEHGFDIVVHSATKYLNGHSDVVAGLAV

VGDNSGLAEKLGYLQNAVGGVLDPFSSFLTLRGIRTLALRMERHSANALQLAEWLEQQPAVERVWFPWLA

SHPHHQLARQQMALPGGMISVVVKGDEGYAERIISKLRWFTLAESLGGVESLVSQPFSMTHASIPLEKRL

ANGITPQLIRLSVGIEDPNDLIADWQQALRAE

>WP\_171819465.1 pyridoxal-phosphate dependent enzyme [Klebsiella pneumoniae]

MVMSLFHSVSDLIGHTPLLQLHKLDTGPCSLFLKLENQNPGGSIKDRVALSMIHEAERQGKLAPGGTIIE

ATAGNTGLGLALIAAQKNYRLILVVPDKMSREKIFHLRALGATVLLTRSDVNKGHPAYYQDYARRLADET

PGAFYIDQFNNDANPLAHATSTAPELYQQLEGDIDAIVVGVGSGGTLGGLQAWFAEHSPKTEFILADPAG

SILADQVDTGRYGETGSWLVEGIGEDFIPPLARLEGVHTAYRVSDCEAFHTARQLLQVEGVLAGSSTGTL

LSAALRYCRTQSRPKRVVTFACDSGNKYLSKMFNDDWMRQQGLIARPEQGDLSDFIALRHDEGATVTAAP

DDTLAAVFTRMRLYDISQLPVLEDGRVVGIVDEWDLIRHVQGDRQRFSLPVSEAMSRHVETLDKRAPESE

LQAILDRGLVAVIADNTRFLGLVTRSDVLTAWRNRVAQ

>WP\_004150912.1 MULTISPECIES: DUF1778 domain-containing protein [Klebsiella]

MPAANSMSIKRETLNLRIKPAERDLIDRAAKARGKNRTDFVLEAARAAAEEALIEQRIIMADPQAYQEFL

ARLDQAPAPNAALRKTMQTPAPWEQEE

>WP\_046042357.1 GNAT family N-acetyltransferase [Klebsiella pneumoniae]

MILAPESLHAGHILTPFCCGIDSMDHWLKQRAMKNQVTGASRTFVCCDDAKVMAYYSLASSAVTTNTAPG

RFRRNMPDPIPVVVLGRLAVDKSLHGKGVGRALVRDAGLRVIQVAETIGIRGMLVHALSDEARDFYLRVG

FEPSPMDPMMLMVTLRDLVNA

>WP\_004188553.1 MULTISPECIES: hypothetical protein [Klebsiella]

MPSILARLSVCIILSLFMVSCSGSFDKTIDYQDAKQMPGYGYIVMDFRLANEMAYGNGYIPGKTNYTISY

KNKGDIFFVDIQHADFRNRILKAYIPYMKGYTLIGIGRSYWYPFFRCDKCDNEPQLKFLYINIVKSVDEA

WCSETTYKNLRSFNAMDGCSQMVGVEESRKVTGDVLITPELKSDFQGMFTPYLKPGR

>WP\_002916694.1 MULTISPECIES: DUF554 domain-containing protein [Klebsiella]

MVTGPFINASAVLVGGVLGALLSQRLPERIRTAMTSIFGLASLGIGILLVIKCANLPVMVLSTLVGTLLG

EICNMEKGINTLVSKLQQLMSAKGKKKASAHESYIQSYVAIIVLFCASGTGVFGAMREGMTGDASILIAK

AFLDFFTATIFACTLGIAVAAISVPMLLIQLTLAACAAIIMPLTTPMMLADFSAVGGMLLVATGLRICGI

KMFAVVNMLPALVLAMPISAAWTLFFA

>WP\_004197024.1 MULTISPECIES: ornithine decarboxylase [Klebsiella]

MKSMHIAASCELVTRLSTHRRVVALDSTDFTDVAAVVISAADSRSGILTLLRRSGFNLPVYLLSETAVDK

PEGVQAVIAGKDQEWLELEAAACDYEARLLPPFFNTLTQYVEMDNSTFACPGHQHGAFFKKHPAGRQFYD

FFGENVFRADMCNADVKLGDLLIHEGSAKHAQKFAAKVFNADKTYFVLNGTSAANKVVTNALLTRGDLVL

FDRNNHKSNHHGALIQAGATPVYLEAARNPFGFIGGIDERCFDEHYLRDLIREAAPEKANASRPFRLAVI

QLGTYDGTVYNARQVVDKIGHLCDYILFDSAWVGYEQFIPMMADCSPLLLELTPDDPGIFVTQSVHKQQA

GFSQTSQIHKKDNHLRGQARFCPHKRLNNAFMLHASTSPFYPLFAALDVNAKIHEGESGRRLWAECVALG

IEARKAIIANCKMIQPFIPPTVAGRPWQDHPTEAIARERRFFSFEPGARWHGFEGYADDQYFVDPCKLLL

TTPGIDAESGEYSEFGIPATILAHYLRENGIVPEKCDLNSILFLLTPAESAEKMAQLVAMLGQFEQHIEA

DTPLADVLPTIYNKYPVRYRDYTLRELCQEMHDLYVSFDVKSLQKEMFRKRSFPRVVMNPQDANHEFIRG

NVELVRLSEAEGRVAAEGALPYPPGVLCVVPGEVWGGAVLRYFLALEEGVNMLPGFSPELQGVYSETDPD

GIKRLYGYVLKG

>WP\_004144787.1 MULTISPECIES: nucleoside permease [Klebsiella]

MNLKLQLKILSFLQFCLWGSWLTTLGSYMFVTLKFDGAAIGAVYSSLGIAAVLMPTLLGIVADKWISAKW

VYAICHLVGALTLYLAAQVTTPGEMFLVILLNSLAYMPTLGLINTISYYRLQSAGLDIVTDFPPIRIWGT

IGFILAMWGVSFSGFELSHMQLYIGATLSVLLTLFTLTLPHIPVANAQRNQSWTEMLGLNAFALFKNKRM

AIFFIFSMMLGAELQITNMFGNTFLHSFDKDPLFAGSFIVEHASVLMSISQISETLFILTIPFFLSRYGI

KNVMLISIVAWMLRFGLFAFGDPTPFGTVLLVLSMIVYGCAFDFFNISGSVFVEKEVRPEIRASAQGMFL

MMTNGFGCILGGMVSGKVVEHFTVEGITDWQSVWLIFAGYSLVLAFAFVALFKYKHVRQPTAAQQSV

>WP\_016529070.1 membrane-bound lytic murein transglycosylase MltC [Klebsiella pneumoniae]

MKKYLALALIAPLLVSCSSSNKNGAEYNEAWVKDTNGFDILMGQFAHNIENIWGYNEVLLAGPKDYVKYT

DQYQTRSHINFDEGTITVETIAGTDPRGRLRQAIVKTLLMGDDPNSIDLYSDVDDIQISKEPFLYGQVVD

NTGASIRWEWRAARFADYLLQTRLKSRNNGLRVVYSITINLVPNHLDKRAHKYLGMVRQASRKYGVDESL

ILAIMQTESSFNPYAVSHADAMGLMQVVQHSAGRDVFRSQGKSGLPSRSYLFDPANNIDTGTAYLAMLNN

VYLAGIDNPTSRRYAVITAYNGGAGSVLRVFSSDKVQAANIINSMAPGDVYQTLTTRHPSAESRRYLYKV

NTAQKSYRRK

>WP\_004105744.1 MULTISPECIES: oxidative damage protection protein [Bacteria]

MSRTIFCTFLQREADGQDFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLSMMNPEHRKLLEQEM

VQFLFEGKDVHIEGYTPPEKQ

>WP\_021314145.1 A/G-specific adenine glycosylase [Klebsiella pneumoniae]

MTFLATQFSAQVLDWYDKYGRKTLPWQIAKTPYKVWLSEVMLQQTQVTTVIPYFERFMARFPTVVDLANA

PLDEVLHLWTGLGYYARARNLHKAAQQVATLHGGEFPRTFDEVAALPGVGRSTAGAILSLSLGQHYPILD

GNVKRVLARCYAVSGWPGKKEVEKRLWDISEEVTPAEGVDRFNQAMMDLGAMVCTRSKPKCELCPLSNGC

VAYANHSWAEYPGKKPKQTLPERTGYFLLMQHGDEVFLSQRPPVGLWGGLFCFPQFADEAELREWLAQRQ

IKADNLTQLTAFRHTFSHFHLDIIPMWLTVHSSGACMDEGNALWYNLAQPPSVGLAAPVERLLQQLKAGA

PV

>WP\_002916627.1 MULTISPECIES: tRNA (guanosine(46)-N7)-methyltransferase TrmB [Klebsiella]

MKNDVISPEFDENGRPLRRIRSFVRRQGRLTKGQQHALDNIWPVMGVEFNDAPLDFAALFGRDAPVTLEI

GFGMGASLVAMAKAKPEQNFLGIEVHSPGVGACLASAEEEGVQNLRVMCHDAVEVLHTMIPDNSLNMVQL

FFPDPWHKARHNKRRIVQPPFAELVKSKLKLGGVFHMATDWEAYAVHMLEVMSSLEGYRNQSASNDYVPR

PESRPVTKFEQRGHRLGHGVWDLMFERVK

>WP\_002916620.1 MULTISPECIES: YggL family protein [Klebsiella]

MAKNRSRRLRKKMHIDEFQELGFSVAWRFPEGTSEEQIDQTVNDLIEEVIEPNKLAFDGSGYLSWEGLIC

MQEIGKCTEEHQAIVRKWLEARKLEDVRTSELFDVWWD

>WP\_002916619.1 MULTISPECIES: DUF2884 domain-containing protein [Klebsiella]

MMRKTLLAVALSVTALSAHADYQCSVTPRDDVILSPQQVQVKGENGDLVIKPDGNLTFNGKAYALSAAQR

EQAQDYQASLRSSLPWIDEGARSRVEKSRKALDKIITEQVGANSSMHGRLTKLDAQLKEQMNRIIERRSD

GLTFHYKAIDQVRADGQQLVNQAMGGILQDSINEMGAKAVLKGGGNPLQGILGSLGGLQTAIQEEWKNQE

ADFQQFGKDVCSRVVSLEDSRKALVGSLK

>WP\_004181281.1 MULTISPECIES: ABC transporter permease [Klebsiella]

MNSKTASHTALDRSDERVRHDEGLFGALRAQITRIKTGDLGTAPVIAGLIVISLVFTFLNPVYIAPNNLV

NLLFDCATVGFISLGIVCVLMLGEIDLSVGSMSGLASAIVGVLWVNAGWPLAGAIAVALACGVAVGLVYA

LLYTRVGMPSFVATLAGLLALLGMQLYILGPSGSINLPYTSPLVRFGQLLVMPGWFSHLMALLPGLAILI

FGLKKRSRRLAANLSAEGVSSLVARAIALTIIFEAAVLYLNQGRGIPWIFGLFVACVMILNYALKRTKWG

RSMFAVGGNREAARRSGINVRAIYVSAFVLCTTLATFGGILAASRLASASQQAGTGDVNLNAIAAAVIGG

TSLFGGRGSAWSALLGIIVIQSISNGLTLLNLPSSLRYIITGAVLAIAVIIDSLARRSRVSHGRA

>WP\_004181271.1 MULTISPECIES: ATP-binding cassette domain-containing protein [Klebsiella]

MPQQQHNSAAGRPILQLRNVSKHFGAVSALTDIELEVHAGEVVALVGDNGAGKSTLVKILAGVHQPTSGT

IEFDGNPVTLDSPGKALEYGIATVFQDLALCENLDVVANLFLGHEISPFQLDEVAMEVKAWTLLQELAAR

IPSVREPVASLSGGQRQTVAIARSLLLNPKIIMLDEPTAALGVAQTAEVLNLIERVRERGLGVIIISHNM

EDVRAVADRIVVLRLGRNKGIFTPDASNQDLVAAITGATENAVSRRVERKSQPTTSGAM

>WP\_016529067.1 sugar ABC transporter substrate-binding protein [Klebsiella pneumoniae]

MNYRNIFITLAALSGTVTASAWSAESATVAFLMPDQASTRYEQHDFPGFKAEMSKLCADCKVIYQNANAN

ASLQQQQFNSVIAQGAKVIVLDPVDSSAAAALVENAQAQGVKVIAYDRPVPDKPADFYVSFDNEGIGYAI

AKSLTDHLKASGVPQDAGVLQINGSPTDAATGLIRDGIHRGLKESGYKTLAEFDTPEWAPPKAQEWTAGQ

VTRFGDKIKGVVAANDGTGGGAIAAFKAAGVQPLPPVTGNDATIAALQLIIAGDQYNTISKPSEIVAAAA

AKVAVDFIQGKKPQASTTLYNTPSQLFTPEVVTAKNIKAEIFDKKIQTWDQVCSGEYAAACQKLGISK

>WP\_016529066.1 MULTISPECIES: radical SAM family heme chaperone HemW [Klebsiella]

MANLPPLSLYIHIPWCVQKCPYCDFNSHALKGEVPHDDYVQHLLNDLQADAHYAQGREIGTIFIGGGTPS

LLSGPAMQTLLDGVRACLPLAAGAEITMEANPGTVEADRFVDYQRAGVNRISIGVQSFSEPKLQRLGRIH

GPEEAKRAARLASGLGLRSFNLDLMHGLPDQSLEEALDDLRQAIALNPPHLSWYQLTIEPNTLFGSRPPV

LPDDDALWDIFEQGHQLLSAAGYQQYETSAYAKPGFQCQHNLNYWRFGDYLGIGCGAHGKITFPDGRILR

TAKTRHPRGYMEGRYLERQHDVEEADKPFEFFMNRFRLLEAAPRAEFSLYTGLDEQVIRQQIDAAIAEGY

LLEDAQNWQITEHGKLFLNSLLELFLSEE

>WP\_002916615.1 MULTISPECIES: XTP/dITP diphosphatase [Klebsiella]

MQKVVLATGNAGKVRELASLLEDFGLDIVAQTELGVDSAEETGLTFIENAILKARHAAQITGLPAIADDS

GLAVDALGGAPGIYSARYSGVDASDQQNLEKLLDALKDVPDDQRQAQFHCVLVYLRHAEDPTPLVCHGSW

PGVITRQAAGHGGFGYDPIFFVPSEGKTAAELSREEKSAISHRGQALKLLLEALRNG

>WP\_016529065.1 DUF167 family protein YggU [Klebsiella pneumoniae]

MSAVETCADGLVLTLYIQPKASRDSIVGVHGDELKVAITAPPVDGQANAHLVKFLAKQFRVAKSQVLIEK

GELGRHKQVKIIAPQQIPTAVAALTE

>WP\_002916613.1 MULTISPECIES: YggT family protein [Klebsiella]

MKTLTFLLSTVIELYTMVVLLRVWMQWARCDFYNPFSQFVVKATQPIVGPLRRIIPAMGPIDSASLLVAF

ILCVIKAIVLFMVITFQPIIWISALLILLKTIGSLIFWVLLLMAIMSWVSQGRSPVEYVLMQLADPLLRP

IRNLLPSMGGIDFSPMVLVLLLYVINMGIAEVLQATGNVLLPGLWMAL

>WP\_016529064.1 YggS family pyridoxal phosphate-dependent enzyme [Klebsiella pneumoniae]

MNDIAHNLAQVRDKISGAAARCGRAPEEVTLLAVSKTKPASAIEEALAAGQRAFGENYVQEGVEKINHFQ

QAGVSGLQWHFIGPLQSNKSRLVAEHFDWCHTVDRLKIATRLNEQRPAHLPPLKVLIQINISDEQSKSGI

PLEALDGLAAEIAELPHLELRGLMAIPAPESEYVRQFAVARQMAVAFARLKTRYPTVDTLSLGMSDDMEA

AIAAGSTMVRIGTAIFGARDYSK

>WP\_004149811.1 MULTISPECIES: type IV pilus twitching motility protein PilT [Klebsiella]

MKLEEIVALSVKHNVSDLHLCNSAAPRWRRQGRLEPAPFPAPDIANLLNDWLDAAQLLHWQEHGQIDFAL

NLACGARLRASAFAHTRGISLVLRLLPEQCPRLDMLGAPPALSELLAEESGLLLVTGATGSGKSTTLAAM

VGHLNQHLDGHILTLEDPVEFIHHSERCLIQQREVGRHCPSFAAALRVALRQDPDVILLGELRDSETIRL

ALTAAETGHLVMATLHTRGAAPAVERLIDVFPAEEKDQVRSQLAGSLCAVLAQKLLPARQGGRVALYELL

VNTPAVANLIREGKVHQLPGVMQTGMQAGMLTFTQSFQQRVAAGAL

>WP\_009308631.1 MULTISPECIES: transcriptional regulator CsgD [Klebsiella]

MINLNGNSSSSRQVTFITHPSIQSKAFASYLSETLMAPVVLQNINKPLAQRLAKDSVILFDIAVSNKKLN

GVWRDIIRLQADNPRLLIINSAQKYELYEMAQWPALYGVFRHDDDESRLIEGIKAVLNGEQTAELSVMHP

AMYAADHASTPVENSPLTERECEILNELRCGATNLDIARALFISENTVRTHLYNVFRKLSVKNRTQAVSW

ANEHLRH

>WP\_002916605.1 MULTISPECIES: Holliday junction resolvase RuvX [Klebsiella]

MSGTFLGFDFGTKSIGVAVGQRITATARPLPALKAQDGKPDWNVIEKLLKEWQPEAVIVGLPLNMDGTEQ

PLTARARNFANKIHGRFGVAILLHDERLSTVEARAGLFEHGGYRALNKGSVDSASAVVILESYFEQSF

>WP\_002916603.1 MULTISPECIES: YqgE/AlgH family protein [Enterobacterales]

MNLQHHFLIAMPALQDPIFRRSVVYICEYNDEGAMGIIINKPLENLQVEGILEKLKIVPEPRNPEIRLDK

PVMLGGPLAEDRGFILHTPPSDFSSSIRISDNTVITTSRDVLETLGTDRQPGNVLVALGYSSWEKGQLEQ

EILDNAWLTAPADQNILFRTPIADRWREAAKLIGIDIVTMPGVAGHA

>WP\_002916600.1 MULTISPECIES: glutathione synthase [Klebsiella]

MIKLGIVMDPIATINIKKDTSFAMLLEAQRRGYELHYMEMNDLYLINGEARARTRTLSVEQNYDKWYDFT

GEQDLPLADLDVILMRKDPPFDTEFIYATYILERAEEKGTLIVNKPQSLRDCNEKLFTAWFSELTPETLV

TRNKAQLKAFWEKHGDIIMKPLDGMGGASIFRVKAGDPNLGVIAETLTELGSRYCMAQNYLPAIKDGDKR

VLVVDGEPVPYCLARIPQGGETRGNLAAGGRGEARPLTESDWEIARRVGPTLKAKGLIFVGLDIIGDRLT

EINVTSPTCVREIEAAFPDISITGMLMDAIERRIDK

>WP\_016530642.1 16S rRNA (uracil(1498)-N(3))-methyltransferase [Klebsiella pneumoniae]

MRIPRIHHPERLIVGSQFALSDDAANHVGRVLRMTTGQHLQLFDGSNQVFDAVITEAGKKNVTVEVLSGE

PDDRESPLHIHLGQVMSRGEKMEFTIQKSIELGVSLITPLFSERCGVKLDAERLQKKIQQWQKIAIAACE

QSGRNVIPEIRPAMQLEAWCAEQDSGLKLNLHPRASASINTLPLPVERVRLLIGPEGGLSAEEIAMTAQY

QFTDILLGPRVLRTETTALTAITALQVRFGDLG

>WP\_002916589.1 MULTISPECIES: deoxyribonuclease I [Klebsiella]

MSRMHVLAVAVLSAAVSGPLAAAGINSFSQAKAAGVKVNADVPGDFYCGCKIDWQGKKGVIDLESCGYKV

RKNENRASRVEWEHVVPAWQFGHQRQCWQEGGRKNCAKDPEYRKMESDMHNLQPAVGEVNGDRGNFMYSQ

WNGGEGQYGQCTMKVDFKDKIAEPPARARGAIARTYFYMRDRYQLNLSRQQTQLFTAWNKQYPVTAWECE

RDERIAKVQGNHNPYVQQACQAQKS

>WP\_016530641.1 SprT family zinc-dependent metalloprotease [Klebsiella pneumoniae]

MKTPRIPIAIQQAVMRSLREHLANANRKLERRYAEPTLVYQQRGTSAGTAWLEKNEIRLNPVLLLENQRE

FIDEVVPHELAHLLVWQHFGRVAPHGKEWKWMMESVLGVPARRTHRFELASVRQNTFPYRCRCQQHQLTV

RRHNRVVRGEATYRCVRCGDLLVAEKQPSELIRNFLI

>WP\_002916587.1 MULTISPECIES: sugar porter family MFS transporter [Klebsiella]

MPDNKKQGRSNKTMTFFVCFLAALAGLLFGLDIGVIAGALPFIANEFQISAHTQEWVVSSMMFGAAVGAV

GSGWLSFKLGRKKSLMIGAILFVAGSLFSAAAPNVEILLVSRVLLGLAVGVASYTAPLYLSEIAPEKIRG

SMISMYQLMITIGILGAYLSDTAFSYSGAWRWMLGVIIIPAVLLLIGVIFLPDSPRWFAAKRRFVDAERV

LLRLRDTSAEAKRELDEIRESLKVKQSGWSLFKDNSNFRRAVFLGILLQVMQQFTGMNVIMYYAPKIFEL

AGYANTTEQMWGTVIVGLTNVLATFIAIGLVDRWGRKPTLILGFIVMAAGMGVLGTMMHIGIHSSTAQYI

AVLMLLMFIVGFAMSAGPLIWVLCSEIQPLKGRDFGITCSTATNWIANMIVGATFLTMLNSLGSANTFWV

YGGLNVLFILLTLWLIPETKNVSLEHIERNLMQGRPLREIGARD

>WP\_004149807.1 MULTISPECIES: methionine adenosyltransferase [Klebsiella]

MAKHLFTSESVSEGHPDKIADQISDAVLDAILEQDPKARVACETYVKTGMVLVGGEITTSAWVDIEEITR

NTVREIGYVHSDMGFDANSCAVLSAIGKQSPDINQGVDRADPLEQGAGDQGLMFGYATNETDVLMPAPVT

YAHRLVQRQAEVRKNGTLPWLRPDAKSQVTFQYDDGKIVGIDAVVLSTQHAEDIDQKSLQEAVMEEIIKP

ILPTEWLNASTKFFINPTGRFVIGGPMGDCGLTGRKIIVDTYGGMARHGGGAFSGKDPSKVDRSAAYAAR

YVAKNIVAAGLADRCEIQVSYAIGVAEPTSIMVETFGTEKVPSEQLTLLVREFFDLRPYGLIQMLDLLHP

IYKETAAYGHFGREHFPWEKTDKAALLREAAGLK

>WP\_223168724.1 MULTISPECIES: protein YqgC [Klebsiella]

MHERDAGCGVLTRDRTTRRIKRKTLVHYLVSPPHRPATGSATSQSYTYRATGATPLRDSVNTDCLTRLEV

APQGHAPCAFLMSRARRFIPRSGVKSKIKMCLFARLSGNFARRVFP

>WP\_002916578.1 MULTISPECIES: acid stress response protein YqgB [Klebsiella]

MNKKPVAQSQNQQIVLGFRTVHGLLSHLWTAIVVNCLTLIIKN

>WP\_004149805.1 MULTISPECIES: biosynthetic arginine decarboxylase [Klebsiella]

MSDDMSMVSPSSAGEHGVLRSMQEVAMSSQEASKMLRTYNIAWWGNNYYDVNELGHISVCPDPDVPEARV

DLAELVKAREAQGQRLPALFCFPQILQHRLRSINAAFKRARESYGYNGDYFLVYPIKVNQHRRVIESLIH

SGEPLGLEAGSKAELMAVLAHAGMTRSVIVCNGYKDREYIRLALVGEKMGHKVYLVIEKMSEIAIVLEEA

ERLNVVPRLGVRARLASQGSGKWQSSGGEKSKFGLAATQVLQLVEILREAGHLESLQLLHFHLGSQMANI

RDIATGVRESARFYVELHKLGVNIQCFDVGGGLGVDYEGTRSQSDCSVNYGLNEYANNIIWAIGDACEEN

GLPHPTVITESGRAVTAHHTVLVSNIIGVERNEYTEATPPAEDAARPLQSMWETWLEMHETGNRRSLREW

LHDSQMDLHDIHIGYSSGTFNLQERAWAEQLYLNMCHEVQKQLDPSNRAHRPIIDELQERMADKIYVNFS

LFQSMPDAWGIDQLFPVMPLEGLNKSPERRAVLLDITCDSDGAIDHYVDGDGIATTMPMPEYDPENPPML

GFFMVGAYQEILGNMHNLFGDTEAVDVFVFPDGSVEVELSDEGDTVADMLQYVQLDPNTLLTQFRDQVKN

TGLDDALQQQFLEEFEAGLYGYTYLEDE

>WP\_002916572.1 MULTISPECIES: agmatinase [Klebsiella]

MSTLGHQYDNSLVSNAFGFLRLPMNFMPYESDADWVITGVPFDMATSGRAGGRHGPAAIRQVSTNLAWEH

NRFPWNFDMRERLNVVDCGDLVYAFGDAREMSEKLQAHAEKLLAAGKRMLSFGGDHFVTLPLLRAHAKHF

GKMALVHFDAHTDTYANGCEFDHGTMFYTAPNEGLIDPNHSVQIGIRTEFDKDNGFTVLDAGQVNDRSVD

DVIAQVKQIVGDMPVYLTFDIDCLDPAFAPGTGTPVIGGLTSDRAIKLVRGLKDLNIVGMDVVEVAPAYD

QSEITALAAATLALEMLYIQAAKKGE

>WP\_004151780.1 MULTISPECIES: M48 family metallopeptidase [Klebsiella]

MKIRSTVLALGIAATLTGCQNMDSNGLLSSGAEAFQAYSLSDAQVKTLSDQACKEMDAKAKIAPANSEYS

QRLNKIAAALGDNINGQPVNYKVYETKDVNAFAMANGCIRVYSGLMDLMNDNEVEAVIGHEMGHVALGHV

KKGMQVALGTNAVRAAAASAGGIVGSLSQSQLGDLGEKLVNSQFSQRQESEADDYSYDLLRKRGINPSGL

ATSFEKLAKLEAGRQSSMFDDHPASEARAQHIRDRMKADGIK

>WP\_002916512.1 MULTISPECIES: erythrose-4-phosphate dehydrogenase [Klebsiella]

MTIRIAINGFGRIGRNVVRALYESGRRAEITVVAINELADAAGIAHLLKYDTSHGRFAWDVRQEREQLFV

GDDAIRLLHEPTIAALPWRELAVDVVLDCTGVYGSREHGEAHLQAGAKKVLFSHPGGNDLDATVVYGVNQ

DELRAGHRIVSNASCTTNCIIPIIKLLDDAYGIESGTVTTIHSAMHDQQVIDAYHPDLRRTRAASQSIIP

VDTKLAAGITRIFPQFNDRFEAIAVRVPTINVTAIDLSVTVKKPVKACEVNQLLQKAAQGAFHGIVDYTE

LPLVSTDFNHDPHSAIVDGTQTRVSGAHLIKTLVWCDNEWGFANRMLDTTLAMAAIGFRFDA

>WP\_002916508.1 MULTISPECIES: phosphoglycerate kinase [Klebsiella]

MSVIKMTDLDLAGKRVFIRADLNVPVKDGKVTSDARIRASLPTIELALKQGAKVMVTSHLGRPTEGEYNE

EFSLLPVVNYLKDKLSNPVRLVKDYLDGVEVAAGELVVLENVRFNKGEKKDDEELSKKYAALCDVFVMDA

FGTAHRAQASTHGIGKFADVACAGPLLAAELDALGKALKEPARPMVAIVGGSKVSTKLTVLDSLSKIADQ

LIVGGGIANTFVAAQGHNVGKSLYEADLVDEAKRLLGTCDIPVPTDVRVATEFSETATATLKSVNDIKDD

EQILDLGDVSAQKLAEILKNAKTILWNGPVGVFEFPNFRKGTEIVANAIADSEGFSIAGGGDTLAAIDLF

GIADKISYISTGGGAFLEFVEGKVLPAVAMLEERAKQ

>WP\_004144748.1 MULTISPECIES: class II fructose-bisphosphate aldolase [Klebsiella]

MSKIFDFVKPGVITGDDVQKVFQVAKENNFALPAVNCVGTDSINAVLEAAAKVRSPVIVQFSNGGAAFIA

GKGVKTDVPQGAAILGAISGAHHVHQMAEHYGVPVILHTDHCAKKLLPWIDGLLDAGEKHFAATGKPLFS

SHMIDLSEESLHENIEICSKYLARMAKMGMTLEIELGCTGGEEDGVDNSHMDASALYTQPEDVDYAYTEL

SKISPRFTIAASFGNVHGVYKPGNVVLTPTILRDSQEYVSKKHNLPHNSLNFVFHGGSGSSAQEIKDSVS

YGVVKMNIDTDTQWATWDGILQYYKANEAYLQGQLGNPKGEDQPNKKYYDPRVWLRAAQTSMVTRLEQAF

KELNAIDVL

>WP\_002916504.1 MULTISPECIES: small-conductance mechanosensitive channel MscS [Klebsiella]

MEDLNVVDSINHAGTWLARNQELLLSYAVNIVAAIAILIVGMIVARVVSNTVNRLMLARKIDATVADFLS

ALVRYAVIAFTLIAALGRVGVQTASVIAVLGAAGLAVGLALQGSLSNLAAGVLLVMFRPFRAGEYVDLGG

VAGTVLNVQIFSTTLRTADGKVVVVPNGKIIAGNIINFSREPARRNEFIIGVAYDADIDKVKQLLTSIIE

SDDRILRDREMTVRLNELGASSVNFVVRVWSKSSDLQNVYWDILERIKREFDANGISFPYPQMDVHVVRL

PEKAE

>WP\_004144747.1 MULTISPECIES: arginine exporter ArgO [Klebsiella]

MFTYYFQGLALGAAMILPLGPQNAFVMNQGIRRQYHLMIALLCAVSDLLLICAGIFGGSALLMQSPWLLA

LVTWGGVAFLLWYGFGALKTAFSQSLELANAEVMQQGRWKIIITMLAVTWLNPHVYLDTFVVLGSLGGQL

AVEPKRWFALGTISASFLWFFGLALLAAWLAPRLRTARAQRIINIVVGAVMWFIAFQLAREGVSHIQALL

N

>WP\_016530384.1 oxidative stress defense protein [Klebsiella pneumoniae]

MKLKVLALAATLGLTTMAAQASELPDGPHIVTSGTASVAAVPDIATLAIEVNVSAKDAASAKKQADDRVA

QYLSFLEKSGIAKKDINSANLRTQPDYDYQNGKSILKGYRAVRTVEVTLRQLDKLNGLLDGALKAGLNEI

RSVSLGVAQPDAYKDKARKAAIDDAVHQAQELAAGFHSKLGPVYSVRYHVSNYQPSPMVRMMKAADAAPV

SAQETYEQATIQFDDQVDVVFELQPAQAAAPANPAKPAETPKPAQ

>WP\_002916497.1 MULTISPECIES: DNA-binding transcriptional regulator ArgP [Klebsiella]

MKRPDYRTLQALDAVIRERGFERAAQKLCITQSAVSQRIKQLENMFGQPLLVRTVPPRPTEQGQKLLALL

RQVELLEEEWLGDEQTGSTPLLLSLAVNADSLATWLLPALANVLSDSPIRLNLQVEDETRTQERLRRGEV

VGAVSIQPQALPSCLVDQLGALDYLFVASKEFAQRYFPNGVTRSALLKAPVVAFDHLDDMHQAFLQQNFD

LPPGSVPCHIVNSSEAFVQLARQGTTCCMIPHLQIEKELNSGELIDLTPGLFQRRMLYWHRFAPESRMMR

RVTDALIDYGHKVLRQD

>WP\_002916495.1 MULTISPECIES: ribose-5-phosphate isomerase RpiA [Klebsiella]

MTQDELKKAVGWAALQYVQPGTIVGVGTGSTAAHFIDALGTMKGQIEGAVSSSDASTEKLKSLGITVFDL

NSVDRLGIYVDGADEINGHMQMIKGGGAALTREKIIASVADKFICIADASKQVDILGKFPLPVEVIPMAR

SAVARQLVKLGGRPEYRQGVVTDNGNVILDVHGLEILDAIALENAINGIPGVVTVGLFANRGADVALIGT

ADGVKTIVK

>WP\_002916493.1 MULTISPECIES: phosphoglycerate dehydrogenase [Klebsiella]

MAKVSLEKDKIKFLLVEGVHQKAIDSLRAAGYTNIEFHKGALDSEQLKASIRDAHFIGLRSRTHLTEEIF

AAAEKLVAVGCFCIGTNQVDLNAAAKRGIPVFNAPFSNTRSVAELVIGELLLMLRGVPEANAKAHRGVWN

KQAVGSFEARGKKLGIIGYGHIGTQLGILAESLGMHVFFYDIENKLPLGNATQVQHLSDLLNMSDVVSLH

VPENASTKNMMGAEELALMKPGALLINASRGTVVDIPALCDALASKHLAGAAIDVFPTEPATNSDPFTSP

LCEFDNVILTPHIGGSTQEAQENIGLEVAGKLAKYSDNGSTLSAVNFPEVSLPLHGGRRLLHIHENRPGV

LTAINQIFAAQSINIAAQYLQTSPQMGYVVIDIEAEEDVAQQALQAMKAIPGTIRARLLF

>WP\_004144746.1 MULTISPECIES: 5-formyltetrahydrofolate cyclo-ligase [Klebsiella]

MTIQPDTLLSRQHIRQQIRDRRRALSPEQQRLFAQQAAERMMAWPPIVLAHNVALFLSFDGELDTQPLID

QLWRAGKRVYLPVLHPFSPGNLLFLHYHPQSQLIVNRLKIREPKLDVRDVLPLAELDVLVTPLVAFDVSG

QRLGMGGGFYDRTLQNWQQYRLQPVGYAHDCQQVDSLPSEEWDIPLPAVITPGKTWCW

>WP\_016531067.1 cell division protein ZapA [Klebsiella pneumoniae]

MSAQPVDLQIFGRSLRVNCPPEQRDALNQAAEDLNQRLQDLKERTRVTNTEQLVFIAALNISYELTQEKA

KTRDYASSMAQRIRMLQQTIEQALLEQGRISEKPGSKFE

>WP\_002916486.1 MULTISPECIES: YecA family protein [Klebsiella]

MSIQNEMPGYNDVDQLLNQQGVGLTPAEMHGLISGLLCGGNTDSSWQPLVHDLTNEGLAFGHELAQALRN

MHSAISDSLDDDGFLFQLYLPEGDAVSVFDRADALAGWVNHFLLGLGVSQPKLDKVKDETGEAIDDLRNI

AQLGYDEDEDQEELEMSLEEIIEYVRVAALLCHDTFARQQPTAPEVRKPTLH

>WP\_016531068.1 Xaa-Pro aminopeptidase [Klebsiella pneumoniae]

MTQQEFLSRRQTLLAQMQPGSAALIFAAPEAVRSADSEYPYRQNSDFWYFTGFNEPEALLVLIKSDETHN

HSVLFNRVRDLTAEIWFGRRLGQEAAPAKLGVDRALAFSEINQQLYQLLNGLDAIYFAQGEYAYADEIVF

NALEKLRKGSRQNLQAPNSVIDWRPIVHEMRLFKSAEELAVMRRAGEITALAHTRAMEKCRPSMFEYQLE

GEILHEFNRHGARFPSYNTIVGGGENGCILHYTENESELRDGDLVLIDAGCEYRGYAGDITRTFPVNGKF

TQPQREIYDIVLESLETALKLYRPGTSICQVNQEVVRIMITGLVRLGILKGEIDELIANNAHRPYFMHGL

SHWLGLDVHDVGNYDTDRSRVLEPGMVLTVEPGLYIATDADVPAQYRGIGIRIEDDIVITEDGNENLTAG

VVKKADEIEALMAAARQS

>WP\_002916482.1 MULTISPECIES: 2-octaprenyl-6-methoxyphenyl hydroxylase [Klebsiella]

MSVLIVGGGMTGATLALAISRLTGGALPVHLIEAQDPHSSRHPGFDDRAIALAAGTCQQLARIGIWQRLA

ERATPIQRVHVSDRGHAGFVNLAAADYGLSALGQVVELHDVGQRLFGLLREAPGVTLHCPAKVEAVSRSQ

ESVSLTLEGGEIINGKLLVAADGSRSALGARCGISWQQQPYEQIAIIANVSTALPHEGRAFERFTEHGPL

AMLPMSQGRCSLVWCHPQSRRDEVQSWSDERFCQELQQAFGWRLGRITHAGKRSVYPLALTTASRAVSHR

LALVGNAAQTLHPIAGQGFNLGLRDVMSLAELLADAHLSGEDVGHYPLLCRYQARRAGDKAATIGVTDGL

VHLFANRWAPLVAGRNVGLMAMELFTPARDALAQRTLGWVPR

>WP\_016530364.1 FAD-dependent 2-octaprenylphenol hydroxylase [Klebsiella pneumoniae]

MQSVDVAIVGGGMVGLAVACGLQGSGLRVAVLEKAEPRPLAADAPPALRVSAINAASEKLLTKLDVWREI

VAQRASCYHGMEVWDKDSFGHISFDDQSMGFSHLGYIIENAVVHHALWQKAQRCADVTLLAPAELQQVAW

GENEAFLSLQDGSMLTARLVIGADGANSWLRNKADIPLTFWDYHHHALVATIRTAEPHQAVARQAFHGDG

ILAFLPLSDPHLCSIVWSLSPGEAQRMQQADETTFNQALNIAFDNRLGLCQLASEREVFPLTGRYARQFA

AHRLALVGDAAHTIHPLAGQGVNLGFMDAAELIDELKRLHAQGKDIGQHLYLRRYERSRKHSAALMLAGM

QGFREMFSGSHPAKKLLRDVGLKLADTLPGVKPQLIRQAMGLNDLPAWLR

>WP\_016530363.1 glycine cleavage system aminomethyltransferase GcvT [Klebsiella pneumoniae]

MAQQTPLYEQHTLCGARMVDFHGWMMPLHYGSQIDEHHAVRGDAGMFDVSHMTIVDFHGSRIREFLRYLL

ANDVAKLTTPGKALYTGMLTASAGVIDDLIVYFLSEDYFRLVVNSATREKDLAWISEQAEPYGLEITVRD

DLSLIAVQGPQAKAKAATLFTDAQRQAVEGMKPFFGVQAGDLFIATTGYTGEAGYEIAMPNEQAADFWRG

LLDAGVKPCGLGARDTLRLEAGMNLYGQEMDEGVSPLAANMGWTIAWEPADRNFIGREALEMQREKDTEQ

LVGLVMTEKGVLRGGLPVRFTDSDGNQKEGIITSGTFSPTLGYSIALARVPAGIGDTAVVQIRNREMPVK

VTKPGFVRNGKAIV

>WP\_002916479.1 MULTISPECIES: glycine cleavage system protein GcvH [Klebsiella]

MSNVPAELKYSKEHEWLRKEADGTYTVGITEHAQELLGDMVFVDLPEVGATVEAGADCAVAESVKAASDI

YAPISGEIVAVNEELNDSPELVNSDPYTDGWIFKIKASDEAQVAALLDAAAYEALLEDE

>WP\_004900541.1 MULTISPECIES: aminomethyl-transferring glycine dehydrogenase [Klebsiella]

MTQTLSQLENRDAFIERHIGPDAQQQQEMLKTVGADSLNALIGQIVPQDIQLATPPQVGDATTEFAALAE

LKAIASRNKRFKSYIGMGYTAVQLPPVIQRNMLENPGWYTAYTPYQPEVSQGRLESLLNFQQVTLDLTGL

DIASASLLDEATAAAEAMAMAKRVSKLKSANRFFVAADVHPQTLDVVRTRAETFGFDVIVDDADKVLDHQ

DVFGVLLQQVGTTGEIHDYSKLIAELKARKVIVSVAADFMALVLLTAPGKQGADIVFGSAQRFGVPMGYG

GPHAAFFAAKDEFKRSMPGRIIGVSKDAAGNTALRMAMQTREQHIRREKANSNICTSQVLLANIASLYAV

FHGPAGLKRIAGRIHRLTDILADGLQKKGLKLRHAHYFDTLCVEVADKAAVLARAEDLQINLRSDIHGAV

GITLDEATTREDVLNLFRAIVGDDHGLDIDTLDKDVALDSRSIPAAMLRDDAILTHPVFNRYHSETEMMR

YMHALERKDLALNQAMIPLGSCTMKLNAAAEMIPITWPEFAELHPFCPVEQAEGYQQMIAQLSDWLVKLT

GYDAVCMQPNSGAQGEYAGLLAIRHYHESRNEGHRDICLIPSSAHGTNPASAQMAGMQVVVVACDKNGNI

DLADLREKAEQAGANLSCIMVTYPSTHGVYEETIREVCEIVHQFGGQVYLDGANMNAQVGITSPGFIGAD

VSHLNLHKTFCIPHGGGGPGMGPIGVKAHLAPFVPGHSVVQIEGMLTRQGAVSAAPFGSASILPISWMYI

RMMGAEGLKQASQNAILNANYIATRLKDAYPVLYTGRDGRVAHECILDIRPLKEETGISELDIAKRLIDF

GFHAPTMSFPVAGTLMVEPTESESKVELDRFIDAMLAIRAEIDRVKAGEWPLEDNPLVNAPHTQGELVGE

WNHPYSRELAVFPAGLHNKYWPTVKRLDDVYGDRNLFCSCVPMSEYQ

>WP\_004174442.1 MULTISPECIES: SDR family oxidoreductase [Klebsiella]

MGIALISGASRGIGRATALLLAQEGYTVAVNYHHNINAATEVVNTIVASGGKATALRADISDEAQVMAMF

EAIDRMGEPLTALVNNAGILFTQCTVESLSAERINRVLATNVTGYFLCCREAVKRMSHRHGGKGGAIVNV

SSAASRLGAPGEYVDYAASKGAVDTLTTGLALEVAAQGIRVNGVRPGLIYTEMHASGGEPGRVDRVKGSL

PMQRGGQPEEVAQAIAWLLSDKASYVTGSFLELAGGK

>WP\_009308618.1 MULTISPECIES: protein disulfide oxidoreductase [Klebsiella]

MASKIRRWLRELAVWLLIGAAVSLAVDYFRQPALPQNVSATSLQTLDGRTLDLNAMSQQKPLLLYVWATW

CGVCRYTTPSVASLAADGGNVLTVALRSGDNAALEKWLTRKKLALPTVNDPSGQLARQWDIQVTPTLVVI

SQGEVKSVTTGWTSSWGMRLRLWLASW

>WP\_009308617.1 MULTISPECIES: thioredoxin domain-containing protein [Klebsiella]

MRAITALLLLCVSAFSFAAPAEEPQSNGNDQLAQLLFNDPNSPRTGAKEPKLTIVSFTDYNCPYCKQFDP

LLEKIVHDNPDIQLIVKLLPFKGQSSVNAAKIALSTWRQQPDKFWALHQRLMAKKGYHDDASIAAAQKKT

ATDSVNIDDKTMDSLKMNLILSQVLNIQGTPATIIGDQMVAGAIPAEDLEGLVKEQLAKARGQ

>WP\_046042370.1 thioredoxin family protein [Klebsiella pneumoniae]

MYMVFRRLLVCLLWLWLPVSQAADSGWLRAADNQHASVRLRAQTESNGDTRLLLDVALEKGWKTYWRSPG

EGGIAPAIAWHTPLEVNWRWPTPQRFDVAGISTQGYHGDVSFPMTLRGKIPPTLSGVLTLSTCSNVCILT

DYPFSLDMTTPAGERFNYDFTRAMGTLPLRDGLTSQLTASYVSGKLTVTARRDAGWQQPALFIDSMEDVD

FGKPSFTTRGDTLTATVPVTDSWGEAAPDLRGKTLSLVLADSGQAQESQVAVAAGSAAPGLALGWVLLMA

LAGGLILNVMPCVLPVLAMKLGSLVQTEGRERGAVRRQFLASVFGIVVSFLALALMMTALRLGNQALGWG

IQFQNPWFIGAMALVMVLFSASLLGLFEIRLSSSASTFLATRGGNGLRGHFWQGAFATLLATPCTAPFLG

TAVSVALVAPLPLLWGIFFAMGIGMSLPWLLIVAWPGLAQRLPRPGRWMNHLRVVLGLMMLGSALWLVSL

LTIHIGRTPVLTLLVMLAIALLVATAWRYRWRTALRAGALAIVVAGAVAFVAQQDGQGPRRDRVNWQPLS

EQAIASALAEHKRVFIDVTADWCVTCKANKYNVLLRDDVQQALLAPDVIALRGDWSRPSADISQFLTARG

SAAVPFNQIYGPELPQGQILPALLDREHLLATLSAAKGK

>WP\_004900527.1 MULTISPECIES: hypothetical protein [Klebsiella]

MIKRQRKAILFVLLACLVVLTCTAQRMAGMHALVMNLTADSPSLQKNQDQAEAPVTPCELSAKSLMAVPP

MLFEGALLAITLLLAVLAAIPPRIERQWPPRVISSPRLRVHLRLCVFRE

>WP\_002916322.1 MULTISPECIES: 6-phospho-beta-glucosidase BglA [Klebsiella]

MKKLTLPKDFLWGGAVAAHQVEGGWDQGGKGPSICDVLTGGAHGVPREITHQVEAGKYYPNHEAVDFYGR

YKEDIKLFAEMGFKCFRTSIAWTRIFPQGDETQPNEEGLKFYDDMFDELLKYNIEPVITLSHFEMPLHLV

QQYGGWTNRKVVDFFVRFAEVVFERYKHKVKYWMTFNEINNQRNWRAPLFGYCCSGVVYTEHDNPEETMY

QVLHHQFVASALAVKAARRINPDMQVGCMLAMVALYPYSCKPEDVMFAQESMRERYVFTDVQLRGYYPSY

VLNEWERRGFNIRMEDGDAQILREGTCAYLGFSYYMTNAVKAEGGTGDAISGFEGSVPNPHVKASDWGWQ

IDPVGLRYSLCELYERYQKPLFIVENGFGAYDKVEADGSINDDYRIDYLRAHIEEMIKAVTYDGVDLLGY

TPWGCIDCVSFTTGQYSKRYGFIYVNKHDDGTGDMSRSRKKSFNWYKEVIASNGENL

>WP\_002916321.1 MULTISPECIES: MurR/RpiR family transcriptional regulator [Klebsiella]

MFSHAAVASLNNLEMMVYHYVIKNRDKVMYMTIRELAEAAGVSTTTVLRFCRKLQCEGYSEFRVRFKLYL

EQNEPQQANIGASEIMSFFKSVNNDEFDELLEQAVDIILASERIIFVGAGTSGALAKYGARFFSNVGKFS

NHIDDPYFPVTNDMARNALAIVLSVSGETEEILRFASQFSLHHCKVMSITSHEHSRLAKLADFNLSWHVP

QTRIGGVYDITTQIPVIYILESLGRKLARKIS

>WP\_004144734.1 MULTISPECIES: N(4)-acetylcytidine aminohydrolase [Enterobacteriaceae]

MQANDITFFQRFQDDILAGRKTITIRDAAESHFKPGDVLRVGRYEDDGYFCTIAVTATSTVTLDTLTEQH

AQQENMTLGQLRQVISDIYPGESQFYVIEFKTL

>WP\_002916317.1 MULTISPECIES: hemolysin III family protein [Klebsiella]

MVRKPLITQGYSLAEEVANSISHGIGLVFGIVGLVLLLVQAADTNASATAIASYSLYGGSMIMLFLASTL

YHAIPHQRAKQWLKKFDHCAIYLLIAGTYTPFLLVGLNSPLAKGLMIVIWSLALLGILFKLTIAHRFKIL

SLVTYLTMGWLSLIVVYQLAVKLAVGGVTLLAVGGVVYSLGVIFYVCKRIPYNHAIWHGFVLGGSVCHFL

AIYLYIGQS

>WP\_016530681.1 tRNA-modifying protein YgfZ [Klebsiella pneumoniae]

MAFTPFPPRQPSSSARLPLTLMTLDDWALATISGPDSEKYLQGQITADVSHLTDAQHLLAAHCDAKGKMW

SNLRVFRREGGFAWIERRSLRDAQLTELKKYAVFSKVTIAANDDLVLLGVAGFQARAALAPLFAALPDAA

TPVVSEGATNLLWFEHPGERFLLVTDVDTANRVTDALRGEAQFNNSQQWLALNIEAGLPVIDSANSGQFI

PQATNLQALGGISFKKGCYTGQEMVARAKFRGANKRALWTLSGTASRVPEAGEDLELKMGDNWRRTGTVL

AAVQLDDGSLMVQVVMNNDMEPDSVFRVRDDAGSLSIKPLPYSLEED

>WP\_002916312.1 MULTISPECIES: FAD assembly factor SdhE [Klebsiella]

MDINNKARIHWACRRGMRELDISIMPFFEYEYDTLSDADKQLFIRLLENDDPDLFNWLMNHGKPADAELQ

RMVTLIQTRNRERGPVAI

>WP\_002916310.1 MULTISPECIES: protein YgfX [Klebsiella]

MVLWQSDLRISWRAQWFSLLLHGVVAALVLLVPWPLSYTPIWLLLLSLVVFDCVRSQRRIHARRGEIKLL

TDSRLRWQNAEWEILGTPWVINSGMLLRLRHVDTRRGQHLWLAADSMDAGEWRDLRRLVLQKPAQE

>WP\_004144730.1 MULTISPECIES: flavodoxin FldB [Klebsiella]

MNIGLFYGSSTCYTEMAAEKIRDIIGPELVTLHNLKDDSPALMSQYDVLILGIPTWDFGEIQEDWEAVWD

QLDTLNLEGKIVALYGMGDQLGYGEWFLDALGMLHDKLATKGVKFVGYWPTEGYEFTSPKPVIADGQLFV

GLALDETNQYDLSDERIQSWCEQILGEMAEHFS

>WP\_046042376.1 site-specific tyrosine recombinase XerD [Klebsiella pneumoniae]

MKQDLALIEQFLDALWLERNLAENTLSAYRRDLTMLVEWLHHRGLSLASVGSDDLQALLAVRQSGGYKAT

STARLLSAVRRFFQHLYREKIRPDDPSALLASPKLPQRLPKDLSEAQVERLLQAPLVEQPLELRDKAMLE

VLYATGLRVSELVGLTMSDISLRQGVLRVVGKGNKERLVPLGEEAVLWVENYLEYGRPWLLNGVASDVLF

PSQRAQQMTRQTFWHRIKHYAVLAGIDSEKLSPHVLRHAFATHLLNHGADLRVVQMLLGHSDLSTTQIYT

HVATERLRQLHQQHHPRA

>WP\_004174456.1 MULTISPECIES: bifunctional protein-disulfide isomerase/oxidoreductase DsbC [Klebsiella]

MKKGLLMFTLLAASLSGTAHADSAAIKQSLAKLGVQSTDIQPSPVSGMSTVLTDSGVLYVTDDGKHIIQG

PMYDVSGAQPVNVTNQLLLGKLNALSNEMIVYKAPKEQHVITVFTDITCGYCHKLHEQMSDYNALGITVR

YLAFPRQGLQSQAEQDMKAIWCAKDRNKALDDAMNGKGVQPASCSVDIAKHYTLGVQMGVNGTPAMVLSN

GMVLPGYQGPKELKAFLDEHKKQTSGN

>WP\_016530103.1 single-stranded-DNA-specific exonuclease RecJ [Klebsiella pneumoniae]

MKQQIQLRRREAVDGVELPADLPPLLQRLYASRGVRSAQELERSVKGMLPWTQLTGVEKAVEMLHDAFQK

GLHIVVVGDFDADGATSTALSVLALRALGYGNVSYLVPNRFEDGYGLSPEVVDQAHARGAQMIMTVDNGI

SSHAGVDHAHALGIPVLVTDHHLPGETLPAAEAIVNPNLRDCDFPSKSLAGVGVAFYLMLALRTFLRDKG

WFDARGIPAPNLGELLDLVALGTVADVVPLDANNRILTWQGLSRIRAGKCRPGIKALLEIANRDPQKLAA

SDLGFALGPRLNAAGRLDDMSVGVALLLCDNIGEARVLANELDALNQTRKEIEQGMQAEALTLCQQLERS

ADTLPGGLAMYHPQWHQGVVGILASRIKERFHRPVIAFAPTGDGTLKGSGRSIQGLHMRDALERLDTLYP

GLILKFGGHAMAAGLSLEEARFEEFQQRFGELVTEWLDPALLQGEVVSDGPLAAAEMSMEVAQMLRDAGP

WGQMFPEPLFDGRFRLLQQRLVGERHLKVMVEPVDGGPLLDGIAFNVDTSIWPDNGVREVQLAYKLDINE

FRGNRSLQLIIDHLWPN

>WP\_095858446.1 MULTISPECIES: peptide chain release factor 2 [Klebsiella]

MFEINPVKNRIQDLTERSDVLRGYLDYDAKKERLEEVNAELEQPDVWNEPERAQALGKERSSLEAIVDTL

DQMSQGLEDVAGLLDLAVEADDEETFNEAVAELDTLEEKLAQLEFRRMFSGEYDSADCYLDIQAGSGGTE

AQDWASMLMRMYLRWAEARGFKTEIIEESEGEVAGIKSVTIKIIGDYAYGWLRTETGVHRLVRKSPFDSG

GRRHTSFSSAFVYPEVEDDIDIEINPADLRIDVYRASGAGGQHVNRTESAVRITHIPTGLVTQCQNDRSQ

HKNKDQAMKQMKAKLYELEMQKKNAEKQAMEDNKSDIGWGSQIRSYVLDDSRIKDLRTGVETRNTQAVLD

GSLDQFIEASLKAGL

>WP\_002916299.1 MULTISPECIES: lysine--tRNA ligase [Klebsiella]

MSEQQAQGADAAIDLNNELKTRREKLAALREQGVAFPNDFRRDHTSDQLHADFDGKENEELEALNVEVAV

AGRMMTRRIMGKASFVTLQDVGGRIQLYVARDDLAEGVYNDQFKKWDLGDIIAARGKLFKTKTGELSIHC

TELRLLTKALRPLPDKFHGLQDQEARYRQRYLDLISNDESRKTFKVRSQILAGIRQFMVGRGFMEVETPM

MQVIPGGASARPFITHHNALDLDMYLRIAPELYLKRLVVGGFERVFEINRNFRNEGISVRHNPEFTMMEL

YMAYADYKDLIELTESLFRTLAQDILGNTEVPYGDQVFDFGKPFEKLTMREAIKKYRPETEMADLDNFDS

AKAIAESIGIKVEKSWGLGRIVTEIFEEVAEAHLIQPTFITEYPAEVSPLARRNDVNPEITDRFEFFIGG

REIGNGFSELNDAEDQAQRFQDQVDAKAAGDDEAMFYDEDYVTALEHGLPPTAGLGIGIDRMVMLFTNSH

TIRDVILFPAMRPQK

>WP\_002916298.1 MULTISPECIES: isopentenyl-diphosphate Delta-isomerase [Klebsiella]

MAGEHVILLDEQDQPAGMLEKYAAHTFDTPLHLAFSCWLFNQQGQLLVTRRSLGKKAWPGVWTNSVCGHP

QQGETFEQAVTRRCRFELGVEISDIAPVHPAFRYRAVAPNGIVENEVCPVYAARVVSEVQPNDDEVMDYQ

WVDLATMLSALAATPWAFSPWMVLEAENRDARQALTDFVARLRG

>WP\_004157874.1 MULTISPECIES: amidase activator ActS [Enterobacteriaceae]

MMKRFYMTLMLAASLVLAGCSSTSDSGGTYTVKRGDTLYGISRTTGTSVRDLARLNNISPPYTIEVGQKL

KLNGSSSTKTTKKKSSSTRTAAVTPSSAVPQSSWPPVGQRCWRWPTSGKVVLPYSTADGGNKGIDIAGTR

GQPVYAAGAGKVVYVGNQLRGYGNLIMIKHSEDYITAYAHNDKLMVNNGQSVKAGQQIATMGSTDADSVR

LHFQIRYRATAIDPLRYLPPQGSKPKC

>WP\_042941128.1 MULTISPECIES: hypothetical protein [Klebsiella]

MDLRGYSFKQHLSDLLLPNNEFYSTVNPAYLNSGGVYVLRSFNDAGQALTIPRVLDDDRDGILYIGMAKL

FCHRTGDLARSFSSQYRQSKHQTGQRYWSDERYQQRYPYEHLKMFMWISDHPATLEQSFFQSYLARFGET

PPLNRI

>WP\_016530105.1 MULTISPECIES: hypothetical protein [Klebsiella]

MDQELIKKLGLEPTHTFNQTSFVNKTKGRLDIDVIMYDEFDKSGVRVAEVTIHDTTERYPPFSREIYLES

RVKV

>WP\_071609135.1 hypothetical protein [Klebsiella pneumoniae]

MPICKQAHRYNSIFINLPYDQGGEGRHKCCGCAYDQGYCAGLARTGQVWVDLTALPDSQAGTVRHKSPQA

AFAEGYRDGVRDSYKQAI

>WP\_023327926.1 MULTISPECIES: recombinase family protein [Klebsiella]

MSRTFAYCRVSTNEQTTENQIMAIRQAGYDILDSRVVSETVSGGVQAMQRRAFANMVDHKLEEGDTLVVL

KLDRLGRDNIDVQQTITMLIERGIKVVSLDLPVRDLSSAEGKLMLQMFSSFAEFEKSRIIERTKEGLERA

KQEGKILGRPVATETRRRVQEAREQGLSQSKAAQSLGLGIATIKRYWNI

>WP\_129015075.1 hypothetical protein [Klebsiella pneumoniae]

MNNYLFCNWHGTYFHGSFINNNSAFTAFCNHQSAAYWDNEGKCIKHLIPQNVGVYARLPLNKDDNIEDVF

SDSKFILCFEGDLLNDYLDCNEVLGLYLFGKINAVQKIYRTR

>WP\_042940720.1 hypothetical protein [Klebsiella pneumoniae]

MKYFTIEQVVEALKTGAARRHQIYDNFAQARYRGFTERASLFKTALEIFDQWKRENKTS

>WP\_162571991.1 MULTISPECIES: hypothetical protein [Enterobacteriaceae]

MNVTFDQETYKDLIYEANLQGLAAPALVARIIRQYIKNQTGPYEGANQPEDLNGKNKR

>WP\_016529417.1 MULTISPECIES: helix-turn-helix domain-containing protein [Enterobacteriaceae]

MGKTKDNYFKSHYDIFKINTINGKKFSISAKSIYSYLKSFSDAGLKVFPSHNEIADTFGITRNAAIKQIE

KLIELGLIERETRPGNCNEYHILTIQIENTAGRTYSENRGTRYEVVGDFGNKSGIVLIEEDNDDLPW

>WP\_016529416.1 MULTISPECIES: hypothetical protein [Enterobacteriaceae]

MGKKKTFEVSINNLPAALKRLDLPAEQVQVIEDYKKQFPFLLEEGENVLVSLDQLWEALDTPYYTRPGTI

PESSGSVKSRSIQQEKQYKRNKFNQWVESVLKEIDGEPFSRMVPTGKTKRKETFVTIEDAKIIAMMAPGE

QGRKIRRYFVTVEKVCKILWQYNLQRNQIEDKSKEVYKLRLAQTGYKGFDVAAKDKVRFNSLVKQIAGAR

NVRETDLENYHHIQHEVFNAMKRGCTDSQILAFYLGDEAA

>WP\_129015076.1 hypothetical protein [Klebsiella pneumoniae]

MSGDSGGQSTPEEQETINSMDGVTWKPRQRYAGFKFNREPLKFECLFDNINEYEGWLEFNRLENEQYQGY

DVDIIDAAYNGITD

>WP\_016531927.1 hypothetical protein [Klebsiella pneumoniae]

MINFEQHKNIVEDFVEQHYPLAHSLMVDSYIDPEAYYSNYQMLLEAMSKLPEHPEFFLEWLLEDDAALYI

NLMELVVITRTIHNVFEQVSP

>WP\_016530284.1 hypothetical protein [Klebsiella pneumoniae]

MVAIHKGVKTFDGKIPVTLLVDDVETANELIKLAKTANVPVVEQEEDLNKSKNKTTQDKLKQIIKNKGVP

NGTN

>WP\_117262243.1 hypothetical protein [Klebsiella pneumoniae]

MALIKFPQPNLSVCDVLSRELNGYSRKVKVFPKIPDCVPGTVIDDSGEIVGSASTSANVVLEYKDADTTP

VAVLVANTNIHIKDFSLVCDDVAKAKELLSADPSVYFSTGNDLPTT

>WP\_016530283.1 major capsid protein [Klebsiella pneumoniae]

MFSYDAYKMVDLAPIFEVAPSEGYLLQNLNIFDKSSSDGIYVMLDRLIEDNKTLLNQPKKRYSFEHDSTA

RTPANSFPVELLHLHREDTVSAADFQKAGRKPGTDVQETMLDIVADYTLKHAKAYKRYVESAYGDALFRG

LVQTPYTQEAPVIDYADSFDAPMMADTITLSNGSTDALEVFNGFLDKISNATDGLWTDVRRVVCFASASF

YNSLRFHASMKSAYQYVDPFNEMNIVYQRKEVLPNVQTFTLPGLSIDVIKVTDPLLTPFIADGTAVMLPV

FQSNTNVYQHLYGPASVDTNLAAAGITQEYFSYQYEKERGEVEIVSEASVLPVNHGTNFSLVITAN

>WP\_016530282.1 hypothetical protein [Klebsiella pneumoniae]

MSGTQITASTLVNKIVYRTDLNSLKKARNDMKKLQQEFSKSNNQVAKVKQQADKQIHQAQIKQQRDIDKQ

QKQTAKQQAADTKAKQNEQKKLAAAQSRAAKIQMQQQAKTAKISENARLAERKALFDIGRLQGLNGTERF

QAIKHAQGLIDSYKNQTITLRDLNQQLSQYLTTQRSIARNNSKQAKQSGKGKKSGSSGWVARNASAILPV

DQLLGPTAAAFLGQQTYQIISGTLAGAIERNQGRKMISSMGLNPLEADAAIQETLKRTGFNMSYEKISDI

SKDVQDKIGQLSLGEWKTDKKTGQSTYSGGGEMGDWLQMMVSRGGYTQQGALKTLQNVKGPVELAVLLEG

LRKSAKLTDSEFTALAEVINDFSYLAKSVDASGQNVIDTMNTMVNSGLALNSQQQKSIDNLSQMSIVFDN

ARNSLGDQFAASFSKGLEDLGINTQNLSSEMGTLVPLVKDLGTGTAQTVKVFKDLLDVLSIITEWKNRLL

GTDKPAEQNIFQQGATFVGESLLPPGVLDMAGKVKAWLTPEGNSVAAQAQSGALINQMMVQTPAMSYQPV

IPDLKADFNLTVNPSPEFGMMVEAVADKRIEWAFDDQNFQINQSILGQ

>WP\_016530281.1 tyrosine-type recombinase/integrase [Klebsiella pneumoniae]

MSIKSQSYLYPTPEGVWMFQIFVPKYMRHIFGGKKLYRKSTGTKDLATAKHFRNHMLIEWKALKEQYCPD

TEERRINNAILELRAQTVMKSPLQAIPTLIEIRDRYADQYKDRRSFSTLAKSARSVEVFLKHLECADIKI

TKIRRSQVALFAMRHIEKKADQTVQNWLTCLGSLYEFARRVHDDIPPDNPFHGHNLEARRTIESYQPFTT

KQLVTLVENAEEELQGVILIGLYSGMRLDEIASLKRDDIVEIEGIRCFNITKSKTKAGVRLVPIHSKALP

IVDRWLSLKSGEYLLPTANRIQRADGKKGPFYSQAFTRLRNKVIPAATNRQCYHSLRGHFITCLDRKGIE

ETRVGTLTGQIEKKAKTEAFRTYSAGPLMRELKQIIELVSYSEIEKGH

>WP\_042941239.1 MFS transporter [Klebsiella pneumoniae]

MTLFSSQPGDEGLPGPARARVMAAIMTTTLMGVFDGTMINIALPSMAQEMQVPASIAVWFANGYLLAAAM

TLAIFAALAARLGYRPVFLAGLTTFTLTSLGCALANKPEVLIGMRVLQGIGGAATLSIAPAILRSVFPGR

LLGRILGFHALLIASSSAIGPVLGGTILHTLSWQWLFAINILPGTLALLLAVRALPRDAIRMQAPFDTVG

AILSALLLGSTIMAANSLQNAISQFGSLCWMALAALSGMAFIWQIRRTGHPLLPPSMFKNERFTLAAFTS

MVAFVSQGITFIALPFLFQSEYGYSPVVSALLFTPWPLGIVLIAPHAGRWADTISAPAISTLGLVIFVVG

LILLATLPARPSMWDICLRSLVCGIGFGCFQSPNNREMLSNVIREHASYASGVLSIMRTFGQCLGAAAVA

VLLAADERSIHVALWSAAAASAVSVVVSASRLRKIAHPAETG

>WP\_016530279.1 LysR family transcriptional regulator [Klebsiella pneumoniae]

MSDPDFNLLVALDILLSEASVAGAARRLNLSTSAMSRTLSRLRDVTGDPILVRAGRNMVLTPWAEATRDR

ARRAVHDARAVLQPSTETFSAQNLARLFTIRANDGFVVAFGPALIAAVADAAPDVCIRFAPKPEKTSRYL

REGLVDLEIGVQSNMGPEIRLQRLFEDRFVGVVRKGHPLAKQAEIGVDDYVAWGHVVASPEGALHGSVDD

ALAELGTKRKIASVVPGFPTALSVALESDLIAMIPALYLLNQQVTDQVHVFELPFKSRRITVSQMWHPRM

ERDPGHRWLREQILAICGVGRSVMTKEPV

>WP\_016530278.1 MULTISPECIES: carboxymuconolactone decarboxylase family protein [Klebsiella]

MKNVIAAAALSLVLSDFAYAHEQRDEAMMKITPSTLADADIQAVSPALARFGREAISNDLWQRDALSARD

RSIVTVAMLIARNQPGELKHYIAVALDSGVTPAEVSEIITHLAFYAGWPNAMSAVSVAKTIFEARGVTAE

ALPAASPTLLPLNEQVEKQRADTVEKNVGPISPGLVKFTADPLFLDLWQRPALTPRDRSLVTVSALIAAG

QSAQIGYHLNRAMDNGLSAEEAGEVVAQAAFYAGWPNAFTAAPVVGEVLRARESKAE

>WP\_002916289.1 MULTISPECIES: aldo/keto reductase [Klebsiella/Raoultella group]

MQYTRLGKSDLLVSRICMGCMGFGDPSTGQHRWTLDETASRDIIRHALEQGINFYDTAIAYQNGSSERYV

GRALREMAKREEVVLATKFLPRTAAQIAEGISGKQAIARSLDQSLRNLGMDYIDLYIYHIWDYNTPVIDV

LEALHTAVTAGKVRAIGISNCYAWQLAKVNALAEREGLTSFVSVQSHYNLIMREDERELFGLCAEEGIAM

TPYSALASGRLSRLEGHTRRAVEDDYARGKYDGTAEQDRIIIARVAELAERHQVSMTEISLAWLLTKVTA

PVIGATQKHHVDGAVNAVALQLSPEDIRYLEEAYQPHVLTGVMAQNTPQAKDHHQVWTR

>WP\_004181226.1 MULTISPECIES: NAD(P)H-dependent oxidoreductase [Klebsiella]

MAHILVVSGHPDLNHSIANATILDELATALPDAEIRRLDWLYPDGKFNIAAEQESLLQADVIVWQFPFSW

YGLPGLMKQWLDEVFVHGFAHGSTAKLGGKKLILSFTTGAPQALYTADGFFGHAIEEYLLPFETTARLCN

LELLAPVYTCGISYADRDADKIAQQKTLAREHAARLIARLNTLVE

>WP\_016530277.1 hypothetical protein [Klebsiella pneumoniae]

MRILCLDIPAPGATLEHYAPHLTAEALHAWGLYKSGFIRDIYFRQDRPGVAIFLECDTVEEANNVMAEFP

LAKSGLLTFECIPLGSFISWENLFSAEF

>WP\_016530276.1 LysR family transcriptional regulator [Klebsiella pneumoniae]

MNNALYNQIRIFQSIAHEGNISAAARKLEITPPSVSNALRLLEEHIGHPLFVRPTRRIELTETGQQLLEQ

TAAAVETLEKSLEIIRDQNQEPSGAVRITLSRFAYLLILKPAMAAFCQQYPGIQLEISVYDGTVNIIEER

FDLGIRFGDILEGGVVARPLMKPFREGLYASSAYLAEYGVPAMPADLHHHRLIGYRFITNNRILPLILND

HGEQLTVEMPGQLISNDIDVMADGIRHGLGIGRLFEPILQLQPDREQFIPVMEDYWKTYPPVYLYYPKNA

GRTKRVKALIDFLIMHAAE

>WP\_023317269.1 hypothetical protein [Klebsiella pneumoniae]

MGRRFIVCIFALVAFSTSAAHGVHGGHNGQSVSAGADGGNGSNGGDIDNSSGRAGCPGGTDPDKHGHFYL

PGTSEPCNPGPQDAEKVGSSR

>WP\_046042393.1 DUF1349 domain-containing protein [Klebsiella pneumoniae]

MQPYFHWINEPAEWRRDADGLTVVTNKHTDFWRHTWYGFERFSGHLYAAEVAGDFTLQAKICADFTTLYD

QAGLMMMADEQTWLKAGIEFNDDAPAIGSVLTLTHSDWATGLFHGDPRTFWLRLTRKGDALRLQYSTDGE

RWPLLRLGYFPPGPVKAGVMCCSPERGGLAVAFQDIQLSPPLDKALHDLS

>WP\_002916282.1 MULTISPECIES: YciI family protein [Enterobacteriaceae]

MSTIYVVVLTYIKPLEEVDRAIPAHIEWLKKGYADGLFLASGRRIPRTGGVILAKCDSRETLQARLSQDP

FQQLGLARTEIIPFEASMASPALQSLL

>WP\_002916281.1 MULTISPECIES: metalloregulator ArsR/SmtB family transcription factor [Enterobacteriaceae]

MSLLPLQLFKNLADETRLGIVLLLKARGELCVCDLCTALAQSQPKISRHLAMLRESGLLLDRKQGKWVHY

RLSPQMPAWAAQVIEQAWLSQQEDVRLMISRLAGGPGCR

>WP\_016530274.1 arsenic transporter [Klebsiella pneumoniae]

MLLAGTIFILTLVLVIWQPRGLGIGWSAAFGAALALATGGVQVADIPVVWHIVWNATATFIAVIIISLLL

DESGFFEWAALHVSRRGRGRGRLLFTWIILLGAAVAALFANDGAALILTPIVIAMLRALGFSKGTMLAFV

MAAGFIADTASLPLVVSNLVNIVSADFFAIGFREYASVMVPVDLAAILTTLAMLHLFFRKDIPPAWDMAL

LKAPATAIKDPATFRTGWGVLLLLLAGFFVLEPLGIPVSAIAALGAGILFAVAKRGRVINTGKVLRGAPW

QIVIFSLGMYLVVYGLRNAGLTDYLTTVLNMLAERGLWAATLGTGILSAFLSSIMNNMPSVLVGALSIDG

STATGTIKEAMIYANVIGCDLGPKITPIGSLATLLWLHVLAQKHITIGWGYYFRCGITMTLPVLLVTLAA

LALRLSFNQP

>WP\_002916278.1 MULTISPECIES: glutaredoxin-dependent arsenate reductase [Klebsiella]

MSITIYHNPDCGTSRNTLALIRNSGAEPTVIYYLETPPSGDELRQLLAAMGIPVRALLRKNVEPYDALGL

AEDRFTDDQIIDFMLQHPILINRPIVTTPQGTRLCRPSEVVLEILTAPQKGAFVKEDGEPVIDAAGQRVK

>WP\_002916277.1 MULTISPECIES: peptide MFS transporter [Klebsiella]

MHSSVNKNESRTFFGHPYPLGSLFFTEMWERFSFYGIRPLLILFMAATVYDGGMGLARENASAIVGIFAG

SMYLAALPGGWLADNWLGQQRAVWYGSILIALGHLSIALSAWLGNDLFFIGLMFIVLGSGLFKTCISVMV

GTLYKKGDARRDGGFSLFYMGINIGSFIAPLISGWLIKSHGWHWGFGIGGIGMLVALIIFRVFAVPSMKR

YDAEVGLDSTWNSPVAKKNGVGAWLLALALGVAVLVTLISLGTIVINPVAVASVLVYVIAASVALYFIWL

FVFAGLNRKERARLLVCFILLVSAAFFWSAFEQKPTSFNLFANDYTNRMIGDFEIPAVWFQSINALFIIL

LAPVFSWAWPALARKNVRPGSMTKFVIGILCAAAGFGLMMLAAQNVLSNGGAGVSPLWLVGSILMLTLGE

LCLSPIGLATMTLLAPERMRGQMMGLWFCASALGNLAAGLIGGHVKADQLSLLPDLFARCSIALLICAAV

LAVLIVPVRRMLENSRSSAAQKSLSNA

>WP\_002916274.1 MULTISPECIES: DUF1889 family protein [Klebsiella]

MPAVIDKALDFIGGMNTSEPVPQSMDESTAKGILKYLKELGVPATPADVAARGQQQGWSAGFTDKVAEWA

ERVAAGERLVIKHPEFFSTYMREELRALV

>WP\_002916272.1 MULTISPECIES: MdtP family multidrug efflux transporter outer membrane subunit [Klebsiella]

MMILPFSARLRGTLFTLTLTLLSGCALIQDEPAQVAIVNPQQAQLAQVIHLANSDWPAARWWEAYDDPQL

NMLINRALQNSPTMQAARLRISQSQSTVELARSAMGLQATAVAAQNRLRITDKSFSWPYSYSLPVDKNGP

WYTLNTVGVGAQLNIDLWGADRARVAAAIGEKNARLAETAGIELDIASSVAQLYFAMQATFQKIALLQEL

EGIARFSVEAHEHRTRRGLEDSVDVANAQAEQLAARQQIISAEGMLTQYRETLRALIGADAQSMPAIHPV

ALPALQETLPPSLSFELLARRPDLQALRGYVTASLSQVDAAKAAFYPHFDIKAFWGYNALSVGDLFKSSF

QQINLLPGLYLPIFDGGRLNANLQSVRTASNILIKQYNQAVLDAVRDVAISSSQLNDLNQQRALQQLKVT

AAQTTTDSARAHYQRGLLSRYAAEEARRAVLAQQLLLLDIEAQRLSTDITLIKALGGGYRGQ

>WP\_032438974.1 multidrug efflux transporter permease subunit MdtO [Klebsiella pneumoniae]

MFPLAHFLRQELRDAPGRASYTLRLTLSCAVLITLFMTLQIPFLAVALIVVFYVSQPNVLMIKLVSVVFF

VTVTVALGGVLLIIKWTYDYPLIRLAASVALFFCALYLMRVLGKLGLAFFVVALAVIYAQTFPSMTSQSE

ILVRLLLWLWVAINTAILVTLLVNACFQQAFPGNQFKARLAGMLHEVARRLAAPDAEAPPTFGETAAQFN

QLQSLFAQASRATPEIAADPQAWRSRLAATLRCYQLTALLQADEADSDDRQQLSQAVLQLKNALSEGPFD

GAIPPLTLSGRGVNRAVLQEMATTLQRLAQGEPVALPQGEVEKAPLLAPDAWRNPAYLHFALKTLLATLI

CYVFYTAADWQGLHTIMLSCVIVAQPGLGATMQKTWLRIGGALLASLLALLLIVFVQPWTDSLTGLLAMS

LPVLALAAWIAAGSERIAYAGIQIGFTFALAFLSWFAPLTNLTELRDRVLGILLGVLVSSIVHLYLWPDS

EAPQLKTRLAALYRRLADCLAAPKEAVPLAPLLVAFTDSEALLHRVRAEPLGTYAHPWPQAKGWPMRATL

AQAEEIARLSEGYRLNATPGDPTLARCAEQLRRYAERIEQEATAPGEQLTAELTNPFGPALAAALAALPD

WGPTPIATEQQAKTS

>WP\_004174502.1 MULTISPECIES: multidrug transporter subunit MdtN [Klebsiella]

MTTSRTSLLRKKWPLLALVLAAILALILVIWQLQTSPETNDAYVYADTIDVVPEVSGRIVEMPIRDNQRV

KKGDLLFRIDPRPYQAMLDDAKARLTTLDAQIMLTQRTIKAQEYNAQSVAAAVERARALVKQTTSTRIRL

EPLVPQGFASQEDLDQARTAEKAARAELEATLLQAKQASAAVTGVDAMVAQRAGVLAQIALAELHLEFTE

VRAPFNGVVVALKTTVGQYASALKPVFTLLDDDRWYVIANFRETDLNNVRPGVAARITVMTNHNRTFNGV

VDSVGSGVLPEGGSVIEGLPLIQKSINWVHVSQRFPVKIAVSDPDPELFRMGASASAVLQP

>WP\_002916204.1 MULTISPECIES: YtcA family lipoprotein [Klebsiella]

MNHIATIARPARLLLVLPLSGCSLSPEIPVLGAAFPGWFFCLLGGAFLLIPCHILITRKGWQPRFSPLVF

SYVALMFLFATLLWFLFFVH

>WP\_016530761.1 (4Fe-4S)-binding protein [Klebsiella pneumoniae]

MDKELLEAGYWAYTGEKIDVYFNTAICQHSGNCVRGSAKLFNLKRKPWIIPNEVDVATVVNVIDTCPSGA

LQYRHK

>WP\_016530762.1 GNAT family N-acetyltransferase [Klebsiella pneumoniae]

MEILEGHNKFYVNNAQGNQVAEIVFVPTGEHLSIIEHTDVDPSLKGQGVGKQLVAKVVEKMRQEQRKIIP

LCPFAKHEFDNTREYDDIRA

>WP\_023287976.1 EAL domain-containing protein [Klebsiella pneumoniae]

MMTDYILSPCSLAARGLSQLMLNAAKRPAELPVEGVSLRELAAVKRIVVYLPDDPLWMLTTLRQAARLLD

EALPPLPMLILSRSPAIWLWQTLLYQVSHPDRLRNIHTAPADLSCAELAHRLENAPRLERLASEAALIHG

KRVVGLTHAELKVILALLQGQTIGEQAQRLGLSQKTLYTQRLAGVKKLVECHPHLAPRFPRTLLPRSPAN

ALTAFEQEWVQAIHDRQVFPVFQPIVDSRSQLQGVEILIRWRHRGQVLHPQTFLPHFRADYTWLLLTAFV

LQEAVQNINEYPGAFYFSVNIPSSLADSDSLLRMVEAARQQLRQPEGVARLVLEYAETIDFRHQSRSAAH

VAQLQRAGVRVMLDDCFSQGSVIFPARRLHFNAYKLDMSIVNDAQHDPKALALIKSLAYYCQLSGSRCVA

EGVDSLAKFTQLKSLGIDRFQGYLFSPPMRREHLPDLIRRFSHQRDPAKR

>WP\_004151788.1 MULTISPECIES: fimbrial protein [Klebsiella]

MKKIIPLFTTLLLLGWSMNAWSFACKTATGATIPIGGGSANVYVNLTPAVNVGQNLVVDLSTQIFCHNDY

PETITDYVTLQRGSAYGGVLSSFSGTVKYNGTSYPFPTTTETARVIYDSRTDKPWPAVLYLTPVSTAGGV

AITAGSLIAVLILHQTNNYNSDSFQFIWNIYANNDVVVPTGGCDVSARDVTVTLPDYPGSMAVPLTVHCA

QSQQLGYYLSGTTADSANAIFTNTASASPAQGIGVQLTRNGSAVPANSTVSLGTVGTSPVNLGLTATYAR

TTGQVTAGNVQSIIGITFVYQ

>WP\_073901412.1 MULTISPECIES: type 1 fimbrial protein [Klebsiella]

MGWLLAGLLTASASLRAADVTLTVNGKVVARPCTVSTVNATVELGDLYTFSLIGAGSASAWHSVALDLSN

CPVGTSRVKATFSGTADSTGYYKNQGTAGNIQLELQNEDGTTLNNGSSQSVQVDETSQSARFPLQVRALS

VNGGATQGTIQAVINVTYTYA

>WP\_004185520.1 MULTISPECIES: type 1 fimbrial protein [Klebsiella]

MRTLQYLLGALFTLGAPAALAADSTIAISGYVRDNACAVAGESKDFTVDLQDNAAKQFYAVGATTPPVPF

RIVLSPCGTSVTAVKVGFTGVADSVNTSLLKLDAGTSAAAGMGVEILDQQQSRLPVNAPSSTMTWTTLTP

GQTNILNFYARLMATQVPVTAGHVNATATFTLEFQ

>WP\_002916192.1 MULTISPECIES: fimbria/pilus periplasmic chaperone [Klebsiella]

MSRQGDNVRKTATMAHGLLAGCVLFAASIFSASAQAGVALGATRVIYPAGQKQVQLAVTNNDDNSTWLIQ

SWVENADGQRDGRFVITPPLFAMQGKKENTLRIIDATNNQLPQDRESLFWMNVKAIPSMDKSKLSDNTLQ

LAIISRIKLYYRPGKLALPPDQAAEKLTFSRSGSSLTLTNPTPYYLTVTELNAGTRILENALVPPMGKTS

VKLPADAGNTITYRTINDYGALTPKMNGVLR

>WP\_016530767.1 type 1 fimbrial protein [Klebsiella pneumoniae]

MQGMKSGLLLLLPPLALAGNHWNVTLPGGSMRFQGLIMASSCRVESGDRQMTVNLGQISSNRFHAVGEDS

NPIPFAIHLQDCSTAVSQHVGVTFHGVADGKNPDVLSVGEGPGIASGIGIALFDSQGQQLPLNRPADRWI

SLYRGPTTLNFVAKYRATGRQVTGGAANAQAWFSLTYQ

>WP\_016530768.1 type 1 fimbrial major subunit FimA [Klebsiella pneumoniae]

MKIKTLAMIVVSALSLSSTAALADTTTVNGGTVHFKGEVVNAACAVDAGSIDQTVQLGQVRSAKLATAGS

TSSAVGFNIQLDDCDTTVATKASVTFAGTAIDSSNTTVLALQNSAAGSATNVGVQILDNTGTPLALDGAT

FSAATTLNDGPNIIPFQARYYATGAATAGIANADATFKVQYE

>WP\_002916189.1 MULTISPECIES: type 1 fimbria switch DNA invertase FimE [Klebsiella]

MNRRRFLTAKEVQAMMQAARQGPTGERDYCLILLAFRHGMRISELLDLHYHDLDLHEGRVNVRRLKNGFS

TIHPLRFDEREAIERWSLVRAGWKAADKTDALFISRRGTALSRQQAYRIIRSAGENAGTVTHTHPHMLRH

ACGYELAERGTDTRLIQDYLGHRNIRHTVRYTASNAARFAGIWERNNLLEEKDQKTKNEITD

>WP\_004151951.1 MULTISPECIES: type 1 fimbria switch DNA invertase FimB [Klebsiella]

MTNNADIKKRNFLTQNEIESLLKAADTGPYAARNYCLTLLCFIHGLRASEICRLRISDIDLAARCVYIHR

LKKGFSTTHPLLDKEIYALKRWLAIRSSWPQAASEWLFLSRKGNPLSRQQFYQIIASSGGLAGLPLEIHP

HMLRHSCGFALANMGIDTRLIQDYLGHRNIRHTVWYTASNAGRFYGIWDNPRDKQRSSLIQ

>WP\_016530769.1 MULTISPECIES: nickel/cobalt transporter [Klebsiella]

MTTPIALRDWRLLAAGCGGLLLLAAAITLHSHWGDFLQWCLATQITLHRYLVMYLLLLNNHQYSGGIWLL

VGAFLYGVLHAVGPGHGKFIVTTYLSTNQESLTAARVVPFLGSLLQGVTAILFVFILAVGLNLAAGDLSA

SRWYVEKISALTIGVFGAYVIFRALQSLWPAKQVIRRLTPAHQHDASCGCGHHGVGQDLQGADWKTRLGV

VLAIGVRPCSGAIMILLFANALGIVSWGIAAVMSMALGTALSILGLSLLVHYARHRTVKRLVTNHRPRPW

LVPLVKILGGLALILFAVGLFFSVVPISANGDFIAAGC

>WP\_002916184.1 MULTISPECIES: MarR family transcriptional regulator [Klebsiella]

MDKSPPIDAVDRILAQWQRERPDLDCSPMGPIGRLKRCAMLLEPQVEVAFTRHDLVRWEFDMLATLRRAG

APFVLSPTQLFSTLMITSGTMTHRLKALEKRGFITRLPNPEDARSMLVALTSAGRERIDAAVETHVDNER

QLLAGLSDGERQQLDQALRVLMRLLETG

>WP\_016530770.1 DMT family transporter [Klebsiella pneumoniae]

MAFLSRNLILDLLLTALAPAIWGTTYIVTSQFLPPDRPFIAALLRVLPAGIALLIWSRRFPQRGEWAKLI

VTGILNIGAFQALLFIAAYRLPGGLAAVIGAIQPLLVMLLAWCVDRQRSPWLAVLSAIAGILGMAMLLLS

PHTVLDPLGIGAAFLGAISMALGTWLSRRWALSLPIVALTGWQLTIGGVVLAPVALIVDPPLHQVTVLQA

AGYLWLCLAGAMLAYGLWFRGIGRLSPVAVSAMSLLSPVTAVVLGWIFLGQKIQGMALMGLIVVLASVLS

IQLALARQAAGAKTKKAP

>WP\_002916131.1 MULTISPECIES: DUF1471 domain-containing protein [Klebsiella]

MKNVKLLAAAGMLSLVSFASFAHPVSVTADTLDSAEAKIATIAKEQGASYHITEAYTGNQVHMTAELSK

>WP\_002916128.1 MULTISPECIES: type 3 fimbria major subunit MrkA [Gammaproteobacteria]

MKKVLLSAAMATAFFGMTAAHAADTTVGGGQVNFFGKVTDVSCTVSVNGQGSDANVYLSPVTLTEVKAAA

ADTYLKPKSFTIDVSNCQAADGTKQDDVSKLGVNWTGGNLLAGATSKQQGYLANTEASGAQNIQLVLSTD

NATALTNKIIPGDSTQPKAKGDASAVADGARFTYYVGYATSAPTTVTTGVVNSYATYEITYQ

>WP\_004211921.1 MULTISPECIES: type 3 fimbria chaperone MrkB [Gammaproteobacteria]

MKRIALFFCFIFSFAAHANNIIVNGTRFIYPGNEKEITVQLSNNADRPALAQAWLDNGDADATPDTITTP

FIITPPISRVDAKSGQTLRIKLGSSAGLAKDKETLWWLNLLEIPPVVANQKNEGQNVLQLAIRSRFKFIY

RPAGLGNRDAAAEKLTLTASGSGLAINNPTPFYITVSRISRDGGKALNSKTVMLAPQSSQTVALSSAVNR

GETLTVNNINDYGADVAVKVAVK

>WP\_000813718.1 MULTISPECIES: type 3 fimbria usher protein MrkC [Gammaproteobacteria]

MKQRSFCPGRLSTAIAIALCCFPPFSSGQENPGTVYQFNDGFIVGSREKVDLSRFSTSAITEGTYSLDVY

TNDEWKGRYDLRIARDKDGRLGVCYTKAMLAQYGIAAEKLNPQLSEQEGYCGSLKSWRNEENVKDNLVQS

SLRLNISVPQIYEDQRLKNYVSPEFWDKGITALNLGWMANAWNSHTSSVGGSDNSSAYLGVNAGLSWDGW

LLKHIGNLNWQQQQGKAHWNSNQTYLQRPIPQLNSIVSGGQIFTNGEFFDTIGLRGVNLSTDDNMFPDGM

RSYAPEIRGVAQSNALVTVRQGSNIIYQTTVPPGPFTLQDVYPSGYGSDLEVSVKEADGSVEVFSVPYAS

VAQLLRPGMTRYALSAGKVDDSALRNKPMLYQATWQHGINNLLTGYTGVTGFDDYQAFLVGTGMNTGIGA

LSFDVTHSRLKSDAHDDSGQSYRATFNRMFTDTQTSIVLAAYRYSTKGYYNLNDALYAVDQEKNSRSNYT

LWRQKNGMTFTVNQNLPDGWGGFYLSGRISDYWNRSGTEKQYQVSYNNSFGRLSWSASAQRVYTPDSSGH

RRDDRISLNFSYPLWFGDNRTANLTSNTSFNNSRFASSQIGINGSLDSENNLNYGVSTTTATGGQHDVAL

NGSYRTPWTTLNGSYSQGEGYRQSGIGASGTMIAHSGGVVLSPESGSTMALIEAKDAAGAMLPGSPGTRV

DSNGYAILPYLRPYRINAVEIDPKGSHDDVAFDRTVAQVVPWEGSVVKVAFGTKVQNNLTLQARQANHEP

LPFAASIFSPDGKEIGVVGQGSMMFISDANAKRAIVKWSGGQCSVDLGQQTTKDSVCR

>WP\_002916123.1 MULTISPECIES: type 3 fimbria adhesin subunit MrkD [Klebsiella]

MSLRKLLTLFIVLMALGTTSSWASCTRLSSPTVMLDMVVGRVVVPPDLPVGSVILTRDWTMSAPGGASYR

CTSGTNRFAAKIVSPGATDLGNKIYSTNVPGIGMRFSRGGATVNIVYPDVFSSRVYNTTNYSLEGSRFTL

QIIKTAATTGSGTLAAGKYTSYDWESGGNPILETYLSANAITVVSPSCSVLSGKNMNVDVGSIRRTDLKG

VGTTAGGKDFNIDLQCSGGLSETGYANISTSFSGTLATSTTATMGALLNEKAGSGMAKGIGIQVLKDGSP

LQFNKKYTVGRLNNQETRYITIPLHARFYQYGPTTSTGEVESHMIFNLTYD

>WP\_002916122.1 MULTISPECIES: type 3 fimbria minor subunit MrkF [Gammaproteobacteria]

MKGLPKNTIAWLLFCGSLAAPSAWGFETNYDRGRVDFAGRVTDISCSVALNGGQHAGSGNVWLAPVSLAE

VHDRGAGAFMKPQPFTLALSNCQLRHDGGAASQDEVRRVSVRWVDGFLLTAVGNENAGYLANTLPDGAQN

IYLALSTNDNNTLDKSNKIVPADPQQNQVRLQESAVSGGLFTYYVGYVSPTPKSATSGPITSWATWELVY

N

>WP\_004144002.1 MULTISPECIES: phosphodiesterase MrkJ [Enterobacteriaceae]

MNTKIFEDNILSRNDIAVRYVFQKMFSPQGTLVAVECLSRFDNLSISPEDFFRHATAAVRERIFLEQLAL

IEKHKAWFLRNHISATINVDDHILNLLRQKDIKAKVAALTCVHFEVTENAENLLHNSLAAWQSPQDTSLW

LDDFGSGYAGINAIRGYHFDYVKIDKDFFWHLMRKESGRQLMDALVTFLSRNHHNVIIEGVESEAHKEWL

QGMEWFAIQGHYWREVSIEQLVADDIAM

>WP\_002916079.1 MULTISPECIES: transcriptional regulator MrkI [Klebsiella]

MLYTNDNLIGHSIYHYLIDSHENATRLSYADVIHEKHLPLAQTIIFNLINKDISAIRIVDLLNALRLSLL

RCQQPVLMVKSDIVGLCRELINFDNAMIISEKSPLTLFSSIVQRAKGVSELPPRGLRKQLSPRECQILEL

LIANNNNKRIAALLGIAHKTVHSHRIHIMQKLGIDNSRTMNQRIAALHQC

>WP\_016530388.1 aldo/keto reductase family oxidoreductase [Klebsiella pneumoniae]

MSSVTLSGRGMLGDRQVYRLGYGAMQLAGPGVFGPPKDPEEAVRVLQAAVEAGINHIDTSDFYGPHVTNQ

LIRKALHPYPDDLCIVTKVSARRDEKGNWLPAMSPAELTQAVEDNLRHLGLEVLEVVNLRSMLSPHGPVE

GSLEAPLATLLELKERGLIRHIGLSNVTAKQVADAQKMTPIVCVQNLYNVAHRADDALVDALAAQHIAWV

PFFPLGGFTPLQAQELNEVAASLEATPMQVALAWLLQRAPNILLIPGTSSRTHLAENIAAAELVLPAEAL

RTLDNIATAARR

>WP\_002916058.1 MULTISPECIES: amino acid permease [Klebsiella]

MSKIWSKEETLWSFALYGTAVGAGTLFLPIQLGSAGAIVLFITALVAWPLTYWPHKALSQFILSANIAPG

TGITGAVNHYYGKKIGNLITGLYFLAFFVVVLIYAVAITNSLAEQVAHRTPMTPGLRALLSLGVVLVLNL

IFLMGRQVTIKVMGFLVFPLIACFLFLSLYLIRDWHPEHLTSQMQFSPQTLHQVWISIPVMVFAFSHTPI

ISTFAIDQQEKHGDLAMGKCKKIMKVAYTIICASVLFFVFSCLLAIPATYIETARDQGVTILSALSMVPG

APGWLAVTGIIVAVVAMSKSFLGTYFGVIEGASEIVKSSLGLLGVRKSRAFNRAMSILLVSAFTFAVCFI

NPNAISMIYAISGPLIAMILFIMPTLSTWLIPALKPYRSVGNAITLVVGLLCVSVMFFG

>WP\_002916056.1 MULTISPECIES: multidrug/biocide efflux PACE transporter [Klebsiella]

MQQTPHQRKTLTERVIHAITFEGLATLILAPTAAWLMQRSVVEMGGLSILLATLAMVWNIIYNAAFDRLW

PVSRFPRQLKVRALHALGFETGFVIIGVTMVAIVLGVSLLQAFMLEIGFMLFFLPYTMAFNWVWDTLRER

VIRHRRPRQTARG

>WP\_002916055.1 MULTISPECIES: LysR family transcriptional regulator [Klebsiella]

MRYSPEALTAFVEAVDSGSFSAAARRLRKSQSTISTAIANLEADLGVILFDRATRQPTLTPQGEQVLSYV

KAILAASERLDELAVSLSGETEPRLTFVLSDTLHPDVLEDLLVQFDRRFPHTEFECLIGEDEDVIDLLQK

SRAQVGLIEARERYPTDIGSTRLPLQTAMGIYVAPGHPLAAQGKVAWDELRSWRELRLSTFLASATEPAA

GQVWSAPNYLLLLSMAAQGFGWCILPSALVAEFAPQGGLVALDIPGWPRAISVDLLWNKKAPPGAAGSWL

RQHLQRRER

>WP\_002916052.1 MULTISPECIES: acetyl-CoA C-acetyltransferase [Klebsiella]

MKDVVIVGALRTPIGCFQGALSRHSAVELGSVVVKALVEKTGIDPHSVDEVILGQVLTAGTGQNPARQSA

IRGGLPNTVSAITINDVCGSGLKALHLATQAIQCGEADVVIAGGQENMSRAPHVLTDSRTGAQLGNSQLI

DSLVHDGLWDAFNDYHMGVTAENLAREFGISRELQDAWALSSQHKARKAIDSGRFRDEIVPVVTEHNGAA

RTVDTDEQPRVDASAEGLASLQPTFDRLGSVTAGNASSINDGAAAVMMMSEAKALELGLPILARIRAFAS

VGVDPALMGIAPVHATRRCLERAGWRLDDVDLIEANEAFAAQAISVGRVLEWDERRVNVNGGAIALGHPI

GASGCRILVSLVHEMIKRDARKGLATLCIGGGQGVALAVERA

>WP\_004143995.1 MULTISPECIES: KdgM family porin OmpK26 [Klebsiella]

MLKRSLVLAALCGMSFAATAVTIDLRHEFIDGGKSDKSNADRVSVSHRFANGLGFTVEAKWRSGGDNGSQ

PYSDVVGNGHEDTISWRWKATSNLFLTPGFTIESNDSRSIYKPHLHAQYSFDNGFYVAARYRYEYTRYPN

NAGKDDDKVNRGDAWAGFVLGDWRTELNYVYARSSEGVSRNDNKPYSQEYNVKVAYKLDNNWSPYGEIGN

VGVNDRSDRQTRFRVGVAYSF

>WP\_002916048.1 MULTISPECIES: PD40 domain-containing protein [Klebsiella]

MAKGMRVKLNYHVSHDPDTGAEVTRLTPPEVTCHRNYFYQKCFFNDGSHLLFAGEFDGHWNYYLLNIASA

EAVQLTEGAGDNTFGGFLSPDDKSLYYVKNDRILLEVNLTTLAEREVYRVSDDWVGYGTWVANSDCSKLV

GIEIAKSDWTPLNDWQIFHDFFHKGPHCRLLRVDLRSGESQVIHEEKIWLGHPIYRPFDDHTVAFCHEGP

HDLVDARMWLVNEDGSHVRKVKAHAPGESCTHEFWVPDGSALIYVSYLKGQQGRTIYRFDPESGVNEALM

TMPACSHLMSNFDGTLLVGDGSGTPVDVKDTGGYSIDNDPWLYVFNVAEKRYFRVARHDTSWATVANSRQ

VTHPHPSFTPDDSAILFSSDKDGKPAIYIAKLPAHPSMLSA

>WP\_002916003.1 MULTISPECIES: 2-dehydro-3-deoxy-D-gluconate 5-dehydrogenase KduD [Klebsiella]

MILDAFSLQGKVAVVSGCDTGLGQGMALGLAEAGCDIVGINIVEPVETIERVTALGRRFLSLTADLRQID

GIPQLLERAVAEFGHIDILVNNAGLIRREDALAFSEKDWDDVMNLNIKSVFFMSQAAAKHFIAQGSGGKI

INIASMLSFQGGIRVPSYTASKSAVMGVTRLLANEWAKHNINVNAIAPGYMATNNTQQLRADEQRSSEIL

DRIPAGRWGLPADLMGPVVFLASSASDYINGYTVAVDGGWLAR

>WP\_002916001.1 MULTISPECIES: sugar porter family MFS transporter [Klebsiella]

MTSISNDSTLSPRTQRDTRRMNWFVSIAAAVAGLLFGLDIGVISGALPFITDHFTLSSQLQEWVVSSMML

GAAIGALFNGWLSFRLGRKYSLMAGAVLFVAGSIGSAFAASVEVLLVARVVLGVAVGIASYTAPLYLSEM

ASENVRGKMISMYQLMVTLGIVLAFLSDTAFSYSGNWRAMLGVLALPAVILIILVVFLPNSPRWLAEKGR

HIEAEEVLRMLRDTSEKARDELNEIRESLKLKQGGWALFKVNRNVRRAVFLGMLLQAMQQFTGMNIIMYY

APRIFKMAGFTTTEQQMIATLVVGLTFMFATFIAVFTVDKAGRKPALKIGFSVMALGTLVLGYCLMQFDN

GTASSGLSWLSVGMTMMCIAGYAMSAAPVVWILCSEIQPLKCRDFGITCSTTTNWVSNMIIGATFLTLLD

AIGAAGTFWLYTALNVAFIGITFWLIPETKNVTLEHIERNLMAGEKLRNIGNR

>WP\_004149647.1 MULTISPECIES: LacI family DNA-binding transcriptional regulator [Klebsiella]

MASLKDVAKLANVSLMTVSRALNTPERLKPETLARVQAAIAETNYVPDLSAKKIRGARATPSTIGVLALD

TVTTPFSVEITLSIEETARAHGWNSFVVNMFSDDRPEAVVDLLLSHRPDGIIFTTMGLRQVPLPEKLLTL

PCVLANCESLSQPVASYIPDDEQGQYDAVKALLAAGYRRPLCLHLPASQPATIRRRRGLERACREAGIEP

DHLSHSYMGQGDEHYHDIPAVVLAHIREGKPGFDSVICGNDRIAFMVYQTLLGQGLRIPQDVAVVGYDNM

VGIGDLFLPPLSTVQLPHYDIGRLSALHIIHGDNHRETRKVASPWLPRASH

>WP\_004143987.1 MULTISPECIES: hypothetical protein [Enterobacteriaceae]

MLRLIFDRDRIFIMLTLTFVINIIYRSESTCVLFFVNVTIIAFL

>WP\_002916000.1 MULTISPECIES: MFS transporter [Klebsiella]

MMKAPHSHSYPLLSALLFFFFVTWSSSGSLLSIWLHQEVGLKAGDTGIIYAVLSVSALFAQVCYGFIQDK

LGLRKHLLWYITALLILSGPAYLLFGHLLKINVLLGSIFGGIYIGLTFNGGIGVLESYTERVARQSQFEF

GRARMWGSLGWAVATFFAGLLFNINPQLNFLVASCSGLVFFILLARLRVSSAPHAMQEAVSGGKVTLEDA

LRLLTLPRFWALVFFVIGTCIYGVYDQQFPVYFSSQFATLQEGNEMYGYLNSFQVFLEAAGMFCAPWLVN

RIGAKNGLIFAGMVMAMRMVASGLVEGPLLISITKLLHAVELPILLVAIFKYNSLNFDKRLSSTLYLVGF

ACTSSIIASVLSPLAGYSYEKYGFAQSYLIMGLLVFCTTFISIFLLRSGKSSADPLVSQPTAI

>WP\_026005853.1 MULTISPECIES: glycoside hydrolase family 32 protein [Klebsiella]

MTYTISRAEQVLQTQRQALNLRWYPHYHLAARAGWINDPNGLVWFDGWYHAFYQHHPYSTQWGPMHWGHA

RSKDLVHWEHLPVALAPEGPEDKDGCFSGSAVVDGDTLALIYTGHKFHGDPGDEANLYQVQCLATSRDGI

HFERQGMVVDTPPGMHHFRDPKVWREGDSWYMIVGAREGDTGQVRLYRSADLRQWQDAGVLDEAESTMGY

MWECPDFFTLNGKRVLMFSPQGMQAAGFSNRNLFQSGYLIGEWQPGQRFIRHGEFREMDNGHDFYAPQSF

ATPDGRRIVIGWLDMWESPLPEQQDGWAGMLSLPRELSLSADDRLQMRPAKEVESLRGAWFPWPVSTLNN

QQTTMVDNCEAMEVNLRWDCARSSAEQYGLRFGDGLRIYVDAQQQRLVLERHYPQYGLCGTRSVPLTAGA

DLNLRIFFDSSSVEVFVNDGEACLSSRIYPQAPRRELALFAWSGSAALTEAGAWQLE

>WP\_004149644.1 MULTISPECIES: carbohydrate porin [Klebsiella]

MNKIWVGCFLTSLYLPSVMAQAPLSLEERLAQMEQRLKATEARAASAEAEIKTLKGQQQAATVARAAPAS

PRLQLNDNGELKFYGDVEFNLDGASRTGSLTSVKTSANKSWAPGDKERWDINGRILLGFDGRRNGADGQY

AGFSVQPLADMDGKMNLDDAVFFFGQQDDWKIKIGRFEAWDMFPLNQDTFIEYSGNTANDLYSDGYGYIY

MMKEGRGRSSSGGNLLFSKTVDNWYFEVNTLVEDGSSLFVDQNYHGNALENRKNVVYVRPVAAWQSGAWS

AAAAIESNLVNNAYGYQSQSGRWVDQSNRTGYGLTMSWNTLKSDPQDGAVVNLSTALLDAADETDFSAGI

NALWHRVELGYIYAHNKIDQFNMAGVTSECDGDCAILAPGRYDIHTLHTSWQLPNIMAMPNFNIYLGAYA

SWLDSTAAKSGNPDERYGARVRFKYFF

>WP\_016531527.1 ABC transporter substrate-binding protein [Klebsiella pneumoniae]

MKNVLISATLSATLGLSAFSSLAQDVDLRMSWWGGNGRHQVTLKALEEFHKQNPDINVKAEYTGWDGHLS

RLTTQIAGGTEPDVMQTNWNWLPIFSKNGDGFYDLNTLKDEIDLSQFDTKELQSTTVNGKLNGIPISVTA

RVFYFNDEAWKKAGIPFPKTWDELMAAGKTFESKLGKQYYPVVLEHQDVLALLNSYMVQKYNQPAIDEKG

RKFSYSKAQWADFFGMYKKLIDSHVMPDTRYYASFGKSNMYEMKPWIQGEWGGTYMWNSTINKYSDNLKP

PAKLVLGEYPMLPGATDAGLFFKPAQMLSIGKSTKNPQAAAKVINFLLNSKEGVDILGLERGVPLSKAAV

TYLTEDGVIKADDPAVSGLKLAQSLPTALPVSPYFDDPQIVAQFGTTLQYIDYGKKSVEEAAEDFQRQTD

RILRRAMR

>WP\_016531528.1 ABC transporter ATP-binding protein [Klebsiella pneumoniae]

MAEVIFNKLEKVYSNGFKAVHGIDLKIADGEFMVIVGPSGCAKSTTLRMLAGLETISDGEVRIGDKIVNN

LAPKSRGIAMVFQNYALYPHMTVRENLAFGLKLSKLPKAQIDRQVEEAAKILELEELLDRLPRQLSGGQA

QRVAVGRAIVKKPDVFLFDEPLSNLDAKLRASMRIRISDLHKQLKKSGKPATTVYVTHDQTEAMTMGDRI

CVMKLGHIMQVDTPDNLYHQPKNMFVAGFIGAPEMNIRPSQLVEHGGRLHLTLGDQRLPLNDRLQSKVET

HKNQQVFFGVRPEFVSLSDEPFAEGSCTGEMVRVENMGHEFFVYLQVAGYELTARIPSDDARPMIAKGLN

RKVYFTFDLNKCHIFDAKTEQNLSL

>WP\_002915996.1 MULTISPECIES: carbohydrate ABC transporter permease [Klebsiella]

MADIQQMAPVMSDADREVARTLRREKVSRVVRYVVLIFVGLLMLYPLAWMFSASFKPNHEIFTTLGLWPA

HATWDGFINGWKTGTEYHFGHYMLNTFKYVIPKVVLTIISSTIVAYGFARFEIPWKKFWFATLITTMLLP

STVLLIPQYLMFREMGMLNSYLPLYLPLAFATQGFFVFMLIQFLRGVPRDMEEAAQIDGCNSIQVLWYVV

VPILKPAIISVALFQFMWSMNDFIGPLIYVYSVDKYPIALALKMSIDVTEGAPWNEILAMASISILPSII

VFFLAQRYFVQGVTSSGIKG

>WP\_002915995.1 MULTISPECIES: sugar ABC transporter permease [Klebsiella]

MNENKLLGLAWISPYIIGLIVFTAFPFVSSFFLSFTEYDLMSPPVFNGIENYRYMLTEDSLFWKSMGVTF

AYVFLTIPLKLAFALGIAFVLNFKLRGIGFFRTAYYIPSILGSSVAIAVLWRALFAIDGLLNSFLAVFGI

DAINWLGEPSLALMSVTLLRVWQFGSAMVIFLAALQNVPQSQYEAAMIDGASKWQMFMKVTVPLITPVIF

FNFIMQTTQAFQEFTGPYVITGGGPTYYTYLFSLYIYDTAFKYFDMGYGAALAWVLFLVVAVFASIAFKS

SKYWVFYSADKGGKNG

>WP\_002915993.1 MULTISPECIES: cupin domain-containing protein [Klebsiella]

MFIFHKDTTLEDLGNGVTRRILAHDGKMMAVEVNFAAGAVGPMHNHPHEQLTYVLSGEFEFTIGEETRVV

SAGDTLYKRPGIMHGCVCLQPGTLLDTFTPIREDFLEG

>WP\_002915992.1 MULTISPECIES: aspartate/glutamate racemase [Klebsiella]

MKTIGLLGGMSWESTIPYYRLINEGVKARLGGLHSASLVLHSVDFHDIEACQSAGDWDRAGEILAEAAVG

LQQAGAEGIVLCTNTMHKVADAIAARCQVPFLHIADATGRAIAAKGQRRVALLGTRYTMEQTFYRGRLQE

QFAIETLIPEADDRAQINQIIFDELCLGTFSEASRDYYLQTIAALAEQGAEGVIFGCTEIGLLVPAELSP

LPVFDTAAIHAEDAVNFMLSAGPTPAA

>WP\_002915991.1 MULTISPECIES: LysR family transcriptional regulator [Klebsiella]

MPAVNLRHIEIFHAVMTTGNLTEAARMLHTSQPTVSRELARFEKVLGLQLFERTRGRLQPTVQGLRLFEE

VQRSWYGLDRIVSAAESLREFRQGELSIACLPVFSQSFLPLLLPPFLARYPEVSLQIVPQESPLLEEWLS

AQRHDLGLTETLHTPAGTERTPLLTLNEVCVLPAGHPLAAQATLTPADFQGENYISLSRTDSYRQLLDAL

FLEHQVKRRMVVETHSAASICAMVRAGAGISVVNPLTALDYADSGVVVRRFSVEVPFTVSLIRPLHRPRS

ALVDAFVAHLQQSLPQILTPLASVLQRA

>WP\_002915990.1 MULTISPECIES: diaminopimelate decarboxylase [Klebsiella]

MPHSLYATDTDLTADNLLRLPAEFGCPVWVYDAQIIRRQIAQLSQFDVVRFAQKACSNIHILRLMREQGV

KVDSVSLGEIERALAAGYDPQQNPEDIVFTADLIDDATLDRVKALQIPVNAGSIDMLSQLGEVSPGHRVW

LRVNPGFGHGHSQKTNTGGENSKHGIWYSHLPAALEVMRRYQLQLVGIHMHIGSGVDYGHLEQVCGAMVR

QVVDFGQDLQAISAGGGLSIPYREGEEAIDTAHYYGLWNRAREQIAAHLGHPVKLEIEPGRFLVAESGVL

VSQVRSVKEMGSRHFVLIDAGFNDLMRPAMYGSYHHITALAGDGRDLSAAPQVETVVAGPLCESGDVFTQ

QEGGKVETRLLPAVAPGDYLVLHDTGAYGASMSSNYNSRPLLPEVLFDGGKARLIRRRQTIQELLALELI

>WP\_004229436.1 MULTISPECIES: LacI family DNA-binding transcriptional regulator [Klebsiella]

MLDVSIRAGVSKATVSRVLNGTGQVKESTRQQVFKAMEELGYRPNFLARSLANQTSNSIGLVVSTFDGFY

FGRLLQQASRQTEAWGKQLIVTDGHDTPEREEEAVQMLADRQCDAIILYTRHMSEKAIMSLINSIAMPLV

VINRDVAQARERCVFFEQQEAAFQAVEYLITQGHRDIACITVPMHTPTGQARLQGYRNALIKHGIEWDPS

RVKYGDSTMTRGYELCRELLDEKARFSALFSCNDDMALGASKALHQAGLRIPQDVSLFGFDDAPSAKWLE

PGLSTVYLPIDNMITTAIDQAIKLANQQPIETIPPFTGTLVLRESVTTGPFFK

>WP\_004174520.1 MULTISPECIES: PTS transporter subunit EIIC [Klebsiella]

MALQDKLIDALGRFATTFNSYRYIMAIKSAFITLMPVIIVGAFSVLISNMVLDPKNGLASFSSLSFLAAL

KPITSALNYATLNFLNIGAVFLIGIELGRINGIKSLFPGLLAVICFICVTPTTVEMMVDGQMHVVKDVLL

RQFSDTRSLFLGMFIAILSVEIYCWLEGRKGLKIKMPDTVPPNVSASFSALIPAIITTTAIATFGFLFHQ

LTGMYLYDAVYQVVQQPLERVVQSLPGILLLMFVAQLFWVIGIHGNQMIKPIREPLLLGAITVNMSAFEQ

GKEVPNIITMPFWDVYMSIGGSGLTIGLLIAVMIATRRKEMKEIAKLSIGPGLFNINEPVIFGMPIMLNP

ILAIPFIITPLVTGSIGYFATLTGFAGKAVVMVPWTTPPLINAWLSTAGSMGAVVTQLICIVVAVLIYLP

FVKIASRRADAAQRQVDNQQTANPV

>WP\_004174521.1 MULTISPECIES: glycoside hydrolase family 1 protein [Klebsiella]

MTTVRMTIPDDFILGAAASAWQTEGWSGKKPGQDSWPDLWYKNDRHVWHNGYGPAVATDFINRFQEDVQL

MKLAGLTHYRTSINWSRFLTDYENVTVDEEYAAYYDQLFDALLANGITPMICLEHYELPGYLLEKYGGWG

SKTVVELFVRYAEKVFARYHPKVTRWFTFNEPIVVQTRVYLDALRWPYEQNTSTWMQWNYHKVLATASVV

KRFRELGYPGTVGCILNPEVTYPRSRAPHDLRAAEIYDLFYNRMFLDPLVHGVWPPELLALLEQHQVTWE

TSEEDLAVIREHTVDELGINLYYPHRVKAPSRAWHPHTPFHPAWYYEPFELPGRRMNASRGWEIYPQIIF

DMAMRIKNDYRNIPWFVAESGMGVENEGQFRNREGVIDDSYRIRFISEHLWHTLRAREAGANCQGYMLWA

FTDNVSPMNAFKNRYGLIEIDLQNHRARRPKASAHWFRQLGERRELVLDIDDEYR

>WP\_002915985.1 MULTISPECIES: GntR family transcriptional regulator [Klebsiella]

MEKAIVPPEKKPYQEIGDDLRAQIAQGRYPVGSRLPPERHIAETYGVSRTIVREALLMLELQGTVDIRQG

SGVYVMRIPHENDSEEEQLLSSDVGPFEILQARQLLESNIAAFAAKMATRADIDNLKRIIEQEQRAIALN

DTAQDNARLFHLVLAGATQNQMLLATVERIWLQMDSSPLWQQFNVHIASRAWRLKWLGDRQTLLAALRRR

DVMGAWQAMWQHLENVKNSLLELSDEDAPDFDGYLFDSVPIFQGKLV

>WP\_046042444.1 GNAT family N-acetyltransferase [Klebsiella pneumoniae]

MTILPLYAAPQFAPQVTDWLWQAFGGETLPRQFFASIVQHSQTAEALPLTFIAVEGEQLLGTIGLWRCDL

ISRQDLFPWLAALFVAPAARGQGLAGKLQRHVIDYARRADFRELYLYSACRDFYERFGWRYIGEGLDYPA

TAVHLYRYDLSPSCGATTE

>WP\_016529841.1 HTH-type transcriptional regulator GalR [Klebsiella pneumoniae]

MATIKDVARLAGVSVATVSRVINNSPKASEASRQSVGAAMETLNYHPNANARALAQQSTETVGLVVGDVS

DPFFGAMVKAVEQVAYRTGNFLLIGNGYHNVQKERQAIEQLIRHRCAALVVHAKMIPDEELAGLMKQIPG

MVLINRILPGYETRCVALDDRYGAWLATRHLIQQGHTRIGYLCSNHDISDAEDRLQGYYAALEESGLPCN

DRLVTFAEPDESGGEQAMTELLGRGRHFSAVACYNDSMAAGAMGVLNDNGIDVPREISLIGFDDVLISRY

IRPRLTTVRYPIVTMATQAAELALALAEQRPAPEITHLFSPTLVRRHSVVAPQEGDKS

>WP\_002915977.1 MULTISPECIES: bifunctional acyl-ACP--phospholipid O-acyltransferase/long-chain-fatty-acid--ACP ligase [Klebsiella]

MLLGFFRLLFKGLYRVRLTGDTQALYQQKVLITPNHVSFLDGILLALFLPVRPVFAVYTSISQRWFMRAL

TPIIDFVPLDPTKPMSIKHLVRLIEQGRPVVIFPEGRISVSGSLMKIYDGAAFVAAKSQATIVPLRIEGA

ELTPFSRLKGLVKRRLFPRIQLHLLPPTHLPMPEAPRARDRRKIAGEMLHQIMMEARMAVRPRETLYESL

LAAQDRFGARKPCVEDINFQPDTYRKLLTKTLFVARILEKYSQPGEKIGLMLPNAGISAAVIFGAIARGR

IPAMMNYTAGVKGLSSAIAAAELNTIFTSRTFLDKGKLWHLPEQLTQVRWVFLEDLKGDITLADKLWIFA

HLLAPRLAQVKQQPEDAAMILFTSGSEGNPKGVVHSHKSLLSNVEQIKTIADFTANDRFMSALPLFHSFG

LTVGLLTPLLTGAEVFLYPSPLHYRVVPELVYDRNCTVLFGTSTFLANYARFANPYDFYRLRYVVAGAEK

LQESTKQLWQDKFGLRILEGYGVTECAPVVSINVPMAAKVGTVGRILPGMDARLLAMPGIDQGGRLQLKG

PNIMKGYLRVENPGVLEAPAAENQHGEMEAGWYDTGDIVTFDEQGYVRIQGRAKRFAKIAGEMISLEMVE

QVALGASPDKMHATAIKQDASKGEALVLFTTDNELTREALLRYARQHGVPELAVPRDIRWLKQLPVLGSG

KPDYVTLKNMVDEAETTHE

>WP\_002915976.1 MULTISPECIES: lysophospholipid transporter LplT [Klebsiella]

MSESVHTNPSLYSKGMLAVICAQFLSAFGDNALLFATLALMKQLYYPEWSQPVLQMLFVGAYILFAPFVG

QFADSFAKGRVMMVANGLKLLGAGCICFGVNPFIGYTLVGIGAAAYSPAKYGILGELTTGDKLVKANGLM

ESSTIAAILLGSMAGGILADWHVLAALIVCALVYGGAVVANLWIPRLPAARPGQSWRFKPMTHSFFSACR

TLWRNGETRFSLMGTSLFWGAGVTLRFLLVIWVPVALGITSNAMPTYLNAMVAVGIVLGAGAAAKLVTLE

TVSRCMPAGILIGIAVIAFAVQQSLLPAFGLLLLLGVFGGFFIVPLNALLQERGKHSVGAGNAIAVQNLG

ENVAMLLMLGLYSLAVSVGVPPVAVGIGFGAVFAVAIAALWVWGRRK

>WP\_002915975.1 MULTISPECIES: NADP(H)-dependent aldo-keto reductase [Klebsiella]

MQYHRIPHSSLEISTLGLGTMTFGEQNSEADAHQQLDYAVANGINLIDVAEMYPVPPRPETQGLTETYVG

NWLAKRGNREKLVLASKVSGPARNNDSSIRPNHVLDRKNIREALHASLKRLQTDYLDLYQVHWPQRPTNC

FGKLGYTWADAAPAVTLLDTLEALTEFQRAGKIRYIGVSNETAFGVMRYLHLADKHDLPRIVTIQNPYSL

LNRSFEVGLAEVSQFEGVELLAYSCLAFGTLTGKYLNGAKPAGARNTLFSRFTRYSSEQSQKAVAAYVDI

AKRHGLDPAQMALAFVRRQPFVASTLLGATTMTQLQANVESLQLELSEEVLAEIEAVHQVYTYPAP

>WP\_016532289.1 YgdI/YgdR family lipoprotein [Klebsiella pneumoniae]

MKKWAVLISAVGLAFSVSGCSSDYVMATEDGRMILTDGKPTVDDDTGLISYEDQQGNKMQINRDDVSQII

KR

>WP\_002915973.1 MULTISPECIES: TerC family protein [Klebsiella]

MLFAWITDPNAWLALGTLTLLEIVLGIDNIIFLSLVVAKLPTAQRAHARRIGLMGAMVMRLALLASIAWV

VKLTNPLFTVFGQEISFRDLILLLGGLFLIWKASKEIHESIEGEEEGLKTNVHSFLGAIVQIMLLDIIFS

LDSVITAVGLSDHLFIMMAAVVIAVGVMMFAARPIGDFVDRHPSVKMLALSFLILVGFTLMLESFDVHVP

KGYIYFAMFFSIAVESLNLLRNKKNPL

>WP\_032440299.1 MULTISPECIES: DNA mismatch repair endonuclease MutH [Klebsiella]

MPAIAPLDSPPQSQEQLLAQARQLAGYSLGELAALAGIPIPRDLKRDKGWTGILLELWLGASAGSKPEQD

FAALGVELKTIPIDSRGRPLETTFVCVAPLTGNSGVTWESSHVRHKLQRVLWIPVEGERTIPLAARRVGA

PLLWSPDEDEERQLRMDWEELMDLIVLGEVERITARHGEVLQLRPKAANSKALTEAIGARGETILTLPRG

FYLKKNFTAALLARHFLLQHD

>WP\_004218186.1 MULTISPECIES: hypothetical protein [Bacteria]

MSLFPSYPTFLWITWCKILFIVSDQFWKTRLHRFHKPHDEFKKPYKS

>WP\_002915936.1 MULTISPECIES: RNA pyrophosphohydrolase [Klebsiella]

MIDDDGYRPNVGIVICNRQGQVMWARRYGQHSWQFPQGGINPGESAEQAMYRELFEEVGLSRKDVRILAS

TRNWLRYKLPKRLVRWDTKPVCIGQKQKWFLLQLIGNDADINMQTSSTPEFDGWRWVSYWYPVRQVVSFK

RDVYRRVMKEFASVTMSLAESAPKPQNAPAYRRKRG

>WP\_002915935.1 MULTISPECIES: phosphoenolpyruvate--protein phosphotransferase [Klebsiella]

MLTRLREIVEKVASAPRLNEALDILVTDVCQAMETEVCSVYLADNDRRCYYLMATRGLKKPRGRTVALAF

DEGLVGLVGRLAEPINLADAQKHPSFKYIPAVKEDRFRAFLGVPIIQRRQLLGVLVVQQRELRQFDESEE

SFLVTLATQMAAILSQSQLNALFGQYRQTRIRALPASSGVAIAEGWMDVSLPLMEQVYEASTLDTASERE

RLTGALEEAANEFRRYSKRYAAGAQKETAAIFDLYSHLLSDARLRRELFAEVDKGAVAEWAVKKIIEKFA

EQFAALSDGYLKERAGDLRTLGQRLLFHLDDSIQGPNTWPARIILVADELSATTLAEVPQDRLAGVVVRD

GAANSHAAIMVRALGIPTVMGADIQPSLLHGHTLIVDGYRGELLVDPEPVLLQEYQRLISEENELSRLAE

DDLQRASELKSGERVKVMLNAGLSPEHEEKLGSFVDGIGLYRTEIPFMLQSGFPSEEEQVAQYQGMLQMF

NSKPVTLRTLDIGADKQLPYMPISEENPCLGWRGIRITLDQPEIFLIQVRAMLRANAATGNLSILLPMVT

SLEEVDEARRLIDRASREVEEMIGYAIPRPRLGVMLEVPSMVFMLPQLASRIDFISVGTNDLTQYLLAVD

RNNTRVASMYDSLHPAVLRALAMIAHDAERFGIDLRLCGEMAGDPMCVTILIGLGYRHLSMNGRSVARVK

YLLRRIDIEEAQELSRRSLDAQMTAEVRHQVAAFMERRGLGGLIRGGR

>WP\_016531632.1 prolipoprotein diacylglyceryl transferase [Klebsiella pneumoniae]

MNSGYLHFPEFDPVIFSLGPASLHWYGLMYLVGFVFAMWLATRRANRPGSGWTKNEVENLLYAGFLGVFL

GGRIGYVLFYNLPVFLADPLYLFRVWDGGMSFHGGLIGVILVMIIFARRTKRTFFQVSDFIAPLIPFGLG

AGRLGNFINGELWGRVDPSFHYTMIFPGSRAEDLALLPTHPEWQSLFDTYGALPRHASQLYELALEGVVL

FLILNLFIRKPRPTGSVSGLFLIGYGLFRIIVEFFRQPDAQFTGGWVQYISMGQILSIPMVLAGIIMMVW

AYRHRPQPQNS

>WP\_004174525.1 MULTISPECIES: thymidylate synthase [Klebsiella]

MKQYLDLMQKVLTEGTPKNDRTGTGTISIFGHQMRFNLQEGFPLVTTKRCHLRSIIHELLWFLQGDTNIA

YLHENNVTIWDEWADENGDLGPVYGKQWRSWPAPDGRHIDQITTVMNQLKNDPDSRRIIVSAWNVGELDK

MALAPCHAFFQFYVADGKLSCQLYQRSCDVFLGLPFNIASYALLVHMVAQQCDLQVGDFVWTGGDTHLYS

NHLEQTHLQLSREPRPLPKLVIKRKPASIFDYRFEDFEIEGYDPHPGIKAPVAI

>WP\_040188384.1 prepilin peptidase-dependent protein [Klebsiella pneumoniae]

MQTFFAYLAGKAIFRHRVRTNRRGILNAMNREHGYTLMETLVTLTLMMILSVGGLYGWQRWQQQQRLWQT

AVQVRDFLVFLRDDANAYNRDRVLRVGQDEAGWCLSAQGEGADCTAGSAFTLRPRWPGITLVGVTPGLGF

YGLRSTAWAGNLRLQSAAGSWSIVISHWGRIRLCRSDSAGGCQ

>WP\_064754486.1 prepilin peptidase-dependent protein [Klebsiella pneumoniae]

MNSRGFSLAEALIAMAIGSLLLMGACRFLPALQRHILRQGEQLALENELWQRVHAVGKHLQRAGYCRGAC

GGAGLELAAGGECLIVRWDANSNGRWETSPAAAAESTGFRLRDGALETLRGASDCRGGGWEKITNPAAIV

VTRFSVQRQVTPGFAPELSVTLAARSAQQTGLTSEVEQRVTGYNL

>WP\_004181182.1 MULTISPECIES: DUF2509 family protein [Klebsiella]

MIRQRGMSSLLMVLLLLTLGSLLLEGLNLQQRALLAQTASETQAIRDTAIAHSALQWGKQQVWSAQVALA

CREQAPQGWRACLRIFGDGSLVLSSASGEVQVWQSGEVRGGQVRFSAHGWSDFCPLREASLCQMP

>WP\_002915888.1 MULTISPECIES: prepilin-type N-terminal cleavage/methylation domain-containing protein [Klebsiella]

MSNALKRQRGFSLPETVLAMALMVLTVTALGGYQRGMAQGIVQLNQTRQLWRDAWRYSQLSAPPSPARGQ

VSRMQTSRQRCVSITVTISRPVAKRVQMTRLHCPVSQ

>WP\_046042461.1 exodeoxyribonuclease V subunit gamma [Klebsiella pneumoniae]

MLRVYHSNRLDVLEALMEFIVERQRLDDPFQAEMVLVQSTGMAQWLQMTLAARFGIAANIEFPLPASFIW

DMFVRVLKDIPGESAFSKQSMSWKLMTLLPQHLEEDDFILLRQYLSDDGDKRKLFQLAARVADLYDQYLV

YRPEWLMRWEAGQRVEGLGDAQQWQAPLWQALVSYTAELGQPQWHRANLYQRFISTLEKADEPPAGLPSR

VFICGISALPPVYLQALQALGKHVDVYVLFTNPCRYYWGDIKDPAFLAKLLSRQRRHHREARALPLFRDT

EQAPGLFNDAGEQDVGNPLLASWGKLGRDYIYLLAGLERYEELDAFVDIAPDNLLHNLQSDILELRNAAV

AGQSAEAFAHSRDKRPLTLDDRSLSIHVCHSPQREVEVLHDRLLAMLEADPTLTPRDIIVMVADIDSYSP

YIQAVFGAASGDRWLPWAISDRRARESHPVLQAFITLLSLPDSRFASEDVLALLDVPVLAARFNITEEGL

RYLRQWVNESGVRWGMDDDNVRELDLPATGQHTWRFGLTRMLLGYAMDSSEGEWQSVLPYDESSGLIAEL

VGNLASLLMQLNLWRRGLAQQRPLAEWLPVCRDLLNDFFLPDSETEAALALIEQQWLAVIDSGLEAQYGE

QVPLTLLRDELAQRLDQQRISQRFLAGPVNICTLMPMRSIPFKVVCLLGMNDGVYPRTLPPLGFDLMSQK

PQRGDRSRRDDDRYLFLEALMSAEQTLYISYIGRSIQDNSERFPSVLVQELVDYIGQSHCLAGDEELDCD

ASEARVKAHITHLHTRMPFDVANFQEDENKSYAREWLAAAGQQGEAHSDFIQPLTAPPIDSLPFDQLLRF

WQHPVRAFFQQRLRVNFRAEEDDIPDDEPFTLEGLSRYQLNQQLLNTLIEEQDVSAMFRRFRAAGELPYG

AFGELVWETQRLEMQALAERVMAERQQAQSMEIDLQCGGVNLTGWLQQVQPDGLLRWRPSLLSVSQGMQL

WLEHLVYCASGGTGESRLFVRKEGEWRFPALAPAEAQAYLNELVDGYLLGMSQPLLLLPESGGAWLKACY

DAEKDVILMDEETQQKARSKFLQTYEGNMVVSGEGADIWYQRLWRSLEPAHYEEIIAQTQRYLLPLYRYH

RSTQI

>WP\_016531296.1 pitrilysin [Klebsiella pneumoniae]

MPRSLWFKVFVVLAALWAPFSQADTGWQPIQETIRKSEKDTRQYQAIRLDNDMVVLLVSDPQAVKSLSAL

VVPVGSLQDPADHQGLAHFLEHMTLMGSQKYPQPDSLAEFLKLHGGSHNASTAPYRTAFYLEVENDALDG

AVDRLADAIAAPLLDKKYADRERNAVNAELTMARTRDGMRMAQVSAETINPAHPAAHFSGGNLETLSDKP

GSPVLDALHTFRDSWYSANLMKAVIYSNKPLPALARMAADTFGRVPNRQISRPEITVPVVTDAQKGIIIH

YVPAMPRKVLRVEFRIDNNSDRFRSKTDELVTYLIGNRSPGTLSDWLQKQGLAEGIRADSDPVVNGNSGV

LAISATLTDKGLAHRDEVTAAIFSYLDLLRTQGIDKRYFDELAHVLALDFRYPSINRDMDYVEWLADTMI

RVPVEHALDVVNIADQYDPQAIKDRLAMMTPQNARIWYISPQEPHNKTAYFVDAPYQVDKISEQTFADWQ

HKSQAIQLQLPALNPYIPDDFTLIKSDKAWPHPQLILDEPTLRVVYAPSQYFASEPKADISLVLRNPQAM

DSARRQVMFALNDYLAGIALDQLSNQAAVGGISFSTGANNGLMVNANGYTQHLPALFSDLLQGYFSYTPT

EEQLEQAKSWYAQMMDSAEKGKAYDQAIMPIQMVSQVPYFQREVRRALLPSITLKEVLDYRANLKTRGRP

ELMVIGNMTADAATTLARQIQQQLGADGNEWCRNKDVVVNRQQLAIFNKAGNSTDSALAAVFAPPNVDEF

SSTAASTLLGQIIQPWFYNQLRTEEQLGYAVFAFPMNVGRQWGMGFLLQSSDKQPAFLWQRFQAFFPTAE

AKLRAMKPEEFAQLQQAVISQMLQAPQTLGDEASKLSKDFDRGNMHFDSRDKVVAQIKLLTPQKLADFFH

QTVVDPQGMTILSQISGSQNGKADYAQPKGGKVWENVSALQQSLPLMRENE

>WP\_046042464.1 exodeoxyribonuclease V subunit beta [Klebsiella pneumoniae]

MTDTAESLDPLRLPLIGERLIEASAGTGKTFTIAALYLRLLLGLGGEAAYPRAISVEELLVVTFTEAATE

ELRGRIRSNIHELRIACLRGESDNPLYSALLAEIADKDDAAKTLLLAERQMDEAAVFTIHGFCQRMLSLN

AFESGMLFEQQLIEDESRLRYQACADFWRRHCYPLTRDIAAVIHDVWKGPRDLLKSLDRWLQGEAPQLKS

PPAPNETLAERHQQIIARIDSLKQQWREQVGEIEGVLENSGLDRRKFNRGNQGKWMEKVNAWAQEETLSY

QLPDALEKFAQSFLLERTKAGGEPPVHPLFSAVESLLASSLTLTDLVLARAMVEIRDAVAREKRRRGELG

FDDMLSRLDEALRGDSGETLASAIRQRFPVAMIDEFQDTDPQQYRIFRRIWRRQPETALLLIGDPKQAIY

AFRGADIFTYMKARGDVAAHYTLDTNWRSSPGMVGSVNRLFSLSDNPFMFHEIPFLPVKAAAKNKGLRFT

VDAADVPAMNVWLMPGDTVGSGDYQTFMAQLCATQIRDWLSAGQRGRALLWRGETSRPVQASDITVLVRN

RLEAAQVREALQTLGIPSVYLSNRDSVFETLEAQELLWLLQAVLAPERENTLRSALATSMFGLTALDIEN

LNQDEQAWDALVEEFSEYRQIWRQRGVMPMLRALMTARHIAENLLATRGGERRLTDILHISELLQEAASQ

LESEHALVRWLAQHIAEPDSNAASQQMRLESDKHLVQIVTIHKSKGLEYPLVWLPFIARFRKQDQAFYHD

RETFAAVLDLGQDEASLELAEAERLAEDLRLLYVALTRAVWHCSLGVAPLSSRKSGNSDFHLSALGRLLQ

AGEAMDAAGLAARLADFCHGDIALQRPGELDLTPWQAPAATIPRLSARELQRRIADDWRVTSYSGLQQHG

FSGGQDLLPRLDVDAAGVGEVVEEPQLTPHQFPRGAAPGTFLHSLFEELDFTQPVPEGWMAEKLQLSGFD

AQWAPVLTDWLGGVLKTRLPGPDIALNQLAAWDKQVEMAFYLPIAQLLTAERLDALIRQYDPLSADTPPL

DFRQVRGMLKGFIDLVFRHEGRYYLLDYKSNWLGEDREAYTRPAMEQAMRAHRYDLQYQLYSLALHRYLR

HRLADYDYDRHFGGVIYLFLRGMDGQEGGQGIFTTRPVRPLIDGLDQLFAGETQEEAS

>WP\_038430860.1 exodeoxyribonuclease V subunit alpha [Klebsiella pneumoniae]

MTFEQLLLAAVEQRLLRPLDVQFALMVAQNDPPAVKLAAALLSRDAGEGHVCLPLSRLSGDEALSGKAGE

IRDRLLAEAGAPEDWPALLLASSAVSCGDAPAPMILCGDRLYLNRMWRNELTVARFFNEANRVLEMDEVR

LASTLNALFPATGETDWQKVAAAVALTRRISVISGGPGTGKTTTVAKLLAALIQIEDSPRCRIRLAAPTG

KAAARLTESLGAALRKLPLTDAQKALIPTEASTLHRLLGAQPGSQRMRYHAGNPLHLDVLVVDEASMIDL

PMMSRLIDALPAHGRVIFLGDRDQLASVEAGAVLGDICAWASSGYTAARAQELTRLTGSPVPAGEGAIAG

ALRDSLCLLQKSYRFGSHSGIGSLARAVNAGARAEVKATLRQPFDDIALHPLSTTEEYEAMLGAAQQGYE

RYLQLRRERAEPQAMLAAFSEFQLLCALREGPYGVSGVNERLEQRLNRQRAIALPRHSRWYDGRPIMISR

NDSALGLFNGDIGIALERNGELRVWFLMPDGAIKSVQPSRLPEHDTAWAMTVHKSQGSEFEHAALILPAR

SVPLVTRELVYTAITRAKRRLSLYADEQVLSQAIVTRTERRSGLAEIFAGREAP

>WP\_016531904.1 hypothetical protein [Klebsiella pneumoniae]

MEPKPNWLVRHINLITTAVALYPWLLMILLLWDNQRHHQHGYAALGAAIAILFLLALTSGMNLLISSLVI

FCARCFTPPLAGGAAVRFFAMNSISALWLIPLFFSY

>WP\_004149616.1 MULTISPECIES: amino-acid N-acetyltransferase [Klebsiella]

MVKERRTELVEGFRHSVPYINAHRGKTFVIMLGGEAIEHENFSNIVNDIGLLHSLGIRLVVVYGARPQID

ANLAEHHHEPVYHKQTRVTDAKTLELVKQAAGMLQLEITARLSMSLNNTPLQGAHINVVSGNFIIAQPLG

VDDGVDYCHSGRIRRIDEEAIHRQLDSGAIVLMGPVAVSVTGESFNLTSEEIATQLAIKLKAEKMIGFCS

SQGVYNQAGEIVSELFPNEAQARVEELEADEDYNSGTVRFLRGAVKACRSGVRRCHLISYQENGALLQEL

FSRDGIGTQIVMESAEQIRRATINDIGGILELISPLEQQGILVRRSREQLEMEIDKFTIIQRDNTTIACA

ALYPFPEEKIGEMACVAVHPDYRSSSRGEVLLERIAAQARQMGLSKLFVLTTRSIHWFQERGFTPVDIDL

LPESKKQMYNYQRRSKVLMADLA

>WP\_004174538.1 MULTISPECIES: N-acetylmuramoyl-L-alanine amidase AmiC [Klebsiella]

MSGNNSGLSRRRLLQGAGAMWLMSVSPVGLAAAARVVAVRVWPASTYTRVTVESNHVLKYRQFALSNPER

VVVDLEGVNLNSVLKGMGGQIRADDPFIKSARVGQFDPQTVRMVFELKQNVKPQLFALAPVAGFKERLVM

DLYPANATDVQDPLLALLEDYNKGDLERQVPPAQSGPQPGKAGRDRPIVIMLDPGHGGEDSGAVGKYRTR

EKDVVLQIARRLRALIDKEGNMKAYMTRNEDVFIPLKVRVAKAQKQRADLFVSIHADAFTSRQPSGSSVF

ALSTKGATSTAAKYLAQTQNASDLIGGVSKSGDRYVDHTMFDMVQSLTIADSLKFGKAVLEKMGNINNLH

KNRVEQAGFAVLKAPDIPSILVETAFISNVEEERKLKTAKFQQEVAESILAGIKAYFADGATLARRG

>WP\_004185485.1 threonine-phosphate decarboxylase CobD [Klebsiella pneumoniae]

MALLKSAHGGNIREAAALLGIAPGELLDFSANINPLGMPASLRQAIVDNPGCAERYPDVEYQQLHQALAA

HHQLPAAHILAGNGETESIFTLVHGLKPRRAMIVIPGFAEYRRALQTVDCEVVEYALRERDGWQLTDAIL

DALTPALDCLFLCTPNNPTGLLPERGLLEAIAQRCRALNISLILDEAFLDFIPDQPGFIPLLAQHPHVWV

LRSLTKFYAIPGLRLGYLLNADAQAVARLRARQMPWSINAYAALAGEIILQDRAYQRATWQWLQEEGARF

YAQLQEMAGLTVWPGRANYLFLRCDRPDFDLQYALLRQHVLIRSCANYPGLDSRYFRVAIRSAEENDQLL

AALRRVLA

>WP\_004193729.1 MULTISPECIES: L-threonine kinase [Klebsiella]

MAVAQCPASCGELIQGWILGSEKLVSCPVDWYSTVEVETGVPRKDERPLSRAMVDQLLAHWGYPPALSQQ

IRITLHSTIPVAKGMASSTADIAATAVATAHHLGHLLDEPTLARLCVALEPTDSTLFRQLTLFDHNTAAT

QIACPPPPALDLLVLESPLTLRTTDYHQLPREPGLLANASRLQLAWEKVQQACHCGNPQLLGEAATISAI

ASQQLLPKPGFDALLDLVESAGLYGLNVAHSGSVVGLLLDRRRHDVEFLQWRLADSDIAAHWPQQHLLAM

VPGGVILQ

>WP\_032104157.1 acetate/propionate family kinase [Klebsiella pneumoniae]

MTYKIMAINAGSSSLKFQLLNMPQGALLCQGLIERIGLPEARFTLKTSAQKWQETLPIADHHEAVTLLLE

ALTGRGILSSLQEIDGVGHRVAHGGERFKDAALVCDDTLREIERLAELAPLHNPVNALGIRLFRQLLPAV

PAVAVFDTAFHQTLAPEAWLYPLPWRYYAELGIRRYGFHGTSHHYVSSALAEKLGVPLSALRVVSCHLGN

GCSVCAIKGGQSVNTSMGFTPQSGVMMGTRSGDIDPSILPWLVEKEGKSAQQLNQLLNNESGLLGVSGVS

SDYRDVEQAADAGNERAALALSLFAERIRATIGSYIMQMGGLDALIFTGGIGENSARARATICRNLHFLG

LALDDEKNQRSATFIQADNALVKVAVINTNEELMIARDVMRLALPQARELAVSA

>WP\_002915858.1 MULTISPECIES: propanediol utilization protein PduV [Klebsiella]

MKRLMLIGPSQCGKTSLTQVLRGETLRYQKTQAIVWTPAAIDTPGEYLENRCLYSALLTSACEADVIALV

LNADAPWSPFSPGFTAPMNRPVIGVITKADLAAPPRLQQVRTWLETAGAGHIFITSALTGDGLDDLFACL

NAEEYQ

>WP\_002915850.1 MULTISPECIES: propanediol utilization microcompartment protein PduU [Gammaproteobacteria]

MEPQTPTERMIQEYVPGKQVTLAHLIANPGKDLFKKLGLPDAVSAIGILTITPSEASIIACDIATKSGAV

EIGFLDRFTGAVVLTGDVSAVEYALRQVTRTLGELMRFTACPITRT

>WP\_046042470.1 propanediol utilization microcompartment protein PduT [Klebsiella pneumoniae]

MTQAIGILELTSIARGMELGDVMLKSANVQLLLCRTLCPGKFLLMLGGDVGAVQQAIAAGTARAGEMLVD

SLVLANIHPSVLPAISGLNVVGQRQAAGIVETWSVAACISAADHAVKAANVTLVRVHMAFGIGGKCYMVV

AGDIADVDNAVTVASDSAGEKGLLVHRAVIP

>WP\_023285520.1 SLBB domain-containing protein [Klebsiella pneumoniae]

MSEAIVPLSSIDAAEIRERVRAAGVVGAGGAGFPTHIKLQARVDTVLVNAAECEPMLKVDQQLMAQQADR

LIRGLGYAMTATGAREGIIALKAKYAPAIAALTPRLPEWARLHILPDVYPAGDEVLTIWLATGRRVPPAA

LPVSVGVVVNNVQTVLNIARAVEQGYPVTRRTLTVNGAVARPLTLAVPLGISLREVLDLAGGATVDDPGF

INGGPMMGSLITSLETPVTKTTGGLLVLPGNHPLIQRRRQDERTLLAIARTVCEQCRLCTDLCPRHLIGH

ELSPHLLVRAVNYRQAATPSLLLSALTCSECNVCESVACPVGISPMRINRLLKRELRAKNLRYDGPLRPA

DEMAKHRLVPVKRLISKLGLDPWYQEAPLTAVEPEVACVTLPLRQHIGISAVPCVAPGERVTRGQLLADI

PADALGAPVHASIDGLVSAITEQAITLVRG

>WP\_016531326.1 1-propanol dehydrogenase PduQ [Klebsiella pneumoniae]

MHTFSLQTRLYSGPGSLAALQRFSHQHIWIVCDGFLARSPLLDRLRAELPASNRVSVFSDITPDPTIHTV

AKGIAQMQALRPQVVIGFGGGSAMDAAKAIVWFSQQGGLPVDTCVAIPTTSGTGSEVTSACVISDPEKGI

KYPLFHEALCPDMAIIDPTLVVSVPPTITAHTGLDALTHALEAWVSPQATDFTDALAEKAVRLVFRALPV

AIHQGDCIATRSKMHNASTLAGMAFSQAGLGLNHAIAHQLGGQFHLPHGLANALLLTAVIRFNAGEPRAA

KRYARLARACRFCPPEAGEQEAFQALLTAVETLKQQCAIPTLKGALQEKYPLFLSRIPAMVPAALADATL

RTNPRPVDGAAIAQLLESLQ

>WP\_016531325.1 CoA-acylating propionaldehyde dehydrogenase PduP [Klebsiella pneumoniae]

MNTAELETLIRTILSEKLAPTPPAPQQEQGIFCDVGSAIDAAHQAFLRYQQCPLKTRSAIISALRETLAP

ELATLAEESATETGMGNKEDKYLKNKAALENTPGIEDLTTSALTGDGGMVLFEYSPFGVIGAVAPSTNPT

ETIINNSISMLAAGNSVYFSPHPGAKKVSLKLIARIEEIAYRCSGIRNLVVTVAEPTFEATQQMMSHPLI

AVLAITGGPGIVAMGMKSGKKMIGAGAGNPPCIVDETADLVKAAEDIISGAAFDYNLPCIAEKSLIVVAS

VADRLIQQMQDFDALLLSRLEADTLRAACLPDGAANKKLVGKSPAALLAAAGLAVPPRPPRLLIAEVEAN

DPWVTCEQLMPVLPIVRVADFDSALALALRVEEGLHHTAIMHSQNVSRLNLAARTLQTSIFVKNGPSYAG

IGVGGEGFTTFTIATPTGEGTTSARTFARLRRCVLTNGFSIR

>WP\_046042475.1 two-domain cob(I)yrinic acid a,c-diamide adenosyltransferase PduO [Klebsiella pneumoniae]

MAIYTRTGDAGSTSLFTGQRVSKTHPRVEAYGTLDELNAMLSLCVCAVAEEEQRTLLEALQQHIFWFSVE

LASDSEQPSPGKRYISSEEIALLEQTIDREMARVPALHQFVLPGRCEAASRLHLARTVARRAERRLVELG

AEVTIRQILLRYLNRLSDCLYALARSEDHAAHQRRLVTEIAARYLAASRSPAPDAPKAQAGSLSFHELHQ

LIRQAIEHARQLQVPVVISIVDAHGTETVTWRMPDALLVSSELAPKKAWTAVAMKTATHELATTVQPGAA

LYGLESHLQGKVVTFGGGYPLWRDGQLIAGLGISGGSVEQDMAIAQAAMAAINVRTHQ

>WP\_002915814.1 MULTISPECIES: ethanolamine utilization protein EutN [Bacteria]

MHLARVTGAVVSTQKSPSLNGKKLLLVRRVSADDDRPILPTSGDEVAVDSVGAGVGELVLLCSGSSARHV

FSGPNEAIDLAVVGIVDSLSR

>WP\_004900288.1 MULTISPECIES: microcompartment protein PduM [Klebsiella]

MNHAMLQRIVEEVAARLRHRALSTATLSVAQLGEADIRSLLCQHASLRIVQVDLPLLEQLAGQRALAAAG

CALHEAMAWGVRVQLTLLPALLPALAVKKLARLPLTFSDPLGQPVRLHAASVLTYADVARFSGGYLVLRR

RPIITALAREAAVARHVQLIKQE

>WP\_002915810.1 MULTISPECIES: phosphate propanoyltransferase [Klebsiella]

MDKQQLASTVNKVLDEMRQRPIPIGISSRHIHLAAADYARLFPAQPIQPKKALLQPGQYAAEQTVTLVGP

KGRLNNVRLLGPLRQTSQVEISRTDARILGIAAPLRMSGNLQGTPGIRLISPFAELELSGGTIVAQRHIH

MSPLDALILRVSHGDSVAVAIEGSDRRLIFDNVAVRVAPDMRLEMHIDTDEANAAGADAAQAWATLVTKP

>WP\_002915808.1 MULTISPECIES: BMC domain-containing protein [Klebsiella]

MKQSLGLLEVSGLALAITCADAMAKAAAITLLALEKTNGSGWMVVKIAGDVASVQAAVMTGAELAERQQG

LVAQKVIARPGEGLLPARVQAPSPAPDVAVTEENTALTDAPSHSTERVTCNLCLDPHCPRQKGDPRSQCL

HAGKRGDA

>WP\_002915806.1 MULTISPECIES: propanediol utilization microcompartment protein PduJ [Klebsiella]

MNNALGLVETKGLVGAIEAADAMVKSANVQLIGYEKIGSGLITVMVRGDVGAVKAAVDAGSAAASVVGEV

KSSHVIPRPHSDVEAILPKSV

>WP\_004174562.1 MULTISPECIES: glycerol dehydratase reactivase beta/small subunit family protein [Klebsiella]

MESSVVAPAIVIAVTDECSEQWRDVLLGIEEEGIPFVLQPQTGGDLIHHAWQAAQRSPLQVGIACDRERL

IVHYKNLPASTPLFSLMYHQNRLARRNTGNNAARLVKGIPFRDRNA

>WP\_004149610.1 MULTISPECIES: diol dehydratase reactivase subunit alpha [Klebsiella]

MRYIAGIDIGNSSTEVALATVDDAGVLNIRHSALAETTGIKGTLRNVFGIQEALTQAAKAAGIQLSDISL

IRINEATPVIGDVAMETITETIITESTMIGHNPKTPGGVGLGVGITITPEALLSCSAGTPYILVVSSAFD

FADVAAMVNAATAAGYQITGIILQQDDGVLVNNRLQQPLPVIDEVQHIDRIPLGMLAAVEVALPGKIIET

LSNPYGIATVFDLNAEETKNIVPMARALIGNRSAVVVKTPSGDVKARAIPAGNLLLIAQGRSVQVDVAAG

AEAIMKAVDGCGKLDNVAGEAGTNIGGMLEHVRQTMAELTNKPAQEIRIQDLLAVDTAVPVSVTGGLAGE

FSLEQAVGIASMVKSDRLQMALIAREIEHKLQIAVQVGGAEAEAAILGALTTPGTTRPLAILDLGAGSTD

ASIINAQGEISATHLAGAGDMVTMIIARELGLEDRYLAEEIKKYPLAKVESLFHLRHEDGSVQFFPSALP

PTVFARVCVVKPDELVPLPGDLPLEKVRAIRRSAKSRVFVTNALRALRQVSPTGNIRDIPFVVLVGGSSL

DFEIPQLVTDALAHYRLVAGRGNIRGCEGPRNAVASGLLLSWQKGGTHGE

>WP\_002915750.1 MULTISPECIES: propanediol dehydratase small subunit PduE [Klebsiella]

MNTDAIESMVRDVLSRMNSLQDGITPAPAAPTNDTVRQPKVSDYPLATRHPEWVKTATNKTLDDLTLENV

LSDRVTAQDMRITPETLRMQAAIAQDAGRDRLAMNFERAAELTAVPDDRILEIYNALRPYRSTQAELLAI

ADDLEHRYQARLCAAFVREAAGLYIERKKLKGDD

>WP\_016529665.1 propanediol dehydratase medium subunit PduD [Klebsiella pneumoniae]

MEINETLLRQIIEEVLVEMKSGADKPVSFSAPAASVASAAPVAVAPVSGDSFLTEIGEAKPGTQQDEVII

AVGPAFGLAQTANIVGIPHKNILREVIAGIEEEGIKARVIRCFKSSDVAFVAVEGNRLSGSGISIGIQSK

GTTVIHQRGLPPLSNQELFPQAPLLTLETYRQIGKNAARYAKRESPQPVPTLNDQMARPKYQAKSAILHI

KETKYVVTGKNPQELRVAL

>WP\_016529664.1 propanediol dehydratase large subunit PduC [Klebsiella pneumoniae]

MRSKRFEALAKRPVNQDGFVKEWIEEGFIAMESPNDPKPSIRIVNGAVTELDGKPVEQFDLIDHFIARYG

INLARAEEVMAMDSVKLANMLCDPNVKRSDIVPLTTAMTPAKIVEVVSHMNVVEMMMAMQKMRARRTPSQ

QAHVTNIKDNPVQIAADAAEGAWRGFDEQETTVAVARYTPFNAIALLVGSQVGRPGVLTQCSLEEATELK

LGMLGHTCYAETISVYGTEPVFTDGDDTPWSKGFLASSYASRGLKMRFTSGSGSEVQMGYAEGKSMLYLE

ARCIYITKAAGVQGLQNGSVSCIGVPSAVPSGIRAVLAENLICSALDLECASSNDQTFTHSDMRRTARLL

MQFLPGTDFISSGYSAVPNYDNMFAGSNEDAEDFDDYNVIQRDLKVDGGLRPVREEDVIAIRNKAARALQ

AVFAGMGLPPITDEEVEAATYAHGSKDMPERNIVEDIKFAQEIINKNRNGLEVVKALAKGGFPDVAQDML

NIQKAKLTGDYLHTSAIIVGEGQVLSAVNDVNDYAGPATGYRLQGERWEEIKNIPGALDPNELG

>WP\_002915739.1 MULTISPECIES: propanediol utilization microcompartment protein PduB [Klebsiella]

MSSNELVEQIMAQVIARVATPEQQALPDTPHPTGETAMAEKSCSLTEFVGTAIGDTLGLVIANVDAALLE

AMKLEKRYRSIGILGARTGAGPHIMAADEAVKATNTEVVSIELPRDTKGGAGHGSLIVLGGNDVSDVKRG

IEVALKELDRTFGDVYGNEAGHIELQYTARASYALEKAFGAPLGRACGIIVGAPASVGVLMADTALKSAN

VEVVAYSSPAHGTSFSNEAILVISGDSGAVRQAVISAREIGKTVLATLGAEPKNDRPSYI

>WP\_002915737.1 MULTISPECIES: propanediol utilization microcompartment protein PduA [Klebsiella]

MQQEALGMVETKGLTAAIEAADAMVKSANVLLVGYERIGSGLVTVIVRGDVGAVKAATDAGAAAARHVGE

VKAVHVIPRPHTDVEKILPKGNSQ

>WP\_009485655.1 MULTISPECIES: propanediol diffusion facilitator PduF [Klebsiella]

MNGSLRAQCIAEFLGTGLFLFFGICCLSALKLTGASLGLWEICIIWGLGISLAVYLTAGISGGHLNPAVT

VALWLFACFPGRKVVPYIVAQVAGAFGGAVLAWILYSTLFTQFETVHHMVRGSLESLQLASIFSTYPAPE

LSIWHAALVEVVITSMLMGMIMALTDDGNGVPKGPLAPLLIGILVAVIGASTGPLTGFAMNPARDFGPKL

FTWFAGWGNIAMTGGRNIPYFIVPIIAPLLGACLGAAIYRFLIANNLPCHTCVEEENTR

>WP\_004181164.1 MULTISPECIES: regulatory protein PocR [Klebsiella]

MISASTLNSELINKIAQDFAQATSLAVVVVNIHGDEISELFNFTPFCQLMRQHPEHSGRCRMSDRCGGLE

ASKKDQLCIYRCHAGLTDFSIPLVIAGHLVGFVLCGQVRLSNDVELVDILNVDDRWQDDPALVQAFRDVP

EMDYSRVIASADLLKLIVENCLKKQLNFVVIKDNPSQNDPAQASRAPSPHDGKMKKALRYIDAHLSDELR

LEDVAAHVYLSPYYFSKLFKKYQGIGFNAWVNQQRMASAKELLCHSDWSIASIARNLGFSQTSYFCKVFR

QTYQVTPQAFRQQINAGSQTESF

>WP\_046042482.1 cobyrinate a,c-diamide synthase [Klebsiella pneumoniae]

MATRRAFILAGTGSGCGKTTVTLGLLSLLQQRGMRVQPCKVGPDYLDTAWHTAISGIASRNLDSFMLPAP

ILNALFTEQLQQADIAVIEGVMGLYDGYGTDPNYCSSAAMAKQLGCPVILLVDGKAVSTSIAATVMGFQH

FDPALDIAGVIVNRVNSDAHFQLLKSAIERYCQVPVLGYVPRVEGVALPERHLGLVTARESVVNQQAWRD

FASLLGRTLDIDRLLALSELAAMPIGEWGEQLAADAGEGLTLALADDEAFNFYYPDNLALLARCGVKMVR

FSPLRDRQLPACQMIWLGGGYPELHAAGLSANHEMLTQLRAAHRRGVAIYAECGGLMYLGTTLEVTSGER

YTMADIIPGHSRMGTRLTRFGYCEAQAQQQTLLAAPGEWLRGHEFHYSDFSPATPAVLACRKQRDGKTLQ

QWQGGWQYGSAFASYLHVHFAQRPTMLNHWLRAARRAL

>WP\_002915724.1 MULTISPECIES: adenosylcobinamide-phosphate synthase CbiB [Klebsiella]

MTLLAWCVAWILDVVIGDPPHWPHPVRWIGRLIAVSQRVVRRVCHSDRALRIGGGVMWLVVIGLTWGVAW

GVLALAHGIHPWLGWLVEVWMIFTALAGRCLAQSAMAVARPLQAGDLAESRHKLSWIVGRDTSQLQPAQI

NRAVVETVAENTVDGIIAPLFFLLLGGAPLAMAYKAVNTLDSMVGYKHEKYRAIGMVSARLDDVANFLPA

RLSWLLLSLAAVLCREDGARALRTGWRDRYQHSSPNCAWPEATVAGALGIRLGGPNDYFGQRVEKPWIGD

AVRDIAVDDISRTIRLMWVASSLALALFIGVRYWLVGAA

>WP\_002915711.1 MULTISPECIES: cobalt-precorrin-8 methylmutase [Klebsiella]

MQYIQQPQAIEAKSFDIISEIIAETRPDYRFASPLHEAIIKRVIHTTADFDWLDILWFSPDALIALSEAL

SRPCTLYTDTTMALSGINKTLLARFGGECRCYISDPRVVREAQSRGMTRSMAAVDIAVQEPGEKVFVFGN

APTALFRLLEHRETAIGGVVGVPVGFVGAAESKAALSESGLPAIAALGRKGGSNVAAAIVNALLYHLREA

Q

>WP\_016531683.1 MULTISPECIES: cobalt-precorrin-5B (C(1))-methyltransferase CbiD [Klebsiella]

MSDQTFDAPVWHHGKALRKGYTTGSCATAAAKVAALMVMRQHLIHQVSIVTPSGVTLCLNVESPHVEGQQ

AVAAIRKDGGDDVDATHGMLIFARVTLNDSGEISLQGGEGIGTVTRKGIGLPTGSPAINRTPRHTIETAV

REAIGPTRGAQVEIFAPEGALRAQKTYNARLGILGGISIIGTTGIVTPMSEESWKRSLSLELEIKRAAGL

ERVVLVPGNHGERFVREQMGIDPQMVVTMSNFVGYMIEEAVRLGFRQIVLIGHPGKLIKIAAGIFHTHSH

IADARMETLVAHLALLGAPLPLLTLVSECDTTEAAMEHIDAWGYQRLYNHLAERICQRVLEMLRFTQQPP

TCDAVLFSFDNQVLGSSRPLAAIARELTC

>WP\_015958917.1 cobalt-precorrin-7 (C(5))-methyltransferase [Klebsiella pneumoniae]

MLTVVGMGPAGLQWLTPAAREAIAAAEALVGGSRHLQQFPDFAGERFALRADMPALLAWIEARTGRRVVV

LASGDPLFYGIGTRLIAHFGRERVQVIPGISAVQYLCARAGIDMNDMWLTSSHGRAVSFDALAAHRKVAM

VTDGRCGPREIAAQLMARGKGHRWMVIGENLAMENERIHWLPVSAVEDEYEMNAVVILDER

>WP\_002915684.1 MULTISPECIES: decarboxylating cobalt-precorrin-6B (C(15))-methyltransferase [Klebsiella]

MKDELFLRGAQVPMTKEAVRALALAKLELHRARHLIDIGAGTGSVSIEAALQNPALRVTAIERQADALRL

LAENRQRFGCDNIAIVAGVAPLAVADKADAIFMGGSGGHLTALIDWSLAQLHPGGRLVMTFILQENLHSA

LAHLRQSGIHEVDCQQLAVSTLATLGSGHYFKPHNPVFVIACQKEENHG

>WP\_046042486.1 cobalt-precorrin-4 methyltransferase [Klebsiella pneumoniae]

MVETFDPHCVWFVGAGPGDRELITLKGYRLLQQAQVVIYAGSLINTELLAYCPPQAECHDSAALHLEQIL

DLMEAGVKAGKTVVRLQTGDVSLYGSVREQGEELTRRGIRWQVVPGVSAFLGAAAELGVEYTVPEVSQSL

IITRLEGRTPVPAREQLEAFASHQTSMAIYLSVQRIHRVAERLVEGGYPATTPVAVIYKATWPERQTVRG

TLADIGDKVRDAGIRKTALILVGPFLGDEYHYSKLYAADFSHEYRKA

>WP\_046042488.1 cobalt-precorrin 5A hydrolase [Klebsiella pneumoniae]

MNTVKPESIALFCLTPGGVRLAKRLAAMLPLTCYTSEALQEEGFIPFNGGFASAAREAFSSFSALIFIGA

TGIAVRVLAPLVNDKLSDPAVVVIDERARHVISLLSGHAGGANALTRYLAGMLDADPVITTATDVNELAA

LDTLAFQLNARMTDFRAAVKTVNQMLVSGKRVGLWCDGEFTGALSRCDRRGFIPVSDLASLPALDALICV

TLRRSLPPLPLPHWKLVPQRVVAGIGCRRDTPCALLSTLLDRQLAAQRLDPLALKAIGSVSLKANEPGLR

QLAHRCRVPFETFSAEALREHEHRFPASSFVRETVGVGSVSGPVAWLLSQGNLSGETLREQGVTITLGVT

H

>WP\_004214523.1 MULTISPECIES: precorrin-3B C(17)-methyltransferase [Klebsiella]

MLSVIGIGPGSQAMMTMEAVEALQAAEIVVGYKTYTHLVKAFTGDKQVIKTGMCKEIERCQAAIELAQAG

HNVALISSGDAGIYGMAGLVLELVNKQQLDIEVRLIPGMTASIAAASLLGAPLMHDFCHISLSDLLTPWP

VIEKRIVAAGEADFVICFYNPRSRGREGHLARAFTLLAASKSADTPVGVVKSAGRKKQEKWLTTLGEMDF

APVDMTSLVIVGNKATYIDNGLMITPRGYAL

>WP\_002915627.1 MULTISPECIES: cobalt-precorrin-6A reductase [Klebsiella]

MNHGDVLVIGGTSDARAICQQLDAADVRYTLSVATPTGERLAGDIRGQIRCGRMEWQQMAEWLRAQRTRW

VIDASHPYAEVVSQNIVRACASVGVLLSRYQRPEQLSDLRHPLLHVVGDLNEACAVARRLGERILLTTGS

KDLAAWRAGLAEKTLLARVLPVPEVVQHCSDLGFGVGEIFALCGPFSAEFNAAFYRQCRADVVVTKASGA

EGGYQEKVQPCLDAGIPCIVITRPAPLVTGDELLQSQADFTARLTRWLSAT

>WP\_016532596.1 MULTISPECIES: sirohydrochlorin cobaltochelatase [Klebsiella]

MKKALLVVSFGTSYHDTREKNIAACERDLAASCPDRTLFRAFTSGMIIRKLQQRDGIHIDTPLQALQKLA

EQGYQDVAIQSLHIINGDEYEKIVREVQSMRPRFQRLTLGAPLLSGHGDYVQLMQALRQQMPPLAATERV

VFMGHGASHHAFAAYACLDHMMAVQGFPARVGAVESYPEVDIVINELSRQGVTGVHLMPLMLVAGDHAIN

DMASDEDDSWKTRFNAAGIPATPWLNGLGENPAVRAMFVAHLQQALNNAMEKAA

>WP\_016532597.1 cobalt-factor II C(20)-methyltransferase [Klebsiella pneumoniae]

MSGKLYALSTGPGAADLITVRAARILGQLDVLYAPAGRKGGDSLALSIVREYLGAHTEVRCCHFPMSADS

AEKEAVWNDVTAALAQEVAAGRQVGFITLGDAMLFSTWVFLLQRIGCPDWLEIVPGVTSFAAIAARAKTP

LAMEQQSLAVISCTAPETDIAAALRQHDSLVLMKVYGRFARIKALLAQAGLLDAALMMSEATLPGEQCWR

RLREVSDDQPLPYFSTILVNKQWEEA

>WP\_008806286.1 MULTISPECIES: cobalt ECF transporter S component CbiM [Klebsiella]

MNQVKSLKQLSYGGLAAAVLLIIVPQEAFAMHIMEGFLPPMWALAWWLLFLPCLWYGLVRLRRIVQEESN

QKVLLALCGAFIFVLSALKIPSVTGSCSHPTGVGLAVILFGPGVVAVLGAIVLLFQALLLAHGGLTTLGA

NGMSMAVIGPMVGYLVWKLACRAGIRRDVGVFLCAMLADLMTYFVTSVQLGVAFPDPATGAGGSILKFMG

IFCLTQIPIAIAEGLLTVMIYDQLTKRRLIAAEGH

>WP\_016532598.1 energy-coupling factor ABC transporter substrate-binding protein [Klebsiella pneumoniae]

MKRPLILLAMVVALMILPFFINHGGEFGGSDGEAESQIQVVAPDYQPWFQPLYEPASGEIESLLFTLQGS

LGAAVIFYILGYARGRQRRDDRV

>WP\_004143925.1 MULTISPECIES: energy-coupling factor ABC transporter transmembrane protein [Klebsiella]

MTGFDRLSYQSRWLQVAPERKFLLWLLLMALAFTLPAWGQALTLALTAALTCWLLRVSFWRWCRWMALPF

GFLLVGVLTIVFSVSRDPQMLLASIRLGAFSIGISAPGLAVAGETFWRSLAAMAATLWLVLNLPFPQLII

LLKRGRVPRLLTEQILLTWRFIFILLDEAMAIHRAQTLRFGYGSVPQGYRSLAMLVGLLFTRVLLRYQQM

STALDIKLYQGDFHL

>WP\_002915614.1 MULTISPECIES: energy-coupling factor ABC transporter ATP-binding protein [Klebsiella]

MLATTDLWFRYQDEPVLKGLTLDFSRHAVTGLVGANGCGKSTLFMNLSGLLRPQQGAVLWQGEALNYSKR

GLLALRQQVATVFQDPDQQIFYTDIDSDIAFSLRNLGVAEEEIARRVDEALTLVDAQGFRQQPIQCLSHG

QKKRVAIAGALVLQARYLLLDEPTAGLDPRGRAQMIAIIRRIVGQGRRVVISSHDIDLIYEVSDAVYVLR

HGEVLAAGDPGEVFACAETMDRAGLTQPWLVKLHSELGLPLCKTEAEFFQRMHNNAIGAIKEAS

>WP\_046042498.1 cobyric acid synthase [Klebsiella pneumoniae]

MTLAVMLQGTASDVGKSVLVAGLCRIFHQDGLRTAPFKSQNMALNSGITPDGKEMGRAQIFQAEAAGIAP

DVRMNPILLKPTSDRQAQVVLMGQVATSMDAVSYHQYKPRLREQILAVYQSLAGEYEALVLEGAGSPAEI

NLRDRDIVNMGMAEMAQCPVILVANIDRGGVFAAIYGTLALLQPQERARVKGVIINKFRGDVALLRSGIE

QIEALTGVPVLGVMPWLDVDLEDEDGVALQAGKYHRTDRRDIDIAVVHLPHIANFTDFNALAAQPDVRVR

YVRDPQALADADLVILPGSKNTLGDLCWLRESGMAHAVEQARQRKVPLLGICGGYQMLGETIIDEVESGL

GAQPGLGVLKTVTHFAQHKTTTQVQATLGSALPDWLADAAGLRVSGYEIHMGETRREAGCPPLLQLHKAG

QAVDDGAISDDGLAFGTYLHGLFDSDAFTRALLNGLRQRKGLAPLDSALEYARYKTRQFDRLAEAMREHI

AIDKIYAIMRQHQEPLC

>WP\_004890028.1 bifunctional adenosylcobinamide kinase/adenosylcobinamide-phosphate guanylyltransferase [Klebsiella pneumoniae]

MLTLVTGGARSGKSRHAEALIADAPQVLYIATSQIFDDEMAARIQHHRDGRPAHWRTAERWQQLDELITP

AIAPAEAILLECITTMVTNLLFALGGDSDPDGWDYAAMEQAIDDEIGVLIAACQRCPAHVVLVTNEVGMG

IVPENRLARHFRDIAGRVNQRLAAAADAVWLVVSGIGVKIK

>WP\_016529969.1 MULTISPECIES: nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase [Klebsiella]

MQNLNTVLRAIPAPDADAMARAQQHIDGLLKPPGSLGRLEALAVQLAGMPGLGGQPQVAKKALLVMCADH

GVWDEGVAISPKAVTAIQAANMTRGTTGVCVLAAQAGAKVHVIDVGIDSEPLPGVVNMRVARGCGNIARG

PAMSREQGQELLLEVMRYTRALAQEGVTLFGVGELGMANTTPAAAIVSVLTGSDAQEVVGIGANLPLAKV

GNKVAVVRRAIAVNQPDPNDGLDVLSKVGGFDLLGMTGVMLGAASCGLPVVLDGFLSYAAALAACQIAPE

VKPYLIPSHYSAEKGARIALAHLGLEPYLNMGMRLGEGSGAALAMPIVEAACAMYHRMGMLAASNIVLPK

G

>WP\_156720420.1 hypothetical protein [Klebsiella pneumoniae]

MAVPVFGGGFAGGRNKKTPLRVFQVVGKKGKSVVFPPLWLSAENQ

>WP\_004181152.1 MULTISPECIES: type VI secretion system baseplate subunit TssE [Klebsiella]

MAASSLFEMLTFSFSGELPLEQVSERDQLILSVMDNMQRIINCRAGTLAHLPDYGLPDLSMIHQGMTAGI

HGLIHQIEETLLRYEPRLSQLRVELQPQPRPGHLNYLIYAQLPDTGWIRFDGIFSAEGRIVLRHLKQQER

A

>WP\_016529968.1 type VI secretion system lipoprotein TssJ [Klebsiella pneumoniae]

MITGVWKYRGKSTNYDTLLMQEEKTLKSDVLAKHTVWMKPAGAVSLNVPLDKETQFIAIVGQFYHPDEQS

NSWRLVLKRDELEADRPRTIELMRSDLRLLPLQDK

>WP\_016531439.1 type VI secretion lipoprotein TssJ, partial [Klebsiella pneumoniae]

MFLTPYKRHAISVLAAVTLLSGCGLTQRVTDGTKEVASAIFYKQIKTLHLDFVSRSALNTDAQDTPLSTM

IHVWQLKTRERFDEAN

>WP\_004181150.1 MULTISPECIES: type VI secretion system baseplate subunit TssG [Klebsiella]

MDRTPQPARTGLTERLAPDINRINFYRFCQLLEQSQPQTPLLGSTTNPADDPVRFRPHPGMGFPVSELKS

VEQDLDHPDAPPTVRTTFLGLYGVDSPLPTAYLDYIAQRRDGHEAMMAFLDIFNHRFITQYYRIWRKYNY

LTSFEPGAVDNISRCLLGLIGLGIPGSENHIATPVSRFLALLSVMRLPTRTAEGITALVRLLAPQTQATV

IPHDPQQIVLPEPAGLSKRSRICLKTRALLGNTGTDVNSQLLMKLYTEDDGEARGWLPGGQLHTDLLVLL

RVYLGWRYQARLQLTLPVSLLPPAQLGNQRVQVSRTGVLRASFAAPVAGTVTVSLGRYQGLMPTSSTRDR

ESVTHVSYTL

>WP\_016531437.1 type VI secretion system baseplate subunit TssF [Klebsiella pneumoniae]

MDDLTQRYYEAEMRYLREAGKEFAQAYPDRAAMLNLDKPGARDPYVERLFEGFAFLMGRLREKLDDDLPE

LTEGLVSLLWPHYLRTIPSLSVVELLTDHRQMKQSETLSDFQVLSRPVGEHRTRCCYSATRDITLLPLAL

PEVSLLYEQDGRSVIRLRFECSPLAGDGSQIDLSRLPLYLNADSPLACALHRALTLGVQQIWFRLPGEER

RTLDGYFSPMGFGKDDPLWPKGESAFSGYQLLLEYFTFREKFMFVALNGLENVVWPAGMSGFEIDVVLAE

SWSHDLPFSTENIRLHCVPVINLFPLEADPLHLSPLENEYLLRPMRIQDGHTEIYSVDNIISSRHTGSQA

YVPFSSFRHRGGMLRHDSPERYYHTRVKRGPSGLHDTWLILGGDAFDIDRLLEDETLSLSLTGTNGQLPR

KALQSTVLDPPVYATQHTLRVRNLCAPTQPCYPPARDRFHWRVLSHLGSNFLSMMDNAEILRGTLALYDW

TESEMNRRRLEAIVDVQHHLIQRFEKGFLLRGVDIQVTLDSNGFAGEGDITLFGELLHRFFALYADIHLF

TQLTLILQPTGKCLQWTEHHSQRVPG

>WP\_223371287.1 hypothetical protein [Klebsiella pneumoniae]

MNSLKMKGYYFLVVLLLTALCGGGYVMYQQQYRMAVHVTPESENDPEWPSKKKWFDASEWLSTPQYIKIN

DFYVINTRYVPIGDLNSDQIIFYLKKGINGSEKRFSELSVLSDLDNQEFRELMKDKLSSEYLETQFDKET

LTPTIDFFLIYFIFNNKRYEVPIRREYSGNKYHYWVLEGSVKKAGYWHERFPASYSYRKYLNK

>WP\_016528833.1 hypothetical protein [Klebsiella pneumoniae]

MLVGKLAYSWEKRGGNFGSLKEINERKIELMTAEQEPVENVQWVTGRDYIVVVAARTKFKDSMGNQYRFV

NCGLRQLRLFPEVNKDNYSIQRIFLMFQQGYVEKGIELINEYVEELSGRVVYVKDKAEFIKFLNSRKDKN

RVIKEMVILCHGIIDTASFDYHHENKGKEKTGEFKSRDVVDVQEAVFDYDAVVTTYACRAGISVDGKDLT

GMDAGQENSPAQKMADCWDVSVRAFEMRSDYSSIYGTKKEIRAAENYEDVIEEYEESLSGYNKKKANGDV

DITPPQKPENYDEMSKRYDDVTARDANAKRGAGPIAPNGAWRMPGTGDSPEGLKEGLQTYQPGEWTL

>WP\_009485635.1 MULTISPECIES: PAAR domain-containing protein [Klebsiella]

MARRLARLGDKTTYGYVASATSSIIDGKKLALNGDRAWCNKCKGMFGIVGTARGWSEDSLFVGNGDRVAC

KCANNQVIATSDLFDE

>WP\_162869795.1 ImpA domain protein [Klebsiella pneumoniae]

MQKNTGTTQMSELLQQLTRNCFSDRDATAVAQEQAALWQSWLLPVTEDSPVGEDPGYHDDFLLMRDEMNK

STAQGLTLTQWESELLFEVKTRQLKLLRLRAHRHADKAALARKMGNLLGTLVVMDPARAAVLCDTQHKD

>WP\_046042502.1 type VI secretion protein VasK [Klebsiella pneumoniae]

MKSANNKLTIIADVLLLLLFAAVLGFIIWRFGDLFGLTGDKNKFYIWLAGIMSFIFLRASWYFSRLYRVR

RERRQSEEQGEYPEKEIRYEPGQRTSLYSELFFHLRDRYGLFWQRQVRLLLVTGEPEQVEAIAPGLTEQR

WQEGDHTVLIYGGKASAEPDTTLLASLKKLRRFRPLDGIIWPLTEKQSTQTAQLDKGWRELGNGGKLLGF

QAPLYLWQVCDDGGYQAGRTLQSVGCLLPERSTPEQLATQLEAQTPQLTEQGMSQLLTNNRHDFLLRLAH

TLTERGIAHWQTVLKPLLAGGAFPSLHLRGLMFSPPLAAVPEAAPHAWLSSLVWAGVTGDNAKGRTVGFP

WLRTALMACFCVLAIWWTGMMTSFFANRALIQETGTHTARAINTRLPLAEQLVALHTLQGELERLQYRIR

HGTPWYQRFGLERNAQLLNTAFPGYAQAANRLVRDVAVAHLQQQLNAFVALSPNSPQRTATGELRYKQLK

ALLMTSRPEKADAAFFSTTLKADNLRYADVTEGTRQSVLPSLLTFWMANLPEHPQWKIAPQPELVGAVRK

ILLRQIGVRNAENTLYQNVLKQVCRNYADMTLADMTGDTQAGSLFGTEQTVPGMFTRQAWEGQVKEAIEQ

VATARREEIDWVLSDRQQDASADISPEALRTRLMERYFTDFAGSWLTFLNSIRWKKEDSLSGVLDQLTLM

ADARQSPLIALTDTVAWQAAAGRESRSLSDSLTQSAKELFSGKEKTPQNTRAAREEEAPTGPMDKTFAPL

LRLTGDKAGGTGDSQLSLQTYLTRVTRVRLKLQQVTNAPDPQEMTQQLAQTVLQGKTVDLTDTRDYGRLI

AASLGEEWSGFGQSLFVRPVEQAWRQVLTPAADSLNRQWQRAIVSHWNQDFAGRYPFKNTPNDASLPLLA

KYLRDDGRISQFIATNLAGVLEREGRYWVADTMNTQGLTVNPAFLRALNRLRDVADTAFASGDAGVHFEL

MAKPARDVMKTHLVIDGQQLEYFNQKERWQRFSWPDEQWQPGASLSWTSTQNMERILADFRGSWSFIRLL

EQAQVTQLDSSSFMLQWQAPDGLPLHYLMRVEQGKGPLALLALKNFRLPGQVFLTGKAISDAEEYRDNAD

E

>WP\_046042504.1 hypothetical protein [Klebsiella pneumoniae]

MAWKRKHIEEPDRPLKIPLYKWLLTFLILSAFLLPLFYLFRDEIIRDNVTLLILFSPLTLCLFLFCLQIY

FYARAMQNYTVIMHNINNINTEWEKWGGRYVSVLGSKLFLPGEVDGSSLSDNQSEVMYGLAVRIDYFRWE

TNDWFSFYTLLIDENDIFNLPVRIAKEFIILTDCNEREYTRMEADFSRVLAEMNIMLPSGSIRLVPSLLF

EQLDAWLKVTEEKIYIVLVLQLNGKENYSDGIVSFLFAADDVVKKYQLDEKARIFRPMVVVADRFDKDLD

IFIDTQKIARNATGLTGDCAGLLPVSGSILQCFNEKEGKLQVDNIHVMESLSGLPGLNSVWLTAALAVSA

ASYQKSDYLMMARYEDDWIITTVHPVEAS

>WP\_016530473.1 hypothetical protein [Klebsiella pneumoniae]

MLKSLLTGLFFIYFLAGNAYAEDYNDIFWGMLKKENQEIVFVRCDSPPLKMKIVRTADANQENIEKAYQT

FNQSKGQSMYFAFIGNVKDTGNGNYVFNMYDVMETKTGRCNLTDALNNWNVSQ

>WP\_009485630.1 MULTISPECIES: hypothetical protein [Klebsiella]

MAILHPQECWLLERAMSVEYYRKRYEAWRALVELCEYQVAEWAKSMPLDIRRRPLYEQIDAVWGGRVLPN

IRGTLKSVHYDFLQRQQNDPNALHSGGNISSDRRGLIDYFPNWMPDVAQKQYQKLLWRAGFYDDLIKDTS

TGYWYEGSLTYYYEESLYGPLALPMQLPLYELDHSVYLREGDPVTIDGLYLPDLLDAGARLMYLRENIPD

AWQGRVRTQYVNDVGQQEYYWEEGAWTKTNWIRIRRVKNRFINVPLEGFFPRGTPEELYNWPQRQQQYIT

EQQRISASSGEPCPHGGEWSIFVEDKPVTVTLEQGELMPEWEDRTMEEEHKQGEKFHVLWSLMARHDGGP

VWVSEAG

>WP\_032104126.1 hypothetical protein [Klebsiella pneumoniae]

MDTDTDLDRALAFYQPPPESWYSGIHKKIEATGQWIWETIQGDFNDNQSTGQVVTGTVISMIPLVDQICD

VRDLVANCMKIKEGNDKKTDTTWAWVAMILTLVGLIPVAGSLIKGIFKVLFNSIRKAALAGKITLKAIDA

AVSLFNRFIDMTVVQATMKYMKIYNPYQYAEKQVRELIAQLNVSVLLTKFDELMEVTGSLLDKAKSWGPE

SIRQPIETTWKLLVSIRSQANTMLEKALAPLNETLEKLAARLRQEGDNYYKAHTGANPHRPTRLKDAEEA

ELLVHNKPDWVDVGVTEKYPGLKQASAEQKSLMRLEKDKEGWPALSEDNIKSFHQMRYVELPQNEKLYRV

LDPASSDNSFCWMREAEFMALKSKSQWRRRFAVWKSWNENGEYVVYTVPPGTTMKVWEGPAASQSRSVTD

NGKNVDIVLEGGGIQIVIDPADLNLNYLGKRQHTGWGYRDFSDEVDMYIGIPQLQTKIFVPEE

>WP\_046042506.1 type VI secretion system tip protein VgrG [Klebsiella pneumoniae]

MDVQNFDHSHHALKIRGLSSGVDVLSFEGKEQLSAPFRYDIQFTSSDKFIAPESVLMQDGAFSLTAPPVQ

GIPTQTPLRTLYGVITGFKQLSSSRDEARYEVRLEPRLALLSRSHQNAIYQNQTVPQIVEKILRERHEMR

GQDFVFNLKSDYPSREQVMQYDEDDLTFISRLLSEVGIWFRFSTDARLKIGVIEFYDDQSGYERGLTLPL

RHPSGMSDSGTEAVWGLNTAYSVVSRSVTTRDYNYREAMAEMTTGQFDVTGGDNTTYGEAYHYADNFLKT

GDKATPESGAFYARIRHERYLNGRAILKGQSTSSLLMPGLEIKVEGNDAPEVFRKGILITGITASAARDR

SYELTFTAIPYSERYGYRPPLIRRPVMAGTLPARVTSTTANDVYAHIDKDGRYRVNLDFDRDTWKPGFES

LWVRQSRPYAGDTYGLHLPLLAGTEVSIAFEDGNPDRPYIAGVKHDSAHTDHVTIQNYKRNVLRTPANNK

IRLDDERGKEHIKVSTEYGGKSQLNLGHLVDAGKQQRGEGFELRTDMWGAIRAKKGVFISADAQEKAQGQ

VLDMQAAITQLENALSIAKSLSQAAEVAKAHGADLDGHTSLNGALSELVKAGIVLSAPEGVGIVSPQGVR

LGSGESSIGLMAGTNIDAGAMEKVTVSAGDAVSVFARKGGIKLYANQGKVEVEAQNERMRLTSRHGMKIS

STEDVVEIEAEKELVLKCGKAYIRLSGGGVEVGGPKNILLKSANVQKMSKAQLPVEMPVLPGKGNYDLSL

DLRDWDGIPIGGAKYTIAFESGAVLSGMLDDKGYALHTNVLPESATVEYEFPEPEPDKPWDPYSSLLASV

DAELGADGQGA

>WP\_016530256.1 OmpA family protein [Klebsiella pneumoniae]

MSRVSNTLKQALLLWSMLLVLALWLGFNQASTAMKFGVTVALIIIAVGLLACWRGKKRQTEADSAWLSRL

PPKTYRQPVVLVCGDAAASLFTENPLRQVAGGLYLHVADEEQLIRQAEVLLADRPAWASQLCVACTVVPV

VHLDMAVLAGRLRRFVGGLATVRRRAGIKVPLLLWSWLPGTGREDDLPWFICAGGKVQVVTPAGESSPTA

WAAQPGTDGSSLRLCHLLRMESLMQWLNQMVLPELNGYPPLAAGMGQAPSLPALEGNLWQTWTTAKTGLT

PEAIPKIGASPLPFPDMMLPLLPRQSGFTPVRRACVAALLMTTVAGVAALCLSATANRSLLLQVSDDLHK

YDAVPADNDAAKAHHLSVLKDDANILDSYFREGEPLRLSLGLYPGERLRQPVWRVIRDYRPPEKKRDVAD

ALPVQSVRLDSMALFDVGQARLKDGSTKVLINALVNIRARPGWLIVVTGYTDTTGNKKANQQLSLRRAEA

VRDWMLQTSDIPATCFAVQGLGESHPAATNDTPEGRAANRRVEISLVPRTDACQDVKQNMLPEPALSQLN

PQGVSAI

>WP\_004181140.1 MULTISPECIES: type VI secretion system protein TssL, short form [Klebsiella]

MTQERKIDIDVLLRDTFLTVVELRQGTSARHGQELYRHCLQQVEGVRERLTAAGFSQQDIEHITYAQCAL

LDETVLSRDVMDDGQMVWLKNPLQSHFFNTLQAGELLYERMKRFLQEPAPTPAVLTCFHRVLLLGFRGRY

QDPESDERQHLIAMFSKRVEPFRVQEDSAVLNVPLTRRQHYLWQSPFCWLLLLMLVLVGVWWGLHSWLNV

LVDELLPTGKS

>WP\_004142901.1 MULTISPECIES: type VI secretion system baseplate subunit TssK [Bacteria]

MKIHRPLWAEGTFLSSQQFQQQARWETYSNNSIAQLGIRHPWGVARVEFDREALALGKLKLRTLRLRFSD

GSLIDSEVSDALPLACDLHTLAVENTAIVVLALPLEHANGGNLGQEKHTERPLRYRQEWHKVQDIYGSDS

EEMAVECHALSLRFAHDNNQDYITCPLARLTRNGQGNWSQDESYIPPLLALSAHIGLVERLDTLLLQLQA

KCRRLMALRRESNQRMADFAVADVSLFWLLNALNSAEPVLSDFLRYPSIHPELVWRELARLAGALLTFSL

EHNVSAIPAYVHDAPASVFPPLFTLLSELLEASLPSRVIALELESLPGNRWKAELHDPRLREEADFYLSV

RSSLPTHVVLQQLPRLCKIGAPDDVTLLVNVALNGVPVVPLTQVPAALPLRLENQYFALDMQSAPAKAML

DAGCCMIYAPGTLGDLKPELFAVLRS

>WP\_004142899.1 MULTISPECIES: hypothetical protein [Klebsiella]

MSAKEHISSSAAMSTMMGSGGIYQSLFKKIHLTVAIHTPLSCLAKSAEDVVMHQPDVQHVKSRWHGLRFL

KCQKQKPDRAVV

>WP\_046042519.1 murein transglycosylase A [Klebsiella pneumoniae]

MKGRWAKYVATGAMLAMLAACSSKPTDRGQQYSDGKFTQPFSLVNQPDADGAPINAGDFSEQVNQIRNAS

PRLYNSQSNVYNALQEWLRAGGDTRTLRQFGIDAWQMQGVDNYGNVQFTGYYTPVVQARHTRQGEFQYPI

YRMPPKRGKLPSRASIYAGALSDNYVLAYSNSLMDNFIMDVQGSGYIDFGDGSPLNFFSYAGKNGWPYRS

IGKVLIDRGEVKKEDMSMQAIREWGEKHSEAEVRELLEQNPSFVFFKPQSFAPVKGASAVPLIGRASVAS

DRSIIPPGTTLLAEVPLLDNNGKFNGQYELRLMVALDVGGAIKGQHFDIYQGIGPDAGHRAGWYNHYGRV

WVLKNAPGAGNVFSG

>WP\_016530752.1 MULTISPECIES: tRNA cyclic N6-threonylcarbamoyladenosine(37) synthase TcdA [Klebsiella]

MSVVISDAWRQRFGGTARLYGEKALRCFADAHVCVVGIGGVGSWAAEALARTGIGAITLIDMDDVCVTNT

NRQIHALSGNVGLAKAEVMAERIRLINPECRVTVVDDFVTPENVAEYLGVGFSYVIDAIDSVRPKAALIA

WCRRYKVPLVTTGGAGGQIDPTQIQVADLAKTIQDPLAAKLRERLKSQFGVVKNSKGKLGVDCVFSTEAL

VYPQADGSVCAMKSTAEGPKRMDCASGFGAATMVTATFGFVAVSHALKKMLAKAQRDAAASGK

>WP\_004142894.1 MULTISPECIES: cysteine desulfurase sulfur acceptor subunit CsdE [Klebsiella]

MTTLHPFGTTITDATLRQIFAPLNQWEDKYRQLILLGKKLPTLTDERKAQAHEIAGCENRVWLGYEEDAE

GRLHFFGDSEGRIVRGLLAVLLTAVEGKTRAGILAQDPLALFDELGLRGQLSASRSQGLSALSEAVLAAA

RER

>WP\_004174604.1 MULTISPECIES: cysteine desulfurase CsdA [Klebsiella]

MNAFNPAHFRAQFPALADAGVYLDSAATALKPLAVIDASDQFYRLSAGNVHRSQFAAAQRLTERYEAARD

RVAAWLNAPSGKDIVWTRGTTEAINMVAQSYVRPRLQPGDEIIVSEAEHHANLVPWLMVAGQTGARVVKL

PLGADRLPDIASLSALITPRSRVLAIGQMSNVTGGCPDLAQAIRLAHAAGMVVMVDGAQGAVHFPADVQA

LDIDFYAFSGHKLYGPTGIGALYGKSELLAAMSPWLGGGKMIAEVSFDGFTPQPAPYGLEAGTPNVAGVI

GLSAALEWLAQSDIGQAENWSRSLASLAEEELAKRPGFRSFRCQQSSLLAFEFEGIHHSDLVTLLAESGI

ALRAGQHCAQPLLAALGVSGTLRASFAPYNTQDDVAALVHAVDRALEILVD

>WP\_002915549.1 MULTISPECIES: YgdI/YgdR family lipoprotein [Enterobacteriaceae]

MTKAAAIISACMLTLGLSACSSNYVMHTNDGRTIVTDGKPQTDNDTGMISYKDAWGNKQQINRSDVKQLG

ELDE

>WP\_002915545.1 MULTISPECIES: glycine cleavage system transcriptional regulator GcvA [Klebsiella]

MSKRLPPLNALRVFDAAARHLSFTRAADELFVTQAAVSHQIKSLEDFLGLKLFRRRNRSLLLTEEGQSYF

QDIKEIFSQLTEATRKLQARSAKGALTVSLLPSFAIQWLVPRLTSFNSAYPGIDVRIQAVDRQEDKLADD

VDVAIFYGRGNWPGLRVEKLYAEYLLPVCSPLLLTGDKALKTPADLAQHTLLHDASRRDWQTYTRQLGLS

HINVQQGPIFSHSAMVLQAAIHGQGVALANNVMAQSEIEAGRLVCPFNDVLVSKNAFYLVCHDSQAELGK

IAAFRQWILAKAASEQEKFRFRYEQ

>WP\_002915543.1 MULTISPECIES: DUF423 domain-containing protein [Klebsiella]

MTSRFMLIFAAISGFIFVALGAFGAHVLSQSLGAAEMAWIHTGLEYQAFHTLAIFGLAVAMQRRISIWFY

WSSVFLALGTVLFSGSLYCLALSHLRLWAFVTPVGGVSFLAGWVLMLIGAIRLKRKGVVHE

>WP\_002915541.1 MULTISPECIES: 23S rRNA (cytidine(2498)-2'-O)-methyltransferase RlmM [Klebsiella]

MNKVVLYCRPGFEKECAAEITDKAARLEVFGFARVKEDSGYVIFEGYQQDDGEKLVRDLPFSSLIFARQM

FVVGELLRDLPPEDRITPIVGMLQGVVEKGGELRVEVADTNESKELMKFCRKFTVPLRAALREAGVLTNY

ETPKRPVVHVFFIAPGCCYTGYSYSNNNSPFYMGIPRLKFPSDAPSRSTLKLEEAFHVFIPADEWDERLA

NGMYAVDLGACPGGWTYQLVKRNMWVSSVDNGPMAQSLMDTGQVTWLREDGFRYRPNRNNISWMVCDMVE

KPAKVAALMAQWLVNGWCRETIFNLKLPMKKRYEEVSQNLAYIQAQLDEHGVNAQIQARQLYHDREEVTV

HVRRLWAAVGGRRDER

>WP\_004142883.1 MULTISPECIES: L-fucose operon activator [Klebsiella]

MKAARQQAIVDLLITHSSLTTETLSKQLNVSRETIRRDLSELQAQGKVLRNHGRAKVIHQRSQDSGDPFH

MRLKSHYAHKADIAREALAWIDEGMVIALDASSTCWYLARQLPDRPLHVFTNSQPICQELAKRDQITLTC

SGGTLQRKYGCYVNPALISQLKSLEIDLFIFSCEGIDPQGALWDSNAFNADFKSILLKRAAQSLLLIDKS

KFNRSGEARIGHLDDVTHIVSDAPQP

>WP\_002915538.1 MULTISPECIES: L-fucose mutarotase [Enterobacteriaceae]

MLKTISPLISPELLKVLAEMGHGDEIIFSDAHFPAHSMGPQVIRADGLRVSDLLQAIIPLFELDSYAPPV

VMMAAVEGDALDPTVEQRYRQALSAQAPCPDIVRIDRFAFYDRAQKAFAIVITGECAKYGNILLKKGVTP

>WP\_016531483.1 L-fuculokinase [Klebsiella pneumoniae]

MKQDVILVLDCGATNVRAMAVDRQGKIIARAAMANASDIAAEKSDWHQWSLEAIMQRFADCCRQIHDQLA

SCTVRGITVTTFGVDGALVDEQGALLYPIISWKCPRTAAVMENISQYMPARQLQQIAGVGAFAFNTLYKL

VWLKENHPQLLAQAHAWLFISSLINHRLTGEFTTDLTMAGTSQMLDLRQRDFSAPILQATGLPRRLFPRL

VEAGQPIGALLPEAAALLGLPVGIPVISAGHDTQFALFGAGAGQDEPVLSSGTWEILMVRSAQVDTSLLC

DYSGSTCELDSQPGRYNPGMQWLASGVLEWVRKLLWSADTPWQTLIDEAQAIPPGAQGVRMQCDLLASQH

AGWQGVTLNTTRGHFYRAALEGLSDQLAQHLQTLEKIGGFRAKELLLVGGGSRNALWNQIKANRLGIPIK

VLDDAETTVAGAAMFGWYGVGEFSSPEQARAQVAYRYRYFWPQTEPELIEEA

>WP\_016531482.1 L-fucose isomerase [Klebsiella pneumoniae]

MKKISLPKIGIRPVIDGRRMGVRESLEAQTMNMAKATAALISEKLRHACGARVECVIADTCIAGMAESAA

CEEKFSSQNVGVTITVTPCWCYGSETIDMDPLRPKAIWGFNGTERPGAVYLAAALAAHSQKGIPAFSIYG

HDVQDADDTSIPADVEEKLLRFARAGLAVASMKGKSYLSLGGVSMGIAGSIVDHNFFESWLGMKVQAVDM

TELRRRIDQKIYDETELEMALAWADKHFRYGEDQNAEQYKRNETQSRAVLKESLLMAMCIRDMMQGNPKL

AEKGLVEESLGYNAIAAGFQGQRHWTDQYPNGDTAEALLNSSFDWNGVREPFVVATENDSLNGVAMLMGH

QLTGTAQVFADVRTYWSPDAVERVTGQPLTGRAEHGIIHLINSGSAALDGSCQQRDAQGNPTMKPHWEIE

QNEADACLAATEWCPAIHEYFRGGGFSSRFLTEGGVPFTMTRVNIIKGLGPVLQIAEGWSVALPKAMHDQ

LDARTNSTWPTTWFAPRLTGKGPFSDVYSVMANWGANHGVLTIGHVGADFITLAAMLRIPVCMHNVEEAK

IYRPSAWAAHGMDIEGQDYRACQNYGPLYKR

>WP\_046042523.1 L-fucose:H+ symporter permease [Klebsiella pneumoniae]

MGNTTIPTQSYRAMESGQSKSYIIPFALLCSLFFLWAVANNLNDILLPQFQQAFTLTNFQAGLIQSAFYF

GYFIIPIPAGMLMKKFSYKAGILTGLFLYACGAALFWPAAEVMNYTLFLIGLFIIAAGLGCLETAANPFV

TVLGPESGGHFRLNLAQTFNSFGAIIAVVFGQSLILSNVPHQPQEVLDKMTPEQLSAWKHCLVLSVQTPY

MIIVAIVLLVALLIVCTRFPSLQSDDHSDSAQSTFFASLTRLMRIRHWRWAVLAQFCYVGAQTACWSYLI

RYAIEEIPGMTAGFAANYLTATMVCFFIGRFTGTWLIRRFAPHNVLAIYAFIAMLLCLLSAFSGGHVGLL

ALTLCSAFMSIQYPTIFSLGIKHLGQDTKYGSSFIVMTIIGGGIVTPVMGFVSDAAGNIPTAELVPALCF

AIIFIFASFRSQAATN

>WP\_002915470.1 MULTISPECIES: L-fuculose-phosphate aldolase [Klebsiella]

MERNRLARQIIDTCLEMTRLGLNQGTAGNVSVRYQGGMLITPTGIPYEKLTEDKIVFIDADGQHEQGKLP

SSEWRFHQAAYQTRPDAQAVVHNHAVHCTAVSILNRPIPAIHYMIAAAGGNSIPCAPYATFGTRELSEHV

AVALKHRKATLLQHHGLIACEASLEKALWLAHEVEVLAQLYLSTLAITDPVPVLDDEAIAIVLEKFKTYG

LRIEE

>WP\_016530415.1 lactaldehyde reductase [Klebsiella pneumoniae]

MANRMILNETAWFGRGAINALTDEAVRRGYRKVLIVTDSTLARCGVAAKVTDKLDAAGLAWDIFSDVIPN

PTIAVVQQGLQAFQRSGADYLIAIGGGSPQDTCKAIGIIQRNPEFANVRSLEGLSPTRQPSVPIFAVPTT

AGTAAEVTINYVITDEEQRRKFVCVDPHDIPQVAFIDADMMDAMPPALKAATGVDALTHAIEGYLTRGAW

ALTDALHLKAIEIIAGALRGSVAGDAGAGEAMALGQYVAGMGFSNVGLGLVHGMAHPLGAFYNTPHGVAN

AILLPHVMRFNAEATGEKYRDIARAMGVRVEALSLTAAREAAVEAVCQLNRDVGIPGHLREVGVRKEDIP

ALAQAALADVCTGGNPREASLADIVGLYQAAW

>WP\_004142871.1 MULTISPECIES: flap endonuclease Xni [Klebsiella]

MAVHLLIVDALNLIRRIHAVQGSPCVDTCLHALEQLIVHSQPTHAVAVFDDEDRAHGWRHQRLPEYKAGR

APMPETLVAEMPALRAAFEQRGIRCWASPGSEADDLAATLAVKVAQAGHQATIVSTDKGYCQLLSPTIRI

RDYFQKRWLDAPFIASEFGVTPEQLADYWGLAGISSSKVPGVAGIGPKSAAQLLNEFQDLEGLYARLAEV

PEKWRKKLAAHQEMAFTCREVARLQTDLQLDGNLQQLRLTR

>WP\_004174618.1 MULTISPECIES: sigma-54-dependent Fis family transcriptional regulator [Klebsiella]

MLNPESPSTAPALIDPASKAFQSLLDKLAPTEATVLIVGETGTGKEVVARYLHHHSARRQQPFLAVNCGA

LTESLAEAELFGHEKGAFTGAQQGQPGWFEAAEGGTLLLDEIGELSLPLQVKLLRVLQEREITRVGSRKA

IKVNVRVIAATHVDLAQAIRERRFREDLYYRLNIAVVPLPPLRQRRQDIPLLAHHFLSLYARRLGRPTLR

LAPESLARLMDYSWPGNIRELENTLHNAVLLSKEEEISPAQLRLATLNDAPGPASDHELDDFIRHQLALP

GEPLWQRVTSALIRHAMAHCDDNQSQAAALLGISRHTLRTQLANLGLIKSRRRPPAPPRAFANAAGADRE

LRIGYQRFGSLGILKARQSLETAFASLGVNVLWSEFPAGPQLLHALACNEIDFGTTGEAPPVFAQASNSE

LMYVAWEPPAPRSVAMVVPQGSDIRQLSDLRGKRIALNKGSNVHWLLLQILEDAGLGLNDVRVVYTPPKY

PLTASDYLAVDAWMMWDPLLSDAEHTGELRVVASGEGRVNNHQFYLSRRDYLAQHGDIMRRLLTELTHTG

QFIDSHRGEAARLLSAELGIDARSLSMALARRSHRPRPMDLSVIRAQQTIADRFYALGLIAKPVPVREAV

WYGEPAPDVIRPLMAVS

>WP\_004219275.1 MULTISPECIES: hypothetical protein [Enterobacteriaceae]

MQMRQRMRGGCAICNSAARRSRFQCIDFKRLIFYSPLA

>WP\_002915347.1 MULTISPECIES: FMNH2-dependent alkanesulfonate monooxygenase [Klebsiella]

MTQQAPDKINVFWFLPTHGDGRYLGTTEGGRPVDLPYLQQVALAADSLGYYGVLIPTGKSCEDSWLVASA

LAPLTRRLRYLVAVRPGLQPPTLAARMAATLDRLSEGRLLINVVTGGDPVENKGDGIFLSHSERYQVTRE

FLDVYTRLLRGEKVDYHGEHIHVEGAEVLFPPVQENGPPLYFGGSSDAAIDVAAEQIDSYLTWGEPPELV

AEKLAVVRERAAARGRTLQYGIRLHVIVRETEEEAWAAADRLIAHLDDDTIAQAQKIFARMDSAGQARMS

ALHQGSRDNLRIAPNLWAGVGLVRGGAGTALVGNPQQVAERIREYQALGISNFIFSGYPHLEEAHRFAEL

VMPLLPLENGASSKARSVNTGPFGETIGGDKRPVRQVSAS

>WP\_046042538.1 FAD/NAD(P)-binding protein [Klebsiella pneumoniae]

MSAEPHIVIIGGGFSGAAVAIELLRLAPNEVRVTLLEPRQSPGAGVAYSTAEPTHRINVPAARMQLAGDE

EGAFDHWYRHQPAFTVDVQALRPDGSVYPQRGQFGRYVAQRFADAAASSGGRLRHLRDRALAFHQGMVTT

DGGLQLKADLLVLAISHPPPSLPAQAEAWRHHPALIANPWQPGALDAIAPHARVAVMGTGLTMADTVATL

DRLGHRGSIVAFSRHGLLSRGNLSGAGTTWPGDYQQGSLRQRLRQIRLDVAYAAQQGLSWQVVLDAVRQQ

GQRIWQALSVADRQRFLRHLRHYWDVHRYRVAPQVAEVLEARQRTGSLQVQAARLLSISGEGETLRLTLA

RRGGGVQTLSVDHLILTTGPAHRALTDSQPFLQDLARRGLIRADALGMGLEVDSRSRAVAEPHVEALPVL

VAGPAARGRFGELMGLPQVADHAADVAAQALLTLGIPQDSRCPAY

>WP\_002915313.1 MULTISPECIES: LLM class flavin-dependent oxidoreductase [Klebsiella]

MSSQREIRLNAFDMNCVGHQSPGLWAHPRDRSWQYKDLEYWVDLARLLERGKFDGLFIADVLGIYDVLNG

SGDAAIRQATQVPVNDPLALITPMALVTEHLGFGLTASLSFEHPYPFARRLSTLDHLTKGRVGWNIVTSY

LESGARNIGQQTQTDHDTRYDYADEYLQVIYKLLEGSWEDGAVLRDRERKIFSDPRKIHPINHQGQFFSV

PGIHLCEPSPQRTPVLYQAGASSRGKQFAAGHAECVFVAAPSKVLLKKTVADIRRRAAEAGRDPHSILIF

NLQTVIVGDTDREAQAKWQEYKQYVSYEGALALLSGWTGIDFGQYQPDQVLKYLHTNAIQSAVEAFSTAD

PNRQWTVQALADWAGIGGFGPLVVGSAQTVADELQSWVEETDVDGFNLAYAVTHETFRDVVELLVPELQK

RGVFKQEYREGTLREKLFGGGPRLAAPHPGASYRRDARTAASVEEKVT

>WP\_020317275.1 MULTISPECIES: ATP-binding cassette domain-containing protein [Klebsiella]

MIAIDDLHKSYRTADGRLSAVLKGLSLQVPERSITAVVGPSGAGKSTLARCISLLEQPDSGSIRINGQDL

SALSGEALRRERRAIGTVFQSSALLSRRTAWENVALPLAWLGVVERDIKARVGELLESVGLSHKADAWPA

QLSGGQRQRIGIARALALRPSVLLADEATSGLDPQATASVLALLKRLRDEYQLAIVLITHEMDAVRTAAD

AVAEIRDGTIVQYGRIEDLLARPDSLLGQQLLPLTPAAATHSDLLLRLSYRWDVPVATDWISRLSQQWGL

QIDLLGGHVEVINGRLAGRLQAGVRFQGERLSPARLQGLLAQLGITAEILDSAPLLREAV

>WP\_015958893.1 MULTISPECIES: ABC transporter permease [Klebsiella]

MKPTVISQDTPWGEIPSLLLPAYGETWLMVAIVMLFVVTLGGLVGVVLFNASPRGLFPHALLYRLLNWVV

NMGRSLPFLVLMAAIIPFTYWLTGTTIGIPAAVVPMIAAGVPFFGRLVENALRELPAEVTAVGVVCGGSR

WQIIASAQLSEAMPALAAAVTLNLVSMIEYSAIAGTIGAGGIGYLAVVYGYQRFDNHIMIATIVALIATI

QLIQFLGDRLVNRLRHTQGNLV

>WP\_002915265.1 MULTISPECIES: MetQ/NlpA family ABC transporter substrate-binding protein [Klebsiella]

MTTEQFELRKARRWPWLAALAVIILLAIAFWWWRGHTQSQQVVFGSTLKIHYEPAMAGEQRIIEYINQHI

APDYGLKLEAVGVQDPVQADRAVAEGQYAGTIYQHQWWLKQVVDANGFALSTTVPVFQWAFGIYSDRYSS

VQALPNGATIVVPDDGANQGQALWLLQRIGLISLDPAVEPRTAKLKNIVGNPHQFVFKELDLLTMPRALN

SVDAAIGYVSQFDAGKVPREKGILFPPAPRTFASQLVIGTPYLSQENIVKLKQAFSDPRIQTWLKTTDDP

LVKDVLVPVSAE

>WP\_016532411.1 MFS transporter [Klebsiella pneumoniae]

MSTLPVDNPGIASVPVSSVGDVARLINSGKEQAKYARMIVFLALGGVFLDAYDLTTLSYGIDDVVREFQL

SPLLTGLVTSSIMVGTIVGNIIGGWLTDKYGRYSVFMADMFFFVISAIAAGLAPNVWVLIGARFLMGIGV

GIDLPVAMSYLAEFSRFAGKGNKAARLAAWCPMWYAASTVCFLIIFGLYFLLPQEHLDWLWRASLLFGAV

PALLIIAVRRRFMNESPLWAANQGDLTSAVRILRDSWGIHAHEVPAAKPAPAPKVSFRVLFEKPYRERTI

VAGVMNICISFEYTAIAFFLPSILAQFLGAGVFETISASLGLNALFAFTGGLLGMHLAWKYPSRHVAIAG

FALQFVALIVLALVGQPHATAGIVLAIAMLGLWLFAEGFGPGAQLMIYPALSYPTAIRATGVGFSRALSG

IGSALALFILPLLQASLGTQMFWVVSLAAIIPIFFLLAVRHEPTREDIDALHE

>WP\_016532410.1 acyl-CoA dehydrogenase family protein [Klebsiella pneumoniae]

MTLLSTGTDYDALAAAFRPIFTRIAQGAAEREQQRILPDEPIRWLKEAGFGTLRIPREKGGWGASLPQLS

ALLIELAQADSNLPQALRAHFAFVEDQLNQPDSAGRDRWFRRFLDGELVGSGWTEIGAVKLGEVNTRVTP

TEGGWRLDGEKFYSTGALYADWIDVFARRSDTASDVIALVSTQQTGVVREDDWDGFGQRLTGSGTTRFTG

ARVETEHVYDFAQRFRYQTAFYQHVLLATLAGIGLAVERDAAQGVKHRSRMYSHGNAAVPRDDAQVLQVV

GQISSWAWATRAAVLQAAESLQQAYVAHVSDDEALIARRNQLAEVEAAQAQVIASDWIPRAATELFNALG

ASDTRTRLALDRHWRNARTVASHNPVIYKARNIGNWLVKGEAPTFIWQIGNGEKTAG

>WP\_002915261.1 MULTISPECIES: aliphatic sulfonate ABC transporter substrate-binding protein [Klebsiella]

MSNRFRPAWLLVLAALSTSALAKAPETVNIGYQKANIFALLKYRGTLDESLKKQGIAVRWVEFPAGPQML

EGLNVGSIDLAATGDAPPAFAQAAQADLVYLAHSPANPKTEAIVVPEQSAIHSVADLKGKRVGLNKGSDV

NYLLVAALEKAGLSYKDITPVYLPPADARAAFQRGAIDAWVIWDPFLAEVETNAKARQIRNAEGLVPHYT

FYLASRKFADTYPETAKQVVDELGKLSAWANSHQDEAAGLLSTSTGLDKAIWLKTLARLPYGAERMTPAV

YNEQQALADTFTRIGLLPVKVDVRSATWSLDKP

>WP\_002915259.1 MULTISPECIES: L-serine ammonia-lyase [Klebsiella]

MISVFDIFKIGIGPSSSHTVGPMKAGKQFTDDLIARGLLAEVSKVVVDVYGSLSLTGKGHHTDIAIIMGL

AGNLPDTVDIDAIPGFIQDVNTHGRLMLANGQHEVDFPVDQCMNFHADNLSLHENGMRITALAGDKVLYS

QTYYSIGGGFIVDEEHFGQTTEAPVAVPYPYKNAADLQRHCRETGLSLSGLMMQNELALHSKEALEQHFA

AVWEVMSAGIERGITTEGVLPGKLRVPRRAAALRRMLVSQDTTNSDPMAVVDWINMFALAVNEENAAGGR

VVTAPTNGACGIVPAVLAYYDKFIRKVNSNSLARYMLVASAIGSLYKMNASISGAEVGCQGEVGVACSMA

AAGLAELLGGSPGQVCIAAEIAMEHNLGLTCDPVAGQVQVPCIERNAIAAVKAVNAARMALRRTSEPRVC

LDKVIETMYETGKDMNAKYRETSRGGLAMKIVACD

>WP\_016531149.1 HAAAP family serine/threonine permease [Klebsiella pneumoniae]

METTQTSTIVSGETRSGWRKTDTMWMLGLYGTAIGAGVLFLPINAGVGGMIPLIIMAILAFPMTFFAHRG

MTRFVLSGKNPGEDITEVVEEHFGVGAGKLITLLYFFAIYPILLVYSVAITNTVETFMAHQLHMTPPPRA

ILSLILIVGMMTIVRFGEQMIVKAMSVLVFPFVIALMVLALYLIPQWNGAALETLSLSGASVTGNGLLMT

LWLAIPVMVFSFNHSPIISSFAVAKREEYGEGAEKKCSSILARAHIMMVLTVMFFVFSCVLSLSPADLAA

AKEQNISILSYLANHFNAPIIAWMAPIIAMIAITKSFLGHYLGAREGFNGMVIKSLRSKGKSIEINKLNK

LTALFMLLTTWIVATLNPSILGMIETLGGPIIAMILFLMPMYAIQKVPAMRKYSGHISNVFVVIMGLIAI

SAIFYSLFS

>WP\_002915258.1 MULTISPECIES: nucleotide 5'-monophosphate nucleosidase PpnN [Klebsiella]

MITHVSPLGSMDMLSQLEVDMLKRTASSDLYQLFRNCSLAVLNSGSLTDNSKELLSRFENFEINVLRRER

GVKLELINPPEDAFVDGRIIRSLQANLFAVLRDILFVYGQIHNTVRFPNLDLESSVHITNLVFSILRNAR

ALHVGEAPNMIVCWGGHSINENEYLYARRVGTQLGLRELNICTGCGPGAMEAPMKGAAVGHAQQRYKDSR

FIGMTEPSIIAAEPPNPLVNELIIMPDIEKRLEAFVRIAHGIIIFPGGVGTAEELLYLLGILMHPDNKAQ

VLPLILTGPKESADYFRVLDEFITHTLGESARRHYRIIIDDPAEVARQMKKAMPLVKESRRETDDAYSFN

WSIRISPDLQMPFDPTHENMANLKLSPDQPVEVLAADLRRAFSGIVAGNVKEVGIQAIEQYGPYKLHGDP

EMMRRMDDLLQGFVAQHRMKLPGGTAYIPCYEIIA